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# A Short Introduction to Galaxy

## Contributors

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## Questions

- What is Galaxy?
- Why should I use Galaxy?
- How do I use Galaxy?
- How can I connect with the Galaxy Community?

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## What is Galaxy?

Speaker Notes

What is Galaxy?



**Data Intensive analysis for everyone**

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- **Data Analysis** platform
- Web-based
- **Easy** to use
- **Free** and Open Source

- Many tools (~8000)
  - Popular (>10.000 publications)
  - Extensive [tutorials](#) available

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.footnote[Homepage: [galaxyproject.org](http://galaxyproject.org)]

## Speaker Notes

- Galaxy is a web based data analysis platform.
  - It is easy to use, and completely free.
  - Galaxy offers over eight thousand analysis tools.
  - Galaxy is widely used. It currently has over ten thousand publications.

# 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, ...



## Speaker Notes

- Data analysis can be very complex.
  - It often requires specialized programming knowledge or command line skills.
  - Galaxy makes this a lot easier by providing a web-based user interface to popular data analysis tools.
  - This means you don't have to install anything, just open your browser and go to Galaxy.
  - Galaxy also helps you make your research reproducible by keeping track of your analysis steps.
  - Galaxy supports many different scientific domains.
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# How do I use Galaxy?

## Speaker Notes

- How do I use Galaxy?
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# Find a Galaxy server

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

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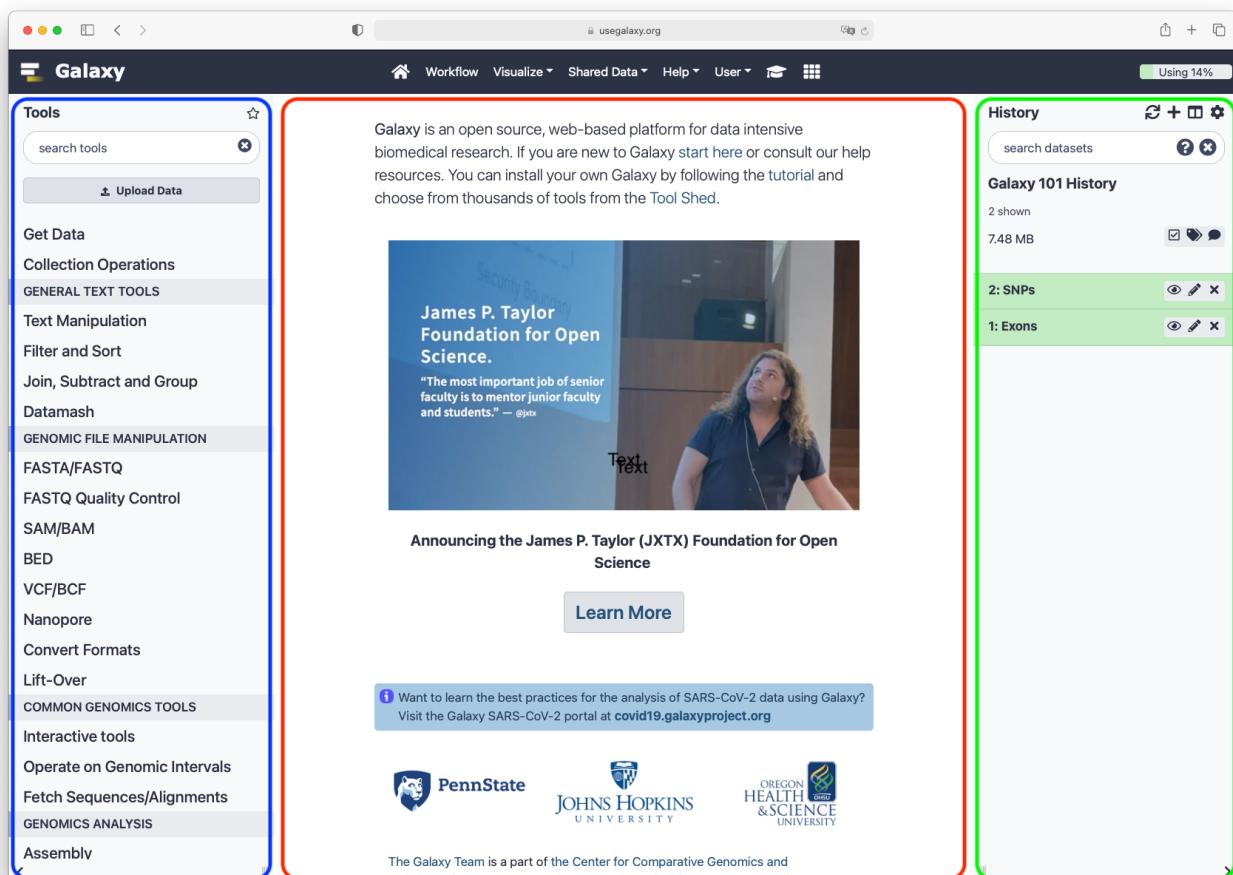
- Many other smaller, often domain-specific Galaxies available
- List of all public Galaxies (125+): [galaxyproject.org/use](http://galaxyproject.org/use)

## Speaker Notes

- There are three main Galaxy servers: Galaxy Main, Galaxy Europe, and Galaxy Australia.
- These three Galaxies have the biggest teams behind them, and offer the most tools and resources.
- You can register an account for free on any of these servers.
- In addition, there are many smaller Galaxy servers to choose from.
- Many of these are domain specific. For example, Galaxy Proteomics focuses on proteomics tools and workflows.
- A lot of universities and other institutions have local private servers.

# The Galaxy Interface

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



## Speaker Notes

- The Galaxy user interface consists of three main parts.
- On the left is the list of available tools.

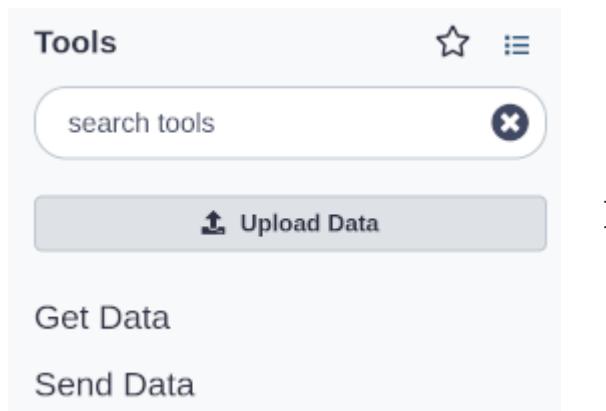
- In the middle panel you will run your analysis tools and view your data and results.
  - On the right is a full record of your analysis history.
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# Uploading data

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

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## Speaker Notes

- The first step of an analysis is to get your data into Galaxy.
  - This can be done in several ways.
  - You can upload files from your computer.
  - Or you can enter an Internet URL, and Galaxy will download the data for you.
  - Furthermore, Galaxy can import data directly from many online data stores such as UCSC, NCBI, and many more.
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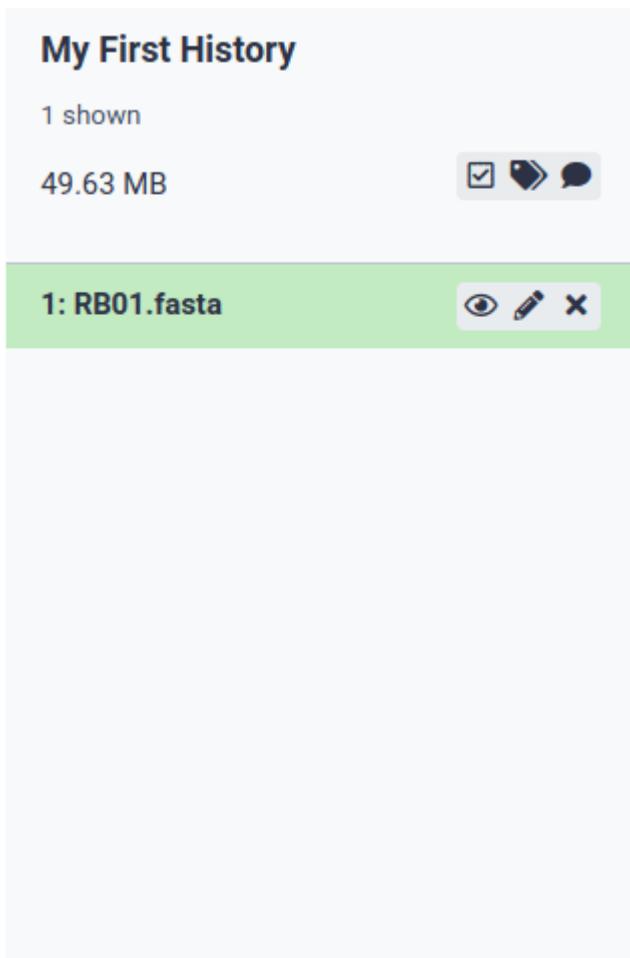
# History

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- 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, ..

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The screenshot shows the Galaxy History interface. At the top, it says "My First History" with "1 shown". Below that, the dataset "1: RB01.fasta" is listed with a size of "49.63 MB". To the right of the dataset name are three icons: a checkmark, a delete symbol, and a speech bubble. A green bar at the bottom of the dataset row contains three icons: an eye, a pencil, and a cross.

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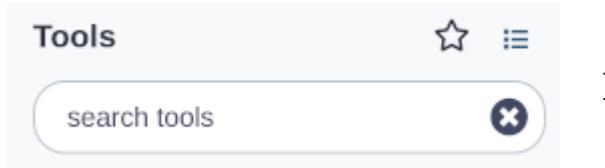
## Speaker Notes

- All files you upload will appear in your history.
- There are 3 button on each dataset in your history.
- The eye icon lets you view the dataset. This will show up in the middle panel of Galaxy.
- The pencil icon allows you to edit the attributes of the file. For example you can change the file name here.
- The cross icon lets you delete the dataset from your history.
- You can also click on the dataset to expand it. This will show more information and more options.

# Finding a tool

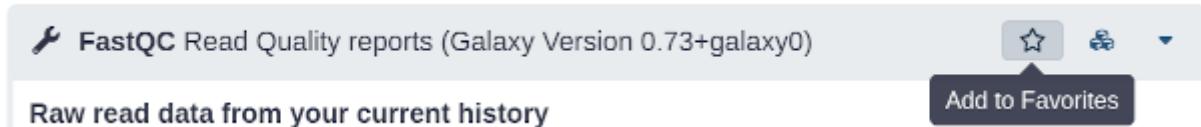
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- Explore tool panel sections
- Enter name in **Tool search** box ]



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- **Star** your favorite tools to make them easier to find



## Speaker Notes

- After your data is uploaded, you are ready to run tools.
- You can find tools by exploring the tool list on the left.
- If you already know the name of the tool you want to use, you can enter this in the search box at the top of the tool panel.
- If you have found a tool you like, you can add it to your favorites by clicking the star at the top of the tool.

# Running a tool

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

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The screenshot shows the 'Sort' tool interface. At the top, there's a title bar with a wrench icon and the text 'Sort data in ascending or descending order (Galaxy Version 1.2.0)'. To the right are a star icon and a dropdown arrow. Below the title, the 'Sort Dataset' section has three input file icons (document, clipboard, folder) followed by a dropdown menu showing '1: 1.bed' with a dropdown arrow. Under 'on column', there's a dropdown menu with a dropdown arrow. The 'with flavor' section has a dropdown menu set to 'Numerical sort' with a dropdown arrow. The 'everything in' section has a dropdown menu set to 'Descending order' with a dropdown arrow. A 'Column selection' section contains a button labeled '+ Insert Column selection'. Below it is a 'Number of header lines to skip' field with the value '0' and up/down arrows. A note says '# characters are already considered as comments and kept'. The 'Email notification' section has a toggle switch set to 'No' and a note saying 'Send an email notification when the job completes.' At the bottom left is a blue 'Execute' button with a checkmark icon.

**i 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.

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## Speaker Notes

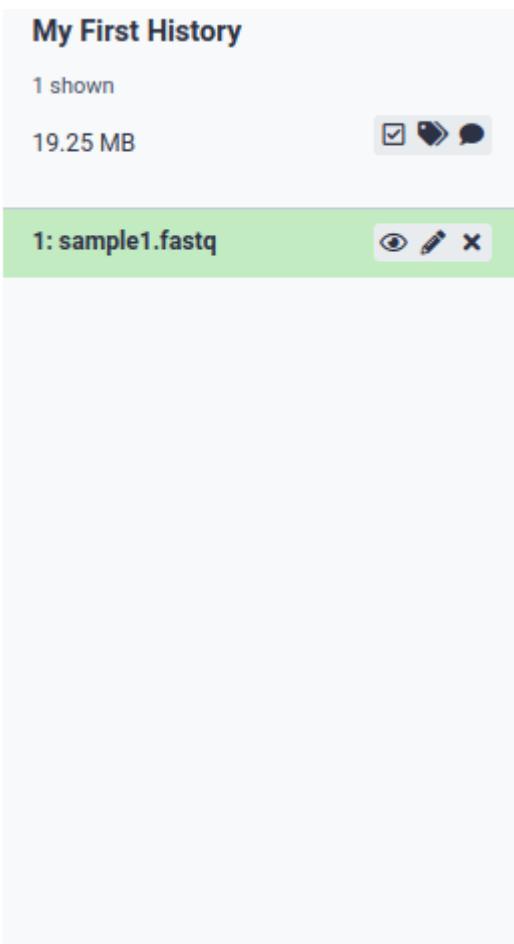
- When you click on a tool, it will show up in the middle panel.
- Here you can select your input files and set the parameters for the tool.
- Then you can hit the Execute button to start the tool.

- Older versions of a tool are usually kept available to ensure reproducibility.
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# Analysis Results

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- 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 ]



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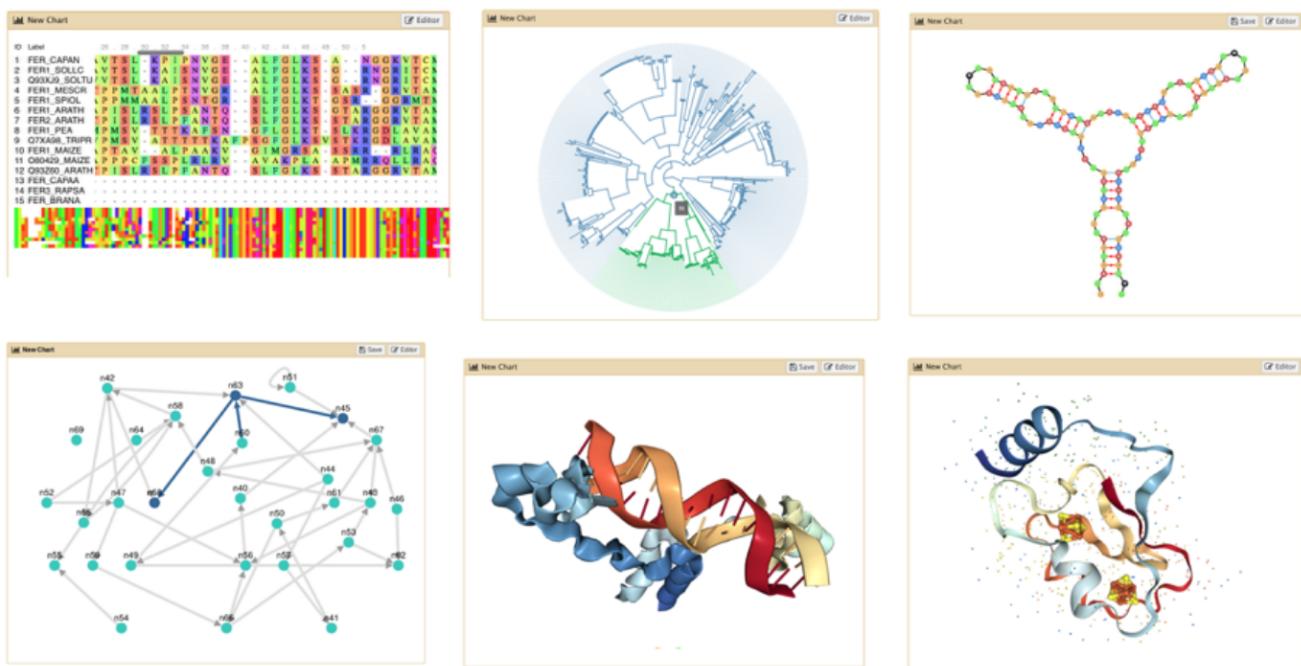
## Speaker Notes

- The results of the analysis will be added to your history.

- You will see these output files go through various states.
  - When a dataset is grey, it means it is waiting to run.
  - When it turns orange, it means the tool is running.
  - When the tool is finished, the outputs will turn green if the tool ran successfully.
  - You can then click on the history item to get more information and options.
  - For example, you can download the file to your computer.
  - Or you can reload the tool with the same parameters.
  - There is also an option to visualize your data.
  - If there was a problem with the tool, it will turn red.
  - You can click on the bug icon to view the error message or submit a error report to the Galaxy administrators.
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## Visualisations

- Galaxy has many options to visualize data



### Speaker Notes

- Galaxy offers several ways to visualize your datasets depending on their format.
  - For example, protein PDB data can be seen in a 3D viewer.
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## Multiple Analyses

- Starting a new analysis? Create a new history +
- You can have as many histories as you want
- Overview of all your histories □

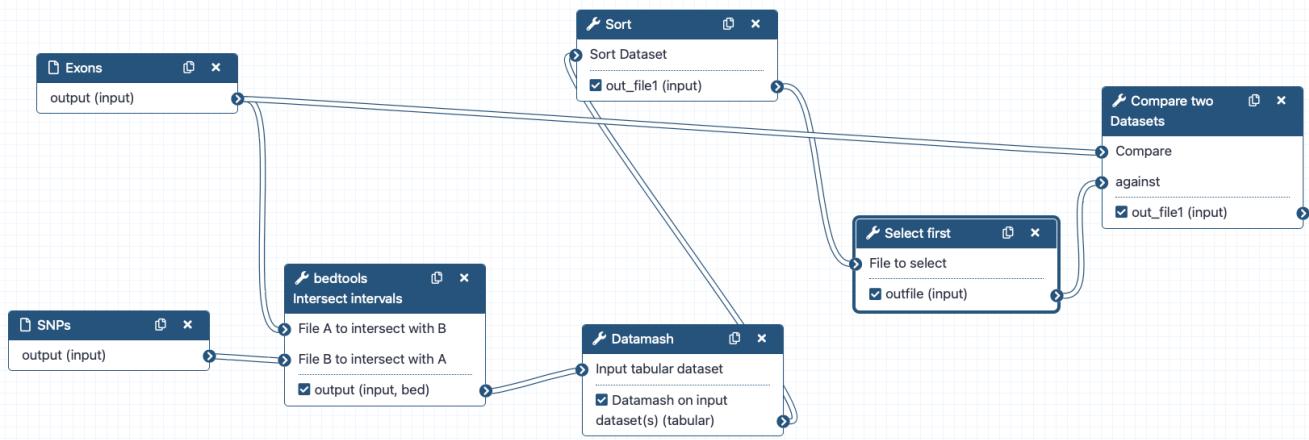
- Good names for your histories help to keep track of your analyses

## Speaker Notes

- When you want to start a new analysis, create a new history using the plus icon at the top of the history panel.
- You can always go back to an old history, and there is no limit on the number of histories you can create.
- An overview of your histories is available where you can easily copy files around.
- Copying datasets instead of re-uploading them let you save on your quota.
- Giving your histories good names will help you keep track of your analyses'

# Workflows

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



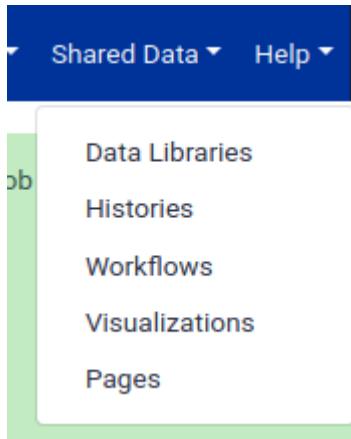
- **Extract** from a history
- **Build manually** with workflow editor
- **Import** a shared workflow

#### Speaker Notes

- Workflows let you run your analyses very easily by connecting tools' outputs and inputs.
- There are multiple ways to create a workflow.
- Workflows can be automatically extracted from a history.
- This means you perform the analysis manually once, and then can easily repeat it on different input data.
- You can also build workflows by hand using the workflow editor to connect the tools.
- Or you can import a workflow somebody else has shared with you.

# 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



## Speaker Notes

- Everything you do in Galaxy can be shared.
  - You can share your history, your workflow, and your visualizations.
  - There are different ways to share your work.
  - You can either share it with specific Galaxy users.
  - Or you can get a share link that you can send to anybody.
  - If you publish your work, it will be visible to everybody.
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# Learning Galaxy

- Galaxy Training Materials ([training.galaxyproject.org](https://training.galaxyproject.org))

**28**

Topics

**265**

Tutorials

**261**

Contributors

# 7.0

Years

## Speaker Notes

- If you would like to learn more about Galaxy, there are a large number of tutorials available.
- These tutorials cover a wide range of scientific domains.

## Getting Help

- **Help Forum** ([help.galaxyproject.org](https://help.galaxyproject.org))

The screenshot shows the GalaxyHelp forum homepage. At the top, there is a navigation bar with links for 'Sign Up', 'Log In', and a menu icon. Below the navigation is a search bar with placeholder text 'search topics, posts, users, or categories' and a magnifying glass icon. Underneath the search bar are several buttons: 'all categories', 'all tags', 'Latest' (which is highlighted in red), 'Top', and 'Categories'. The main content area displays two forum posts:

Topic	Category	Users	Replies	Views	Activity
<a href="#">Troubleshooting resources for errors or unexpected results</a> 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... <a href="#">read more</a>	usegalaxy.org support		1	85	7d
<a href="#">Welcome to Galaxy Community Help</a> For assistance with a specific Galaxy server please post into appropriate category.			1	75	15d

- **Chat on Matrix**

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

## Speaker Notes

- If you get stuck, there are ways to get help.
- You can ask your questions on the help forum.
- Or you can chat with the community on Matrix.

## Join an event

- Many Galaxy events across the globe
- Event Horizon: [galaxyproject.org/events](https://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

## Speaker Notes

- There are frequent Galaxy events all around the world.
- You can find upcoming events on the Galaxy Event Horizon.

## 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

## Thank you!

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

contributors!



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The [Galaxy Training Network](#) provides researchers with online training materials, connects them with local trainers, and helps promoting open data analysis practices worldwide.

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