

Introduction to Galaxy

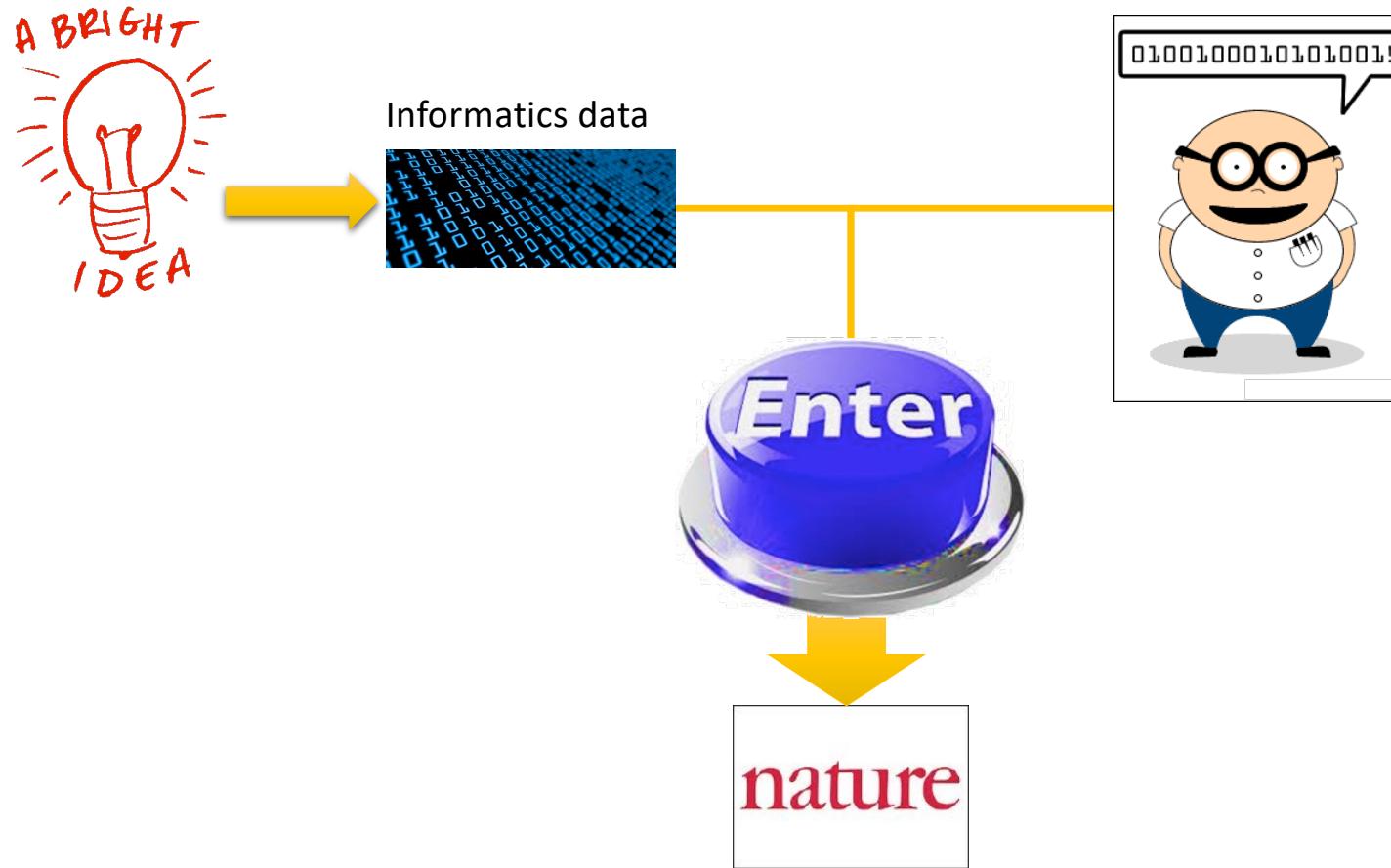
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Guidelines

- Analyzing biological data with informatics tools
- Presentation of the Galaxy project
- Description of the main features of the Galaxy platform

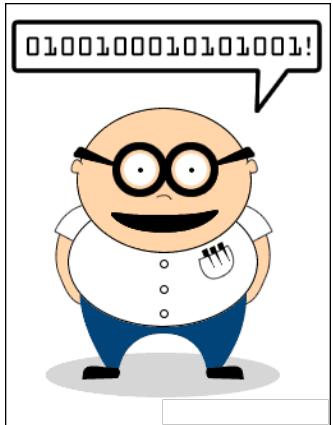
Analyzing biological data with informatics tools

Bioinformatics analyses



Bioinformatics analyses

Scripts, softwares



```
#!/usr/bin/perl

use strict;
use warnings;
use Getopt::Long;

## Date : 22 fev 2011
## Author : Stephanie Le Gras

## Objectives :

my $num_arg = scalar @ARGV;
my $progrname = "ExtractID.pl";
my $input;
my $out;
my $id;

my $result = GetOptions(
    "id=s" => \$id,
    "out=s"      => \$out,
    "input=s"     => \$input,
);

my $usage = <<END;
Usage: $progrname --id=FILENAME --out=FILENAME --input=FILENAME
END

die $usage unless ($result);
my @files = @ARGV;
die "Enter at least two files\n$usage" if ( $num_arg < 2 );
die $usage if ( $num_arg == 0 );

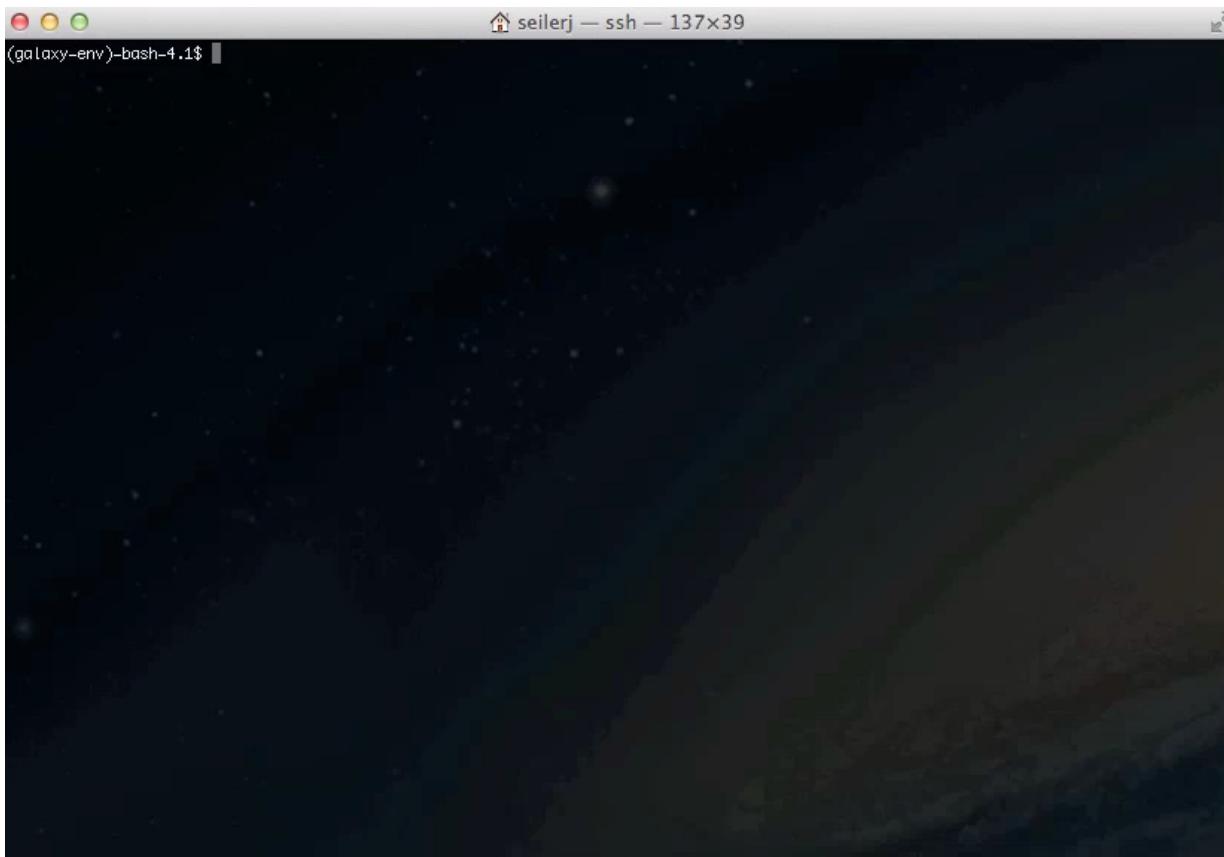
my %ids;
$out = ( defined $out ) ? $out : "results.txt";

## first, every lines of each files are put in the hash table ids. Variant ids are used as keys of the
## hash table and it contains a table.
```

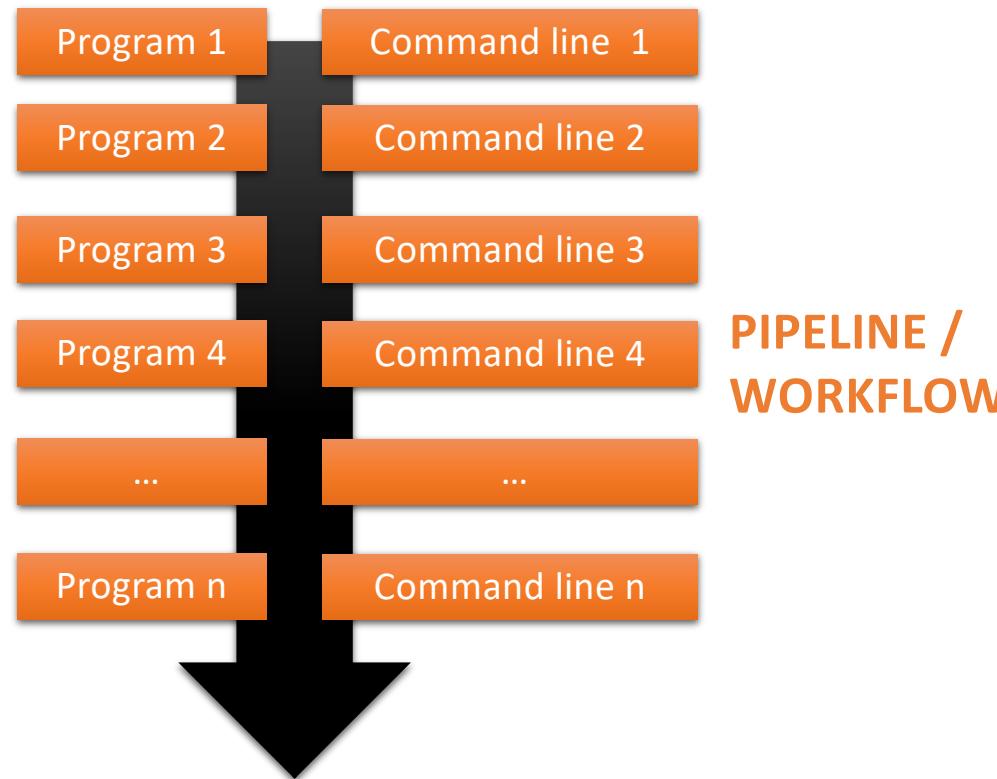
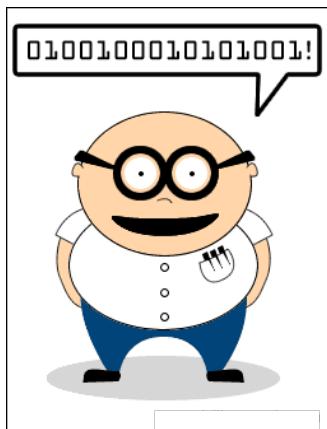
Command line

```
macs14 -t treatment.sort.bed -c control.bed -f BED -g mm --name=name1 --llocal=50000
--slocal=5000 > macs1.nohup 2>&1 &
```

Bioinformatics analyses



Bioinformatics analyses



Galaxy ?





Galaxy PROJECT

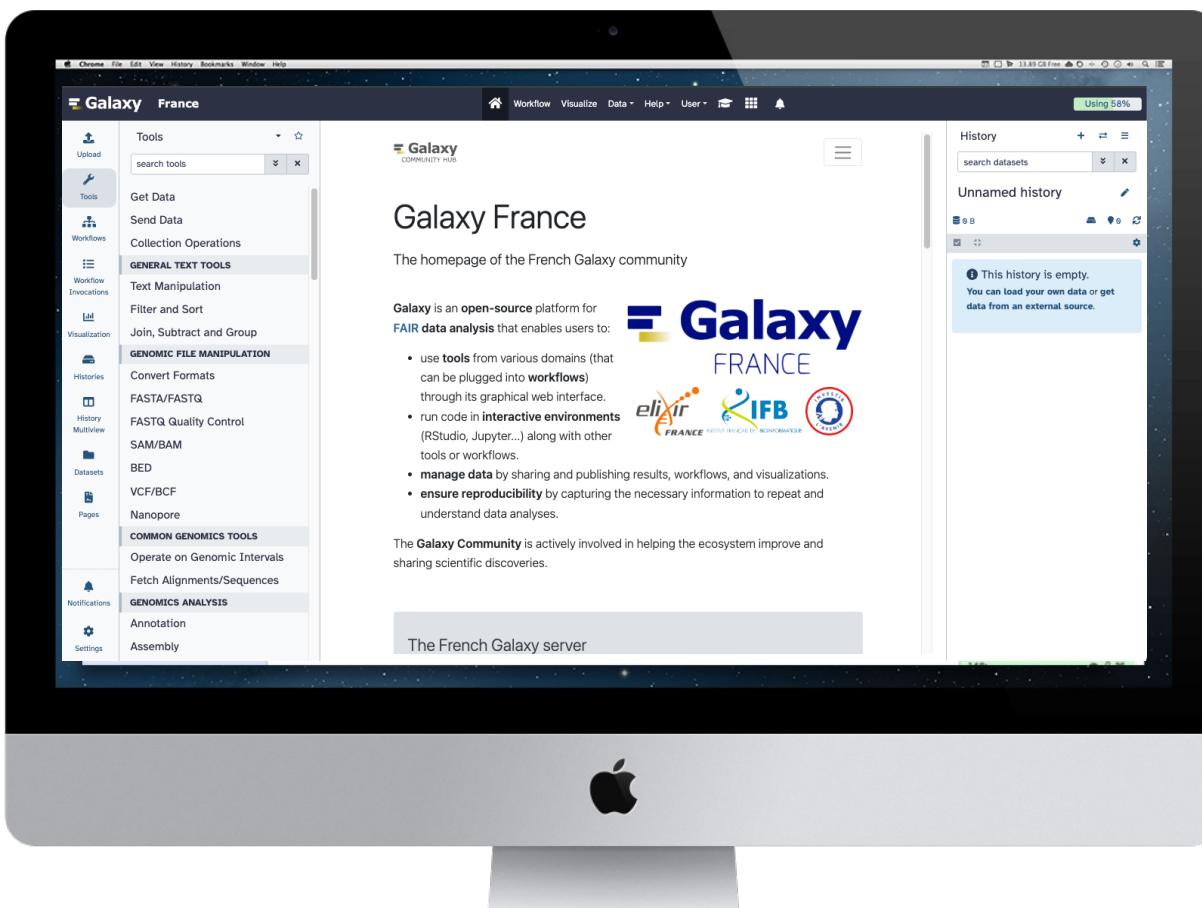
The Galaxy project

Galaxy is a **computing platform** that enables people to run complex bioinformatics tools on a **compute cluster** through a simple web interface.

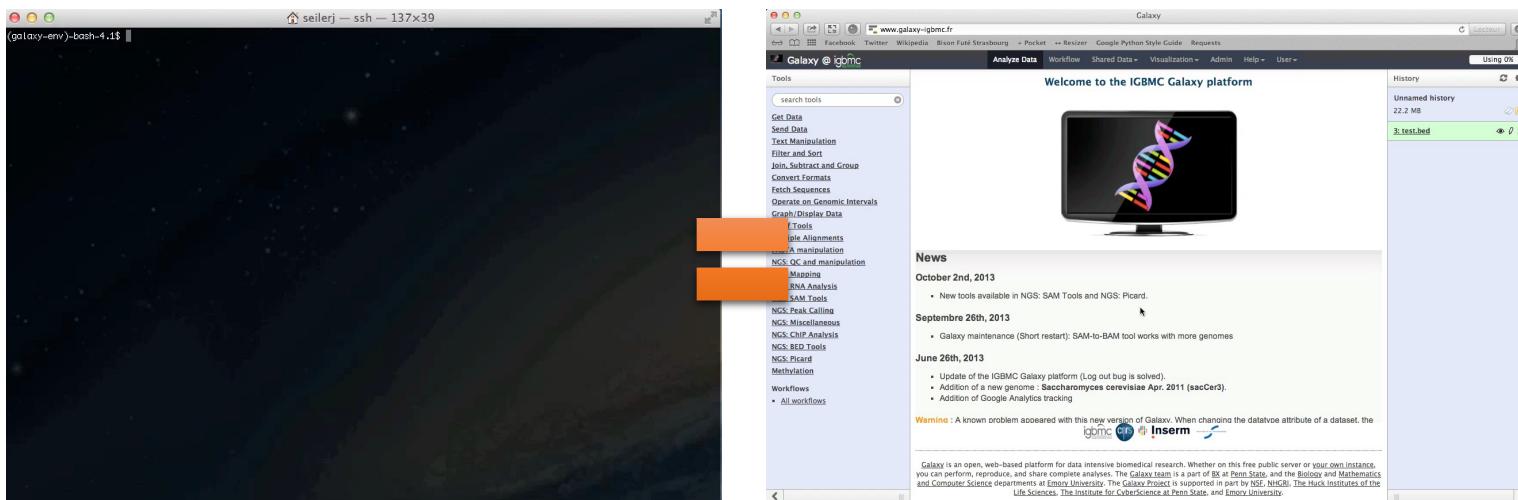


National
Human Genome
Research Institute

This is Galaxy



Running analyses with tools



Galaxy philosophy

- **Perform**, and **share** complete analysis
- **No programming skills** required
- **Open source** and **free** solution
- **Very large** and **active** community
- **Reproducibility/Usability/Transparency**

How to use Galaxy

Use Galaxy

- **Public servers**
- **Local servers**
- Clouds (Public, Commercial or Academic)
- Docker
- Virtual Machines

Galaxy public servers

- Galaxy Project's public server (<https://usegalaxy.org/>) (3)
- There are several public remote Galaxy instances worldwide (137)
 - Genomics Servers
 - Domain Servers
 - Tool Publishing Servers

Public Galaxy Servers list :
<https://galaxyproject.org/use/>
Last Update on: 2024, December 10th

Galaxy public servers

- All analyses are run on remote computing infrastructures
- No need to have a Supercomputer to use Galaxy
- Web browser



Use Galaxy

	UseGalaxy Servers	Public Servers	Tlaas	Academic Clouds	Commercial Clouds	Containers	VMs	Local
Free to use	Yes	Yes	Yes	Yes ¹	No	Yes	Yes	Yes
Uses your local compute infrastructure	No	No	No	No	No	Yes ²	Yes ²	Yes
Datasets total > 250GB (including intermediate)	No	? ⁵	Yes	Yes	Yes	Yes ³	Yes ³	Yes
Computational requirements are similarly large	No	? ⁵	Yes	Yes	Yes	Yes ³	Yes ³	Yes
Share Galaxy objects outside your organization	Yes	Yes	Yes	Yes	Yes	Yes ⁴	Yes ⁴	Yes ⁵
Install custom tools and reference genomes	No	No	No	Yes ⁵	Yes	Yes	Yes	Yes
Have absolute data security requirements	No	No	No	? ⁵	? ⁵	? ⁵	? ⁵	Yes

¹ Depends on provider, and if you are eligible for the service

² These technologies can be deployed on clouds or locally.

³ Depends on the size of the system you are running it on.

⁴ With these technologies you can save the server and share the entire platform with them.

⁵ Depends on configuration.

* Tlaas: Training Infrastructure as a Service

- <https://galaxyproject.org/use/>
 - 167 resources for using Galaxy (Last Update on: 2024, September 24th)

Galaxy public servers

Your research institute



Connect to Galaxy web site through
a web browser
(<https://usegalaxy.org/>)

Download and
upload of the data

Remote instance of Galaxy



Run analyses



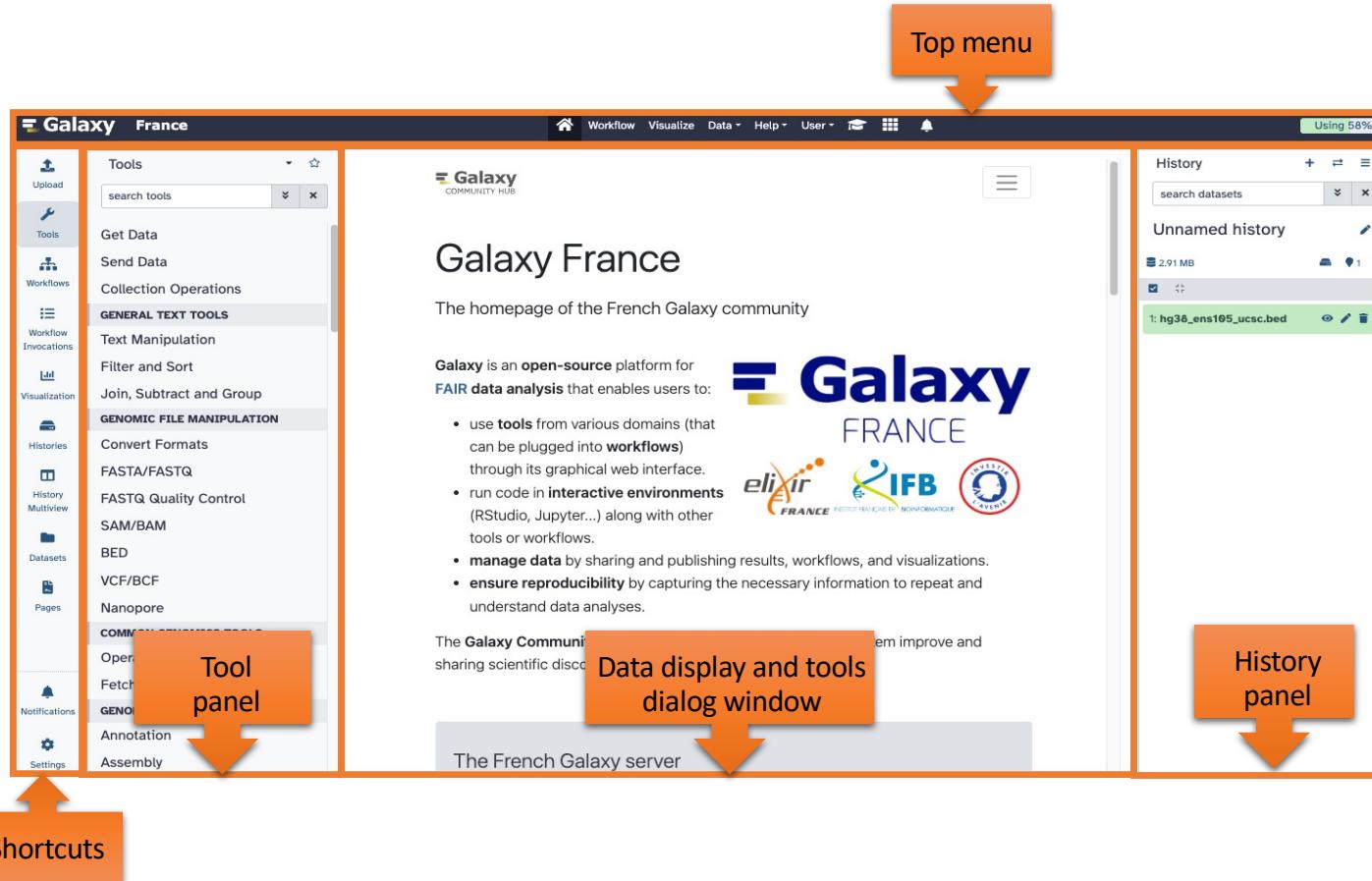
Galaxy local server

- Run a local production Galaxy because you want to
 - install and use tools unavailable on public Galaxies
 - use sensitive data (e.g. clinical)
 - process large datasets that are too big for public Galaxies
 - Develop Galaxy tools
 - Develop Galaxy itself

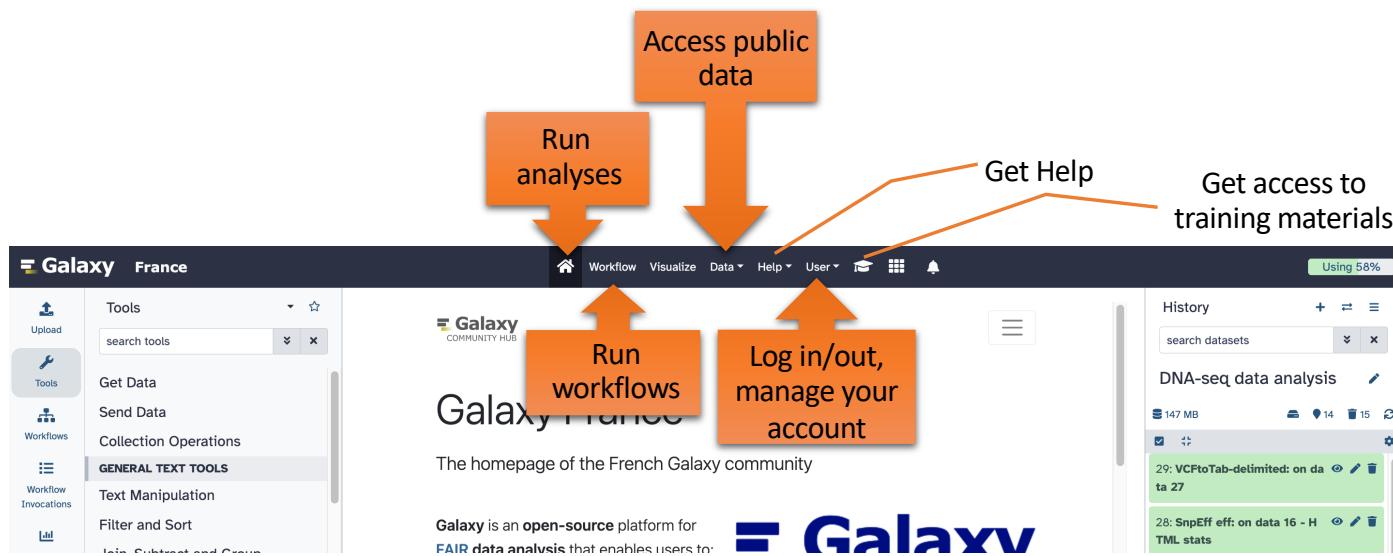


Description of the main features of Galaxy

Galaxy web interface



Top menu



Hands
On

Exercise 1

History

The screenshot displays the Galaxy France web application. On the left, a sidebar menu lists various tools and features: Upload, Tools, Workflows, Workflow Invocations, Visualization, Histories, History Multiview, Datasets, Pages, Notifications, and Settings. The main content area shows the "Galaxy France" homepage, which includes a search bar, navigation links for Workflow, Visualize, Data, Help, User, and a bell icon, along with a "Using 58%" status indicator. The homepage text describes Galaxy as an open-source platform for FAIR data analysis, highlighting its use of tools, workflows, interactive environments, data management, and reproducibility. It also mentions the active involvement of the Galaxy Community in improving the ecosystem. Logos for elixir FRANCE, IFB Institut Français de Bioinformatique, and INSTITUT CÉRÈS are displayed. A callout box on the right, titled "History panel" and "Keep track of each job run", highlights the "History" section of the interface, which is shown in a separate window. This history window has a search bar and a message stating "This history is empty. You can load your own data or get data from an external source."

History

The screenshot shows the 'History/Dataset options' menu, which includes:

- A search bar labeled 'search datasets'.
- A 'History' section with a 'History name' field containing 'Unnamed history' and a size indicator '0 B'.
- An info message: 'This history is empty. You can load your own data or get data from an external source.'
- Three icons: a checkmark, a plus sign, and a gear.
- Three buttons: a plus sign, a double equals sign, and a three-dot ellipsis.
- Text: 'Select and switch to another history' and 'Create new history'.
- A right-click context menu:
 - 'Show Histories Side-by-Side' (highlighted with an orange border)
 - 'Resume Paused Jobs'
 - 'Copy this History'
 - 'Delete this History'
 - 'Export Tool Citations'
 - 'Export History to File'
 - 'Archive History'
 - 'Extract Workflow'
 - 'Show Invocations'
- Bottom section:
 - 'Share or Publish'
 - 'Set Permissions'
 - 'Make Private'

View all histories

The screenshot shows the Galaxy History Multiview interface. On the left, a sidebar lists various history items:

- Unnamed history (3 items, about 1 hour ago)
- DNA-seq data analysis (29 items, about 1 hour ago)
- Neuro-epigenetics train... (17 items, about 2 months ago)
- Copy of 'Neuro-epigenetic...' (5 items, about 2 months ago)
- ChIP-seq data analysis (26 items, 2 months ago)
- RNA-seq data analysis (0 items, 2 months ago)
- RNAseq vs ChIPseq (4 items, 2 months ago)
- RNAseq data analysis (44 items, 2 months ago)
- Copy of 'NGS data anal...' (65 items, 3 months ago)
- RNAseq data analysis (65 items, 3 months ago)

The main area displays two histories:

Unnamed history (last edited about 1 hour ago):

- 39.5 MB
- 3: CaptureDesign_chr4.bed
- 2: CRN-107_11-R2.fastq.gz
- 1: CRN-107_11-R1.fastq.gz
- Add Tags
- 18.5 MB format fastqsanger.gz, database hg19 uploaded fastqsanger.gz file
- @HWI-ST1136:79:HS026:2:1105:11935 TAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAC+ @?DDADDFDF

DNA-seq data analysis (last edited about 1 hour ago):

- 147 MB
- 29: VCFtoTab-delimited: on data 27
- 28: SnpEff eff: on data 16 - HTML stats
- 27: SnpEff eff: on data 16
- 16: FreeBayes on data 15 and data 14 (variants)
- 15: CaptureDesign_chr4.bed
- 14: MarkDuplicates on data 12: BAM
- 13: MarkDuplicates on data 12: tabular
- 12: Map with BWA-MEM on data 3 and data 2 (mapped reads in BAM format)
- 11: FastQC on data 3: RawData
- 10: FastQC on data 3: Webpage
- 9: FastQC on data 2: RawData
- 8: FastQC on data 2: Webpage

At the bottom, there are buttons for "Switch to", "Current History", and "Hide".

**Hands
On**

Exercise 2

Import data into Galaxy

- Your own data (from your computer)
- Shared data / data libraries
- Shared data / histories
- Data from external sources

Import your own data to Galaxy

The screenshot shows the Galaxy web interface. On the left is a vertical sidebar with icons for Upload, Tools, Workflows, Workflow Invocations, Visualization, Histories, History Multiview, Datasets, Pages, Notifications, and Settings. The 'Upload' icon is highlighted with an orange arrow pointing from the text 'Display the utility used to upload local files'. The main area is titled 'Download from web or upload from disk' and shows a table with one item: CRN-107_11-R1.fastq. The table columns are Name, Size, Type, Genome, Settings, and Status. The file name is CRN-107_11-R1.fastq, size is 18.5 MB, type is Auto-detected, genome is set to Additional ..., and status is 0% complete. Orange arrows point from the text labels 'Name of the dataset', 'Size of the dataset', 'File format', and 'Genome' to the corresponding table columns. At the bottom are buttons for Choose local files, Choose remote files, Paste/Fetch data, Start, Pause, Reset, and Close.

Display the utility used to upload local files

Name of the dataset

Size of the dataset

File format

Genome

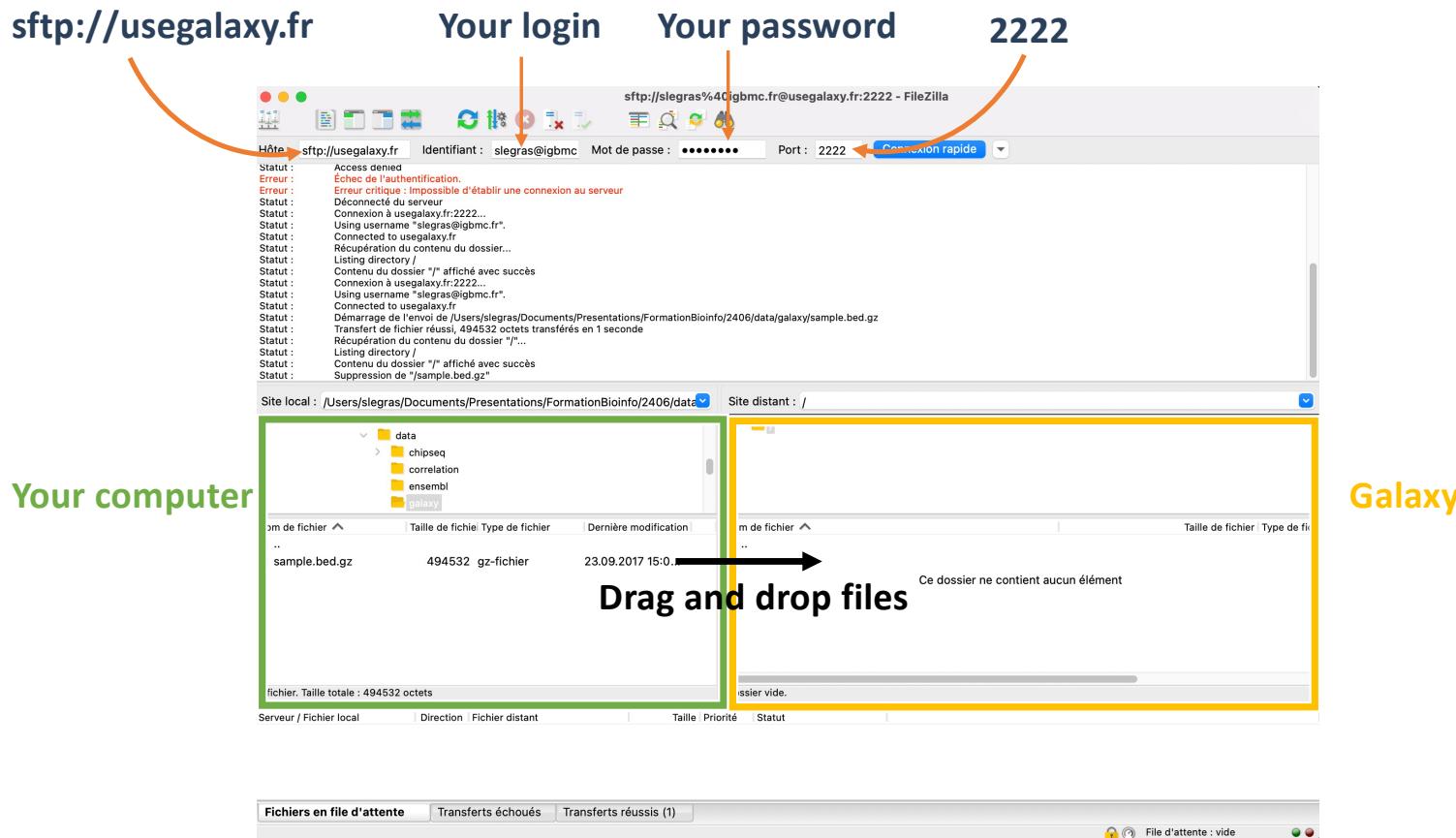
Name	Size	Type	Genome	Settings	Status
CRN-107_11-R1.fastq	18.5 MB	Auto-de...	Additional ...	0%	

Type (set all): Auto-detect Genome (set all): Additional ...

Choose local files Choose remote files Paste/Fetch data Start Pause Reset Close

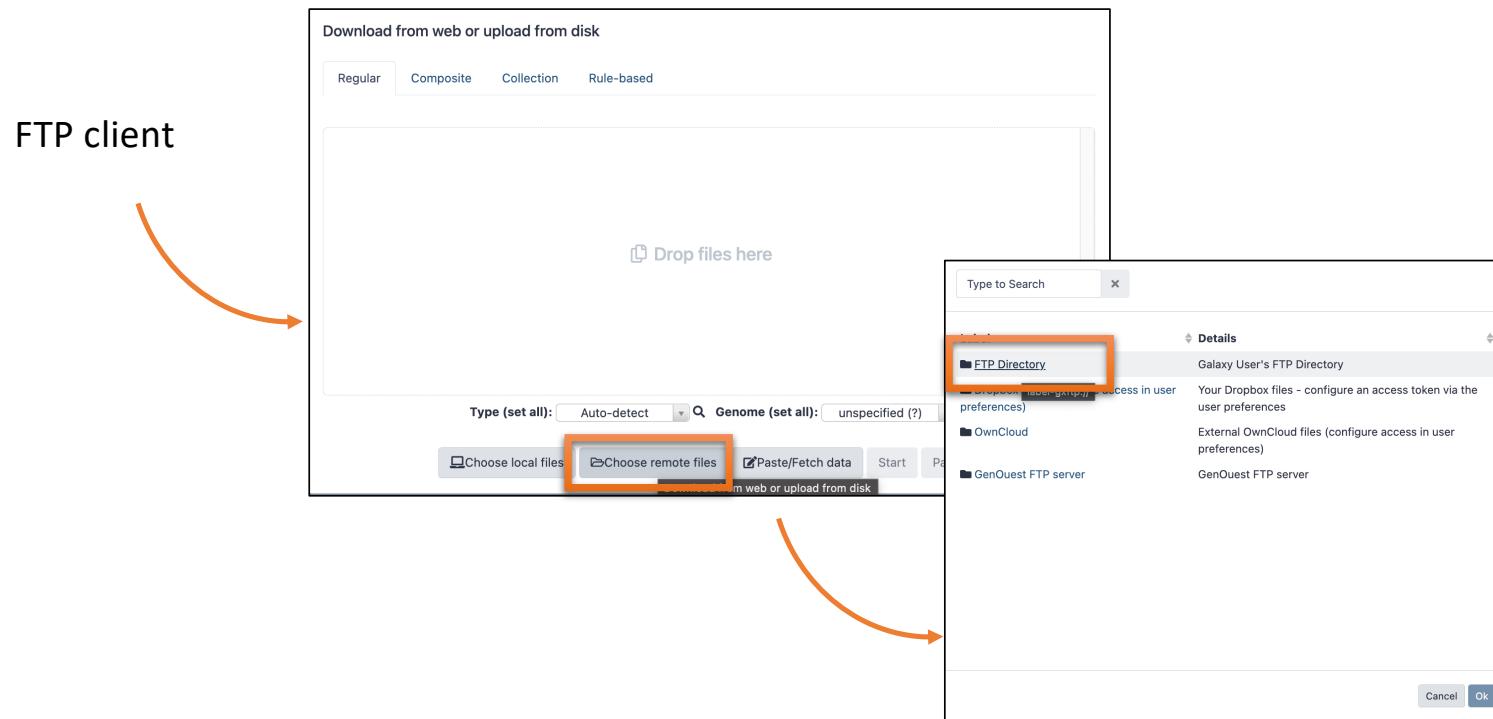
Import your own data to Galaxy (ftp - 1)

- For big files (>1GB) use FTP



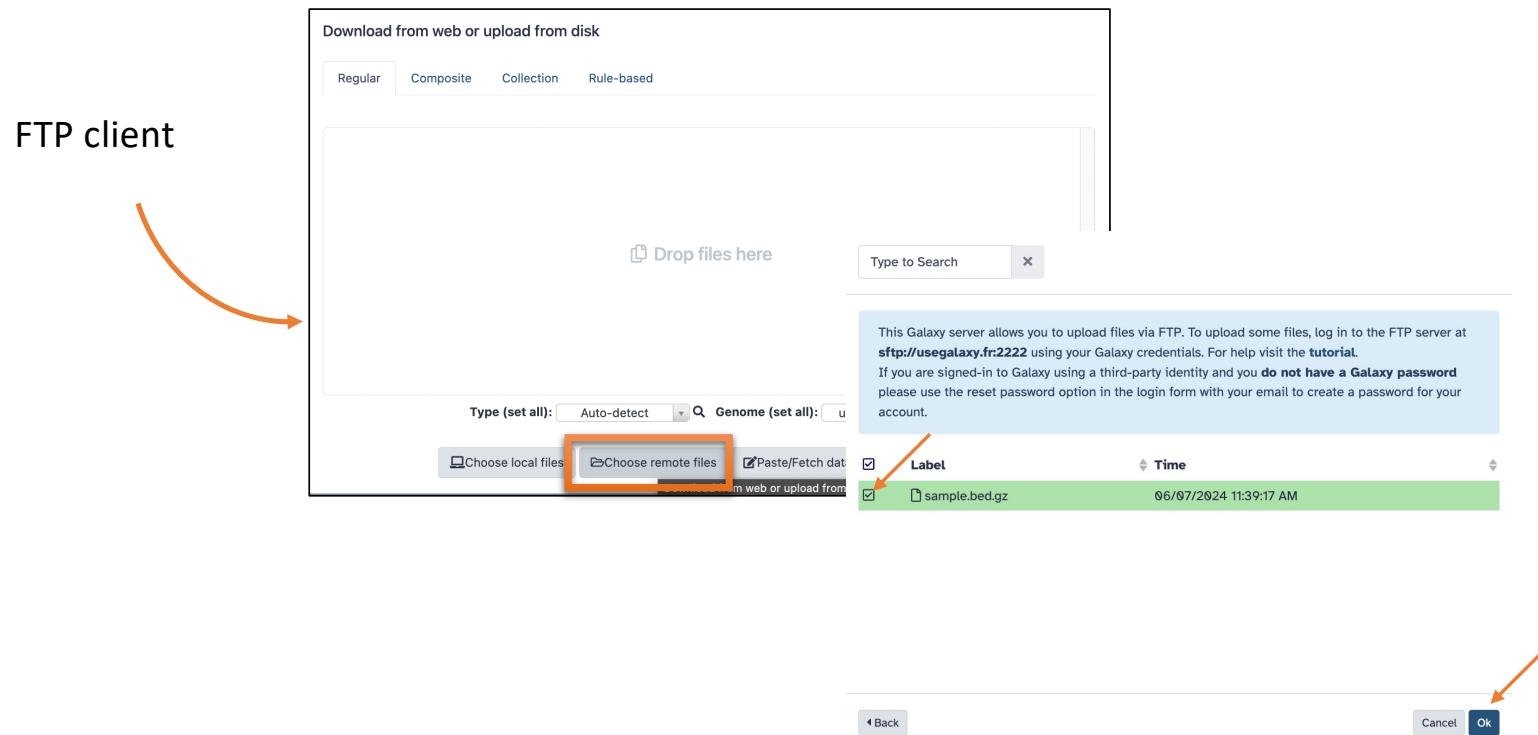
Import your own data to Galaxy (ftp - 2)

- For big files (>1GB) use FTP



Import your own data to Galaxy (ftp - 3)

- For big files (>1GB) use FTP



Import shared data (Data Libraries)

The screenshot shows the Galaxy France web interface. The top navigation bar includes links for Home, Workflow, Visualize, Data, Help, User, and a bell icon. A dropdown menu for 'Data' is open, showing options: Datasets, Histories, Pages, Visualizations, Workflows, and Workflow Invocations. The 'Data Libraries' option is highlighted with a blue box and an orange arrow labeled '1.' pointing to it. Another orange arrow labeled '2.' points to the 'EBAAI A&A 2022' library entry in the main list, which is also highlighted with a red box.

List of data libraries

Name	Description
Agrocampus_2024	Datasets for agrocampus 2024
CATI BARIC	Formations du CATI BARIC (INRAE)
covid-19	
DU agents infectieux 2024	DU "les Agents Infectieux à l'Ere de la ... (more) DU "les Agents Infectieux à l'Ere de la ... (more)
EBAAI A&A 2022	École EBAAI Assemblage & Annotation sept ... (more)
Formation BIGOMICS	BIGOMICS, Génomique comparative, Montpel ... (more)
Formation M2 Agro Rennes	Formation M2 Agro Rennes
Formation REacTION	Formation du réseau INRAE REacTION
Formation sRNA 2022	Data for Formation sRNA 2022
GTN - Material	Galaxy Training Network Material Galaxy Training Network Material. See ht ... (more)

Import shared data (Data Libraries)

The screenshot shows the Galaxy web interface with the following steps highlighted:

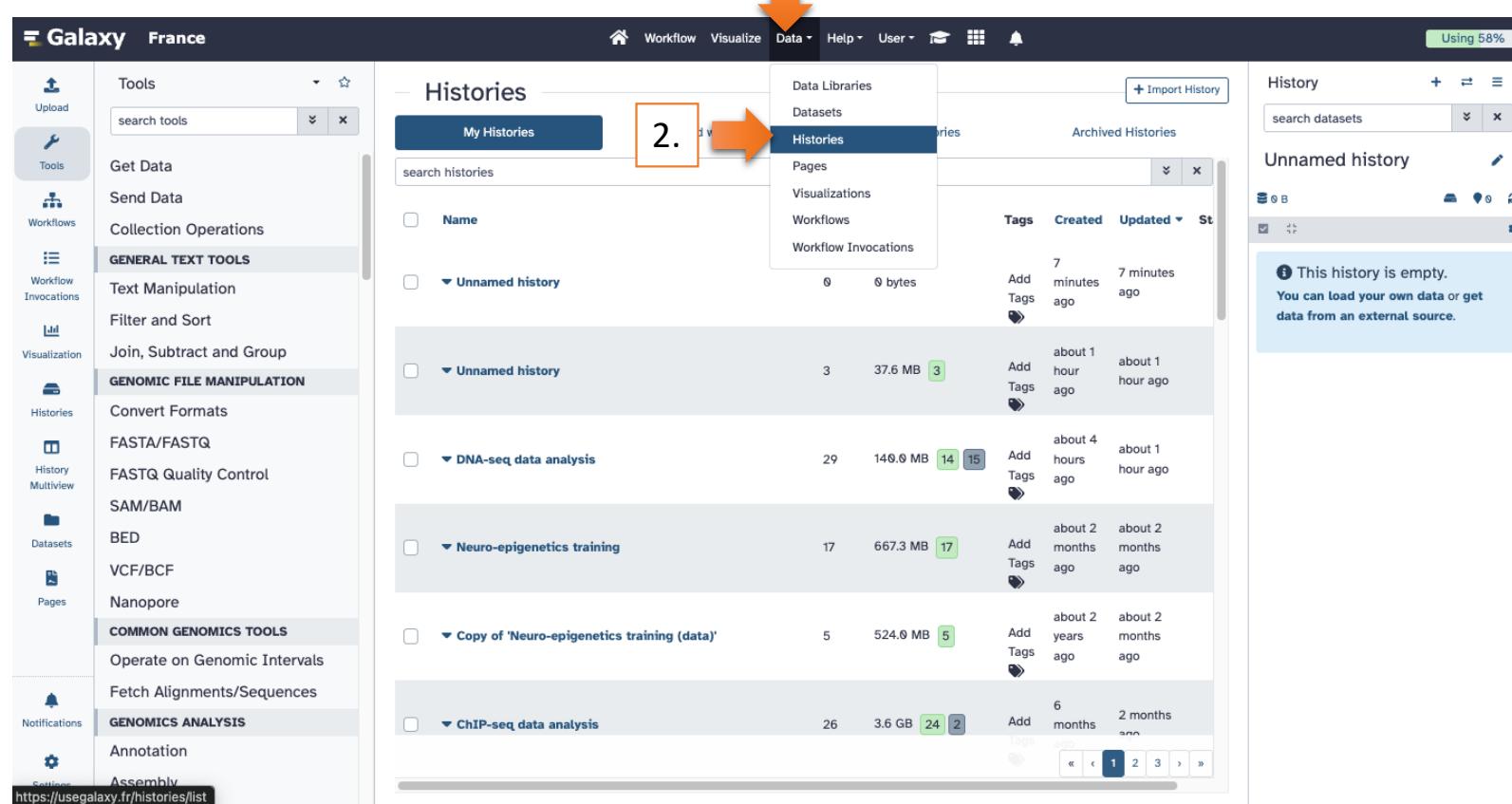
- 1. Select dataset**: An orange arrow points to the "DatasetSalmonella_metadata (1).csv" entry in the list of datasets.
- 2. Add selected dataset to history**: Another orange arrow points to the "Add to History" button in the top right corner of the main content area.

The interface includes a sidebar with various tools and a main content area displaying a list of datasets from a library. A history panel on the right shows an empty history named "Unnamed history".

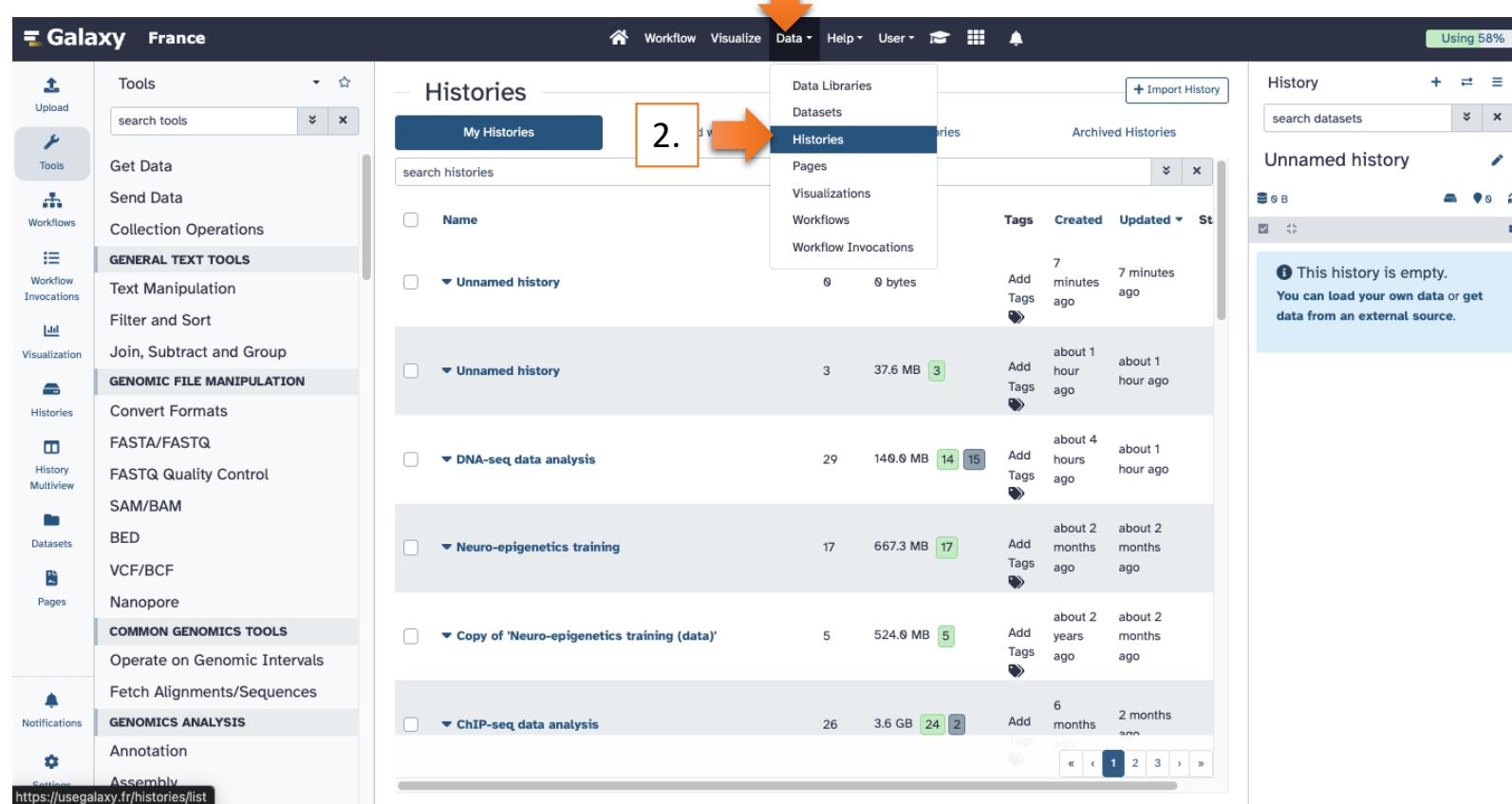
Name	Description
Assembly	Data for assembly
Comparative genomics	data for comparative genomics
Eukaryotic annotation	
Functional annotation	Protein sequence datasets
Polishing	Data for assembly polishing
Prokaryotic annotation	Data for prokaryotic annotation track
Prokaryotic assembly	Data for prokaryotic assembly
DatasetSalmonella_metadata (1).csv	uploaded txt file

Import shared data (Histories)

1.



2.



The screenshot shows the Galaxy web interface with the following details:

- Header:** Galaxy France, Workflow, Visualize, Data (highlighted with an orange arrow), Help, User, Settings, Using 58%.
- Left Sidebar:** Upload, Tools (selected), Get Data, Send Data, Workflows, Workflow Invocations, Visualization, Histories (selected), Datasets, Pages, Notifications, Settings.
- Middle Panel:** Histories (selected).
 - Submenu:** My Histories, search histories, Name, Unnamed history, DNA-seq data analysis, Neuro-epigenetics training, Copy of 'Neuro-epigenetics training (data)', ChIP-seq data analysis.
 - Table:** Shows history details: Name, Size, Number of datasets, Last modified, Created, Updated.
- Right Panel:** History (selected).
 - Submenu:** search datasets, Unnamed history.
 - Content:** This history is empty. You can load your own data or get data from an external source.

Import shared data (Histories)

The screenshot shows the Galaxy web interface with the title "Galaxy France". The left sidebar contains navigation links for Upload, Tools, Workflows, Workflow Invocations, Visualization, Histories, History Multiview, Datasets, Pages, Notifications, and Settings. The main content area is titled "Histories" and displays a list of histories. The list includes:

Name	Items	Size	Tags	Created	Updated
Unnamed history	0	0 bytes	Add Tags	7 minutes ago	7 minutes ago
Unnamed history	3	37.6 MB	[3]	about 1 hour ago	about 1 hour ago
DNA-seq data analysis	29	140.0 MB	[14] [15]	Add Tags	about 4 hours ago
Neuro-epigenetics training	17	667.3 MB	[17]	Add Tags	about 2 months ago
Copy of 'Neuro-epigenetics training (data)'	5	524.0 MB	[5]	Add Tags	about 2 years ago
CHIP-seq data analysis	26	3.6 GB	[24] [2]	Add Tags	6 months ago

There are three tabs at the top of the list: "My Histories" (selected), "Shared with Me", and "Public Histories". A "History" panel on the right shows an empty history named "Unnamed history" with a message: "This history is empty. You can load your own data or get data from an external source." The status bar at the bottom right indicates "Using 58%".

Import public data

The diagram illustrates the process of importing public data. It features two main interface screenshots: the Galaxy France web interface on the left and the UCSC Main Table Browser on the right.

Galaxy France Interface:

- Left sidebar:** Includes icons for Upload, Tools (selected), Workflows, Workflow Invocations, Visualization, Histories, and History Multiview.
- Top bar:** Shows the Galaxy logo and "France".
- Tools panel:** A search bar with "search tools" placeholder, a dropdown arrow, and a close button. Below it is a list of available tools:
 - NCBI Accession Download:** Download sequences from GenBank/RefSeq by accession through the NCBI ENTREZ API.
 - Download and Generate Pileup:** Format from NCBI SRA.
 - Get species occurrences data:** from GBIF, OBIS, ALA, iNAT and others.
 - BARIC Archive:** Toulouse and Rennes.
 - Upload File:** from your computer.
 - UCSC Main table browser**
 - UCSC Archaea table browser**
 - EBI SRA ENA SRA**

A vertical orange line with arrows points from the "Tools" section of the Galaxy interface to the "Table Browser" section of the UCSC interface.

UCSC Main Table Browser:

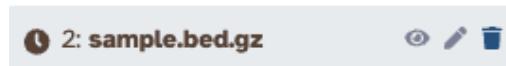
- Top navigation:** Genomes, Genome Browser, Tools, Mirrors, Downloads, My Data, Projects, Help, About Us.
- Section headers:** Table Browser, Using the Table Browser.
- Form fields:** clade: Mammal, genome: Mouse, assembly: Dec. 2011 (GRCm38/mm10), group: Variation and Repeats, track: RepeatMasker, table: rmask, data format description.
- Region selection:** Define region of interest, region: genome (radio button selected), position: chr12:56,694,976-56,714,605, lookup, define regions.
- Optional controls:** filter: create, intersection: create.
- Retrieval options:** Retrieve and display data, output format: BED - browser extensible data, Send output to: Galaxy, GREAT, output filename: mm39_rmask.fasta.gz, file type returned: plain text, gzip compressed.
- Help section:** Using the Table Browser, brief descriptions of controls.

**Hands
On**

Exercise 3

Datasets/Jobs in the History

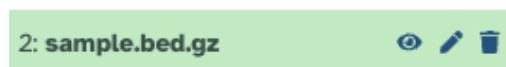
Grey: the job is waiting to run



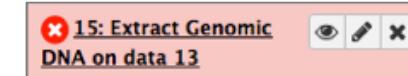
Orange: the job is running



Green: the job is successfully done



Red: the job encountered a problem



Datasets/Jobs in the History

The screenshot shows a dataset card for a file named "sample.bed.gz". The card has a green header and footer and a white central area. At the top right are icons for eye, edit, and delete. Below the header, there are three sections: "32,561 regions", "format bed, database mm9", and "uploaded bed file". The bottom section displays a table of genomic coordinates:

1.Chrom	2.Start	3.End	4.Name
chr1	193580486	193580686	chr1-193457322
chr1	64972363	64972563	chr1-64860165-
chr1	134238383	134238583	chr1-134169452
chr1	51991430	51991630	chr1-51879231-
chr1	53880739	53880939	chr1-53768540-

Annotations with orange arrows point to specific parts of the card:

- An arrow from the text "Number of lines in the file or size of the file" points to the "32,561 regions" text.
- An arrow from the text "Format" points to the "format bed, database mm9" text.
- An arrow from the text "If the dataset is a text file, the first lines of the file are displayed" points to the table below.
- An arrow from the text "Genome" points to the "chr1" entries in the table.

Datasets/Jobs in the History

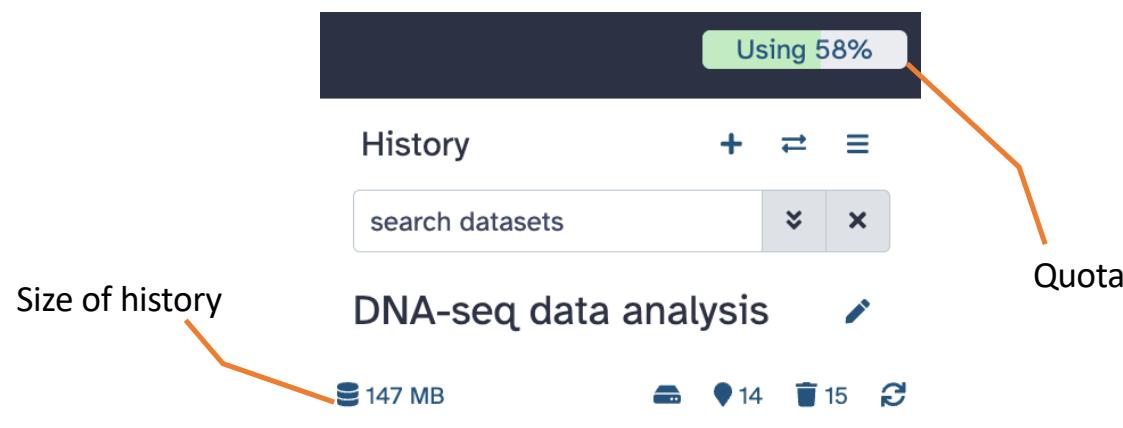
A screenshot of a Galaxy dataset history card for a file named "1: sample.bed.gz". The card has a green header and footer and a white central area. At the top right are icons for eye (View), edit, and delete. Below the header, the dataset name is shown, followed by "32,561 regions", "format bed, database mm9", and "uploaded bed file". A table below shows genomic coordinates:

1.Chrom	2.Start	3.End	4.Name
chr1	193580486	193580686	chr1-193457322
chr1	64972363	64972563	chr1-64860165-
chr1	134238383	134238583	chr1-134169452
chr1	51991430	51991630	chr1-51879231-
chr1	53880739	53880939	chr1-53768540-

Annotations with orange arrows point to various parts of the card:

- "View dataset (if possible) in the middle panel of Galaxy" points to the eye icon.
- "Download dataset" points to the download icon in the toolbar.
- "Edit attributes of the dataset (change name, format, genome, permission)" points to the edit icon.
- "Delete dataset" points to the delete icon.

Size of histories and quota



**Hands
On**

Exercise 4

Tool Panel / Run analyses

The screenshot shows the Galaxy France web interface. On the left, a vertical sidebar menu is displayed, with the 'Tools' icon highlighted. An orange arrow points from the text 'Show/hide Tool panel' to this icon. Another orange arrow points from the text 'Tool panel' to the 'Tools' icon. The main content area displays the 'Galaxy France' homepage, which includes the Galaxy logo, logos for elixir FRANCE, IFB, and INRAE, and a summary of Galaxy's features. To the right of the homepage is a 'History' panel titled 'Unnamed history', which is currently empty.

Show/hide Tool panel

Tool panel

Galaxy France

The homepage of the French Galaxy community

Galaxy is an open-source platform for FAIR data analysis that enables users to:

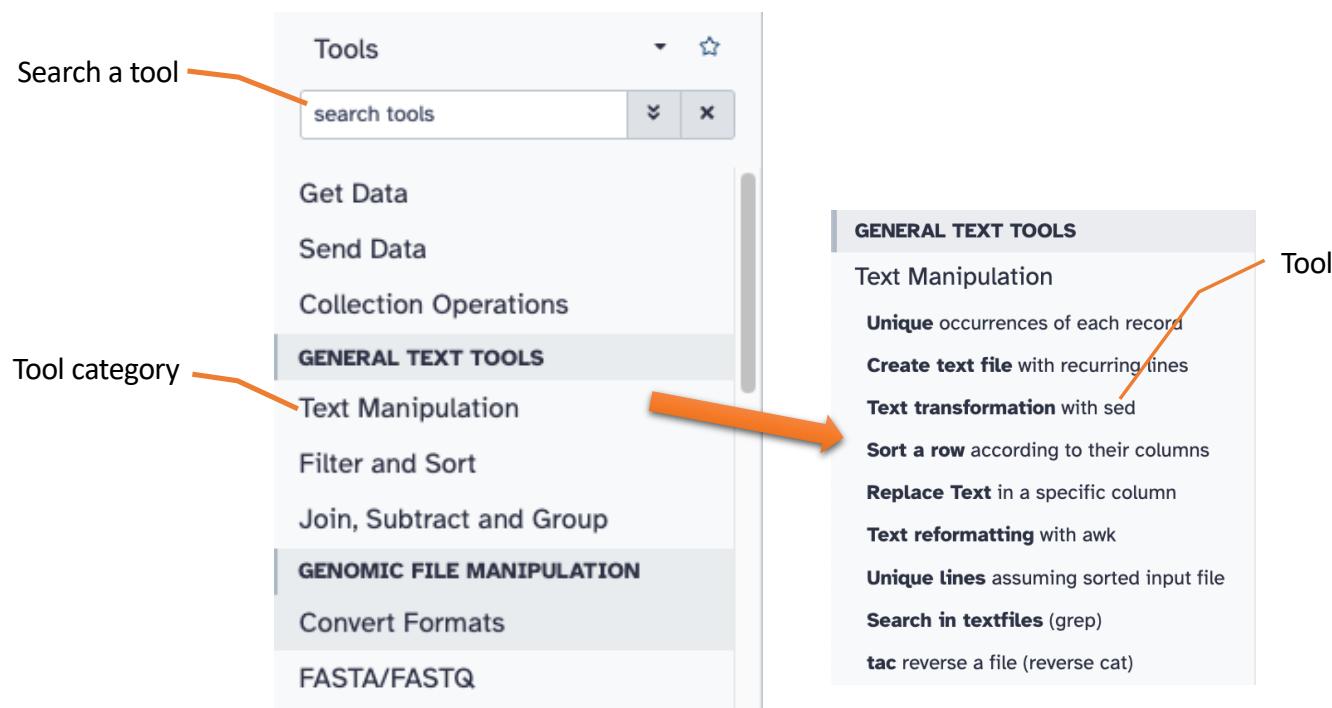
- use tools from various domains (that can be plugged into workflows) through its graphical web interface.
- run code in interactive environments (RStudio, Jupyter...) along with other tools or workflows.
- manage data by sharing and publishing results, workflows, and visualizations.
- ensure reproducibility by capturing the necessary information to repeat and understand data analyses.

The Galaxy Community is actively involved in helping the ecosystem improve and sharing scientific discoveries.

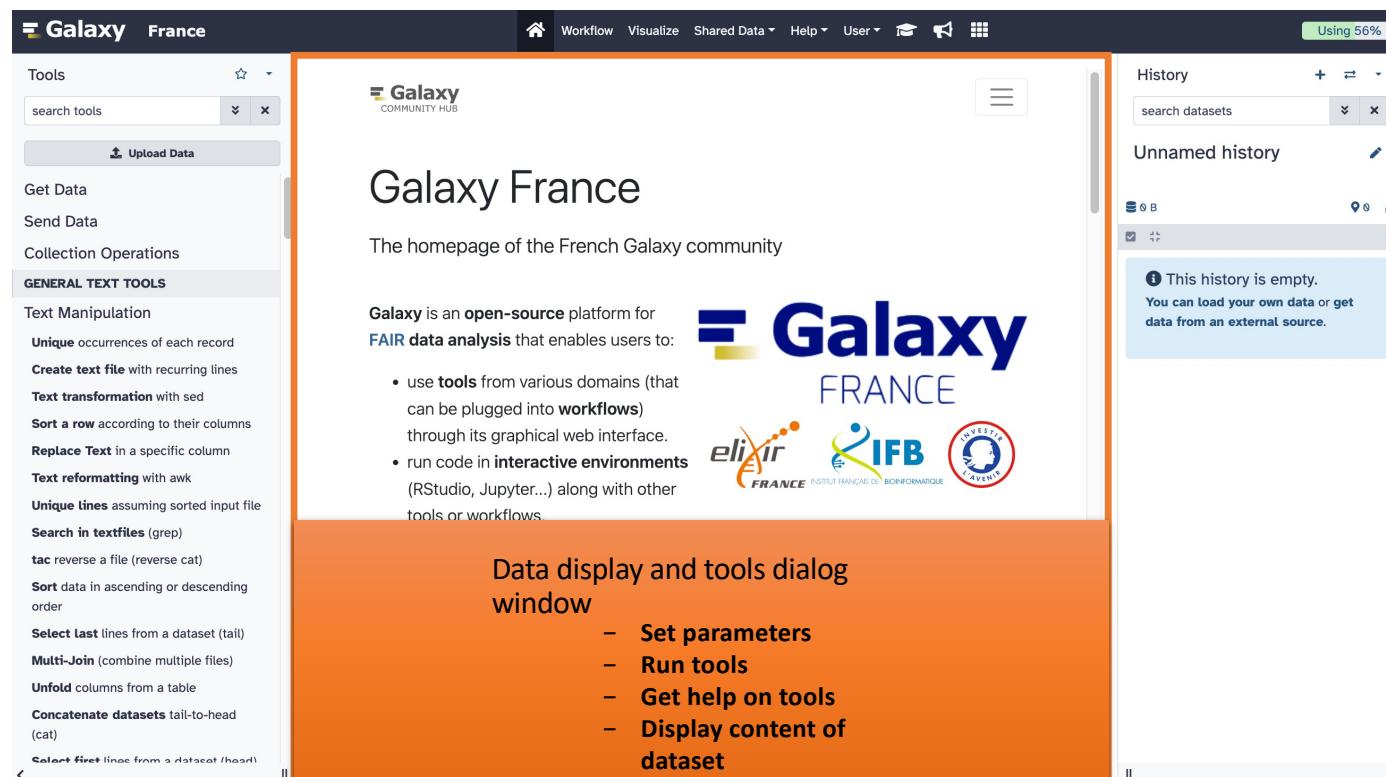
The French Galaxy server

The French Galaxy server <https://galaxy.ifr.fr> is maintained by IFR INNOC Cluster Task force. Please

Tool Panel / Run analyses



Tools dialog window



**Hands
On**

Exercise 5

**Hands
On**

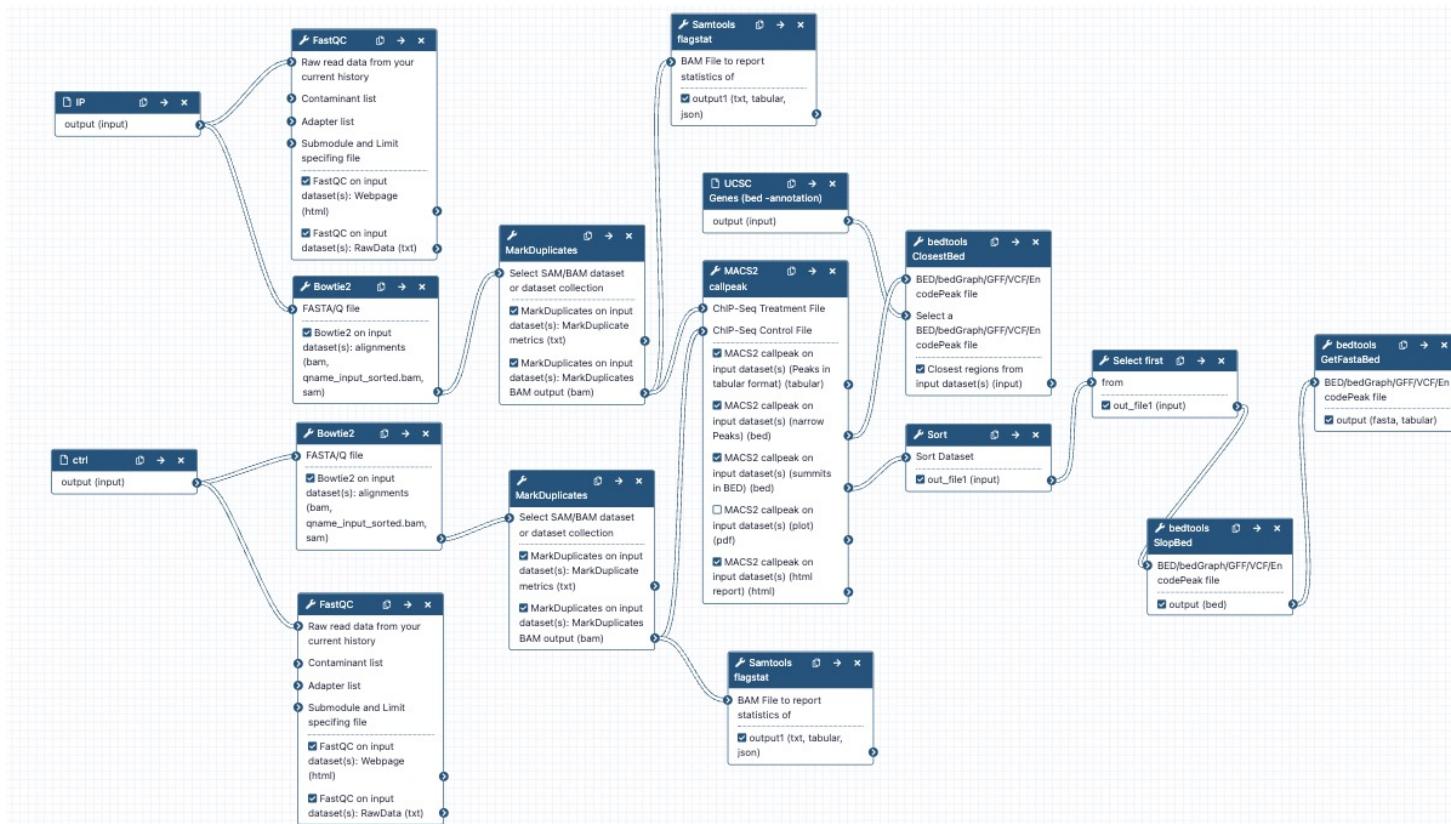
Exercise 6

Workflow

**Hands
On**

Exercise 7

Galaxy workflow



Galaxy workflows

- Workflow:
 - Analysis protocol with several steps (tools)
 - The output of a step is used as the input of the next so file formats between two steps should be compatible!
- Workflows are often made general so that they can be run on various datasets
- Some of the parameters are pre-defined while others are set at runtime

Workflows

The screenshot shows the Galaxy France homepage. The top navigation bar includes links for Home, Workflow (which is highlighted with an orange box), Visualize, Data, Help, User, and a search bar. The main content area features the Galaxy France logo and a brief introduction. On the left, a sidebar lists various tools and services: Upload, Tools, Workflows (which is also highlighted with an orange box), Workflow Invocations, Visualization, Histories, History Multiview, Datasets, Pages, Notifications, and Settings. The right side of the page displays a history panel titled 'History' with an empty dataset list and a message encouraging users to load their own data or get data from an external source. Logos for ELIXIR-FR, IFB, and INVESTISSE are visible at the bottom.

Galaxy France

The homepage of the French Galaxy community

Galaxy is an **open-source** platform for **FAIR** data analysis that enables users to:

- use **tools** from various domains (that can be plugged into **workflows**) through its graphical web interface.
- run code in **interactive environments** (RStudio, Jupyter...) along with other tools or workflows.
- manage data** by sharing and publishing results, workflows, and visualizations.
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The **Galaxy Community** is actively involved in helping the ecosystem improve and sharing scientific discoveries.

The French Galaxy server

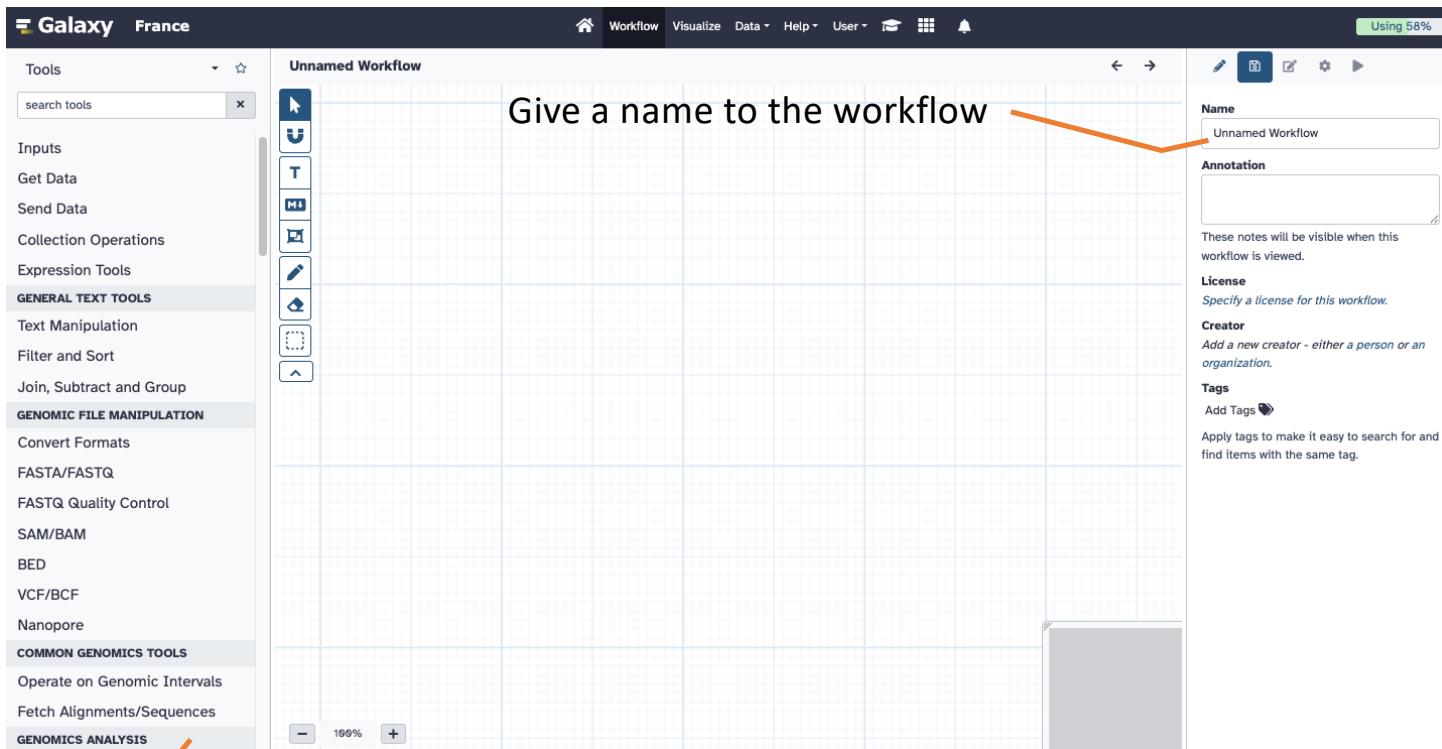
The French Galaxy server [UseGalaxy.fr](#) is maintained by **IFB** NNCR Cluster Task force. Please check our [Terms of Use](#) and [data retention policy](#) before using the server. We offer thousands of tools, increased quota on temporary basis, and compute infrastructure for trainers through Training Infrastructure as a Service (TaaS).

Workflows

The screenshot shows the Galaxy web interface with the following details:

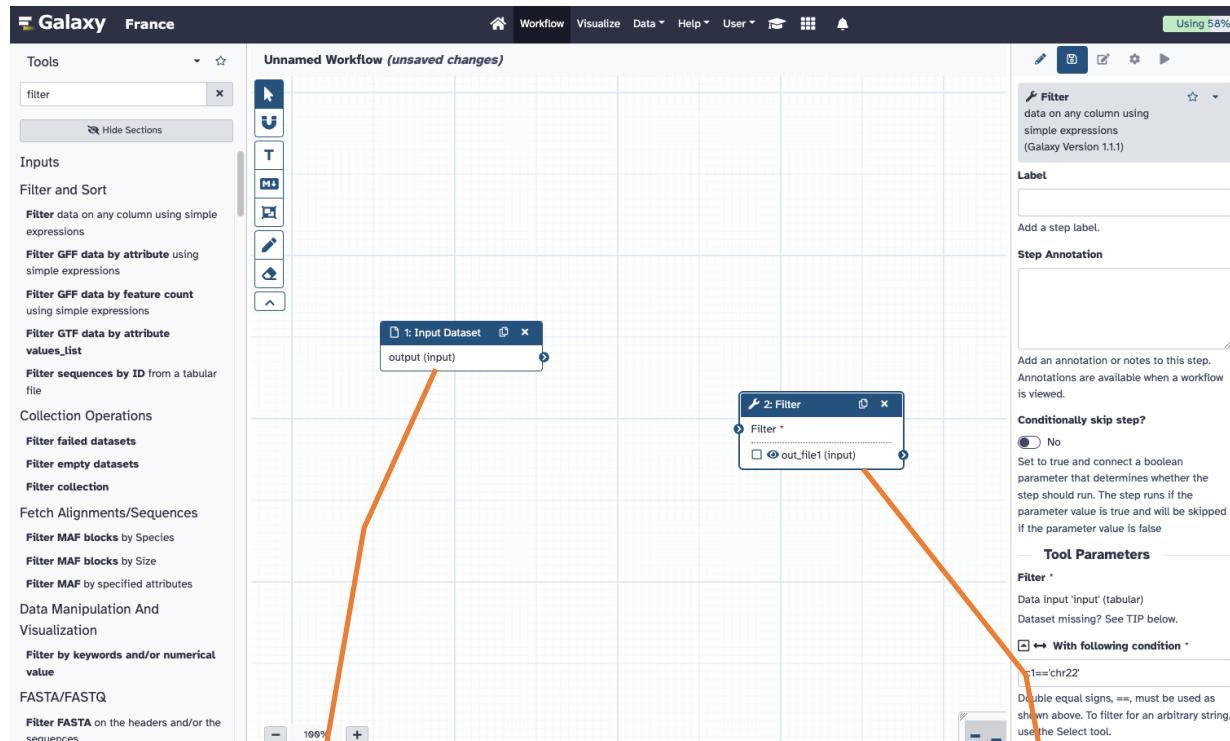
- Header:** Galaxy France, Workflow, Visualize, Data, Help, User, Import, Using 58%.
- Left Sidebar:** Upload, Tools, Workflows (selected), Workflow Invocations, Visualization, Histories, History Multiview, Datasets, Pages, Notifications, Settings.
- Main Content:** "Workflows" section.
 - My workflows:** DNA-seq data analysis (edited 43 minutes ago), ChIP-seq data analysis workflow (11 juin 2024) (edited 3 months ago), BED Ensembl to BED UCSC (edited over 1 year ago), BED Ensembl to BED UCSC (edited over 1 year ago), Run "Prepare RNA-seq data for seqMINER" (edited over 1 year ago).
 - Workflows shared with me:** DNA-seq data analysis (edited about 4 hours ago), DNA-seq workflow (edited 12 months ago).
 - Public workflows:** (empty)
- Right Sidebar:** History (search datasets, Unnamed history, This history is empty, You can load your own data or get data from an external source).
- Bottom Right:** Create workflows button (highlighted by a red box).

Workflow creation



Add tools or input datasets to the workflow

Workflow creation

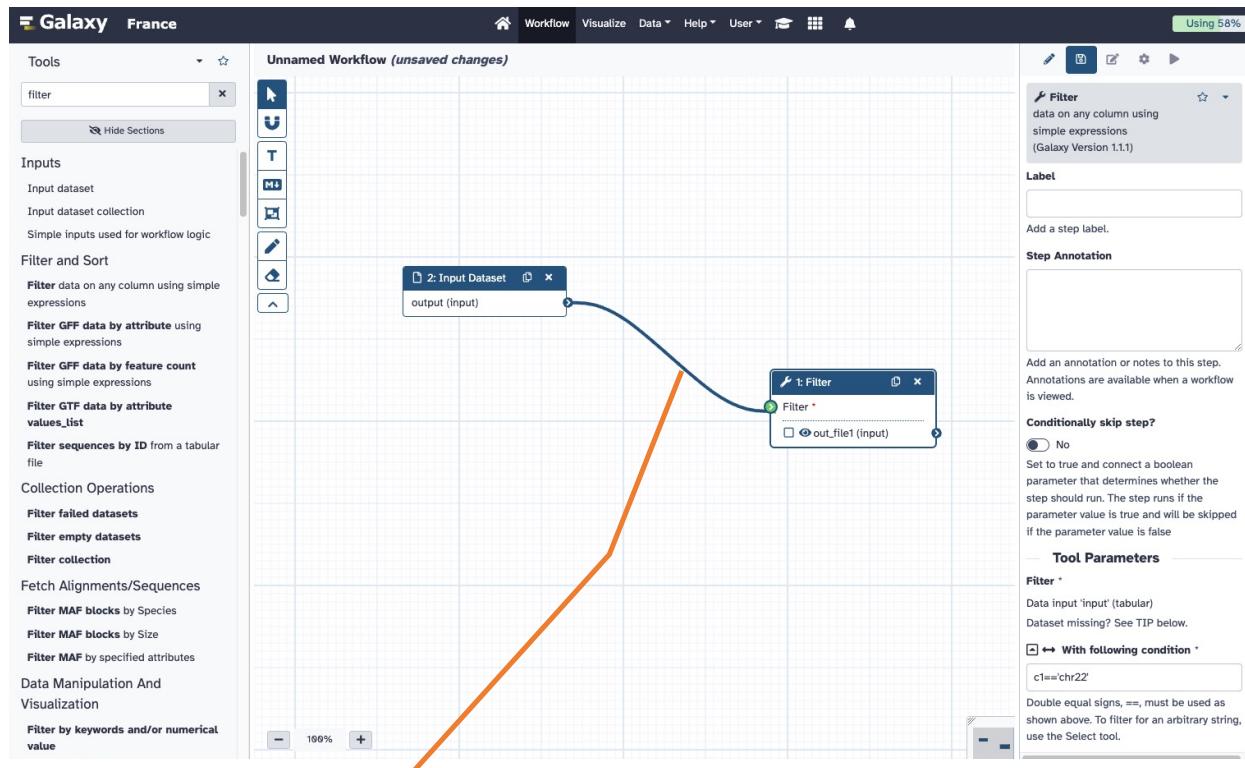


Input dataset.

Most of the time, a workflow starts with an input dataset to which analyses are applied. In Galaxy, the file format of the input dataset will be limited to the input file format of the subsequent step

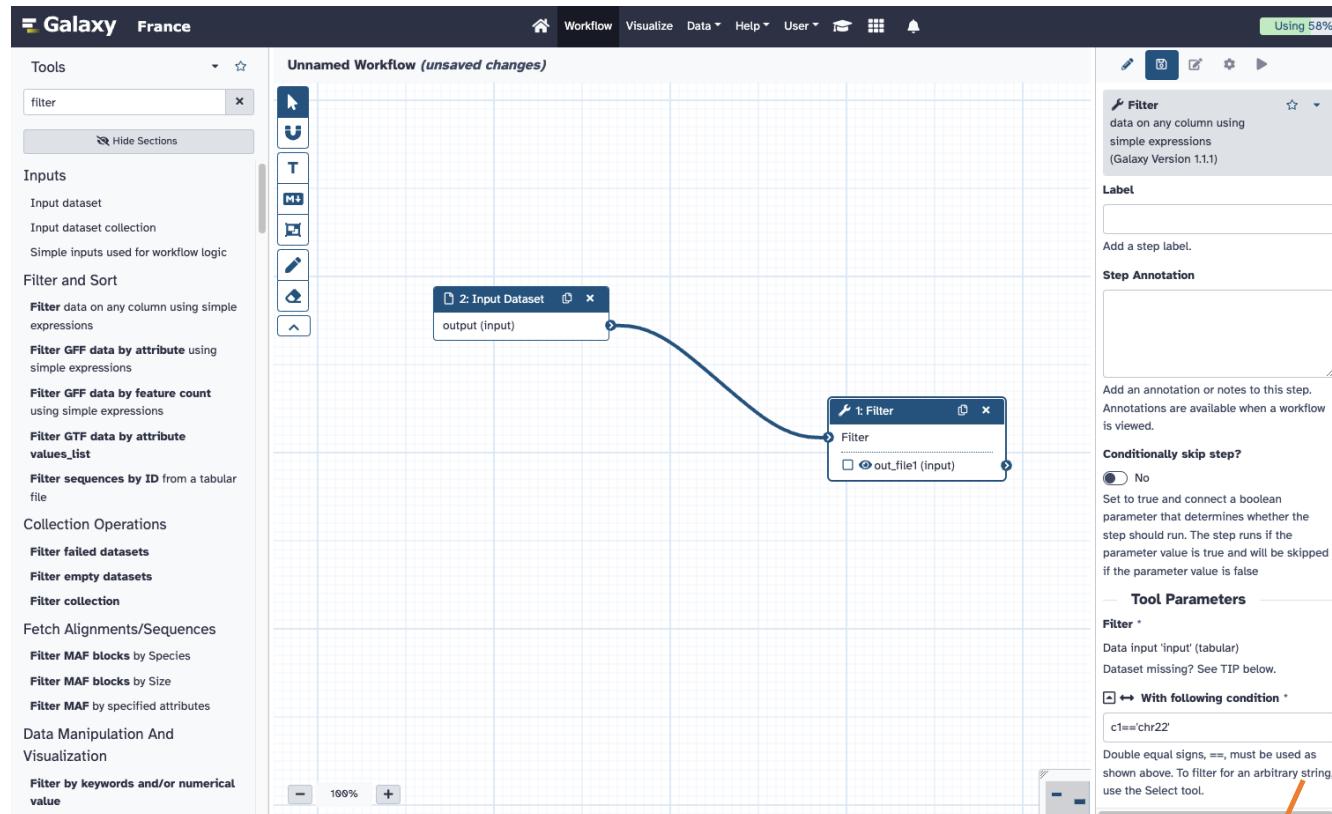
Tool to be run

Workflow creation

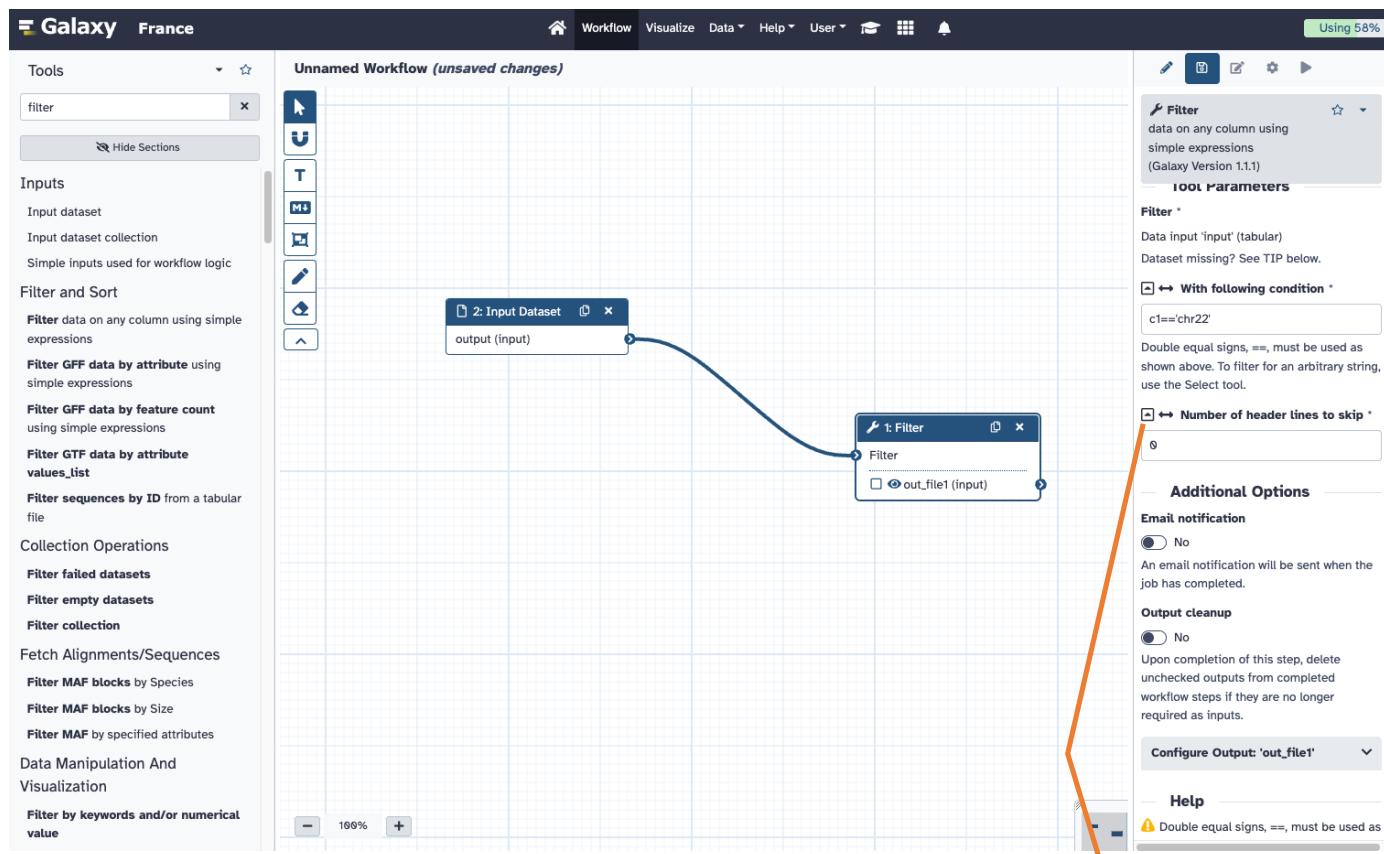


If two steps can be linked together,
the link between the two boxes is
green

Workflow creation

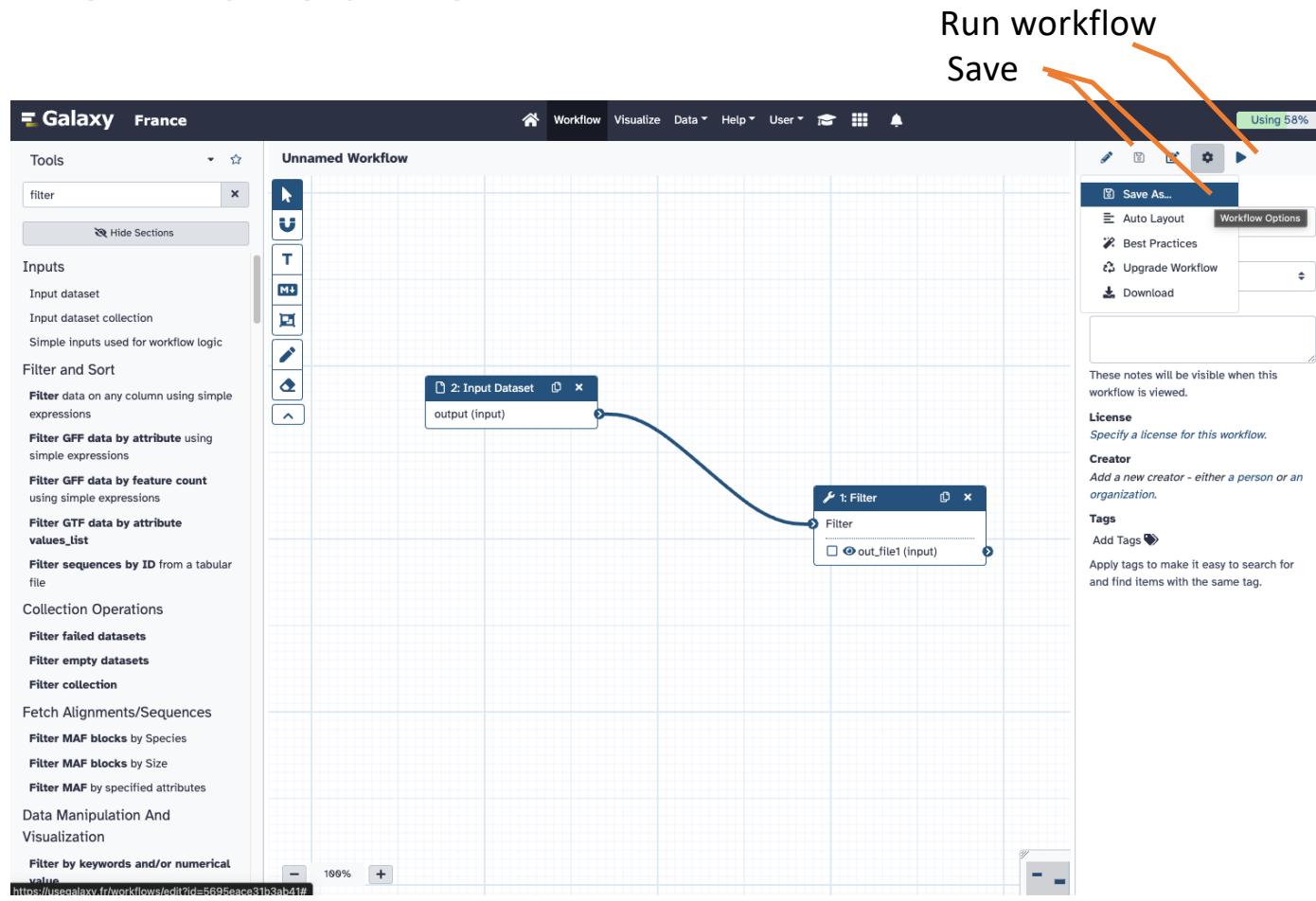


Workflow creation



Click to get the parameter to be set at runtime

Workflow creation



Run workflow

The screenshot shows the Galaxy web interface with two main panels. The top panel displays a list of workflows under the 'Workflows' tab. An orange arrow labeled '1.' points to the 'Workflow' tab in the top navigation bar. Another orange arrow labeled '2.' points to a specific workflow named 'DNA-seq data analysis'. The bottom panel shows the details of this workflow, titled 'Workflow: BED Ensembl to BED UCSC (version: 5)'. It includes a 'Run Workflow' button and a 'History Options' section. A third orange arrow labeled '3.' points to the 'Run Workflow' button. To the right of the bottom panel, three callout boxes provide instructions:

- 3. Run workflow**
- 1. Set input file(s).
Found in current history!**
- 2. Set parameters**

The 'History' sidebar on the right shows an empty history with a message: 'This history is empty. You can load your own data or get data from an external source.'

**Hands
On**

Exercise 8

**Hands
On**

Exercise 9

Privacy

- By default datasets, workflows, histories are private to the user that generated/uploaded them.
- They can be shared across Galaxy users (of the same Galaxy instance) or via links