

WEBINAR SERIES

Galaxy Resources for...



Please remain muted unless you're invited to speak by the Chair.



Please use "Q&A" to raise questions during the presentation.



Please use the "hand-raising function" to indicate you would like to contribute directly



Please use "Chat" for further comments or discussions.



This session will be recorded.



Researchers

April 14

WEBINAR SERIES

 **Galaxy**

**Resources
for...**

**Tool
Developers**



May 12



**Educators
& Trainers**

April 28

**Admin &
Infrastructure
Providers**



May 26

Galaxy Resources for Educators & Trainers

April 28, 2021

Saskia Hiltemann (Erasmus Medical Center)

Subina Mehta (University of Minnesota)

Miaomiao Zhou (Avans Hogeschool)

Christine Cucinotta (Fred Hutchinson Cancer Center)

Bérénice Batut (University of Freiburg)





Outline

- **Galaxy Training Network (GTN) for Instructors** - Saskia Hiltemann
- **Examples of teaching with Galaxy**
 - **Remote and Hybrid training** - Saskia Hiltemann & Helena Rasche
 - **Teaching with Galaxy in a High School Setting** - Christine Cucinotta
 - **GTN Training in a University Setting** - Miaomiao Zhou
 - **GTN Training for Research Scientists** - Subina Mehta
 - **Galaxy for teaching pupils and citizens** - Bérénice Batut
- **Q & A**



GTN for Instructors

Saskia Hiltemann, Bérénice Batut, Helena Rasche





Why use Galaxy for Teaching?

Galaxy is an **amazing** teaching platform



Focus on the science, not the technical details of tools



No installation required, only requirement is a browser



Huge **library** of free, **high quality tutorials**



Visualizations of results and workflows



Share data with students, and have them share their work back.



Enable **remote teaching** & **follow their progress** with TlaaS



Wait, there's more..



Lots of tools available, ~8000 in the Galaxy Tool shed



Combine Galaxy with **programming environments** e.g. Jupyter and Rstudio



Shared data libraries for sharing input datasets



Interactive tools such as genome browsers, visualisation tools



Large **community of Galaxy instructors**



GTN Catalog of Tutorials

Contributors ? Help

Extras

Edit on GitHub

GTN statistics

Panel Metrics

Large number of tutorials

Many different **scientific topics**

Free to use for anybody

Also suitable for **self-study**

Anybody can **contribute**
updates and new tutorials

Community-driven

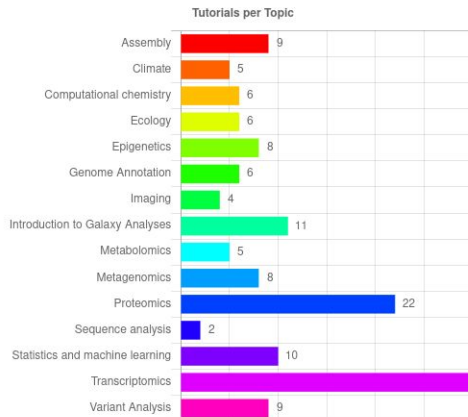
GTN Statistics

21 Topics

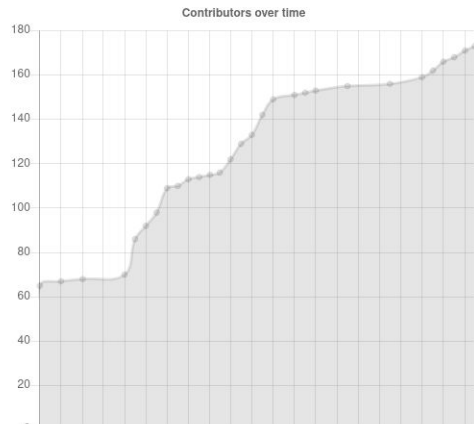
196 Tutorials

176 Contributors

16 Scientific Topics



Growing Community



training.galaxyproject.org/stats



GTN Catalog of Tutorials

training.galaxyproject.org



Welcome to Galaxy Training!

Collection of tutorials developed and maintained by the worldwide Galaxy community

Galaxy for Scientists

Topic	Tutorials
Introduction to Galaxy Analyses	10
Assembly	9
Climate	4
Computational chemistry	6
Ecology	6
Epigenetics	6
Genome Annotation	5
Imaging	4
Metabolomics	4
Metagenomics	7
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Statistics and machine learning	11
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Variant Analysis	8
Visualisation	2

Galaxy Tips & Tricks

Topic	Tutorials
Using Galaxy and Managing your Data	17

Galaxy for Developers and Admins

Topic	Tutorials
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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](#) or our [Frequently Asked Questions](#)

Galaxy for Contributors and Instructors

Topic	Tutorials
Contributing to the Galaxy Training Material	11
Teaching and Hosting Galaxy training	6

Welcome to the GTN!

New to the GTN? This video gives an introduction to what it's all about.



Video created by Geert Bonamie.

Meet & Join the Galaxy Community!

Find out how you can become part of the Galaxy community



Video created by Beatriz Serrano-Solano

The latest GTN news

Read about new tutorials, features, events and more!

Apr 10, 2021 📖 New Tutorials: Whole transcriptome analysis of Arabidopsis thaliana
Apr 6, 2021 🔊 New Feature: Video Player
Mar 30, 2021 📖 New Tutorial: Downstream Single-cell RNA Plant analysis with ScanPy
Mar 24, 2021 📖 New Tutorials: Genome assembly of a MRSA genome

GTN Tweets





GTN Tutorials

Follow a “scientific story”

Often recreating a **published analysis**

Step-by-step guide through the analysis

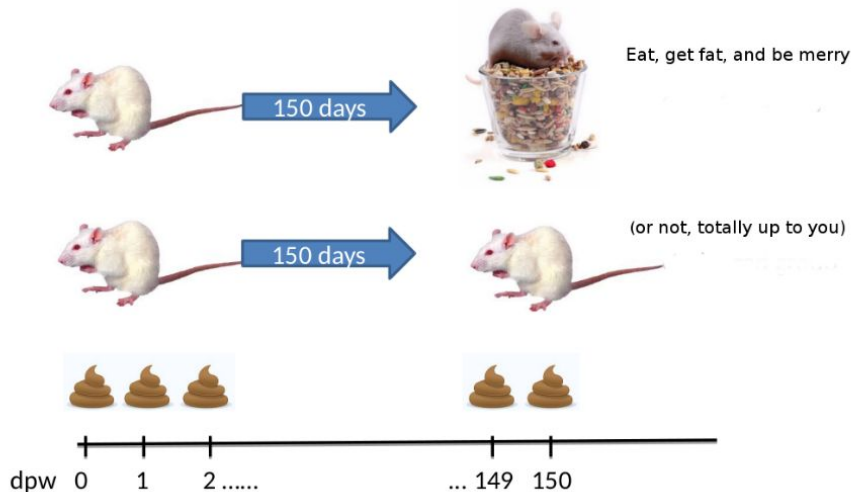
Hands-on sections mixed with scientific and technical **background**

Understanding our input data

In this tutorial we use the [dataset generated by the Schloss lab](#) to illustrate [their MiSeq SOP](#).

They [describe the experiment](#) as follows:

"The Schloss lab is interested in understanding the effect of normal variation in the gut microbiome on host health. To that end, we collected fresh feces from mice on a daily basis for 365 days post weaning. During the first 150 days post weaning (dpw), nothing was done to our mice except allow them to eat, get fat, and be merry. We were curious whether the rapid change in weight observed during the first 10 dpw affected the stability microbiome compared to the microbiome observed between days 140 and 150."





GTN Tutorials

Designed for teaching

Each tutorial includes metadata:

- Questions addressed in the lesson
- Learning objectives of the lesson
- Prerequisite knowledge
- Supporting materials
- Difficulty level
- Time estimate
- Key points
- References for further learning

Overview

? Questions

- How to perform quality control of NGS raw data (FASTQ)?
- What are the quality parameters to check for a dataset?
- How to improve the quality of a dataset?

🎯 Objectives

- Manipulate FASTQ files
- Assess quality from a FASTQ file
- Use FastQC tool
- Understand FastQC output
- Use tools for quality correction
- Use a tool to aggregate FastQC output
- Process single-end and paired-end data

✅ Requirements

- [Introduction to Galaxy Analyses](#)

🕒 **Time estimation:** 1 hour 30 minutes

🎓 **Level:** Introductory 🎓 🎓 🎓

📎 Supporting Materials

[📄 Slides](#) [📁 Datasets](#) [🔗 Workflows](#) [🔧 Tours](#) [🌐 Available on these](#)

📅 **Last modification:** Mar 12, 2021



GTN Tutorials

Designed for teaching

Formative assessments in the form of **question** boxes (with **solutions**) scattered throughout the tutorial

- For self-assessment and for instructors to assess the participants' understanding

? Question

1. What are the 4 main features of each read in a fastq file.
2. What does the `_1` and `_2` mean in your filenames?

👁 Solution

1. The following:
 - A `@` followed by a name and sometimes information of the read
 - A nucleotide sequence
 - A `+` (optional followed by the name)
 - The quality score per base of nucleotide sequence (Each symbol to be explained later)
2. Forward and reverse reads, by convention, are labelled `_1` and `_2`, to be `_r1 / _r2`.



GTN-in-Galaxy



Graduation cap icon on top menu

Access all GTN tutorials

Jump back and forth between Galaxy and the tutorial

Great for small screens

New! Click on tool name in tutorial to quickly open it in Galaxy

The screenshot displays the Galaxy Europe web interface. At the top, a blue header bar contains the 'Galaxy Europe' logo and navigation links: 'Analyze Data', 'Workflow', 'Visualize', 'Shared Data', 'Help', 'User', and a graduation cap icon. A status bar below the header indicates 'Using 320.0 G'. A notification banner states: '[20/04/2021, 12:30] Interactive tools can be scheduled again.'

The main interface is divided into three panels:

- Left Panel (Tools):** Features a search bar, an 'Upload Data' button, and a list of tool categories: 'Get Data', 'Send Data', 'Collection Operations', 'GENERAL TEXT TOOLS' (highlighted), 'Text Manipulation', 'Filter and Sort', 'Join, Subtract and Group', 'GENOMIC FILE MANIPULATION' (highlighted), 'Convert Formats', 'FASTQ/FASTQ', 'FASTQ Quality Control', 'Quality Control', 'SAM/BAM', and 'BED'.
- Center Panel:** Displays a 'COVID-19 Research!' announcement with links to the 'Galaxy SARS-CoV-2 portal', 'ENA', and 'COVID-19 dedicated training materials'. Below this is a quote from Prof. Stephen Hawking and a 'News' section with articles dated April 19, 17, and 15, 2021, including 'The Galaxy community involved in several ELIXIR Implementation Studies' and 'GCC2021 Abstract Submission is open'.
- Right Panel (History):** Shows a 'test: Astrid: Unicycler - Hybrid - v3.3' dataset with 15 shown and 110 hidden datasets, totaling 2.46 GB. Below this is a list of recent datasets, including '125: ABRicate List - list of databases', '124: ABRicate List - list of databases', '123: Top hits', '121: Circos Plot', '94: Genome Browser', '66: Join two Datasets on data 65 and data 64', and '52: Sequence Lengths'. Each entry includes a 'hybrid' or 'unicycler' tag and icons for viewing, editing, and deleting.



Support for Instructors

- Slides have **speaker notes** to help you prepare
- **Video slides** generated based on speaker notes
 - Using text-to-speech
 - Example: [Short intro to Galaxy](#)
- **FAQ page** for tutorials (new!)
 - See common questions and their answers to prepare for teaching
 - Add additional questions here after teaching to help other instructors!

The screenshot shows the Galaxy Training! interface with two tabs: 'Lesson' and 'Slides'. Under the 'Lesson' tab, there is a list of lessons: 'Introduction to Galaxy' and 'A short introduction to Galaxy'. Each lesson has a small icon and a dropdown arrow. Under the 'Slides' tab, there is a list of slides: 'Introduction to Galaxy' and 'A short introduction to Galaxy'. Each slide has a small icon, a dropdown arrow, and a share icon.

The screenshot shows a Galaxy Training! slide. The top part features the Galaxy Training Network logo and the title 'A Short Introduction to Galaxy' by Saskia Hiltemann and Helene Rasche. Below the title, it says 'Tip: press p to view the presenter notes'. The bottom part of the slide is titled 'Questions' and lists four common questions: 'What is Galaxy?', 'Why should I use Galaxy?', 'How do I use Galaxy?', and 'How can I connect with the Galaxy Community?'. The right side of the slide shows the 'NOTES FOR CURRENT SLIDE' section, which contains presenter notes and a timer showing '0:00:00'.

The screenshot shows the Galaxy Training! FAQ page. The page has a dark header with the Galaxy Training! logo and navigation links: 'Contributors', 'Help', 'Extras', and 'Search Tutorials'. The main content area is titled 'Frequently Asked Questions' and is divided into two sections: 'Analysis' and 'Collections'. The 'Analysis' section has a heading 'Results may vary' and a tip: 'Your results may be slightly different from the ones presented in this tutorial due to differing versions of tools, reference data, external databases, or because of stochastic processes in the algorithms.' The 'Collections' section has a heading 'Adding a tag to a collection' and a tip: 'Tip: Adding a tag to a collection'. Below this, there is a heading 'Creating a dataset collection' and a tip: 'Tip: Creating a dataset collection'.

All thanks to **175+** contributors

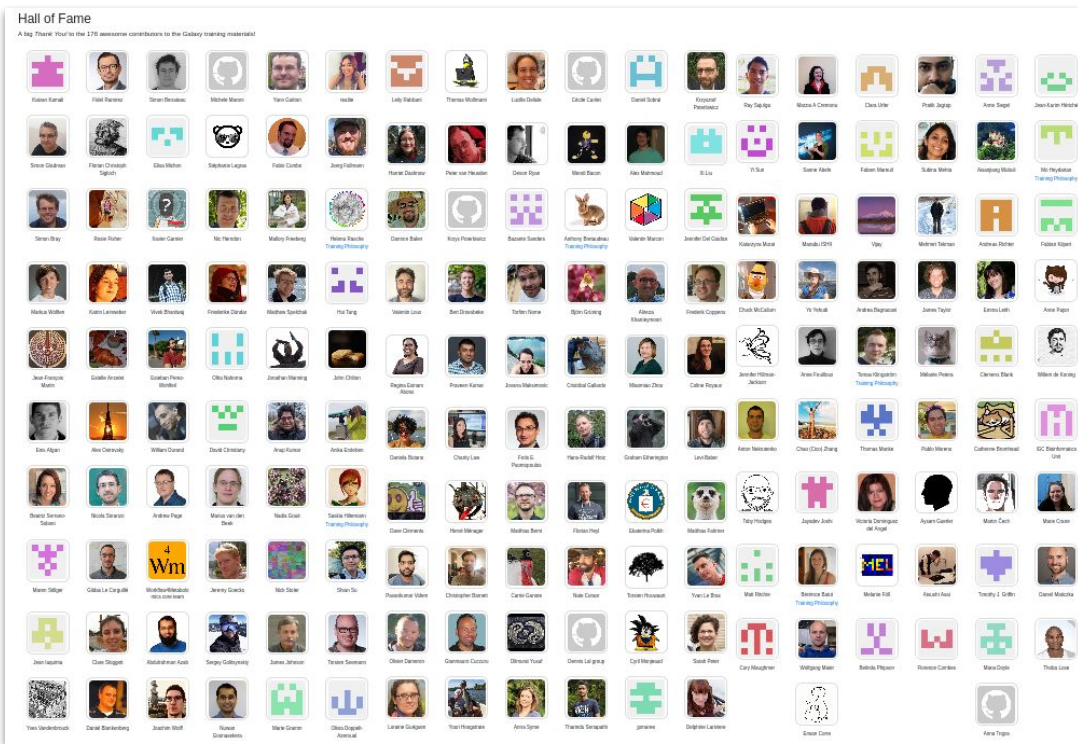
Together we keep materials
up-to-date

New **tutorials** added regularly

New **topics** added regularly


New **features** added regularly

training.galaxyproject.org/hall-of-fame






Which Galaxy to use?


- You do not need to set up your own Galaxy server
- Each tutorial is **annotated** with a list of public Galaxy servers where it can be run

 Galaxy Training! Introduction to Galaxy Analyses Help

Galaxy 101

By:  Saskia Hiltermann  Nicola Soranzo  Cler  Björn
 Helena Rasche


Overview



 **Questions**

- Which coding exon has the highest number of single nucleotide variants?



 **Objectives**

- Familiarize yourself with the basics of Galaxy
- Learn how to obtain data from external sources
- Learn how to run tools
- Learn how histories work
- Learn how to create a workflow
- Learn how to share your work

 **Time estimation:** 1 hour

 **Level:** Introductory   

 **Supporting Materials**

 [Topic Overview slides](#)  [Datasets](#)  [Workflows](#)  [Available on these Galaxies](#) 

 **Last modification:** Mar 23, 2021

 Docker image
CLIP-Explorer
Galaxy Africa
Galaxy Test
Galaxy@GenOuest
HiCEXplorer
Human Cell Atlas
Metagenomics
NanoGalaxy
Single Cell Omics workbench
Street Science
UseGalaxy.be
UseGalaxy.eu
UseGalaxy.fr
UseGalaxy.no
UseGalaxy.org (Main)
UseGalaxy.org.au
Virology



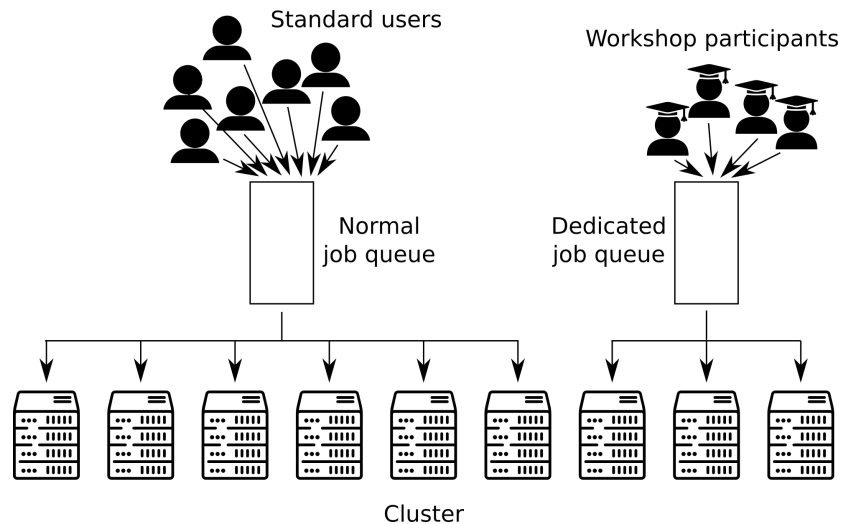
TlaaS: Training Infrastructure as a Service

Galaxy EU offers TlaaS

- Dedicated resources for your workshop
- Dashboard to monitor students progress

How does it work?

- Apply (for free)
- Provide some information
 - dates, number of participants, tutorials used, etc
- You will get a special workshop **join link**
 - Students click this link once at start of event
- Optional: write a blog post describing how it went!
- **Coming soon!** also on Galaxy Main and Galaxy Australia!



TlaaS

Apply now: usegalaxy.eu/tiaas



TlaaS Dashboard

- Overview of status of everybody in the TlaaS group
 - Which tools have been run?
 - How many times a tool was run?
 - Success, Failed, Running, Queued?
-
- See approximately how far people are
 - Are we losing anybody?

Especially handy for online training

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	93

Overview by Tool

Tool	New	Queued	Ok	Error
bgruening/trim_galore/trim_galore/0.4.3.1	0	0	6	0
iuc/featurecounts/featurecounts/1.6.4	0	0	27	0
devteam/bowtie2/bowtie2/2.3.4.3	0	0	27	0
iuc/nanoplot/nanoplot/1.13.0	0	0	2	0
devteam/fastqc/fastqc/0.72+galaxy1	0	0	10	0
lparsons/cutadapt/cutadapt/1.16.5	0	0	1	0
iuc/hisat2/hisat2/2.1.0+galaxy4	0	0	6	0
upload1	0	0	5	0
CONVERTER_gz_to_uncompressed	0	0	1	0
devteam/samtool_filter2/samtool_filter2/1.8	0	0	6	0
iuc/multiqc/multiqc/1.7	0	0	2	0

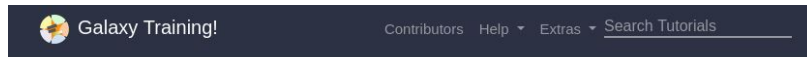
Queue

User	Created	Tool	State	Job Runner ID
9be9d8	2019-06-17 14:16:26	iuc/multiqc/multiqc/1.7	ok	859583
a81b3a	2019-06-17 14:14:38	devteam/samtool_filter2/samtool_filter2/1.8	ok	859579
a81b3a	2019-06-17 14:14:38	devteam/samtool_filter2/samtool_filter2/1.8	ok	859580
a81b3a	2019-06-17 14:14:38	devteam/samtool_filter2/samtool_filter2/1.8	ok	859578
a81b3a	2019-06-17 14:14:15	devteam/samtool_filter2/samtool_filter2/1.8	ok	859576
a81b3a	2019-06-17 14:14:15	devteam/samtool_filter2/samtool_filter2/1.8	ok	859575
a81b3a	2019-06-17 14:14:15	devteam/samtool_filter2/samtool_filter2/1.8	ok	859577
0c1d9c	2019-06-17 14:10:15	iuc/multiqc/multiqc/1.7	ok	859592
0c1d9c	2019-06-17 14:10:15	iuc/multiqc/multiqc/1.7	ok	859592



GTN Tutorials for Workshop Organizers

- **Checklists for workshop organizers**
 - Before, during & after event
- **Tips & Tricks for instructors**
- **How to request TlaaS**
- **Workshop kickoff slides**
- **How to configure your own Galaxy server with all the tutorial requirements**
 - We provide Docker images supporting all tutorials in a topic



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

Q X

Lesson	Slides	Hands-on
Galaxy Admin Training		▾
Organizing a workshop		▾
Running a workshop as instructor		▾
Set up a Galaxy for Training		▾
UseGalaxy.eu's Training Infrastructure as a Service		▾
Workshop Kickoff		▾



GTN Tutorials for Contributors

Want to create your own tutorial?
Great! We are happy to help!

Tutorials available

- How to write GTN tutorials
- How to write GTN slides
 - Including automated video slides
- How to use Github



Galaxy Training!

Contributors

Help ▾

Extras ▾

Search Tutorials

Contributing to the Galaxy Training Material

Galaxy is a great solution to train the bioinformatics concepts: numerous bioinformatics tools are available (more than 7,000 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

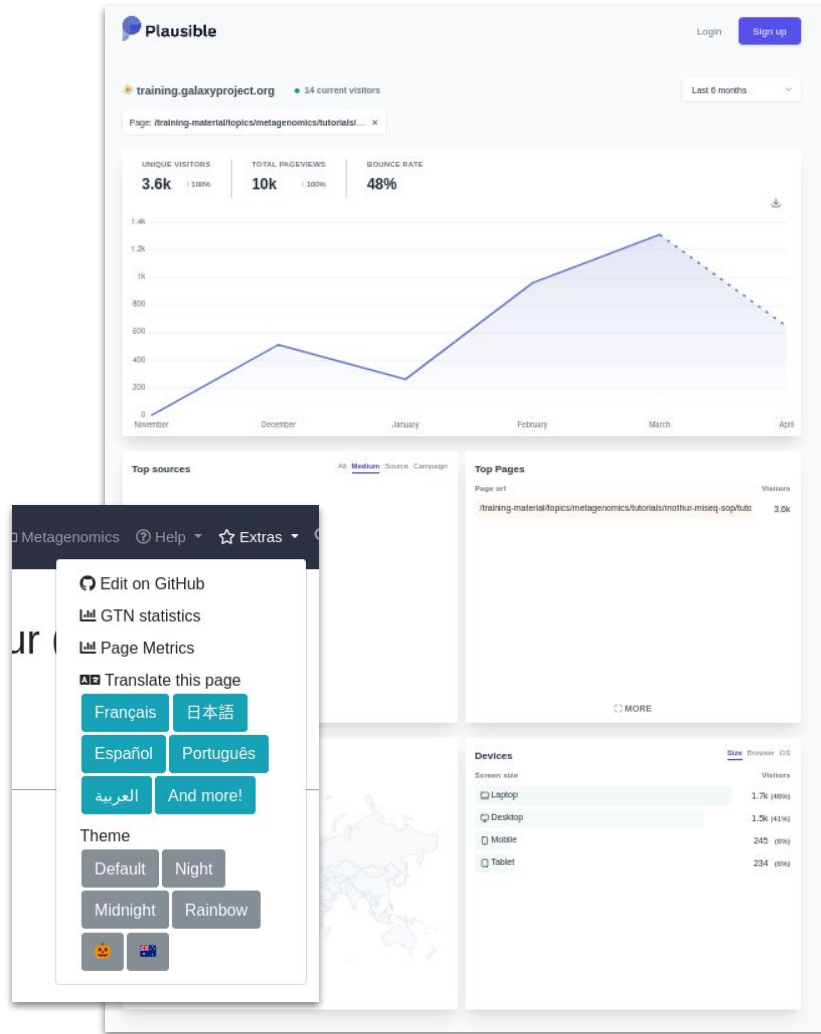
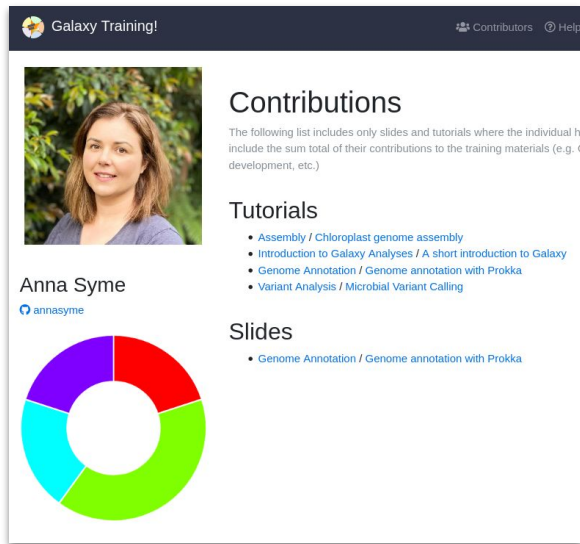
Writing Tutorials

These will take you from zero to hero in writing Galaxy Training Materials.

Lesson	Slides	Hands-on	Galaxy instances
Creating a new tutorial		▾	▾
Creating content in Markdown		▾	
Creating Slides	▾		
Running the Galaxy Training material website locally		▾	
Tools, Data, and Workflows for tutorials		▾	

GTN for Contributors

- Get credit for your contributions
- See how much your tutorial is being used
 - “Extras” menu -> Page Metrics



GTN Community and Support

Engage with other Galaxy instructors!

- Share our experiences
- Get help using and creating GTN materials or organizing your event
- Need instructors or helpers for your event? Ask the community!

Gitter chat: gitter.im/Galaxy-Training-Network/Lobby

Galaxy events page: galaxyproject.org/events (add your training event here!)

Each pair, take the
mapping base call differs
derived by combining

OPEN CHAT

The screenshot shows the Gitter chat interface for the Galaxy Training Network Lobby. The header bar includes the lobby icon, the name "Galaxy Training Network/Lobby", the URL "https://training.galaxyproject.org", and navigation icons for messages, a globe, a star, settings, and a user profile. The chat area on the left displays three messages: a thank you from @aless78, a question from @nomadscientist about an icon, and a response from @shiltemann about fontawesome icons. On the right, a "PEOPLE" sidebar shows a grid of 24 user avatars, with an "ADD" button and a link to "SEE ALL (314 PEOPLE)".

Galaxy Training Network/Lobby <https://training.galaxyproject.org>

[m] [Globe] [Star] [Settings] [User Profile]

MESSAGES

@aless78 @aless78 Mar 16 19:51
I will for sure! thanks!

Wendi Bacon @nomadscientist Mar 17 11:56

Is there an {% icon XXX???? %} for this image?

Saskia Hiltmann @shiltemann Mar 17 11:57
I don't believe so. If there are ever new icons you want to add, we can make anything from <https://fontawesome.com/>
available to use with the {% icon XX %} tag in the GTN

PEOPLE

ADD SEE ALL (314 PEOPLE)



GTN Feedback



Give us your feedback!

- Did you use Galaxy and/or the GTN for teaching? Let us know how it went [here](#)
- Have other comments or suggestions? Start a discussion [here](#)
- How can Galaxy be improved to facilitate teaching? Comment [here](#)

The screenshot shows the GitHub interface for the `galaxyproject/training-material` repository. The top navigation bar includes links for Code, Issues (114), Pull requests (33), Discussions (active), Actions, Projects (12), Security, and Insights. On the right, there are buttons for Unwatch (48), Unstar (197), and Fork (475). The main content area displays three discussion cards:

- General**: "Welcome to GTN Discussions!" by shiltemann.
- Instructors**: "Workshop Instructor Feedback" by hexylena.
- Instructors**: "Optimizing Galaxy for Teachin..." by shiltemann.

At the bottom, there is a search bar labeled "Search all discussions", filters for "New", "Top: All", "Answered", and "Unanswered", and a "New discussion" button.



GTN Collaboration Fests

Every 3 months on 3rd Thursday

Community calls in 3 time zones

- Ask your questions
- Learn how to develop tutorials
- Discuss with other instructors

All day support in Gitter

- Work on your tutorials and get help from us
- Prepare your workshop and ask us anything
- Help us improve the GTN materials



Next CoFest: May 20, 2021. Everybody Welcome! See [here](#) for more info



Examples of Galaxy Training in Various Educational Settings

Examples from community members using Galaxy for teaching

Remote and hybrid trainings - reaching participants across a distance

High Schools - Fostering an interest in science

University - Preparing for a career in science

Research Institutes - Keeping up to date with the latest developments in the field

Citizen Science - Outreach to general public



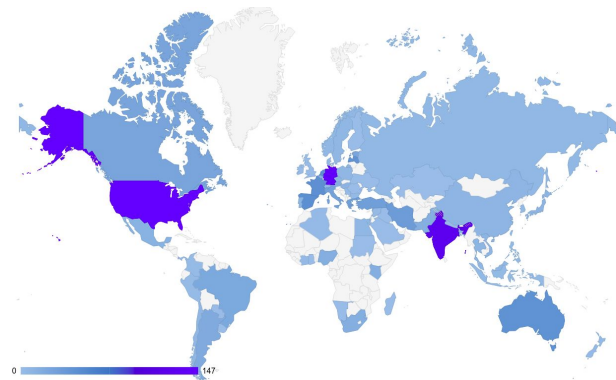
Remote Global Training: GTN Smörgåsbord

Saskia Hiltemann & Helena Rasche



Remote Training: Smörgåsbord event

- Global 5-day, 24/7 continuous event (all time zones)
- 1200 registrations from 78 countries
- Asynchronous format
 - Pre-recorded videos (40+ sessions, 25+ hours of video tutorials)
 - Slack chat for support
 - Participants start, stop, pause whenever they want
 - Everything remains available after event
- 60+ instructors, 25+ presenters
- Great format during pandemics
- Will become an annual event



Read our [blog post](#)



GTN Video Catalog

All videos from Smorgasbord event still available online on the [course webpage](#) and [YouTube](#)

- Feel free to re-use videos for your own events!
- We will run a similar event during the [Galaxy Conference this summer](#) (with lots of extra content!)

Future Plans:

- “Shopping cart” for building your own remote training event from available videos
- With **event support** (website, Slack space, communications plan, registration forms, event report template, ..)

GTN Smörgåsbord 2021 - A Global Galaxy Course



Welcome & Practical Information

Welcome & Course Information	↕
Get set up for the course	↕
Meet & Join the Galaxy Community!	↕

Day 1: Introduction to Galaxy and NGS analysis

Today we start by introducing the Galaxy Platform, and show you how to analyze your NGS data using Galaxy. Today we have a mixture of lectures, demos, and hands-on tutorials.

Icebreaker: Introduce yourself in Slack!	↕
A Very Short Introduction to Galaxy	↕
Your First Galaxy Analysis	↕
Demo: NGS Data Logistics using SARS-CoV-2 data	↕
Quality Control: Intro	↕
Quality Control: Hands-on!	↕
Mapping: Introduction	↕
Mapping: Hands-on!	↕
Genome Assembly: Introduction	↕
Genome Assembly: Hands-on!	↕
Wrap up & Socialize	↕

Day 2: Introduction to RNA-Seq analysis with Galaxy and R

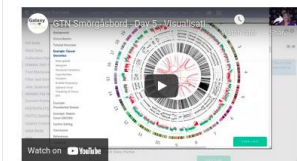
Today we dive into (bulk) RNA-seq analysis. We will walk you through an end-to-end analysis and Galaxy, and show you how to perform downstream analysis on the results using Rstudio in Galaxy.

Icebreaker: Say Hi in Slack!	↕
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Circos Visualisation in Galaxy: Intro

Circos Visualisation in Galaxy: Hands-on!

Video Tutorial



Video Length: 50m
Subtitles By: Beatriz Serrano-Solano, Helena Rasche, Saskia Hiltmann, Alireza Khanfeymouri
Description: Circos is a popular tool for creating circular graphs to display genomic data. In this tutorial you will create a Circos plot for a cancer dataset

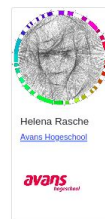
Supported Servers

- [Use Galaxy.org.au](#)
- [Use Galaxy.eu](#)
- [Use Galaxy.org](#)

Supporting Materials

- **Tutorial: Visualisation with Circos**
- **Video: Watch it on YouTube**
- **FAQ Document** - Have a question about this training? Check here to see if it has already been answered
- **Ask an Instructor** - Have question about the training? Did you run into a problem? Just wanna chat? Ask away on Slack! (Channel: [#gtc_circos-visualisation](#))
- **Finished the session?** - Let us know that you've finished it, and what you thought of it! On Slack: Channel: [#gtc_circos-visualisation](#)! Thank!
- **Enjoyed it?** - Like the video on YouTube, Tweet, and follow the GTN on Twitter! [@galaxytraining](#)

Genome Annotation: Annotation of a prokaryotic genome: Slides

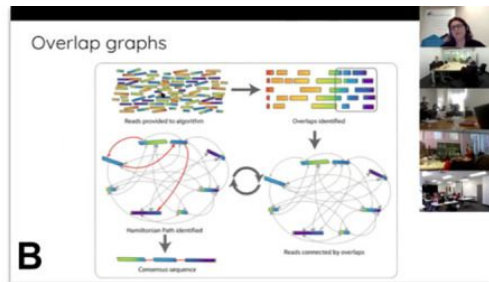
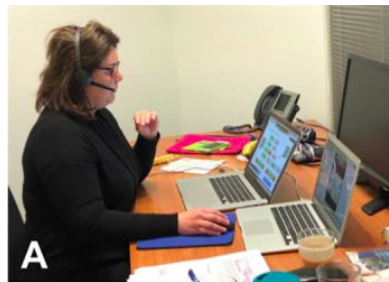


Hybrid Training: Australian BioCommons & Gallantries

Australian Biocommons: Christina Hall, Anna Syme & Australian BioCommons team
Gallantries: Saskia Hiltemann, Helena Rasche, Bérénice Batut, Fotis Psomopoulos, Anthony Bretaudeau, Yvan le Bras

Hybrid Training: Australian BioCommons

- Australia is a very big place, travel is not easy
- **Combination** of **remote** and **in-person** format
- **Livestream** to multiple classrooms across the region
- **One presenter** in front of a camera, **on-site instructors** to help participants
- Dedicated helpers to **communicate** with presenter (e.g. “slow down”, “repeat”, “explain in more detail”)
- **Discussion** boards using Google Docs



DOI: [10.1371/journal.pcbi.1008715](https://doi.org/10.1371/journal.pcbi.1008715)



Hybrid Training: Gallantries

Galaxy meets [The Carpentries](#) - Combine Galaxy analysis with R and Python *inside* Galaxy!

Set of RNA-seq Gallantries tutorials available in GTN

Will be expanded to include more topics in the coming years



With the support of the
Erasmus+ Programme
of the European Union



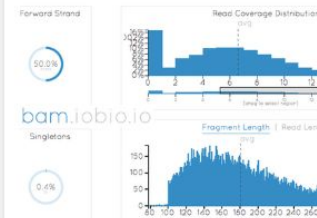
Jupyter lab for Python, R and Julia



RStudio with basic R packages

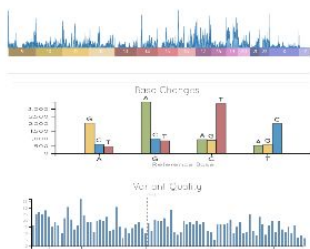


SPARQL query interface



BAM IOBIO

Examine sequence alignment in seconds

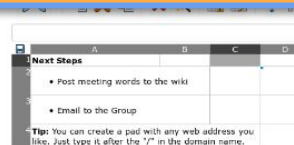


VCF IOBIO

Examine your variant file in seconds



Explore single-cell transcriptomics data



Ethercalc

A web spreadsheet



Visualise large biological datasets
(microbiomes, metagenomes, etc.)

live.usegalaxy.eu

History



search datasets



RStudio Demo

8 shown, 5 deleted

220.36 KB



17: Pasted Entry



16: workspace.RHistory



15: workspace.RData



11: workspace.RHistory



10: workspace.RData



9: jupyter-vs-rstudio.png



8: all.png



4: its.tsv





Thanks!

I will be available for the Q&A session at the end of this webinar

Teaching with Galaxy in a High School Setting

Christine Cucinotta - Fred Hutchinson
Cancer Research Center





See other slide deck

For slides on this topic

GTN Training in a University Setting

Miaomiao Zhou - Avans Hogeschool, Breda,
The Netherlands.





Biomedicine lab technology

Year 2:

- Half-wet half-dry semester project on drug resistant bacteria identification
 - 4 wet-lab sessions with drug-resistant bacterial strain sequencing (ONT MinION)
 - 6 dry-lab sessions with Galaxy based NGS data analysis
- Tailor-made Galaxy tutorials
 - <https://galaxyproject.github.io/training-material/topics/assembly/tutorials/mrsa-illumina/tutorial.html>
 - <https://galaxyproject.github.io/training-material/topics/assembly/tutorials/mrsa-nanopore/tutorial.html>
- 16 students, 20 weeks
 - Goal: analyze your own NGS data and find the source of drug resistance



Biomedicine lab technology

Year 3:

- Galaxy based RNA-seq courses

Smörgåsbord videos and training materials

Week 1	When?	Activity	Materials	Source	Specifics / Tools
Pre-processing	Preparation	Pre recorded video lecture:	youtube video via link	https://www.youtube.com/watch?v=gKkS_tztw_Q	
	In class	Overview of the course	Powerpoint	Blackboard (course)	
		Galaxy training: import data, quality control	Online tutorial	https://training.galaxyproject.org/training-material/topics/transcriptomics/tutorials/ref-based/tutorial.html	Quality control (FASTQC); Trimming (Cutadapt / Trimmomatic)
	Self - study	R Training:	Online computer based hands-on training	www.datacamp.com	Introduction to R
Week 2	When?	Activity	Materials	Source	Specifics / Tools
Mapping and assembly	Preparation	Pre recorded video lecture:	youtube video via link	https://youtu.be/7FhHb8EV3EU	Mapping
	In class	Lecture transcriptome	Powerpoint	Blackboard (course)	Assembly
		Galaxy training: Mapping	Online tutorial	https://training.galaxyproject.org/training-material/topics/transcriptomics/tutorials/ref-based/tutorial.html	Mapping (RNASTAR)
		Galaxy training: Assembly	Blackboard tutorial	Blackboard (course)	Assembly (StringTie)

Students build workflows by following the GTN materials.

Each person receives a novel dataset as the input data for the final assignment (apply your own workflow!)



Comenius: big data in biology education

Project subsidy: comenius teaching fellowship dossiernummer 405.19865.246

- 18 months project
- Use Galaxy to teach big data to biology teachers
- Teachers, teaching assistants and students learn side by side
- Subjects:
 - NGS
 - Metabolomics (LC-MS/Proteomics)



ABCDs:Avans BootCamp of Data skills

- 5 year's long term project
- Upgrade teacher's data skills
- Upgrade the complete curriculum with data-education
- Upgrade dry-lab facilities
 - Dedicated galaxy.bioinformatics-atgm.nl

GTN Training for Research Scientists




Subina Mehta - University of Minnesota



GTN training



WHY?

- ◆ Introduce new topics. 
- ◆ To keep everyone up-to-date with latest tools  available.
- ◆ Introduce collaboration/fostering interest regarding your approach. 



HOW?



Demo

- Can use their own instance.
- Trainees can learn at their own pace.



Hands-on/ in person

- Request for infrastructure-TlaaS to use Galaxy EU.
- Step by step instructions.
- Mention the need for bringing their laptops.

 Docker image
CLIP-Explorer
Galaxy Africa
Galaxy Test
Galaxy@GenOuest
HiCEplorer
Human Cell Atlas
Metagenomics
NanoGalaxy
Single Cell Omics workbench
Street Science
UseGalaxy.be
UseGalaxy.eu
UseGalaxy.fr
UseGalaxy.no
UseGalaxy.org (Main)
UseGalaxy.org.au
Virology

Plan your training

Familiarize yourself with the tutorial and tools involved - if training available or else develop your own!

Galaxy Training!

MetagenomicsHelpExportSearch Tutorials

Metatranscriptomics analysis using microbiome RNA-seq data (short)

By: Pratik Jagtap Subina Mehta Ray Sajulge Bérénice Batut Emma Leith Praveen Kumar Saskia Hittmann

Overview

Questions

- How to analyze metatranscriptomics data?
- What information can be extracted of metatranscriptomics data?
- How to assign taxa and function to the identified sequences?

Objectives

- Choose the best approach to analyze metatranscriptomics data
- Understand the functional microbiome characterization using metatranscriptomic results
- Understand where metatranscriptomics fits in 'multi-omic' analysis of microbiomes
- Visualise a community structure

Requirements

- Introduction to Galaxy Analysis

Time estimation: 3 hours

Level: Introductory

Supporting Materials

Topic Overview slides

Datasets

Workflows

Available on these Galaxies

Last modification: Feb 14, 2020

Overview

Introduction

Data aligned

Preprocessing

Extraction of the community profile

Extract the functional information

Combine taxonomic and functional information

Conclusion

Frequently Asked Questions

References

Feedback

Citing this Tutorial

Overview

In this tutorial we will perform a metatranscriptomics analysis based on the ASAM workflow (Batut et al. 2018), using data from Kunath et al. 2018.

Note: Two versions of this tutorial

Because this tutorial consists of many steps, we have made two versions of it, one long and one short. This is the **shortened version**. Instead of running each tool individually, we will employ workflows to run groups of analysis steps (e.g. data cleaning) at once. If you would like the more in-depth discussion of each step, please see the longer version of tutorial. You can also **switch** between the long and short version at the start of any section.

Introduction

Microbiomes play a critical role in host health, disease, and the environment. The study of microbiota and microbial communities has been facilitated by the evolution of technologies, specifically the sequencing techniques. We can now study the microbiome dynamics by investigating the DNA content (metagenomics), RNA expression (metatranscriptomics), protein expression (metaproteomics) or small molecules (metabolomics).

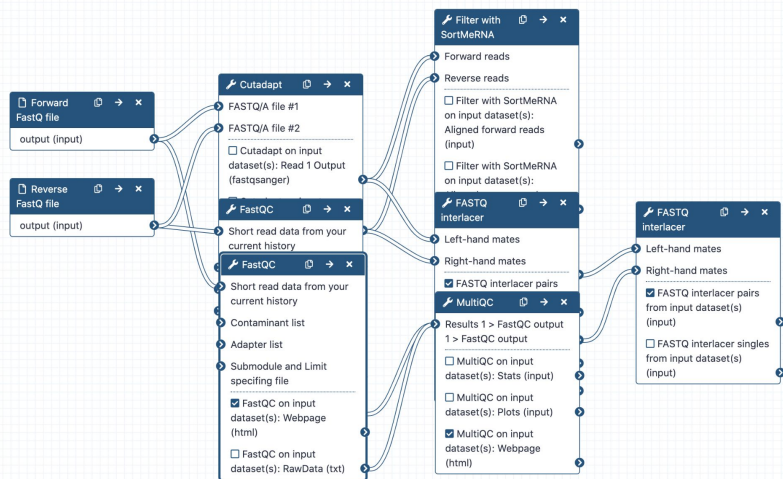
Microbial community



Before training.....

Test the tutorial/workflows

Workflow 1: Preprocessing [Metatranscriptomics]



Prepare example histories!

Name	Annotation	Owner	Community Rating
History3:Functional_Information_Metatranscriptomics		galaxyp	★★★★★
History2:Community_Profile_Metatranscriptomics		galaxyp	★★★★★
History1: Preprocessing_Metatranscriptomics		galaxyp	★★★★★
Input_Metatranscriptomics_GTN		galaxyp	★★★★★

While training.....

- Give users enough time to follow the tutorial.
- Mention basics
 - a. Galaxy
 - b. Basic background
 - c. Talk slowly
 - d. Allow time for Q&A





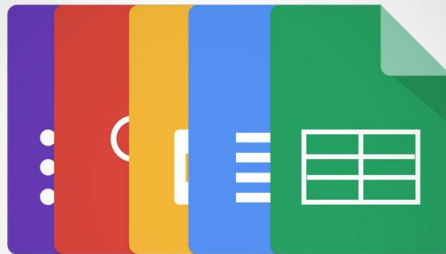
Q&A for trainees



slack



GITTER



Google docs



After training.....

GTN feedback

Feedback

Did you use this material as an instructor? Feel free to give us feedback on [how it went](#).

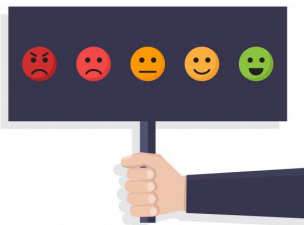
Help us improve this content!

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?



Feel free to ask
for Feedback!

Too fast???

Too Slow???



Forms

Informative??

Where can I
improve??



Take home message

1. GTN training - user friendly and step by step instructions
2. Preparation! Preparation! Preparation!
3. Testing workflows and Time management
4. User communication during and after the training
5. Feedback and improvement

If you have any questions, contact- smehta@umn.edu

Galaxy for teaching pupils and citizens

Bérénice Batut - University of Freiburg





BeerDEcoded by the

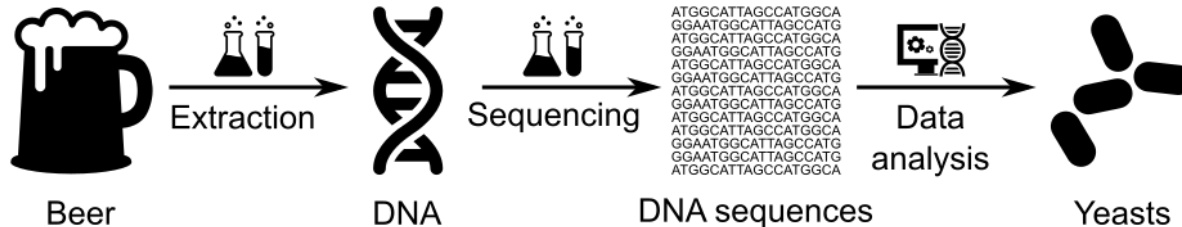


An immersion into biology, bioinformatics & sciences via beer and their yeasts

Purpose: Introduction of biology and genomics to a broad audience.

Pupils and citizens learn about DNA, sequencing technologies, bioinformatics, open science, possible application, and the impact of all of it on everyone's life.

Process: 1-2 days (or divided over several days) practical workshop on beer decoding



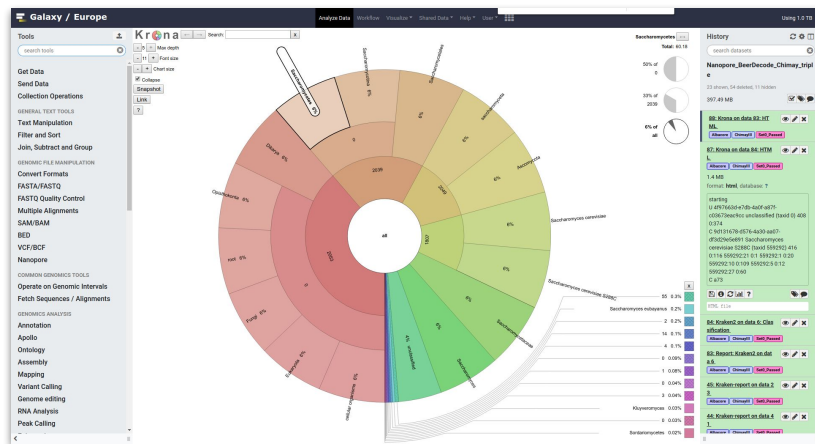
BeerDEcoded by the



streetscience.usegalaxy.eu

Tools & Workflows

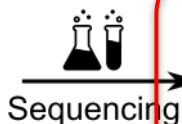
Data in shared data libraries



Beer



DNA



```
ATGGCATTAGCCATGGCA
GGAATGGCATTAGCCATG
ATGGCATTAGCCATGGCA
GGAATGGCATTAGCCATG
ATGGCATTAGCCATGGCA
GGAATGGCATTAGCCATG
ATGGCATTAGCCATGGCA
GGAATGGCATTAGCCATG
ATGGCATTAGCCATGGCA
GGAATGGCATTAGCCATG
ATGGCATTAGCCATGGCA
GGAATGGCATTAGCCATG
ATGGCATTAGCCATGGCA
GGAATGGCATTAGCCATG
ATGGCATTAGCCATGGCA
```

DNA sequences



Yeasts

Acknowledgements





Thanks to

- Funders
- You!
- Today's presenters
- Galaxy Training Network Contributors (all 176 of you)



Appendix



Watch: Welcome to the GTN!

