

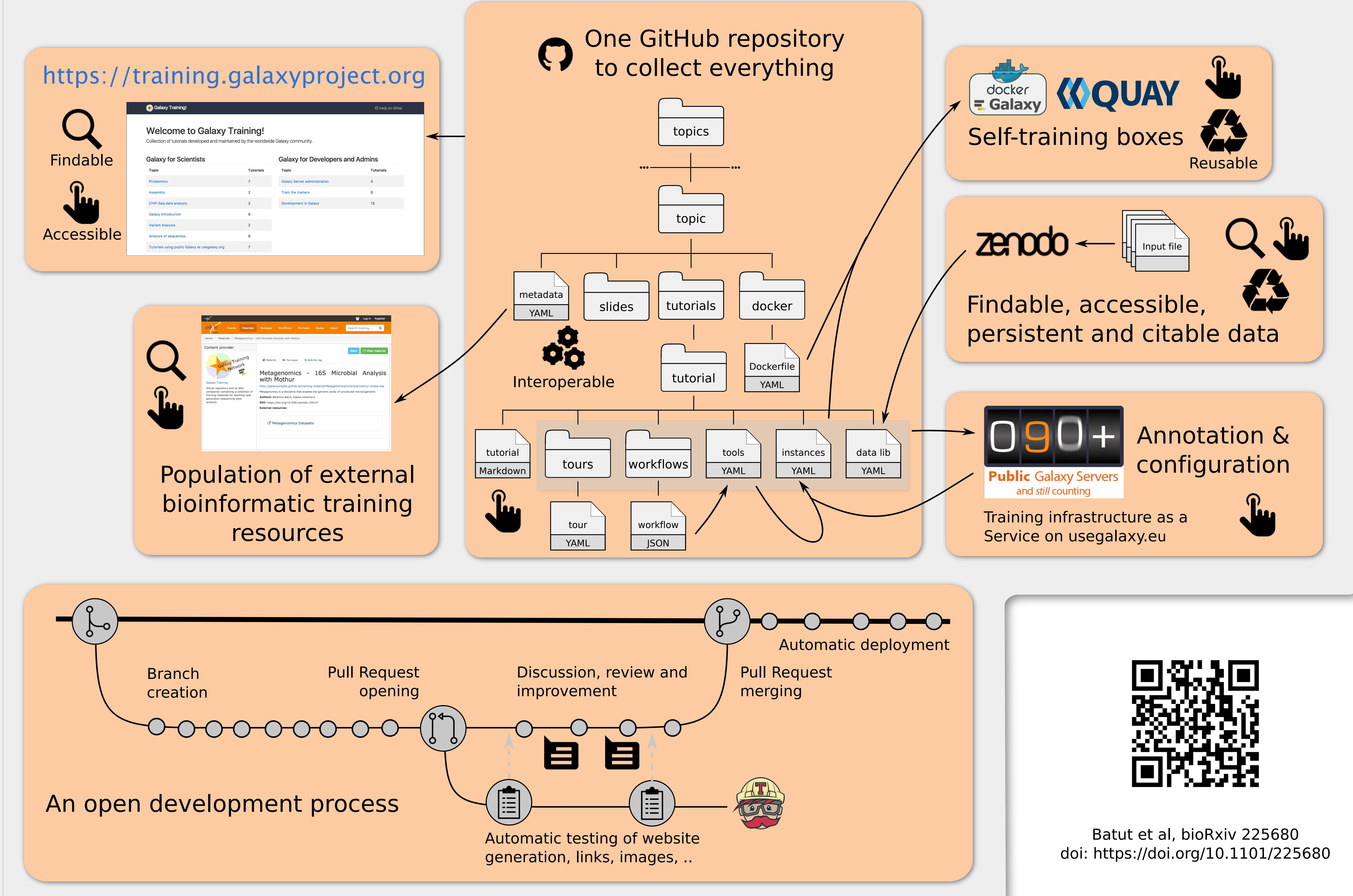
Community-Driven Training for Biological Data Analysis with the Galaxy Training Network

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The primary problem with the explosion of biomedical datasets is not the data itself, not computational resources, and not the required storage space, but the general lack of trained and skilled researchers to manipulate and analyze these 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

The screenshot displays two separate Galaxy interfaces. The left interface is a "Galaxy Training!" window showing a "Quality control" section. It includes a "Hands-on: Quality control" section with steps 1 through 5, each with sub-instructions and a "Tip" box. Step 1 involves running FastQC on FASTQ files. Step 2 involves inspecting a generated webpage for sample GSM461177_1. Step 3 involves aggregating FastQC reports with MultiQC. Step 4 involves inspecting MultiQC webpage output. Step 5 involves treating sequence quality with Trim Galore!.

The right interface is a "Galaxy | Europe" window showing the "FastQC Read Quality reports (Galaxy Version 0.67)" tool. The tool's documentation page is displayed, featuring a sidebar of "Tools" and a main content area with sections like "Short read data from your current history", "Contaminant list", and "Submodule and Limit specifying file". A "Execute" button is present. Below the tool description, there are sections for "Purpose" (explaining FastQC's aim to provide quality control checks) and "FastQC" (describing it as a Galaxy wrapper for the FastQC package). The rightmost portion of the interface shows a "History" panel listing four datasets from Zenodo.org.

Community driven

A growing community

Support & Discussions

The screenshot shows a real-time chat interface for the Galaxy Training Network. The top bar includes the title "Galaxy Training Network/Lobby" and a link to the mailing list page. The main area displays a conversation log with messages from various users, each accompanied by a small profile picture. The messages cover topics such as build pipelines, slide content changes, and specific features like the Metagenomics tutorial. On the right side, there are sections for "PEOPLE" (listing user profiles) and "ACTIVITY" (listing recent pull requests and code changes). A sidebar at the bottom provides navigation links for the chat and other parts of the platform.

Gildas Le Corguillé @lecorguille May 31 16:01

John Chilton @jmchilton Jun 01 21:11

I tried checking out build_pipeline and now only the usegalaxy tutorials show up in my training site
Not admin or dev tutorials at all - any ideas?

Björn Grüning @bgruening Jun 01 21:12

This branch is not yet working ... @dannom needs to finish up his metsmith build magic

John Chilton @jmchilton Jun 01 21:18

Are there slide content changes or just restructuring and metadata reorganization in that branch?

Dannom Baker @dannom Jun 01 21:18

Yep, the build_Blocked Plug-in contains a full reorganization of the content, which doesn't build quite yet. (but that's where we'll want new stuff for now)
I wouldn't guess there are likely conflicting slide content changes

Björn Grüning @bgruening Jun 01 21:22

Afaik there are no content changes, just the build procedure and the organisation.

Victoria Dominguez del Angel @vdda Jun 02 16:15

I'm with Berenice, please take care 😊

Slugger70 @Slugger70 Jun 05 12:20

Hi all, Torsten Seemann came up with an idea after looking at the GTN website. He would like to see tags on the various tutorials for things like Eukaryotic vs prokaryotic specific, or virus etc etc... I reckon it's a good idea.

Björn Grüning @bgruening Jun 05 12:29

We need more tags, also for supported Galaxy instance etc ...

Slugger70 @Slugger70 Jun 05 12:32

I agree. Minimum Galaxy version at least.

Yvan Le Bras @yvanlebras Jun 05 12:50

+1

Mallory Freeberg @malloryfreeberg Jun 05 16:04

+1
Also willing to help with this 😊

Slugger70 @Slugger70 Jun 05 16:07

Could be something to add at the hackathon?

Mallory Freeberg @malloryfreeberg Jun 05 16:08

Absolutely, I'll add it to suggested data hack topics

Mallory Freeberg @malloryfreeberg Jun 05 16:16

Click here to type a chat message. Supports GitHub flavoured markdown.

PEOPLE

SEE ALL (50 PEOPLE)

ACTIVITY

shitemann on general_metagenomics_tutorial update tutorial (compare) 01:04

nsoranzo commented #358 Jun 15

shitemann on master Add authors of introduction.sli... Merge pull request #359 from ns... (compare) Jun 15

shitemann closed #359 Jun 15

nsoranzo opened #359 Jun 15

shitemann on fix-slides change slide deck type (compare) Jun 15

shitemann synchronize #358 Jun 15

shitemann opened #358 Jun 15

shitemann on fix-slides change slide deck type (compare) Jun 15

nsoranzo commented #354 Jun 15

shitemann on general_metagenomics_tutorial start updating amplicon part (compare) Jun 15

Community events

