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Galaxy and training 2019 updates from the Galaxy Training Network

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Galaxy and Training

2019 updates from the Galaxy Training Network



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

Bérénice Batut and the Galaxy Training Network

Galaxy Community Conference - July 2019



The learner's path

Galaxy workshops






Galaxy Event Horizon

Upcoming (and past) events with Galaxy-related content.

The events listed here are also available in the [Galaxy Events Google Calendar](#). The [Galaxy Other Events Google Calendar](#) lists additional events that are relevant to the Galaxy Community, but that are not known to feature significant Galaxy content.

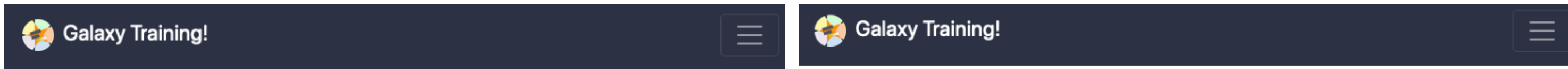
If you know of any event that should be added to this page and/or to the Galaxy Event Calendar, please add it here or send it to outreach@galaxyproject.org. For events prior to this year, see the [Events Archive](#).

Upcoming Events

Date	Topic/Event	Venue/Location	Contact
July 1st 2019	2019 Galaxy Community Conference (GCC2019)	Freiburg, Germany	 Organizers 
July 2nd 2019	Galaxy @ JOBIM 2019	Nantes, France	 Presenters
July 3rd 2019	An introduction to Galaxy with the NeCTAR Genomics Virtual Laboratory	2019 Winter School in Mathematical & Computational Biology, Brisbane, Queensland, Australia	 Igor Makunin 

<https://galaxyproject.org/events/>

Tutorials from Galaxy Training Material



Galaxy 101

By: Saskia Hiltemann, Nicola Soranzo, Clemens Blank, Anton Nekrutenko, Björn Grüning, Anne Pajon, Helena Rasche

Mapping

By: Joachim Wolff, Bérénice Batut, Helena Rasche

The screenshot displays two overlapping tutorial pages from the Galaxy Training Material. The left page is titled 'Quality Control' and is authored by Bérénice Batut. It includes a sidebar with 'Questions', 'Objectives', 'Time estimation', 'Level: Introduction', and 'Supporting Materials'. The main content area lists questions, objectives, and requirements. The right page is titled 'Reference-based RNA-Seq data analysis' and is authored by Bérénice Batut, Mallory Freeberg, Mo Heydarian, Anika Erleben, Pavankumar Videm, Clemens Blank, Maria Doyle, Nicola Soranzo, and Peter van Heusden. It also features a sidebar and a main content area with questions, objectives, and requirements. Both pages have a 'Galaxy Training!' header with a menu icon.
























<https://training.galaxyproject.org/>

Back to lab



Back to data

18 Transcriptomics tutorials

RNA-Seq reads to counts collections mouse QC	 ▾			
RNA-seq counts to genes limma-voom mouse QC	 ▾			
RNA-seq genes to pathways mouse	 ▾			
Reference-based RNA-Seq data analysis	 ▾			
Small Non-coding RNA Clustering using BlockClust	 ▾			
Understanding Barcodes single-cell	 ▾			
Visualization of RNA-Seq results with CummeRbund		 ▾		 
Visualization of RNA-Seq results with Volcano Plot				
Visualization of RNA-Seq results with heatmap2				

🎓 Do you want to extend your knowledge? Follow one of our recommended follow-up trainings:

- [Transcriptomics](#)
 - Reference-based RNA-Seq data analysis: [laptop icon](#) [hands-on](#)
- [ChIP-Seq data analysis](#)
 - Formation of the Super-Structures on the Inactive X: [GitHub icon](#) [slides](#) - [laptop icon](#) [hands-on](#)

Learning path

Learning more?

- 18 topics
 - 4 new topics: Metabolomics, Computational Chemistry, Data manipulation, User Interface and Features
- 140+ tutorials
 - 66 new tutorials
 - 16 new tutorials for new topics
 - Migration of 23 admin tutorials
 - 27 new tutorials in existing topics

Learning more?

Data Manipulation

A collection of microtutorials explaining data manipulation within Galaxy

Material

Lesson

Slides

Hands-on

Collections: Multisample Analysis



Collections: Rule Based Uploader



Collections: Using dataset collection



Data: Getting data into Galaxy



Group tags for complex experimental designs

Name tags for following complex histories



Search on TeSS

FAQ

Chat on Gitter

Discuss on Galaxy Help

Search of the website on TeSS

Levels

FR

JA

ES

PT

AR

Automatic translation



From learner to teacher

How to teach using Galaxy?

Teaching and Hosting Galaxy training

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 people without any computer science skills, it trains to use technology, outlining available resources and efforts that have made them accessible to researchers, it is scalable.

The Galaxy community via the Galaxy Training Network supports instructors and workshop organizers using with a series of recommendations (tutorials below) and regular discussion meetings.

You can additionally [read about our training philosophies](#).

Material

Lesson

Organizing a workshop

Running a workshop as instructor

Set up a Galaxy for Training

UseGalaxy.eu's Training Infrastructure as a Service

Workshop Kickoff

6 tutorials

Training Philosophies

We all teach in different ways, share your training philosophy and help other instructors find the way that is best for them!

Read their stories below:

- [Bérénice Batut](#)
- [Mo Heydarian](#)
- [Saskia Hiltemann](#)
- [Helena Rasche](#)
- [Tomas Klingstrom](#)
- [Anthony Bretaudeau](#)

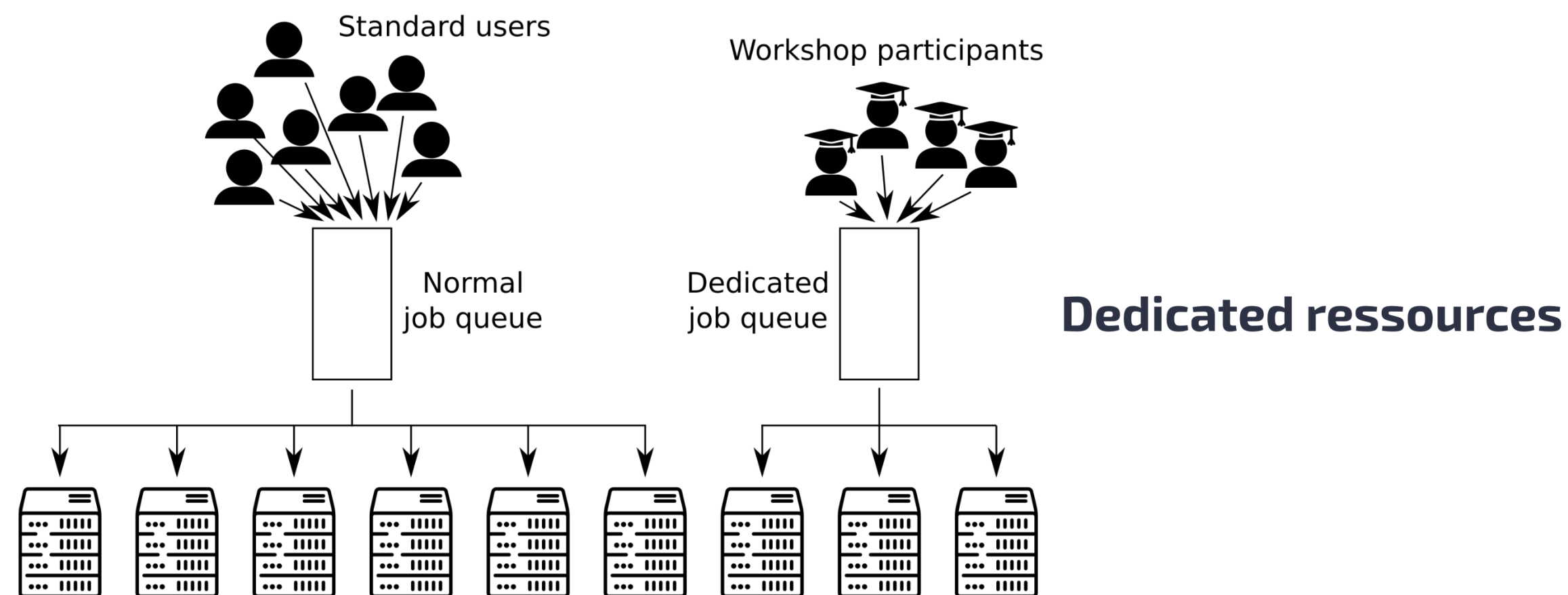
Bérénice Batut

When I am giving a training using Galaxy (e.g. ref-based RNA-seq), I usually give a 10-20 min introduction to RNA, RNA-seq using the slides that in the transcriptomics topic.

Then I switch to the tutorial. I show the participants where to find the tutorial on the training material website. I introduce the tutorial story: explain that we want to reproduce an analysis from a paper, introduce this paper, talk about the datasets/samples we will use.

Teaching practices of 6 trainers

Galaxy + Training = TlaaS



Overview
About
 This page gives you a brief overview of the current status of the trainees. Please note the following:

- Only jobs created in the last 3 hours are shown
- This includes jobs they run outside of the context of the course (as we cannot tell which are which)
- The username is essentially random but will be consistent within a one day period

State Overview

State	Count
ok	8
queued	6

Queue

User	Created	Tool	State	Job Runner ID
e4c7b1	2019-06-21 09:05:34	devteam/fastqc/fastqc/0.72+galaxy1	queued	None
e4c7b1	2019-06-21 09:05:33	devteam/fastqc/fastqc/0.72+galaxy1	queued	None
e4c7b1	2019-06-21 09:05:33	devteam/fastqc/fastqc/0.72+galaxy1	queued	None
e4c7b1	2019-06-21 09:05:18	devteam/fastqc/fastqc/0.72+galaxy1	queued	None
e4c7b1	2019-06-21 09:05:18	devteam/fastqc/fastqc/0.72+galaxy1	queued	None
e4c7b1	2019-06-21 09:05:18	devteam/fastqc/fastqc/0.72+galaxy1	queued	None
d7d09d	2019-06-21 08:34:00	devteam/fastqc/fastqc/0.72+galaxy1	ok	891099
d7d09d	2019-06-21 08:34:00	devteam/fastqc/fastqc/0.72+galaxy1	ok	891101
d7d09d	2019-06-21 08:33:59	devteam/fastqc/fastqc/0.72+galaxy1	ok	891098
d7d09d	2019-06-21 08:33:59	devteam/fastqc/fastqc/0.72+galaxy1	ok	891097
d7d09d	2019-06-21 08:33:52	devteam/fastqc/fastqc/0.72+galaxy1	ok	891102

Overview by Tool

Tool	New	Queued	Running	Ok	Error
devteam/fastqc/fastqc/0.72+galaxy1	0	6	0	5	0
upload1	0	0	0	3	0

Status dashboard

UseGalaxy.eu Workflow Testing

Based off of [jmchilton's template](#), except running tests against UseGalaxy.eu

Testing

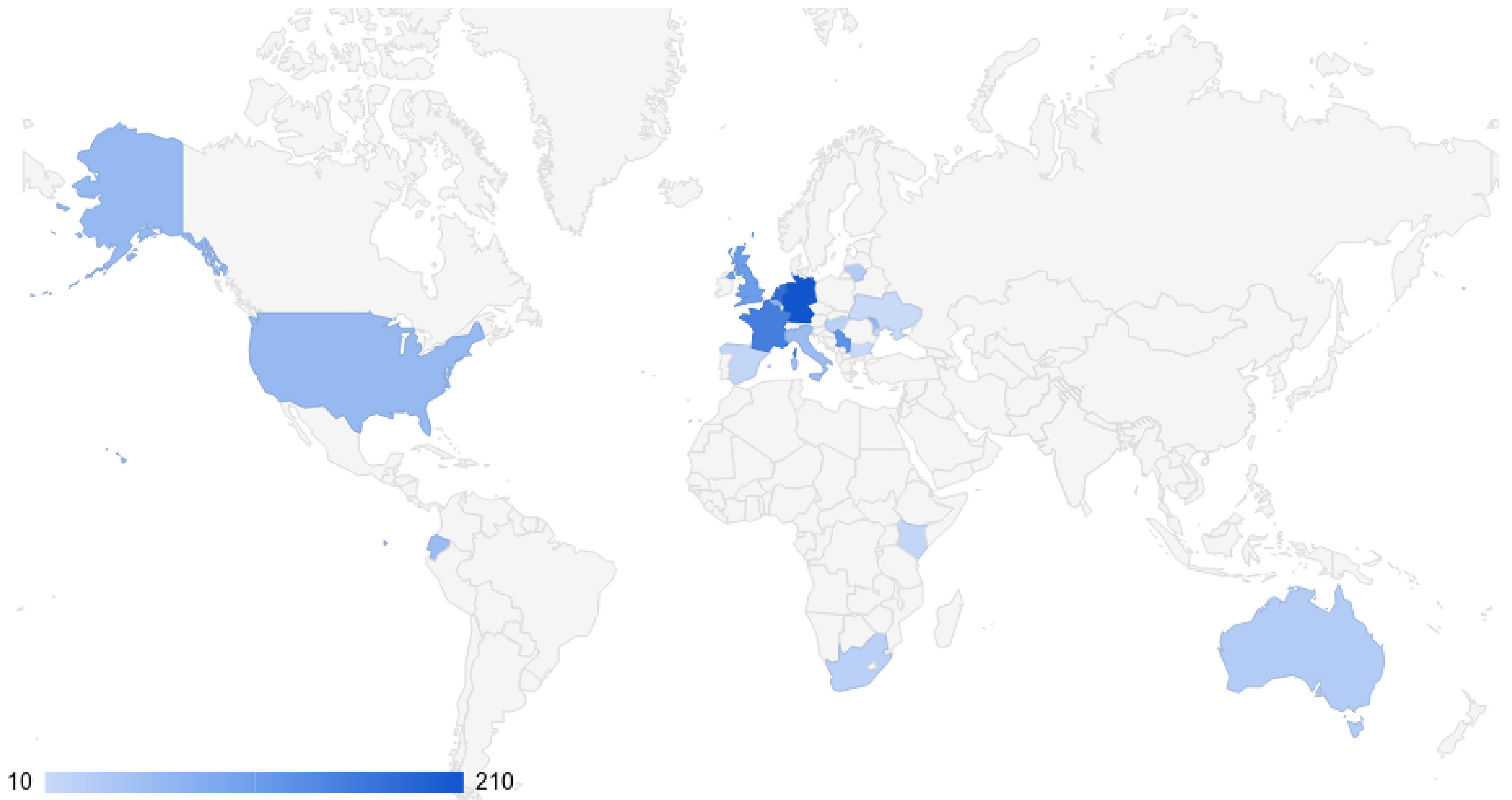
We are **automatically running** these workflows against UseGalaxy.eu

Workflow	Status
training/chip-seq/formation_of_super_structures_on_xi/formation_of_super_structures_on_xi.ga	build passing
training/proteomics/metaproteomics/metaproteomics.ga	build passing
training/proteomics/protein-id-sg-ps/protein-id-sg-ps.ga	build passing
training/proteomics/protein_quant_sil/protein_quant_sil.ga	build passing
training/sequence-analysis/mapping/mapping.ga	build passing
training/sequence-analysis/quality-control/quality_control.ga	build passing
training/statistics/machine_learning/regression/gradient_boosting_regression.ga	build passing
training/transcriptomics/ref-based/ref_based.ga	build failing
training/transcriptomics/small_ncrna_clustering/blockclust_workflow.ga	build failing

Automated workflow testing

<https://galaxyproject.eu/tiaas>

60+ training - 1,200 participants



Number of people trained per country

<https://galaxyproject.eu/tiaas>

Becoming a contributor

A collection of tutorials developed and maintained
by the worldwide Galaxy community

training.galaxyproject.org



learn on our infrastructure
galaxyproject.eu/tiaas

contribute on GitHub

Online CoFest and community calls



- Every 3 months
- One day of CoFest
- 2 community calls
- Next one: August, 15th

A Training Development Kit

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 people without any computer science skills, it trains to use technology, outlining available resources and efforts that have made them accessible to researchers, it is scalable.

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

Lesson

Overview of the Galaxy Training Material

Contributing with GitHub via command-line

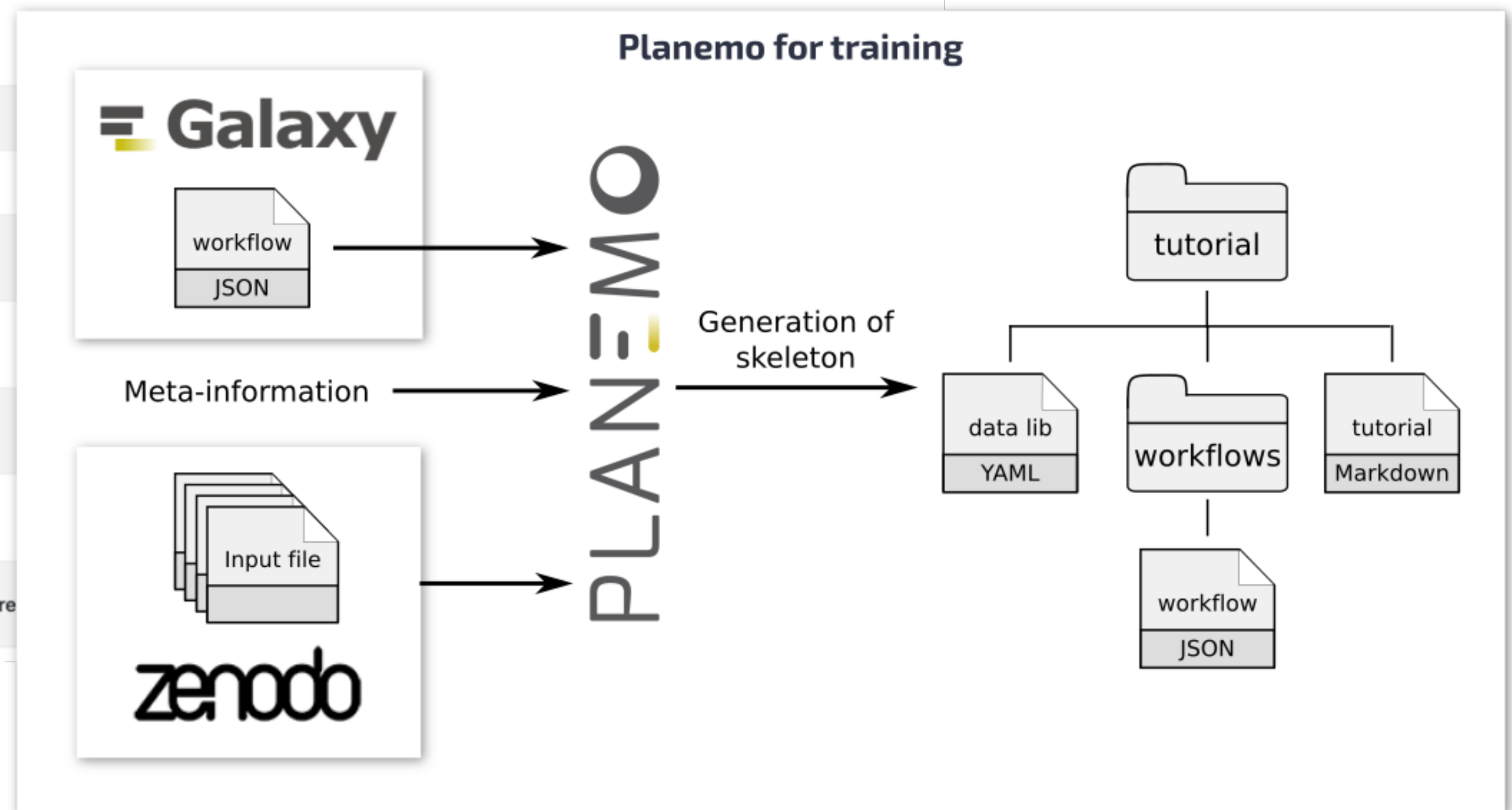
Contributing with GitHub via its interface

Creating a new tutorial

Creating a new tutorial - Creating Interactive Galaxy Tours

Creating a new tutorial - Defining the technical infrastructure

10 tutorials



Feedbacks

👏 Congratulations on successfully completing this tutorial!

Help us improve this content!

Your feedback helps us improve this tutorial and will be considered in future revisions.

This feedback should be ONLY ABOUT THE MANUAL; if you encountered problems with the Galaxy server or if tools were missing, please contact the administrators of the Galaxy server you were using.

We do not store any personal identifying information.

How much did you like this tutorial?

1 2 3 4 5

🙄 ❤️

Direct feedback form at the end of each tutorial

Automatic submission to GitHub

Tutorial Feedback #989

Edit New issue

📌 Open shiltemann opened this issue on Aug 28, 2018 · 305 comments

shiltemann on Aug 28, 2018 Member + 👤 ✎ ⋮ Assignees – assign yourself ⚙️

This issue will collect all feedback submitted via the feedback form at the end of each tutorial

👤 3 🏷️ 📁

shiltemann referenced this issue on Aug 28, 2018

Embed a short feedback form at the bottom of the tutorial #988 Merged

shiltemann on Aug 28, 2018 + edited Author Member + 👤 ✎ ⋮

New GTN feedback received (extended form)

Which GTN tutorial did you complete?: assembly with velvet

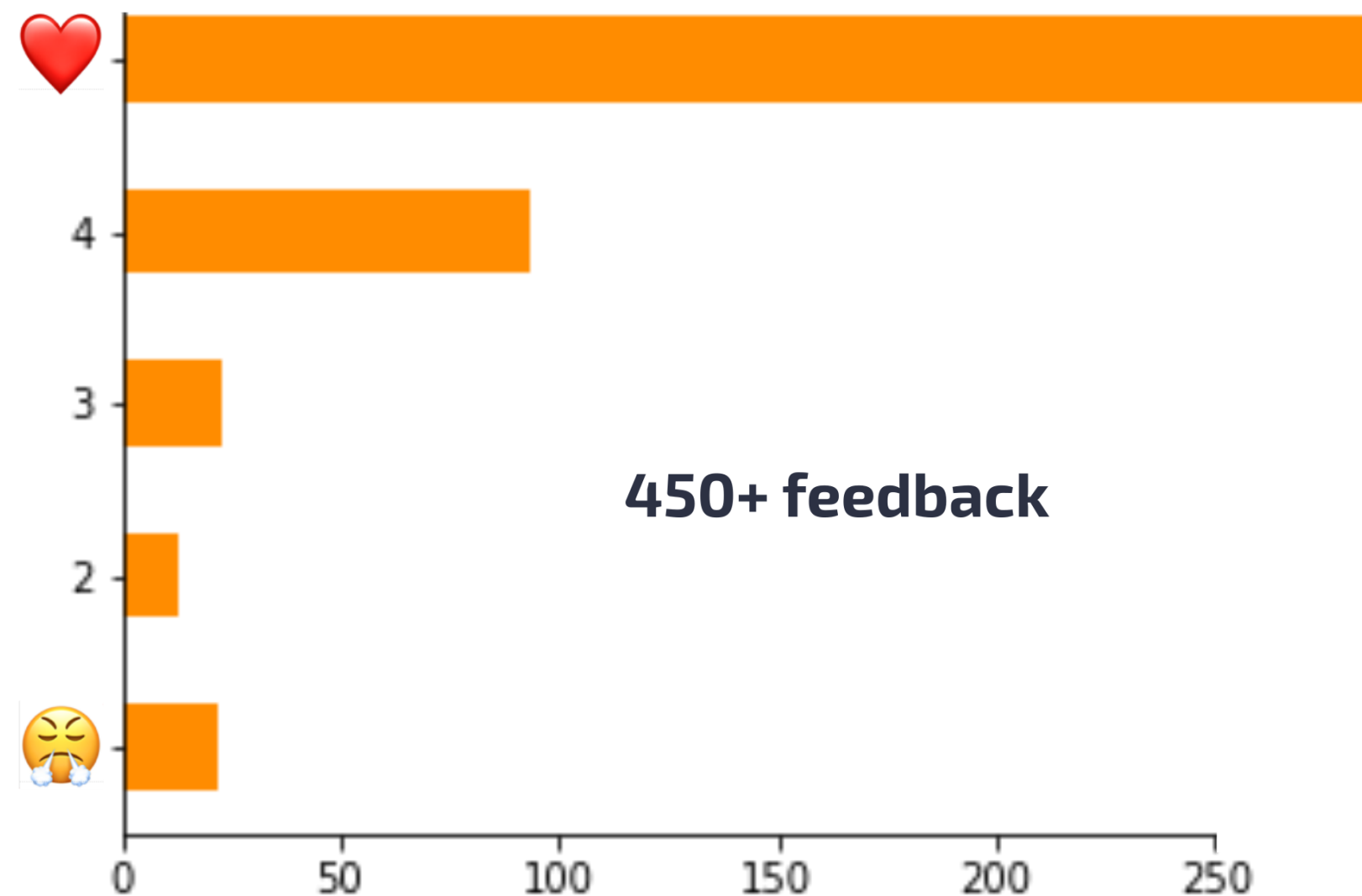
How did you use this tutorial?: I took the tutorial on my own.

Notifications Customize

🔊 Unsubscribe

📄 Mark as unread

3 participants 👤 👤 👤

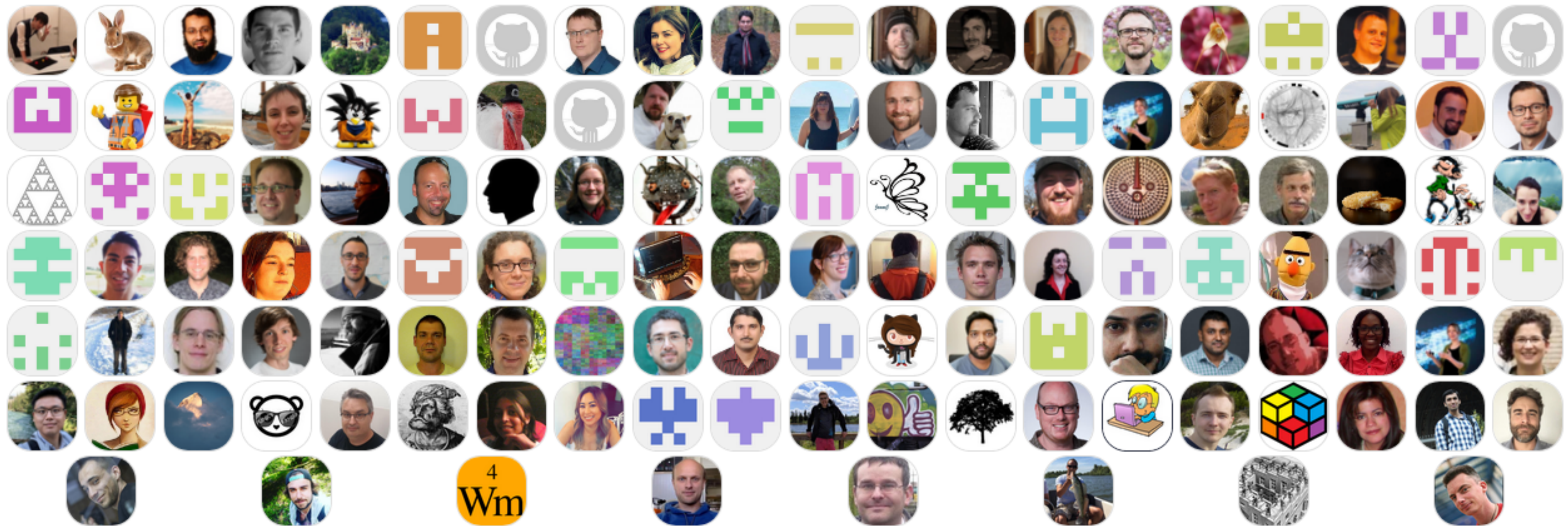


Community of contributors

120+ contributors - 46 new ones

Hall of Fame

A big *Thank You!* to the 128 awesome contributors to the Galaxy training materials!

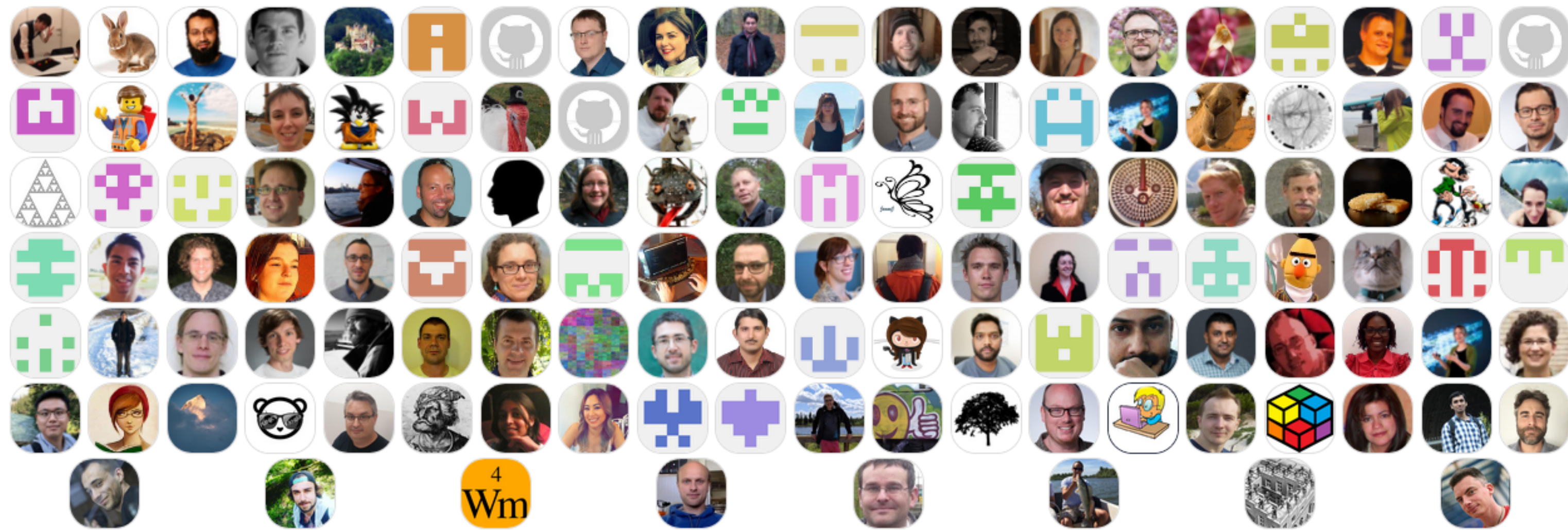


<https://training.galaxyproject.org/hall-of-fame>

Thank you!

Hall of Fame

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training.galaxyproject.org

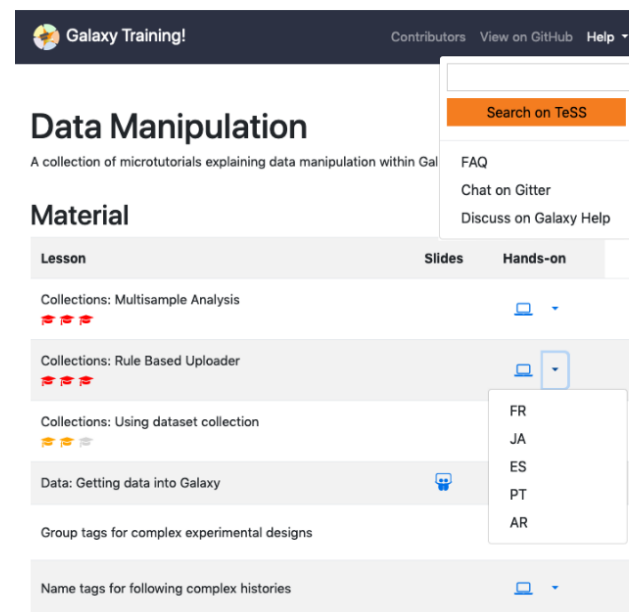


2019 updates

New content

4 new topics: Metabolomics, Computational chemistry, Data manipulation, User Interface and Features
66 new tutorials: 16 tutorials for new topics, migration of 23 admin tutorials, 27 new tutorials in existing topics
Many updated tutorials

Features for users



Search engine for the website

Levels

Automatic translation

Table of content

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Direct feedback form submitted as GitHub issue
 450+ feedback

Support for instructors

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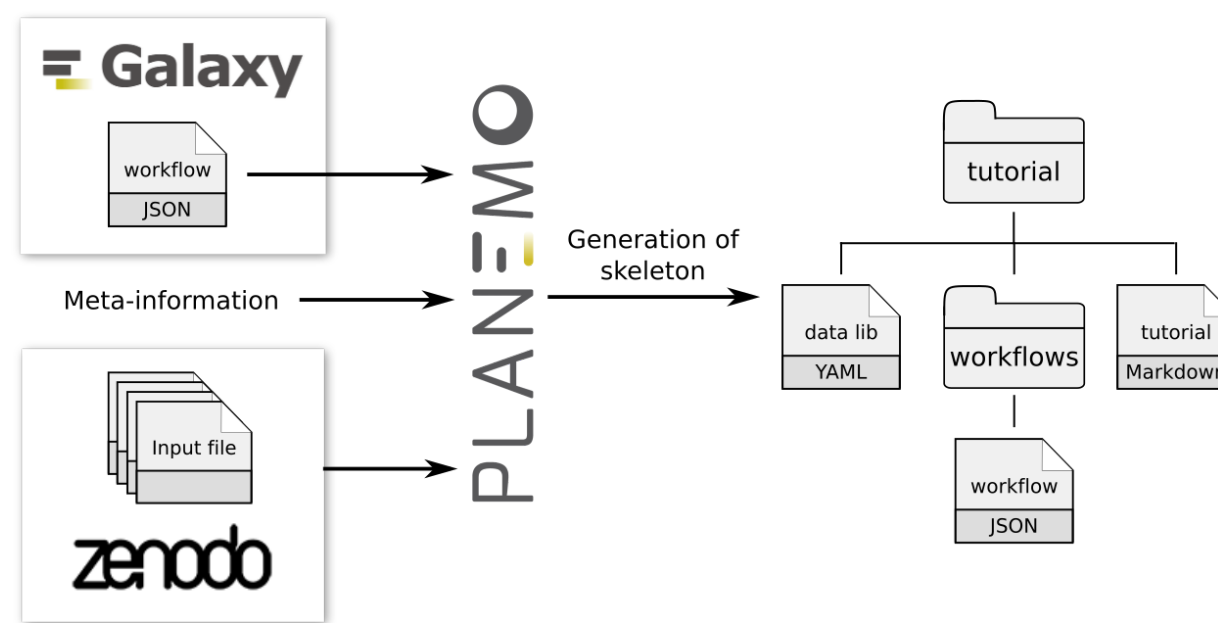
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Training Development Kit



Community



Online, every 3 months

46 new contributors

Maintainers

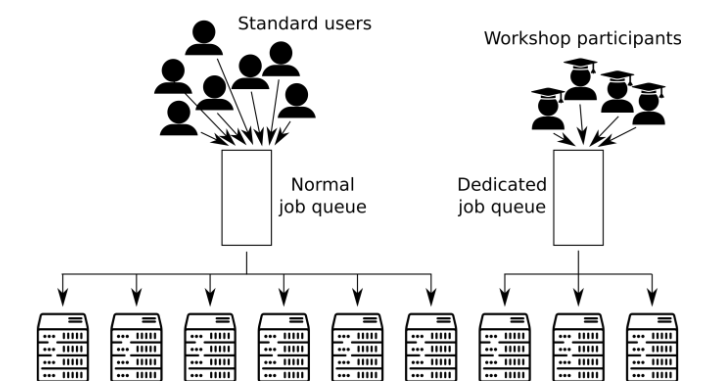
This material is maintained by:

Yan Le Bras, Bérénice Batut
 For any question related to **Genome annotation with Prokka**

Contributors

By: Anna Syme, Torsten Seemann, Simon Gladman

Better visibility for contributors



Dedicated resources

Status dashboard

UseGalaxy.eu Workflow Testing

Automated workflow testing

