

Misconceptions about Galaxy debunked by the (French) Galaxy Community

*Romane LIBOUBAN, Eva MERCIER, Thomas CHAUSSEPIED, Bérénice BATUT,
Anthony BRETAUDEAU, Gildas LE CORGUILLÉ*

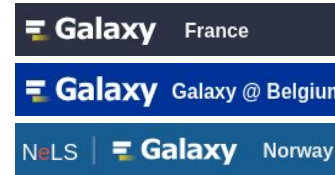


Galaxy project

Galaxy is a world-wide community



Regional Galaxy servers



Public servers

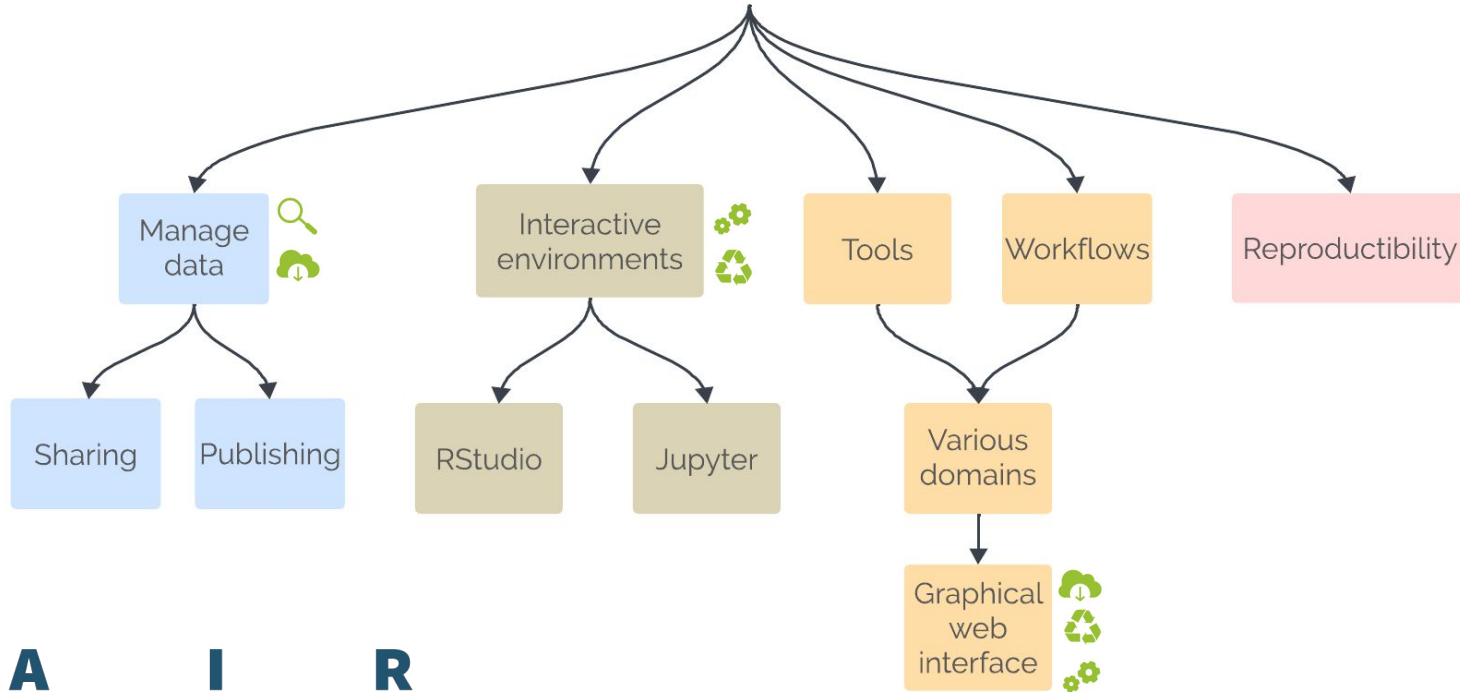


Subdomain servers



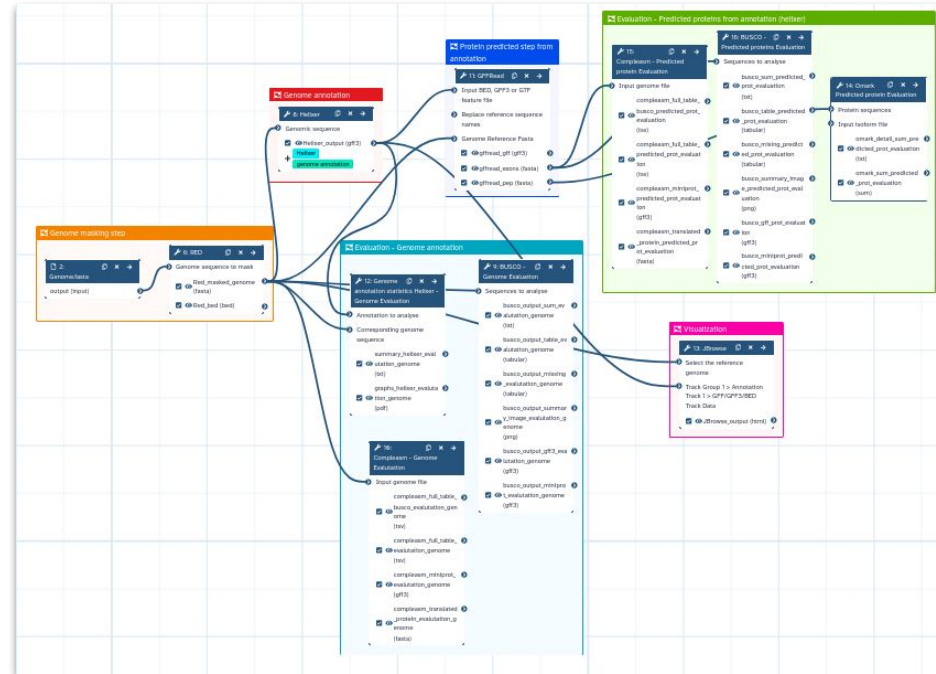
<https://galaxyproject.org/use/>

Galaxy PROJECT



Workflows

- A series of tools and datasets actions that run in sequences as a batch operation
- **Generated** from a history or **Created** using the workflow editor
- **Reproducibility**
 - Import from one instance to another
 - Import and upload to [WorkflowHub](https://www.workflowhub.eu/) and/or [Dockstore](https://dockstore.org/)
- Can be executed using the API



<https://galaxyproject.org/learn/advanced-workflow/>

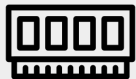
Workflow manager

	Galaxy	Nextflow	Snakemake	Airflow
Application	User interface	Command line	Command line	Web user interface
Complexity	Ease of use	Average (requires skills in scripting and container management)	Average (Need to manage dependencies and conda environments)	High (due to configuration)
Workflow management	User interface for building and running workflows	Using scripts to define and run workflows	Using scripts to define and execute workflows	Definition of workflows using DAGs (Directed Acyclic Graphs)

Core Cluster



8300
cores

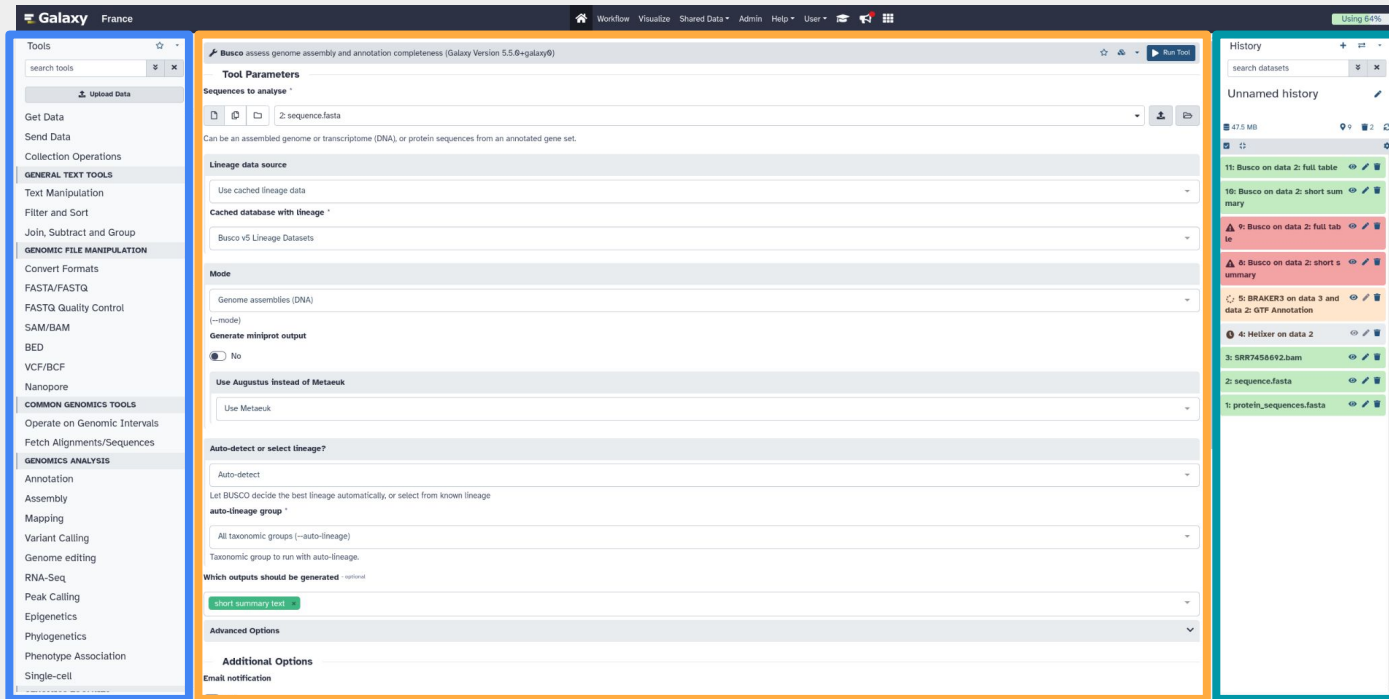


52 Tb
RAM



2 Pb

Galaxy PROJECT



The screenshot displays the Galaxy web interface for a BUSCO analysis tool. The interface is divided into three main sections:

- Tools List (Left):** A sidebar menu with a search bar and a list of tool categories including 'GENERAL TEXT TOOLS', 'GENOMIC FILE MANIPULATION', 'COMMON GENOMICS TOOLS', and 'GENOMICS ANALYSIS'.
- Tool Forms/Result Viewer (Center):** The main workspace showing the 'Busco assess genome assembly and annotation completeness' tool form. It includes sections for 'Tool Parameters', 'Sequences to analyse', 'Lineage data source', 'Mode', 'Generate miniprot output', 'Auto-detect or select lineage?', and 'Advanced Options'.
- History (Right):** A sidebar showing a list of previous jobs, including '11: Busco on data 2: full table', '10: Busco on data 2: short summary', and '1: protein_sequences.fasta'.

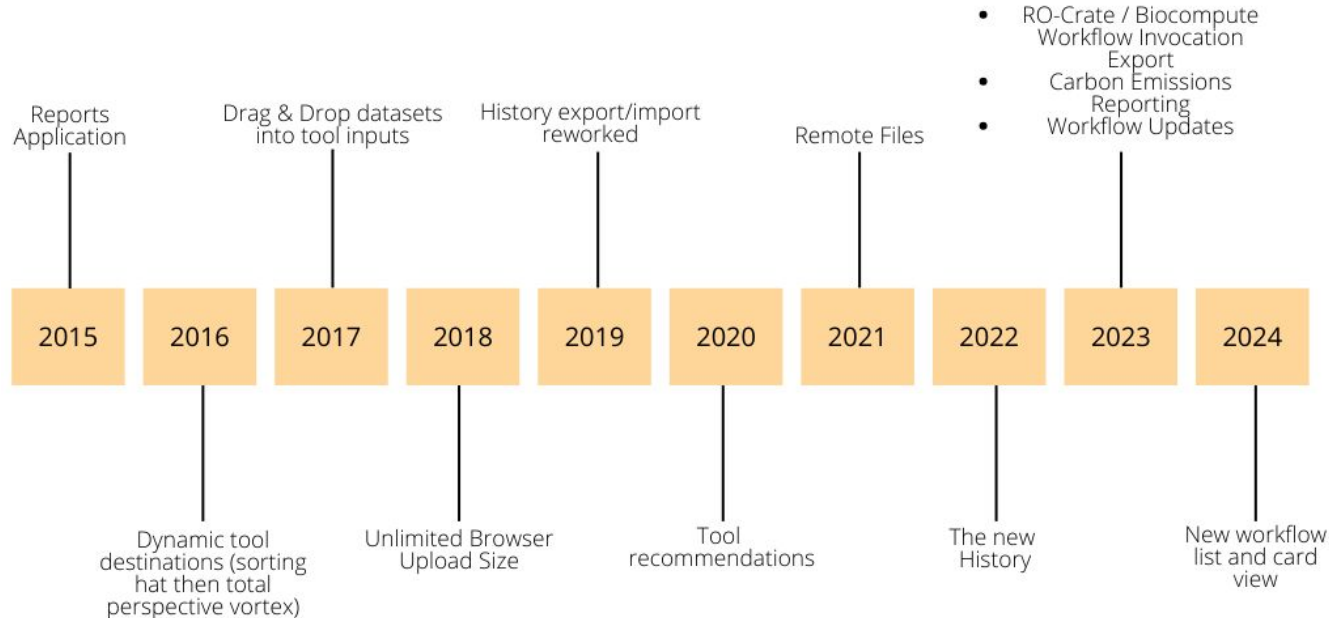
Tools List

Tool Forms/Result Viewer

History

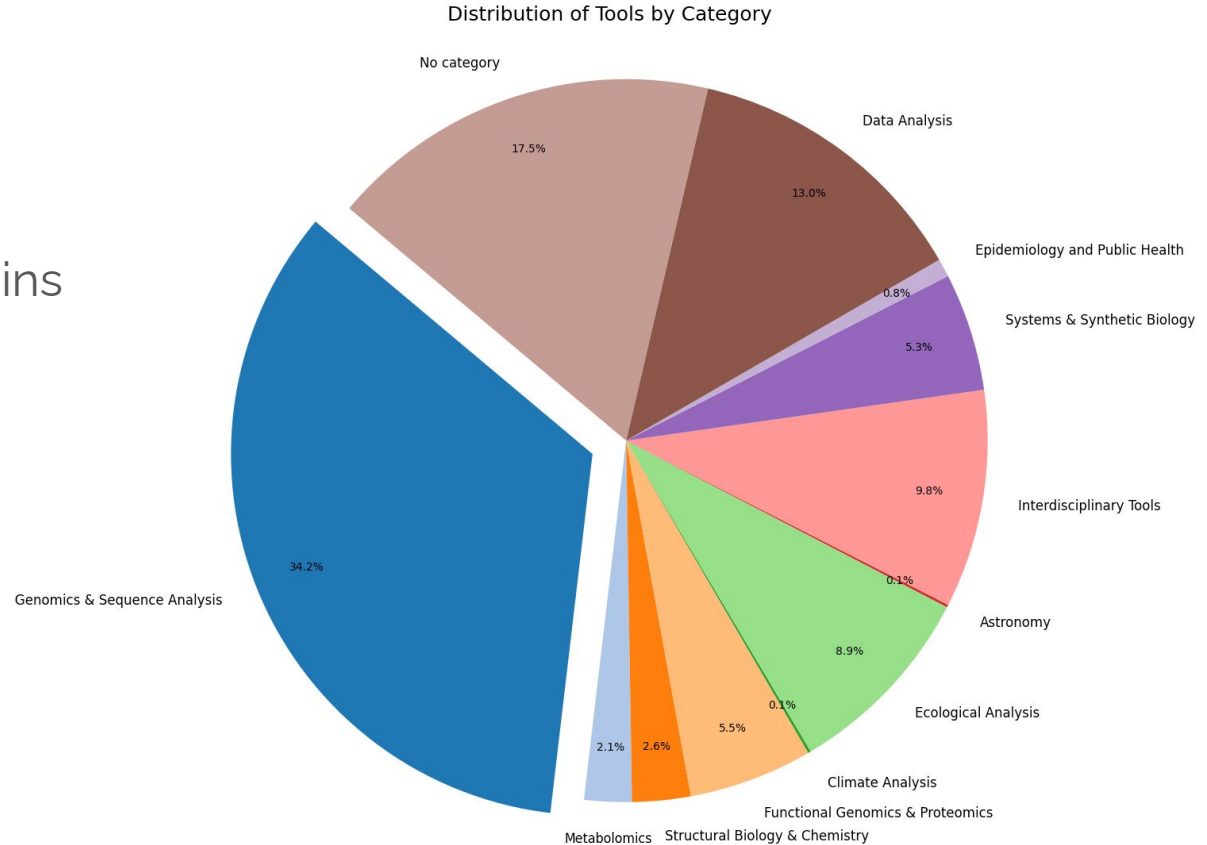
Why are there misconceptions on Galaxy?

- Beginning of 2005
 - Errors
 - Not stable
- In constant evolution
 - Major changes over the last 10 years



“Galaxy is only useful for genome scientists”

- 9.95k+ tools
- 3.5k tools on EU
- 1.8k+ tools on .FR
- Various scientific domains



“Galaxy offers nothing to technically capable informaticians who can write their own analysis code”

- **API** ([Application Programming Interface](#))
 - Accessible by programmatically through shell scripts and other programs
 - Allows
 - Connecting a Galaxy instance directly
 - Running a workflows against multiple datasets
- Workflow manager

“Galaxy offers nothing to technically capable informaticians who can write their own analysis code”

- **API** ([Application Programming Interface](#))
 - Accessible by programmatically through shell scripts and other programs
 - Allows
 - Connecting a Galaxy instance directly
 - Running a workflows against multiple datasets
- Workflow manager
- Resources
 - CPU core
 - RAM
 - GPU
 - Tools

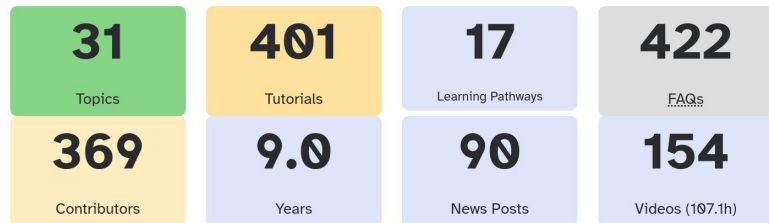
No need to configure the necessary computing resources or worry about resolving dependencies

“Galaxy is hard to learn and hard to use”

Galaxy Training Network (GTN)

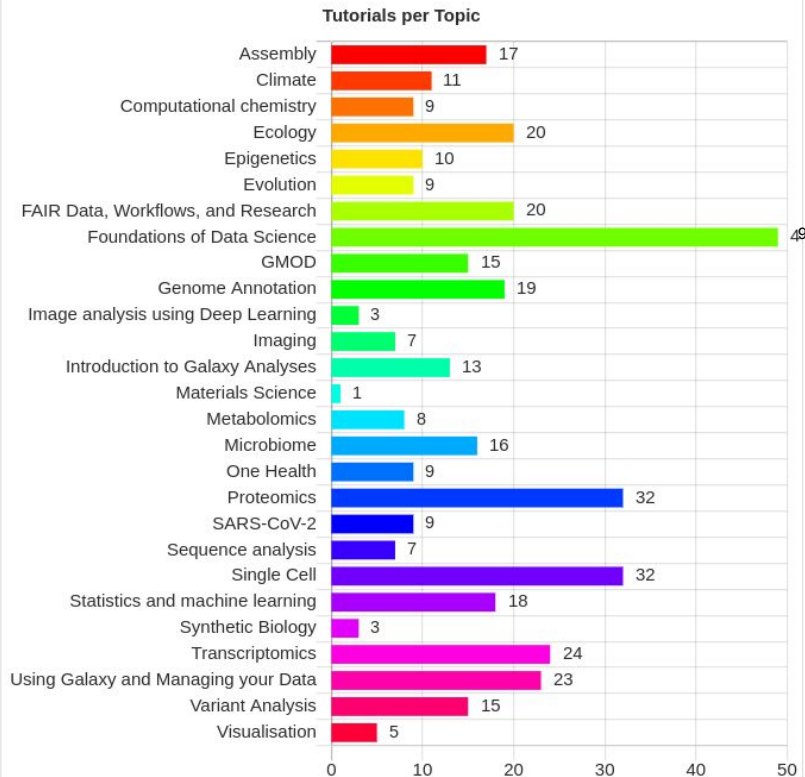
(<https://training.galaxyproject.org/training-material/>)

GTN Statistics



The screenshot shows the Galaxy Training! website. At the top, there is a navigation bar with links for Contributors, Learning Pathways, Help, Settings, and Search Tutorials. The main heading is "Welcome to Galaxy Training!" followed by a sub-heading "Collection of tutorials developed and maintained by the worldwide Galaxy community". Below this, there are sections for "Galaxy for Scientists" (with a quickstart guide), "Start Here" (with a list of topics and tutorial counts), "Not sure where to start?" (with a "Start Learning" button), "Upcoming Events" (with a "See all events" button), and "Scientific Fields" (with a list of fields and tutorial counts). At the bottom, there is a section for "The latest GTN news" with a RSS icon.

27 Scientific Topics



“Galaxy is hard to learn and hard to use”

Training Infrastructure as a Service

Since 2022 (on .FR)



80 events



1.9k+ taught students



We are proud to provide Training Infrastructure as a Service (TlaaS) for the Galaxy training community. You provide the training, we provide the infrastructure and cover all costs.

Why TlaaS?



All costs are covered by our funding agencies.



Priority job queue to service your training event effectively. See our [Event Dashboard](#).



No maintenance or administration required.



[Official Galaxy Training materials](#) are regularly tested and highly reliable.

Eligibility

We have access to large computing capacity, some of which is dedicated to provide training for our service. Anyone who provides training using Galaxy is eligible to request the use of this service.

Please register **at least 7 days** before your event in order to be approved!

[Apply now](#)

“Galaxy is only useful for teaching, not real scientific analyses”

- 12k+ publications related to Galaxy
 - 30 papers/weeks

JOURNAL ARTICLE

RNPomics: Defining the ncRNA transcriptome by cDNA library generation from ribonucleo-protein particles

Mathieu Rederstorff , Stephan H. Bernhart, Andrea Tanzer, Marek Zywicki, Katrin Perfler, Melanie Lukasser, Ivo L. Hofacker, Alexander Hüttenhofer 

Nucleic Acids Research, Volume 38, Issue 10, 1 June 2010, Page e113,
<https://doi.org/10.1093/nar/gkq057>

Published: 11 February 2010 **Article history** ▾

Low concentrations of copper oxide nanoparticles alter microbial community structure and function of sediment biofilms

Lingzhan Miao , Peifang Wang , Jun Hou , Yu Yao, Zhilin Liu, Songqi Liu

Show more ▾

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<https://doi.org/10.1016/j.scitotenv.2018.10.354> ↗

Get rights and content ↗

A framework for collaborative analysis of ENCODE data: Making large-scale analyses biologist-friendly

Daniel Blankenberg, James Taylor, Ian Schenck, Jianbin He, Yi Zhang, Matthew Ghent, Narayanan Veeraghavan, Istvan Albert, Webb Miller, Kateryna D. Makova, Ross C. Hardison, and Anton Nekrutenko¹

 Author Affiliations

Article | Published: 13 May 2024

Nanoparticles for inducing Gaucher disease-like damage in cancer cells

Chunyan Yue, Wenjing Lu, Shuxin Fan, Zhusheng Huang, Jiaying Yang, Hong Dong, Xiaojun Zhang, Yuxin Shang, Wenjia Lai, Dandan Li, Tiejun Dong, Ahu Yuan, Jinhui Wu, Lifeng Kang & Yiqiao Hu 

Nature Nanotechnology (2024) | [Cite this article](#)

4051 Accesses | 10 Altmetric | [Metrics](#)

Open Access **Article**

In Vivo Comparative Study on Acute and Sub-acute Biological Effects Induced by Ultrafine Particles of Different Anthropogenic Sources in BALB/c Mice

by Francesca Farina^{1,2,†}, Elena Lonati^{1,†} , Chiara Milani¹ , Luca Massimino³ , Elisa Ballarini¹, Elisabetta Donzelli¹ , Luca Crippa¹, Paola Marmiroli¹, Laura Botto¹, Paola Antonia Corsetto⁴ , Giulio Sancini^{1,2}, Alessandra Bulbarelli^{1,2} and Paola Palestini^{1,2,*} 

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³ Division of Neuroscience, San Raffaele scientific institute, 20121 Milan, Italy

⁴ Department of Pharmacological and Biomolecular Sciences, University of Milan, 20100 Milano, Italy

* Author to whom correspondence should be addressed.

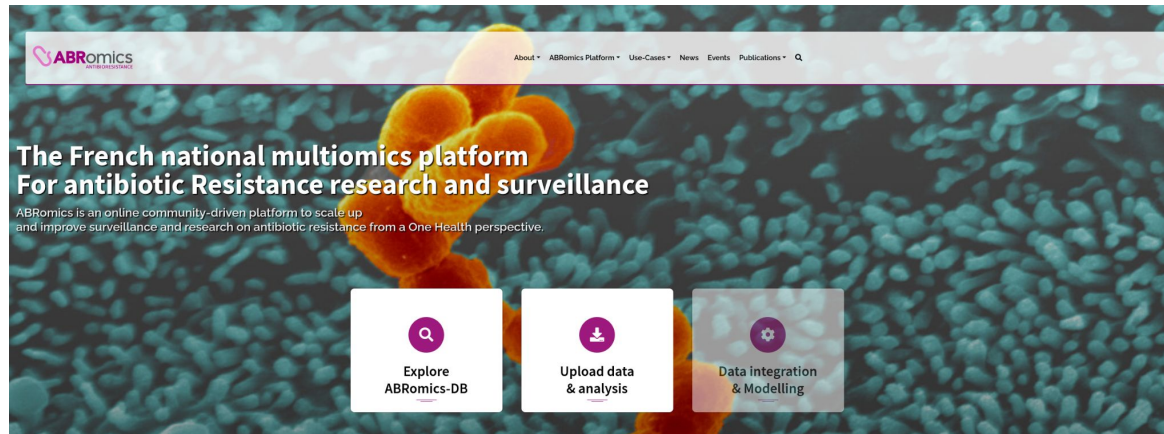
† These authors contributed equally to this work.

Int. J. Mol. Sci. **2019**, *20*(11), 2805; <https://doi.org/10.3390/ijms20112805>

Submission received: 19 April 2019 / Revised: 31 May 2019 / Accepted: 4 June 2019 / Published: 8 June 2019

“Galaxy is only useful for teaching, not real scientific analyses”

- ABRomics
 - Surveillance platform
 - Integrated multi-omics platform for antibiotic resistance research and public health surveillance
 - Poster (presented by Julie Lao): ***ABRomics: A Galaxy-based one health antimicrobial resistance platform***



“Galaxy is neither popular with, nor widely used by real scientists”

 **Galaxy**
EUROPE



98k+ users



71M jobs

 **Galaxy**
FRANCE

Launch: 2019



7k+ users



4.5M+ jobs

On the last year:



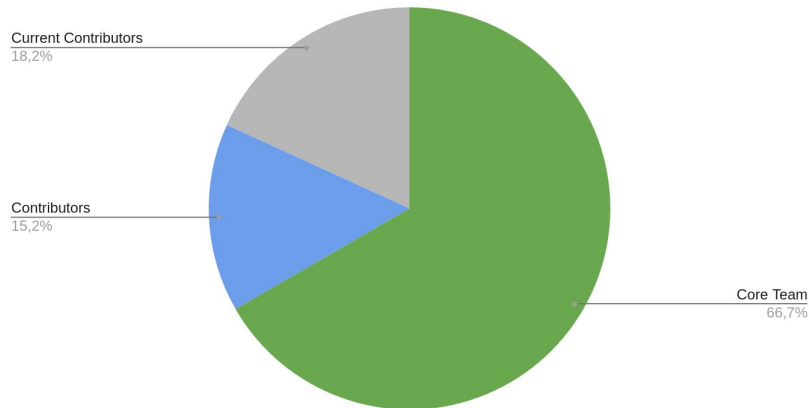
3k active users



1.5M+ Jobs

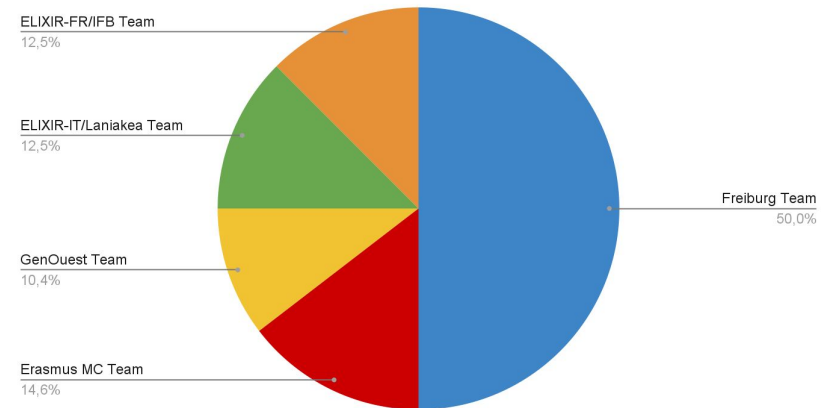
“Galaxy is free, so it cannot be good because professional engineers are not being paid to fix bugs and develop enhancements”

US Team ([33 contacts](#))



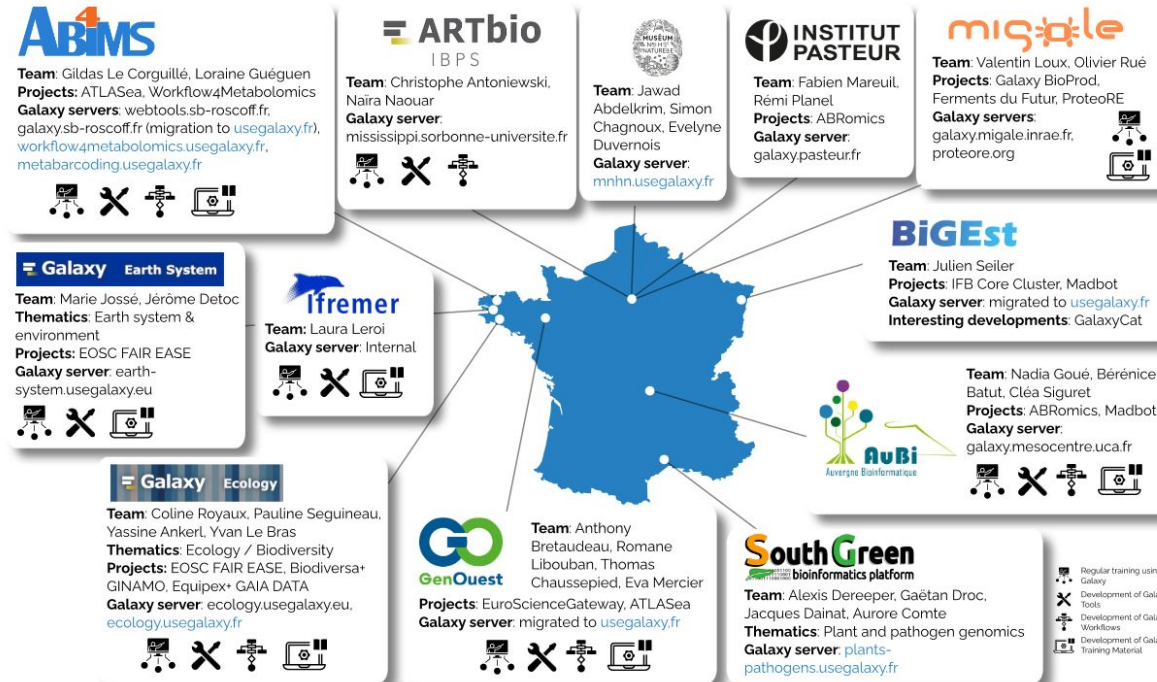
EU team ([48 contacts](#))

<https://usegalaxy-eu.github.io/people>



“Galaxy is free, so it cannot be good because professional engineers are not being paid to fix bugs and develop enhancements”

FR Team



“Galaxy is free, so there cannot be professional staff offering quick and helpful support”

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- Forum GalaxyHelp: <https://help.galaxyproject.org/>

GalaxyHelp

Sign Up Log In

How to get faster help with your question

Everyone is welcome to post a new question for community help. Be sure to provide enough context!

Consider [FAQ: Sharing your History](#) or posting content from the Job Details [I](#) view as described in [FAQ: Troubleshooting errors](#).

While a shared Galaxy history provides most technical details, situational context can also help! See [FAQ: What information should I include when reporting a problem?](#)

categories tags Latest Categories Docs

Topic	Replies	Views	Activity
⚠ Troubleshooting resources for errors or unexpected results queued-gray-datasets resources share-or-publish troubleshooting Troubleshooting How to review your work in Galaxy, and how to ask for help! Review the full Dataset Details of your job, including inputs, parameters and logs in summary format directly in the application us... read more	5	9.9k	Nov 2018
Inoperative Account on EU Server usegalaxy.eu support server-admin troubleshooting	1	16	7h
⚠ MP3 files not recognised	3	24	19h

OMSK proteome quality assessment (Galaxy Version 0.1.6-galaxy2)

Nothing selected

A semi-annotated file, listing all isoforms of each gene, with one gene per line.

Only compute a list of conserved HOGs

Yes

Can be used to obtain a set of genes on which to train (-c)

OMSK database *

Merzosa-v2.8.0

Taxonomic Identifier *

NCBI taxid corresponding to the input proteome (-t)

Taxonomic rank *

(-r)

Which outputs should be generated *

Detailed summary

switch to column select

Additional Options

Email notification

Yes

Send an email notification when the job completes.

Pin Tool

Help

OMSK is a software for proteome quality assessment. It provides measures of proteome completeness, characterizes the consistency of all protein coding genes with regard to their homologs, and identifies the presence of contamination from other species.

OMSK documentation

Help Forum

There are no questions on the Help Forum [about this tool](#).

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“Galaxy is free, so there cannot be professional staff offering quick and helpful support”

- Galaxy report

The screenshot displays the Galaxy web interface. The top navigation bar includes 'Galaxy France' and various menu items like 'Workflow', 'Visualize', 'Shared Data', 'Admin', 'Help', and 'User'. The main content area is titled 'Dataset Error Report' and contains the following sections:

- Dataset Error Report:** An error occurred while running the tool `toolshed.g2.bx.psu.edu/repos/genouest/braker3/braker3/3.0.0+galaxy0`.
- Troubleshooting:** There are a number of helpful resources to self diagnose and correct problems. Start here: [My job ended with an error. What can I do?](#)
- Issue Report:** Your email address is `romane.libouban@irisa.fr`. Please provide detailed information on the activities leading to this issue:
 - Hi, I'm having a problem. There doesn't seem to be enough memory allocated for the Braker3 tool.
 - Best regards, [Romane Libouban](#)

A 'Report' button is visible below the issue report text. On the right side, the 'History' panel shows a list of jobs:

- 81: Miniprot index on data 62 (Success)
- 80: Miniprot index on data 62 (Success)
- 79: Miniprot index on data 62 (Success)
- 78: BRAKER3 on data 4, data 9, and data 1: GTF Annotation (Failure)
 - Error message: An error occurred with this dataset: format gtf, database ?
 - Reason: This job was terminated because it used more memory than it was allocated. Please click the bug icon to report this.
- 77: Helixer on data 1 (Success)
- 76: Helixer on data 1 (Failure)

“Galaxy is free, so there cannot be professional staff offering quick and helpful support”

- Forum: <https://community.france-bioinformatique.fr/>
 - 13.1k+ messages for 2.1K subjects
- Multiple categories
 - workflow4metabolomics
 - galaxy
 - emergen
 - proteore
 - more

IFB Community Support

Bienvenue sur la plateforme communautaire de l'IFB Core Cluster

L'équipe de support du Cluster IFB Core est actuellement en effectif limité. Nous essayons de vous répondre rapidement, mais il est possible que nous mettions plus de temps à répondre à vos demandes. Merci de votre compréhension

Découvrez comment publier un message ou contacter en direct un groupe, consulter [notre documentation](#) de prise en main

Welcome to the IFB Core Cluster community platform

The IFB Core Cluster support team is currently short-staffed. We try to respond to you promptly, but it may take us longer to respond to your requests. Thank you for your understanding.

Find out how to publish a message or contact a group live, consult [our documentation](#) to get started

toutes les catégories | toutes les étiquettes | **Catégories** | Récents | Nouveaux (5) | Non lu (1) | Top | + Créer un sujet

Catégorie	Sujets	Récents
Galaxy For any questions, issues and request regarding usegalaxy.fr and its subdomains * usegalaxy.fr	201	🚩 FTP usegalaxy.fr oct. '21 1 non lu 3 nouveaux 🚩 README: before request a Galaxy quota extension janv. '21 Bakta Exception: diamond error error code: -11 22 min
Support scientifique et technique Get help on a scientific thematic, a workflow, a software or a parameter. Nextflow Snakemake	103	1 nouveau AlphaFold 2.3.2 - Relaxation : No compatible CUDA device is av... 1 j SortMeRNA - Problème d'allocation de mémoire 7 j Point de montage de /shared/projects dans l'explorateur de fichi... 29 avr.
Workflow4Metabolomics This category is dedicated to any questions, issues and requests regarding workflow4metabolomics.usegalaxy.fr . LCMS Instance GCMS MSMS NMR	160	🚩 Troubleshooting - Workflows sept. '20 🚩 Troubleshooting - Galaxy mai '20 📄 Demande augmentation espace de stockage 6 h
IFB Core Cluster Gestion de comptes et de projets Demande de logiciel ou de banque de données 1 nouveau Support IFB Core Cluster Cluster - FAQ	1,7 k	1 nouveau 📄 Accès à la demande à la partition gpu 9 h 📄 Installation smc++ 10 h Update Nextflow 22 h
Espace Formation/Training Cet espace est dédié aux formateurs (leurs questions à l'équipe de support, et les échanges entre formateurs)	4	Formation 2409_ubx_hts 27 févr. Utilisation comptes invités formation 22 janv. 📄 Demande d'ouverture de session pour formation FROGS m... sept. '23
RSAT This channel aims at facilitating interactions between users and developers of the software suite Regulatory Sequence Analysis Tools (RSAT; http://rsat.eu). The support will cover questions about the usage of the tool, bug reports, suggestions for improvement, request for new functionalities, direc...	4	RSAT Matrix Clustering Error oct. '23 Ouverture d'un port pour accès mysql à DB Ensemble mars '22 📄 RSAT Metazoa isn't loading juin '20

“Galaxy is free, so there cannot be professional staff offering quick and helpful support”

The French support team



Cléa
Siguret



Thomas
Chaussepied



Romane
Libouban



Eva
Mercier



Julien
Seiler



Bérénice
Batut



Gildas Le
Corguillé



Anthony
Bretaudeau

“Galaxy is free, so there cannot be useful documentation since nobody is paid to write, maintain or deliver it”

- [Galaxy Training Network \(GTN\)](#)
- [Galaxy doc](#)
- [Planemo doc](#)
- [OPenAPI doc](#)
- [Bioblend doc](#)

Planemo
latest

Search docs

- Quick Start
- Installation
- Configuration
- Virtual Appliance
- Building Galaxy Tools
- Building Common Workflow Language Tools
- Publishing to the Tool Shed
- Test Format
- Best Practices for Maintaining Galaxy Workflows
- Running Galaxy workflows
- Automating Galaxy Workflows
- Autoupdating tools
- Commands
- FAQs
- Galaxy Tool Framework Changes
- Code of Conduct
- Contributing
- Project Governance
- Release Checklist

Read the Docs v: latest

/ Welcome to Planemo's documentation! Edit on GitHub

Welcome to Planemo's documentation!

Contents:

- Quick Start
 - Obtaining
 - Basics - Galaxy
 - Basics - Common Workflow Language
 - Tool Shed
 - Conda
 - Docker and Containers
- Installation
 - pip
 - Conda (Experimental)
- Configuration
- Virtual Appliance
 - Quick Links
 - The Setup
 - Launching the Appliance
 - Building the Appliance
- Building Galaxy Tools
 - ...using Planemo

Galaxy Project
24.0

Search docs

- RELEASE NOTES
 - Releases
- ADMIN DOCUMENTATION
 - Administration
 - Special topics
- DEVELOPER DOCUMENTATION
 - Development

Galaxy Documentation View page source

Galaxy Documentation

Galaxy is an open, web-based platform for accessible, reproducible, and transparent computational biomedical research.

For more information on the Galaxy Project, please visit the <https://galaxyproject.org>

This site contains documentation for administrators and developers. For user documentation, and admin and developer tutorials, please visit the [Galaxy Training Network](#).

The community also maintains a list of awesome Galaxy resources related to all aspects of Galaxy.

- Release Notes
- Admin Documentation
- Developer Documentation
- About Project

Release Notes

- Releases
 - 24.0 Galaxy Release (March 2024)
 - 23.2 Galaxy Release (January 2024)
 - 23.1 Galaxy Release (June 2023)
 - 23.0 Galaxy Release (April 2023)
 - May 2022 Galaxy Release (v 22.05)
 - January 2022 Galaxy Release (v 22.01)
 - September 2021 Galaxy Release (v 21.09)
 - May 2021 Galaxy Release (v 21.05)
 - January 2021 Galaxy Release (v 21.01)

“Galaxy cannot be sustainable in the long run, because no commercial organisation is managing it”

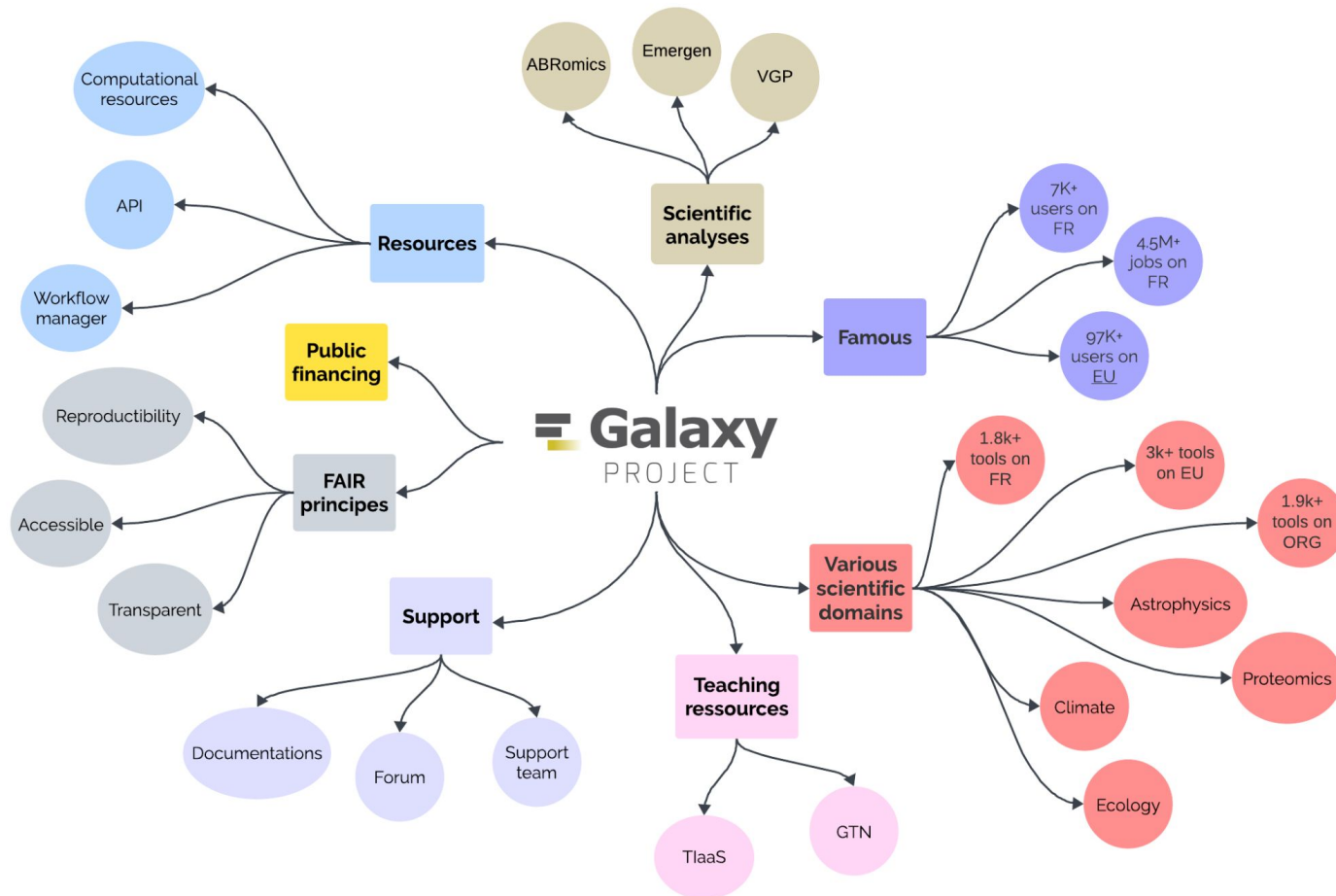
European Financing



French financing



Galaxy benefits



Convinced? Join the community!

See you on **12 July** for the **Galaxy
Working Group meeting**

Mailing list: bit.ly/galaxy-gt



 **Galaxy**
FRANCE



