

A — Pre-requisites: History

les mardis de la grenouille — FROGS 4.1

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Where to use Galaxy?

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

The image displays three vertical panels, each representing a different Galaxy installation location. Each panel lists technical specifications and provides navigation buttons.

- Genotoul Bioinfo:**
 - Location: **Toulouse**
 - Compute (#CPU HT*): **6224**
 - Storage (#TB): **4400**
 - RAM (#GB): **36500**
 - RAM/core (#GB): **5.56**
 - GPU (#Card): **1**
- mig:ole:**
 - Location: **Jouy en Josas**
 - Compute (#CPU HT*): **1016**
 - Storage (#TB): **350**
 - RAM (#GB): **7000**
 - RAM/core (#GB): **6.89**
 - GPU (#Card): **-**
- IFB CORE:**
 - Location: **Orsay (IDRIS)**
 - Compute (#CPU HT*): **4300**
 - Storage (#TB): **2400**
 - RAM (#GB): **20008**
 - RAM/core (#GB): **4.65**
 - GPU (#Card): **-**

Each panel includes a 'Demande de compte' button, a 'Support communautaire' button, and a 'Documentation' button. The bottom of each panel features the Galaxy logo and, for the IFB CORE panel, logos for R Studio and GitLab.



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 Platform: 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.

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.](#)

Login

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

Exercise

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

Galaxy France

Workflow Visualize Données parta

Tools

search tools

Show panel options

Upload Data

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

1

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](#)

Fichier Édition Affichage Historique Marque-pages Outils Aide

Galaxy GTDB: Multi- alfben Micro Comn hifi-m Index of /f Jaweb auth0.open EZ

https://metabarcoding.usegalaxy.fr

Les plus visités 22 Messengerie #Temps Galaxy-Prod Galaxy-dev Galaxy | France GitHub FROGS: home FROGS - Hac

Galaxy France

Workflow Visualize Donn

Tools

Full Tool Panel

...by Ontology

EDAM Operations

EDAM Topics

Metabarcoding: FROGS

✓ **Metabarcoding: FROGS 4.1.0**

FROGS_2 Clustering swarm Single-linkage clustering on sequences

FROGS_Cluster_Stat Process some metrics on clusters

Show panel options

2

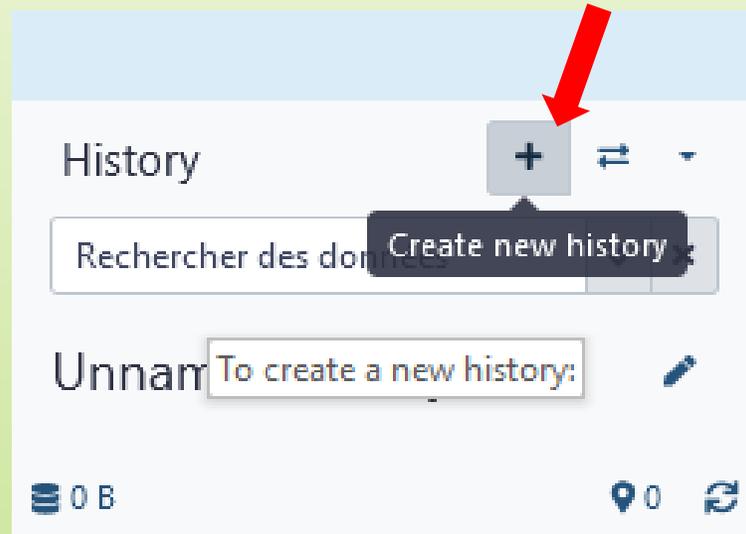
Welcome to metabarcoding.usegalaxy.fr

• 06/06/2023: usegalaxy.fr is now running the **23.0 release** of Galaxy. Please check the [23.0 user rel](#)

Choose the last version 4.1.0

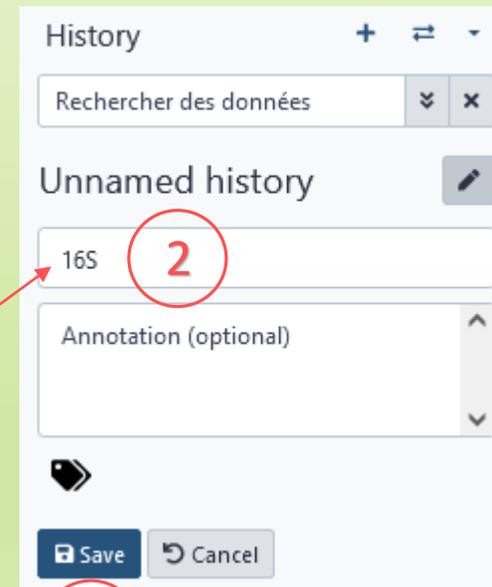
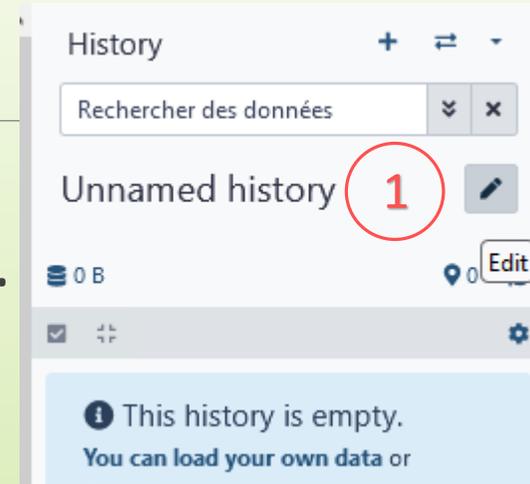
To create a new history:

- Click on the plus.



To rename a history:

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



3

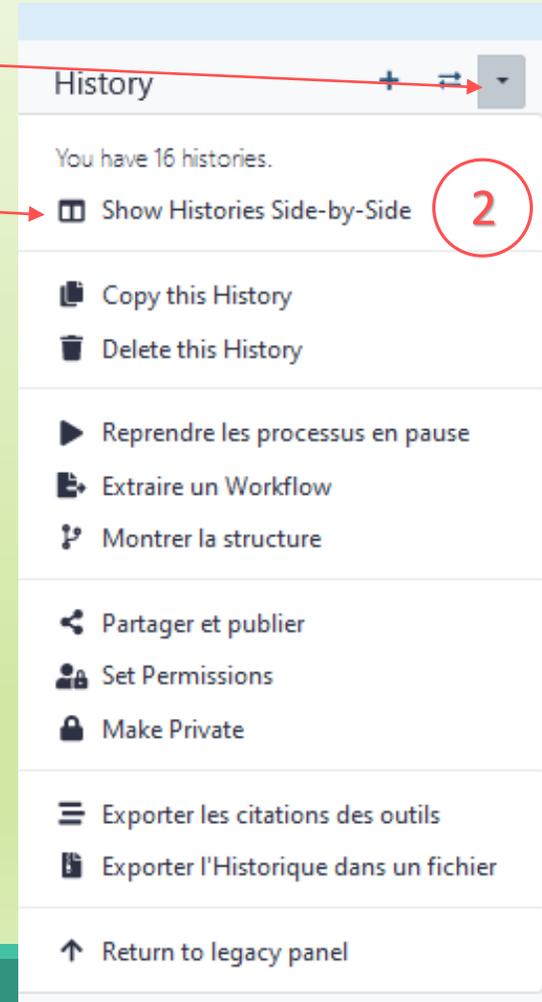


Exercise

- 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

.fasta

16S

36.5 MB

No data found for selected filter.

- 37 : FROGS OTU Filters: otuFilter_sequences.fasta
- 27 : FROGS Affiliation Filters: affiliationFilters_sequences.fasta
- 15 : FROGS OTU Filters: otuFilter_sequences.fasta
- 10 : FROGS Remove chimera: non_chimera.fasta
- 6 : FROGS Clustering swarm: seed_sequences.fasta
- 3 : FROGS Pre-process: dereplicated.fasta
- 56 : FROGS ITSx: ITSx_sequences.fasta
- 55 : FROGS ITSx: no ITS_sequences.fasta
- 52 : FROGS ITSx: ITSx_sequences.fasta
- 51 : FROGS ITSx: no ITS_sequences.fasta
- 48 : FROGS ITSx: ITSx_sequences.fasta
- 47 : FROGS ITSx: no ITS_sequences.fasta
- 44 : FROGS ITSx: ITSx_sequences.fasta
- 43 : FROGS ITSx: no ITS_sequences.fasta
- 42 : Galaxy29-[FROGS_4_Cluster_filters_clusterFilters_sequences.fasta].fasta
- 35 : FROGSFUNC_step1_placeseqs: frogfunc_placeseqs.fasta
- 25 : FROGS ITSx: ITSx_sequences.fasta

Select histories

Switch to Hide

Switch to Hide

Switch to Hide

Search dataset among displayed history by keywords

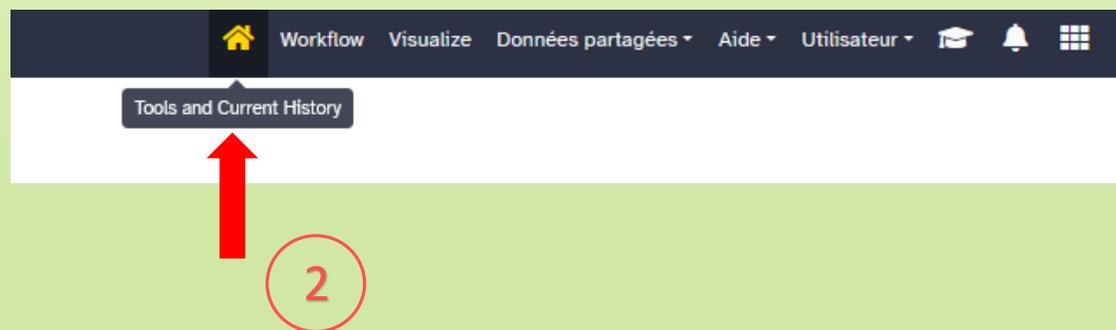
Switch to pass this history as your current history

Search among all your histories

Switch current history

1. When you are several histories, switch to the history named « 16S » as current history

2. You can click on “home” to go back to the main interface.



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:
http://genoweb.toulouse.inra.fr/~formation/15_FROGS/Webinar_data/

Index of /~formation/15_FROGS/Webinar_data

<u>Name</u>	<u>Last modified</u>	<u>Size</u>	<u>Description</u>
 Parent Directory	-	-	-
 replicate information chaillou.tsv	2023-03-31 10:50	310	
 metadata chaillou.tsv	2023-03-31 10:50	1.4K	
 chaillou withprimers 64renamedsamples V1V3 10000seq R1R2.tar.gz	07-Mar-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

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

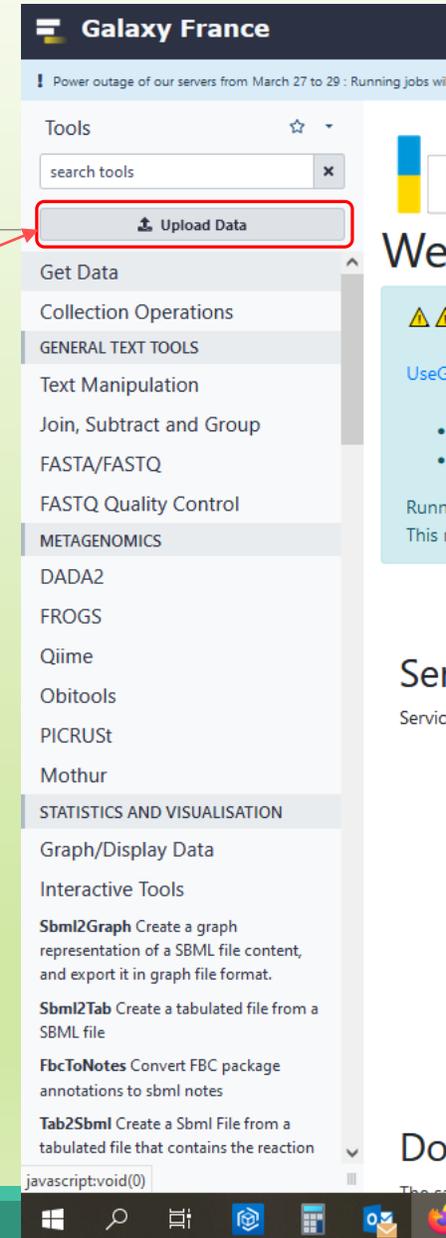


- By URL



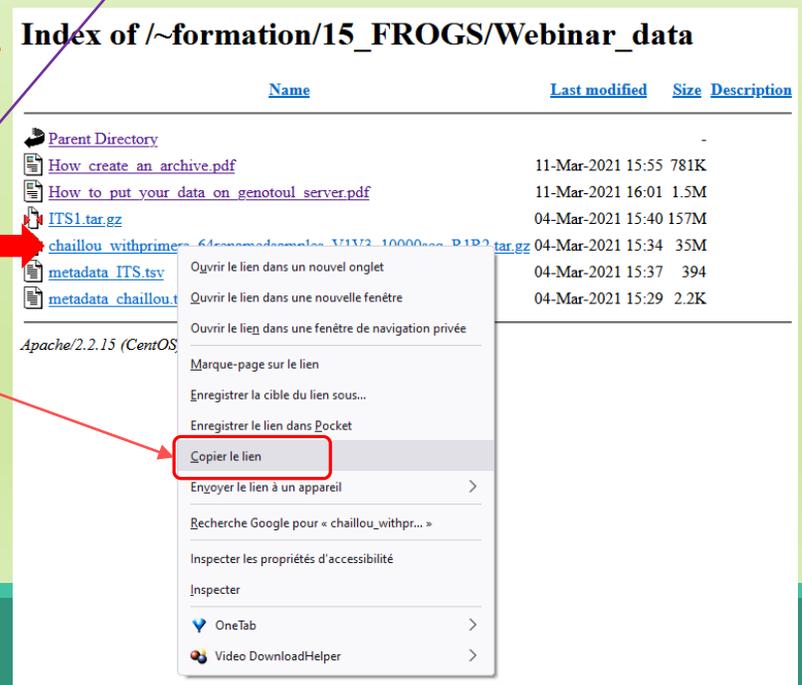
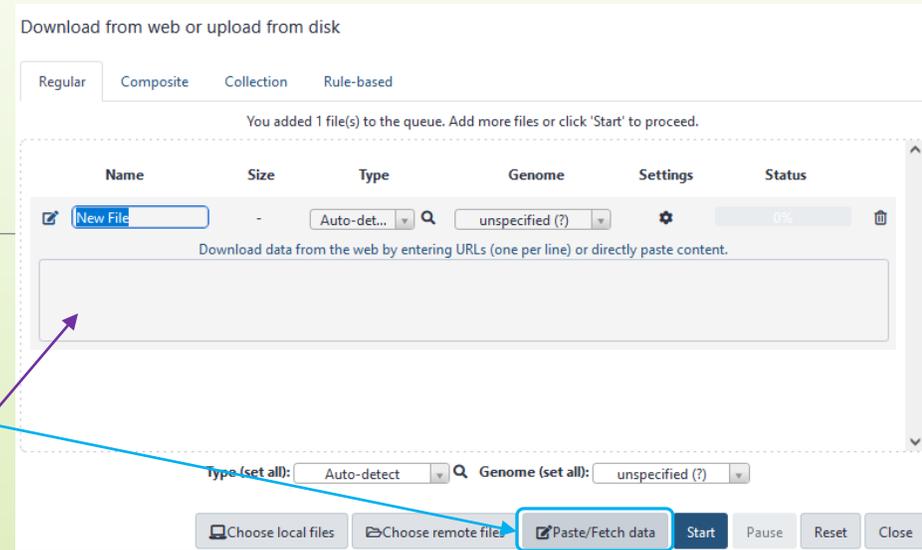
16S history creation

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



16S history creation

3. Click on **Paste/Fetch Data**
4. Collect your data address on [http://genoweb.toulouse.inra.fr/~formation/15 FROGS/Webinar data/](http://genoweb.toulouse.inra.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

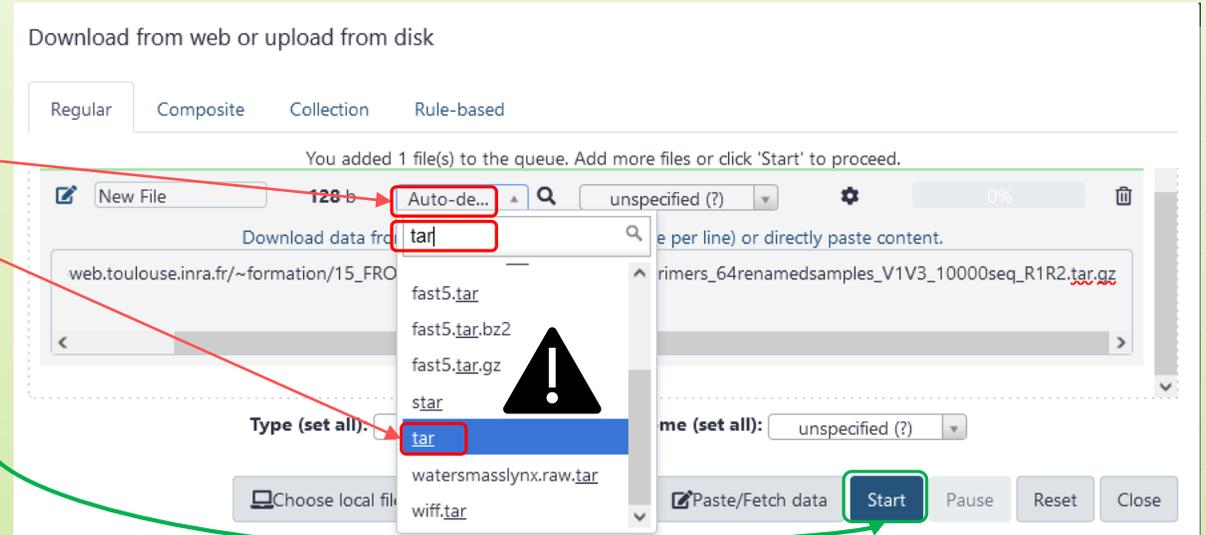


16S history creation

7.  Change the data type!

8. Click on Start

9. Start again with the file metadata_chaillou.tsv



Index of /~formation/15_FROGS/Webinar_data

	Name	Last modified	Size
	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	36K
	metadata_chaillou.tsv	04-Mar-2021 15:29	2.2K

**Remember to
change your
data type to TSV**

ITS history creation

Create a new history for ITS:

http://genoweb.toulouse.inra.fr/~formation/15_FROGS/Webinar_data/

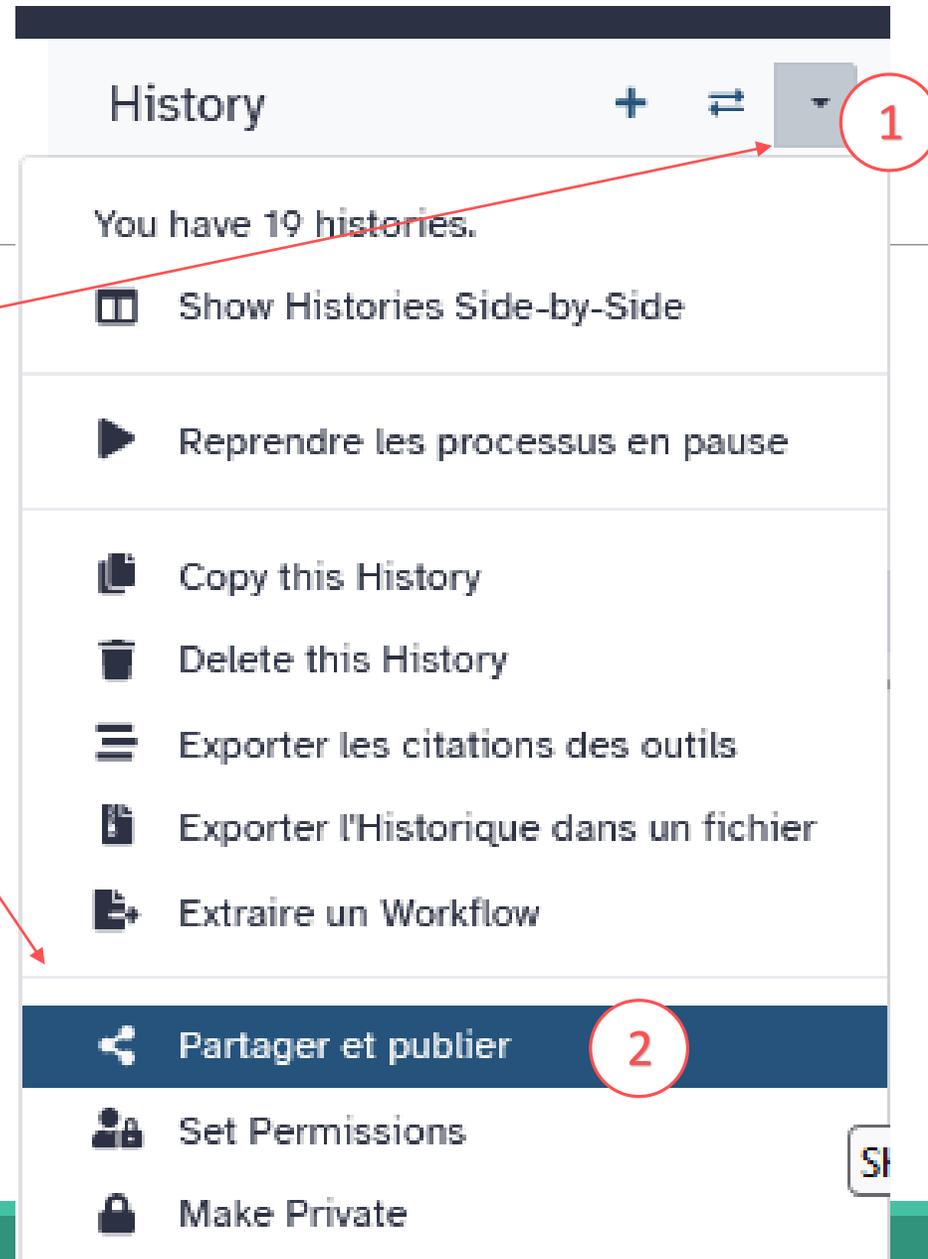
Index of /~formation/15_FROGS/Webinar_data

<u>Name</u>	<u>Last modified</u>	<u>Size</u>	<u>Description</u>
 Parent Directory		-	
 replicate information chaillou.tsv	24-May-2022 23:01	1.5K	
 metadata chaillou.tsv	04-Mar-2021 15:29	2.2K	
 chaillou withprimers 64renamedsamples V1V3 10000seq R1R2.tar.gz	04-Mar-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	

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

To share click on and enter a user

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 ✕

Cancel Save

To unshare click on the cross

History + ⇄ ▾

Rechercher des données ▾ ✕

test FROGSFUNC ✎

8.64 MB 11 ↻

⇄ ⚙

11 : FROGSFUNC_step2_cop 👁 ✎ 🗑
ynumbers: frogsfunc_copyn
umbers_marker.tsv

10 : FROGSFUNC_step2_co 👁 ✎ 🗑
pynumbers: frogsfunc_copy
numbers_predicted_functio
ns.tsv

Share a history

Share or Publish History `test frogs sans clustering`

- Make History accessible
- Make History publicly available in Published Histories

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

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

Practice: share a history

SHARE 16S HISTORY WITH TRAINERS

Share your data with us

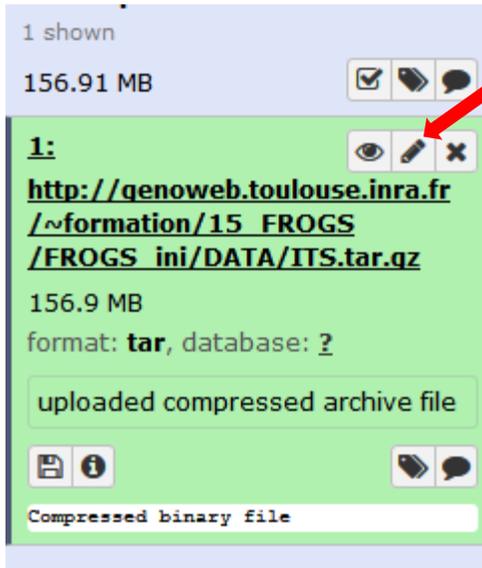


- When your history “16S” is ready and contains the 2 files
 1. chaillou_withprimers_64renamedsamples_V1V3_10000seq_R1R2.tar.gz
 2. metadata_chaillou.tsv
- Then share with `geraldine.pascal@inrae.fr`
- Contact me by email geraldine.pascal@inrae.fr when it is done.

Other useful things

To rename a dataset

Click here to display attributes and change the name.



1 shown
156.91 MB

1:
http://genoweb.toulouse.inra.fr/~formation/15_FROGS/FROGS_ini/DATA/ITS.tar.qz
156.9 MB
format: **tar**, database: ?
uploaded compressed archive file
Compressed binary file

To rename a dataset

Change the name here

The screenshot shows a web interface for editing a dataset. At the top, there are three tabs: 'Attributes' (selected), 'Convert', and 'Permissions'. Below the tabs, the 'Name' field contains the text 'FROGS_2 Clustering swarm: seed_sequences.fasta'. Underneath is the 'Info' section, which includes a '## Application' field with the value 'Software :/shared/ibfstor1/galaxy/mutable-data/dependencies/_cor'. Below that is an 'Annotation' section with a text area and a note: 'Add an annotation or notes to a dataset; annotations are available wh'. At the bottom, there is a 'Database/Build' field with the value 'unspecified (?)'. At the very bottom, there are two buttons: 'Save' and 'Auto-detect'. Three red arrows originate from the blue callout box 'Change the name here': one points to the 'Attributes' tab, one points to the 'Name' text input field, and one points to the 'Save' button.

To change the datatype

Attributes Convert Permissions

Convert

Target datatype

tabular (using 'Convert FASTA to Tabular')

This will create a new dataset with the contents of this dataset

Create Dataset

Datatypes

New Type

fasta

This will change the datatype of the existing dataset but not modify its contents

Save Auto-detect

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

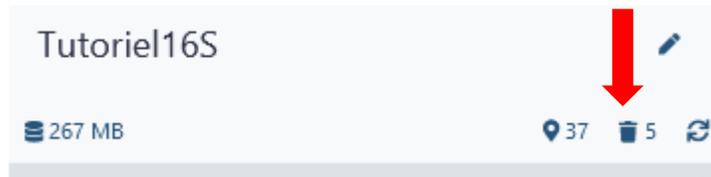
To delete a dataset

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

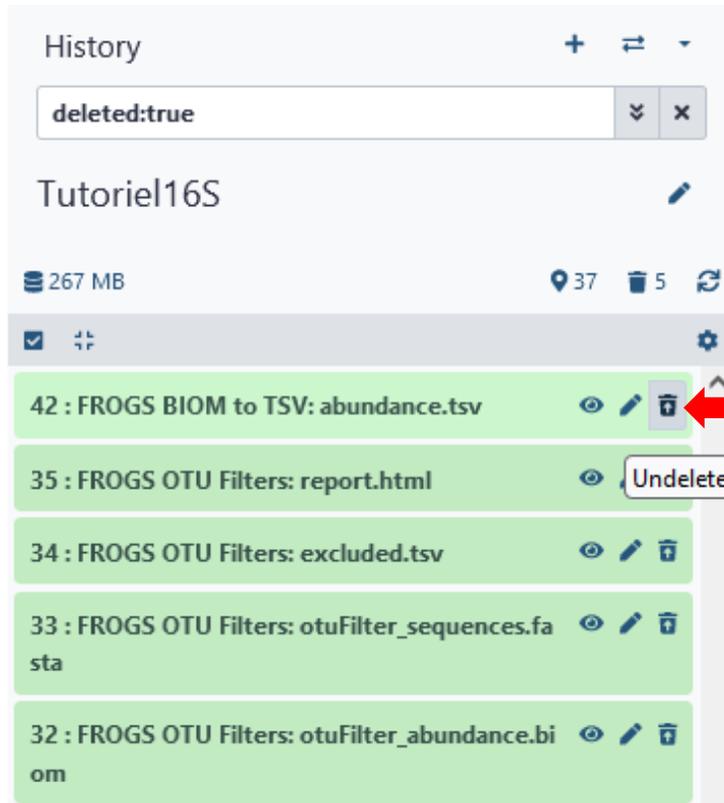


Click here to see deleted dataset.



Here the complete list of 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

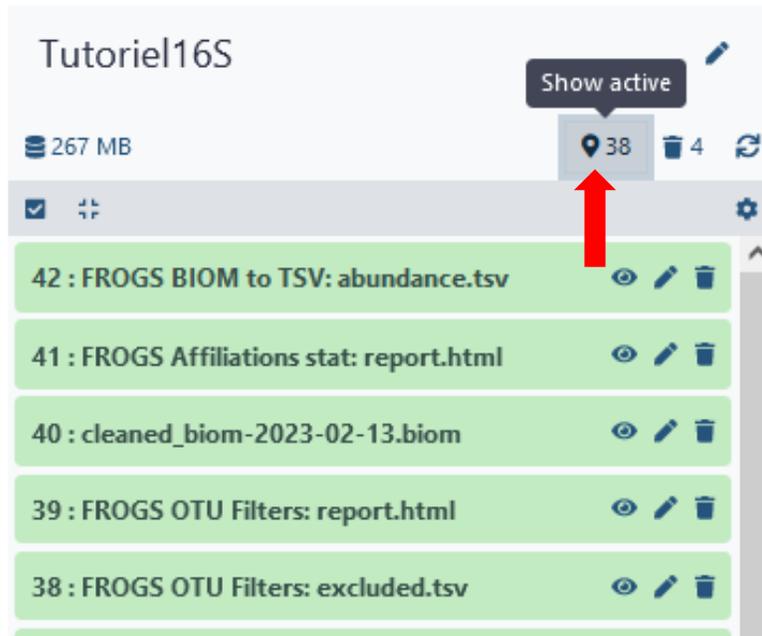
33 : FROGS OTU Filters: otuFilter_sequences.fasta

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



Click here to see again your active history

Thank you for following this first step,
see you on Tuesday 16 January!
