

Plot with scipy (Galaxy Version 1.4.4+galaxy0)

Annotated data matrix

Method used for plotting

Embeddings: Scatter plot in UMAP basis, using 'pl.umap'

(method)

Keys for annotations of observations/cells or variables/genes

louvain

One or a list of comma-separated index or key from either '.obs' or '.var' (color)

Use 'raw' attribute of input if present

Yes No

(use\_raw)

Show edges?

No

(edges)

Show arrows?

Yes No

It requires to run 'tl.rna\_velocity' before. (arrows)

Sort order?

Yes No

For continuous annotations used as color parameter, plot data points with higher values on top of others. (sort\_order)

Categorical observation annotations, comma-separated

108: Plot (pl.umap) on data 107  
69.9 KB format: png, database: ?  
import scipy as sc  
import pandas as pd  
import numpy as np  
  
adata = sc.read('anndata.h5ad')  
  
sc.pl.umap(  
 adata,  
 show=False,  
  
 color=[louvain],  
 use\_raw=False,  
  
 image=True  
)  
  
Image in png format  
107: Manipulate AnnData

# Data-Driven Research for Everyone with the European Galaxy Instance!

Galaxy is an **open, web-based** platform for **data driven 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 to add user-supplied annotation.

## Scalable

Galaxy scales for thousands of users. It runs on a large cluster and on the cloud.



**Thousands of documented and maintained tools**



**10,000+ users**



**Free registration for all users**



**250 GB per user by default and more on request**



**Training capacities on demand and online**



## Online training material at [training.galaxyproject.org](http://training.galaxyproject.org)

150+ slides, hands-on tutorials, designed for both self-training and workshops

Technical support with tools, data, and tested workflows on [usegalaxy.eu](http://usegalaxy.eu)

Topics: Sequence analysis, Transcriptomics, Assembly, Epigenetics, Metagenomics, Proteomics, Variant analysis, Metabolomics, Imaging, Ecology, Computation chemistry, Statistics & machine learning, etc

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

Dedicated on-demand infrastructure for all trainees during workshops

Free, no need for Galaxy maintenance or administration

Official Galaxy Training Materials guaranteed to work

Details on [galaxyproject.eu/tiaas](http://galaxyproject.eu/tiaas)

## An European project

### Distributed compute resources

Pulsar

Openly managed infrastructure via [Github.com/usegalaxy-eu](https://github.com/usegalaxy-eu)

### Distributed compute resources



[galaxyproject.eu](http://galaxyproject.eu)

[contact@usegalaxy.eu](mailto:contact@usegalaxy.eu)

[gitter.im/usegalaxy-eu/Lobby](https://gitter.im/usegalaxy-eu/Lobby)

[usegalaxy-eu](https://github.com/usegalaxy-eu)

[@galaxyproject](https://twitter.com/galaxyproject)



# Thousands of Tools

## Genomics, HTS

**Quality control:** FastQC, MultiQC, Trim Galore!, etc  
**Alignment:** BLAST, Diamond, etc  
**Mapping:** Bowtie2, STAR, HISAT2, BWA, segemehl, minimap2, etc  
**Assembly:** Unicycler, SPades, Quast, Flye, Canu, etc  
**Annotation:** SortMeRNA, Aragorn, Roary, Prokka, Augustus, KOBAS, Glimmer, antiSMASH, etc  
**Transcriptomics:** FeatureCounts, DESeq2, Trinity, Salmon, etc  
**RNA:** LOCARNA, RNAfold, RNAnz, 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  
**Metagenomics:** MetaPhlAn2, HUMAnN2, VSearch, QIIME, Mothur, MEGAHit, MetaSpades, etc  
**Single-cell:** Scanpy, Scatter, Seurat, Race-ID, etc  
**Nanopore:** Porechop, Nanopolish, Nanoplot

## File and metatools

**Get data:** USCS, Uniprot  
**Send data:** GenomeSpace Exporter  
**Convert**

## Text tools

Text manipulation  
Filter and Sort  
Join, Subtract and Group

## Proteomics, Metabolomics, Chemistry

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

## Statistics & Machine learning

skit-learn

## Climate & Ecology

Copernicus Essential climate variables, etc  
GIS data handling: GDAL suite, etc  
Animal detection on acoustic recording  
Phenology & trend computation

Galaxy / Single Cell Omics    Analyze Data    Workflow    Visualize    Shared Data    Help    Login or Register   

Using 0 bytes

Tools

Collection

GENERAL TOOLS

Text Manipulation

Filter and Sort

Join, Subtract and Group

Convert

FASTQ Quality

BED

COMMON COMMANDS

Operate on Data

Annotation

Mapping

RNA-Seq

Picard

Domain-specific European Galaxies

Welcome to the world of Single Cell Omics

Domain-specific versions of `usegalaxy.eu` server

Set of curated tools, standardized high-quality workflows and training focused on one specific domain

Dedicated interface but same server on the back with user data

Several European Galaxies to foster communities

annotation.usegalaxy.eu, cheminformatics.usegalaxy.eu, climate.usegalaxy.eu, clipseq.usegalaxy.eu, ecology.usegalaxy.eu, imaging.usegalaxy.eu, metabolomics.usegalaxy.eu, metagenomics.usegalaxy.eu, nanopore.usegalaxy.eu, plants.usegalaxy.eu, proteomics.usegalaxy.eu, rna.usegalaxy.eu, singlecell.usegalaxy.eu, etc

Get started

Are you new to Galaxy, or returning after a long time, and looking for help to get started? Take a guided tour through the Galaxy tutorial.

History

search datasets

Unnamed history

(empty)

your own data or get data from an external source



## Virtualization for Sensitive Data

For sensitive (biomedical) data and users with internet limitation

## 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

**Data Analysis for any Scientist**

**No programming knowledge required**  
Access Galaxy and its tools with a web browser at [usegalaxy.eu](http://usegalaxy.eu)  
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

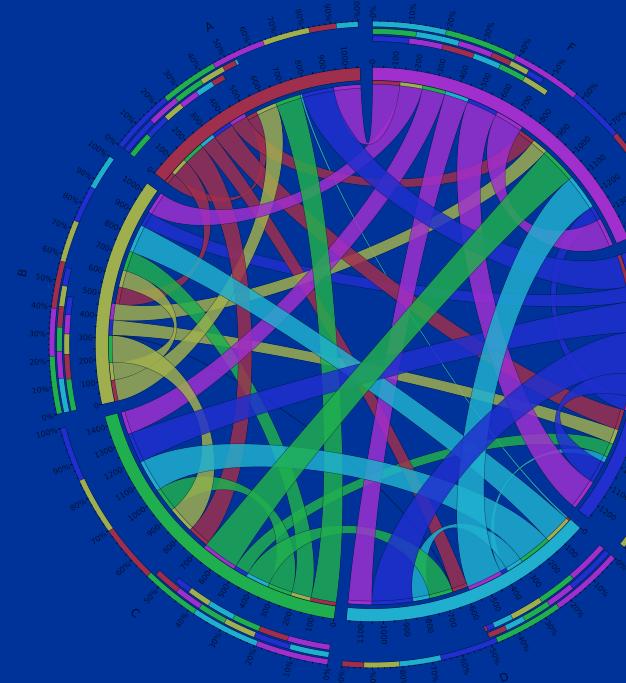
Development of novel analyses right in the interface with Interactive Tools via [live.usegalaxy.eu](http://live.usegalaxy.eu): Jupyter lab, RStudio, Ethercalc, cellxgene, etc.

Programmatic access via an API to leverage cluster usage and data storage to scale beyond the visual interface and to automate the analyses

## Visualization & Data Interpretation

### Instantaneous publication-ready visualizations

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



### Interactive visualizations for digging deeper

Integrated Genome Browser, Trackster JBrowse, Circos, IGV, UCSC, Phinch, pyGenomeTrack, KRONA, etc

## Reproducibility & Transparency

### Histories to track analysis

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

### Powerful workflow system

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

## Tools and reference data

Fixed versions of thousands of tools, managed by Bioconda and BioContainers  
6+TB of reference data providing access to 100+ of reference genomes