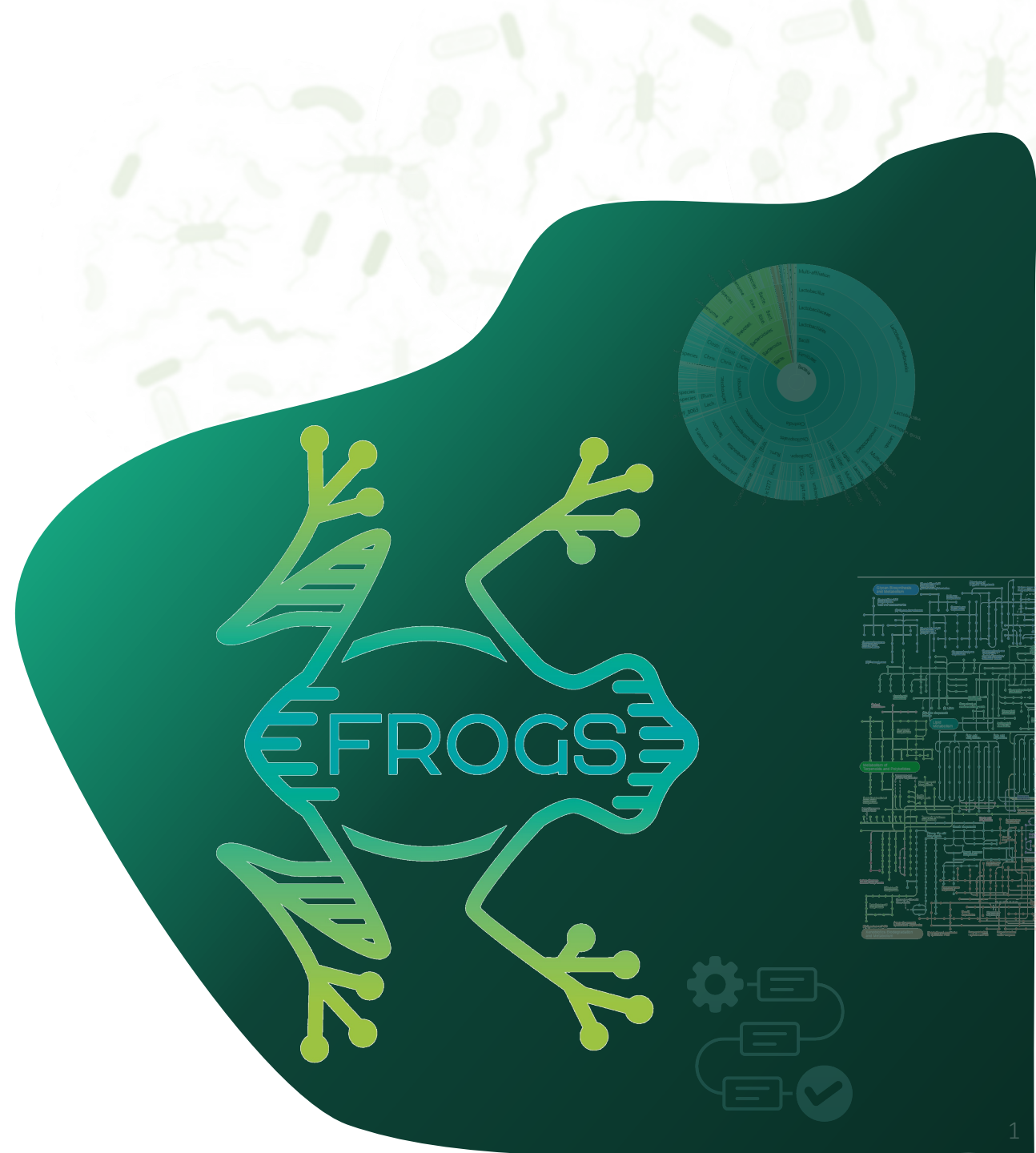


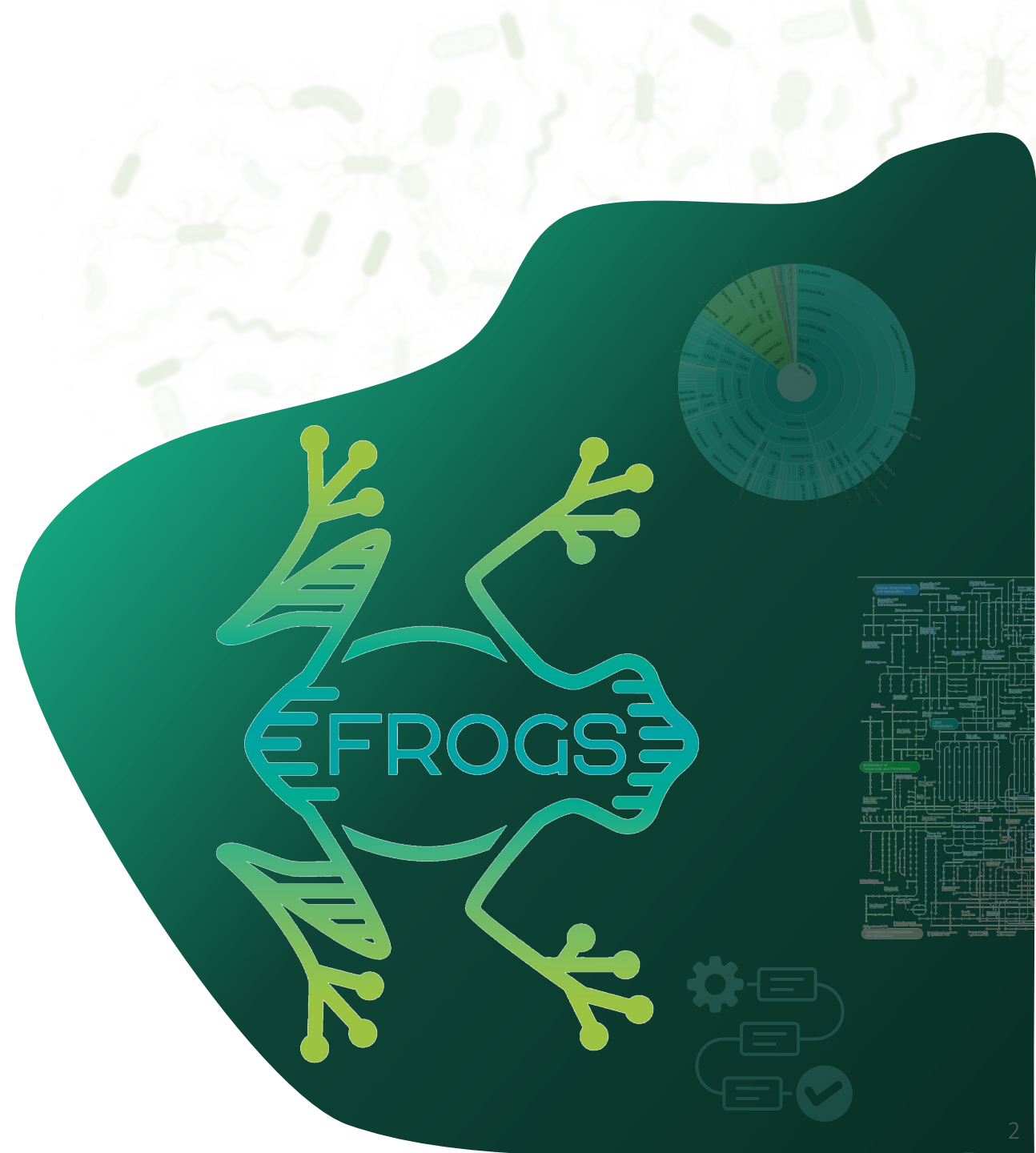
Get Started with Galaxy

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Maëlle POMIÈS & Olivier RUÉ



Get Started with Galaxy

Overview of the Galaxy platform



Overview of the Galaxy platform

FROGS is hosted on the **Galaxy platform**, an open-source web environment designed to make bioinformatics analysis **accessible, transparent, and reproducible**. Originally developed at Penn State University, Johns Hopkins University, Oregon Health & Science University, and the Cleveland Clinic, Galaxy has grown thanks to substantial contributions from an active international community.

As a web-based platform, Galaxy allows users to perform complex analyses without installing any software or writing code. Its versatile workflows make it easy to combine and reproduce tools for different sequencing projects.

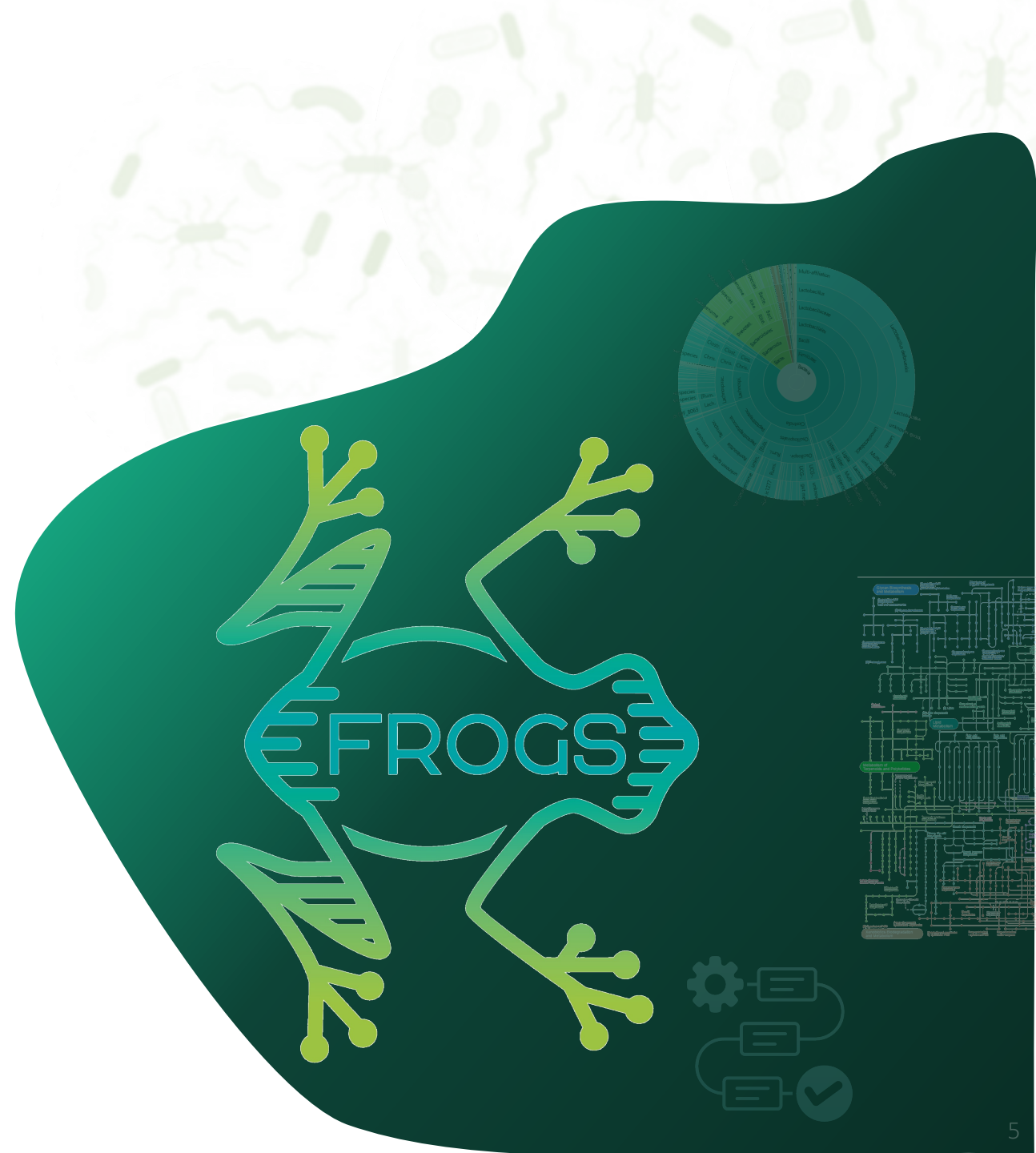
Overview of the Galaxy platform

- **Accessibility:** Users with no programming experience can easily upload or retrieve data, run workflows like FROGS, and visualize results directly in their browser.
- **Reproducibility:** Galaxy automatically records all parameters and inputs, so any analysis can be fully understood, reviewed, or repeated by others.
- **Transparency:** Users can share or publish their entire analyses — including histories, workflows, and visualizations — or even create Galaxy “Pages” to document methods for publications.

Together, these features make Galaxy an ideal platform for deploying FROGS and ensuring that every analysis is both reliable and shareable.

Get Started with Galaxy

Accessing the platform

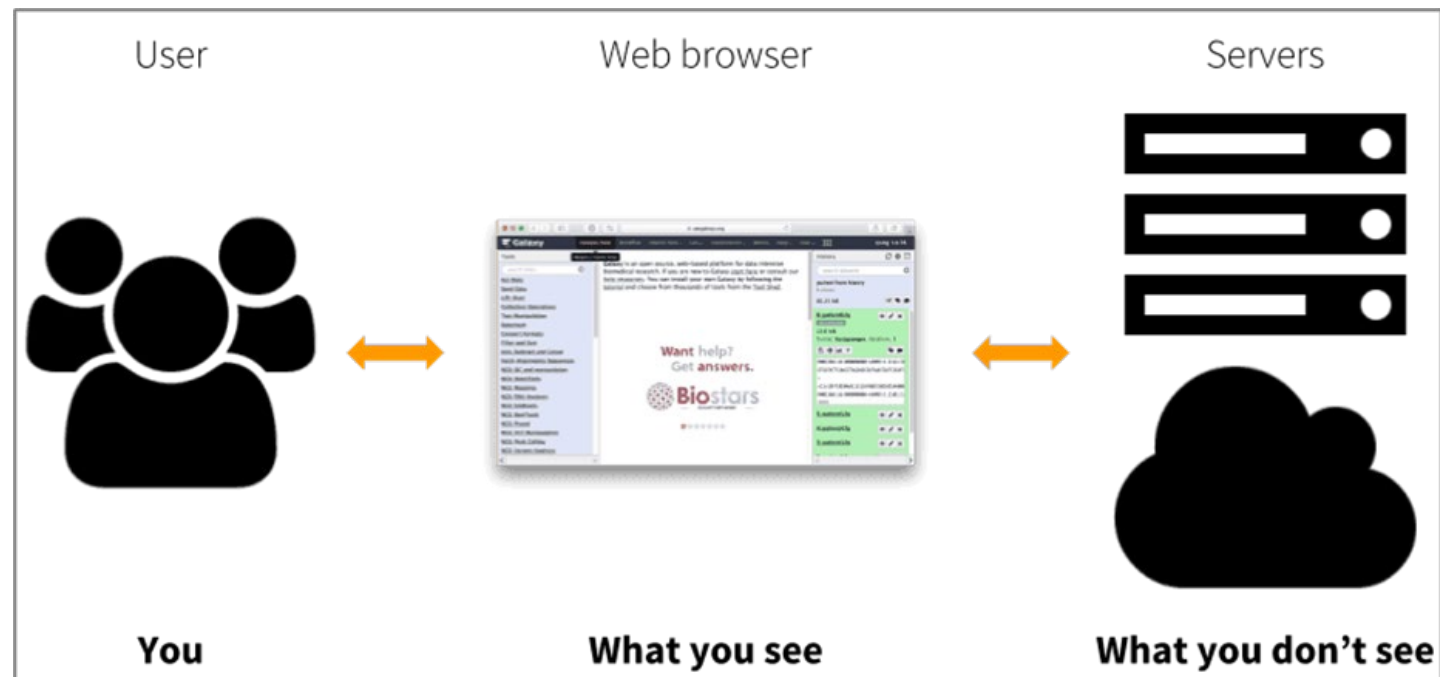


Accessing the platform

When using FROGS on the Galaxy platform, nothing runs on your own computer.

All computations are executed on remote servers, so your computer is only used to access the web interface.

This means you can run analyses without worrying about your computer's power or operating system — you only need a web browser and an internet connection.



FROGS is hosted on three main partner platforms

- Genotoul Bioinfo/Sigenae (INRAE Toulouse) <https://vm-galaxy-prod.toulouse.inrae.fr>
- Migale (INRAE Jouy-en-Josas) <https://galaxy.migale.inra.fr>
- IFB Core (French Bioinformatics Institute) <https://metabarcoding.usegalaxy.fr>

⚠ Important

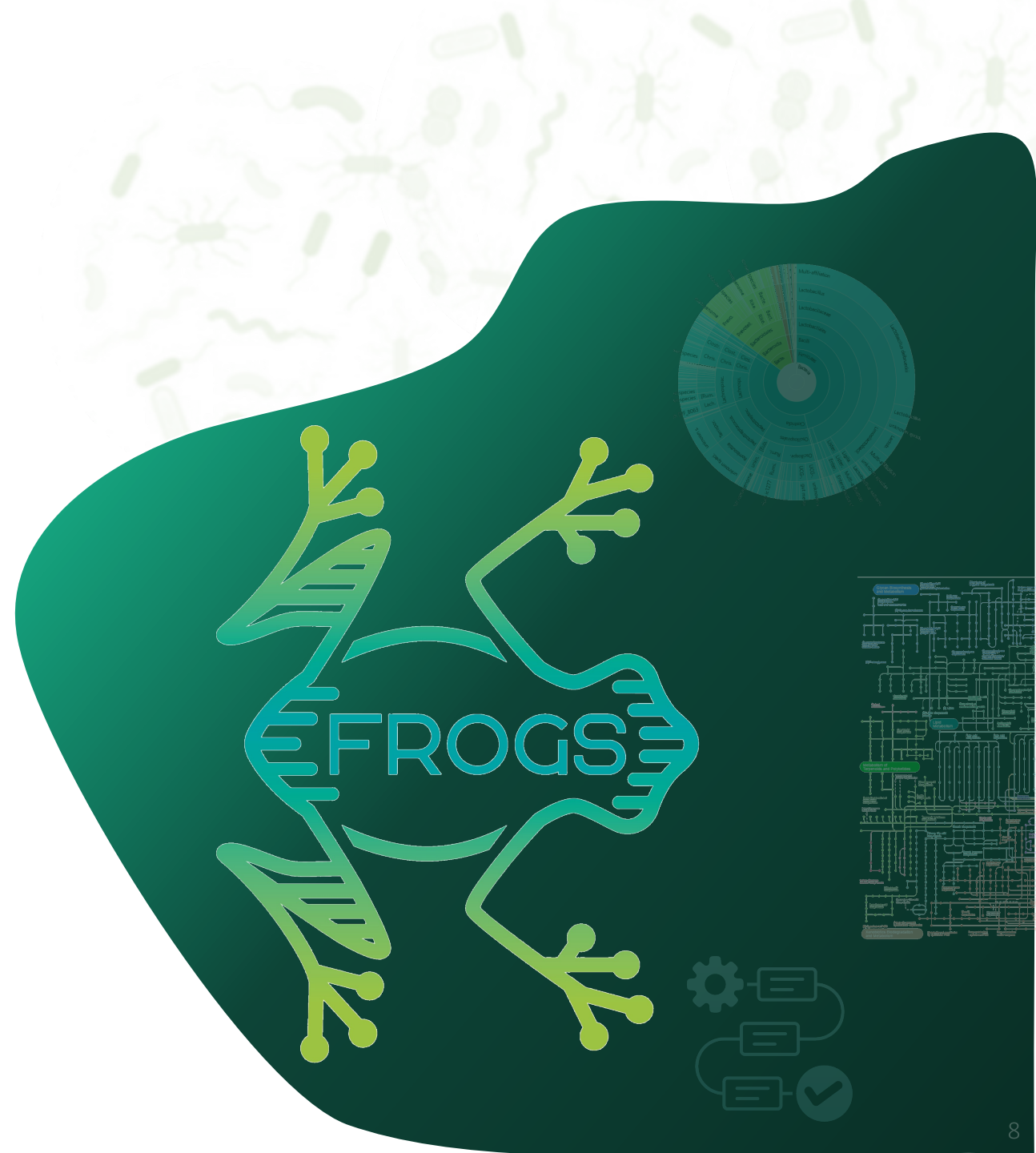
Each Galaxy platform operates **independently**. FROGS is available on several Galaxy instances but these **platforms are not connected to each other**.

This means that:

- Your data are stored only on the platform you are using and are **not shared with other Galaxy servers**.
- Tools and workflows may **differ slightly between platforms**; some tools available on one FROGS Galaxy instance may not exist elsewhere.
- Each instance relies on its own computing cluster, so **job performance and storage capacity can vary** from one platform to another.

Get Started with Galaxy

The Galaxy Interface



The Galaxy Interface Layout

The Galaxy web interface is divided into **four main panels**, each with a distinct role.

The screenshot displays the Galaxy web interface with four main panels highlighted by green callouts:

- The activity bar:** Located on the left, it contains navigation links for Upload, Tools, Multiview, Datasets, and Admin.
- The tool panel:** Located in the upper left, it shows a search bar and a list of tools under the heading "Tools".
- The central panel:** The main workspace, currently displaying the "FROGS-5 Core dev ASV reconstruction and taxonomic annotation" tool parameters.
- The History panel:** Located on the right, it shows a list of recent jobs and datasets, including "Test 1.b Géraldine" and "59: FROGS-5 Core dev".

The Galaxy Interface Layout

The Activity Bar

The activity bar enhances the user experience by providing quick access to essential Galaxy features: you can **upload files**, open **tools** and **workflows**, or switch between your **histories** and ongoing analyses.

The screenshot shows the Galaxy web interface. On the left is the 'The activity bar' (a vertical sidebar) containing icons for Upload, Tools, Multiview, Datasets, More, and Admin. The main area is divided into three panels: 'The tool panel' (left, showing a list of tools like 'FROGS-5 Core dev ASV reconstruction and taxonomic annotation'), 'The central panel' (middle, showing the configuration for the selected tool, including input type and sample information), and 'The History panel' (right, showing a list of recent workflows and datasets). The interface is titled 'Galaxy' at the top left and 'Using 1.7 GB' at the top right.

The Galaxy Interface Layout

The screenshot shows the Galaxy web interface. On the left is the 'activity bar' with icons for Upload, Tools, Multiview, Datasets, More, and Admin. The 'Tools' panel is open, showing a search bar and a list of tool categories: Get Data, Send Data, Collection Operations, Lift-Over, Text Manipulation, Operate on Genomic Intervals, Statistics, Graph/Display Data, Phenotype Association, and FROGS_dev. The 'FROGS-5 Core dev' tool is selected, showing its description and input options. The central panel displays the tool's configuration, including input type, sample files, and samples. The right panel shows the 'History' of previous tool runs.

The activity bar

The tool panel

The central panel

The History panel

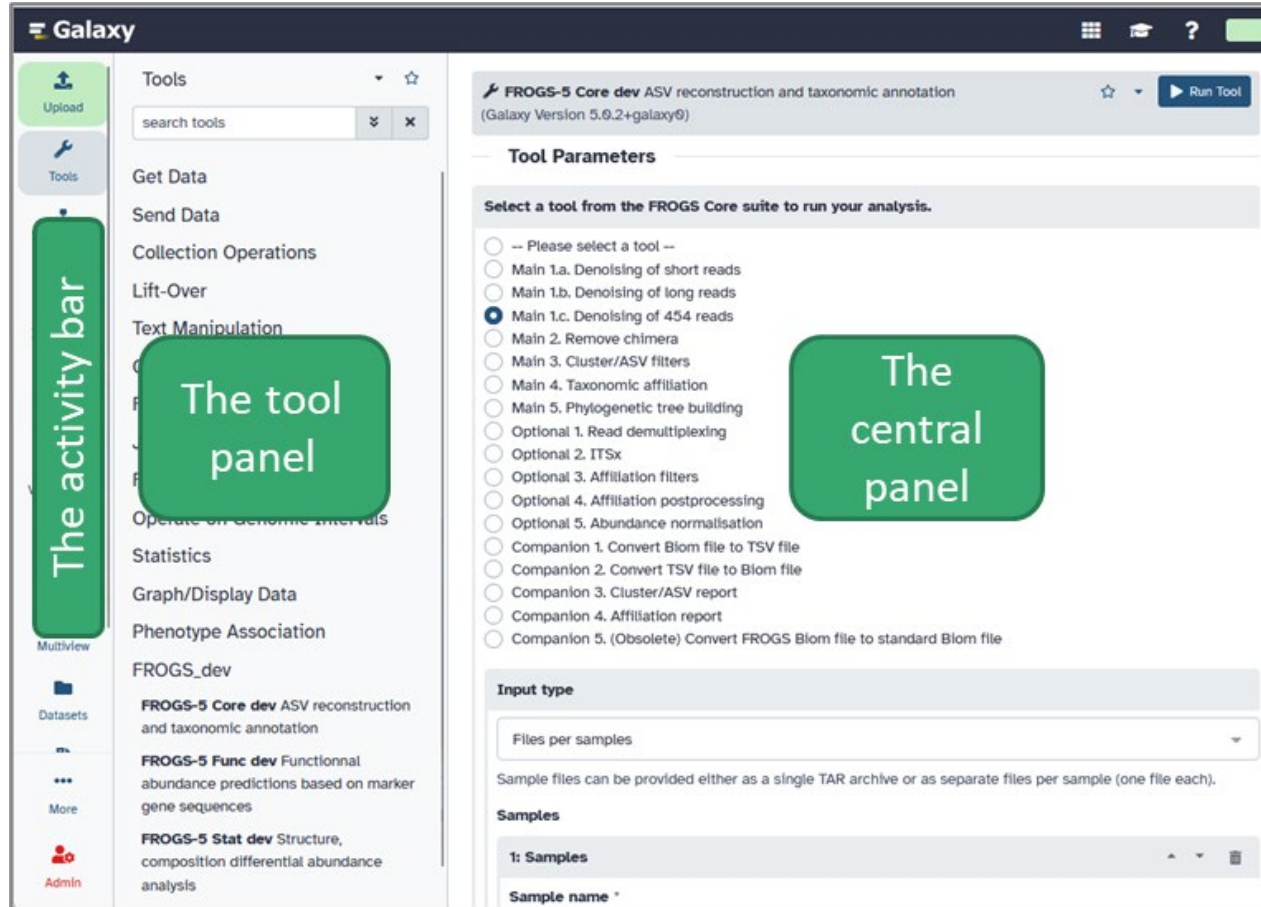
The Tools Panel

This panel lists all the **available tools** on your Galaxy platform. Tools are organized into categories (for example: *FASTQ Quality Control*, *FROGS Core*, *Qiime*, etc.).

When you click on a tool's name, its description and parameter options appear in the central panel.

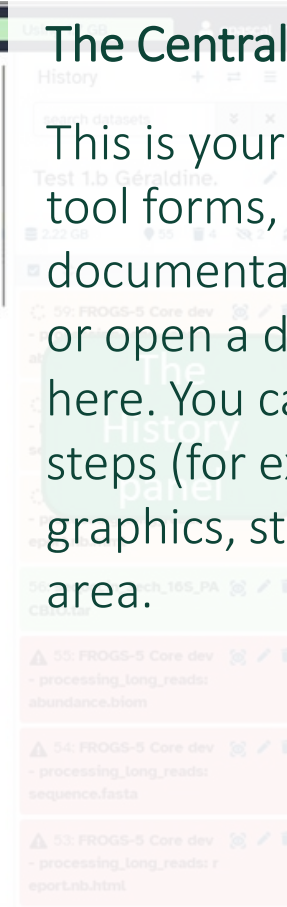
Tip: Use the search bar at the top of the Tools panel to quickly find any tool by name or keyword.

The Galaxy Interface Layout

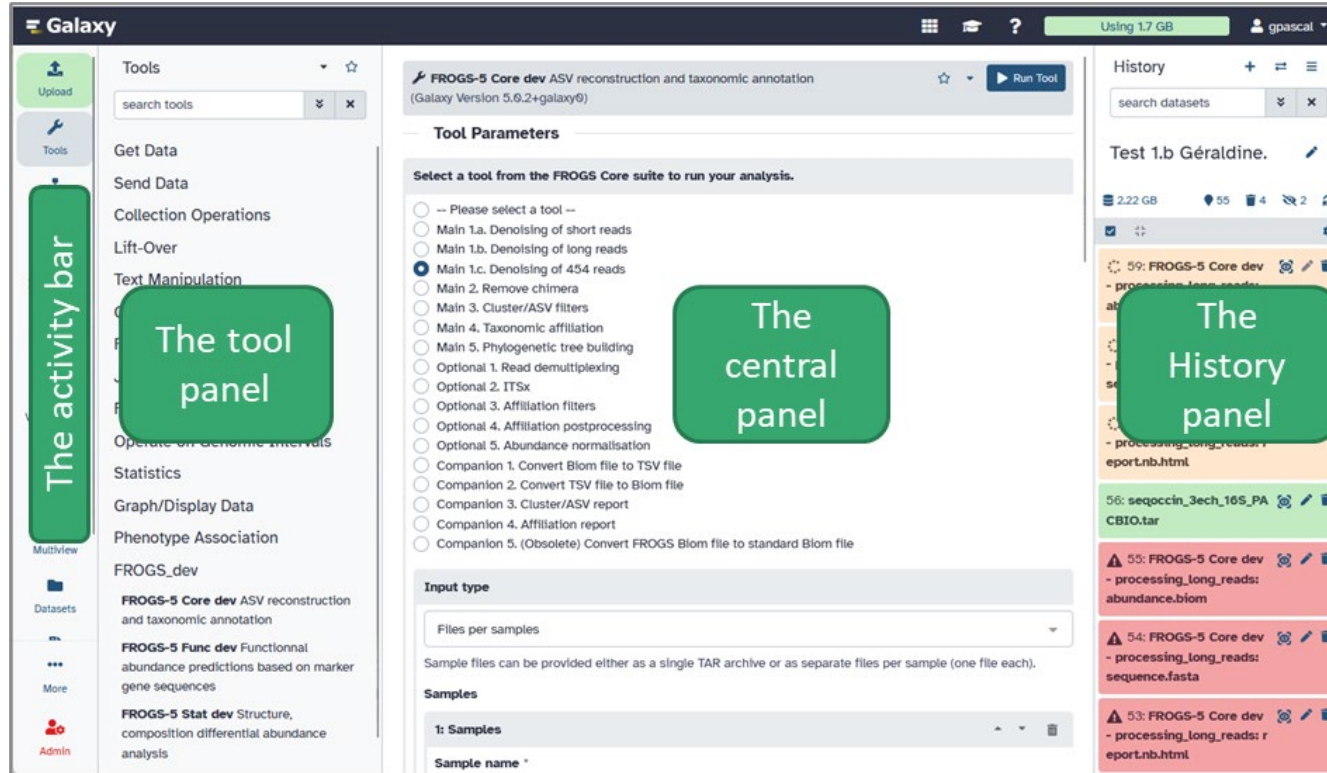


The Central Panel (in the middle)

This is your **main working area**. It displays tool forms, results, visualizations, and documentation. Whenever you launch a tool or open a dataset, the details are shown here. You can also view the output of FROGS steps (for example, abundance tables, graphics, statistics report) directly in this area.



The Galaxy Interface Layout



The History Panel (on the right)

The History panel keeps track of all your **datasets, analyses, and results**. Each time you run a tool, its output appears here as a new dataset — color-coded to show its status:

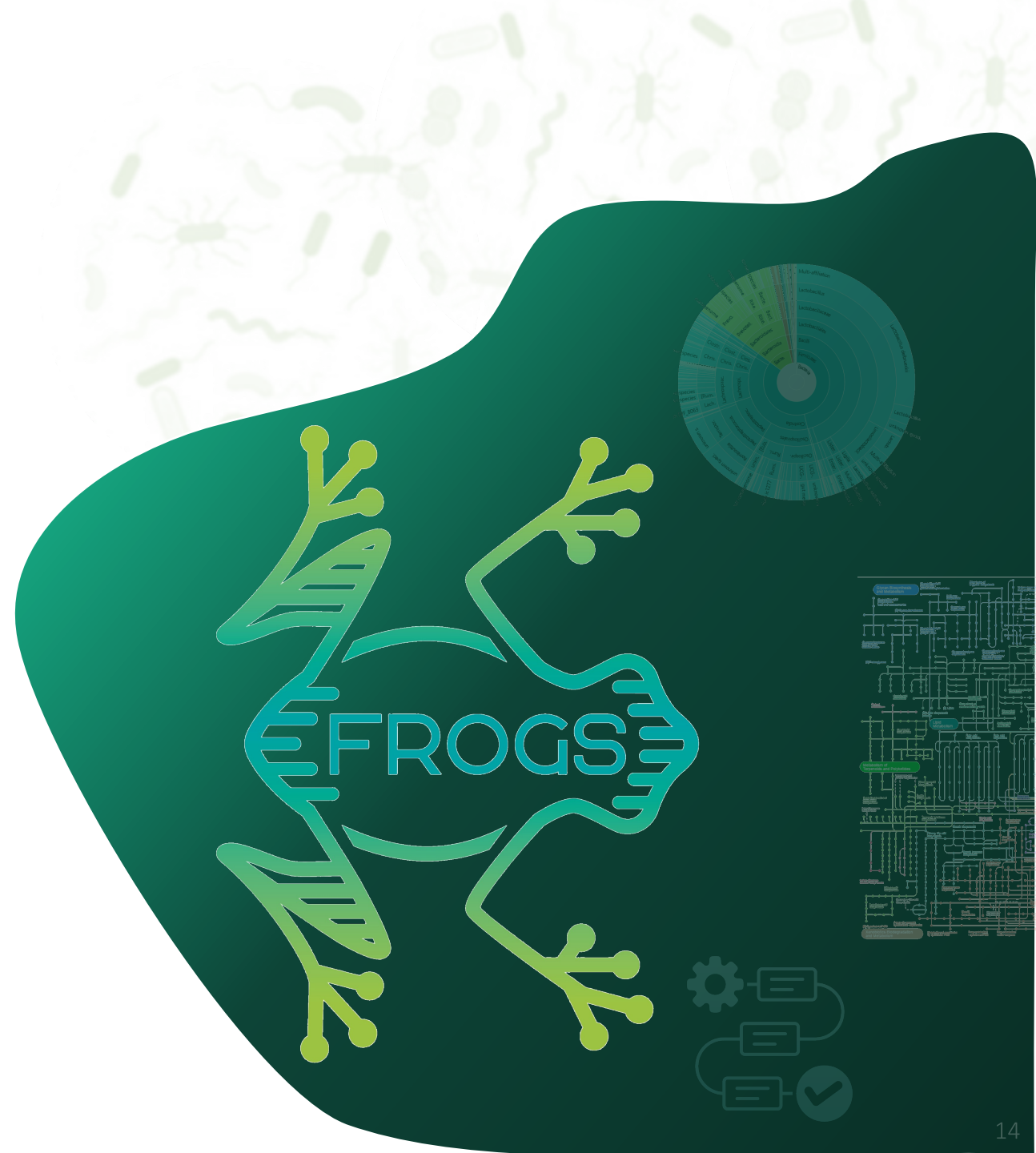
-  Grey = waiting for server response
-  Orange = running
-  Green = finished successfully
-  Red = failed

Histories are **automatically saved** and can be renamed, shared, duplicated, or downloaded.

Tip: You can click on a dataset name to view details or click the eye icon to preview its content.

Get Started with Galaxy

Create a *.tar* archive with your data



Why package your data into a .tar archive?

Uploading files one by one is slow, tedious, and error-prone.

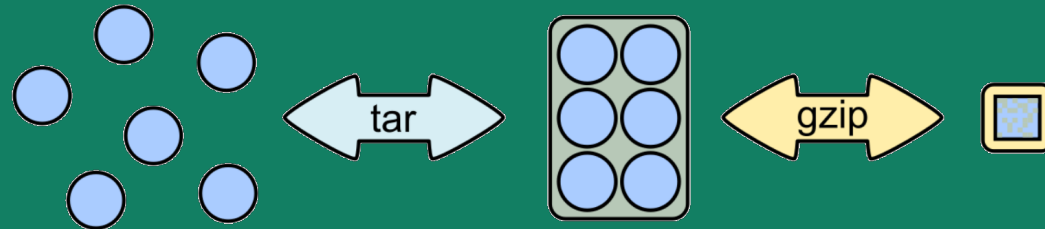
A better solution is to bundle your files into a single tar archive.

This makes the upload faster, cleaner, and much less likely to fail.

What is a .tar.gz file?

.tar bundles multiple files and folders in a single package

.gz compresses that package to reduce its size (effective if .fastq are not compressed)



How to package your data into a .tar archive?

Several solutions exists:

- without command lines: 7-zip (Windows only)
- with command lines: for macOS, Unix (or Windows with mobaXterm)

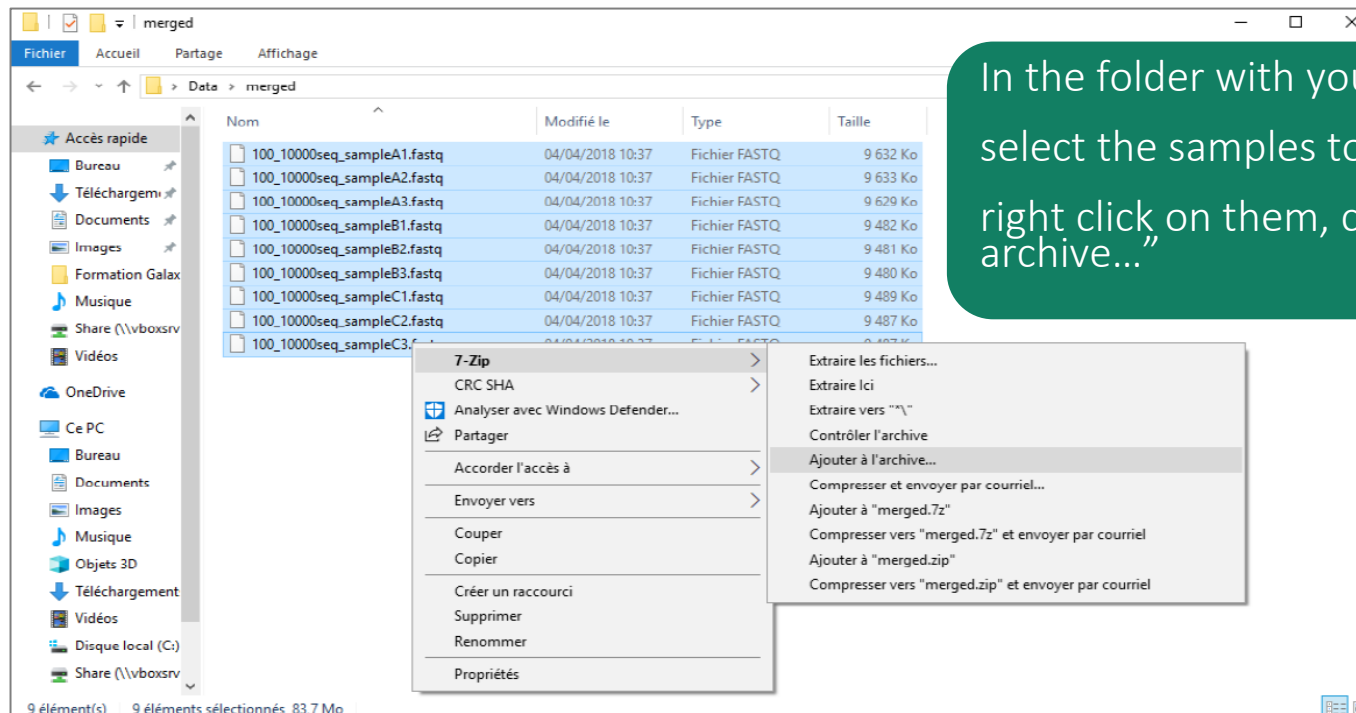
Create a tar file with 7-Zip (Windows)



7-ZIP is an open-source file archiver which can archive and compress files.

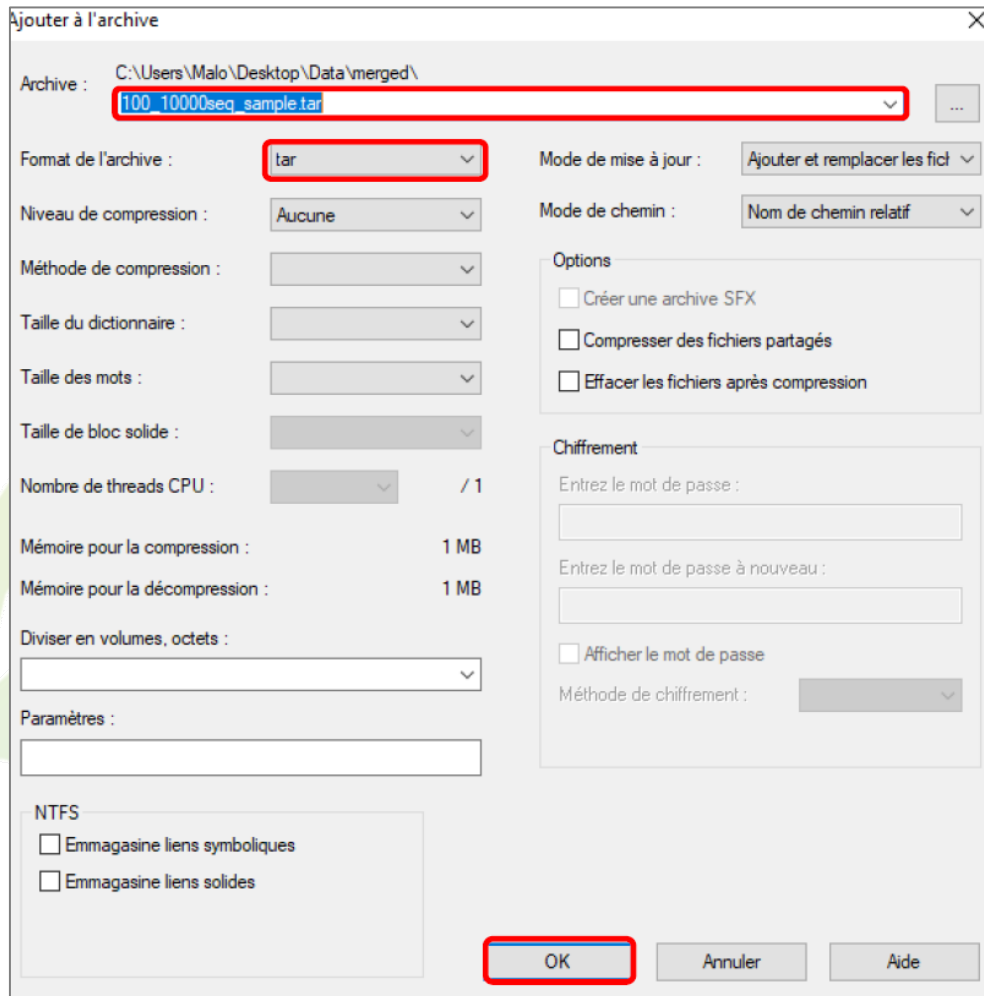
You can download it at: <https://www.7-zip.org/>

After installation, 7-Zip appears in the right-click context menu on files :



In the folder with your data,
select the samples to bundle
right click on them, choose 7-Zip, “add to
archive...”

Create a tar file with 7-Zip (Windows)



Choose a name for your archive (ending with .tar)

Choose “tar” as archive format

Click on OK

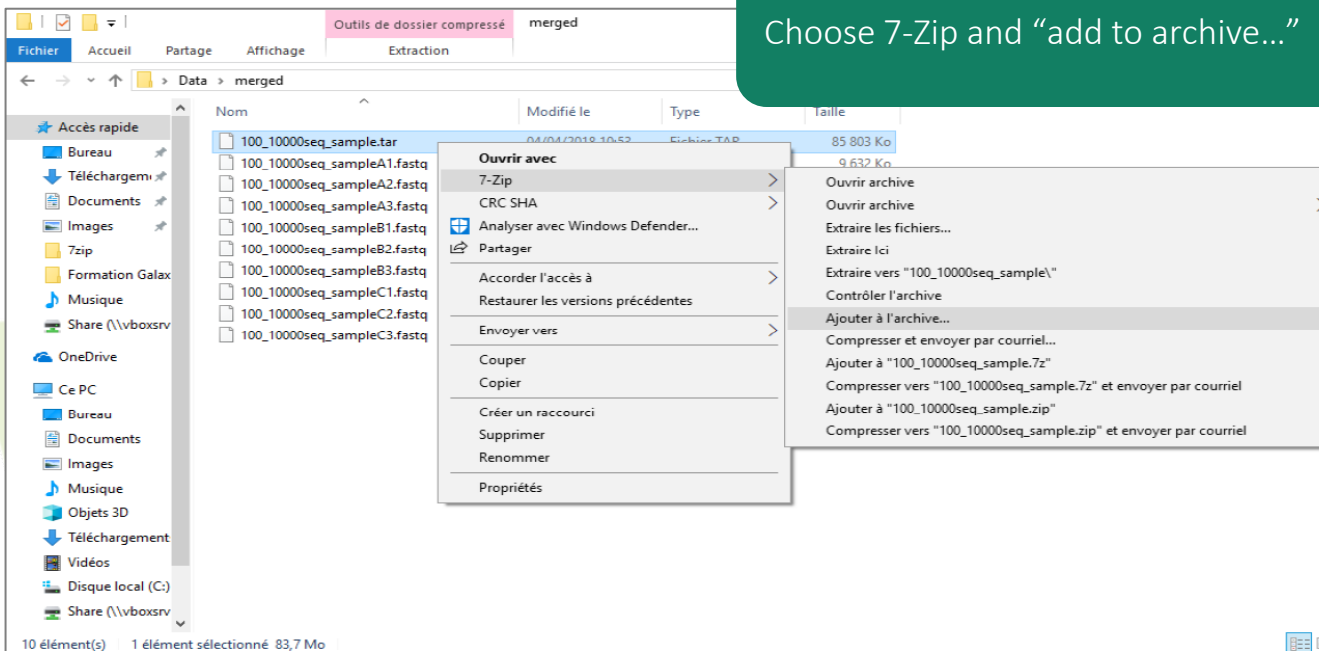
It creates a .tar archive which is not compressed.

If it needs to be compressed
(if the .fastq files were not already compressed in
.fastq.gz format) it is required to compress it in a
second step

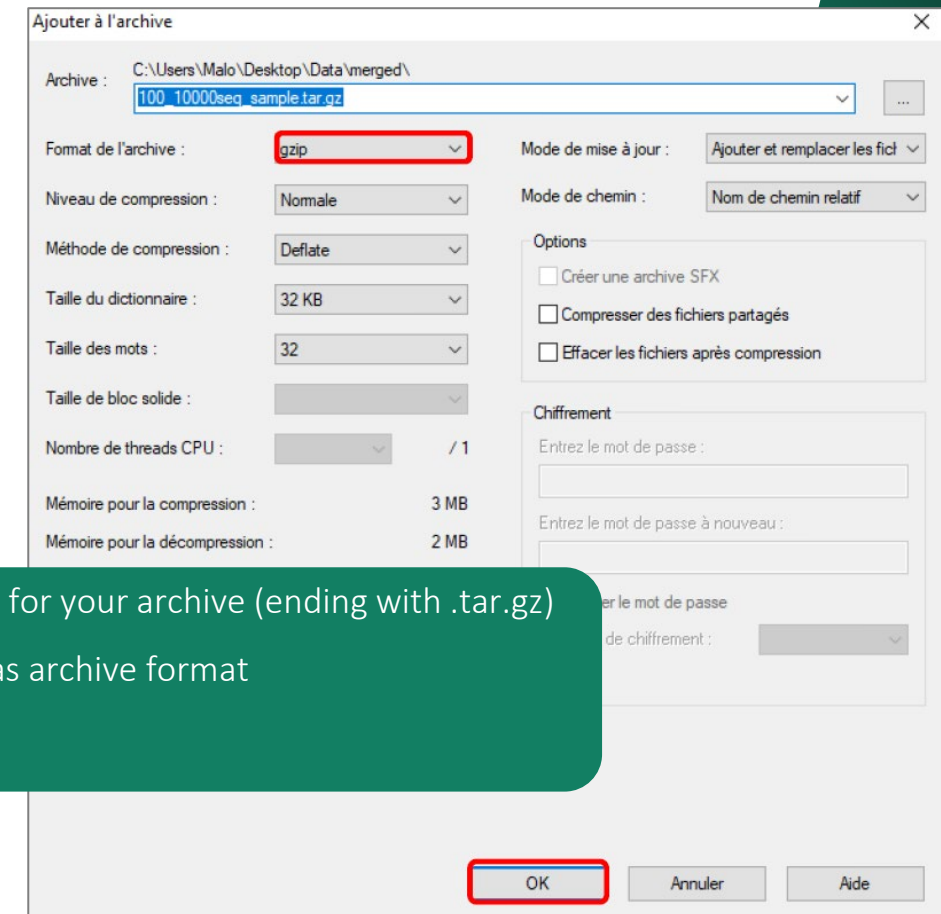
Create a tar file with 7-Zip (Windows)



Right click your newly created .tar archive.
Choose 7-Zip and “add to archive...”



Choose a name for your archive (ending with .tar.gz)
Choose “gzip” as archive format
Click on OK



You now have a .tar.gz unique file containing all your data.

Create a tar file in command line

The tar software, which gave its name to the .tar format, is accessible through command-line.

Once located in the folder containing your data (using `cd` and `ls` to navigate):

```
tar -czv -f YourArchiveName.tar.gz *.fastq
```

```
tar -czv -f YourArchiveName.tar.gz
```

```
tar -czv -f YourArchiveName.tar.gz *.fq
```

```
tar -czv -f YourArchiveName.tar.gz *.fq.gz
```

run tar

use options:

- c: create archive
- z: use gzip compression
- v: list processed files

name of the output file

According to your file names,
choose the files to archive:
*.fq.gz means “any chain of
characters followed by .fq.gz”



macOS native tar installation
can generate archives
corrupted for other OS

Create a tar file with macOS

The tar software is natively available in the macOS Terminal, and thus there is no “point-and-click”, open-source and free solution to create an archive.

⚠ Warning: macOS native tar implementation can introduce UTF-8 encoding problems when archives created on macOS are read on other operating systems.

You need to use install and use GNU-tar:

```
> brew install gnu-tar
```

If brew (an installation manager) is not yet installed first install it using:

```
/bin/bash -c "$(curl -fsSL https://raw.githubusercontent.com/Homebrew/install/HEAD/install.sh)"
```

Once installed, use gtar the same way than tar on the previous slide:

```
> gtar -czv -f YourArchiveName.tar.gz *.fq.gz
```

run GNU-tar

(re)Naming your files

The filenames returned by sequencing platform usually contains a lot of machine-generated elements (sequencer, run or lane IDs), plus the `_R1` and `_R2` suffixes for the forward or reverse reads.

These names will be directly used by FROGS, thus a good practice is to clean and shorten them as much as possible before the archive creation.

*Warning: keep the `_R1` and `_R2`, which are required in downstream analyses.
You should not have any other `_R1` or `_R2` than machine-suffixes in your naming.*

It can be done with command line or with renaming tools such as *ant renamer*:

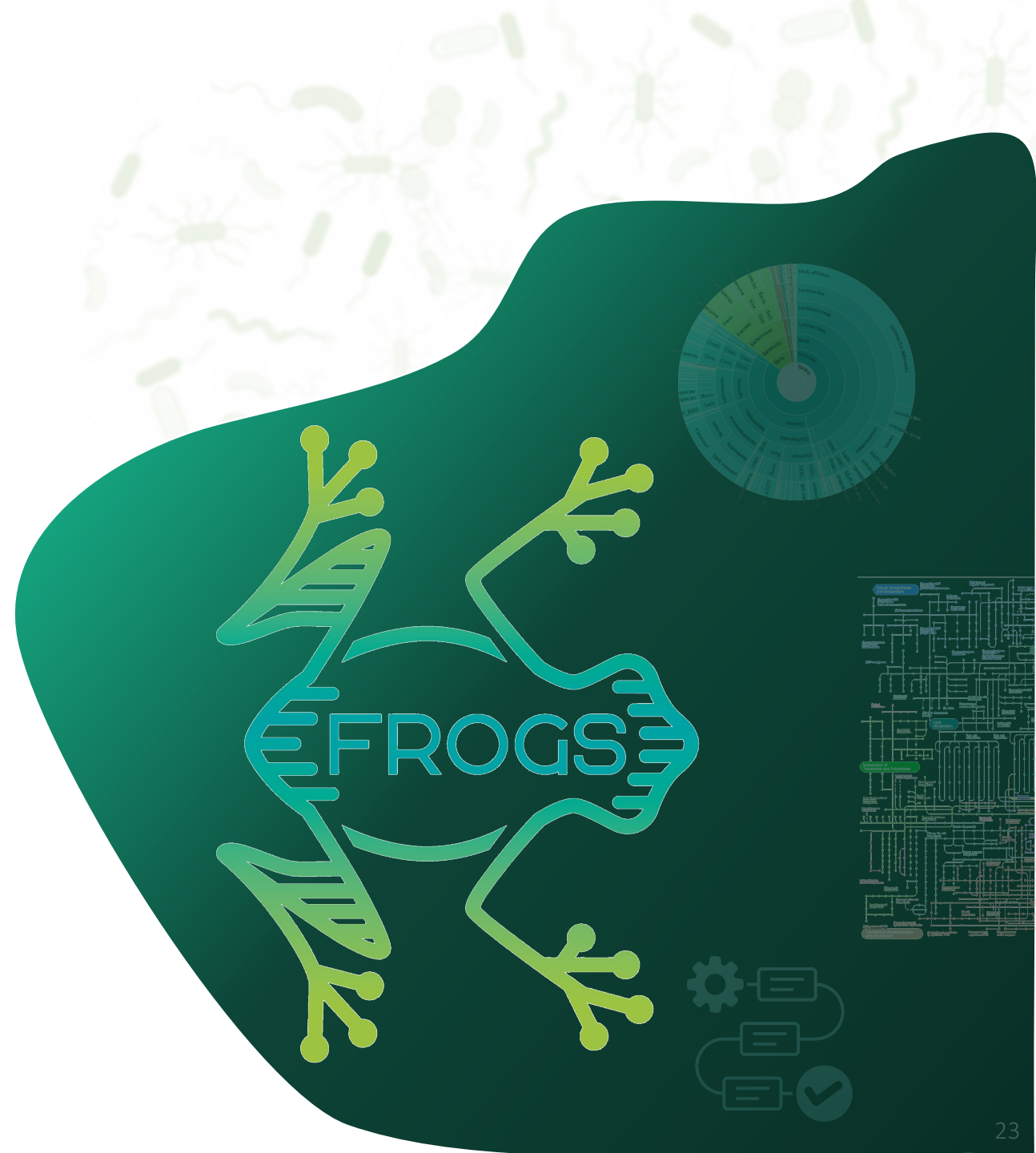
<https://antp.be/software/renamer/fr>

http://update.antp.be/renamer/antrenamer2_install.exe

Documentation: https://documentation.help/Ant-Renamer-2-fr/actions_fr.html

Get Started with Galaxy

Uploading your data



Uploading your data

Importing your data into Galaxy

Before running FROGS, you need to import your input files into Galaxy.

These are typically your **raw sequencing reads** in FASTQ format (single-end or paired-end).

How to upload your data

In the **Activity bar** (left side), click “**Upload**”.

Choose **one** of the following options:

- **Choose local file** – drag and drop files or select them manually.

or

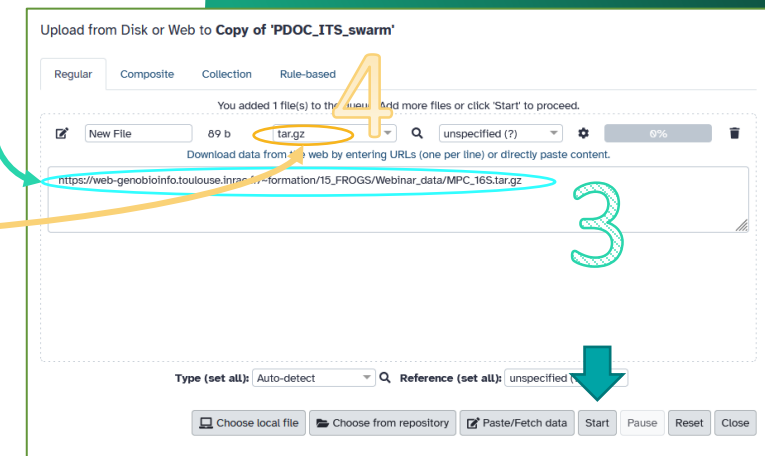
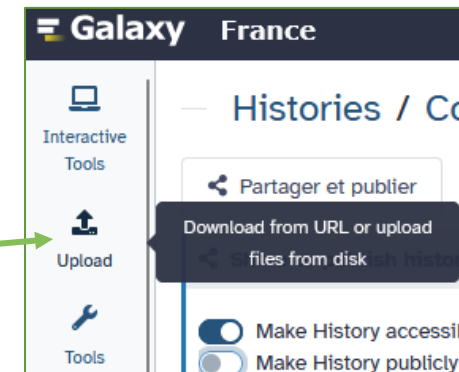
- **Paste/Fetch data** – paste a link/url to an online dataset.

Once uploaded, the files will appear in the **History panel** (on the right).

Their status will change from grey → orange → green when the upload is complete.

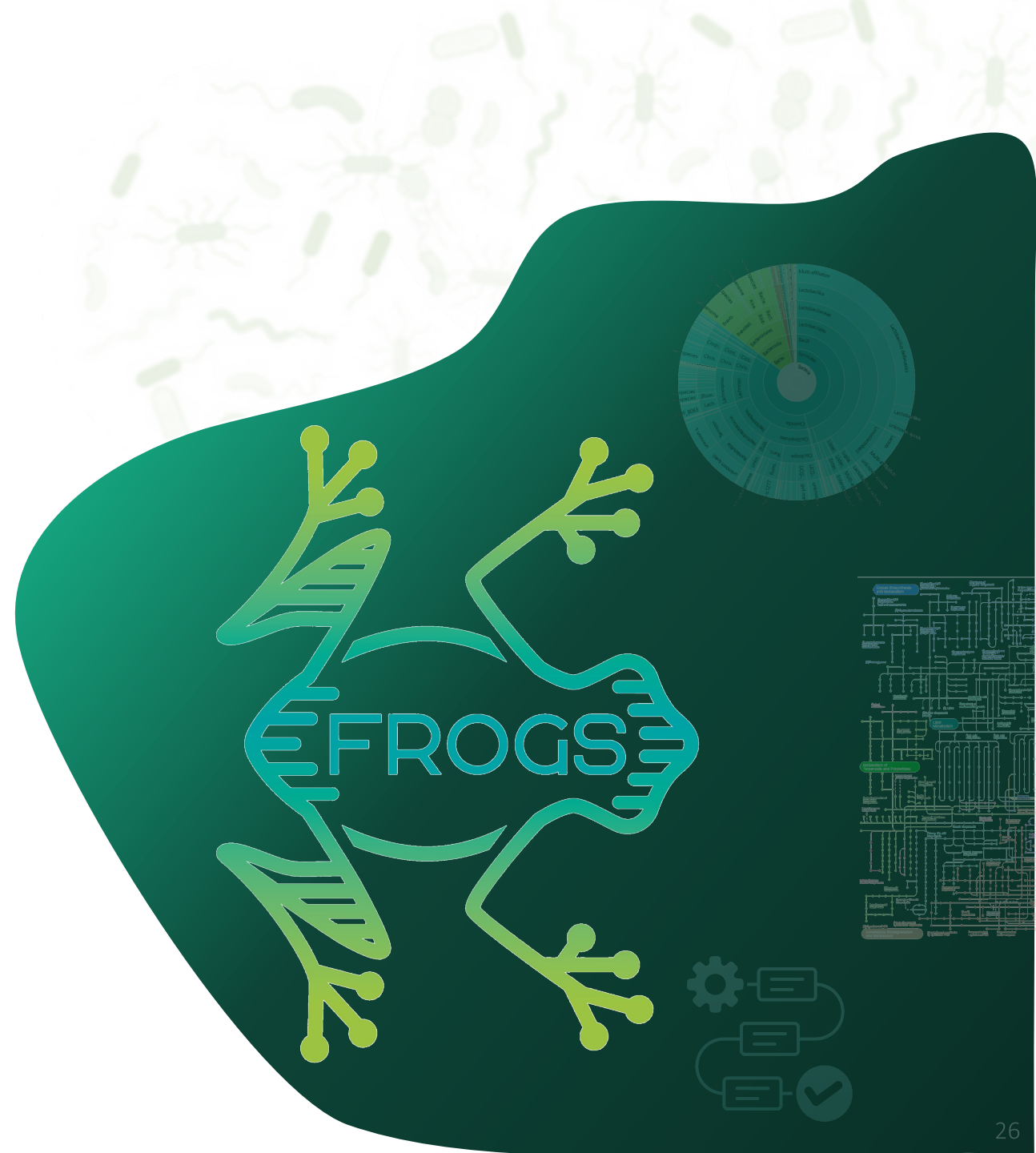
⚠ Important reminders

- Make sure your data correspond to the correct **datatype** (tar.gz, tsv, fastq.gz, etc.).
- Tips: after uploading, if the datatype is incorrect, you can edit the metadata by clicking the  (Edit attributes) icon.



Get Started with Galaxy

The tool
interface



The tool interface

Every Galaxy tool — including each step of the FROGS workflow — is presented through a **tool form** in the central panel.

This interface allows you to select input data, adjust parameters, and start analyses.

A tool form is divided into several key sections:

Input datasets:

You can select one or more datasets from your history as inputs.

For example, in *FROGS Core Main 1.a*, you choose your raw FASTQ files.

Parameters:

Below the inputs, you can configure tool-specific options such as quality thresholds, clustering methods, or reference databases.

Default parameters are already optimized for most use cases but can be adjusted if needed.

Run Tool button:

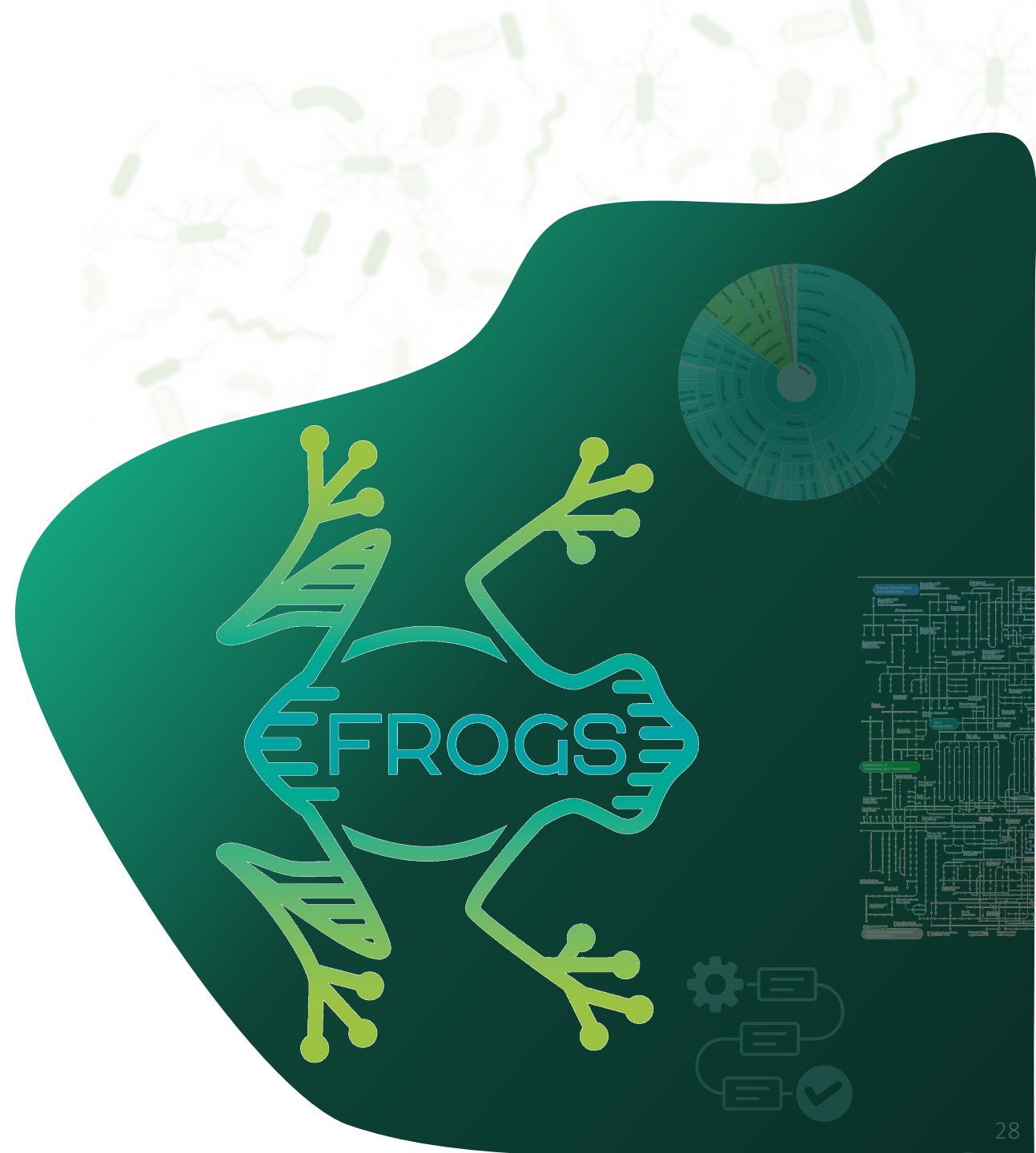
Once your inputs and parameters are set, click **“Run Tool”** to start the job.

The analysis will execute on the Galaxy server, and the resulting output datasets will appear in your **History panel**.

N.B.: New tool versions can be installed without removing old ones to ensure reproducibility.

Get Started with Galaxy

Running an analysis



Running an analysis

Once your data are uploaded, you can start a FROGS analysis using the available workflow or individual tools.

To launch FROGS tools:

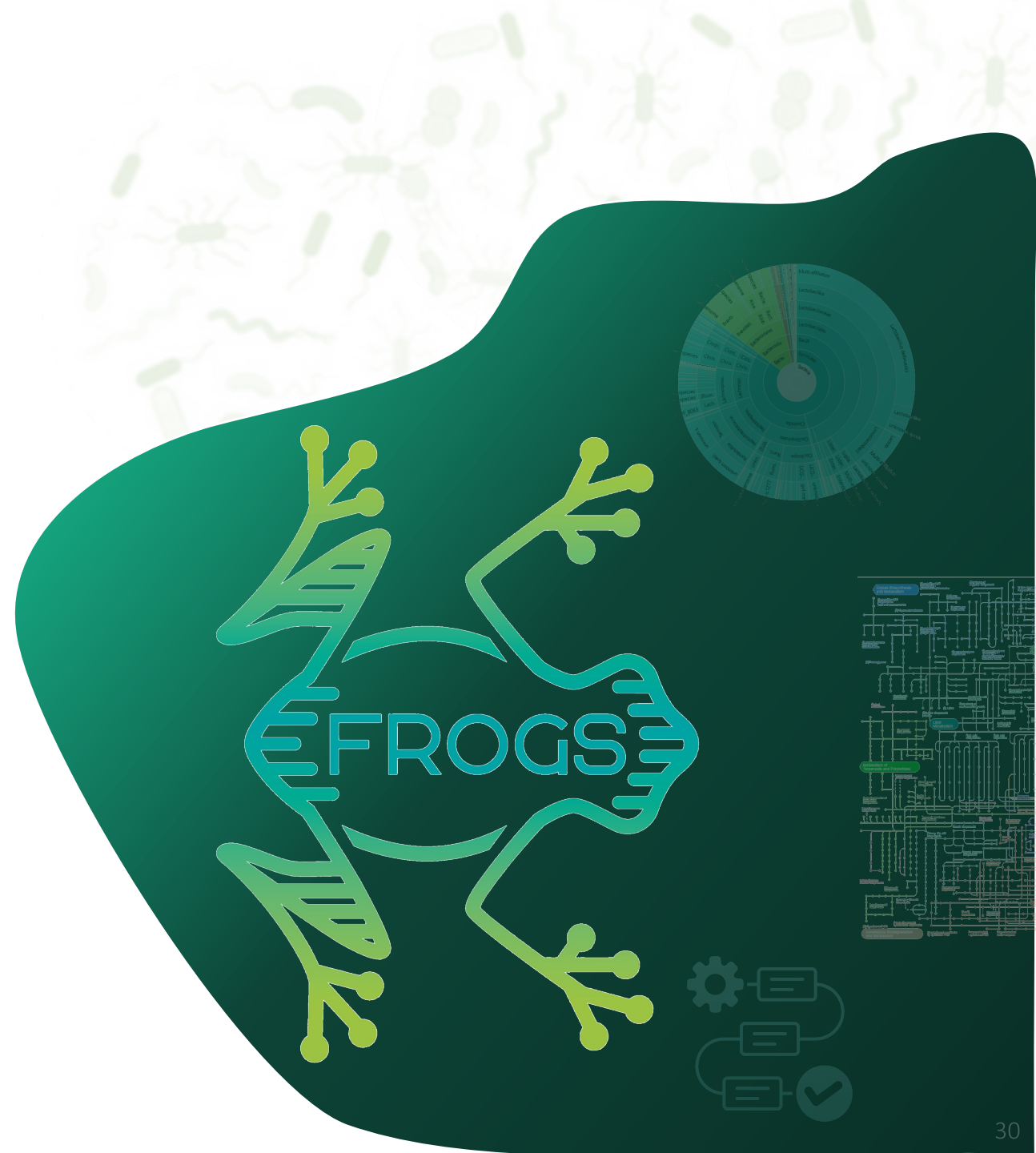
1. In the Tools panel, open the category FROGS (or similar, depending on your Galaxy instance).
2. Click on a tool of FROGS Core, FROGS Stat, FROGS Func, or another tool adapted to your analysis.
3. In the central panel, select your input datasets (*e.g.* FASTQ files or abundance table).
4. Adjust parameters if needed — default values are usually well suited for standard datasets.
5. Click on the Run tool button.

Galaxy will automatically run each step in sequence. You can follow the progress in the History panel, where outputs will appear one by one. Each tool works independently and generates new datasets that can be used as inputs for the next step.

Tip: If a step fails (red color), click on the dataset to read the error message by clicking on the bug  and check input compatibility or parameter settings. If you do not understand where the error is, contact frogs-support@inrae.fr.

Get Started with Galaxy

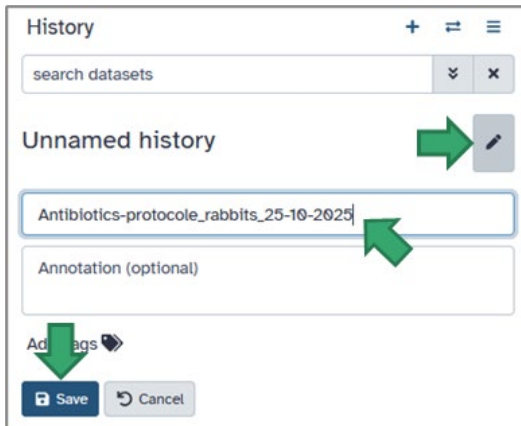
Managing your histories



Creating and organizing histories

You can rename your current history by clicking on its title or on the pencil (top of the History panel).

1



To create a new one, click on the cross icon at the top of the right panel.

2

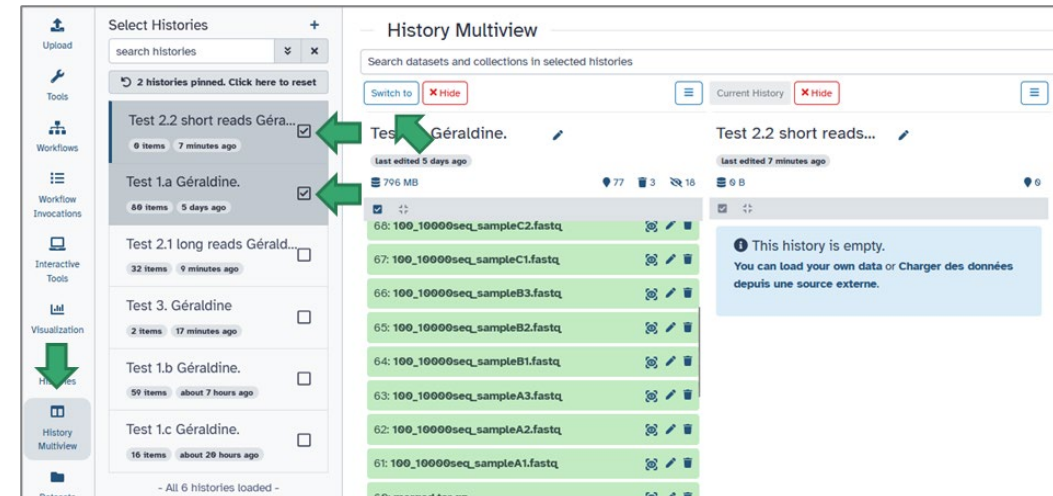


You can easily switch between histories from:

1. the **double arrow** on the top of the History panel
2. the **activity bar**. Simply select the **History Multiview** module.



3



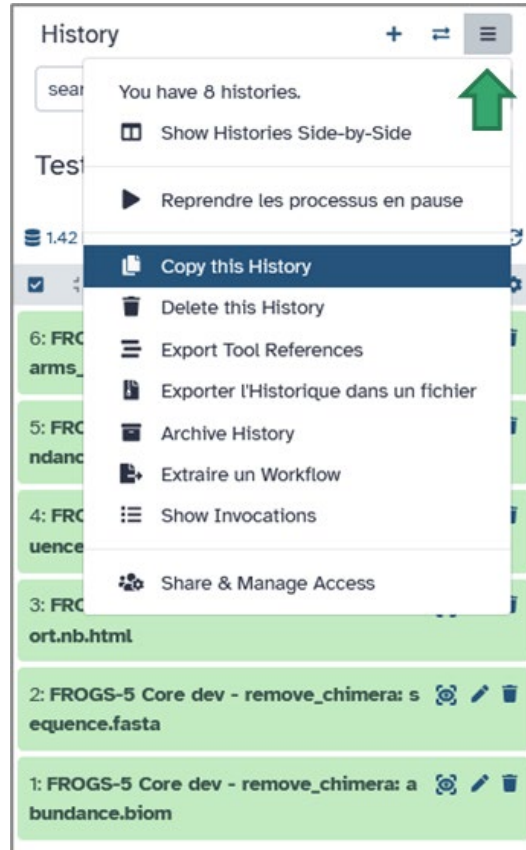
Duplicating and cleaning histories

Each history can be duplicated to reuse previous analyses.

Click the history options icon → **Copy History**. You can then modify parameters or rerun analyses without altering the original version.

Via the **activity bar**, by selecting **Histories**, you will have access to many useful options.

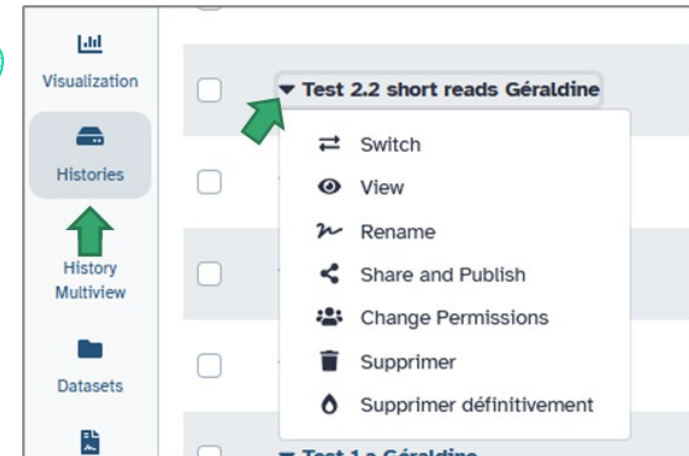
1



2



3



Viewing and re-running tools

Clicking on a dataset allows you to:

1. Inspect metadata and outputs.
2. View the tool parameters used to generate it, click on “i”.
3. Re-run the same tool with identical or modified parameters using the Re-run button — ensuring complete reproducibility.

The screenshot displays the Galaxy interface for a tool named "4: FROGS-5 Core dev - remove_chimera: sequence.fasta". The interface is divided into a green header area and a white content area. In the green area, there is a section for "Add Tags" and a line indicating "6,023 sequences" with a circled "1" next to it. Below this, it says "format **fasta**, génome de référence ?". The white area contains a section titled "## Application" with details about the software path and conda environment. Below this, there are two circular icons: a blue "i" icon and a green "r" icon, both with circled numbers "2" and "3" respectively. The bottom part of the white area shows sequence data with headers like ">Cluster_1 reference=otu_00162 position=1..300" and ">Cluster_2 reference=otu_01101 position=1..300". A circled "1" is placed next to the first sequence header. The entire interface is framed by a dark green border.

4: FROGS-5 Core dev - remove_chimera: sequence.fasta

Add Tags

6,023 sequences 1

format **fasta**, génome de référence ?

Application

Software ./galaxydata/galaxy2025/galaxy02/galaxy/database/dependencies/
_conda: nys/mull _v1-

2 3

1

>Cluster_1 reference=otu_00162 position=1..300

GAACGCTGGCGGCGTGCCTAATACATGCAAGTCGAACGAACGGATAAAGAGCTTGCTCTTTGAAGTTAGTGGCGGACGGGTGAGT

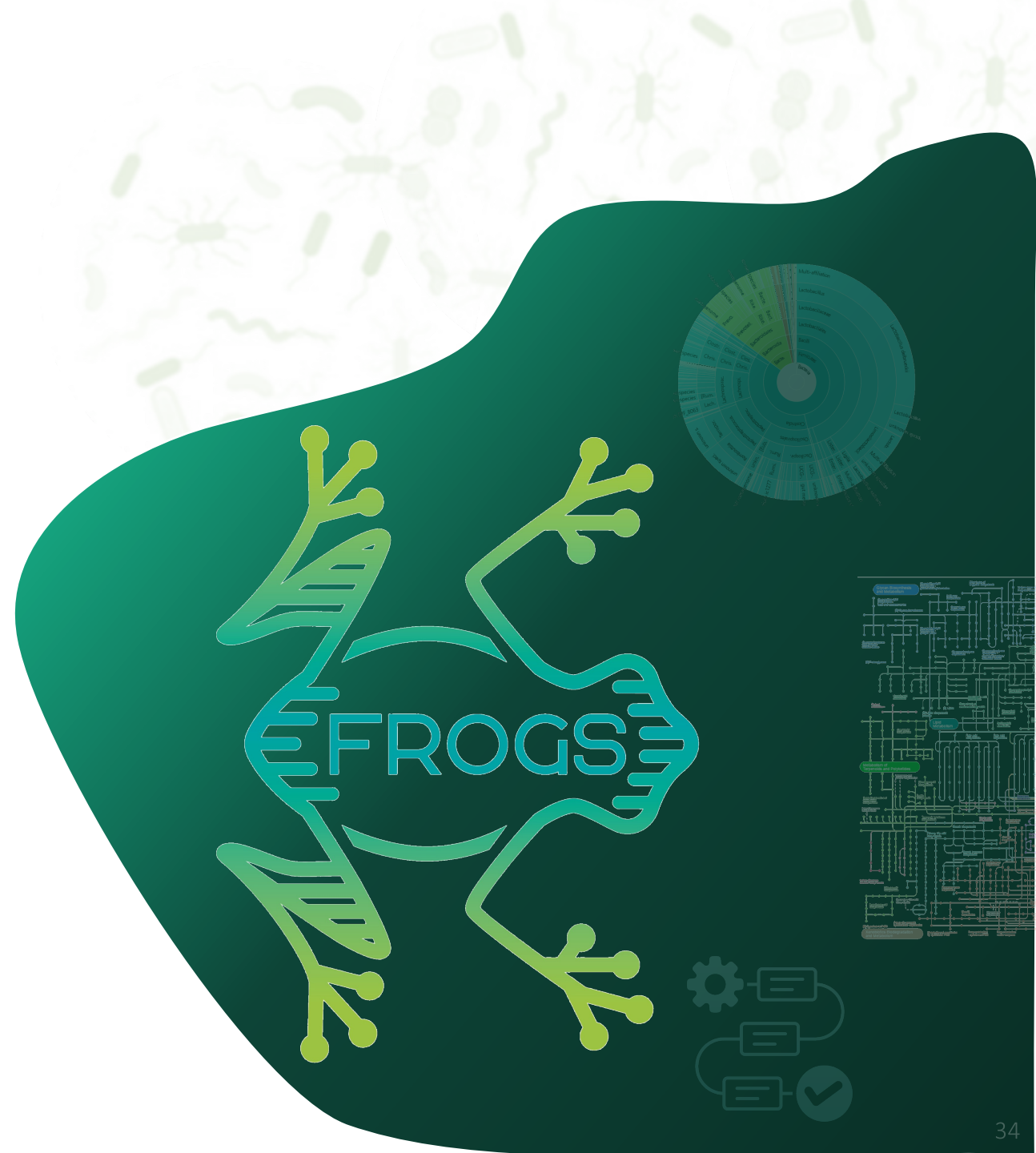
CGREGATCCATAGCCGACCTGAGAGGGTGATCGGCCACATTGGGACTGAGACACGGCCAACTCCTACGGGAGGCAGCAGTAGGGAAT

>Cluster_2 reference=otu_01101 position=1..300

ATTGAACGCTGGCGGCGGCGTGCCTAATACATGCAAGTCGAGCGGTAACAGATTGATAGCTTGCTATCAATGCTGACGAGCGGCGGACGGGT

Get Started with Galaxy

Saving, sharing,
and exporting
your work



Saving and exporting

Your histories are automatically saved on the server, but you can also export them locally:

Open the **History options** menu → **Export to file**. This generates an archive (in .tar.gz) containing all datasets and workflow information, which you can download and re-import later or share with collaborators.

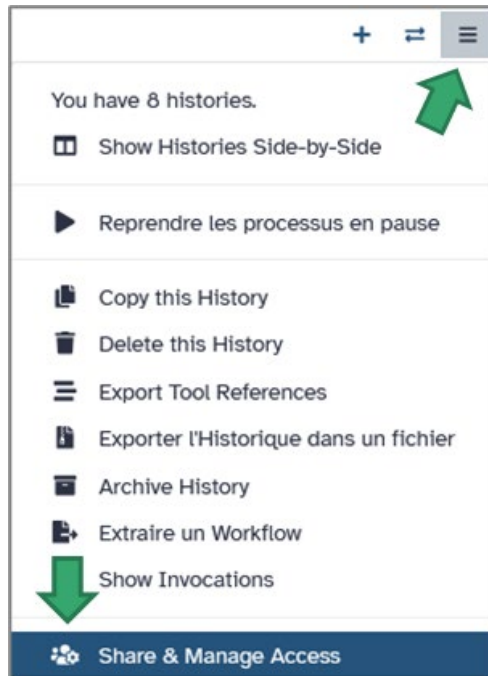
You can also export individual datasets *via* their specific menu → **Download**.



Sharing with collaborators

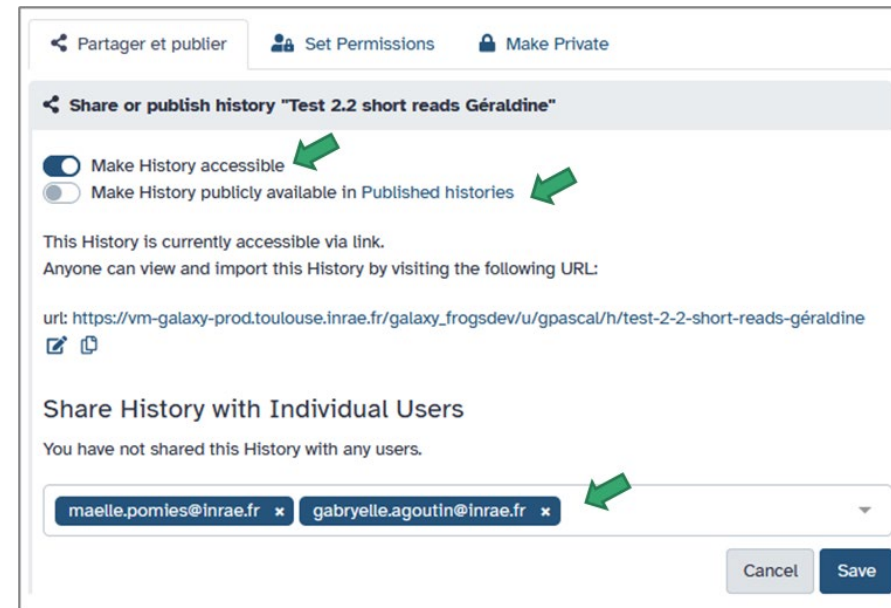
Galaxy makes it easy to share your work.

From the **History options**, select **Share & manage access**.



You can then:

- Generate a **private link** to share with specific collaborators.
- Make the history **public** so it's visible to anyone on the platform.
- Share it directly with another registered Galaxy user (by username or email).

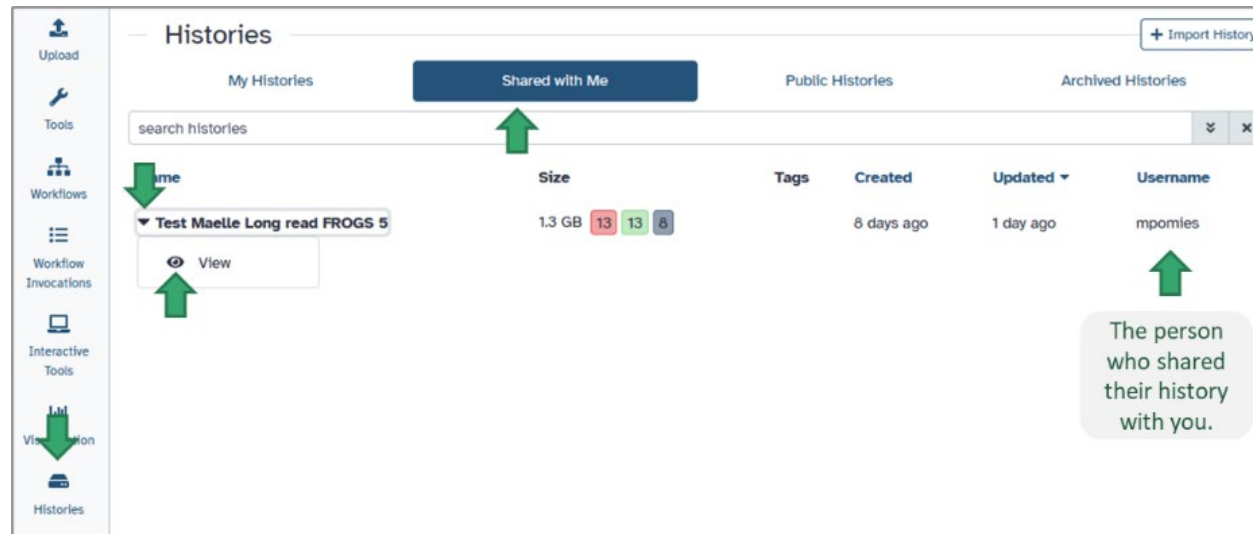


When shared, others can view, copy, or re-run your analyses — ensuring transparency and reproducibility.

Working with shared histories

When another Galaxy user shares a history with you, it appears under your **Histories menu** but is not editable. You can view all datasets, inspect parameters, and even re-run tools, but you cannot directly modify the shared version.

To open a shared history: Go to the **Histories module** on the activity bar. Select **Histories shared with me**. Click on the history name to see it in your central panel.



You will see all datasets and workflow steps exactly as they were produced by the owner, including tool versions, parameters, and metadata.

Working with shared histories

If you want to **reuse or modify** the shared analysis: Click on **View** the shared history and **Import this history**.

Galaxy will create a personal copy in your own account. You can then rename it, delete or add datasets, adjust parameters, or re-run the workflow using your own data.

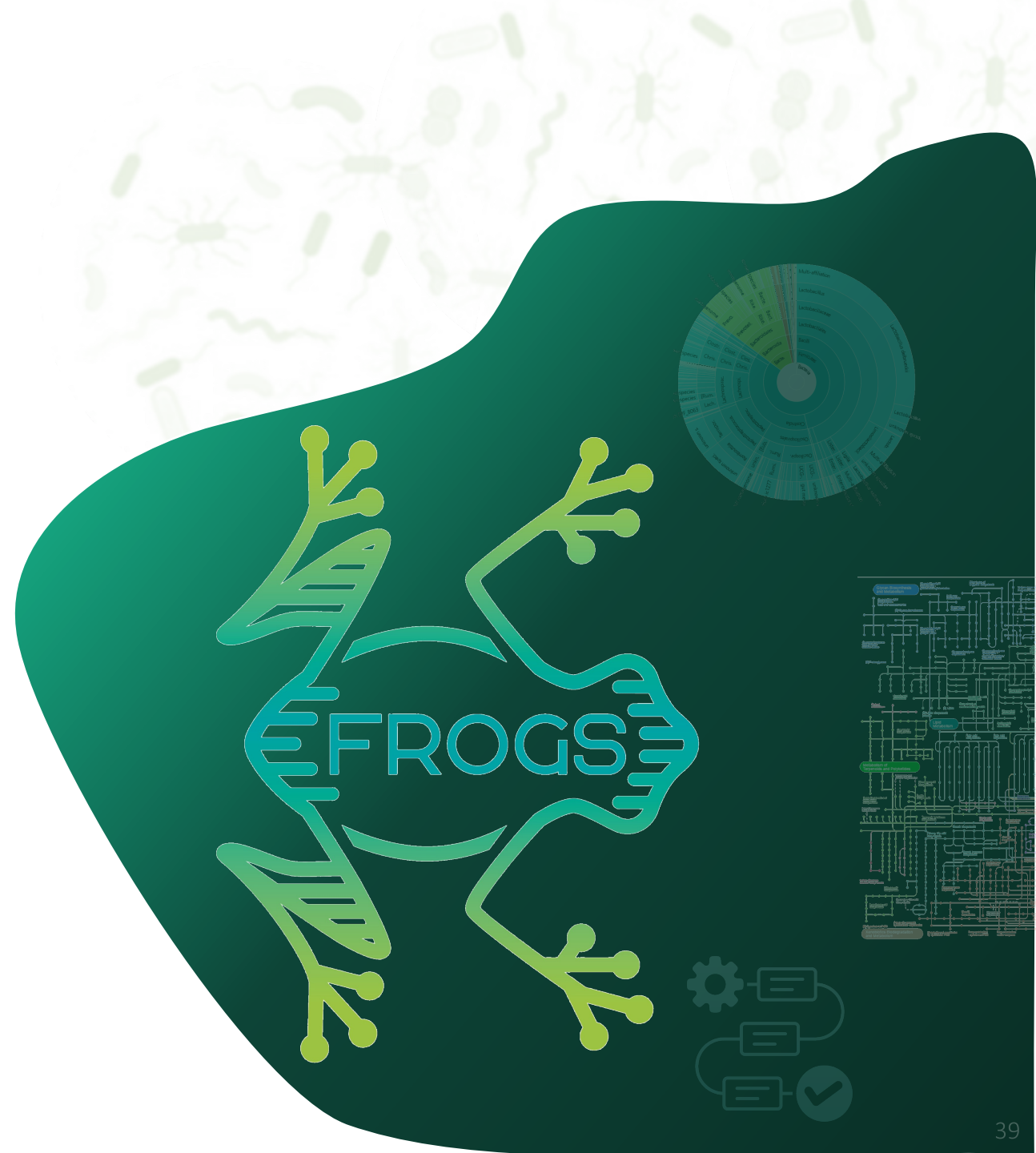
When the owner modifies their history, you will see the history update when it is shared.

A screenshot of a dialog box titled 'Copying History: ITS'. It contains a text input field with the title 'FROGS_ITS_forest_soil_25_10_2025' and a green checkmark. Below the input field, there is a section titled 'Choose which datasets from the original history to include.' with two radio button options: 'Copy only the active, non-deleted datasets.' and 'Copy all datasets including deleted ones.' The second option is selected. At the bottom right, there are two buttons: 'Cancel' and 'Copier l'Histoire'.

Note: Any changes you make to your copy will not affect the owner's history. You can, in turn, share your modified copy with others using the same **Share or Publish** options.

Get Started with Galaxy

Building
workflows from
your histories



From history to workflow

Once you've completed an analysis and are satisfied with the results: Open your **History option** (on the top of the right panel).

Choose **Extract Workflow**. Galaxy will display a new page showing all the tools that were run in this history, in their exact order.

Selecting the relevant steps

In the workflow extraction view: Each line corresponds to a tool execution from your history. You can **select** or **deselect** individual steps to include only those you need.

For example, you may skip data import or statistical steps if they are not required for automation.

The following list contains each tool that was run to create the datasets in your current history. Please select those that you wish to include in the workflow.

Tools which cannot be run interactively and thus cannot be incorporated into a workflow will be shown in gray.

Workflow name
Workflow constructed from history 'FROGS_ITS_forest_soil_25_10_2025'

Create Workflow Check all Uncheck all

Tool	History items created
Data Fetch <i>This tool cannot be used in workflows</i>	1 ITS_fast.tar.gz ☐ Treat as input dataset ITS_fast.tar.gz
FROGS-5 Core dev ☒ Include "FROGS-5 Core dev" in workflow All job outputs have been deleted	2 FROGS-5 Core dev - processing_short_reads: report.nb.html
FROGS-5 Core dev ☒ Include "FROGS-5 Core dev" in workflow All job outputs have been deleted	3 FROGS-5 Core dev - processing_short_reads: sequence.fasta
	4 FROGS-5 Core dev - processing_short_reads: abundance.biom
	5 FROGS-5 Core dev - processing_short_reads: swarms_composition.txt
	6 FROGS-5 Core dev - remove_chimera: report.nb.html
	7 FROGS-5 Core dev - remove_chimera: sequence.fasta
	8 FROGS-5 Core dev - remove_chimera: abundance.biom
	9 FROGS-5 Core dev - remove_chimera: swarms_composition.txt
	10 FROGS-5 Core dev - processing_short_reads: report.nb.html
	11 FROGS-5 Core dev - processing_short_reads: sequence.fasta
	12 FROGS-5 Core dev - processing_short_reads: abundance.biom
	13 FROGS-5 Core dev - processing_short_reads: swarms_composition.txt

Give your workflow a **clear, descriptive name** (e.g. *Workflow constructed from history 'FROGS_ITS_forest_soil_25_10_2025'*), then click **Create Workflow**.

Your new workflow will appear in the **Workflow menu** (accessible from the activity bar).

Workflows + Create Import

My workflows Workflows shared with me Public workflows

Search my workflows by query or use the advanced filtering options

☐ Select all Sort by: Name Update time Filter: ☐ Show deleted ☒ Show bookmarked Display: ☐ ☐

☐ Workflow constructed from history 'FROGS_ITS_forest_soil_25_10_2025'

Add Tags

☒ less than a minute ago

☐ Edit ☐

Editing and customizing your workflow

Once your workflow is created, you can modify it using Galaxy's **Workflow Editor**:

Open the **Workflow menu** (activity bar).

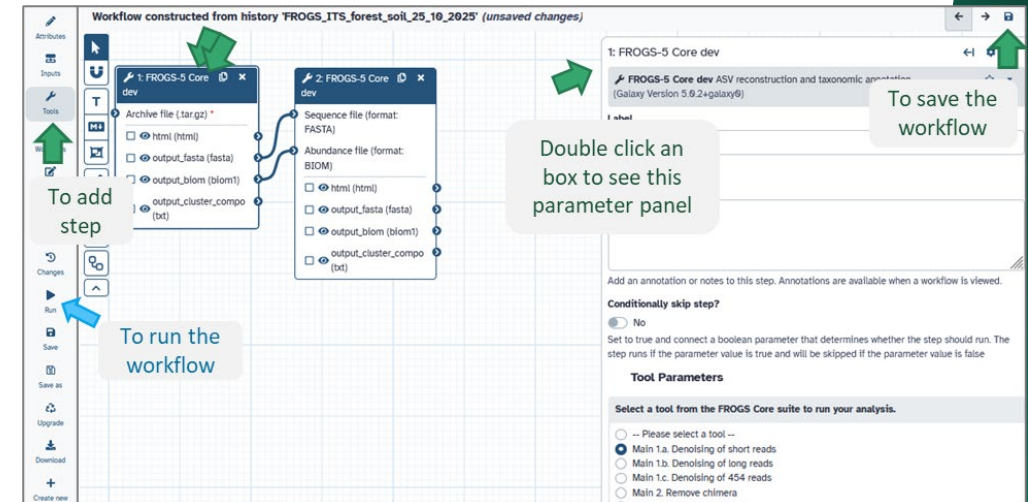
Click on your workflow name → **Edit**



In the editor:

- Tools are shown as boxes connected by arrows (representing data flow).
- You can drag and drop tools, change parameter defaults, or add/remove steps.
- Each connection indicates how the output of one tool becomes the input of another.
- **Don't forget to save !**

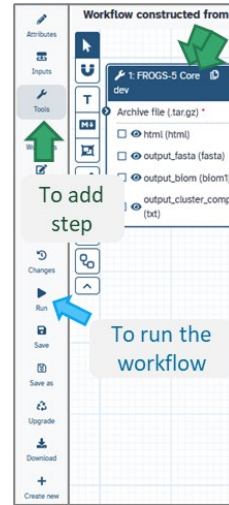
Tip: Double-click a tool box to adjust its default parameters — this can save you time when re-running the workflow later.



Running your workflow

To use your newly created workflow:

Click **Run on the activity bar** next to your workflow panel.



In the History panel (on the right), **select your input datasets** from your current history (or another — click on switch to history).

Adjust parameters (on the central panel) if necessary, then **click Run Workflow** (on the top of the central panel).

Galaxy will **execute all steps automatically**, following the same sequence as in your original analysis.

Outputs will appear in your current history.

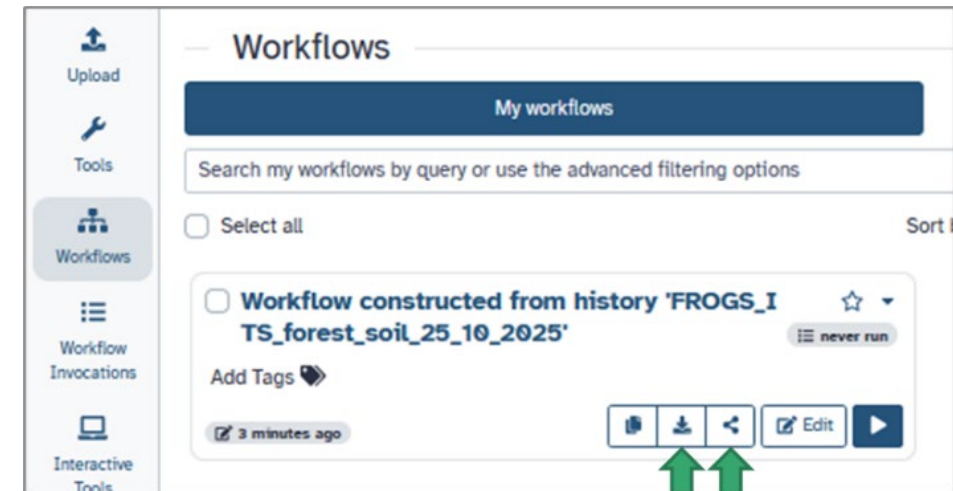


Sharing and reusing workflows

Workflows can be **shared, exported, or published** just like histories: From the **Workflow menu**, click **Share** or **Download**.

You can:

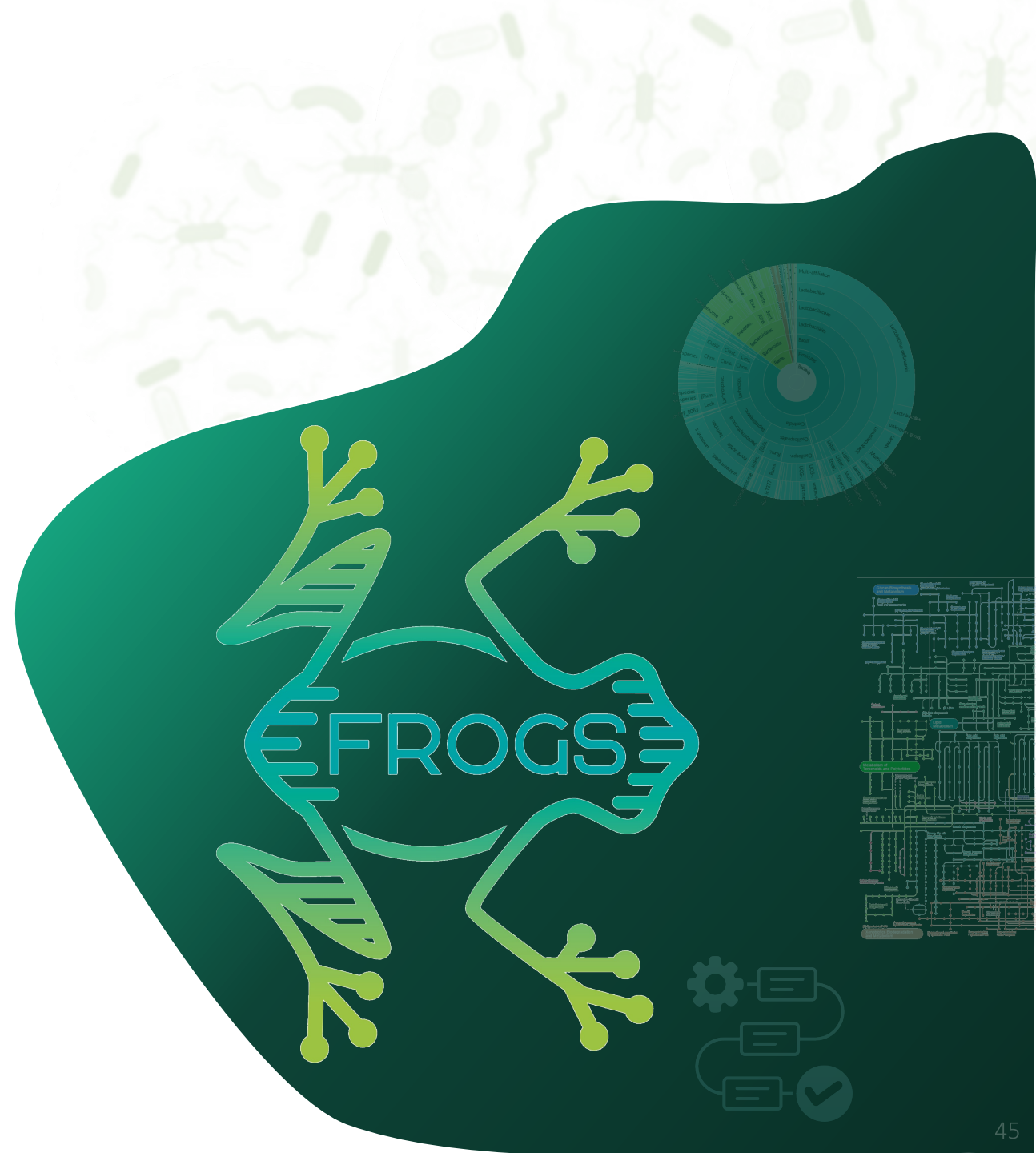
- Share a private link with collaborators.
- Publish the workflow on your Galaxy instance for the community.
- Download it as a .ga file and import it on another Galaxy server.



This is particularly useful for collaborative projects using FROGS, as all parameters, tool versions, and connections remain identical — ensuring perfect reproducibility.

Get Started with Galaxy

Best practices
for stable
analyses



Best practices for stable analyses

- **Organize your histories:** Keep one history per project or dataset to avoid confusion.
- **Use clear dataset names:** Short, informative names (*e.g.* “Soil_16S_PACBIO_summer2025”) help track inputs and results.
- **Avoid special characters or spaces** in dataset names — use underscores _ instead.
- **Regularly clean up old histories** or purge deleted datasets to free storage space.
- **Document your workflows:** Save and name your customized workflows clearly (*e.g.* “FROGS_pipeline_v5_customparams”).
- **Use the Re-run option** rather than reconfiguring tools from scratch — it guarantees parameter consistency.

Now, we will prepare the histories using the data sets that are useful for training purposes.



We need to connect to the Galaxy platform.

We need to create histories.

We need to download the datasets.

Practice session

We need to connect to the Galaxy platform.

- Go to https://vm-galaxy-prod.toulouse.inrae.fr/galaxy_fmt04/
- Enter your login and your password (c.f. mail)

Only
for this
training
!



Welcome to Galaxy, please log in

Public Name or Email Address

Password

[Forgot password? Click here to reset your password.](#)

Login

Don't have an account? Registration for this Galaxy instance is disabled. Please contact an administrator for assistance.



- Visit the Galaxy Platform.
- Look at the tool list.
- Display only FROGS tools.
- Display all tools concerning fastq files.

search tools



Only
for this
training
!

Practice session

We need to connect to the Galaxy platform.

- Go to <https://metabarcoding.usegalaxy.fr>
- Enter your login and your password

For your
daily usage
after the
training



Welcome to Galaxy, please log in

Public Name or Email Address

Password

[Forgot password? Click here to reset your password.](#)

Login

Don't have an account? Registration for this Galaxy instance is disabled. Please contact an administrator for assistance.

Practice session

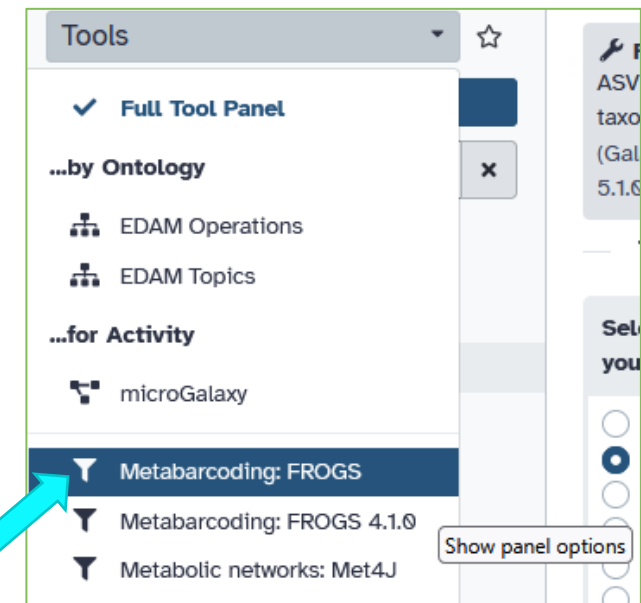
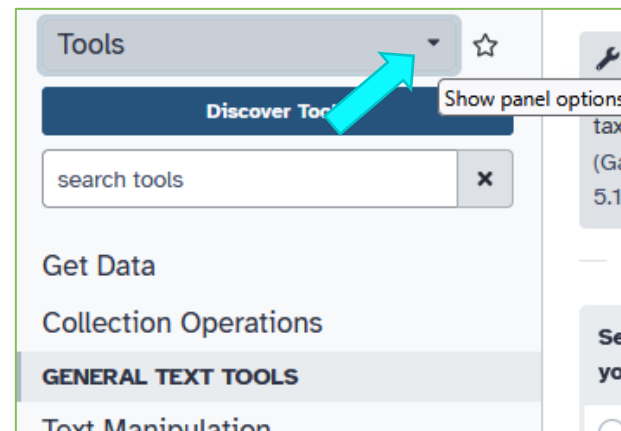
For your
daily usage
after the
training



- Visit the Galaxy Platform.
- Look at the tool list.
- Display only FROGS tools.
- Display all tools concerning fastq files.

- Display the FROGS panel and choose FROGS

search tools



Practice session

We need to create histories.



Create a new history.

History

+ ↔ ≡

⌵ ✕

Rename this history.

Unnamed history ✎

Add Tags 🏷️

💾 Save ↺ Cancel

Unnamed history ✎

Add Tags 🏷️

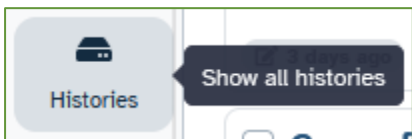
💾 Save ↺ Cancel

Practice session



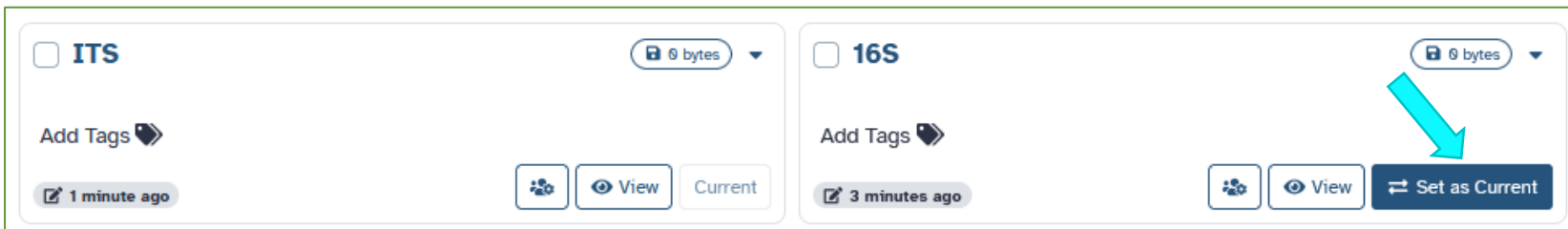
Create another history named “ITS”.

Look the 2 histories.



Look the 2 histories.

Return on the 16S history.



Practice session

We need to download the datasets.



Together, we will examine what these files represent and the nature of this data. However, please note that this is an analysis of cheese samples and includes data from both 16S and ITS metabarcoding sequencing of the same samples. The metadata is therefore identical for both sets of sequence data.

Practice session

We need to download the datasets.



16S data are here :

https://web-genobioinfo.toulouse.inrae.fr/~formation/15_FROGS/31_September2026/

You have to upload

- MPC_16S.tar.gz: the data file
- MPC_complete_metadata.tsv: the metadata file

Do not hesitate to open the TAR archive, look at the sample names and see the sequences...

To upload files, you can follow protocol described in [these slides](#).

Get Started
with Galaxy

Uploading your
data



Practice session

We need to download the datasets.

Return in the ITS history

ITS data are here :

https://web-genobioinfo.toulouse.inrae.fr/~formation/15_FROGS/31_September2026/



You have to upload

- MPC_ITS.tar.gz: the data file
- MPC_complete_metadata.tsv: the metadata file

Practice session

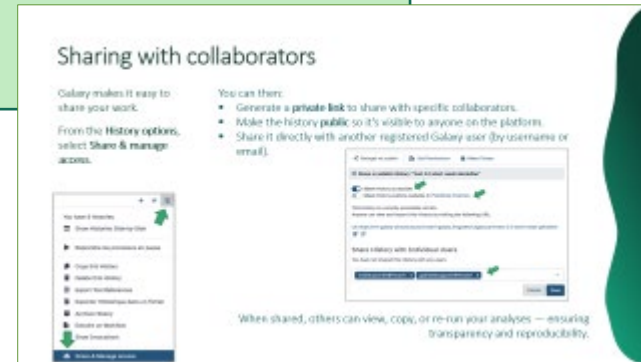
Your histories should now be ready.



Please share them with us.

`formation01@ici.la` ✕

You can refer to [this slide](#).



And please send us an email to let us know when everything is OK.



frogs-training@inrae.fr

Thank you for
following this first
step.
See you on monday
28th September!

Your trainers:
Géraldine & Lucas

