

Community-Driven Training for Biological Data Analysis with the Galaxy Training Network



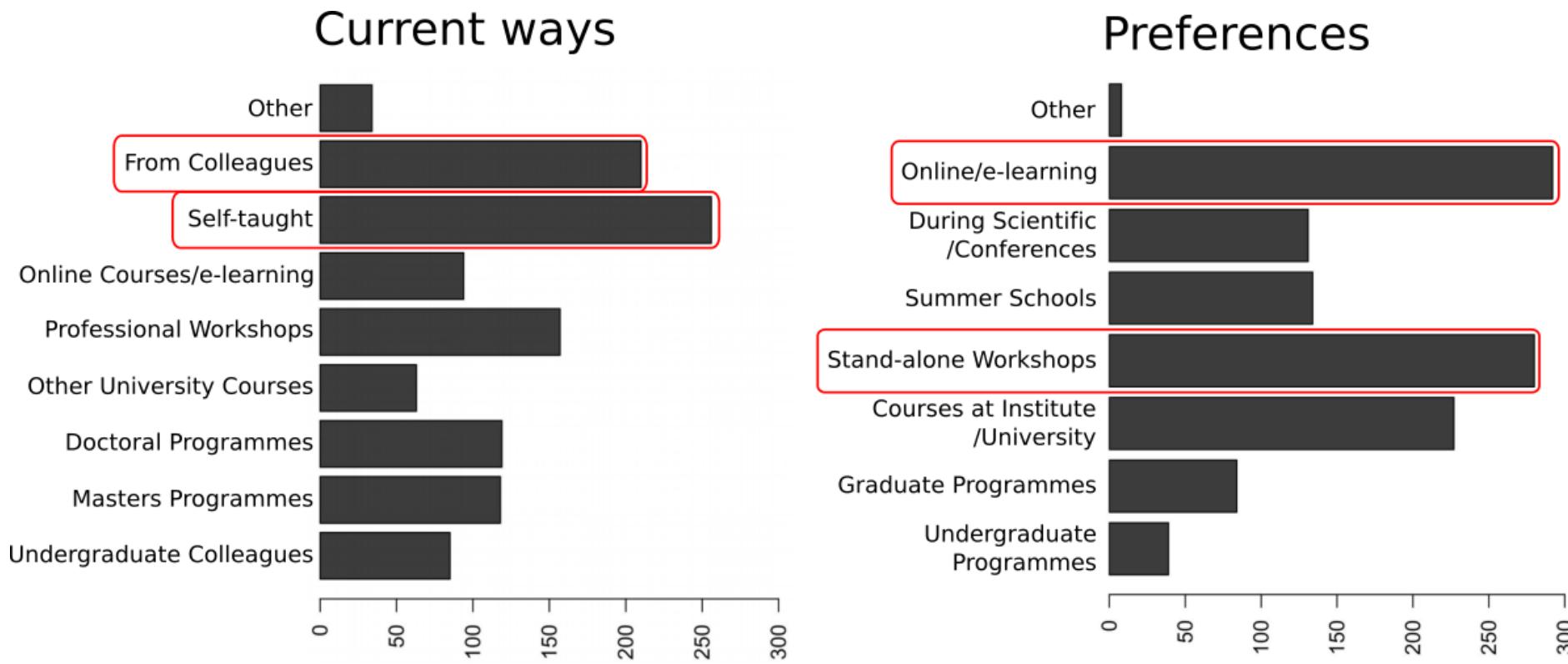
Picture from Bérénice Batut - Icons from the Noun Project and Flaticon

Bérénice Batut

CarpentryCon - May 2018

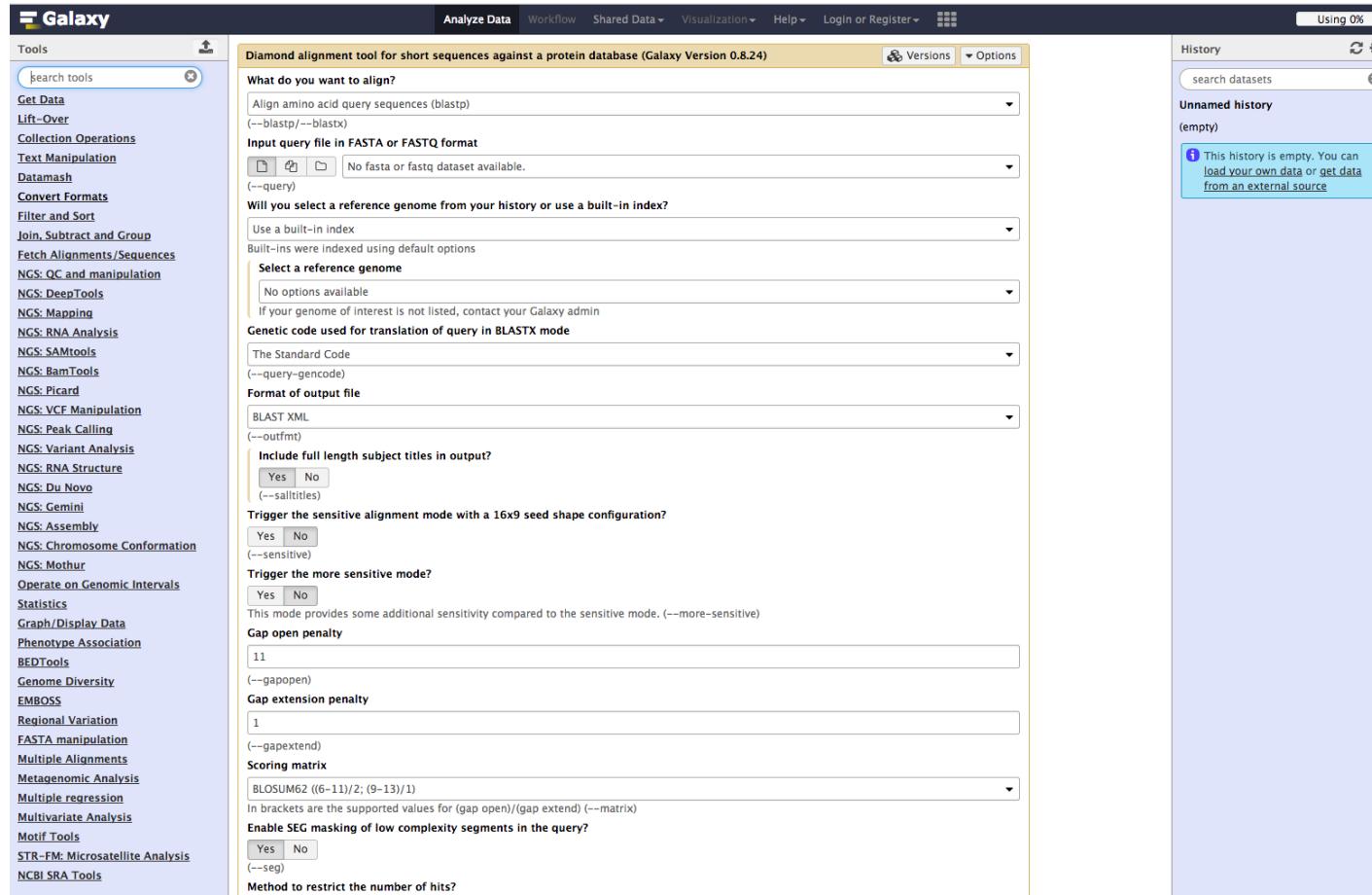
Need and demand for bioinformatic training

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



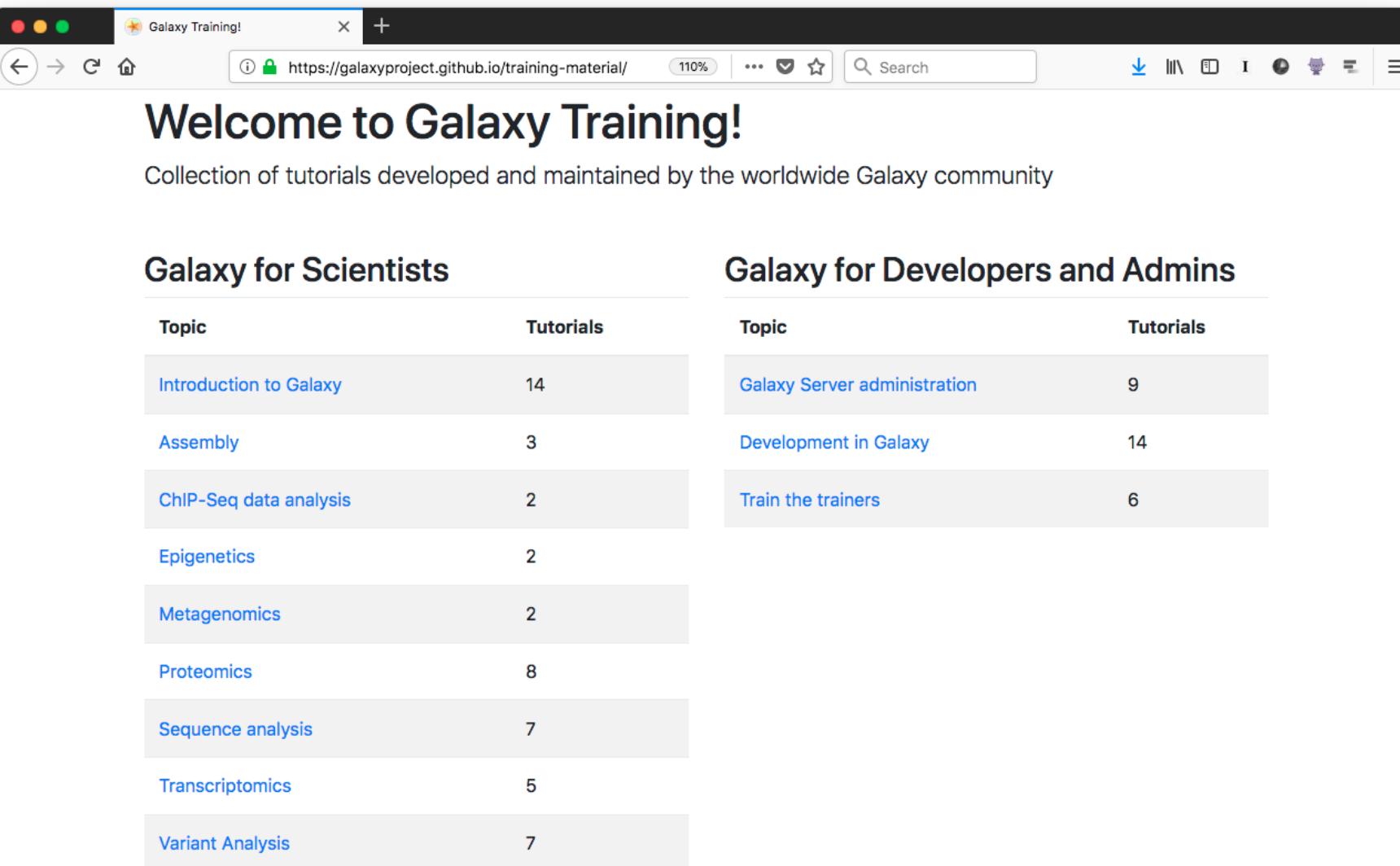
Graphs of Brazas et al, 2017

Galaxy: a great solution !



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

Online training material covering many topics



The screenshot shows a web browser window titled "Galaxy Training!" with the URL <https://galaxyproject.github.io/training-material/>. The page features a "Welcome to Galaxy Training!" header and a subtitle "Collection of tutorials developed and maintained by the worldwide Galaxy community". Below this, there are two main sections: "Galaxy for Scientists" and "Galaxy for Developers and Admins", each containing a list of topics and their corresponding tutorial counts.

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

Topic	Tutorials
Galaxy Server administration	9
Development in Galaxy	14
Train the trainers	6

<https://training.galaxyproject.org>

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

The image displays two side-by-side screenshots of a Galaxy web interface. The left screenshot shows a 'Hands-on: Quality control' tutorial with steps 1 through 5. Step 1 details how to run FastQC on FASTQ files. Step 2 instructs inspecting a generated webpage for sample 'GSM461177_1'. Step 3 covers MultiQC aggregation. Step 4 involves inspecting MultiQC output. Step 5 discusses Trim Galore! treatment. A 'Tip' section in step 2 advises selecting multiple files by holding the CTRL or COMMAND key. Step 2 also includes a 'Questions' section asking about read length, with an option to 'Click to view answers'. The right screenshot shows the 'FastQC Read Quality reports (Galaxy)' tool details. It includes sections for 'Short read data from your current history' (with a dropdown menu for file types like fastq, fastq.gz, etc.), 'Contaminant list' (with a dropdown menu for 'Nothing selected'), and 'Submodule and Limit specifying file' (with a dropdown menu for 'Nothing selected'). A large 'Execute' button is present. Below these are sections for 'Purpose' (describing FastQC's aim to provide quality control checks) and 'FastQC' (noting it's a Galaxy wrapper for the FastQC package). The Galaxy header at the top shows the title 'Galaxy' and various navigation options.

Hands-on: Quality control

1. **FastQC**: Run FastQC on the FASTQ files to control the quality of the reads
 - "Short read data from your current history"
 - Click on "Multiple datasets"
 - Select all raw datasets
2. Inspect on the generated webpage for [GSM461177_1](#) sample

Questions
What is the read length?
▶ Click to view answers
3. **MultiQC**: Aggregate the FastQC reports with
 - "Which tool was used generate logs?" to [FastQC](#)
 - "Type of FastQC output?" to [Raw data](#)
 - "FastQC output" to the generated [Raw data](#) files (multiple datasets)
4. Inspect the webpage output from MultiQC

Questions
What is the quality for the sequences for the different files?
▶ Click to view answers
5. **Trim Galore!**: Treat for the quality of sequences by running Trim Galore! with
 - "Is this library paired- or single-end?" to [Paired-end](#)

FastQC Read Quality reports (Galaxy)

Purpose
FastQC aims to provide a simple way to do some quality control checks on raw sequence data coming from high throughput sequencing pipelines. It provides a modular set of analyses which you can use to give a quick impression of whether your data has any problems of which you should be aware before doing any further analysis.
The main functions of FastQC are:

- Import of data from BAM, SAM or FastQ/FastQ.gz files (any variant),
- Providing a quick overview to tell you in which areas there may be problems
- Summary graphs and tables to quickly assess your data
- Export of results to an HTML based permanent report
- Offline operation to allow automated generation of reports without running the interactive application

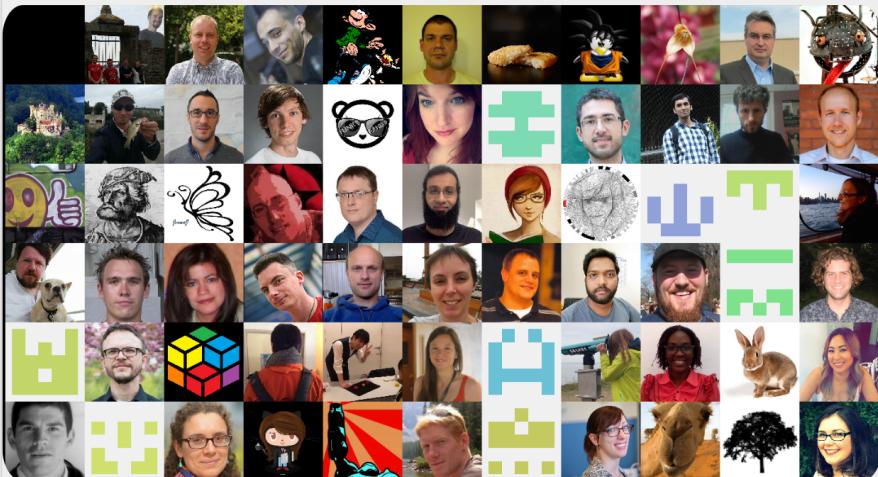
FastQC
This is a Galaxy wrapper. It merely exposes the external package [FastQC](#) which is documented at [FastQC](#). Kindly acknowledge it as well as this

An effective training infrastructure

- Interactive learning platform
- Support for current research problems
- Usable for effective training for individual users & instructors
- FAIR (Findable, Accessible, Interoperable, Reusable) and Open
- Technical support (tools, data, etc)
- Community driven (content creation and maintenance)

Community-driven

A growing community



>70 contributors!

Support & Discussions

The screenshot shows a GitHub repository page for 'Galaxy Training Network/Lobby'. The page displays a list of issues and pull requests. One issue, titled 'More tags for Galaxy instance etc...', discusses the need for more tags and data hack topics. Another issue, titled 'Help with this topic', asks for assistance with a specific topic. The repository has over 600 contributors.

Real time chat
Galaxy-Training-Network/Lobby

Community events

10.16



05.17 06.17

ELIXIR/
GOLET/
GTN

Galaxy
Community
Conference

05.18 06.18 08.18 11.18

ELIXIR/
GTN

Galaxy
Community
Conference



Thank you!

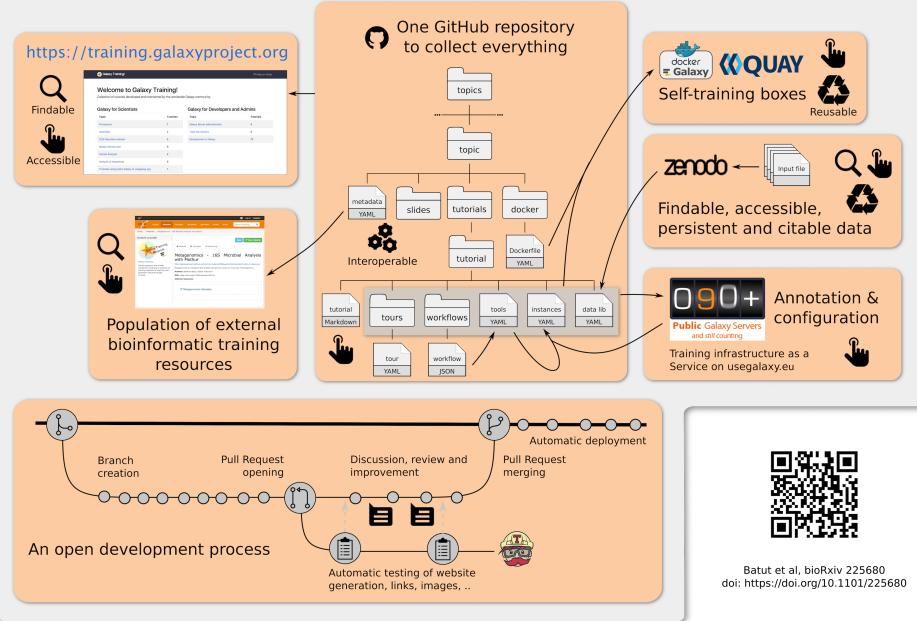
Community-Driven Training for Biological Data Analysis with the Galaxy Training Network

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The primary problem with the explosion of biomedical datasets is not the data itself, nor computational resources, nor the required storage space, but the general lack of trained and skilled researchers to manipulate and analyze this data. Eliminating this problem requires development of comprehensive educational resources. Here we present a community-driven framework that enables modern, interactive teaching of data analytics in life sciences and facilitates the development of training materials.



A newly developed and already used Galaxy Training infrastructure



Interactive training

Community driven

A growing community >60 contributors!

Support & Discussions

Real time chat Galaxy-Training-Network/Lobby

Community events

10.16 05.17 06.17 05.18 06.18 08.18 11.18

ELIXIR/ GOBLETS/GTN Galaxy Community Conference ELIXIR/ Galaxy GTN/ Community Conference

Icons by The Noun Project, Flaticon and icon8

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Rx Community-driven data analysis training for biology

 training.galaxyproject.org



github.com/galaxyproject/training-material

