

Wellcome Genome Campus | OC3_1-16_Overview_of_Galaxy

A short introduction to Galaxy-- what is galaxy? Why should I use galaxy? How do I use galaxy? How can I connect with the Galaxy community? What is galaxy?

Galaxy is a web-based data analysis platform. It is easy to use and completely free. Galaxy offers over 8,000 analysis tools. Galaxy is widely used. It currently has over 10,000 publications. Data analysis can be very complex. It often requires specialised 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 instal 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. How do I use galaxy? 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 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.

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. All files you upload will appear in your history.

There are three buttons on each data set in your history. The eye icon lets you view the data set. 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 data set from your history. You can also click on the data set to expand it. This will show more information and more options.

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 a 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 favourites by clicking the star at the top of the tool. 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. The results of the analysis will be added to your history. You will see these output files go through various states.

When a data set 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 visualise 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 an error report to the Galaxy administrators.

Galaxy offers several ways to visualise your data sets, depending on their format. For example, protein PDB data can be seen in a 3D viewer. 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 data sets instead of uploading them lets you save on your quota. Giving your histories good names will help you keep track of your analyses. 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. Everything you do in Galaxy can be shared. You can share your history, your workflow, and your visualisations. 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.

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

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 for watching.