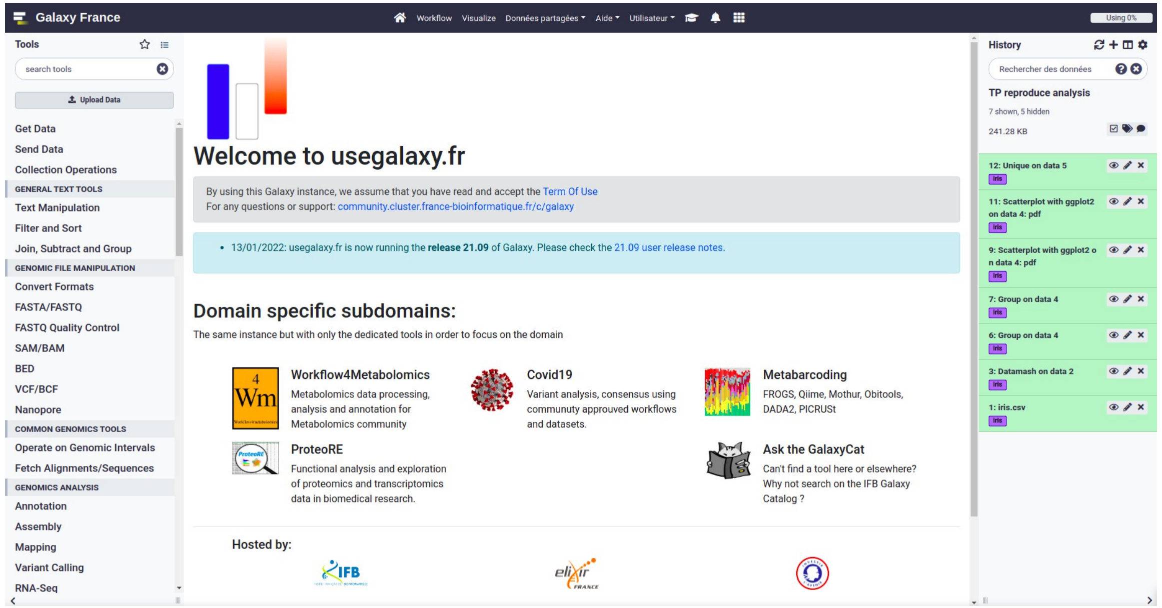
A general introduction to Galaxy

What is Galaxy?

- Galaxy is a WEB application for data analysis focused on biological applications.



Welcome to usegalaxy.fr

By using this Galaxy instance, we assume that you have read and accept the Term Of Use
For any questions or support: community.cluster.france-bioinformatique.fr/c/galaxy

- 13/01/2022: usegalaxy.fr is now running the **release 21.09** of Galaxy. Please check the 21.09 user release notes.

Domain specific subdomains:

The same instance but with only the dedicated tools in order to focus on the domain

Workflow4Metabolomics
Metabolomics data processing, analysis and annotation for Metabolomics community

Covid19
Variant analysis, consensus using communuty approuved workflows and datasets.

Metabarcoding
FROGS, Qiime, Mothur, Obitools, DADA2, PICRUSt

ProteoRE
Functional analysis and exploration of proteomics and transcriptomics data in biomedical research.

Ask the GalaxyCat
Can't find a tool here or elsewhere? Why not search on the IFB Galaxy Catalog ?

Hosted by:

- Galaxy offers common ground for biologists and bioinformaticians!

Why Galaxy?

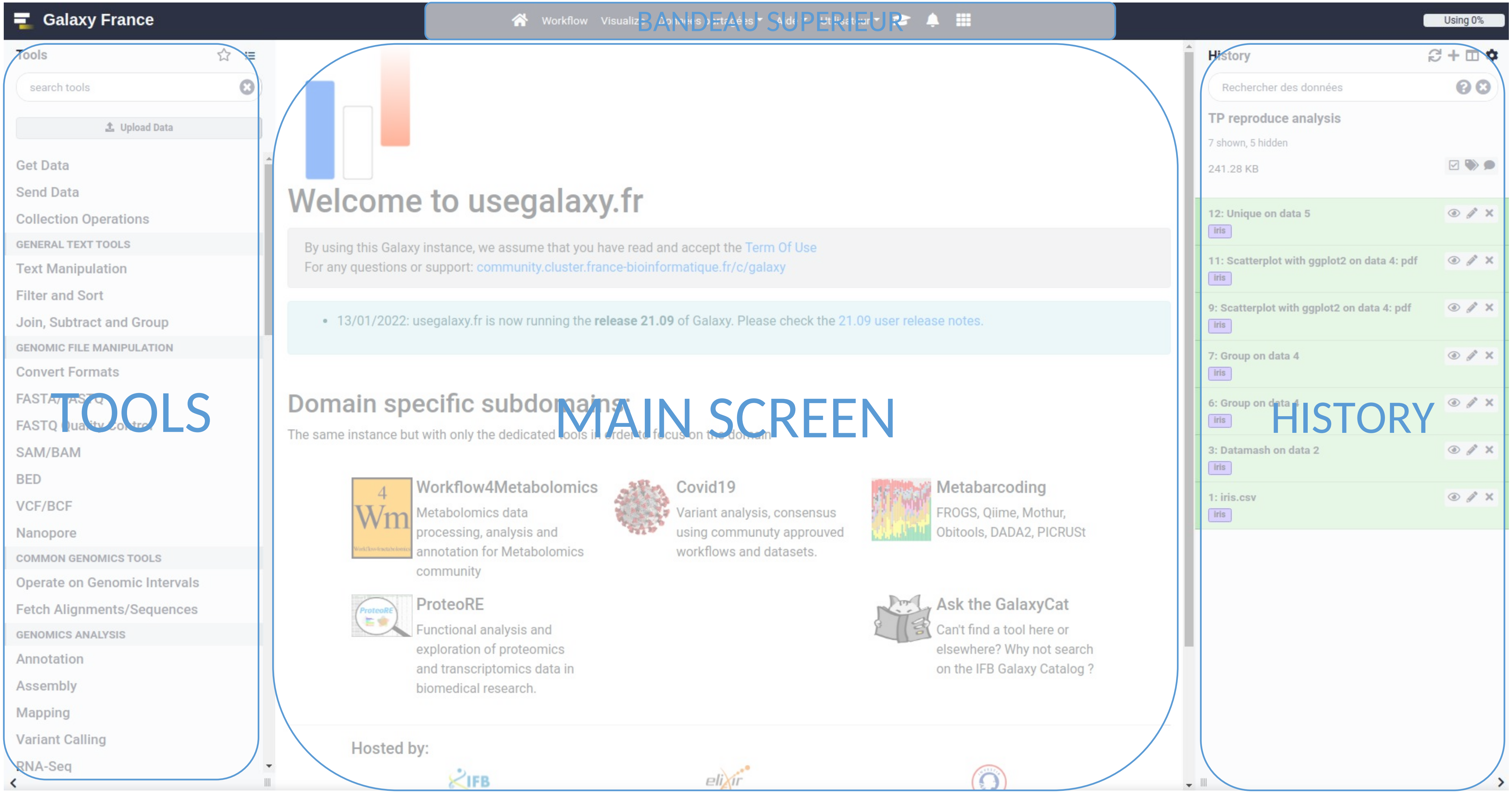
- “The Galaxy Project: Online bioinformatics analysis for **ALMOST** everyone”
- Avoids the dogma: bioinformatics = command line
- Allows to focus on the biological question and analysis, not on syntax and tool installation
- Allows to chain tools to create workflows
- Allows to track and archive all analyses
- Increased reproducibility
- Easy sharing

Connection to a Galaxy instance

A lot of public instances exist :

- https://usegalaxy.org/
- https://usegalaxy.fr/
- https://usegalaxy.eu/
- …

There are also specialized instances with thematic tools (metabolomics, single cells, plants, etc.).



BANDEAU SUPERIEUR

TOOLS

MAIN SCREEN

HISTORY

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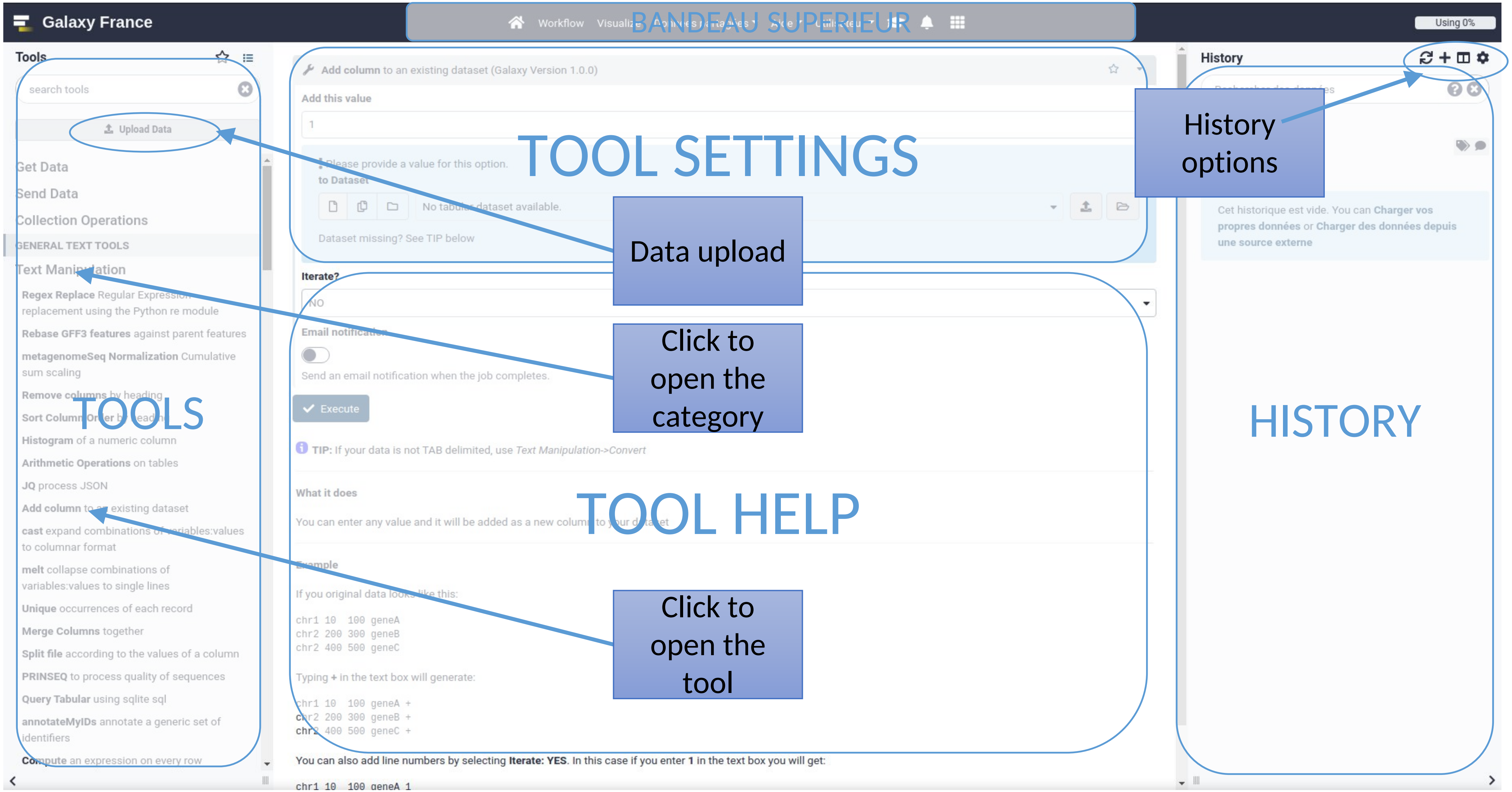


Regex Replace Regular Expression replacement using the Python re module

Rebase GFF3 features against parent features

metagenomeSeq Normalization Cumulative sum scaling

Remove columns by heading

Sort Column Order by heading

Histogram of a numeric column

Arithmetic Operations on tables

JQ process JSON

Add column to an existing dataset

cast expand combinations of variables:values to columnar format

melt collapse combinations of variables:values to single lines

Unique occurrences of each record

Merge Columns together

Split file according to the values of a column

PRINSEQ to process quality of sequences

Query Tabular using sqlite sql

annotateMyIDs annotate a generic set of identifiers

Compute an expression on every row

Add column to an existing dataset (Galaxy Version 1.0.0)

Add this value

1

Please provide a value for this option.

to Dataset

No tabular dataset available.

Dataset missing? See TIP below

Iterate?

NO

Email notification

Send an email notification when the job completes.

TIP: If your data is not TAB delimited, use *Text Manipulation->Convert*

What it does

You can enter any value and it will be added as a new column to your dataset

Example

If you original data looks like this:

```
chr1 10  100 geneA
chr2 200 300 geneB
chr2 400 500 geneC
```

Typing **+** in the text box will generate:

```
chr1 10  100 geneA +
chr2 200 300 geneB +
chr2 400 500 geneC +
```

You can also add line numbers by selecting **Iterate: YES**. In this case if you enter **1** in the text box you will get:

```
chr1 10  100 geneA 1
```

Cet historique est vide. You can **Charger vos propres données** or **Charger des données depuis une source externe**

BANDEAU SUPERIEUR

TOOL SETTINGS

History options

Data upload

Click to open the category

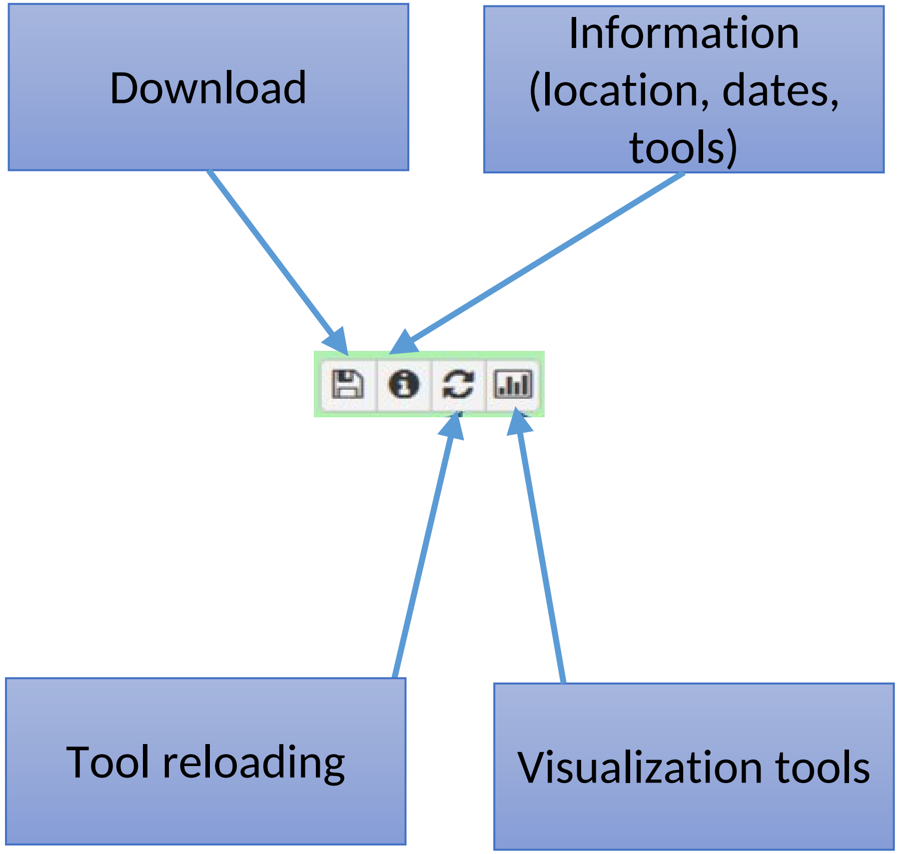
TOOLS

TOOL HELP

Click to open the tool

HISTORY

Datasets

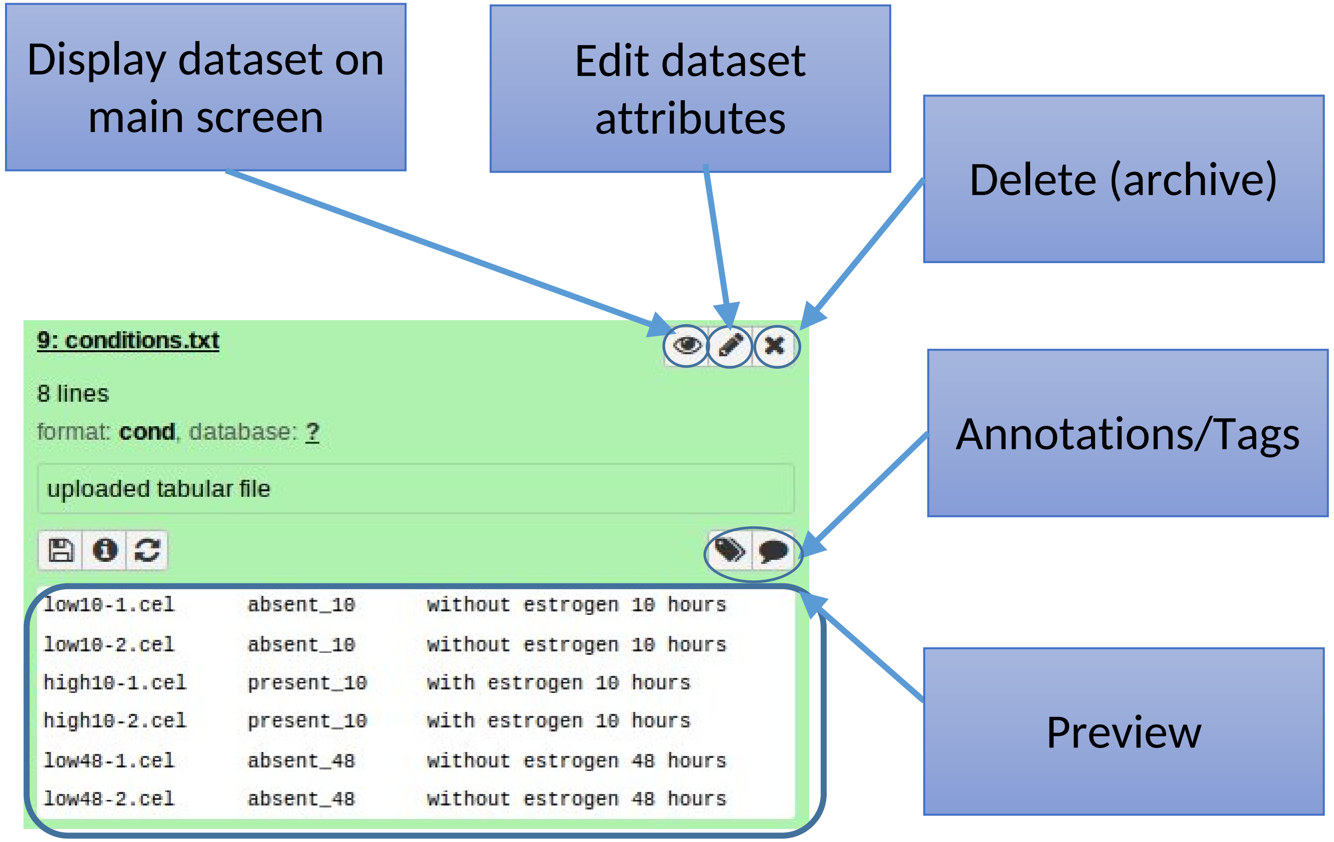


Download

Information (location, dates, tools)

Tool reloading

Visualization tools



Display dataset on main screen

Edit dataset attributes

Delete (archive)

Annotations/Tags

Preview

9: conditions.txt

8 lines

format: **cond**, database: ?

uploaded tabular file

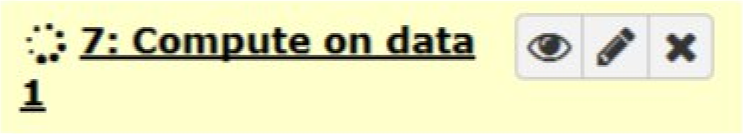
low10-1.cel	absent_10	without estrogen 10 hours
low10-2.cel	absent_10	without estrogen 10 hours
high10-1.cel	present_10	with estrogen 10 hours
high10-2.cel	present_10	with estrogen 10 hours
low48-1.cel	absent_48	without estrogen 48 hours
low48-2.cel	absent_48	without estrogen 48 hours

Dataset status

In queue

6: Compute on data 1

In progress

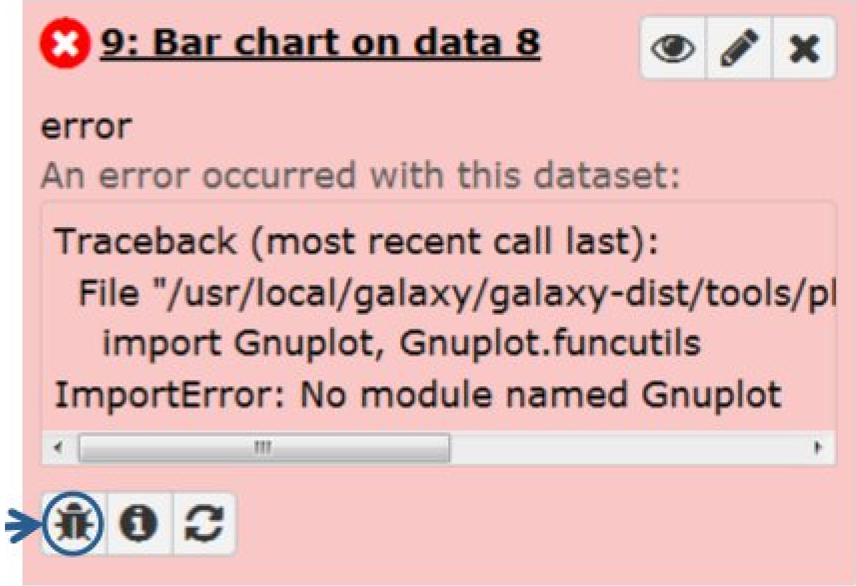


7: Compute on data 1

Successfully finished

7: Compute on data 1

Finished with error



9: Bar chart on data 8

error

An error occurred with this dataset:

```
Traceback (most recent call last):
  File "/usr/local/galaxy/galaxy-dist/tools/pl
    import Gnuplot, Gnuplot.funcutils
ImportError: No module named Gnuplot
```

File formats (datatypes)

- Generic formats:
  - tabulated format, Excel, HTML, xml, jpg, zip...
- Standard bioinformatics formats:
  - FASTQ, FASTA, SAM/BAM, bed, GFF...

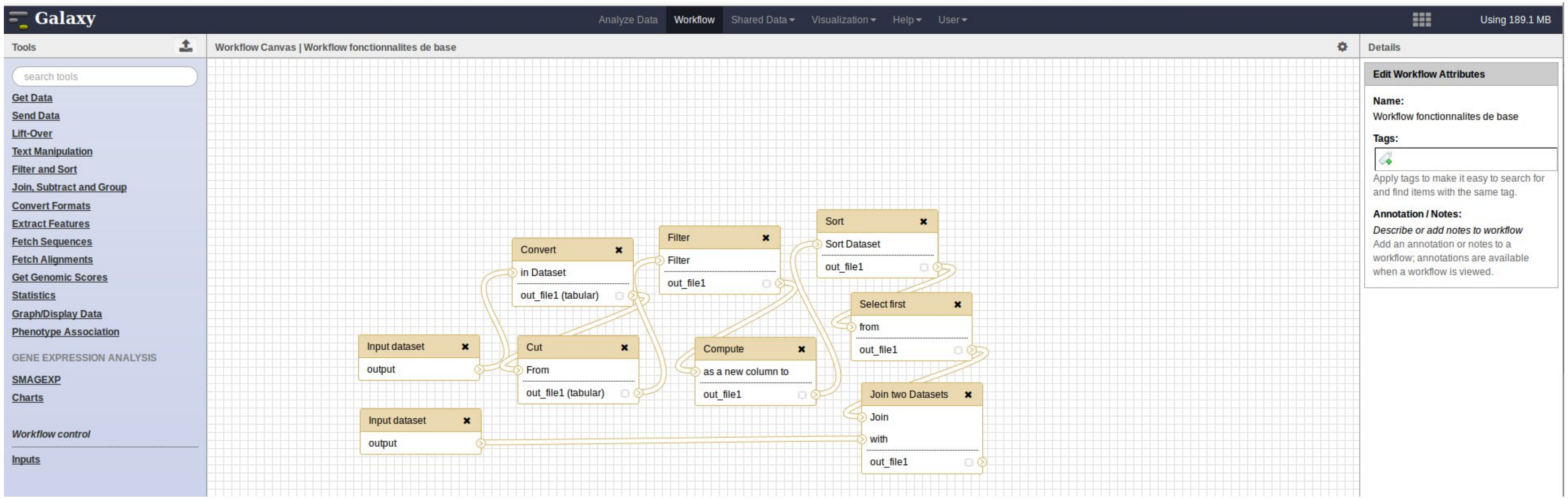
Tools

- Generic tools
  - manipulation of text files, spreadsheets...

- Standard bioinformatics tools
  - DNA-seq, RNA-seq, ChiP-seq, variant identification, metagenomics...

- Many tools can be installed from the Toolshed (~App store)
  - 10,556 tools available as of 17/06/2025

Workflows



Name:
Workflow fonctionnalites de base

Tags:
Apply tags to make it easy to search for and find items with the same tag.

Annotation / Notes:
Describe or add notes to workflow
Add an annotation or notes to a workflow; annotations are available when a workflow is viewed.

- Automate repetitive analyses
- Standardize analysis pipelines
- Easy to share
- Easy to reproduce