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

Please use the “hand-raising function” to indicate you would like to contribute directly.

This session will be recorded.

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

Please use “Chat” for further comments or discussions.
WEBINAR SERIES

Galaxy
Resources for...

Researchers
April 14

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 TIaaS
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

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

Contributors over time

training.galaxyproject.org/stats
Welcome to Galaxy Training!
Collection of tutorials developed and maintained by the worldwide Galaxy community

<table>
<thead>
<tr>
<th>Galaxy for Scientists</th>
<th>Galaxy Tips &amp; Tricks</th>
</tr>
</thead>
<tbody>
<tr>
<td>Topic</td>
<td>Tutorials</td>
</tr>
<tr>
<td>Introduction to Galaxy Analysis</td>
<td>10</td>
</tr>
<tr>
<td>Assembly</td>
<td>9</td>
</tr>
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<td>Climate</td>
<td>4</td>
</tr>
<tr>
<td>Computational chemistry</td>
<td>6</td>
</tr>
<tr>
<td>Ecology</td>
<td>6</td>
</tr>
<tr>
<td>Epigenetics</td>
<td>6</td>
</tr>
<tr>
<td>Genome Annotation</td>
<td>5</td>
</tr>
<tr>
<td>Imaging</td>
<td>4</td>
</tr>
<tr>
<td>Metabolomics</td>
<td>4</td>
</tr>
<tr>
<td>Metagenomics</td>
<td>7</td>
</tr>
<tr>
<td>Proteomics</td>
<td>21</td>
</tr>
<tr>
<td>Sequence analysis</td>
<td>2</td>
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<tr>
<td>Statistics and machine learning</td>
<td>11</td>
</tr>
<tr>
<td>Transcriptomics</td>
<td>29</td>
</tr>
<tr>
<td>Variant Analysis</td>
<td>6</td>
</tr>
<tr>
<td>Visualization</td>
<td>2</td>
</tr>
</tbody>
</table>

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 comments-11: 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 Developers and Admins

<table>
<thead>
<tr>
<th>Topic</th>
<th>Tutorials</th>
</tr>
</thead>
<tbody>
<tr>
<td>Galaxy Server administration</td>
<td>37</td>
</tr>
<tr>
<td>Development in Galaxy</td>
<td>13</td>
</tr>
</tbody>
</table>

The latest GTN news
Read about new tutorials, features, events and more!

<table>
<thead>
<tr>
<th>Date</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Apr 10, 2021</td>
<td>New Tutorials: Whole transcriptome analysis of Arabidopsis thaliana</td>
</tr>
<tr>
<td>Apr 6, 2021</td>
<td>New Feature: Video Player</td>
</tr>
<tr>
<td>May 31, 2021</td>
<td>New Tutorials: Genome assembly of a MRSA genome</td>
</tr>
</tbody>
</table>

Meet & Join the Galaxy Community!
Find out how you can become part of the Galaxy community

GTN Tweets

Tweets by @galaxyproject

Australian BioCommons
@Abcomum
There's still time to sign up for this week's PlantBiology workshop with @amayre and @MelBolH.

Get hands-on experience with assembling, polishing and visualising a chloroplast genome using @GalaxyAustralia.

21 April 2021 1 - 4pm AEST biocommons.org.au/events/plantg...
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
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

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 be explained later)

2. Forward and reverse reads, by convention, are labelled \_1 \_2, \_r1 / \_r2.
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

"Anyone, anywhere in the world should have free, unhindered access to not just my research, but to the research of every great and enquiring mind across the spectrum of human understanding." — Prof. Stephen Hawking
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!
A Real Community Effort!

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
**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!

Apply now: [usegalaxy.eu/tiaas](usegalaxy.eu/tiaas)
# TIaaS Dashboard

- Overview of status of everybody in the TIaaS 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

## Galaxy Training Infrastructure as a Service

### 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 ran 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

<table>
<thead>
<tr>
<th>State</th>
<th>Count</th>
</tr>
</thead>
<tbody>
<tr>
<td>ok</td>
<td>10</td>
</tr>
</tbody>
</table>

### Queue

<table>
<thead>
<tr>
<th>User</th>
<th>Created</th>
<th>Tool</th>
<th>State</th>
<th>Job/Runner ID</th>
</tr>
</thead>
<tbody>
<tr>
<td>s073</td>
<td>2019-06-17 14:16:26</td>
<td>lvis/multiqc/multiqc1.7</td>
<td>ok</td>
<td>899583</td>
</tr>
<tr>
<td>s073</td>
<td>2019-06-17 14:14:38</td>
<td>devteam/samtools_filter2/samtools_filter2/1.8</td>
<td>ok</td>
<td>899579</td>
</tr>
<tr>
<td>s073</td>
<td>2019-06-17 14:14:38</td>
<td>devteam/samtools_filter2/samtools_filter2/1.8</td>
<td>ok</td>
<td>899580</td>
</tr>
<tr>
<td>s073</td>
<td>2019-06-17 14:14:38</td>
<td>devteam/samtools_filter2/samtools_filter2/1.8</td>
<td>ok</td>
<td>899578</td>
</tr>
<tr>
<td>s073</td>
<td>2019-06-17 14:14:15</td>
<td>devteam/samtools_filter2/samtools_filter2/1.8</td>
<td>ok</td>
<td>899576</td>
</tr>
<tr>
<td>s073</td>
<td>2019-06-17 14:14:15</td>
<td>devteam/samtools_filter2/samtools_filter2/1.8</td>
<td>ok</td>
<td>899575</td>
</tr>
<tr>
<td>s073</td>
<td>2019-06-17 14:14:15</td>
<td>devteam/samtools_filter2/samtools_filter2/1.8</td>
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<td>899574</td>
</tr>
<tr>
<td>s073</td>
<td>2019-06-17 14:14:15</td>
<td>devteam/samtools_filter2/samtools_filter2/1.8</td>
<td>ok</td>
<td>899572</td>
</tr>
</tbody>
</table>
GTN Tutorials for Workshop Organizers

- Checklists for workshop organizers
  - Before, during & after event

- Tips & Tricks for instructors

- How to request TIaaS

- 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.

<table>
<thead>
<tr>
<th>Material</th>
<th>Slides</th>
<th>Hands-on</th>
</tr>
</thead>
<tbody>
<tr>
<td>Galaxy Admin Training</td>
<td>![Slides](Galaxy Training Admin)</td>
<td>![Hands-on](Galaxy Training Admin)</td>
</tr>
<tr>
<td>Organizing a workshop</td>
<td>![Slides](organizing Galaxy)</td>
<td>![Hands-on](organizing Galaxy)</td>
</tr>
<tr>
<td>Running a workshop as instructor</td>
<td>![Slides](running Galaxy)</td>
<td>![Hands-on](running Galaxy)</td>
</tr>
<tr>
<td>Set up a Galaxy for Training</td>
<td>![Slides](setup Galaxy)</td>
<td>![Hands-on](setup Galaxy)</td>
</tr>
<tr>
<td>UseGalaxy.eu’s Training Infrastructure as a Service</td>
<td>![Slides](Infrastructure Galaxy)</td>
<td>![Hands-on](Infrastructure Galaxy)</td>
</tr>
</tbody>
</table>
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

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 decide 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.

<table>
<thead>
<tr>
<th>Lesson</th>
<th>Slides</th>
<th>Hands-on</th>
<th>Galaxy Instances</th>
</tr>
</thead>
<tbody>
<tr>
<td>Creating a new tutorial</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Creating content in Markdown</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Creating Slides</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Running the Galaxy Training material website locally</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Tools, Data, and Workflows for tutorials</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
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](gitter.im/Galaxy-Training-Network/Lobby)
Galaxy events page:  [galaxyproject.org/events](galaxyproject.org/events) (add your training event here!)
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](#).
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, ..)
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](http://10.1371/journal.pcbi.1008715)
Hybrid Training: 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
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

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-illumina/tutorial.html)
  - [https://galaxyproject.github.io/training-material/topics/assembly/tutorials/mrsa-nanopore/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

<table>
<thead>
<tr>
<th>Week</th>
<th>When?</th>
<th>Activity</th>
<th>Materials</th>
<th>Source</th>
<th>Specifics / Tools</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Pre-processing</td>
<td>Preparation</td>
<td>Pre recorded video lecture: Youtube video via link</td>
<td><a href="https://www.youtube.com/watch?v=sB5_ttBQ">https://www.youtube.com/watch?v=sB5_ttBQ</a></td>
<td>Blackboard (course)</td>
</tr>
<tr>
<td></td>
<td>In class</td>
<td>Overview of the course</td>
<td>Powerpoint</td>
<td></td>
<td>Quality control (FASTQC); Trimming (Cutadapt / Trimomatic)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Galaxy training: import data, quality control</td>
<td>Online tutorial</td>
<td><a href="https://training.galaxyproject.org/training-material/topics/transcriptomics/tutorials/ref-based/tutorial.html">https://training.galaxyproject.org/training-material/topics/transcriptomics/tutorials/ref-based/tutorial.html</a></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Self-study</td>
<td>R Training</td>
<td>Online computer based hands-on training</td>
<td><a href="http://www.datacamp.com">www.datacamp.com</a></td>
<td>Introduction to R</td>
</tr>
<tr>
<td>2</td>
<td>mapping and assembly</td>
<td>Preparation</td>
<td>Pre recorded video lecture: Youtube video via link</td>
<td><a href="https://youtu.be/3Hh86V3ZEU">https://youtu.be/3Hh86V3ZEU</a></td>
<td>Mapping</td>
</tr>
<tr>
<td></td>
<td>In class</td>
<td>Galaxy training: Mapping</td>
<td>Lecture transcriptome</td>
<td>Galaxy training: Mapping</td>
<td>Powerpoint</td>
</tr>
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<td></td>
</tr>
</tbody>
</table>

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-TIaaS to use Galaxy EU.
  ● Step by step instructions.
  ● Mention the need for bringing their laptops.
Plan your training

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

Test the tutorial/workflows

Prepare example histories!
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

Feel free to ask for Feedback!

Too fast???
Too Slow???
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
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 Street Science Community

streetscience.usegalaxy.eu

Tools & Workflows

Data in shared data libraries

Beer → Extraction → DNA → Sequencing → DNA sequences → Data analysis → Yeasts
Acknowledgements
Thanks to

- Funders
- You!
- Today’s presenters
- Galaxy Training Network Contributors (all 176 of you)
Watch: Welcome to the GTN!

bit.ly/galaxy_training_network