# A - Training on Galaxy: Metabarcoding

Mai 2025 - webinar

# GALAXY Practice

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# Objectives of the 1$^{st}$ part

- Learn the basics of Galaxy
- Prepare the 1 dataset for FROGS formation

# What is Galaxy?

# Galaxy software framework

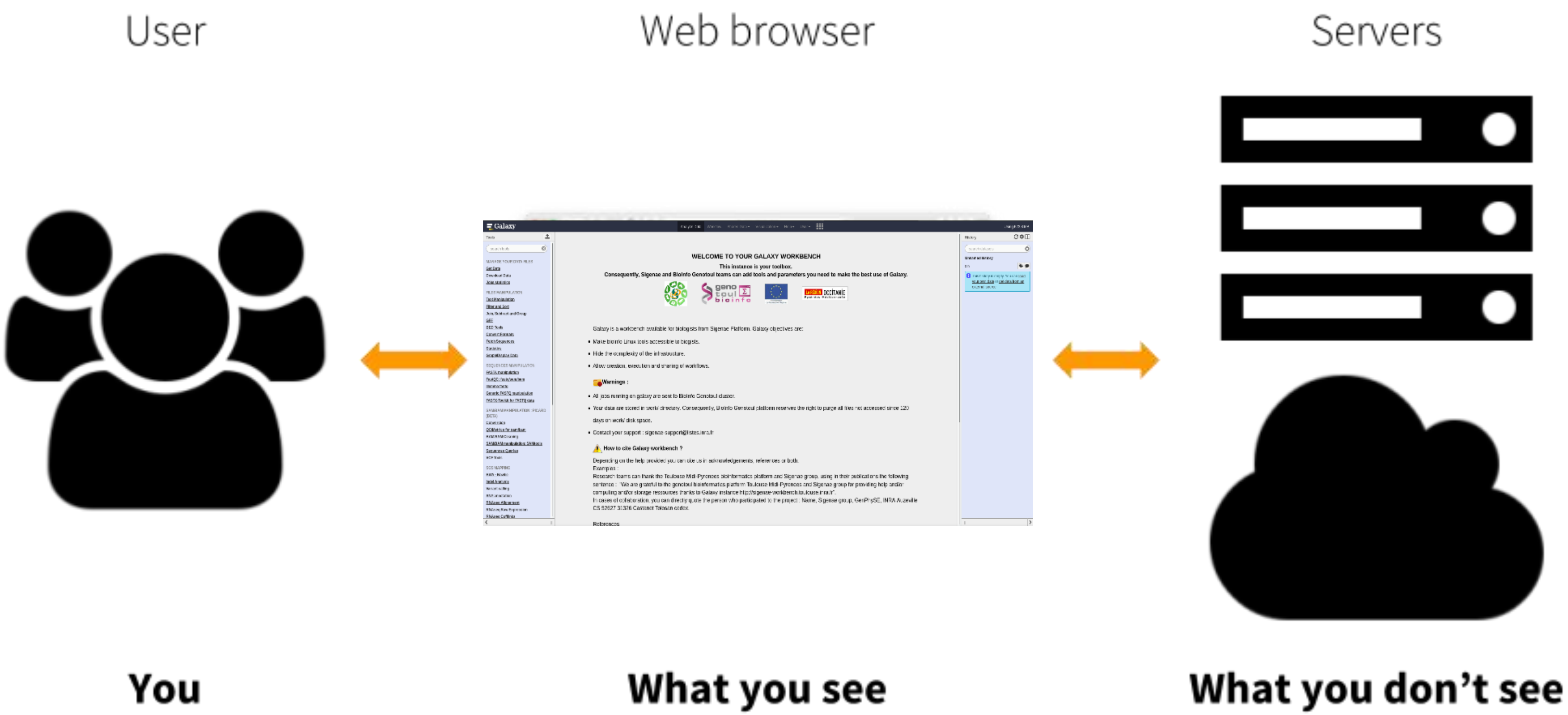
- Galaxy is an overlay that allows researchers without computer expertise to perform computational analyses online, automate them and share the results easily.

- Developed by the Galaxy Team Project.

- Relies on a computational infrastructure (Server).

- Open source

# Galaxy software framework



User

Web browser

Servers

Galaxy

WELCOME TO YOUR GALAXY WORKBENCH

This instance is your toolbox.

Consequently, Sigenae and BioInfo Genotoul teams can add tools and parameters you need to make the best use of Galaxy.

Galaxy is a workbench available for biologists from Sigenae Platform. Galaxy objectives are:

- Make bioinfo Linux tools accessible to biologists.
- Hide the complexity of the infrastructure.
- Allow creation, execution and sharing of workflows.

Warnings :

- All jobs running on galaxy are sent to BioInfo Genotoul cluster.
- Your data are stored in work/ directory. Consequently, BioInfo Genotoul platform reserves the right to purge all files not accessed since 120 days on work/ disk space.
- Contact your support : sigenae-support@listes.inra.fr

How to cite Galaxy workbench ?

Depending on the help provided you can cite us in acknowledgements, references or both.
Examples :
Research teams can thank the Toulouse Midi-Pyrenees bioinformatics platform and Sigenae group, using in their publications the following sentence : "We are grateful to the genotoul bioinformatics platform Toulouse Midi-Pyrenees and Sigenae group for providing help and/or computing and/or storage ressources thanks to Galaxy instance http://sigenae-workbench.toulouse.inra.fr".
In cases of collaboration, you can directly quote the person who participated to the project : Name, Sigenae group, GenPhySE, INRA Auzeville CS 52627 31326 Castanet Tolosan cedex.

References

**You**

**What you see**

**What you don't see**

https://galaxyproject.org/tutorials/g101/

# Where to use Galaxy?

- Galaxy software can be installed and run on powerful server farms (Cluster) or on your individual PC.

- Location : **Toulouse**
- Compute (#CPU HT*) : **6224**
- Storage (#TB) : **4400**
- RAM (#GB) : **36500**
- RAM/core (#GB) : **5.56**
- GPU (#Card) : **1**

- Location : **Jouy en Josas**
- Compute (#CPU HT*) : **1016**
- Storage (#TB) : **350**
- RAM (#GB) : **7000**
- RAM/core (#GB) : **6.89**
- GPU (#Card) : -

- Location : **Orsay (IDRIS)**
- Compute (#CPU HT*) : **4300**
- Storage (#TB) : **2400**
- RAM (#GB) : **20008**
- RAM/core (#GB) : **4.65**
- GPU (#Card) : -

# Where to use Galaxy?

- The Toulouse Galaxy platform: https://vm-galaxy-prod.toulouse.inrae.fr
- Institut Français Bioinformatique IFB (national server): https://metabarcoding.usegalaxy.fr
- Migale Plateform: galaxy.migale.inra.fr
- Others…

⚠ The different platforms of Galaxy are not connected together

- Galaxy is installed on many clusters across the world.
- Some tools are in our Galaxy platform but not in other platforms.
- Your data is not shared with other Galaxy platforms than ours.

# Exemple of Galaxy platforms

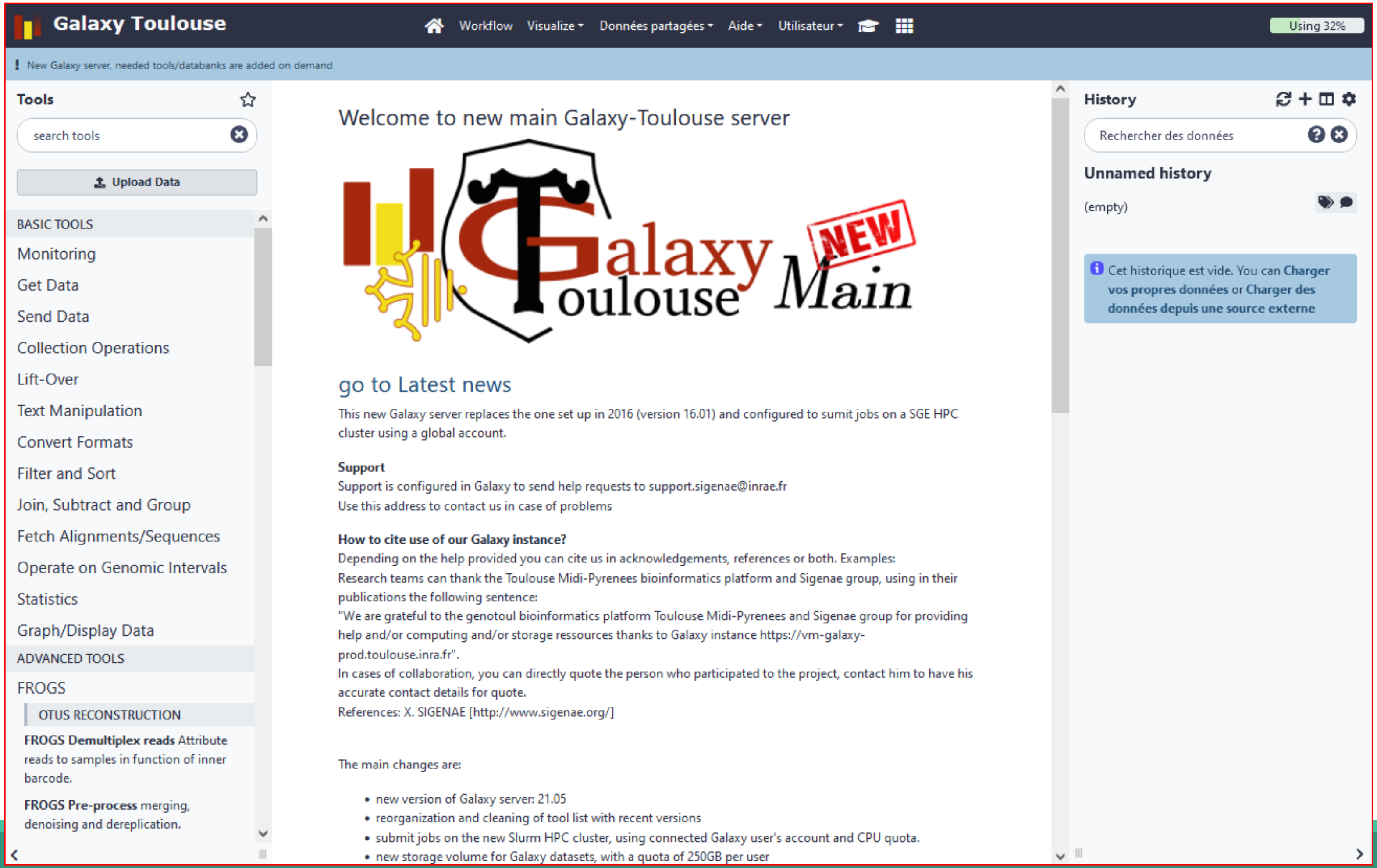
Welcome to the Migale Galaxy instance!

Global load of the nodes dedicated to Galaxy jobs

What's new

- **28th January 2021:** Added Parnsnp in Section *Phylogenyy*.
- **28th January 2021:** Added ECTyper in Section *Genome Annotation*.
- **14th January 2021:** Added Filter SPAdes Output in Section *Assembly*.
- **27th November 2020:** Added Seqtk in Section *FAST/FASTQ Manipulation*.
- **27th November 2020:** Added SeqSero in Section *Genome Annotation*.
- **23d November 2020:** Added staramr in Section *Genome Annotation*.
- **2nd October 2020:** Added Shovill in Section *Assembly*.
- **27th July 2020:** Added Progressive Mauve in Section *Multiple Alignements*.
- **27th July 2020:** Added Mummer4 in Section *Multiple Alignements*.
- **24th July 2020:** Added NCBI accession Download in Section *Get Data*.

# Exemple of Galaxy platforms



! New Galaxy server, needed tools/databanks are added on demand

**FROGS Demultiplex reads** Attribute reads to samples in function of inner barcode.

**FROGS Pre-process** merging, denoising and dereplication.

Welcome to new main Galaxy-Toulouse server

go to Latest news

This new Galaxy server replaces the one set up in 2016 (version 16.01) and configured to sumit jobs on a SGE HPC cluster using a global account.

**Support**
Support is configured in Galaxy to send help requests to support.sigenae@inrae.fr
Use this address to contact us in case of problems

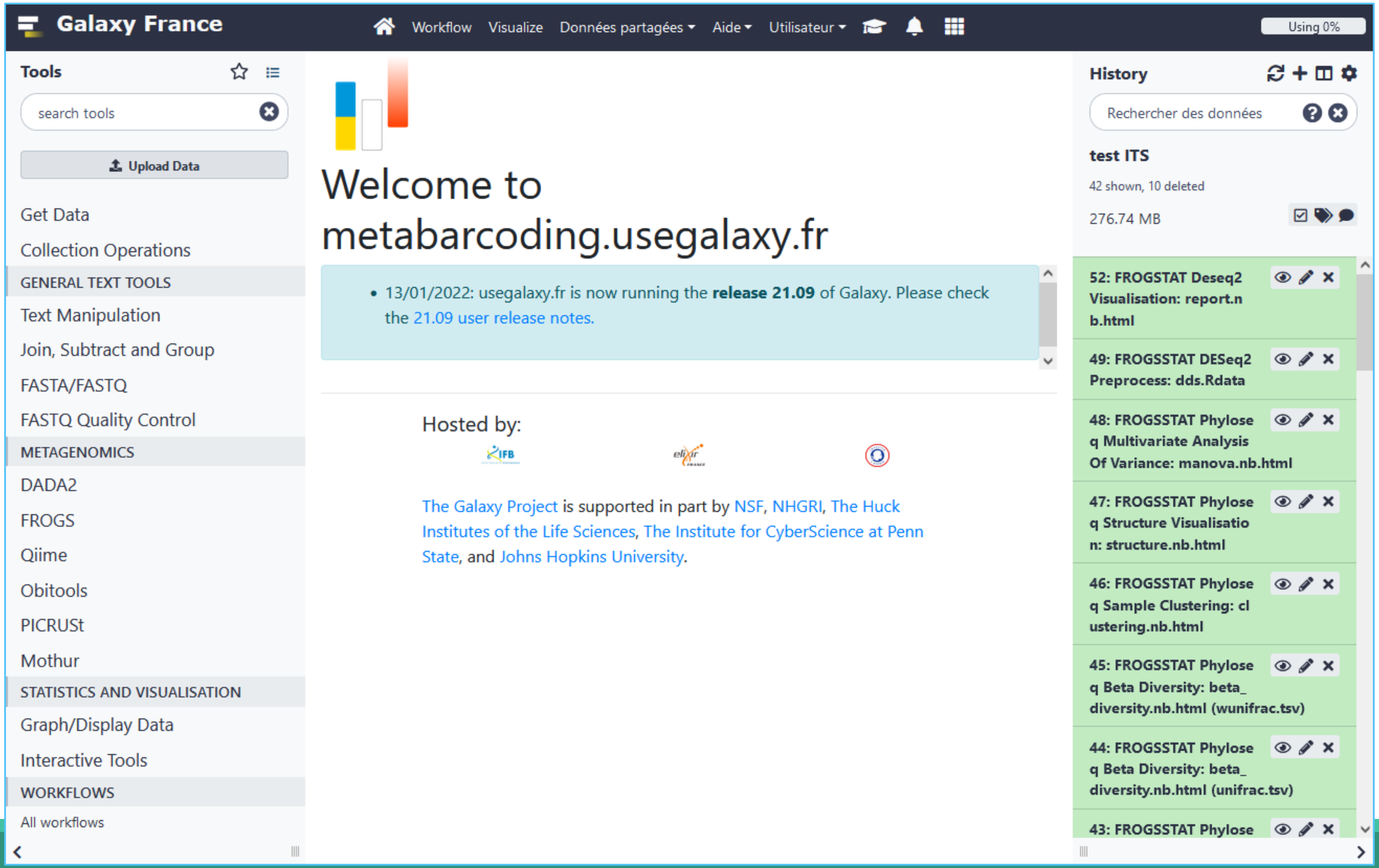
**How to cite use of our Galaxy instance?**
Depending on the help provided you can cite us in acknowledgements, references or both. Examples:
Research teams can thank the Toulouse Midi-Pyrenees bioinformatics platform and Sigenae group, using in their publications the following sentence:
"We are grateful to the genotoul bioinformatics platform Toulouse Midi-Pyrenees and Sigenae group for providing help and/or computing and/or storage ressources thanks to Galaxy instance https://vm-galaxy-prod.toulouse.inra.fr".
In cases of collaboration, you can directly quote the person who participated to the project, contact him to have his accurate contact details for quote.
References: X. SIGENAE [http://www.sigenae.org/]

The main changes are:

- new version of Galaxy server: 21.05
- reorganization and cleaning of tool list with recent versions
- submit jobs on the new Slurm HPC cluster, using connected Galaxy user's account and CPU quota.
- new storage volume for Galaxy datasets, with a quota of 250GB per user

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

# Exemple of Galaxy platforms



Welcome to metabarcoding.usegalaxy.fr

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

Hosted by:

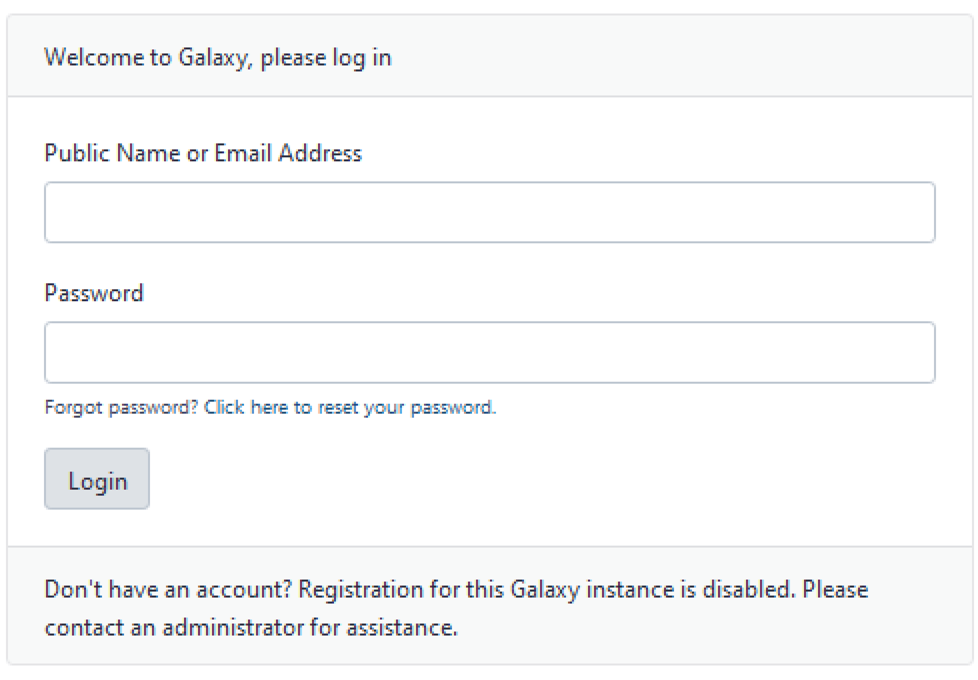
The Galaxy Project is supported in part by NSF, NHGRI, The Huck Institutes of the Life Sciences, The Institute for CyberScience at Penn State, and Johns Hopkins University.

# Practice:

CONNECT TO GALAXY WORKBENCH

# Exercise

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



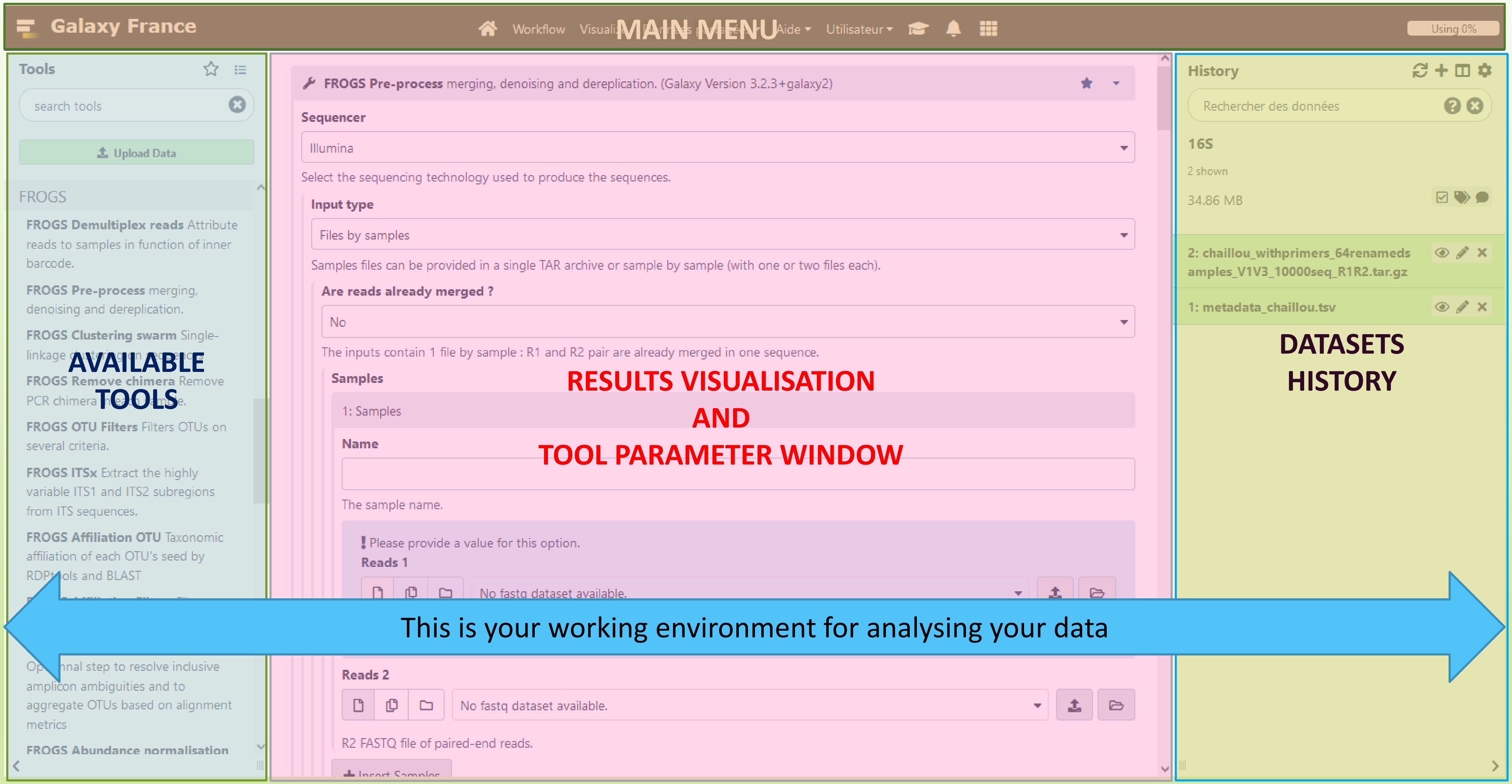
Welcome to Galaxy, please log in

Public Name or Email Address

Password

Forgot password? Click here to reset your password.

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



MAIN MENU

AVAILABLE TOOLS

RESULTS VISUALISATION
AND
TOOL PARAMETER WINDOW

DATASETS HISTORY

This is your working environment for analysing your data

FROGS

**FROGS Demultiplex reads** Attribute reads to samples in function of inner barcode.

**FROGS Pre-process** merging, denoising and dereplication.

**FROGS Clustering swarm** Single-linkage clustering on sequences.

**FROGS Remove chimera** Remove PCR chimera in each sample.

**FROGS OTU Filters** Filters OTUs on several criteria.

**FROGS ITSx** Extract the highly variable ITS1 and ITS2 subregions from ITS sequences.

**FROGS Affiliation OTU** Taxonomic affiliation of each OTU's seed by RDPtools and BLAST

Optional step to resolve inclusive amplicon ambiguities and to aggregate OTUs based on alignment metrics

**FROGS Abundance normalisation**

**FROGS Pre-process** merging, denoising and dereplication. (Galaxy Version 3.2.3+galaxy2)

**Sequencer**

Illumina

Select the sequencing technology used to produce the sequences.

**Input type**

Files by samples

Samples files can be provided in a single TAR archive or sample by sample (with one or two files each).

**Are reads already merged ?**

No

The inputs contain 1 file by sample : R1 and R2 pair are already merged in one sequence.

**Samples**

1: Samples

**Name**

The sample name.

! Please provide a value for this option.

**Reads 1**

No fastq dataset available.

**Reads 2**

No fastq dataset available.

R2 FASTQ file of paired-end reads.

Insert Samples

**16S**

2 shown

34.86 MB

**2: chaillou_withprimers_64renamedsamples_V1V3_10000seq_R1R2.tar.gz**

**1: metadata_chaillou.tsv**

# Vocabulary of Galaxy

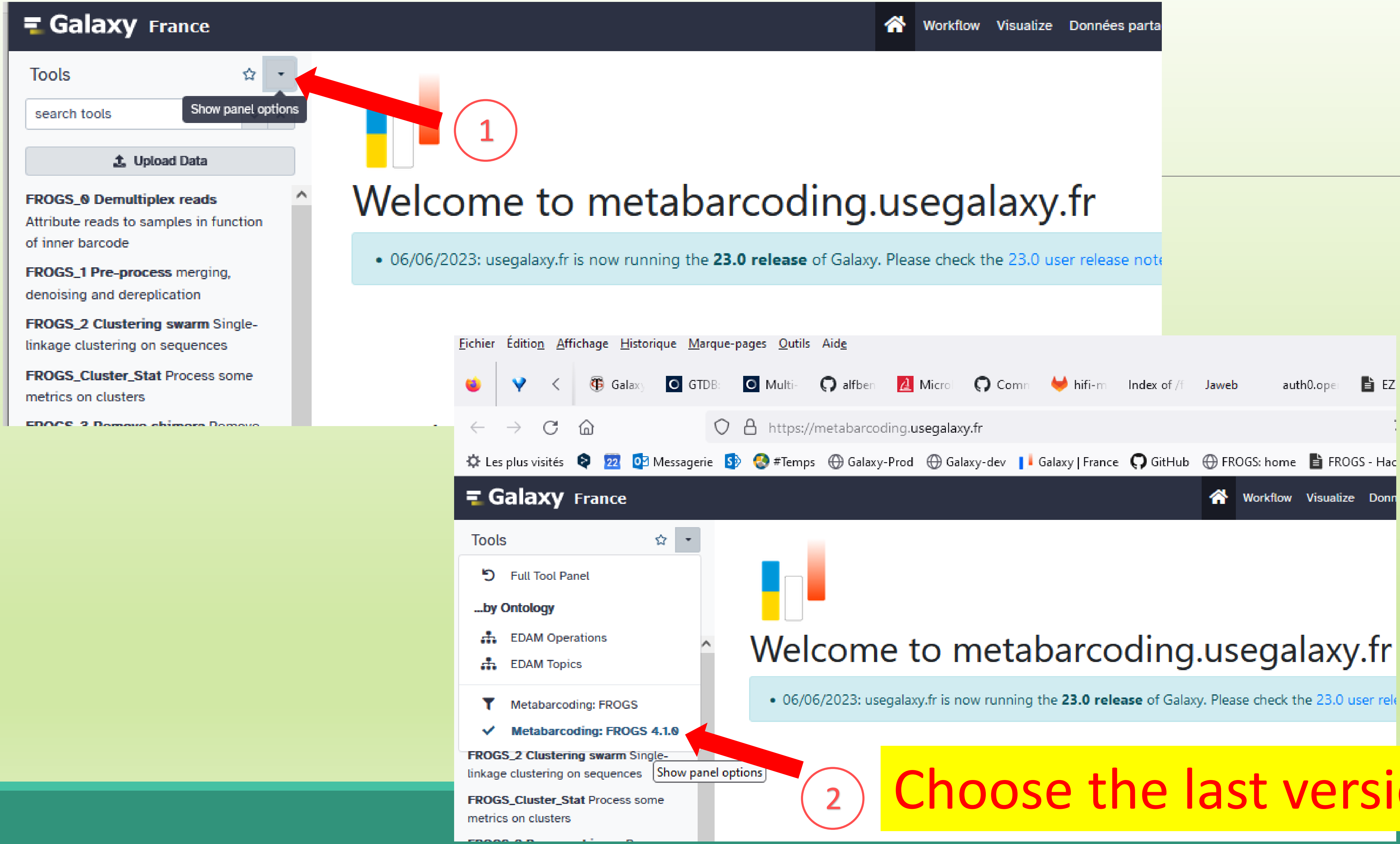
- **Tools:**
  - A tool has a function which is explained when you click on it.
  - Each Galaxy platform has its own tools.
- **Datasets:**
  - A dataset is a file, uploaded to Galaxy by you or produced by a tool.
  - Be careful: a dataset has a datatype.
- **Histories:**
  - A tool generates datasets and these datasets are stored in the current history.
  - Everything is permanently saved.
  - If you log off your computer or browser, it’s ok, everything will keep running and be saved!

# Pratice:

DISCOVER GALAXY

# Exercise

1. Visit the Galaxy Platform.
2. Look at the tool list.
3. Display only FROGS tools.
4. Display all tools concerning fastq files.



**FROGS_0 Demultiplex reads** Attribute reads to samples in function of inner barcode

**FROGS_1 Pre-process** merging, denoising and dereplication

**FROGS_2 Clustering swarm** Single-linkage clustering on sequences

**FROGS_Cluster_Stat** Process some metrics on clusters

Welcome to metabarcoding.usegalaxy.fr

- 06/06/2023: usegalaxy.fr is now running the **23.0 release** of Galaxy. Please check the 23.0 user release note

Choose the last version 4.1.

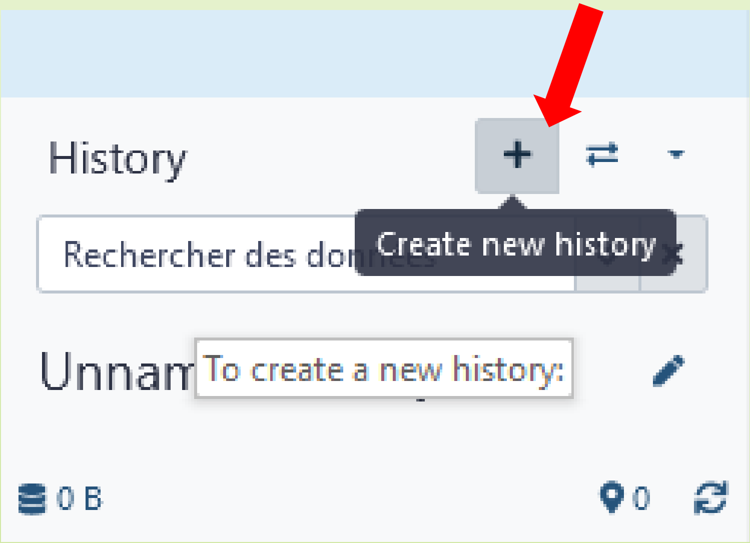
# Manipulate Histories

# Practice:

## CREATE THE NECESSARY HISTORY FOR FROGS TRAINING

# To create a new history:

- Click on the plus.



History

Rechercher des données

Create new history

Unnamed history

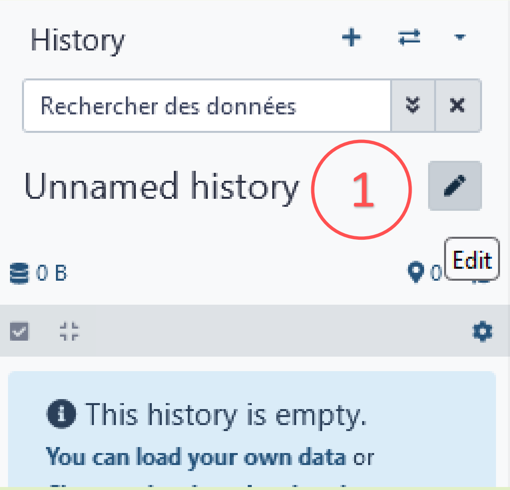
To create a new history:

0 B

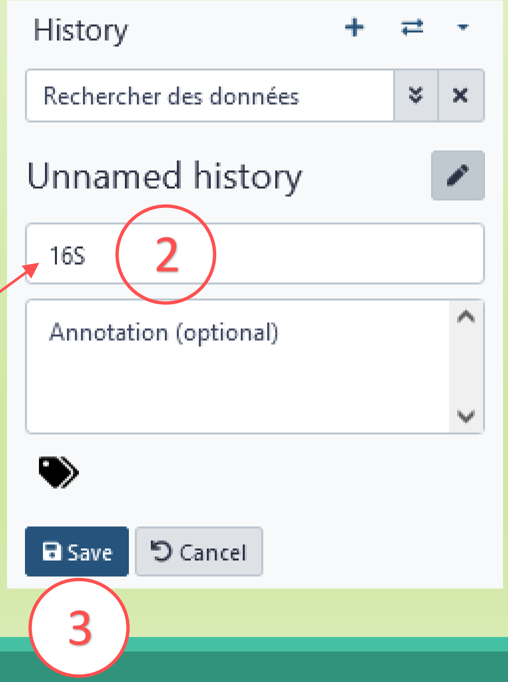
0

# To rename a history:

- Click on the pen ✏ next to “Unnamed history” (top right).
- Enter « 16S ».
- Hit « Enter » to validate.



This history is empty.
You can load your own data or



16S

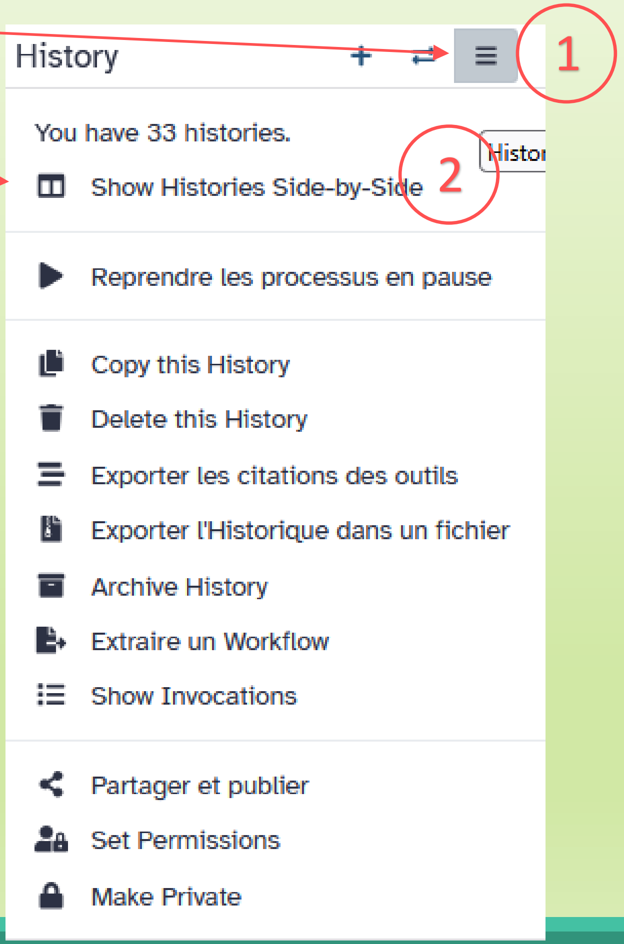
⚠ Don’t use special characters or accents!

# Exercise

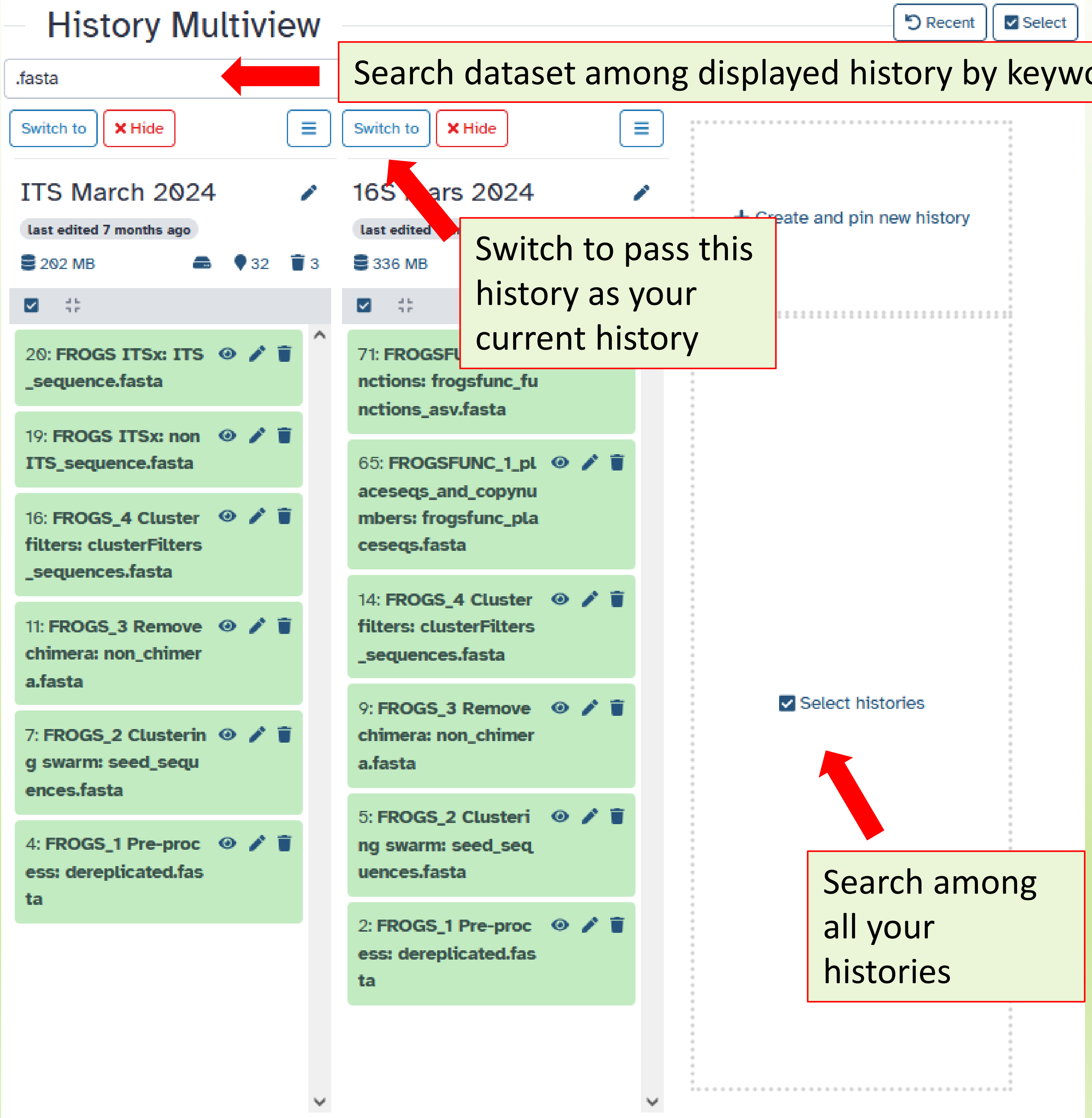
- Create another history as before with 16S. This new history will be named **ITS**

# How to list all histories?

1. To view all histories, click on this arrow
2. And click on



# Explore the « View all histories » section



## History Multiview

**ITS March 2024**

last edited 7 months ago

202 MB · 32 · 3

- 20: FROGS ITSx: ITS_sequence.fasta
- 19: FROGS ITSx: non ITS_sequence.fasta
- 16: FROGS_4 Cluster filters: clusterFilters_sequences.fasta
- 11: FROGS_3 Remove chimera: non_chimera.fasta
- 7: FROGS_2 Clustering swarm: seed_sequences.fasta
- 4: FROGS_1 Pre-process: dereplicated.fasta

**16S ars 2024**

last edited

336 MB

- 71: FROGSFU nctions: frogsfunc_functions_asv.fasta
- 65: FROGSFUNC_1_placeseqs_and_copynumbers: frogsfunc_placeseqs.fasta
- 14: FROGS_4 Cluster filters: clusterFilters_sequences.fasta
- 9: FROGS_3 Remove chimera: non_chimera.fasta
- 5: FROGS_2 Clustering swarm: seed_sequences.fasta
- 2: FROGS_1 Pre-process: dereplicated.fasta

Search dataset among displayed history by keywords

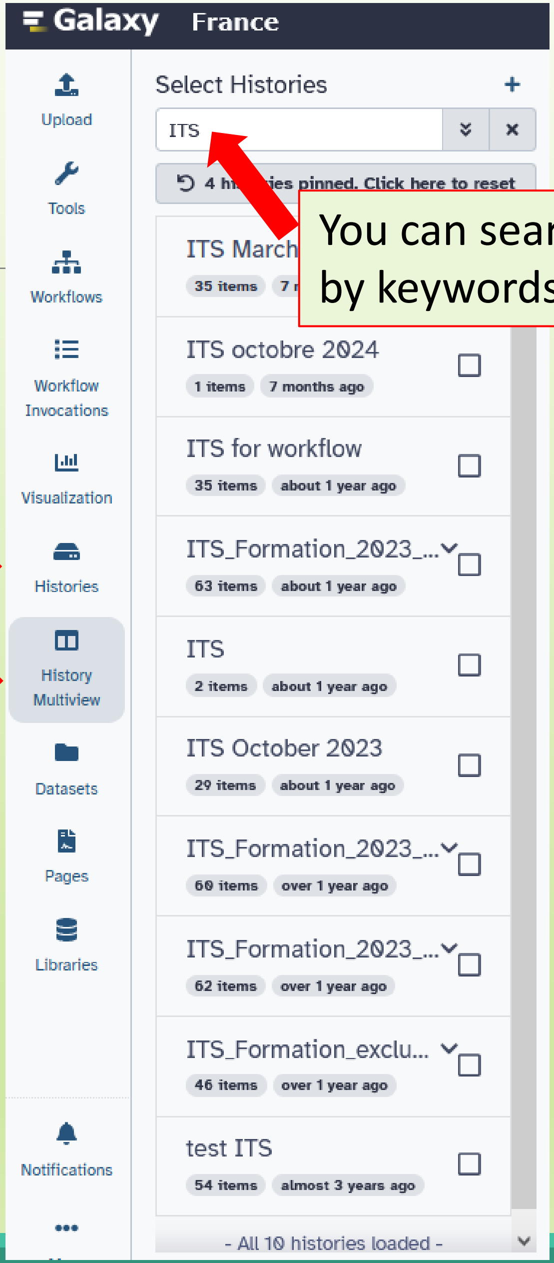
Switch to pass this history as your current history

Search among all your histories

# Choose your current history

1. To work on the good histoiries, navigate thanks to the sidebar

OR



Select Histories

ITS

4 hi ies pinned. Click here to reset

ITS March
35 items 7

ITS octobre 2024 ☐
1 items 7 months ago

ITS for workflow ☐
35 items about 1 year ago

ITS_Formation_2023_... ☐
63 items about 1 year ago

ITS ☐
2 items about 1 year ago

ITS October 2023 ☐
29 items about 1 year ago

ITS_Formation_2023_... ☐
60 items over 1 year ago

ITS_Formation_2023_... ☐
62 items over 1 year ago

ITS_Formation_exclu... ☐
46 items over 1 year ago

test ITS ☐
54 items almost 3 years ago

- All 10 histories loaded -

You can search by keywords

# Data import

# How to import your data to Galaxy ?

- Several ways to upload your data to Galaxy:
  - From your computer

drag-and-drop files

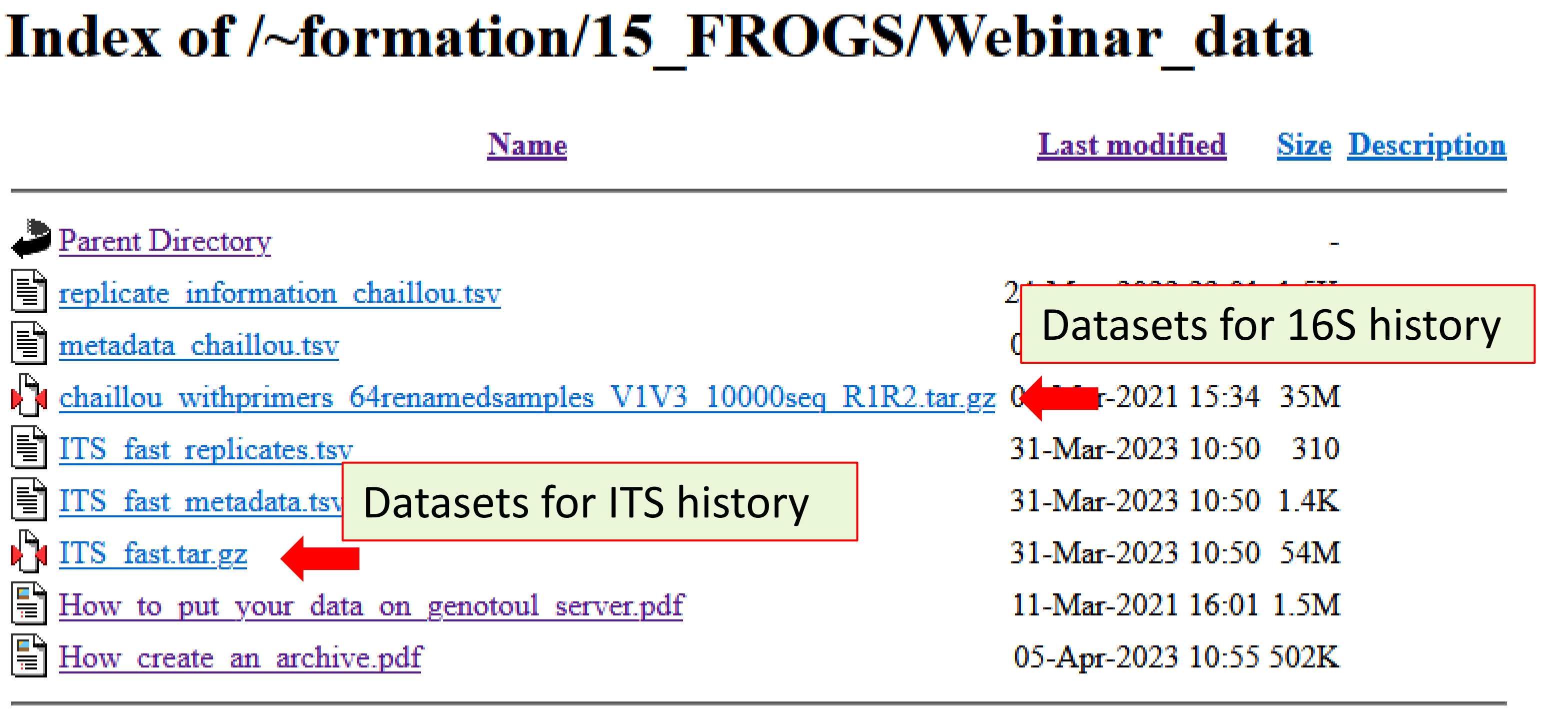
  - By URL

Paste an url

  - Shared by other users of Galaxy

# Formation data

- All the training data are online on: https://web-genobioinfo.toulouse.inrae.fr/~formation/15_FROGS/Webinar_data/



## Index of /~formation/15_FROGS/Webinar_data

| Name | Last modified | Size | Description |
|---|---|---|---|
| Parent Directory | | - | |
| replicate_information_chaillou.tsv | 2 | | |
| metadata_chaillou.tsv | 0 | | |
| chaillou_withprimers_64renamedsamples_V1V3_10000seq_R1R2.tar.gz | 0 r-2021 15:34 | 35M | |
| ITS_fast_replicates.tsv | 31-Mar-2023 10:50 | 310 | |
| ITS_fast_metadata.tsv | 31-Mar-2023 10:50 | 1.4K | |
| ITS_fast.tar.gz | 31-Mar-2023 10:50 | 54M | |
| How_to_put_your_data_on_genotoul_server.pdf | 11-Mar-2021 16:01 | 1.5M | |
| How_create_an_archive.pdf | 05-Apr-2023 10:55 | 502K | |

Datasets for 16S history

Datasets for ITS history

All samples are in archive .tar.gz

# Remark: how create an archive ?

**Not for this session**, but for your own data, it will be important to know how create an archive.

**To learn how create an archive**
https://web-genobioinfo.toulouse.inrae.fr/~formation/15_FROGS/Webinar_data/How_create_an_archive.pdf

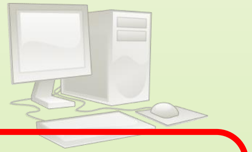
Create an archive is
always possible !
It is our recommendation.

# Practice: 16S history

## UPLOAD FILE FROM AN URL

# How to import your data to Galaxy ?

- Several ways to upload your data to Galaxy:
  - From your computer

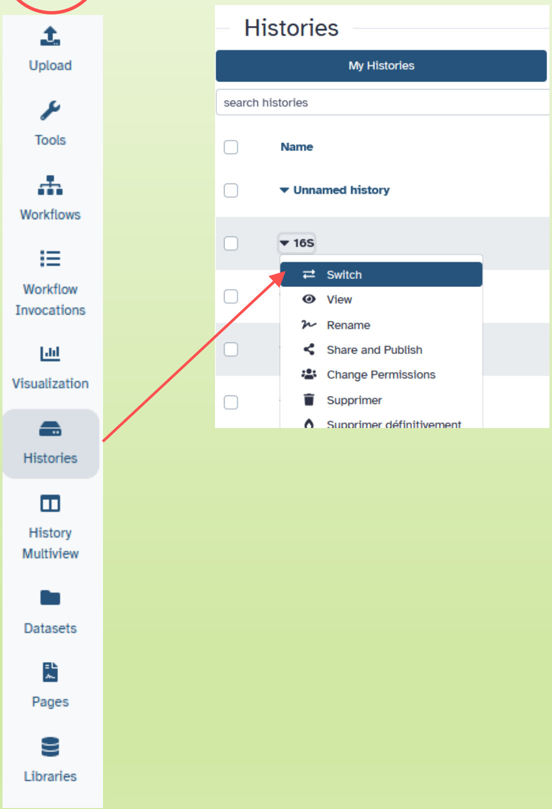


  - By URL

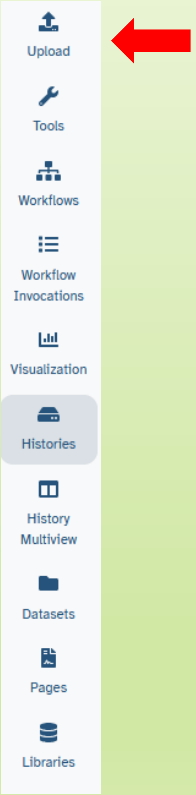
# 16S history creation

1. In your current history "**16S**" (If it not the case, switch to 16S history)
2. Go to **Upload Data** on the left panel

1

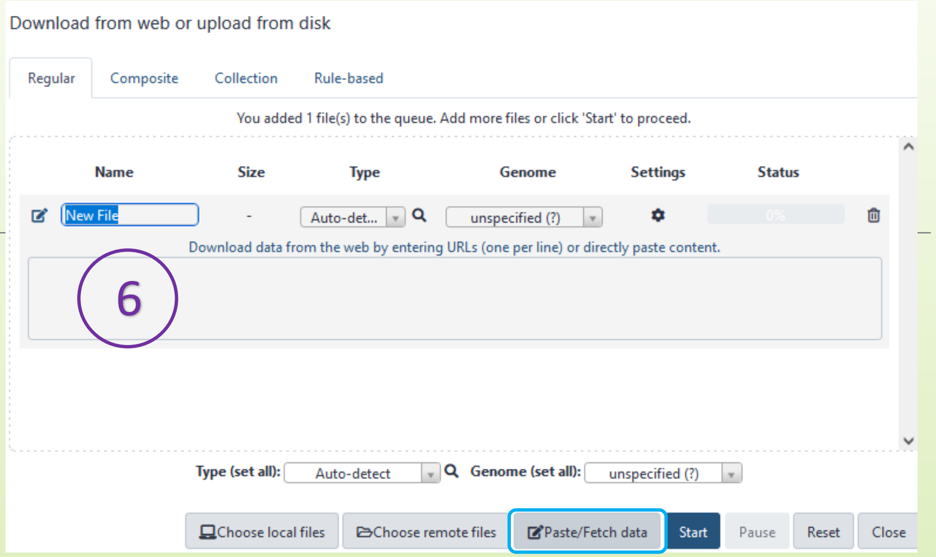


2



# 16S history creation

3. Click on **Paste/Fetch Data**



Download from web or upload from disk

You added 1 file(s) to the queue. Add more files or click 'Start' to proceed.

| Name | Size | Type | Genome | Settings | Status |
|---|---|---|---|---|---|
| New File | - | Auto-det... | unspecified (?) | | 0% |

Download data from the web by entering URLs (one per line) or directly paste content.

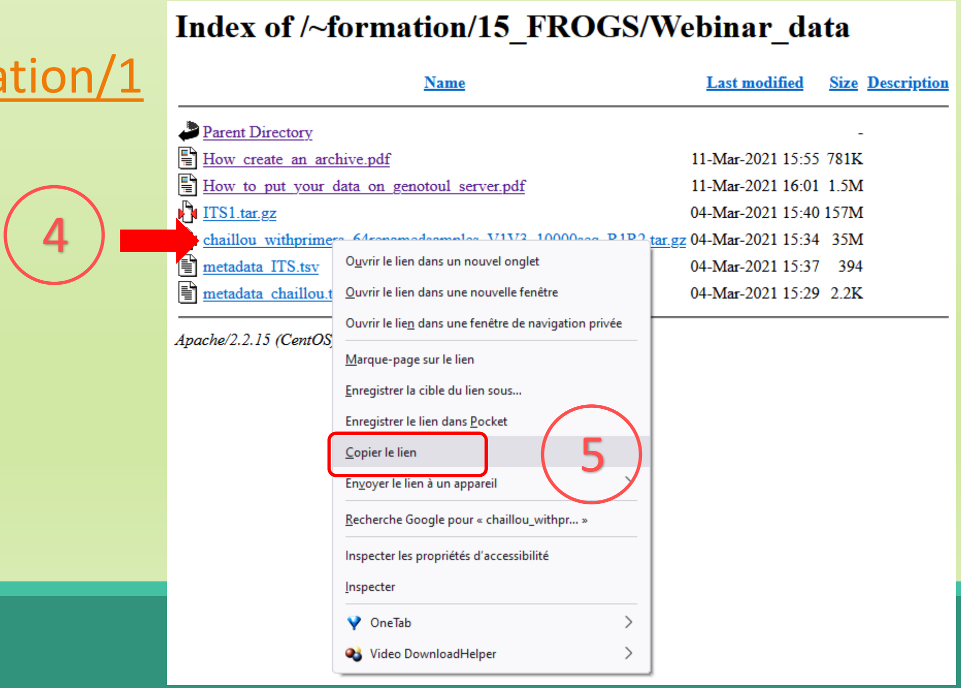
Type (set all): Auto-detect Genome (set all): unspecified (?)

4. Collect your data address on [https://web-genobioinfo.toulouse.inrae.fr/~formation/15_FROGS/Webinar_data/](https://web-genobioinfo.toulouse.inrae.fr/~formation/15_FROGS/Webinar_data/)

   Click right on the name file

5. Copy the address of the link

6. Paste the link in the grey window



**Index of /~formation/15_FROGS/Webinar_data**

| Name | Last modified | Size | Description |
|---|---|---|---|
| Parent Directory | | - | |
| How_create_an_archive.pdf | 11-Mar-2021 15:55 | 781K | |
| How_to_put_your_data_on_genotoul_server.pdf | 11-Mar-2021 16:01 | 1.5M | |
| ITS1.tar.gz | 04-Mar-2021 15:40 | 157M | |
| chaillou_withprimers_64renamedsamples_V1V3_10000seq_R1R2.tar.gz | 04-Mar-2021 15:34 | 35M | |
| metadata_ITS.tsv | 04-Mar-2021 15:37 | 394 | |
| metadata_chaillou.t | 04-Mar-2021 15:29 | 2.2K | |

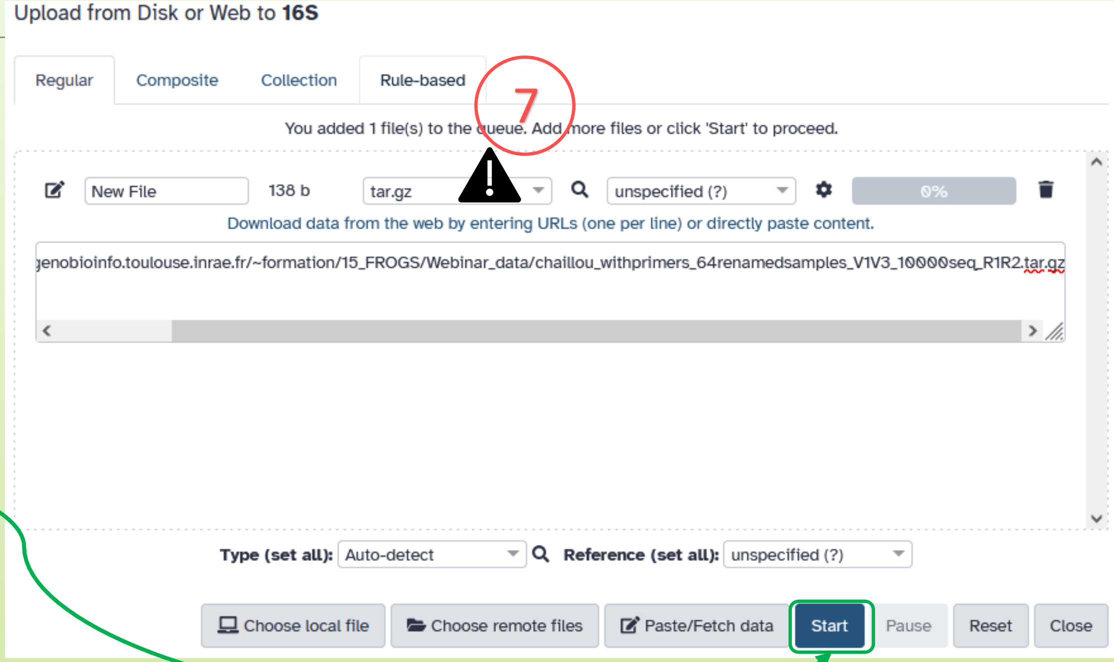
*Apache/2.2.15 (CentOS*

# 16S history creation

7. ⚠ Change the data type!

8. Click on Start

9. Start again with the file metadata_chaillou.tsv



Upload from Disk or Web to **16S**

You added 1 file(s) to the queue. Add more files or click 'Start' to proceed.

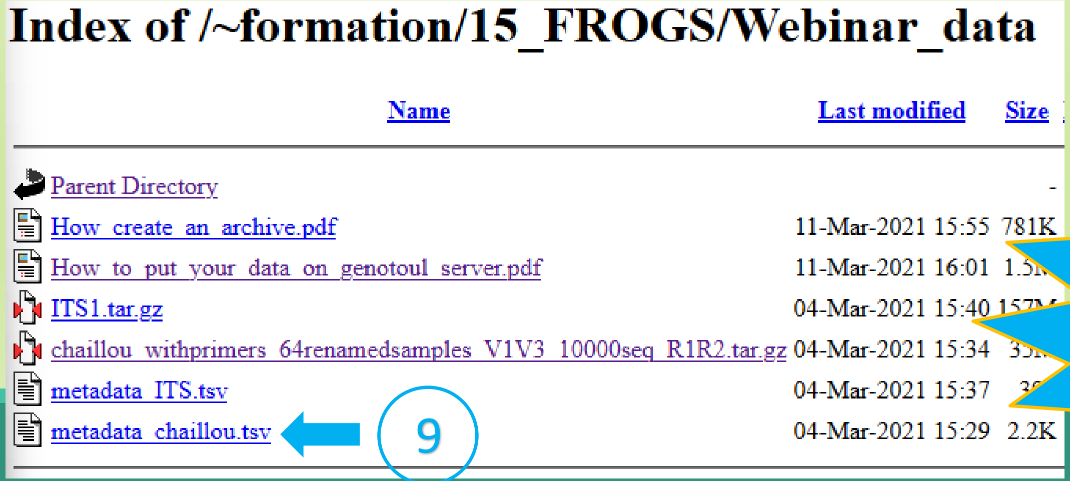
New File | 138 b | tar.gz | unspecified (?) | 0%

Download data from the web by entering URLs (one per line) or directly paste content.

genobioinfo.toulouse.inrae.fr/~formation/15_FROGS/Webinar_data/chaillou_withprimers_64renamedsamples_V1V3_10000seq_R1R2.tar.gz

**Type (set all):** Auto-detect **Reference (set all):** unspecified (?)

8



# Index of /~formation/15_FROGS/Webinar_data

| Name | Last modified | Size |
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| How_create_an_archive.pdf | 11-Mar-2021 15:55 | 781K |
| How_to_put_your_data_on_genotoul_server.pdf | 11-Mar-2021 16:01 | 1.5 |
| ITS1.tar.gz | 04-Mar-2021 15:40 | 157 |
| chaillou_withprimers_64renamedsamples_V1V3_10000seq_R1R2.tar.gz | 04-Mar-2021 15:34 | 35 |
| metadata_ITS.tsv | 04-Mar-2021 15:37 | 3 |
| metadata_chaillou.tsv | 04-Mar-2021 15:29 | 2.2K |

9

Remember to change your data type to TSV

# Share a History

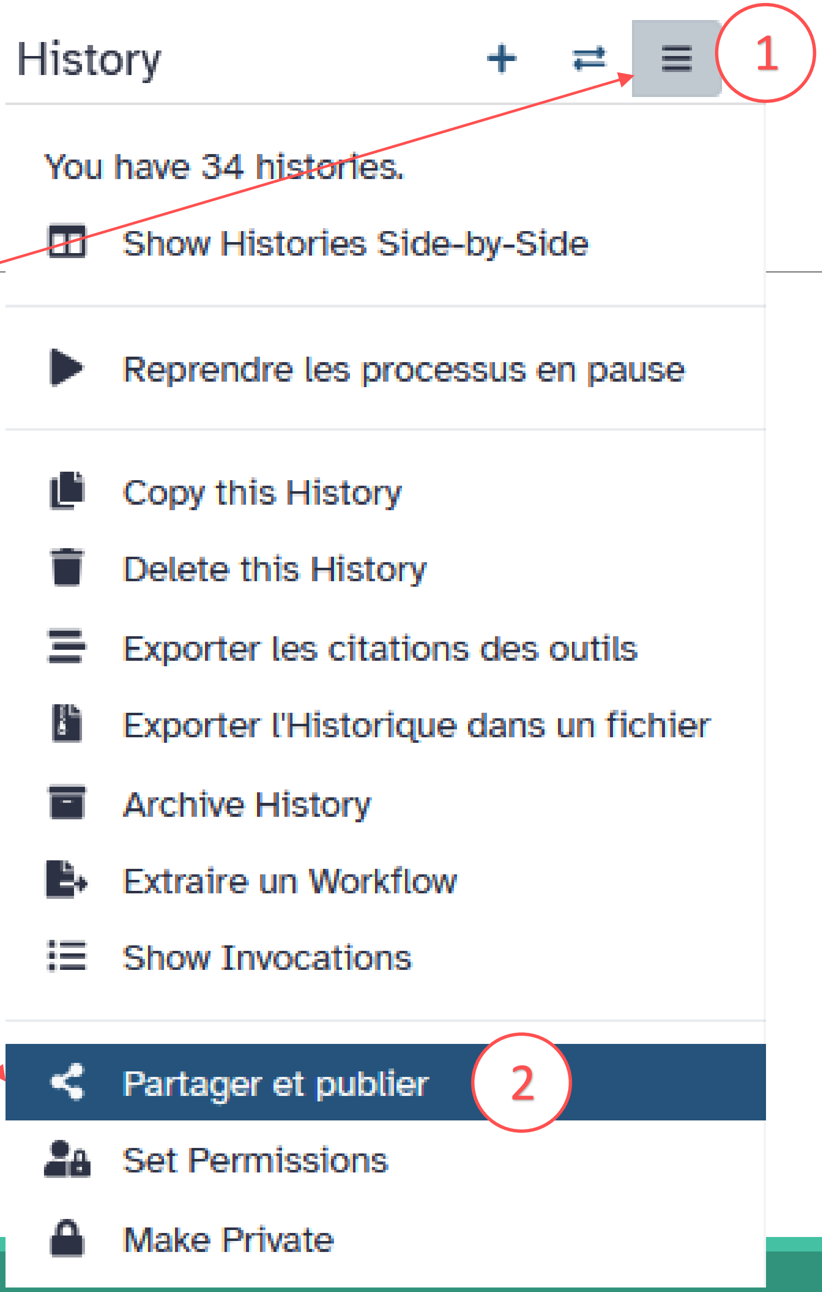
# Share a history

- You can share a history with another Galaxy user:
  - For working with your colleague.
  - For support, so we can help you better and faster.
- You can import shared history to your account too.

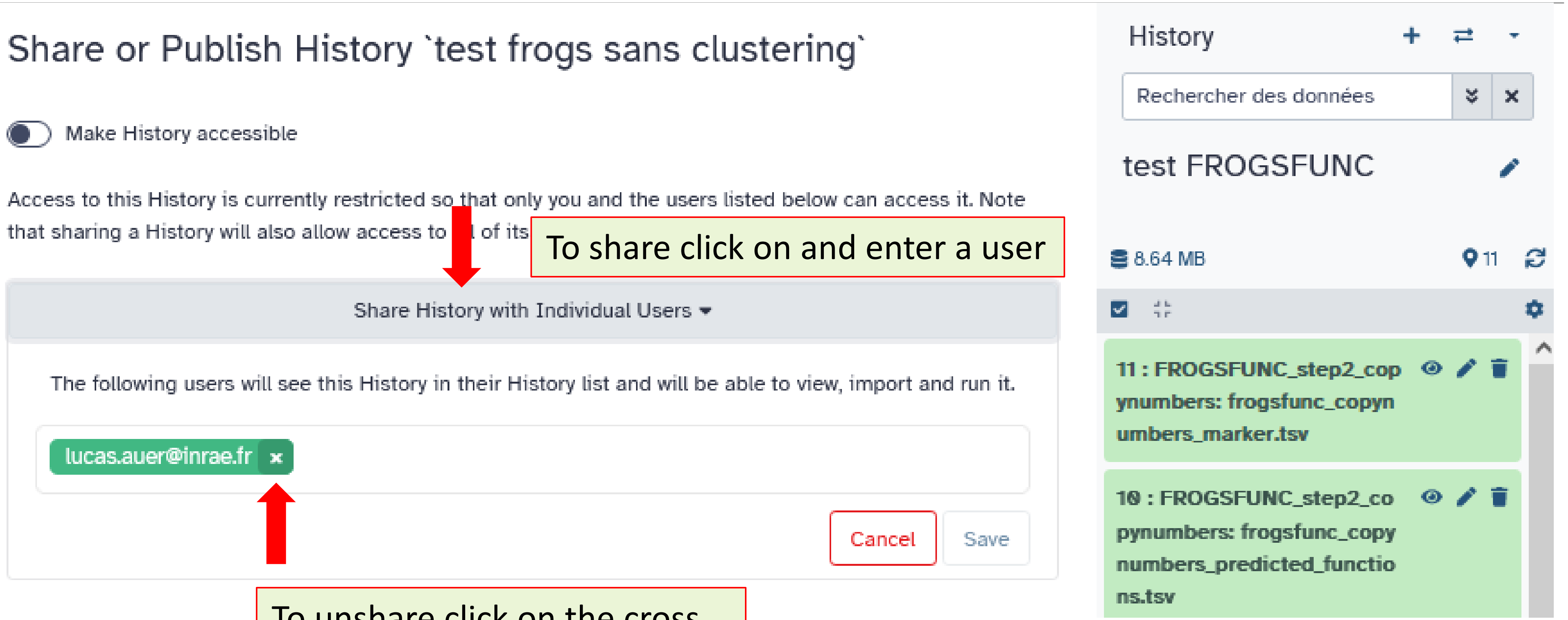
# Share a history

To share an history

1. Click on this arrow
2. Click on share and publish



# Share a history



Share or Publish History `test frogs sans clustering`

Make History accessible

Access to this History is currently restricted so that only you and the users listed below can access it. Note that sharing a History will also allow access to all of its

Share History with Individual Users ▾

The following users will see this History in their History list and will be able to view, import and run it.

lucas.auer@inrae.fr ×

To share click on and enter a user

To unshare click on the cross

# Share a history

## Share or Publish History `test frogs sans clustering`

Make History accessible

Make History publicly available in Published Histories

This History is currently **accessible via link.**

Anyone can view and import this History by visiting the following URL:

url: https://metabarcoding.usegalaxy.fr/u/geraldine.pascal/h/test-frogs-sans-clustering

to make your history public and visible to the whole world, click here

# Practice: share a history

SHARE 16S AND ITS HISTORIES WITH TRAINERS

# Share your data with us

- When your history “16S” is ready and contains the 2 files
  1. chaillou_withprimers_64renamedsamples_V1V3_10000seq_R1R2.tar.gz
  2. metadata_chaillou.tsv
- Then share with

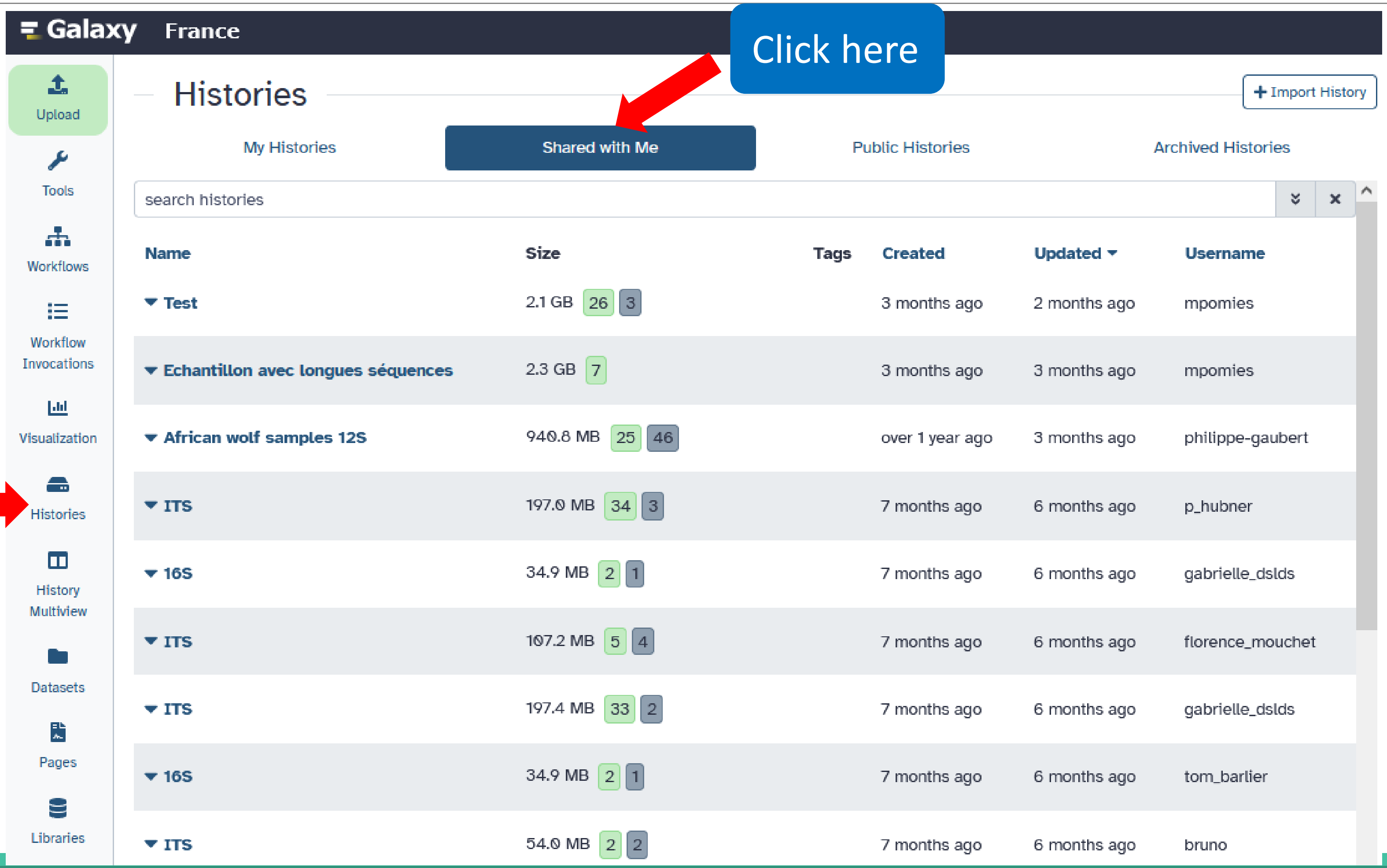
lucas.auer@inrae.fr ×

geraldine.pascal@inrae.fr ×

- Start again with the “ITS” history
- Contact us by email frogs-training@inrae.fr when it is done.

# Other useful things

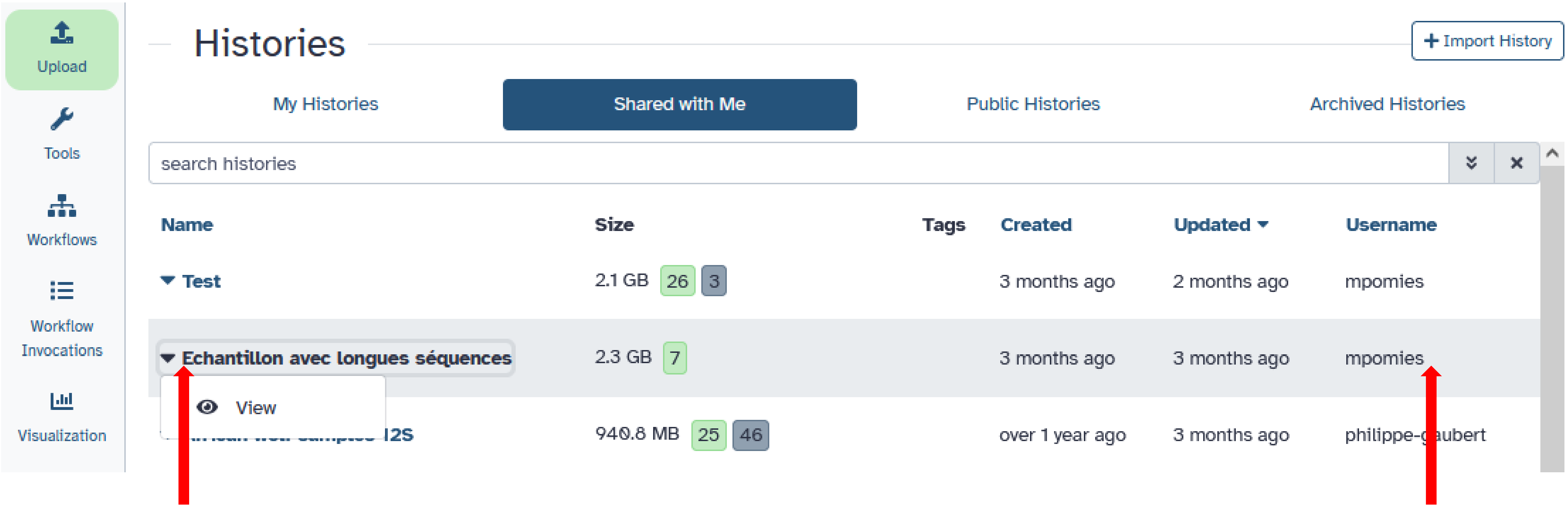
# Import a shared history



Click here

Click here

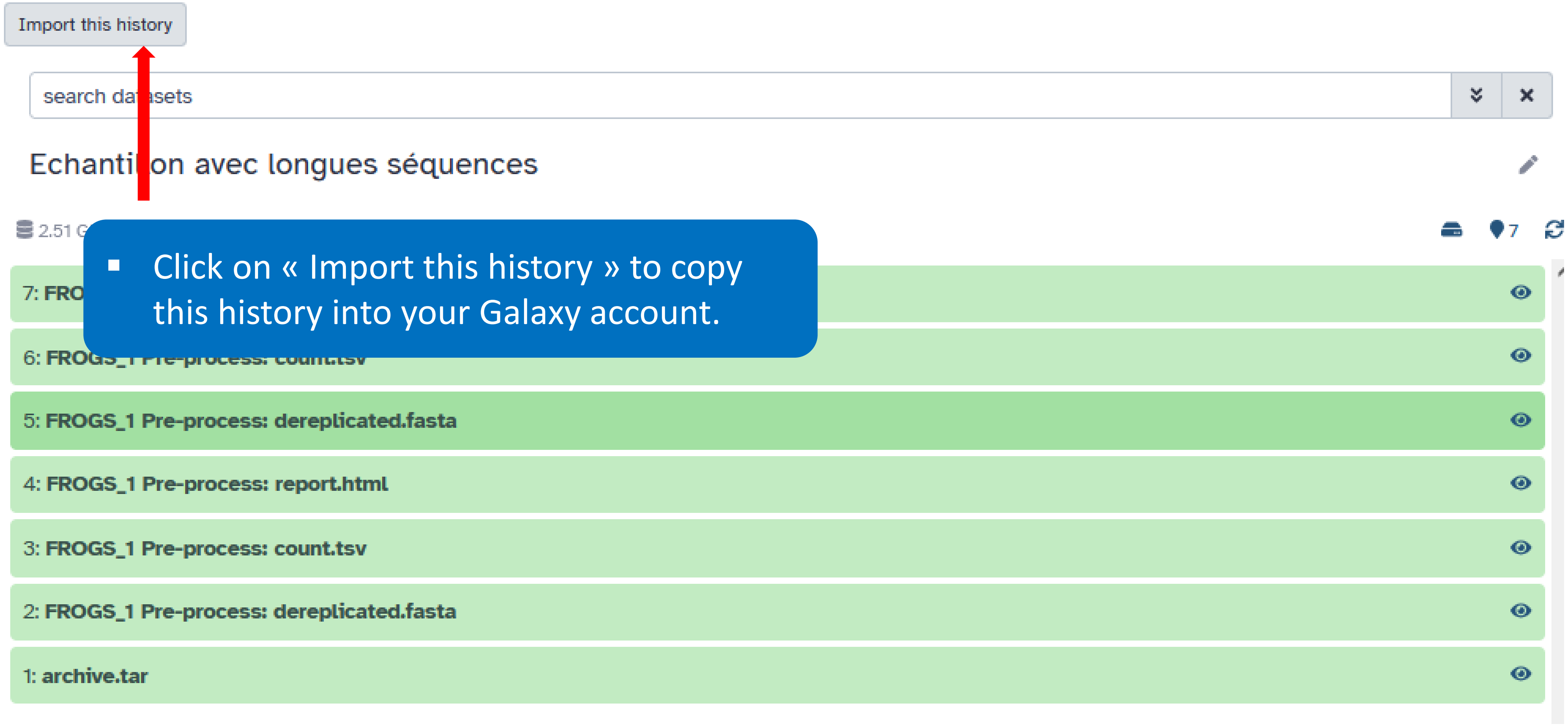
| Name | Size | Tags | Created | Updated ▾ | Username |
|---|---|---|---|---|---|
| ▾ Test | 2.1 GB 26 3 | | 3 months ago | 2 months ago | mpomies |
| ▾ Echantillon avec longues séquences | 2.3 GB 7 | | 3 months ago | 3 months ago | mpomies |
| ▾ African wolf samples 12S | 940.8 MB 25 46 | | over 1 year ago | 3 months ago | philippe-gaubert |
| ▾ ITS | 197.0 MB 34 3 | | 7 months ago | 6 months ago | p_hubner |
| ▾ 16S | 34.9 MB 2 1 | | 7 months ago | 6 months ago | gabrielle_dslds |
| ▾ ITS | 107.2 MB 5 4 | | 7 months ago | 6 months ago | florence_mouchet |
| ▾ ITS | 197.4 MB 33 2 | | 7 months ago | 6 months ago | gabrielle_dslds |
| ▾ 16S | 34.9 MB 2 1 | | 7 months ago | 6 months ago | tom_barlier |
| ▾ ITS | 54.0 MB 2 2 | | 7 months ago | 6 months ago | bruno |



| Name | Size | Tags | Created | Updated | Username |
|---|---|---|---|---|---|
| Test | 2.1 GB 26 3 | | 3 months ago | 2 months ago | mpomies |
| Echantillon avec longues séquences | 2.3 GB 7 | | 3 months ago | 3 months ago | mpomies |
| 12S | 940.8 MB 25 46 | | over 1 year ago | 3 months ago | philippe-gaubert |

- Click on the name and click on « View » to see an history into your Galaxy account.

The person who shared the history.



Echantillon avec longues séquences

2.51 G

7

7: FRO

6: FROGS_1 Pre-process: count.tsv

5: FROGS_1 Pre-process: dereplicated.fasta

4: FROGS_1 Pre-process: report.html

3: FROGS_1 Pre-process: count.tsv

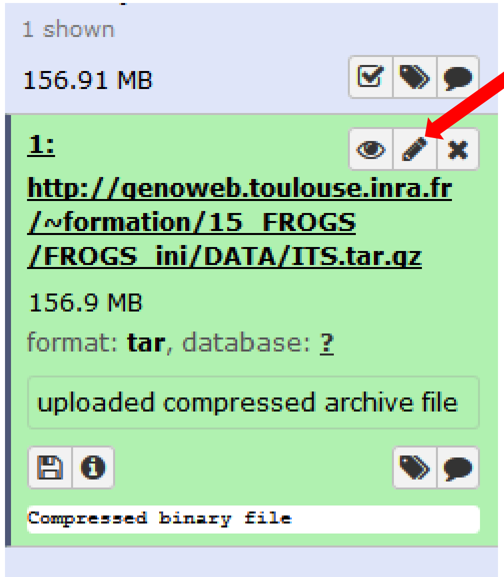
2: FROGS_1 Pre-process: dereplicated.fasta

1: archive.tar

- Click on « Import this history » to copy this history into your Galaxy account.

# How manipulate datasets

# To rename a dataset



1 shown

156.91 MB

**1: http://genoweb.toulouse.inra.fr/~formation/15_FROGS/FROGS_ini/DATA/ITS.tar.gz**

156.9 MB

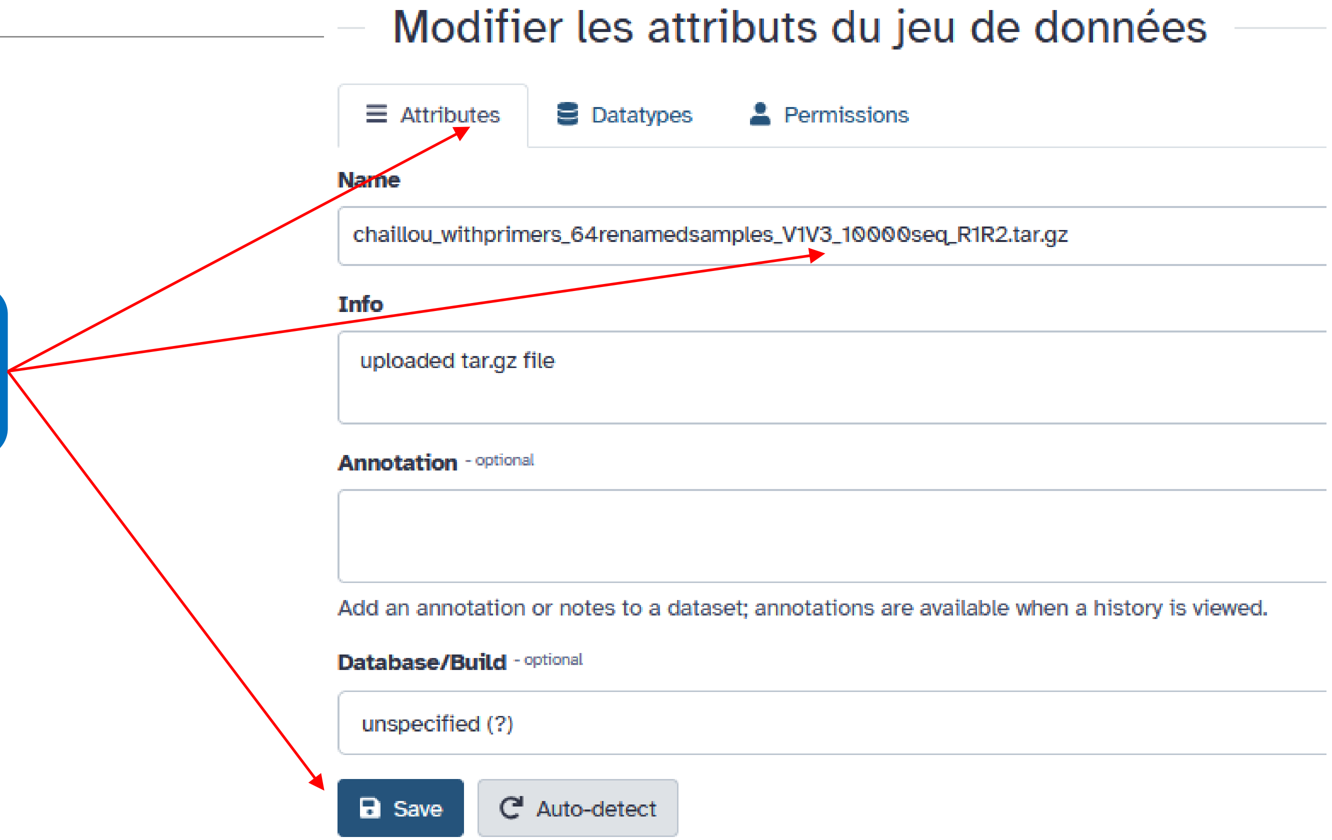
format: **tar**, database: ?

uploaded compressed archive file

```
Compressed binary file
```

Click here to display attributes and change the name.

# To rename a dataset



## Modifier les attributs du jeu de données

**Name**

chaillou_withprimers_64renamedsamples_V1V3_10000seq_R1R2.tar.gz

**Info**

uploaded tar.gz file

**Annotation** - optional

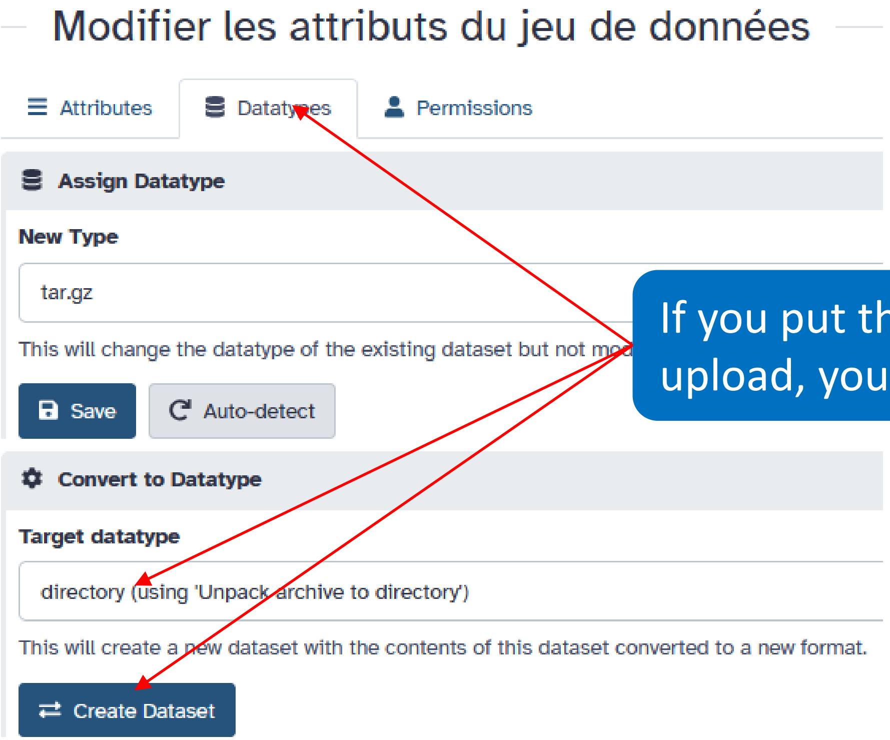
Add an annotation or notes to a dataset; annotations are available when a history is viewed.

**Database/Build** - optional

unspecified (?)

Change the name here

# To change the datatype



Modifier les attributs du jeu de données

**Assign Datatype**

**New Type**

tar.gz

This will change the datatype of the existing dataset but not mo

**Convert to Datatype**

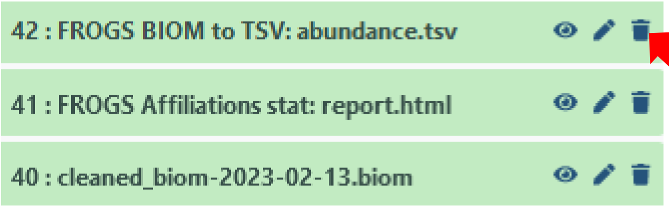
**Target datatype**

directory (using 'Unpack archive to directory')

This will create a new dataset with the contents of this dataset converted to a new format.

If you put the wrong datatype in during the upload, you can change it here.

# To delete a dataset



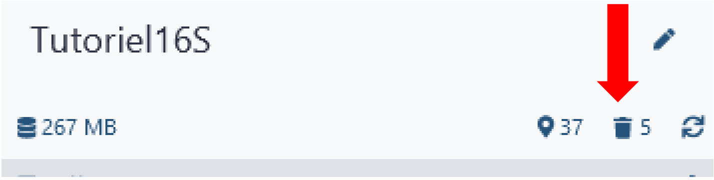
42 : FROGS BIOM to TSV: abundance.tsv

41 : FROGS Affiliations stat: report.html

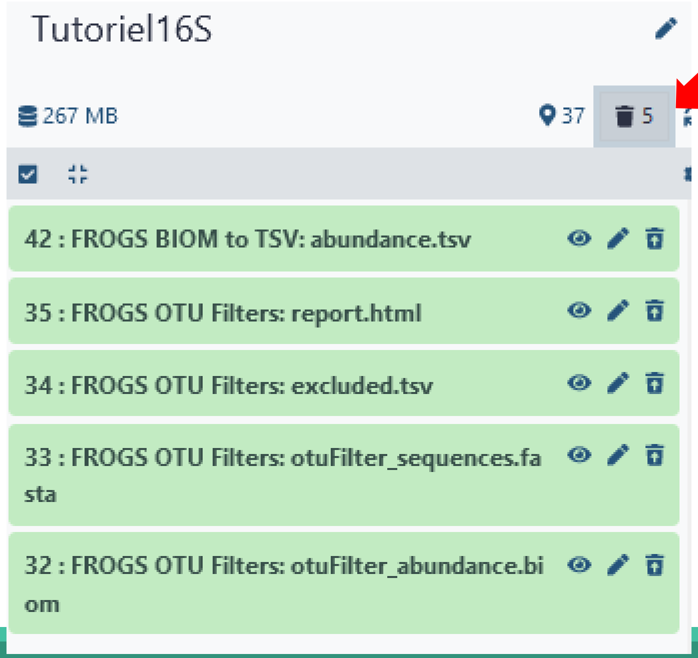
40 : cleaned_biom-2023-02-13.biom

Click here to delete a dataset.

# To see deleted dataset



Click here to see the deleted dataset.



42 : FROGS BIOM to TSV: abundance.tsv

35 : FROGS OTU Filters: report.html

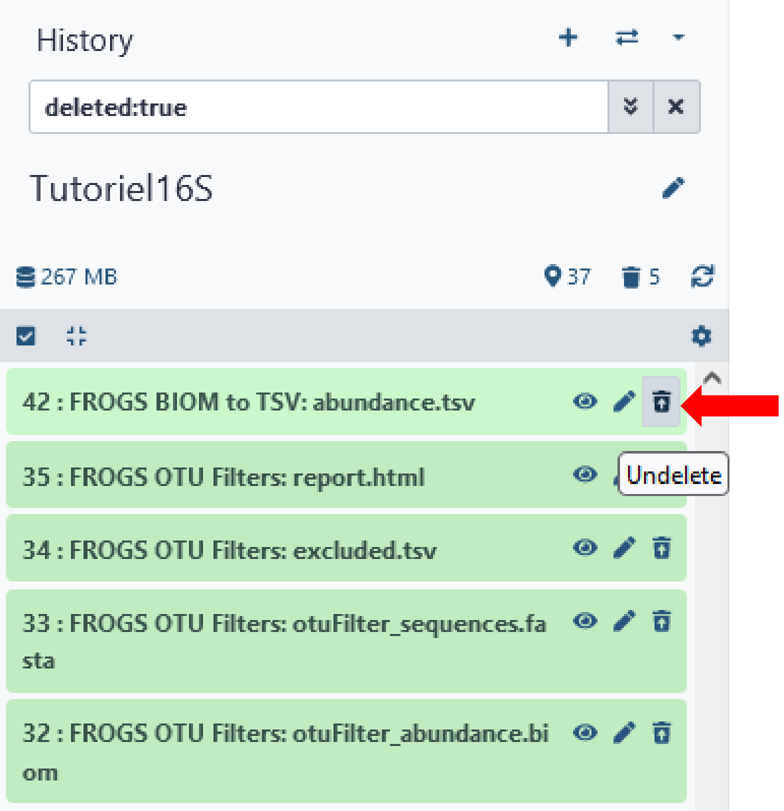
34 : FROGS OTU Filters: excluded.tsv

33 : FROGS OTU Filters: otuFilter_sequences.fasta

32 : FROGS OTU Filters: otuFilter_abundance.biom

Here the complete list of the deleted dataset.

# To undelete dataset



History

deleted:true

Tutoriel16S

267 MB 37 5

42 : FROGS BIOM to TSV: abundance.tsv

35 : FROGS OTU Filters: report.html

34 : FROGS OTU Filters: excluded.tsv

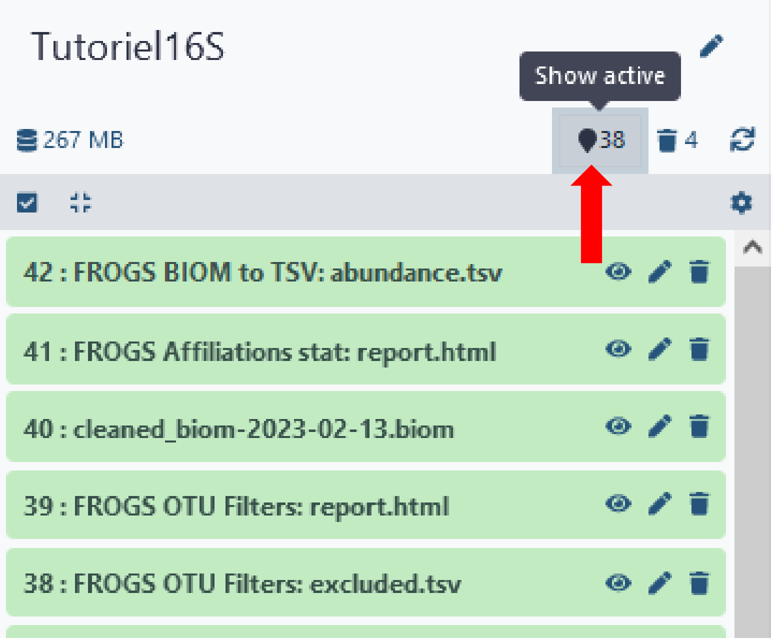
33 : FROGS OTU Filters: otuFilter_sequences.fasta

32 : FROGS OTU Filters: otuFilter_abundance.biom

Click here and this file return into the history

Nothing is deleted in Galaxy until you delete it permanently (=purge).

# To undelete dataset


Tutoriel16S

Show active

267 MB

38

4

42 : FROGS BIOM to TSV: abundance.tsv

41 : FROGS Affiliations stat: report.html

40 : cleaned_biom-2023-02-13.biom

39 : FROGS OTU Filters: report.html

38 : FROGS OTU Filters: excluded.tsv

Click here to sea again your active history

# How to cite Galaxy workbench?

For Genotoul Bioinfo:

- Research teams can thank the Toulouse Occitanie bioinformatics platform and Sigenae group, using in their publications the following sentence :  " We are grateful to the genotoul bioinformatics platform Toulouse Occitanie (Bioinfo Genotoul, doi: 10.15454/1.5572369328961167E12) and Sigenae group for providing help and/or computing and/or storage ressources thanks to Galaxy instance http://sigenae-workbench.toulouse.inra.fr".

- In cases of collaboration, you can directly quote the person who participated to the project : Name, Sigenae group, GenPhySE, INRAE Auzeville CS 52627 31326 Castanet Tolosan cedex.

For IFB:

- We are grateful to the Institut Français de Bioinformatique (ANR-11-INBS-0013) for providing help and/or computing and/or storage resources.

For Migale:

- Research teams that have used Migale services are expected to thank the Migale bioinformatics facility in the publications of their analyses with the following sentence: "We are grateful to the INRAE MIGALE bioinformatics facility (MIGALE, INRAE, 2020. Migale bioinformatics Facility, doi: 10.15454/1.5572390655343293E12) for providing help and/or computing and/or storage resources"

- In cases of collaboration, you can directly quote the person who participated to the project with the two following affiliations: Université Paris-Saclay, INRAE, MaIAGE, 78350, Jouy-en-Josas, France Université Paris-Saclay, INRAE, BioinfOmics, MIGALE bioinformatics facility, 78350, Jouy-en-Josas, France

# Thank you for following this first step, see you on Monday 12 May!

YOUR TRAINERS:

GÉRALDINE & LUCAS