

Galaxy PROJECT

Data Driven Research for Everyone

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

Accessible

Users can easily configure and run tools without the need to write code, all via an user-friendly web-based interface.

Reproducible

Galaxy captures the full metadata required so that any user cannot only understand but also reproduce the complete computational analysis.

Transparent

Users can extract, share and publish analyses via interactive, web-based documents that can enhance analyses with user-supplied annotation.

Scalable

Galaxy scales for thousands of users. It can run on a local computer, on a large cluster or on the cloud.



The European Galaxy Instance!

by



- Thousands of documented and maintained tools
- Free registration
- 250 GB per user
- Training capacities on demand and online

Data Analysis for any Scientist

No programming knowledge required

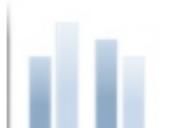
Access Galaxy and its tools with a web browser
Powerful data analyses, to replace Excel habits

Powerful computational infrastructure

Computation automatically performed on a cluster and on the de.NBI cloud
250 GB of storage for analyses, more on request

From beginners to advanced users

Programmatic access to usegalaxy.eu via its API to leverage cluster usage and data storage to scale beyond the visual interface and to automate the analyses
Development of novel analyses right in the interface with Galaxy Interactive Environments: Jupyter notebooks, Ethercalc, HiCBrowser, etc.



Bar diagram
(NVD3)



Horizontal
(NVD3)



Visualization & Data Interpretation

Instantaneous publication-ready visualizations

Charts: bar diagram, line charts, box plots, heatmaps, etc
Scatterplot, Venn diagrams, and more



Scatter plot
(NVD3)



Stacked area
(NVD3)

Interactive visualizations for digging deeper

Integrated Genome Browser: Trackster
Phinch for BIOM files, Circos, JBrowser, IGV, IGB, UCSC, etc



Clustered



Venn Diagram
(benfre...)



Our Services

usegalaxy.eu: the European server

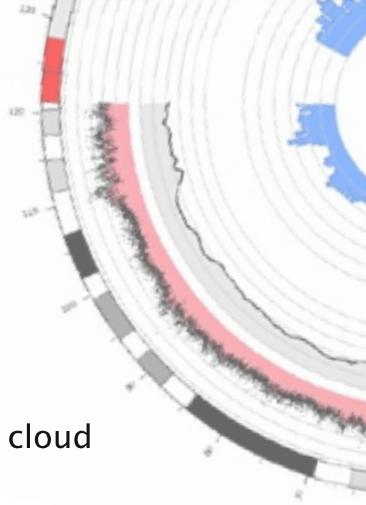
Free access to bioinformatics tools
Regular updates of tools and analysis pipelines

Tool development and integration

Maintenance, adaptation, and optimization of existing Galaxy tools
Development of new tools and integration into Galaxy

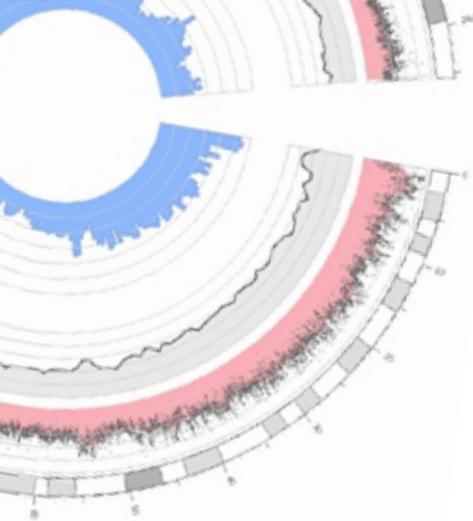
Data analysis

Team with experience in different fields (RNA-Seq, ChIP-Seq, Metagenomics, WES, WGBS, HiC, etc)
Collaboration with a world-wide community of scientists





Tools for any Bioinformatics Analysis



File and metatools

Get data: UCSC, Uniprot
Send data: GenomeSpace Exporter
Convert

Genomics, HTS

Quality control: FastQC, MultiQC, Trim Galore!, etc
Alignment: BLAST, Diamond, etc
Mapping: Bowtie2, STAR, HISAT2, BWA, segemehl, etc
Assembly: Unicycler, SPades, Quast, etc
Transcriptomics: FeatureCounts, DESeq2, Trinity, Salmon, etc
RNA: LocARNA, RNAfold, RNAAz, RNAPlot, etc
Variant Calling: FreeBayes, Gemini, VCFTools, SnpEff, etc
Peak Calling: MACS2, Piranha, PEAKachu, etc
Epigenetics: Bismark, metilene, bwameth, MethylDackel, etc
deepTools, SAM Tools, HicExplorer, Picard, EMBOSS, etc

Text tools

Text manipulation
Filter and Sort
Join, Subtract and Group
Statistics

Metagenomics

MetaPhlAn2, HUMAN2, VSearch, ...
QIIME, Mothur
MEGAHIT, MetaSpades, ...

Annotation, ontologies

SortMeRNA, Aragorn, Roary, Prokka, Augustus, KOBAS, Glimmer, antiSMASH, etc

Proteomics, Metabolomics, Chemistry

OpenMS, PeptideShaker, SearchGUI, MADLIquant, etc
Jmol Editor, Docking, etc
OpenBabel, ChemFP, OMG, QED, etc



Reproducibility & Transparency

Histories

Foundation of reproducibility and transparency in Galaxy
Capture inputs, parameters, and versions of the used tools
Sharable with everyone or specific groups

Powerful workflow system

Extraction of workflows from histories or from scratch with drag-and-drop
Downloadable and sharable with everyone, no vendor lock-in

Tools and reference data

Fixed versions of thousands of tools, managed by Bioconda and BioContainers
4 TB of reference data available on usegalaxy.eu providing access
to hundreds of reference genomes



Virtualization for Sensitive Data

For sensitive (biomedical) data and users with internet limitation,
we offer a virtualized Galaxy

Virtualization of Galaxy via the Galaxy Docker project

Full-fledged Galaxy installation with all dependencies
Easily extendable bases images with tools, data and workflows

Customized flavors to meet different needs

Installation of community-maintained curated sets of tools, workflows, data and
training materials



We care for bioinformatics training



Workshops

Bi-annual week-long workshops in Freiburg covering HTS data analyses:
Introduction to Galaxy and HTS, RNA-Seq, ChIP-Seq, HiC, MethylC-Seq, etc
Training around the world on demand
Training for developers and administrators

Online training material at training.galaxyproject.org

Slides, tutorials with hands-on material and interactive tours
Designed for both self-training and workshops
Technical support with tools, data, virtualized instances
Topics: Sequence analysis, Transcriptomics, ChIP-Seq, Assembly, Epigenetics,
Metagenomics, Proteomics, Variant analysis, Metabolomics, etc

Hackathons

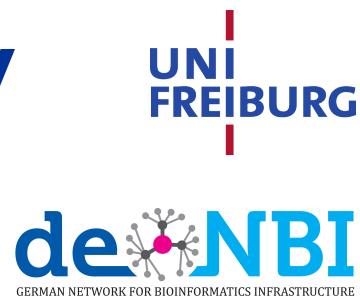
Hackathons for developing new, or improving existing techniques, tools, training materials, etc
Numerous hackathons per year on site or online
Close cooperation with de.NBI, ELIXIR, GOBLET, and the Galaxy community

TIaaS: Training Infrastructure as a Service on usegalaxy.eu

Dedicated on-demand infrastructure for all trainees during workshops



usegalaxy.eu/freiburg
 freiburg@usegalaxy.eu
 [usegalaxy-eu](https://github.com/usegalaxy-eu)
 [@galaxyproject](https://twitter.com/galaxyproject)



Get more information about our team: usegalaxy.eu/freiburg/people