

# 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 a 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, a large cluster or 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



## Our Services

### `usegalaxy.eu`: the European server

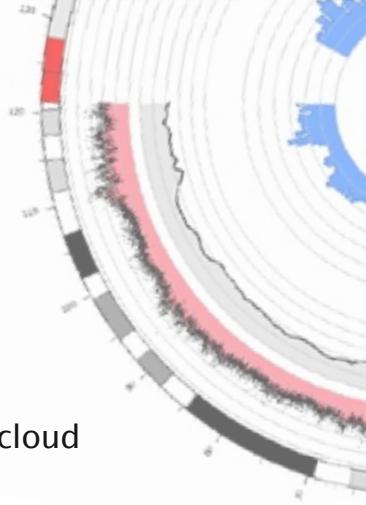
Free access to bioinformatics tools  
Regular updates of tools and analysis pipelines

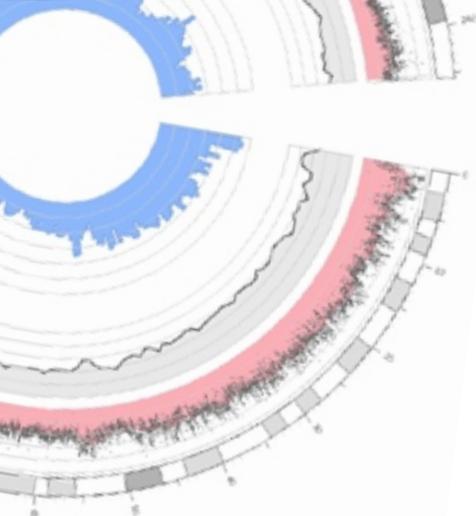
### Tool development and integration

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, HUMAnN2, 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](http://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](http://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 onsite or online  
Close cooperation with de.NBI, ELIXIR, GOBLET, and the Galaxy community

## TlaaS: Training Infrastructure as a Service on [usegalaxy.eu](http://usegalaxy.eu)

Dedicated on-demand infrastructure for all trainees during workshops



🏠 [galaxyproject.eu/freiburg](http://galaxyproject.eu/freiburg)  
✉️ [contact@usegalaxy.eu](mailto:contact@usegalaxy.eu)  
🔗 [usegalaxy-eu](https://usegalaxy-eu)  
🐦 [galaxyproject](https://galaxyproject)



Get more information about our team: [galaxyproject.eu/freiburg/people](http://galaxyproject.eu/freiburg/people)