

Galaxy training material



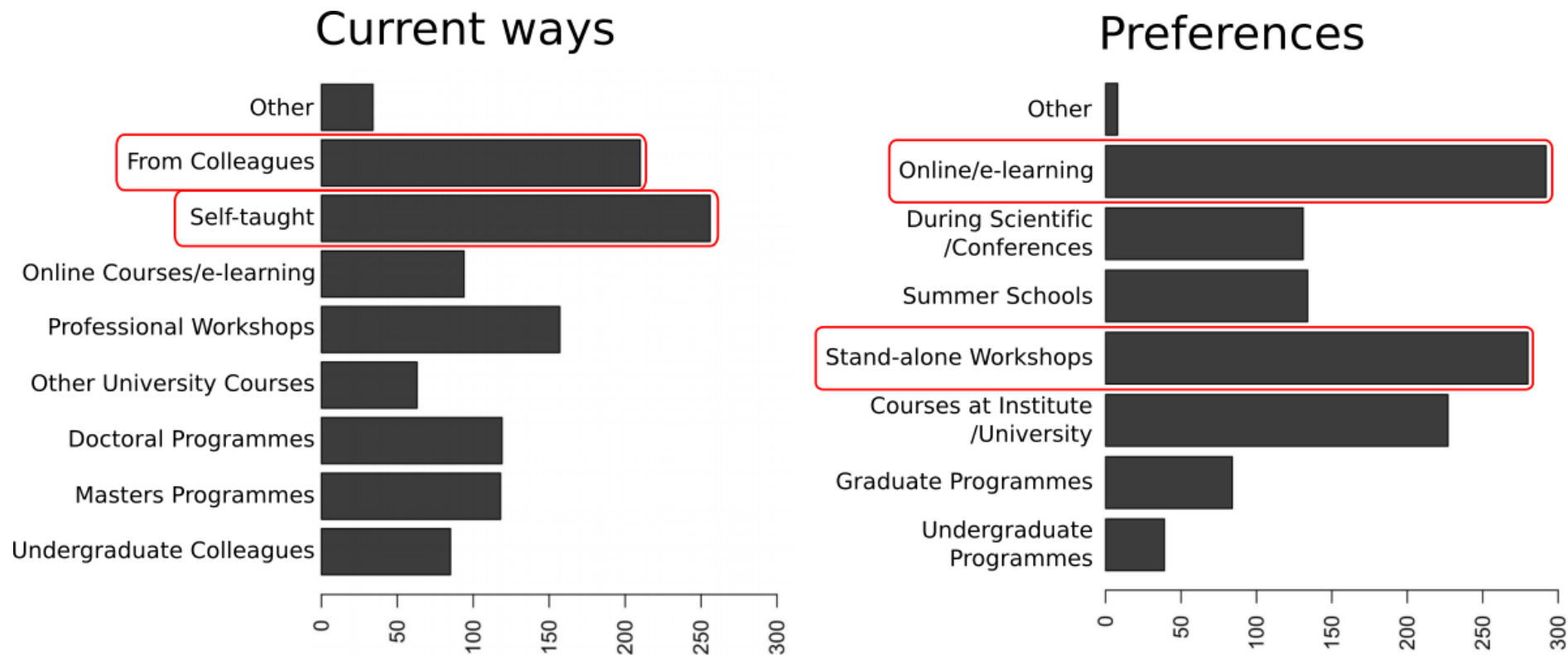
Picture from Bérénice Batut - Icons from the Noun Project and Flaticon

Bérénice Batut, Saskia Hiltemann, The Galaxy Training Network

Biohackathon - Paris - November 2018

Need and demand for bioinformatic training

Bioinformatics has become too central to biology to be left to specialist bioinformaticians



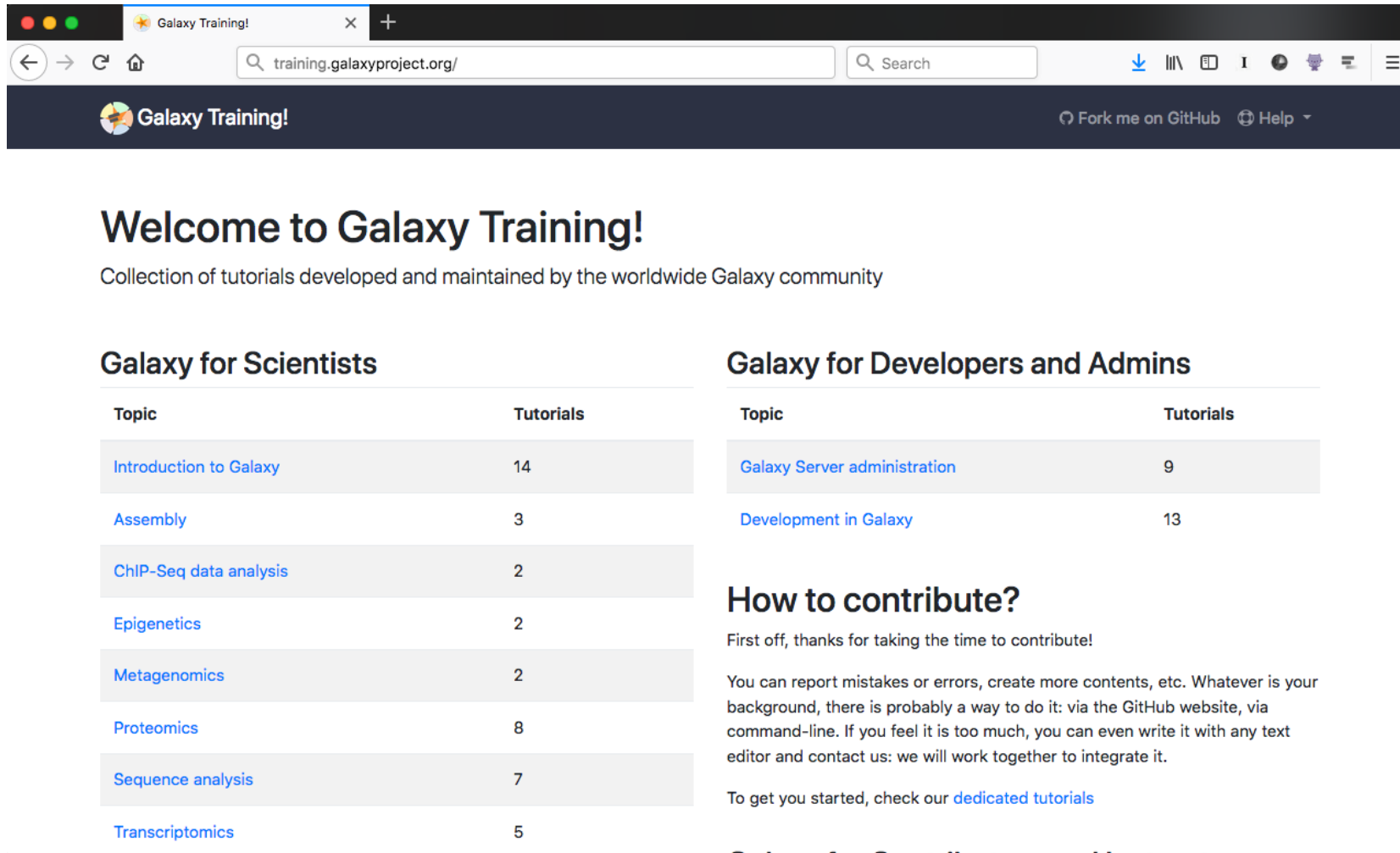
Graphs of [Brazas et al, 2017](#)

Galaxy: a great solution !

The screenshot displays the Galaxy web interface. The top navigation bar includes links for 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', 'Login or Register', and a 'Using 0%' status indicator. On the left, a 'Tools' sidebar lists various bioinformatics tools categorized by function, such as 'Get Data', 'Collection Operations', 'Text Manipulation', 'Convert Formats', 'Filter and Sort', 'Join, Subtract and Group', 'Fetch Alignments/Sequences', 'NGS: QC and manipulation', 'NGS: DeepTools', 'NGS: Mapping', 'NGS: RNA Analysis', 'NGS: SAMtools', 'NGS: BamTools', 'NGS: Picard', 'NGS: VCF Manipulation', 'NGS: Peak Calling', 'NGS: Variant Analysis', 'NGS: RNA Structure', 'NGS: Du Novo', 'NGS: Gemini', 'NGS: Assembly', 'NGS: Chromosome Conformation', 'NGS: Mothur', 'Operate on Genomic Intervals', 'Statistics', 'Graph/Display Data', 'Phenotype Association', 'BEDTools', 'Genome Diversity', 'EMBOSS', 'Regional Variation', 'FASTA manipulation', 'Multiple Alignments', 'Metagenomic Analysis', 'Multiple regression', 'Multivariate Analysis', 'Motif Tools', 'STR-FM: Microsatellite Analysis', and 'NCBI SRA Tools'. The main content area shows the 'Diamond alignment tool for short sequences against a protein database (Galaxy Version 0.8.24)'. The tool's configuration page includes several sections: 'What do you want to align?' with a dropdown for 'Align amino acid query sequences (blastp)'; 'Input query file in FASTA or FASTQ format' with a file upload button and a dropdown for 'No fasta or fastq dataset available'; 'Will you select a reference genome from your history or use a built-in index?' with a dropdown for 'Use a built-in index'; 'Select a reference genome' with a dropdown for 'No options available'; 'Genetic code used for translation of query in BLASTX mode' with a dropdown for 'The Standard Code'; 'Format of output file' with a dropdown for 'BLAST XML'; 'Include full length subject titles in output?' with 'Yes' and 'No' radio buttons; 'Trigger the sensitive alignment mode with a 16x9 seed shape configuration?' with 'Yes' and 'No' radio buttons; 'Trigger the more sensitive mode?' with 'Yes' and 'No' radio buttons; 'Gap open penalty' with a text input field containing '11'; 'Gap extension penalty' with a text input field containing '1'; 'Scoring matrix' with a dropdown for 'BLOSUM62 ((6-11)/2; (9-13)/1)'; 'Enable SEG masking of low complexity segments in the query?' with 'Yes' and 'No' radio buttons; and 'Method to restrict the number of hits?' with a dropdown. On the right, a 'History' sidebar shows an 'Unnamed history (empty)' with a message: 'This history is empty. You can load your own data or get data from an external source'.

- Web interface for numerous bioinformatics tools
- No issue with computer configuration during training

Online training material covering many current research topics



The screenshot shows the Galaxy Training! website in a web browser. The browser's address bar displays 'training.galaxyproject.org/'. The website's header includes the 'Galaxy Training!' logo and a navigation bar with links to 'Fork me on GitHub' and 'Help'. The main content area features a large heading 'Welcome to Galaxy Training!' followed by a subtitle 'Collection of tutorials developed and maintained by the worldwide Galaxy community'. Below this, there are two columns of content. The left column is titled 'Galaxy for Scientists' and contains a table with two columns: 'Topic' and 'Tutorials'. The right column is titled 'Galaxy for Developers and Admins' and contains a similar table. Below these tables, there is a section titled 'How to contribute?' with a paragraph of text and a link to 'dedicated tutorials'.

Topic	Tutorials
Introduction to Galaxy	14
Assembly	3
ChIP-Seq data analysis	2
Epigenetics	2
Metagenomics	2
Proteomics	8
Sequence analysis	7
Transcriptomics	5

Topic	Tutorials
Galaxy Server administration	9
Development in Galaxy	13

How to contribute?

First off, thanks for taking the time to contribute!

You can report mistakes or errors, create more contents, etc. Whatever is your background, there is probably a way to do it: via the GitHub website, via command-line. If you feel it is too much, you can even write it with any text editor and contact us: we will work together to integrate it.

To get you started, check our [dedicated tutorials](#)

<https://training.galaxyproject.org>

Interactive learning via hands-on tutorials built around a "research story"

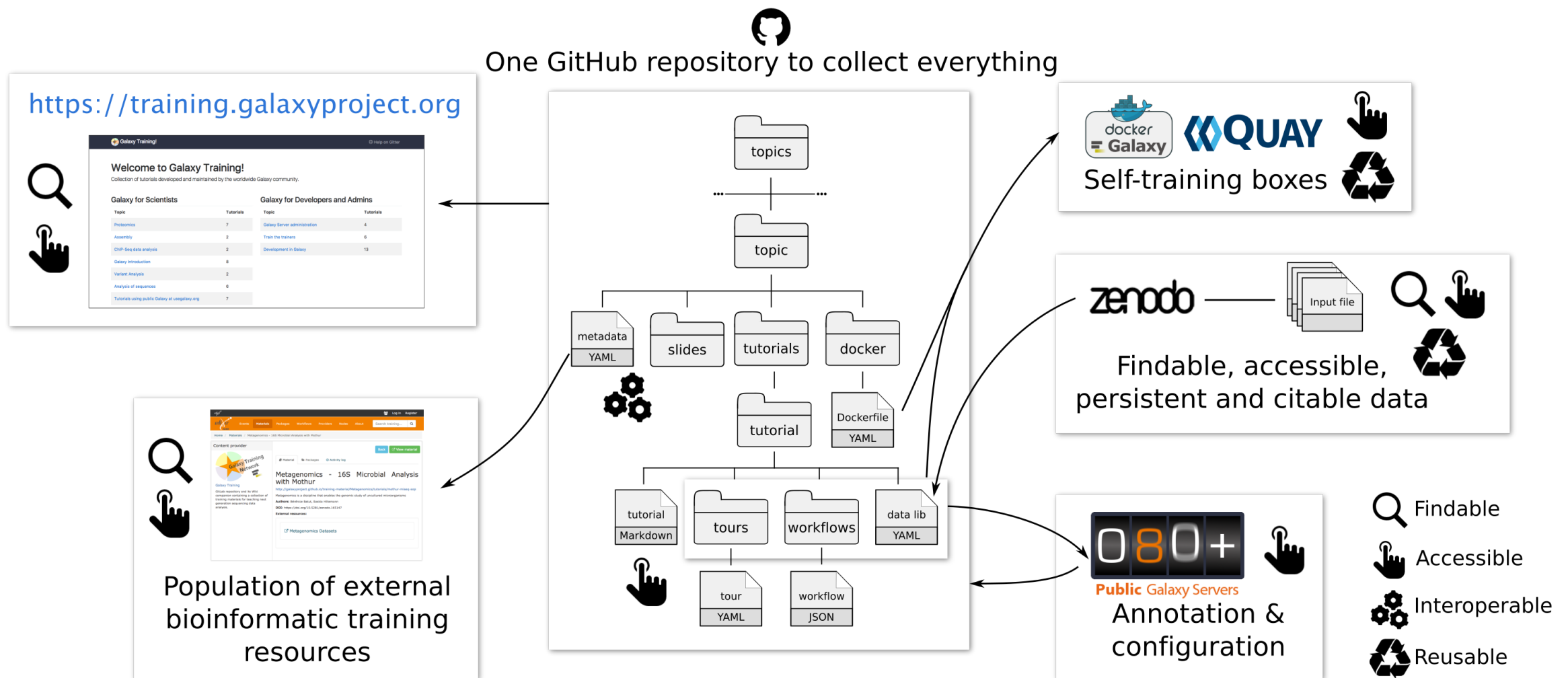
The image displays two side-by-side screenshots illustrating an interactive learning environment for bioinformatics.

Left Screenshot (Tutorial Page): This is a web page titled "Hands-on: Quality control" from the Galaxy Training! project. It provides a step-by-step guide for performing quality control. The first step involves using **FastQC** with specific parameters, including selecting "Short read data from your current history" as input. A tip box suggests selecting multiple datasets. The second step is to inspect the output of FastQC for a specific sample (GSM461177). A "Questions" section asks "What is the read length?" with a "Solution" button. The third step involves using **MultiQC** to aggregate the FastQC reports, with instructions on selecting the correct tool and output type.

Right Screenshot (Galaxy Interface): This is a screenshot of the Galaxy web interface. The "Tools" panel on the left shows the "fastqc" tool selected under "NGS: QC and manipulation". The main panel displays the "FastQC Read Quality reports (Galaxy Version 0.69)" tool configuration. It shows options for selecting input data (currently empty), a contaminant list, and a submodule/limit specifying file. The "Execute" button is visible. The right sidebar shows the "History" panel with a list of datasets, including those generated by FastQC for the GSM461177 sample.

Usable for effective training for individual users & instructors

An effective (FAIR) training infrastructure



Community-driven

A growing community



>100 contributors!

Support

Contributing to the Galaxy Training Material

Galaxy is a great solution to train the bioinformatics concepts: numerous bioinformatics tools are available (almost 5,000 in the Toolshed), it can be used by anyone without any computer science skills. It aims to use technology, making available resources and efforts that have made them accessible to researchers. It is possible.

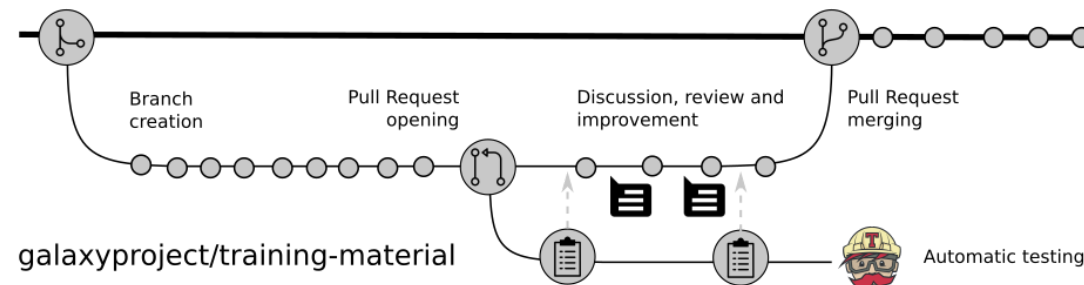
In 2016, the Galaxy Training Network decided to set up a new infrastructure for delivering easily Galaxy related training material. The idea was to develop something open and online based on a community effort, as always in Galaxy.

Material	Slides	Hands-on
Lesson		
Overview of the Galaxy Training Material		
Contributing with GitLab via command-line		
Contributing with GitLab via its interface		
Creating a new tutorial		
Creating a new tutorial - Creating Interactive Galaxy Tours		
Creating a new tutorial - Defining the technical infrastructure		
Creating a new tutorial - Slides		
Creating a new tutorial - Writing content in Markdown		

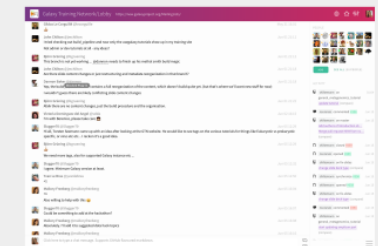
Tutorials to contribute



An open development process

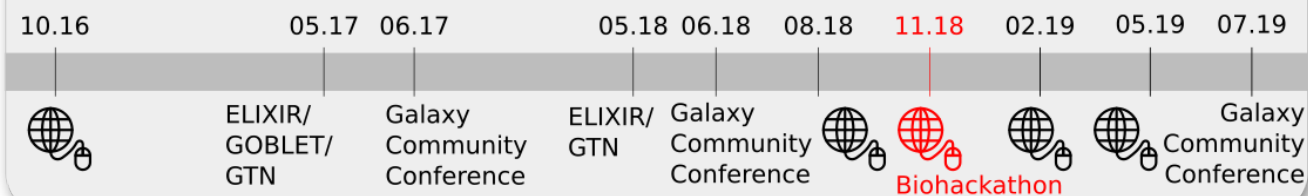


Discussions







Real time chat
Galaxy-Training-Network/Lobby

Community events: CoFests and calls



Many ideas for this week!

CoFest

-  Content
 - New topics, new tutorials
 - Training handbook
-  Global infrastructure
 - FAIRness evaluation of the training
 - Support for automatic translated content
-  Technical support
 - Workflow testing
 - Docker images
-  Community
 - More visibility for training events
 - Instructors

Join us for this hackathon!

 training.galaxyproject.org

 github.com/galaxyproject/training-material

Thank you!

