



A - Training on Galaxy: Metabarcoding

Decembre 2021 - webinar

GALAXY Practice

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Objectives of the 1st part

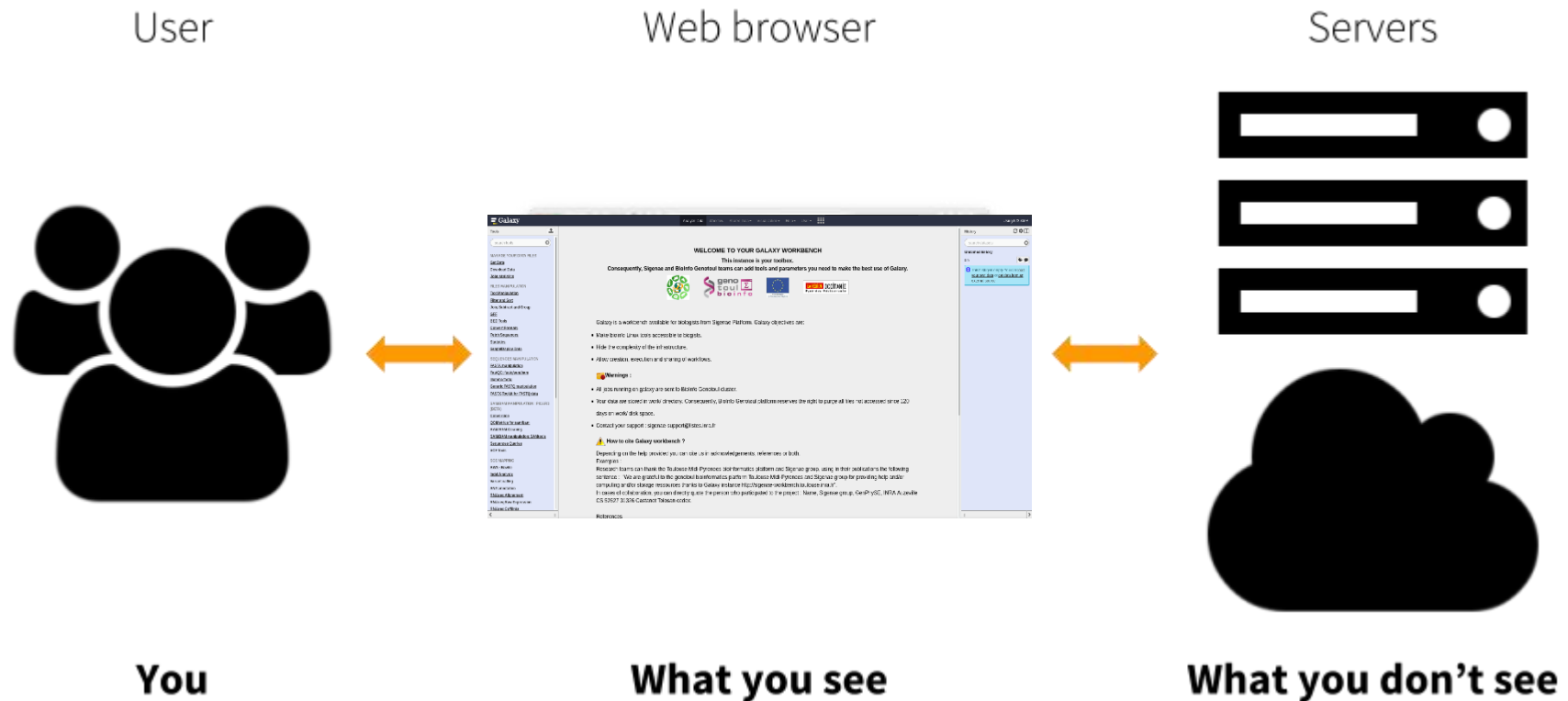
- Learn the basics of Galaxy
- Prepare the 2 datasets for FROGS formation

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



<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.

- Genotoul Bioinfo



- Cluster: Many computers tightly connected that work together
- High performance computer:
 - More than 5000 cores
 - 34 TB of RAM
 - More than 1 Peta Byte (1024 TB) of hard drive



Where to use Galaxy?

- The Toulouse Galaxy platform is https://vm-galaxy-prod.toulouse.inra.fr/Galaxy_menu/galaxy-sigenae.html

 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 2 INRAE Galaxy platforms

Galaxy Migale Analyse de données Workflow Visualize Données partagées Aide Authentication

Tools search tools

Get Data
Collection Operations
BASIC TOOLS
Text Manipulation
Convert Formats
Filter and Sort
Join, Subtract and Group
Statistics
Multiple Alignments
ncbi_blast
NGS TOOLS
Quality control
FASTQ manipulation
Mapping
RNAseq
Variant calling
Variant analyses
Migale Tools
SEQUENCE ANALYSIS TOOLS
GENOME ANALYSIS TOOLS
Genome annotation
METAGENOMICS TOOLS
Metabarcoding
METAPROTEOMICS TOOLS
Send Data
Lift-Over

migale
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 *Phylogeny*.
- **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 [staram](#) 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 2 INRAE Galaxy platforms

Galaxy | Analyze Data | Workflow | Shared Data | Visualization | Help | User | Using 0%

Tools | search tools

MANAGE YOUR DATA FILES
[Get Data](#)
[Download Data](#)
[Jobs statistics](#)

FILES MANIPULATION
[Text Manipulation](#)
[Filter and Sort](#)
[Join, Subtract and Group](#)
[GFF](#)
[BED Tools](#)
[Convert Formats](#)
[Fetch Sequences](#)
[Statistics](#)
[Graph/Display Data](#)

SEQUENCES MANIPULATION
[FASTA manipulation](#)
[FastQC: fastq/sam/bam](#)
[Illumina fastq](#)
[Generic FASTQ manipulation](#)
[FASTX-Toolkit for FASTQ data](#)

SAMBAM MANIPULATION : PICARD (BETA)
[Conversion](#)
[QC/Metrics for sam/bam](#)
[BAM/SAM Cleaning](#)
[SAMBAM manipulation: SAMtools](#)
[Sequences Queries](#)
[VCF Tools](#)

SGS MAPPING
[BWA - Bowtie](#)
[Indel Analysis](#)
[Variant calling](#)
[SNP annotation](#)
[RNAseq Alignment](#)
[RNAseq Raw Expression](#)
[RNAseq Cufflinks](#)

Genotoul Bioinfo | European Union | LA REGION OCCITANIE Pyrénées-Méditerranée

Welcome on Galaxy Sigene / BioInfo Genotoul.
Contact your support : support.sigene@inra.fr

Ready to use Workflows

- 1/ [FROGS - Find, Rapidly, Otus with Galaxy Solution](#)
- 2/ [Tax4Fun workflow](#)
- 3/ [Function Table for Tax4Fun matrix workflow](#)

Galaxy News

- 1/ How to use [datasets collections](#) ?
- 2/ How to [upload several files in Galaxy](#) ?
- 3/ New tools : [Tax4Fun \(manual\)](#), [VIP \(manual\)](#), [Salmon](#), [multiQC](#).
- 4/ Tools availables for [virologie analyses](#)
- 5/ [Virology tools](#)
- 6/ How to use [Function Table tool](#) ?
- 7/ How to [export](#) and [import](#) your histories ?

E-learning
<https://inra.classilio.com/Login>
2 e-learning availables : [Galaxy initiation](#) and [Quality sequences analysis](#)
Training resources : [BioInfo Genotoul / Sigene](#)

History | search datasets | 33 b | 3: seq1.fasta | 2: seq2.fasta | 1: seq3.fasta

Old version

Exemple of 2 INRAE Galaxy platforms

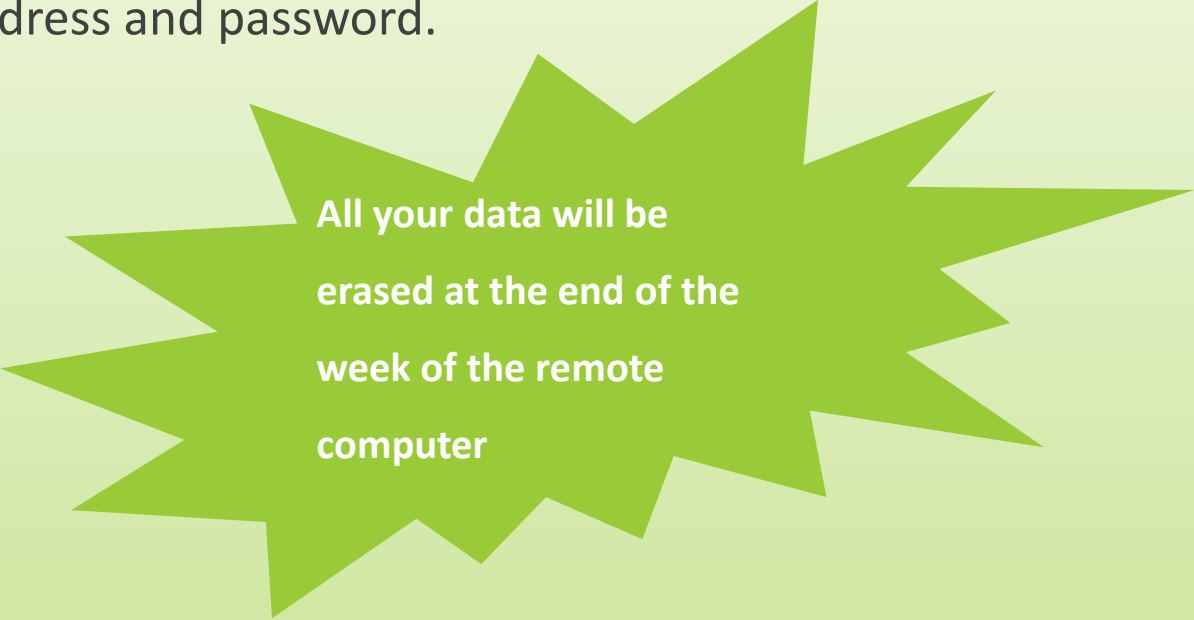
The screenshot shows the Galaxy Toulouse web interface. The header includes the logo, navigation menu (Workflow, Visualize, Données partagées, Aide, Utilisateur), and a 'Using 0%' indicator. A notification bar states: 'New Galaxy server, needed tools/databanks are added on demand'. The left sidebar contains a 'Tools' section with a search bar and an 'Upload Data' button, followed by a list of tool categories like 'Get Data', 'Send Data', 'Collection Operations', etc. The main content area features a large graphic with the text 'Galaxy Toulouse Main' and a red 'NEW' stamp. Below the graphic, a welcome message reads: 'Welcome to new main Galaxy-Toulouse server'. A paragraph explains that this new server replaces the 2016 version and is configured for a new HPC cluster. A bulleted list details the main changes: new Galaxy server version (21.05), reorganization of the tool list, submission on a new Slurm HPC cluster, and increased storage volume (250GB per user). Further text explains that histories from the old server are not present and provides instructions on how to import data. A right sidebar shows a 'History' section with a search bar and a message: 'Cet historique est vide. You can Charger vos propres données or Charger des données depuis une source externe'. A yellow starburst graphic with the text 'New version' is overlaid on the bottom right of the screenshot.

Practice:

CONNECT TO OUR GALAXY WORKBENCH

Exercise

Ask trainers for the address and password.

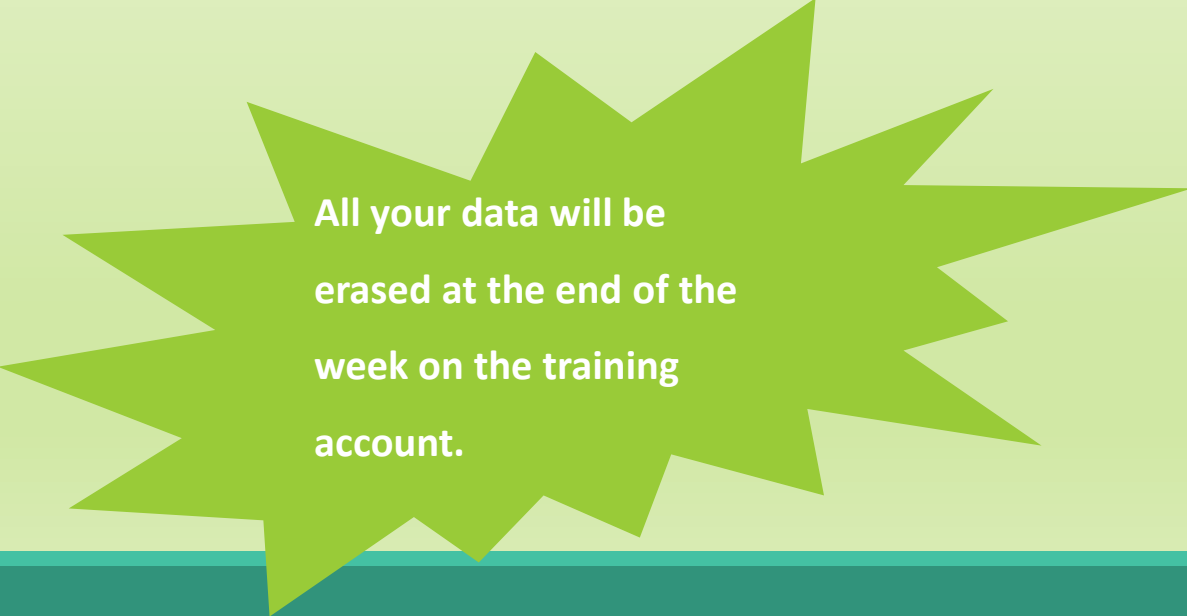


**All your data will be
erased at the end of the
week of the remote
computer**

Exercise

During this training, even you have a personal account, don't use it !
We use training accounts for more facilities


If you don't have a personal account, you can request a personal account later on :
<http://bioinfo.genotoul.fr/index.php/ask-for/create-an-account/>



All your data will be
erased at the end of the
week on the training
account.

Exercise

Our Galaxy platform is: https://vm-galaxy-prod.toulouse.inra.fr/Galaxy_menu/galaxy-sigenae.html



Before starting, check if your browser is not already connected to a Galaxy account. If this is the case, log out or use a private browser window!
Risk of data duplication

Exercise

Our Galaxy platform is: https://vm-galaxy-prod.toulouse.inra.fr/Galaxy_menu/galaxy-sigenae.html

For the formation, you must choose OLD version

Be careful, to fully login you must enter your credentials twice:

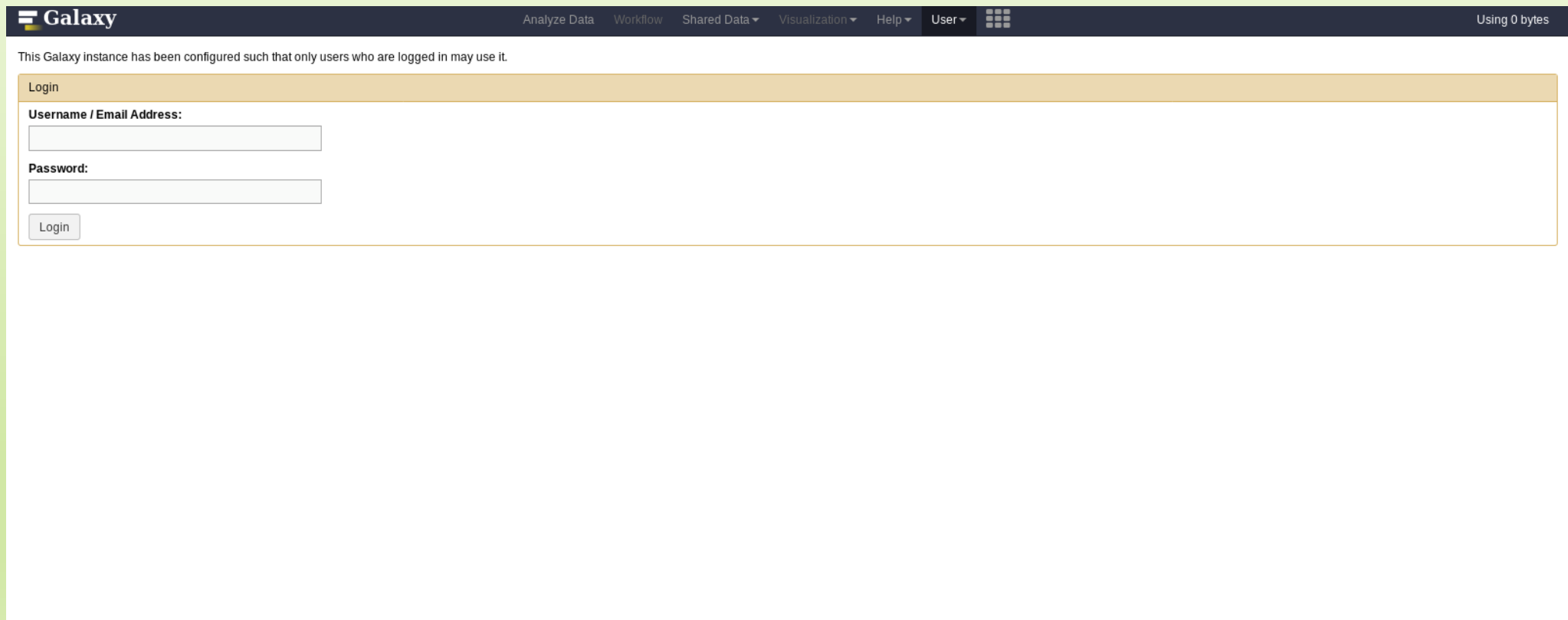
- The first time in this pop-up window:



The screenshot shows a standard Windows-style dialog box with a title bar that reads "Authentification requise". On the left side of the dialog, there is a key icon. The main text area contains the following message: "Le site http://galaxy-workbench.toulouse.inra.fr demande un nom d'utilisateur et un mot de passe. Le site indique : « Please enter your Genotoul LDAP password »". Below this text, there are two input fields: the first is labeled "Utilisateur :" and the second is labeled "Mot de passe :". At the bottom right of the dialog, there are two buttons: "Annuler" and "OK".

Exercise

- And a second time, in the browser:



The screenshot shows the Galaxy web interface. At the top, there is a dark navigation bar with the Galaxy logo on the left and several menu items: 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User'. On the far right of the navigation bar, it says 'Using 0 bytes'. Below the navigation bar, a message reads: 'This Galaxy instance has been configured such that only users who are logged in may use it.' Below this message is a 'Login' form. The form has a title 'Login' and two input fields: 'Username / Email Address:' and 'Password:'. A 'Login' button is located below the password field.

Galaxy
Analyze Data Workflow Shared Data Visualization Help User
Using 0%

Tools

search tools

MANAGE YOUR DATA FILES

[Get Data](#)

[Download Data](#)

[Jobs statistics](#)

FILES MANIPULATION

[Text Manipulation](#)

[Filter and Sort](#)

[Join, Subtract and Group](#)

[GFF](#)

[BED Tools](#)

[Convert Formats](#)

[Fetch Sequences](#)

[Statistics](#)

[Graphical Analysis](#)

SEQUENCES MANIPULATION

[FASTA manipulation](#)

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[Variant calling](#)

[SNP annotation](#)

[RNAseq Alignment](#)

[RNAseq Raw Expression](#)

[RNAseq Cufflinks](#)



RESULTS VISUALISATION —AND— TOOL PARAMETER WINDOW

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 Sigeneae group, using in their publications the following sentence : "We are grateful to the genotoul bioinformatics platform Toulouse Midi-Pyrenees and Sigeneae group for providing help and/or computing and/or storage resources thanks to Galaxy Instance <http://sigeneae-workbench.toulouse.inra.fr>".


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

References
X. SIGENAE [<http://www.sigeneae.org/>]




Ready to use Workflows

- 1/ FROGS - Find, Rapidly, Otus with Galaxy Solution
- 2/ Tax4Fun workflow
- 3/ Function Table for Tax4Fun matrix workflow



Galaxy News

- 1/ How to use [datasets collections](#) ?
- 2/ How to [upload several files in Galaxy](#) ?
- 3/ New tools : Tax4Fun ([manual](#)), VIP ([manual](#)), Salmon, multiQC.
- 4/ Tools availables for [virologie analyses](#)
- 5/ Virology tools
- 6/ How to use [Function Table tool](#) ?



E-learning

<https://inra.classilio.com/Login>

2 e-learning availables : Galaxy initiation and Quality sequences analysis

History

search datasets

Data Collection

3 shown

33 b

3: seq1.fasta

2: seq2.fasta

1: seq3.fasta

DATASETS HISTORY

AVAILABLE TOOLS

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:

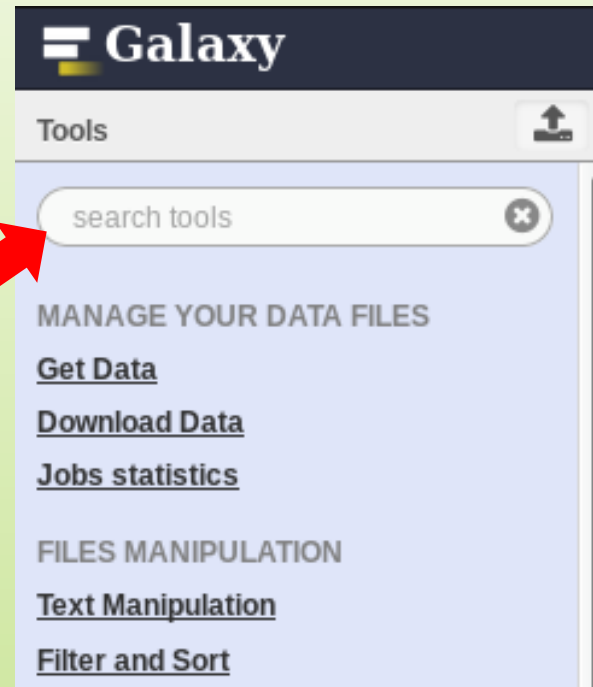
DISCOVER GALAXY

Exercise

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

Exercise

Search a tool by name.



If you search FROGS? You find 2 versions (3.0 and 3.2). You have to use 3.2.

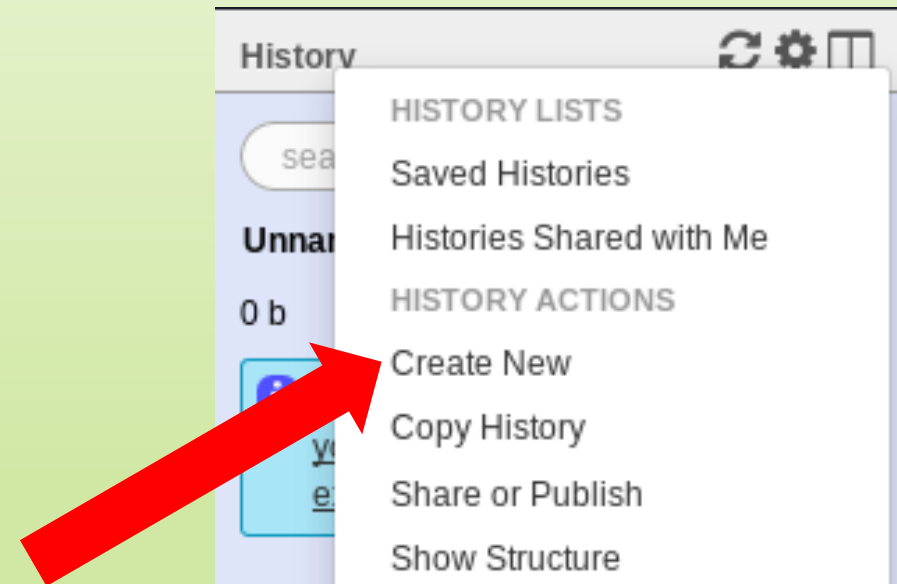
Manipulate Histories

Practice:

CREATE THE 2 HISTORIES NEEDED FOR THE FROGS FORMATION

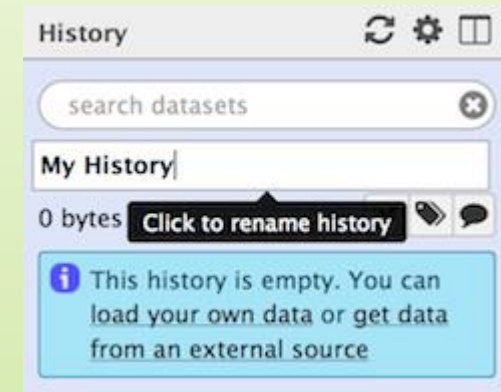
To create a new history:

- Click on the wheel.
- Click on « create new ».



To rename a history:

- Click on the history name (at the top).
- Enter « 16S ».
- Hit « **Enter** » to validate.



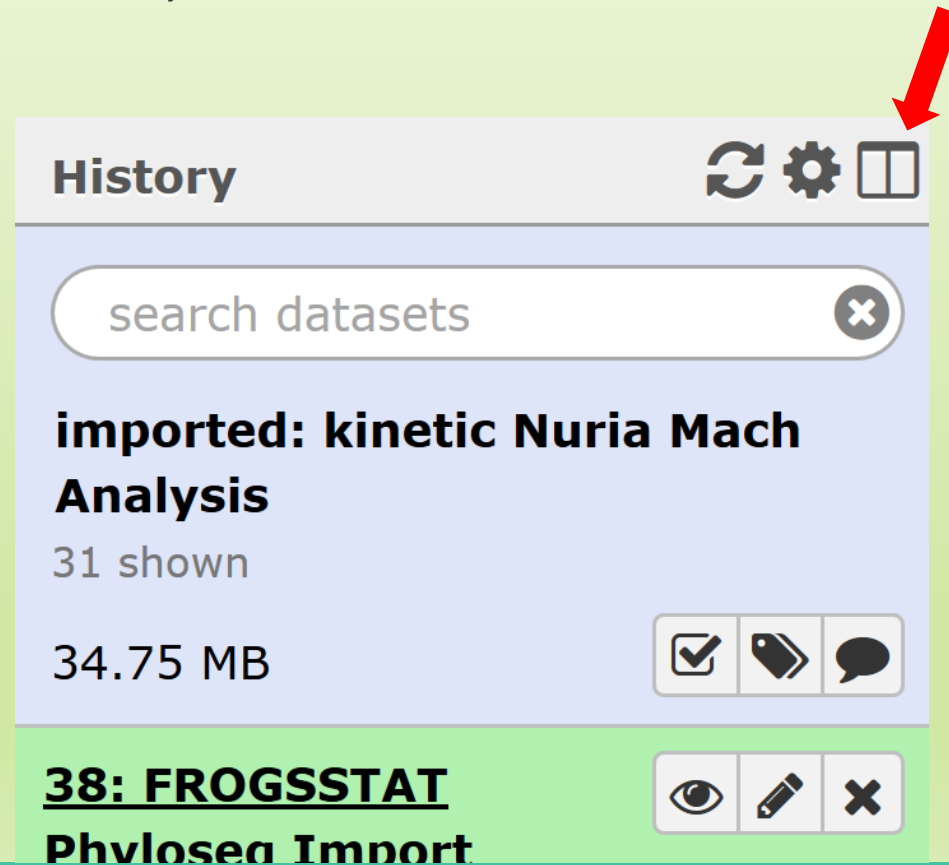
Don't use special
characters or
accents!

Exercise

- Create another history named ITS
- Switch to the history named « 16S » as current history.
- Go back to the main interface.

How to list all histories?

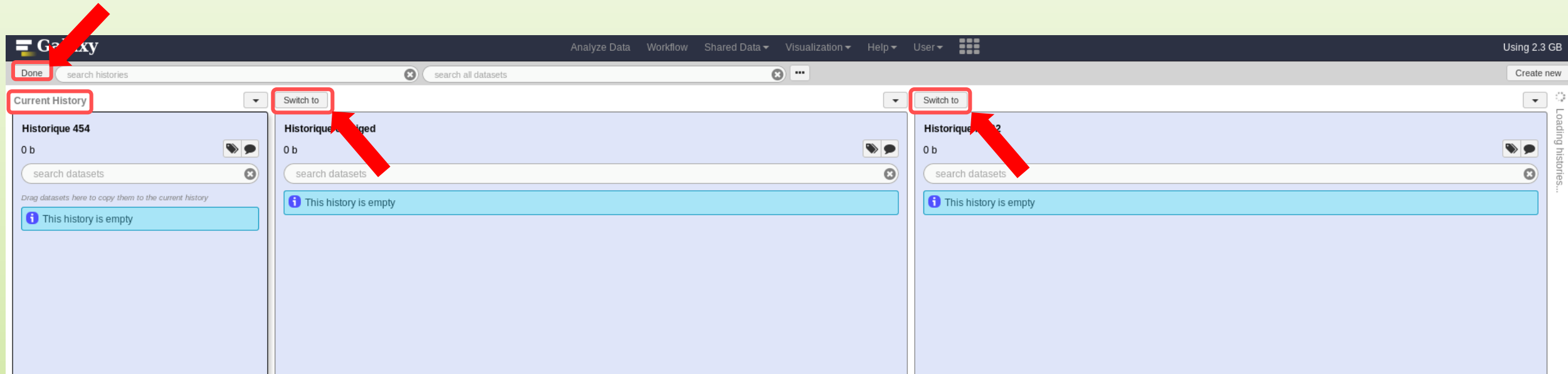
- To view all histories, click on this icon.



Explore the « View all histories » section

The screenshot displays the Galaxy web interface. At the top, the navigation bar includes the Galaxy logo and menu items: Analyze Data, Workflow, Shared Data, Visualization, Help, and User. Below the navigation bar, there are search bars for 'search histories' and 'search all datasets', along with a 'Create new' button. The main content area shows three history panels. The first panel is titled 'Current History' and contains a dropdown menu (highlighted with a red box) and a 'Switch to' button. The second panel is titled 'Test Ta Thi's tools' and contains a context menu (also highlighted with a red box) with options: Copy, Delete, and Purge. The third panel is titled 'Copy of 'full ph...' by 'maria.bernard...' and contains a 'Switch to' button. The interface also shows dataset search bars and icons for copying, deleting, and purging datasets.

Switch current history



- Switch to the history named « ITS » as current history.
- Click on “Done” 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



- By URL



- From Genotoul Bioinfo clusters








- 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		-	
 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.tsv	04-Mar-2021 15:29	2.2K	

All samples are in archive .tar.gz

Above all: how create an archive ?

To learn how create an archive

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

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

How to import your data to Galaxy ?

- Several ways to upload your data to Galaxy:

- From your computer



- By URL



We will learn how to import data with these 2 modalities.

- From Genotoul Bioinfo clusters



- Shared by other users of Galaxy



Practice

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



- From Genotoul Bioinfo clusters



- Shared by other users of Galaxy



Upload file from URL

1. In your current history “16S”
2. Go to **Get Data > Upload File from your computer**
3. Click on **Paste/Fetch Data**
4. Copy the address of the file:
http://genoweb.toulouse.inra.fr/~formation/15_FROGS/Webinar_data/chaillou_withprimers_64renamedsamples_V1V3_10000seq_R1R2.tar.gz
5. Change the type!
6. Click on Start
7. You can put one address per line for multiple uploads

Download from web or upload from disk

Regular Composite

Name	Size	Type	Genome	Settings	Status
New File	128 b	tar	unspecified (?)		100% ✓

You can tell Galaxy to download data from web by entering URL in this box (one per line). You can also directly paste the contents of a file.

```
http://genoweb.toulouse.inra.fr/~formation/15_FROGS/Webinar_data/chaillou_withprimers_64renamedsamples_V1V3_10000seq_R1R2.tar.gz
```

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

Choose local file Paste/Fetch data Pause Reset Start Close

Upload file from URL

The screenshot shows a web interface with a 'History' header. Below the header is a search bar containing the text 'search datasets'. Underneath the search bar, there is a section titled '16S' with the text '1 shown' and '34.85 MB'. To the right of this section are three icons: a checkmark, a folder, and a speech bubble. Below this, a specific file entry is highlighted in green. The entry is labeled '1:' and contains the following URL: http://genoweb.toulouse.inra.fr/~formation/15_FROGS/Webinar_data/chaillou_withprimers_64r_enamedsamples_V1V3_10000seq_R1R2.tar.gz. To the right of the URL are three icons: an eye, a pencil, and an 'X'.

Practice:

UPLOAD FILE FROM YOUR COMPUTER

How to import your data to Galaxy ?

- Several ways to upload your data to Galaxy:

- From your computer



- By URL



- From Genotoul Bioinfo clusters



- Shared by other users of Galaxy



Upload a local file

- To simulate that you have already the file on your own computer, download the file “metadata_Chailou.tsv” as:


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

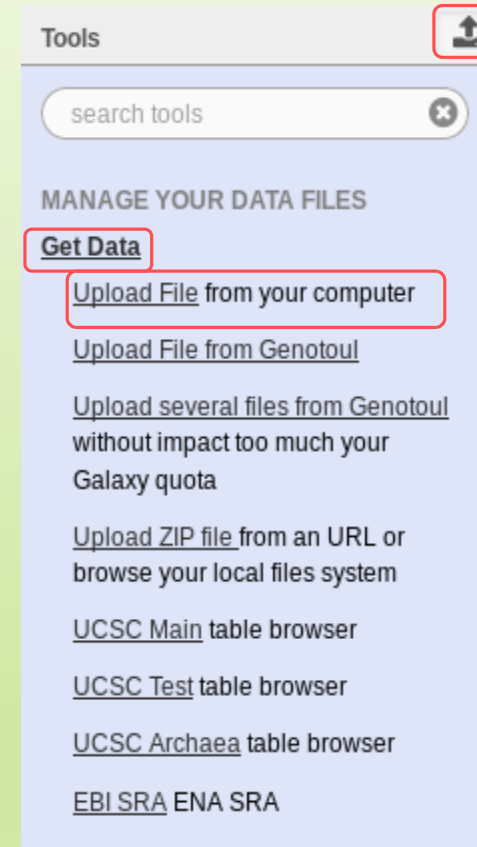


<u>Name</u>	<u>Last modified</u>	<u>Size</u>	<u>Description</u>
Parent Directory	-	-	-
ITS1.tar.gz	04-Mar-2021 15:40	157M	
chailou_withprimers_64renamedsamples_V1V3_10000seq_R1R2.tar.gz	04-Mar-2021 15:34	35M	
metadata ITS.tsv	04-Mar-2021 15:37	394	
metadata_chailou.tsv	04-Mar-2021 15:29	2.2K	

Upload a local file

- In Galaxy, your current history must be 16S
- Click on the « Get Data » tool.
- Upload file from your computer.

 For files smaller than 2 GB for old generations of galaxy platform



Upload a local file

Download from web or upload from disk

Regular Composite

Drop files here

Click here to choose a file on your hard drive.

Type (set all): Genome (set all):

The image shows a software interface for uploading files. At the top, there's a title "Download from web or upload from disk" and two tabs: "Regular" (selected) and "Composite". Below the tabs is a large dashed-line box containing the text "Drop files here". A blue callout box with white text says "Click here to choose a file on your hard drive." with a red arrow pointing to the "Choose local file" button in the bottom toolbar. The toolbar also includes a search icon, a "Genome" dropdown menu, and buttons for "Pause", "Reset", "Start", and "Close".

Upload a local file

The datatype of a file indicates the content of it.

.tsv = tabular

.fastq = fastq

.tar or .tar.gz = tar

Select the type corresponding to your file.

Do not trust blindly
the auto-detect!

1. Select the type of file (Do not leave on Auto-Detect!).

2. Select your other files the same way.

3. Begin upload.

Download from web or upload from disk

Regular Composite

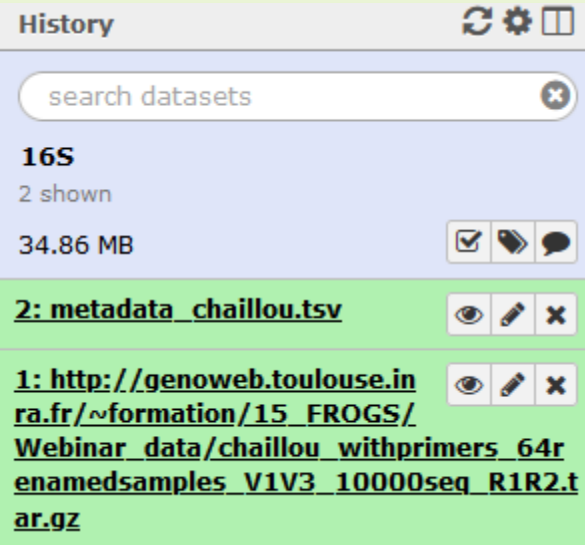
Name	Size	Type	Genome	Settings	Status
metadata_chaillou.tsv	2.2 KB	tabular	unspecified (?)		100% ✓

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

Choose local file Paste/Fetch data Pause Reset Start Close

On new galaxy choose 'tsv'

Upload a local file



History ↻ ⚙ 🗑

search datasets ✕

16S
2 shown
34.86 MB ☑ 📄 💬

2: metadata_chaillou.tsv 👁 📝 ✕

1: http://genoweb.toulouse.inra.fr/~formation/15_FROGS/Webinar_data/chaillou_withprimers_64r_enamedsamples_V1V3_10000seq_R1R2.tar.gz 👁 📝 ✕

Create and fill yourself the ITS history

Get data form here:

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>
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
chailou withprimers 64renamedsamples V1V3 10000seq R1R2.tar.gz	04-Mar-2021 15:34	35M
metadata ITS.tsv	04-Mar-2021 15:37	394
metadata chailou.tsv	04-Mar-2021 15:29	2.2K

Download from web or upload from disk

Regular Composite

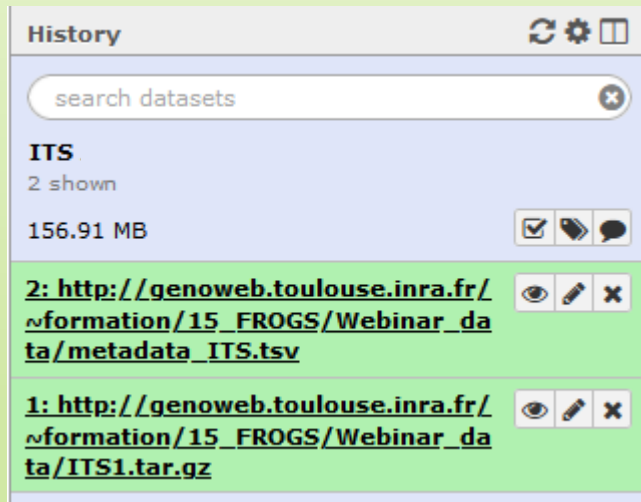
Name	Size	Type	Genome	Settings	Status
New File	76 b	tar	unspecified (?)		100% ✓
You can tell Galaxy to download data from web by entering URL in this box (one per line). You can also directly paste the contents of a file.					
http://genoweb.toulouse.inra.fr/~formation/15_FROGS/Webinar_data/ITS1.tar.gz					
New File	81 b	tabular	unspecified (?)		100% ✓
You can tell Galaxy to download data from web by entering URL in this box (one per line). You can also directly paste the contents of a file.					
http://genoweb.toulouse.inra.fr/~formation/15_FROGS/Webinar_data/metadata_ITS.tsv					

Type (set all): Genome (set all):

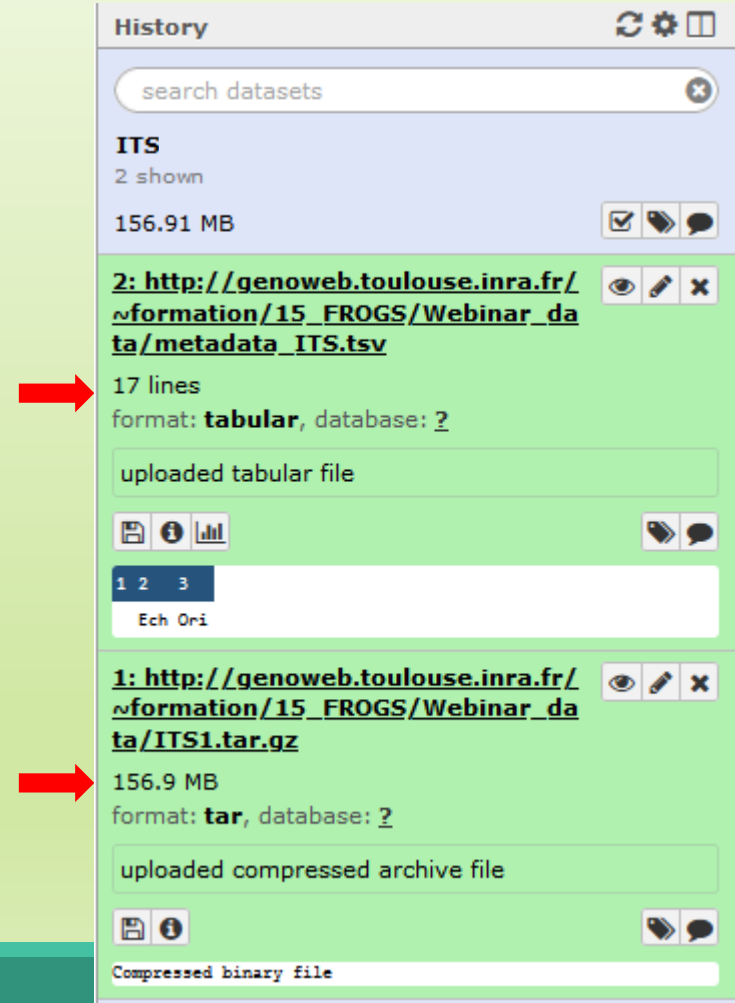
On new galaxy
choose 'tsv'

Create and fill yourself the ITS history

You have to obtain your second history:



The screenshot shows the 'History' panel with a search bar and two entries. The top entry is highlighted in green and contains the URL: http://genoweb.toulouse.inra.fr/~information/15_FROGS/Webinar_data/metadata_ITS.tsv. The bottom entry is also highlighted in green and contains the URL: http://genoweb.toulouse.inra.fr/~information/15_FROGS/Webinar_data/ITS1.tar.gz. The panel also displays 'ITS', '2 shown', and '156.91 MB'.



This screenshot provides a detailed view of the 'History' panel. A red arrow points to the second entry, which is highlighted in green and contains the URL: http://genoweb.toulouse.inra.fr/~information/15_FROGS/Webinar_data/metadata_ITS.tsv. Below the URL, it shows '17 lines' and 'format: tabular, database: ?'. A text box below contains 'uploaded tabular file'. Another red arrow points to the first entry, which is also highlighted in green and contains the URL: http://genoweb.toulouse.inra.fr/~information/15_FROGS/Webinar_data/ITS1.tar.gz. Below the URL, it shows '156.9 MB' and 'format: tar, database: ?'. A text box below contains 'uploaded compressed archive file'. At the bottom, a text box contains 'Compressed binary file'. The panel also displays 'ITS', '2 shown', and '156.91 MB'.

How to import your data to Galaxy ?

- Several ways to upload your data to Galaxy:

- From your computer



- By URL



- From Genotoul Bioinfo clusters



- Shared by other users of Galaxy



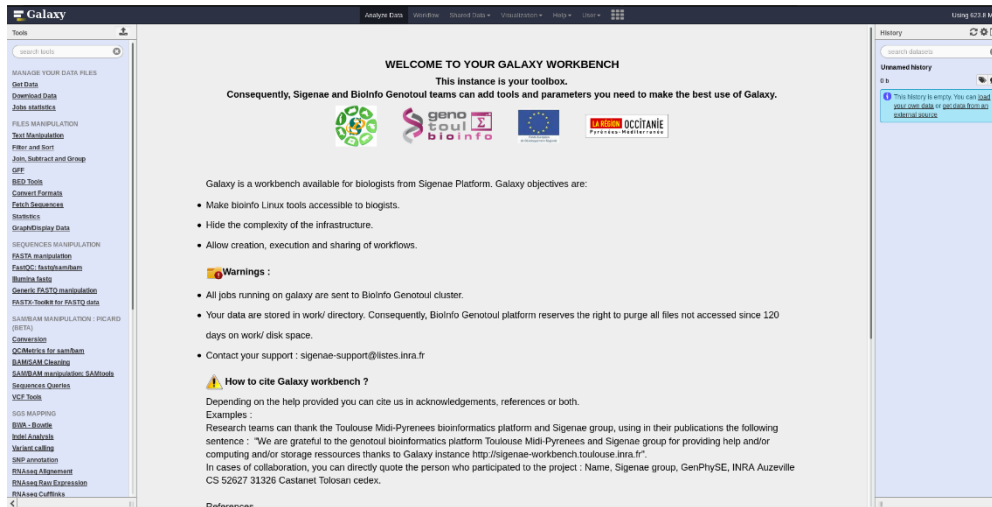
Upload your data from Genotoul

To download data from the server « Genotoul of Bioinformatics of Toulouse », you must already have your data on this server.

To learn how put your data on genotoul

[http://genoweb.toulouse.inra.fr/~formation/15_FROGS/Webinar_data/How to put your data on genotoul server.pdf](http://genoweb.toulouse.inra.fr/~formation/15_FROGS/Webinar_data/How_to_put_your_data_on_genotoul_server.pdf)

Advantage to put your data on Genotoul:



1TB of space



/work: 1TB (1024GB) of space
/save: 250GB of space

- This method allows you to have more space disk and to upload bigger files.
- Files not used in the last 180 days can be purged at any time.

Tools

search tools

MANAGE YOUR DATA FILES

Get Data

[Upload File from your computer](#)[Upload File from Genotoul](#)[Upload several files from Genotoul](#)[Upload ZIP file from an URL or browse your local files system](#)[UCSC Main table browser](#)[UCSC Test table browser](#)[UCSC Archaea table browser](#)[EBI SRA](#) [ENA SRA](#)

Download Data

Jobs statistics

FILES MANIPULATION

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SEQUENCES MANIPULATION

[FASTA manipulation](#)

Upload File from Genotoul (Galaxy Version 1.0.0)

Options

Path to file

Path must be like : /work/USERNAME/somewhere/afile

File type

Bam

Execute

Help

This program does

Path to file

This must be an absolute

valid path : /work/LinuxUserName/galaxy/file.extension
invalid path : /home/LinuxUserName/work/galaxy/file.extension

⚠ To use this tool and to maintain the confidentiality of yours directories:

1. Create a "galaxy" directory in your work : `mkdir galaxy`
2. `chmod a+x /work/LinuxUserName`

Example : `drwxr-x--x 4 smaman sigenae 16384 mar 9 14:15 /work/smaman`

3. `chmod a+r /work/LinuxUserName/dataGalaxy.fasta`

ℹ Thanks to the fact that this tool requires you to enter your filepath (without "browse" button), you can manage your data privacy.

For example, if your data to download in Galaxy are: /work/LinuxUserName/galaxy/data.fasta:

1. Add "x" rights to "others" on /work/LinuxUserName/ and on galaxy/

It is not useful that "others" have "r" rights of these directories.

- Switch to a new history.
- Next go to Get Data > Upload File from Genotoul.

History

search datasets

ITS

0 b

ℹ This history is empty. You can [load your own data](#) or [get data from an external source](#)

Tools

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FASTA manipulation

Upload File from Genotoul (Galaxy Version 1.0.0) Options

Path to file

 Path must be like : /work/USERNAME/somewhere/afile

File type

Execute

write your file address

Don't forget to change the Datatype!

What it does
 This program allows you to use a file stored in your genotoul work directory and optimize Galaxy work space by creating symlinks.

Path to file
 This must be an absolute path to a file located in your genotoul work directory. The path must start with **/work/YOUR_USER_NAME/blablabla.extension**

valid path : /work/LinuxUserName/galaxy/file.extension
 invalid path : /home/LinuxUserName/work/galaxy/file.extension

⚠ To use this tool and to maintain the confidentiality of yours directories:

1. Create a "galaxy" directory in your work : `mkdir galaxy`
2. `chmod a+x /work/LinuxUserName`

Example : `drwxr-x--x 4 smaman sigenae 16384 mar 9 14:15 /work/smaman`

3. `chmod a+r /work/LinuxUserName/dataGalaxy.fasta`

📄 Thanks to the fact that this tool requires you to enter your filepath (without "browse" button), you can manage your data privacy.
 For example, if your data to download in Galaxy are: /work/LinuxUserName/galaxy/data.fasta:

1. Add "x" rights to "others" on /work/LinuxUserName/ and on galaxy/

It is not useful that "others" have "r" rights of these directories.

History

search datasets

ITS
 1 shown
 1.5 MB

1: /work/formation/FROGS/ITS.tar.gz

5,613 lines
 format: tar.gz, database: ?

Epilog : job finished at Fri Mar 5 11:37:55 CET 2021

complete-ADN-1_R1.fastq.gz

Tools



search tools

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SEQUENCES MANIPULATION

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Upload File from Genotoul (Galaxy Version 1.0.0)

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Path must be like : /work/USERNAME/somewhere/afile

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What it does

This program allows you to use a file stored in your genotoul work directory and optimize Galaxy work space by creating symlinks.

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This must be an absolute path to a file located in your genotoul work directory. The path must start with **/work/YOUR_USER_NAME/blablabla.extension**

valid path : /work/LinuxUserName/galaxy/file.extension
invalid path : /home/LinuxUserName/work/galaxy/file.extension

To use this tool and to make

1. Create a "galaxy" dire
2. chmod a+x /work/Linu

Example : drwxr-x--x 4 smaman sigenae 16384 mar 9 14:15 /work/smaman

3. chmod a+r /work/LinuxUserName/dataGalaxy.fasta

Thanks to the fact that this tool requires you to enter your filepath (without "browse" button), you can manage your data privacy.

For example, if your data to download in Galaxy are: /work/LinuxUserName/galaxy/data.fasta:

1. Add "x" rights to "others" on /work/LinuxUserName/ and on galaxy/

It is not useful that "others" have "r" rights of these directories.

After executing, the file is imported into Galaxy.

History

search datasets

ITS

1 shown

1.5 MB

[1: /work/gpascal/FROGS_Formation/ITS.tar.gz](#)

5,613 lines

format: tar.gz, database: ?

Epilog : job finished at Thu Mar 4 17:12:09 CET 2021

complexe-ADN-1_R1.fastq.gz

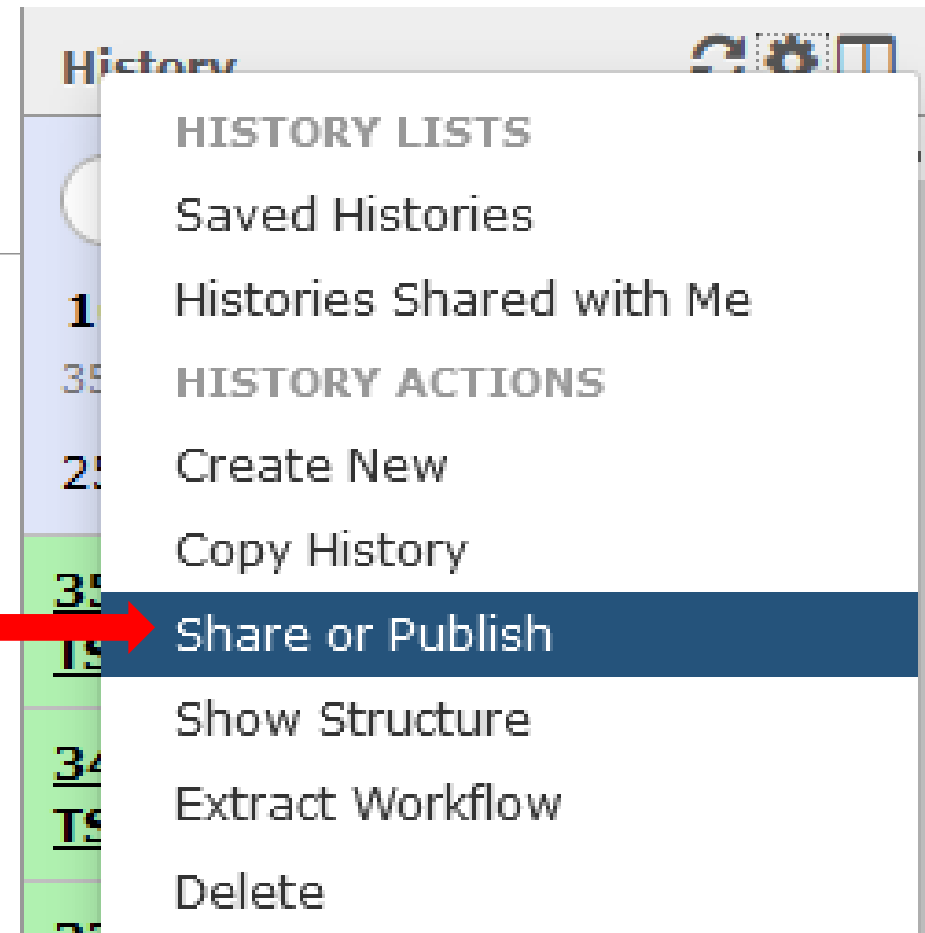
Share a History

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 an history

Click on the wheel and click here.



Share an history

Share or Publish History '16S'

Make History Accessible via Link and Publish It

This history is currently restricted so that only you and the users listed below can access it. You can:

Make History Accessible via Link

Generates a web link that you can share with other people so that they can view and import the history.

Make History Accessible and Publish

Makes the history accessible via link (see above) and publishes the history to Galaxy's [Published Histories](#) section, where it is publicly listed and searchable.

Share History with Individual Users

You have not shared this history with any users.

Share with a user



[Back to Histories List](#)

Tools



search tools



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SEQUENCES MANIPULATION

[FASTA manipulation](#)[FastQC: fastq/sam/bam](#)[Illumina fastq](#)[Generic FASTQ manipulation](#)[FASTX-Toolkit for FASTQ data](#)

SAM/BAM MANIPULATION : PICARD (BETA)

[Conversion](#)[QC/Metrics for sam/bam](#)[BAM/SAM Cleaning](#)[SAM/BAM manipulation: SAMtools](#)[Sequences Queries](#)[VCF Tools](#)

Share 1 histories

Histories to be shared:

History Name	Number of Datasets
Historique R1R2	3

Galaxy user emails with which to share histories

Select a user

Enter a Galaxy user email address or a comma-separated list of addresses if sharing with multiple users

Submit

- Enter an email address from a Galaxy user.
- Auto-completion helps you to find your co-worker

History



search datasets



Historique R1R2

3 shown

126.19 MB

**3: Upload several files from Genotoul (sampleA_R2)****2: Upload several files from Genotoul (sampleA_R1)****1: Upload several files from Genotoul**

empty

format: **txt**, database: ?

Epilog : job finished at Tue Jun 27 22:53:52 CEST 2017



Share 1 histories

Histories to be shared:

History Name

ITS June 2021

Number of Datasets

26

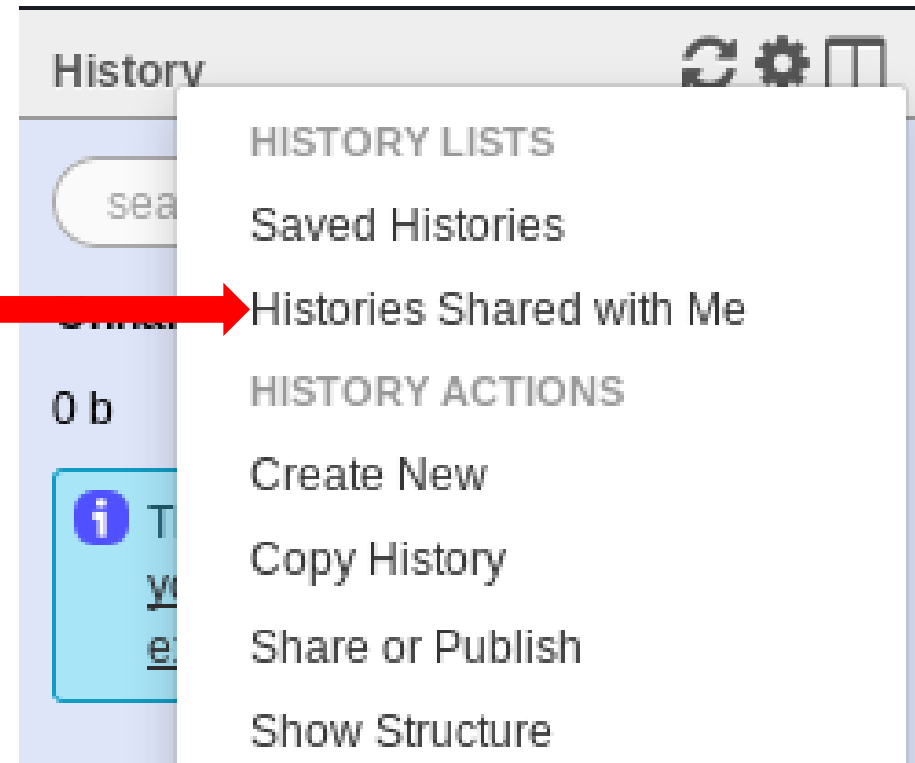
Galaxy user emails with which to share histories

comma-separated list of addresses if sharing with multiple users

- You must click on the address in the dropdown menu.
- Click on submit.
- The history will appear in your co-worker's history.

Import a shared history

Click on the wheel and click here.



Tools



Histories shared with you by others

<input type="checkbox"/>	Name	Datasets	Created	Last Updated	Shared by
<input type="checkbox"/>	chaillou_2021	53 4	Feb 17, 2021	Feb 19, 2021	laurent.cauquil@inra.fr
<input type="checkbox"/>	ForestSoil iTags	54 3	Jul 09, 2020	Jul 10, 2020	auer@insa-toulouse.fr

For 0 selected histories:

- Check the box and click on « Copy » to import an history into your Galaxy account.

Name of the history.

The person who shared the history.

History



search datasets

Historique R1R2

3 shown

126.19 MB



3: Upload several files from Genotoul (sampleA_R2)



2: Upload several files from Genotoul (sampleA_R1)



1: Upload several files from Genotoul



empty

format: txt, database: ?

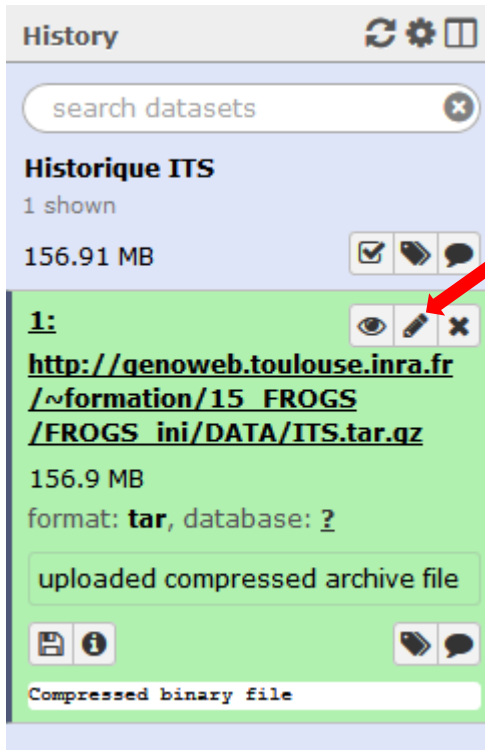
Epilog : job finished at Tue Jun 27 22:53:52 CEST 2017



How manipulate datasets

To rename a dataset

- Switch to ITS history



Click here to display attributes and change the name.

To rename a dataset

Change the name here
and call it « ITS1.tar.gz »

Attributes Convert Format Datatype Permissions

Edit Attributes

Name:

Info:

Annotation / Notes:

Add an annotation or notes to a dataset; annotations are available when editing a dataset.

Database/Build:

Save

Auto-detect

This will inspect the dataset and attempt to correct the above column values.

To change the datatype

Attributes Convert Format Datatype Permissions

Edit Attributes

Name:

Info:

Annotation / Notes:

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

Database/Build:

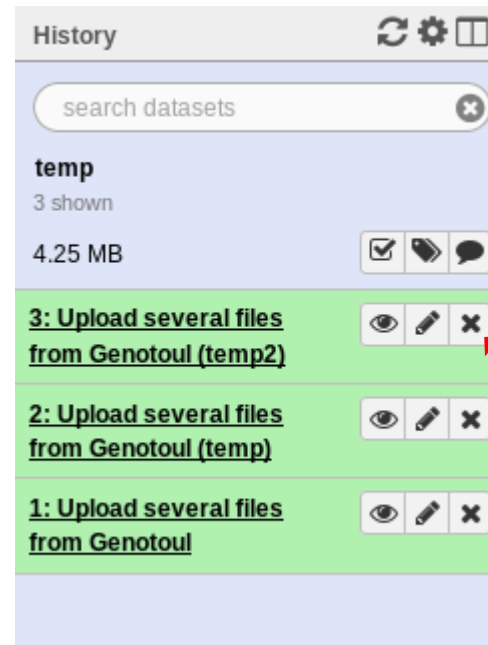
Save

Auto-detect

This will inspect the dataset and attempt to correct the above column values if they are not accurate.

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

To delete a dataset



Click here to delete a dataset.

To delete a dataset

Click here.

temp
2 shown, [1 deleted](#)
4.25 MB

2: Upload several files from Genotoul (temp)

1: Upload several files from Genotoul

History

search datasets

temp
3 shown, [hide deleted](#)
4.25 MB

3: Upload several files from Genotoul (temp2)

2: Upload several files from Genotoul (temp)

1: Upload several files from Genotoul

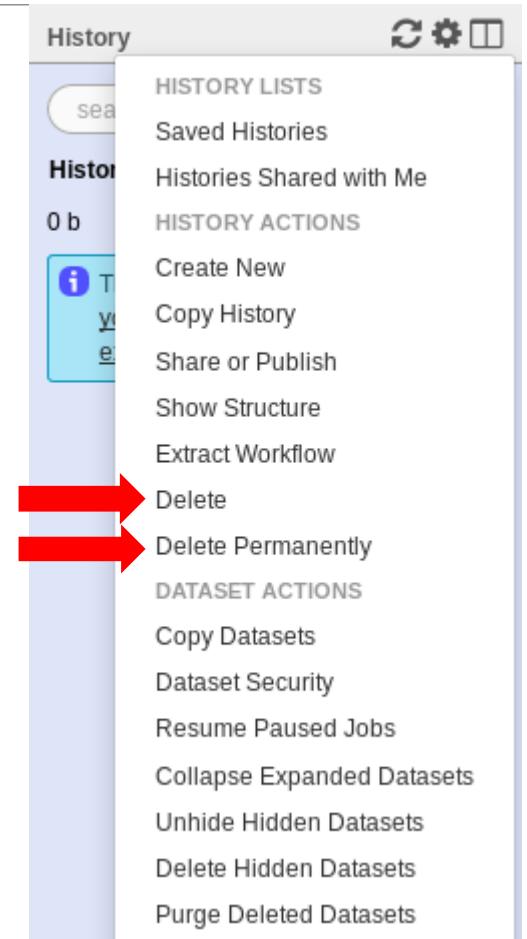
This dataset has been deleted
Undelete it
[Permanently remove it from disk](#)

Delete this dataset permanently.

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

How to delete a history?

- Stay in the temp history.
- Click on the wheel.
- Click on delete.
- A deleted item on Galaxy is recoverable.
- To definitively delete it:
click on « Delete Permanently ».



Other tools available on Galaxy

- Text Manipulation
- Filter and Sort data
- FASTA manipulation

Galaxy support

- Mail: support.sigena@inrae.fr
- If you need more training about bioinformatics and Galaxy, please connect to Sigena e-learning platform:
<http://sig-learning.toulouse.inra.fr/>

How to cite Galaxy?

- Goecks, J, Nekrutenko, A, Taylor, J and The Galaxy Team. "*Galaxy: a comprehensive approach for supporting accessible, reproducible, and transparent computational research in the life sciences.*" Genome Biol. 2010 Aug 25;11(8):R86.
- Blankenberg D, Von Kuster G, Coraor N, Ananda G, Lazarus R, Mangan M, Nekrutenko A, Taylor J. "*Galaxy: a web-based genome analysis tool for experimentalists*". Current Protocols in Molecular Biology. 2010 Jan; Chapter 19:Unit 19.10.1-21.
- Giardine B, Riemer C, Hardison RC, Burhans R, Elnitski L, Shah P, Zhang Y, Blankenberg D, Albert I, Taylor J, Miller W, Kent WJ, Nekrutenko A. "*Galaxy: a platform for interactive large-scale genome analysis.*" Genome Research. 2005 Oct; 15(10):1451-5.

How to cite Genotoul Galaxy workbench?

- 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.