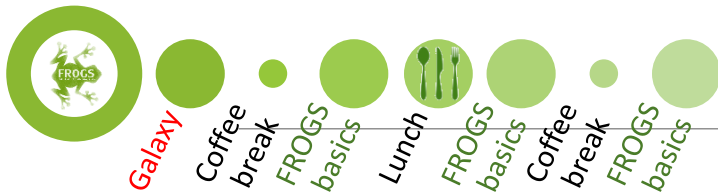


Monday



9 am to 4.30pm



2 short coffee breaks morning and afternoon

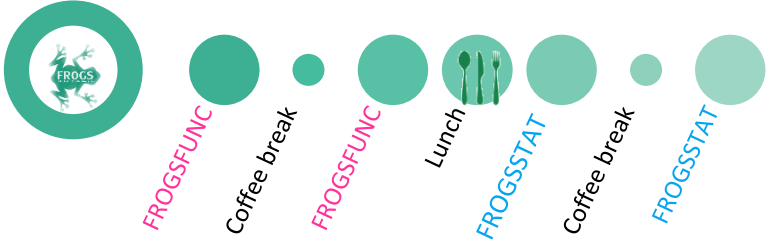


Lunch
12 to 1.30 pm ?

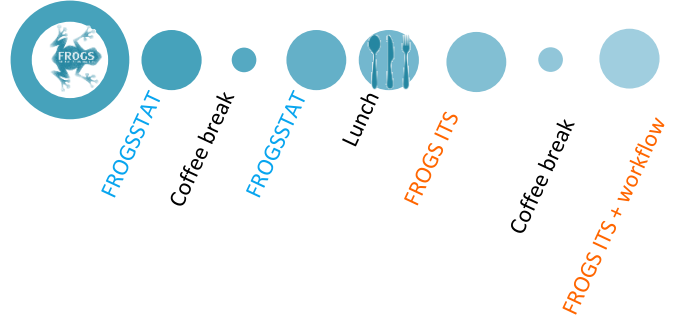
Tuesday



Wednesday



Thursday





A - Training on Galaxy: Metabarcoding

October 2022 - webinar

GALAXY Practice

LUCAS AUER, MARIA BERNARD, LAURENT CAUQUIL, VINCENT DARBOT, MAHENDRA MARIADASSOU, GÉRALDINE PASCAL & OLIVIER RUÉ

Objectives of the 1st part

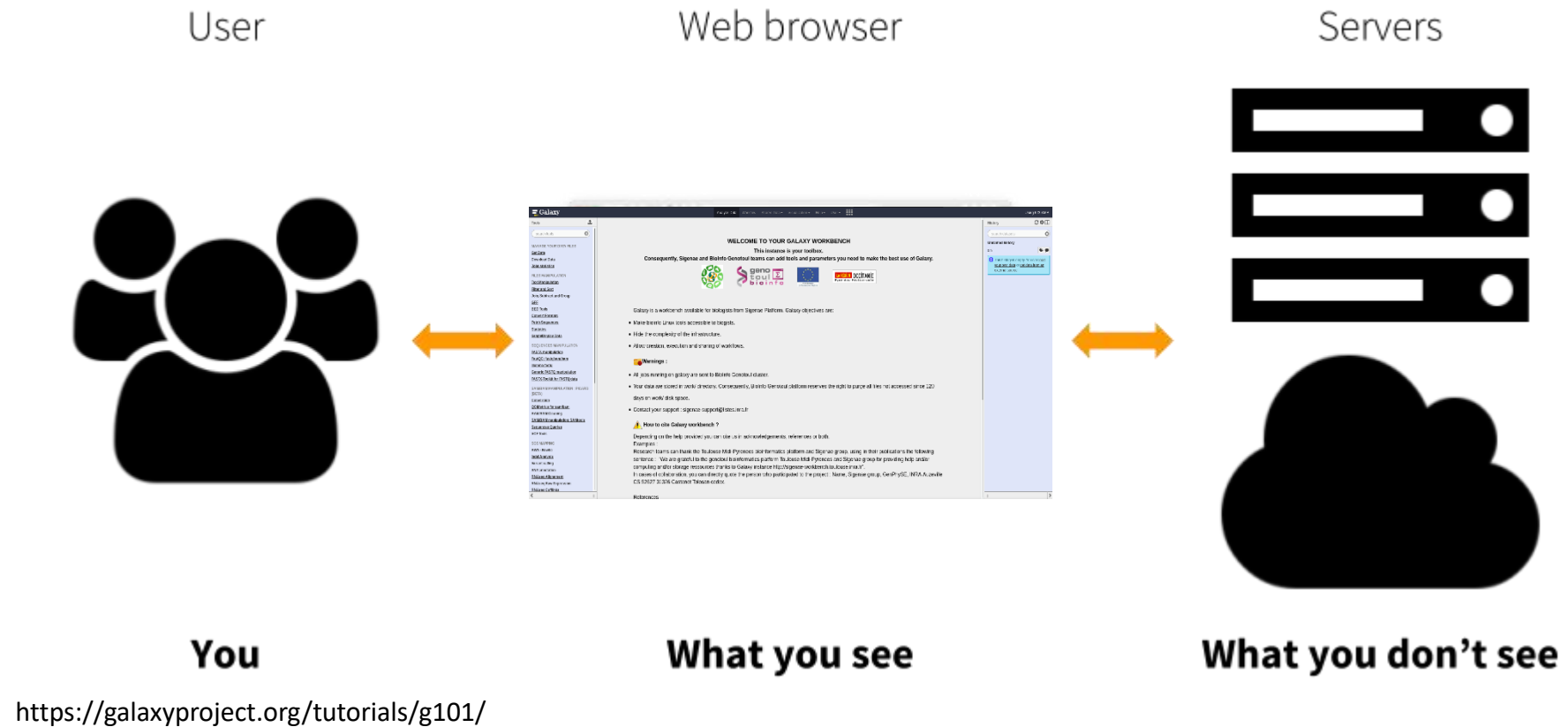
- Learn the basics of Galaxy
- Prepare the 2 datasets for FROGS formation

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



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

Exemple of Galaxy platforms

Galaxy Migale Analyse de données Workflow Visualize Données partagées Aide Authentification

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 Alignments*.
- **27th July 2020:** Added [Mummer4](#) in Section *Multiple Alignments*.
- **24th July 2020:** Added [NCBI accession Download](#) in Section *Get Data*.

Exemple of Galaxy platforms

The screenshot displays the Galaxy Toulouse web interface. At the top, the navigation bar includes the logo, the name 'Galaxy Toulouse', and menu items: 'Workflow', 'Visualize', 'Données partagées', 'Aide', 'Utilisateur', and a grid icon. A status indicator on the right shows 'Using 32%'. Below the navigation bar, a message states: 'New Galaxy server, needed tools/databanks are added on demand'. The main content area features a large logo for 'Galaxy Toulouse Main' with a 'NEW' stamp, and a welcome message: 'Welcome to new main Galaxy-Toulouse server'. Below the logo, there are sections for 'go to Latest news', 'Support', 'How to cite use of our Galaxy instance?', and 'The main changes are:'. The left sidebar contains a 'Tools' section with a search bar and an 'Upload Data' button, followed by categories: 'BASIC TOOLS' (Monitoring, Get Data, Send Data, Collection Operations, Lift-Over, Text Manipulation, Convert Formats, Filter and Sort, Join, Subtract and Group, Fetch Alignments/Sequences, Operate on Genomic Intervals, Statistics, Graph/Display Data), 'ADVANCED TOOLS', and 'FROGS' (OTUS RECONSTRUCTION, FROGS Demultiplex reads, FROGS Pre-process merging). The 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'.

Galaxy Toulouse Workflow Visualize Données partagées Aide Utilisateur Using 32%

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

Tools search tools Upload Data

BASIC TOOLS

- Monitoring
- Get Data
- Send Data
- Collection Operations
- Lift-Over
- Text Manipulation
- Convert Formats
- Filter and Sort
- Join, Subtract and Group
- Fetch Alignments/Sequences
- Operate on Genomic Intervals
- Statistics
- Graph/Display Data

ADVANCED TOOLS

FROGS

- OTUS RECONSTRUCTION
- 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

Galaxy Toulouse Main NEW

[go to Latest news](#)

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

Support

Support is configured in Galaxy to send help requests to support.sigena@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 Sigena group, using in their publications the following sentence:
"We are grateful to the genotoul bioinformatics platform Toulouse Midi-Pyrenees and Sigena group for providing help and/or computing and/or storage resources 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.sigena.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

History Rechercher des données

Unnamed history (empty)

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

Exemple of Galaxy platforms

The screenshot displays the Galaxy France web interface. At the top, the navigation bar includes 'Workflow', 'Visualize', 'Données partagées', 'Aide', 'Utilisateur', and a 'Using 0%' indicator. The left sidebar contains a 'Tools' section with a search bar and an 'Upload Data' button, followed by categories like 'Get Data', 'Collection Operations', 'GENERAL TEXT TOOLS', 'METAGENOMICS', 'STATISTICS AND VISUALISATION', and 'WORKFLOWS'. The central area features a 'Welcome to metabarcoding.usegalaxy.fr' message and a notification about the release 21.09. Below this, it lists the hosting institutions: IFB, eLife, and the University of Pennsylvania. The right sidebar shows a 'History' panel with a search bar and a list of recent jobs, including '52: FROGSSTAT Deseq2' and '49: FROGSSTAT DESeq2'.

Practice:

CONNECT TO GALAXY WORKBENCH

Exercise

- 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.

Tools ☆ ☰

search tools ✕

Upload 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 in parallel.
- FROGS Remove chimera** Remove PCR chimera from OTUs.
- 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
- FROGS Affiliation Filters** Filters OTUs on several affiliation criteria.
- FROGS Affiliation postprocess** Optionnal step to resolve inclusive amplicon ambiguities and to aggregate OTUs based on alignment metrics
- FROGS Abundance normalisation**

AVAILABLE TOOLS

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

▾ ⬆️ 📁

R1 FASTQ file of paired-end reads.

Reads 2

▾ ⬆️ 📁

R2 FASTQ file of paired-end reads.

Insert Samples

RESULTS VISUALISATION AND TOOL PARAMETER WINDOW

History ↺ + 🗑️ ⚙️

Rechercher des données ? ✕

16S

2 shown

34.86 MB ☑️ 📁 🗨️

2: chaillou_withprimers_64renamedsamples_V1V3_10000seq_R1R2.tar.gz 👁️ ✎️ ✕

1: metadata_chaillou.tsv 👁️ ✎️ ✕

DATASETS HISTORY

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:

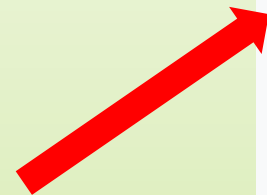
DISCOVER GALAXY

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.



Tools ☆

 ✕

⬆️ Upload Data

👁️ Show Sections

FROGS BIOM to std BIOM Converts a FROGS BIOM in fully compatible BIOM.

FROGSSTAT Phyloseq Structure Visualisation with heatmap plot and ordination plot

FROGS TSV_to_BIOM Converts a TSV file in a BIOM file.

FROGS Affiliation Filters Filters OTUs on several affiliation criteria.

FROGS Tree Reconstruction of phylogenetic tree



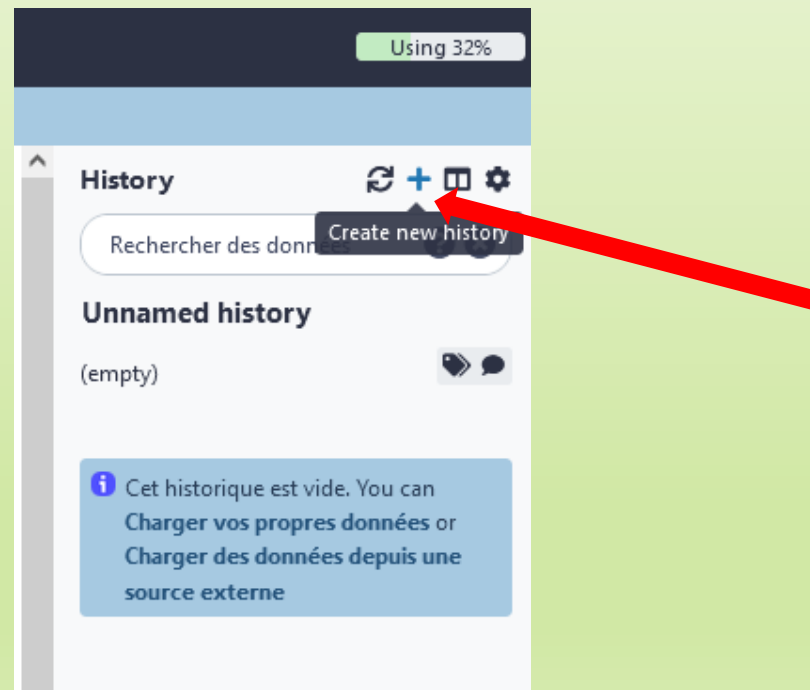
Manipulate Histories

Practice:

CREATE THE 2 HISTORIES NEEDED FOR THE FROGS FORMATION

To create a new history:

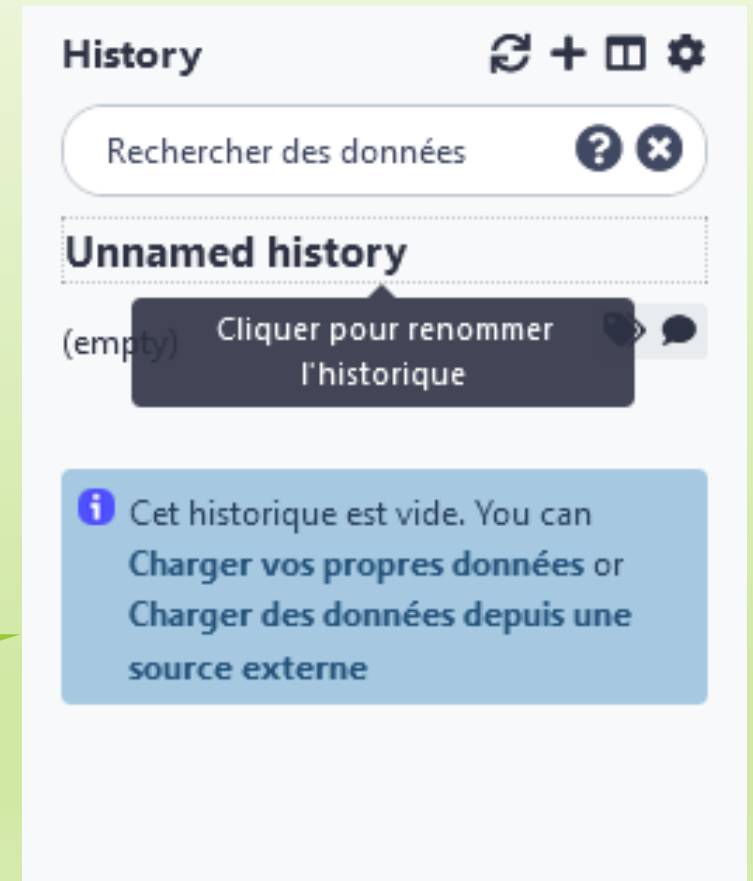
- Click on the plus.



To rename a history:

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

Don't use special characters or accents!

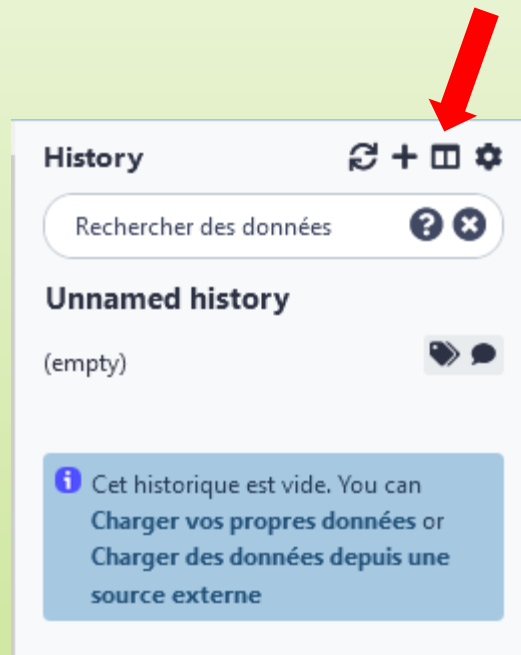


Exercise

- 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?

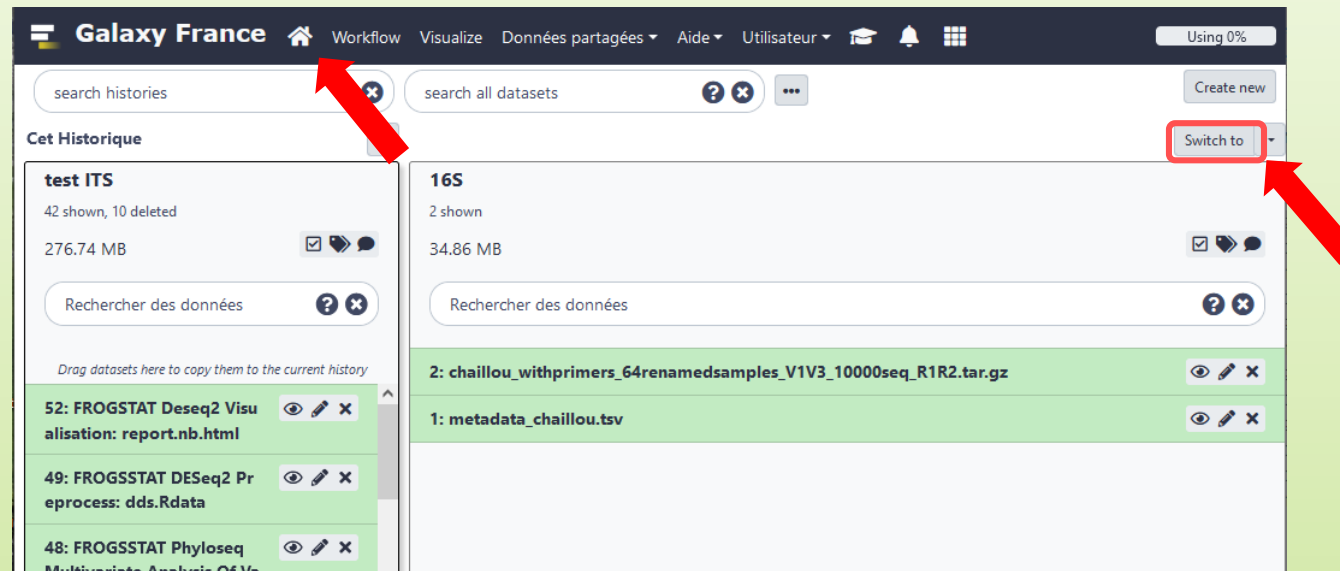
- To view all histories, click on this icon.



Explore the « View all histories » section

The screenshot displays the Galaxy France web interface. At the top, there is a navigation bar with the logo and menu items: Workflow, Visualize, Données partagées, Aide, Utilisateur, and a grid icon. A status indicator on the right shows 'Using 0%'. Below the navigation bar, there are two search bars: 'search histories' and 'search all datasets'. A 'Create new' button is located to the right of the search bars. The main content area is titled 'Cet Historique' and features a dropdown menu (highlighted with a red box) that opens a context menu with options: Copy, Delete, and Purge (also highlighted with a red box). To the right of the dropdown is a 'Switch to' button (also highlighted with a red box). The interface shows two history panels. The left panel, titled 'test ITS', contains a list of datasets with details like '42 shown, 10 deleted' and '276.74 MB'. The right panel, titled '16S', shows '2 shown' and '34.86 MB'. Both panels have search bars and icons for viewing, editing, and deleting datasets. The dataset list in the right panel includes '2: chaillou_withprimers_64renamedsamples_V1V3_10000seq_R1R2.tar.gz' and '1: metadata_chaillou.tsv'.

Switch current history



- Switch to the history named « 16S » as current history.
- 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



- 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



drag-and-drop files

- By URL



Paste an url

- 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

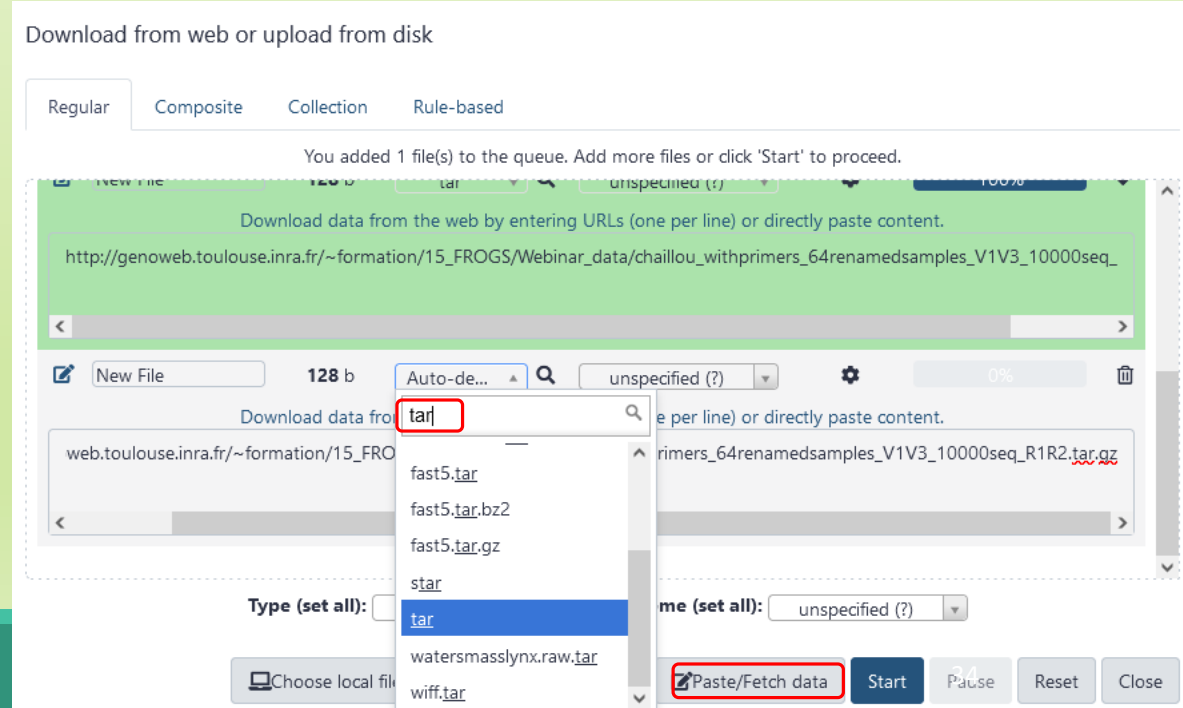
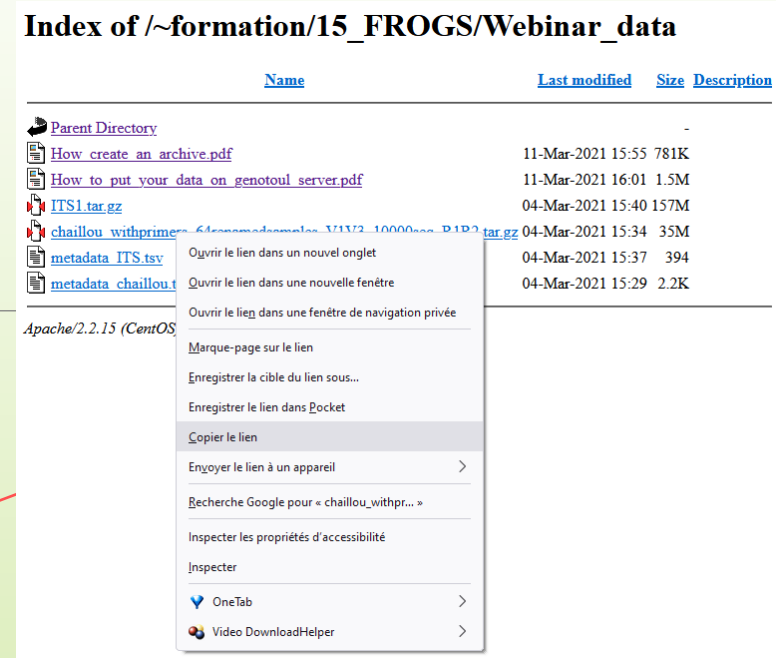


- Shared by other users of Galaxy



16S history creation

1. In your current history “16S”
2. Go to **Get Data > Upload File from your computer**
3. Click on **Paste/Fetch Data**
4. Click right on the name file
5. Copy the address of the link
6. Paste the address
7. Change the data type!
8. Click on Start
9. You can put one address per line for multiple uploads
10. Start again with the second file



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

	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
	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 Collection Rule-based

Name	Size	Type	Genome	Settings	Status
<input checked="" type="checkbox"/> New File	76 b	tar	unspecified (?)		100%
Download data from the web by entering URLs (one per line) or directly paste content.					
http://genoweb.toulouse.inra.fr/~formation/15_FROGS/Webinar_data/ITS1.tar.gz					
<input checked="" type="checkbox"/> New File	81 b	tsv	unspecified (?)		100%
Download data from the web by entering URLs (one per line) or directly paste content.					
http://genoweb.toulouse.inra.fr/~formation/15_FROGS/Webinar_data/metadata_ITS.tsv					

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



Create and fill yourself the ITS history

You have to obtain your second history:

54: metadata_ITS.tsv 16 lines, 1 comments
format: **tsv**, génome de référence: ?

1.	2.Ech	3.Ori
	Ech	Ori
echantillon1-1	1	alim
echantillon1-2	1	alim
echantillon1-3	1	alim
echantillon2-1	2	alim

53: ITS1.tar.gz 156.9 MB
format: **tar**, génome de référence: ?

Compressed binary file

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.

The image shows a software interface with a 'History' panel. The panel has a dark header with 'Using 0%' and a light body with the word 'History' and four icons: a refresh icon, a plus icon, a square icon, and a gear icon. A context menu is open over the gear icon, listing various actions. A blue callout box with the text 'Click on the wheel and click here.' has a red arrow pointing to the gear icon. Another red arrow points from the callout box to the 'Partager et publier' option in the context menu.

History Actions

- Copy
- Partager et publier
- Montrer la structure Partager et publier
- Extraire un Workflow
- Set Permissions
- Make Private
- Reprendre les processus en pause

Actions sur les jeux de données

- Copier des jeux de données
- Réduire les données étendues
- Afficher les données cachées
- Supprimer les données cachées
- Purger les données supprimées

Télécharger

- Exporter les citations des outils
- Exporter l'Historique dans un fichier

Beta Features

- Use Beta History Panel

Share an history

The screenshot shows a software interface with a dark navigation bar at the top containing icons for home, workflow, visualize, shared data, help, user, and a grid. A green status bar on the right indicates 'Using 32%'. Below the navigation bar, the main content area is titled 'Share or Publish History `Jeu test pour tuto 16S`'. It features a toggle switch for 'Make History accessible', a paragraph explaining access restrictions, and a section for sharing with individual users. A list of email addresses is provided, each with a 'Remove' button. A red arrow points to a 'Share with a user' button. On the right side, a 'History' panel displays a search bar, the title 'Jeu test pour tuto 16S', and a list of history items with icons for view, edit, and delete.

Workflow Visualize Données partagées Aide Utilisateur Using 32%

Share or Publish History `Jeu test pour tuto 16S`

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 datasets.

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.

Email

olivier.rue@inrae.fr

maria.bernard@inrae.fr

vincent.darbot@inrae.fr

patrice.dehais@inrae.fr

History

Rechercher des données

Jeu test pour tuto 16S

47 shown, 13 deleted

281.06 MB

- 60: FROGSSTAT DESeq2 Preprocess: dds.Rdata
- 59: FROGSSTAT DESeq2 Preprocess: dds.Rdata
- 56: FROGSSTAT DESeq2 Preprocess: dds.Rdata
- 55: FROGSSTAT Phyloseq Multivariate Analysis Of Variance: manova.nb.html
- 54: FROGSSTAT Phyloseq Sample Clustering: clustering.nb.html

Import a shared history

The screenshot shows the Galaxy Toulouse web interface. At the top, the navigation bar includes the Galaxy Toulouse logo, a home icon, and menu items for Workflow, Visualize, Données partagées, Aide, and Utilisateur. A red arrow points from a blue 'Click here' box to the Utilisateur menu. Below the navigation bar, a light blue banner displays a message: 'New Galaxy server, needed tools/databanks are added on demand'. On the left, a 'Tools' sidebar contains a search box, an 'Upload Data' button, and a list of categories including 'BASIC TOOLS', 'Monitoring', 'Get Data', and 'Send Data'. On the right, the user menu is open, showing the user's name 'Authentifié en tant que geraldine.pascal@inrae.fr', 'Préférences', 'Mes génomes Builds de référence', 'Déconnexion', 'Datasets', 'Histories', 'Histories shared with me', 'Pages', 'Workflow Invocations', and 'Visualisations'. A second red arrow points from another blue 'Click here' box to the 'Histories shared with me' option.

Histories shared with you by others

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: Copy Unshare

Name of the history.

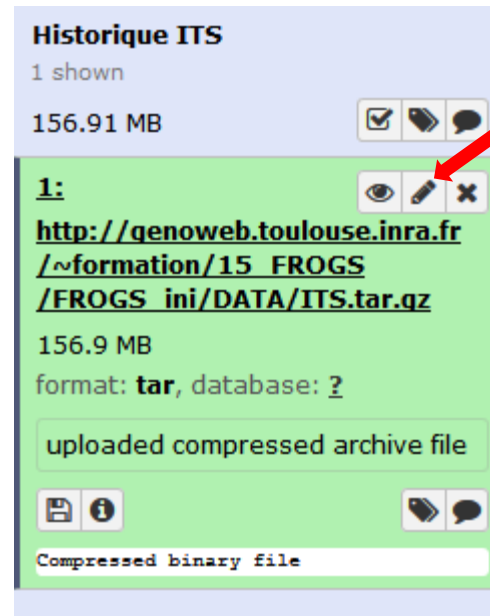
Check the box and click on « Copy » to import an history into your Galaxy account.

The person who shared the history.

How manipulate datasets

To rename a dataset

- Switch to ITS history



Historique ITS
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

Click here to display attributes and change the name.

To rename a dataset

Change the name here

Edit dataset attributes

Attributes

Convert

Datatypes

Permissions

Editer les attributs

Convertir en un nouveau
format de données

Auto-detect

Save

Name

FROGS Pre-process: count.tsv

Info

Application

Software: preprocess.py (version: 3.2.3)

Command: /galaxydata/galaxy2021/galaxy01/galaxy/database/dependencies/_conda/envs/mulled-

v1.81e0e76624e2492f20000d51de285ef751406605e2dede0f71ba6e0b0129202/bin/preprocess.pyillumina_output.derep

Annotation

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

Database/Build

----- Additional Species Are Below -----

Number of comment lines

To change the datatype

Edit dataset attributes

Attributes

Convert

Datatypes

Permissions

Changer le format de données

Detect datatype

Changer le format de données

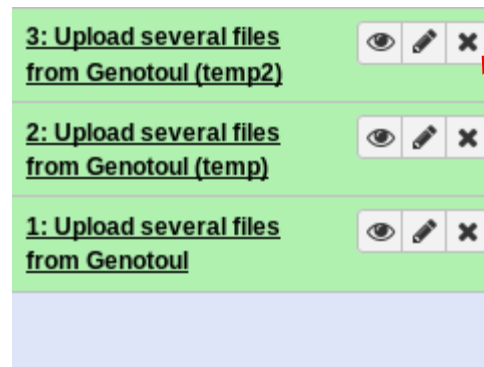
New Type

tsv

This will change the datatype of the existing dataset but not modify its content. Use this if Galaxy has incorrectly guessed the type of your dataset.

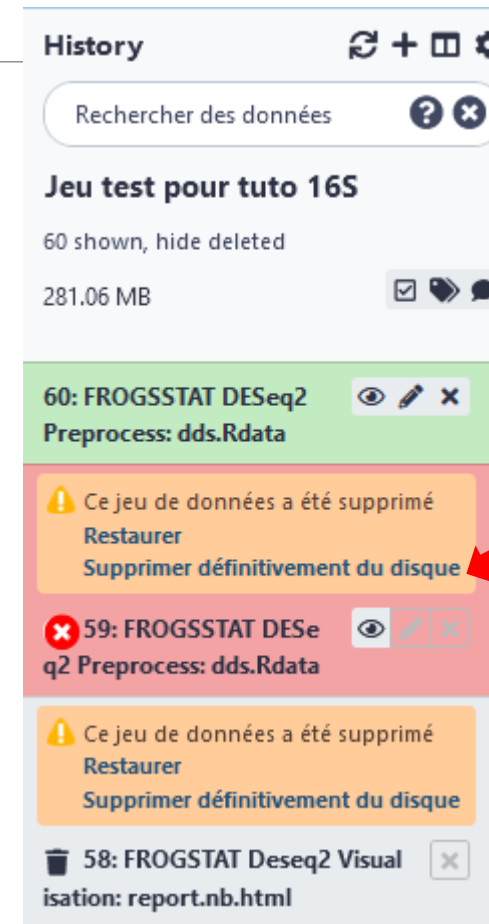
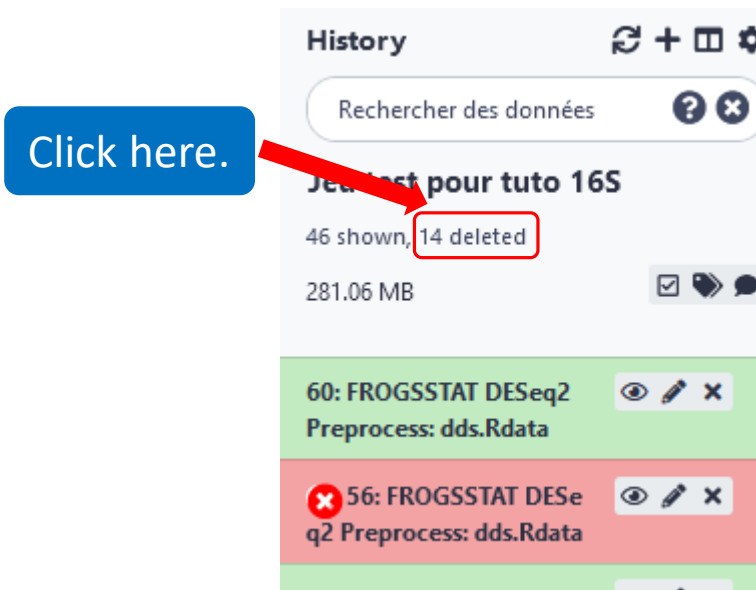
If you put the wrong datatype in during the upload, you can change it here.

To delete a dataset



Click here to delete a dataset.

To delete a dataset



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

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