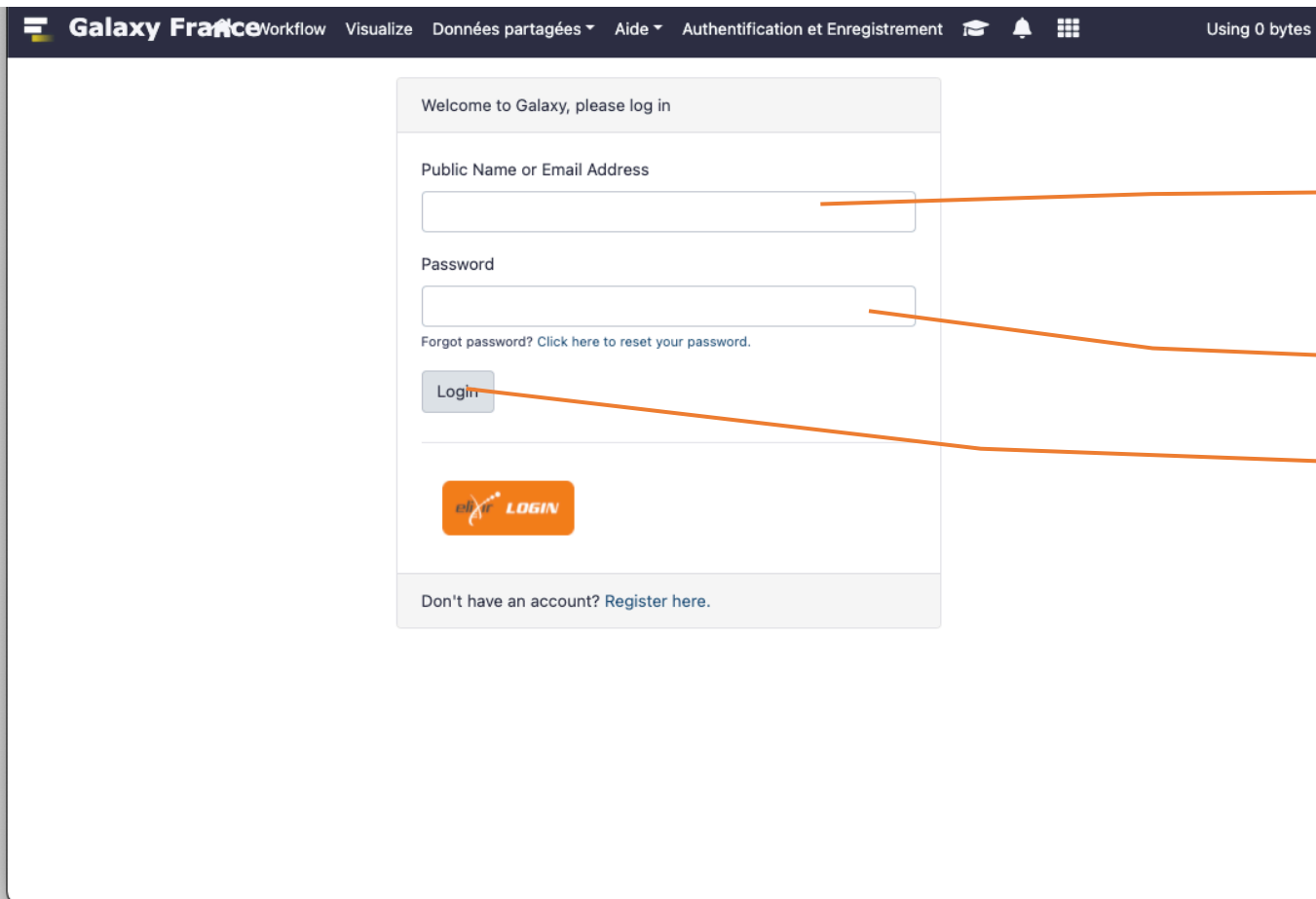


Introduction to Galaxy (answers to questions)

Stéphanie Le Gras
(slegras@igbmc.fr)

Answer 1 : Log in

- Go to <https://usegalaxy.fr/>



The screenshot shows the Galaxy France login interface. At the top, there is a dark navigation bar with the text "Galaxy France" and several menu items: "Workflow", "Visualize", "Données partagées", "Aide", and "Authentification et Enregistrement". On the right side of the navigation bar, it says "Using 0 bytes". Below the navigation bar, the main content area has a light gray background. At the top of this area, it says "Welcome to Galaxy, please log in". Below this, there are two input fields: "Public Name or Email Address" and "Password". Below the password field, there is a link that says "Forgot password? Click here to reset your password." Below the link, there is a "Login" button. Below the "Login" button, there is a large orange button with the text "LOGIN" and a small icon. At the bottom of the login form, there is a link that says "Don't have an account? Register here." Three orange lines point from the right side of the image to the input fields and the "Login" button, with corresponding text labels: "Enter your login", "Enter your password", and "Click on Login".

Enter your login

Enter your password

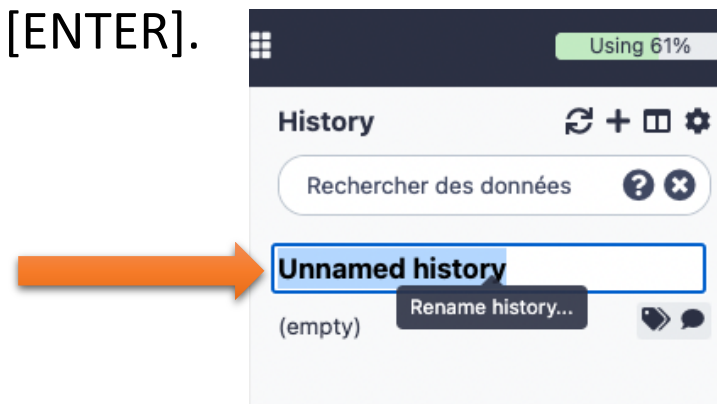
Click on Login

Answer 2 : History

- Create a new history



- Change the name of the new history to “RNA-seq data analysis” by clicking on “Unnamed history” on top of the history panel. Then type “RNA-seq data analysis” and [ENTER].



Answer 3 : Import data to Galaxy

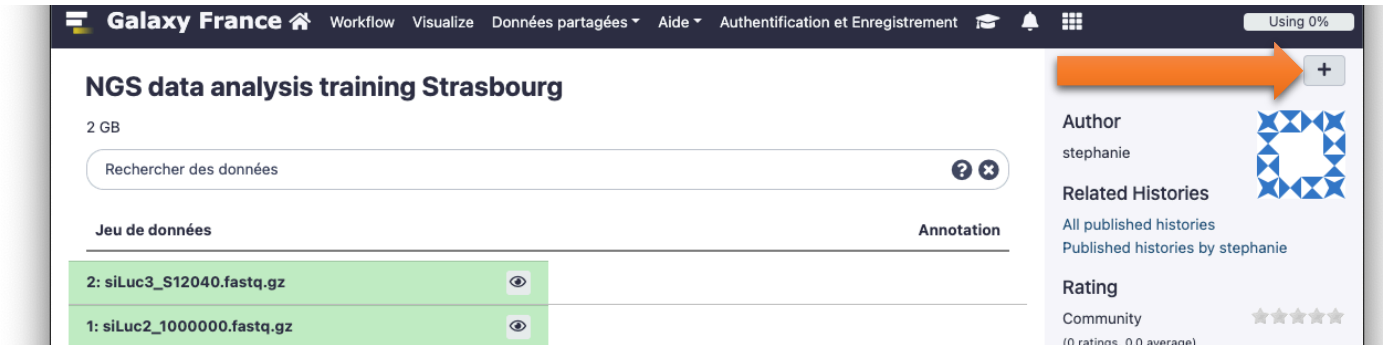
- 1.
 - Go to Shared data (top menu) > Histories.
 - Search « NGS data analysis training Strasbourg ».

The screenshot shows the Galaxy France interface. The top navigation bar includes 'Galaxy France', 'Workflow', 'Visualize', 'Données partagées', 'Aide', 'Authentification et Enregistrement', and 'Using 0%'. The left sidebar contains a 'Tools' section with a search bar and an 'Upload Data' button. Below this is a list of tool categories, including 'Get Data', 'Collection Operations', 'GENERAL TEXT TOOLS', 'Text Manipulation', 'Filter and Sort', 'Join, Subtract and Group', 'GENOMIC FILE MANIPULATION', 'Convert Formats', 'FASTA/FASTQ', 'FASTQ Quality Control', 'SAM/BAM', 'BED', 'VCF/BCF', 'Nanopore', 'COMMON GENOMICS TOOLS', 'Operate on Genomic Intervals', 'Fetch Alignments/Sequences', and 'GENOMICS ANALYSIS'. An orange arrow points to the search bar in the 'Tools' section. The main content area is titled 'Published Histories' and features a search bar with the text 'search name, annotation, owner'. Below the search bar is a table of published histories. The table has three columns: 'Name', 'Annotation', and 'Owner'. The first row is highlighted in blue and contains the text 'NGS data analysis training Strasbourg', 'stephanie'. The other rows are: 'galaxy101', 'lgueuen'; 'Rustenholtz - GW', 'dc244f268e'; 'RNASeq GW BV - Rustenholtz', 'dc244f268e'; 'RNASeq RI MIM - Rustenholtz', 'dc244f268e'; 'RNASeq RI BV - Rustenholtz', 'dc244f268e'; 'Rustenholtz - RI', 'dc244f268e'; 'ABIMS - Galaxy initiation 2022 - datasets - public', 'lgueuen'; 'Rustenholtz - IGV', 'dc244f268e'; 'Rustenholtz - DE Sangiovese', 'dc244f268e'; 'Rustenholtz - DE Barbera Refosco', 'dc244f268e'; 'RNASeq GW MIM - Rustenholtz', 'dc244f268e'; 'GCMS_For_WF', 'yguilton44'; 'TP RNAseq billie Initial datasets', 'c0d111ceec2'; and 'ARTIC v3', 'lecorguille'. The right sidebar is titled 'History' and contains a search bar with the text 'Rechercher des données'. Below the search bar is the text 'Unnamed history (empty)'. A blue box contains the text: 'Cet historique est vide. You can Charger vos propres données or Charger des données depuis une source externe'.

Name	Annotation	Owner
NGS data analysis training Strasbourg		stephanie
galaxy101		lgueuen
Rustenholtz - GW		dc244f268e
RNASeq GW BV - Rustenholtz		dc244f268e
RNASeq RI MIM - Rustenholtz		dc244f268e
RNASeq RI BV - Rustenholtz		dc244f268e
Rustenholtz - RI		dc244f268e
ABIMS - Galaxy initiation 2022 - datasets - public		lgueuen
Rustenholtz - IGV		dc244f268e
Rustenholtz - DE Sangiovese		dc244f268e
Rustenholtz - DE Barbera Refosco		dc244f268e
RNASeq GW MIM - Rustenholtz		dc244f268e
GCMS_For_WF		yguilton44
TP RNAseq billie Initial datasets		c0d111ceec2
ARTIC v3	Auxiliary datasets for analysis of ARTIC (v3) SARS-CoV-2 data	lecorguille

Answer 3 : Import data to Galaxy

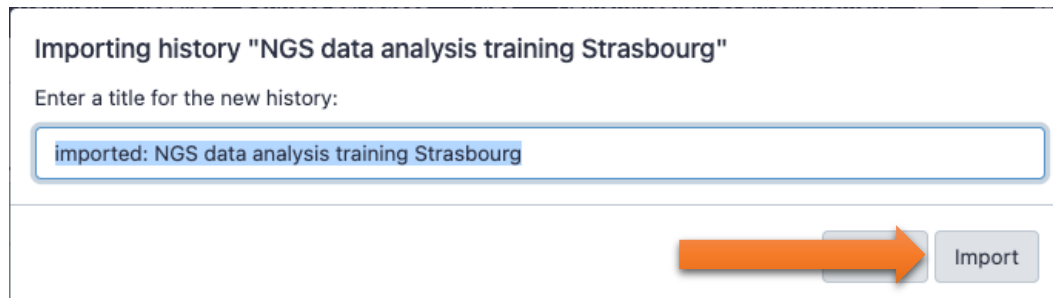
- Click on « **NGS data analysis training Strasbourg** »
- Click on 



The screenshot shows the Galaxy France interface. The main heading is "NGS data analysis training Strasbourg" with a size of "2 GB". Below this is a search bar labeled "Rechercher des données". Underneath, there are two data sets listed in a table:

Jeu de données	Annotation
2: siLuc3_S12040.fastq.gz	
1: siLuc2_1000000.fastq.gz	

On the right side, there is a sidebar with a plus icon at the top, an author profile for "stephanie", and a "Related Histories" section. An orange arrow points to the plus icon.



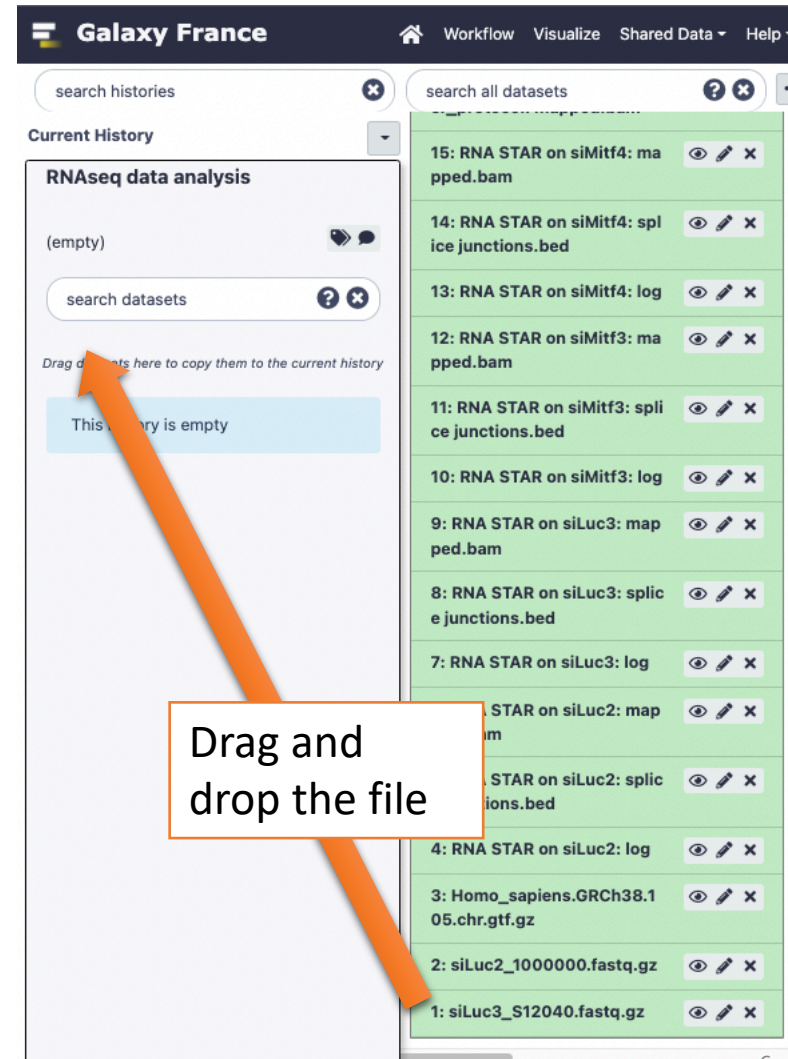
The dialog box is titled "Importing history 'NGS data analysis training Strasbourg'". It prompts the user to "Enter a title for the new history:". The input field contains the text "imported: NGS data analysis training Strasbourg". Below the input field is an "Import" button. An orange arrow points to the "Import" button.

- Click on Import

Answer 3 : Import data to Galaxy

- Use the tool "View all histories" 

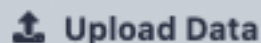
then:



Answer 3 : Import data to Galaxy

• 2

- Click on the button to display the drag and drop utility

 Upload Data




- Drag and drop the file [sample.bed.gz](#) into the opened window.
 - **Type:** bed
 - **Genome:** Mouse July 2007 (NCBI37/mm9) (mm9)

Download from web or upload from disk

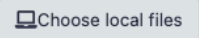
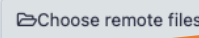

Download from web or upload from disk

Regular Composite Collection Rule-based

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

Name	Size	Type	Genome	Settings	Status
 sample.bed.gz	482.9 KB	bed	Mouse July 200...		0% 

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

   **Start** Pause Reset Close

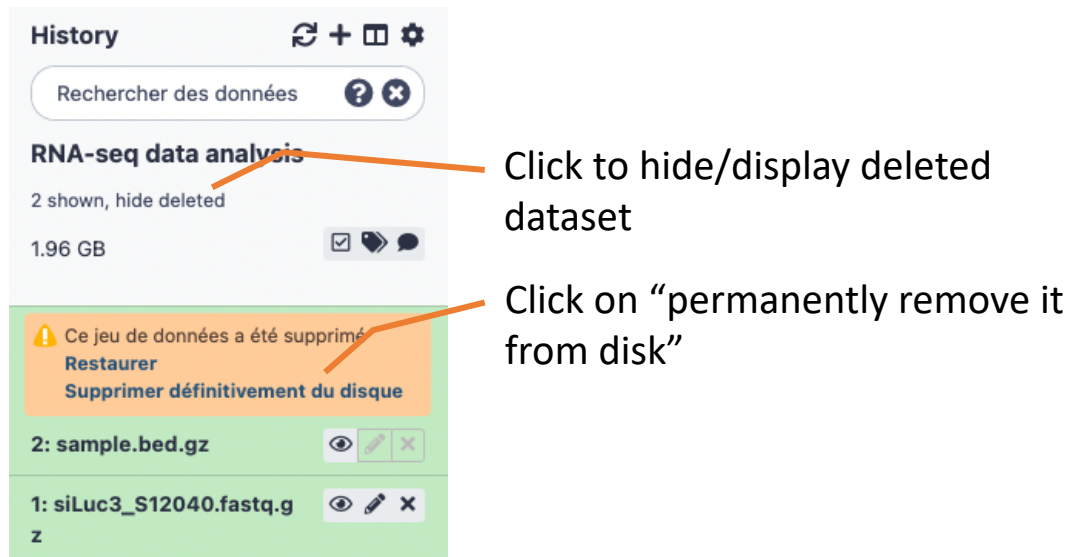
- Click on Start
- Click on Close to close the upload utility


Answer 4: remove dataset

- 1. Click on the  of the dataset in the history



- 2.
 - A)



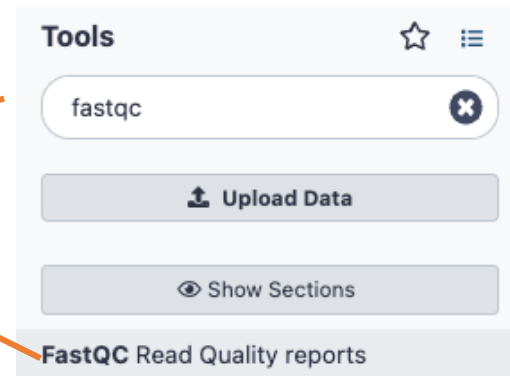
- B) Click on "hide deleted"
- NOTE: to permanently remove from disk multiple deleted datasets, click on the History option button  and select "Purge deleted datasets"

Answer 5 : Running a tool

1. Search “fastqc” in the list or using the search field of the tool panel.


Enter: “fastqc”

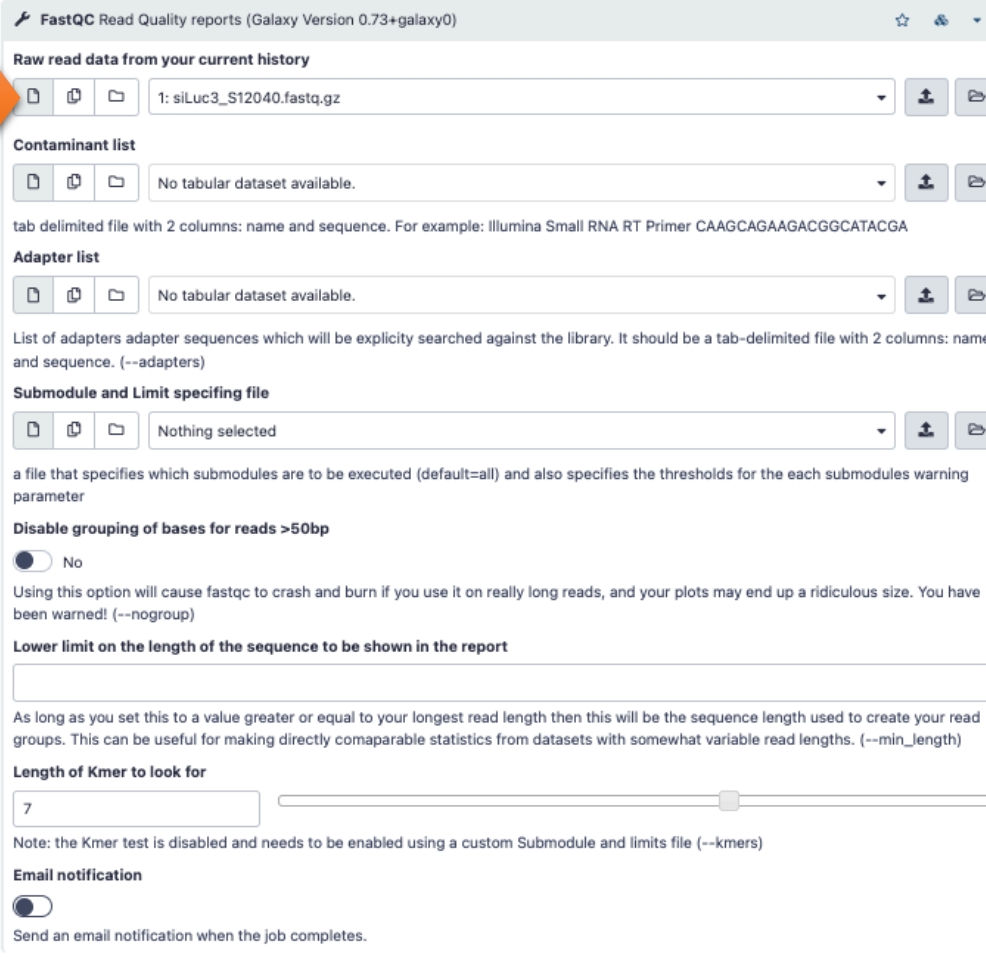
Click on the tool name



Answer 5 : Running a tool

2. Select the file to analyze and click on Execute

1. 



FastQC Read Quality reports (Galaxy Version 0.73+galaxy0)

Raw read data from your current history

1: siLuc3_S12040.fastq.gz

Contaminant list

No tabular dataset available.

tab delimited file with 2 columns: name and sequence. For example: Illumina Small RNA RT Primer CAAGCAGAAGACGGCATACGA

Adapter list

No tabular dataset available.

List of adapters adapter sequences which will be explicitly searched against the library. It should be a tab-delimited file with 2 columns: name and sequence. (--adapters)

Submodule and Limit specifying file

Nothing selected

a file that specifies which submodules are to be executed (default=all) and also specifies the thresholds for the each submodules warning parameter

Disable grouping of bases for reads >50bp

No

Using this option will cause fastqc to crash and burn if you use it on really long reads, and your plots may end up a ridiculous size. You have been warned! (--nogroup)

Lower limit on the length of the sequence to be shown in the report

As long as you set this to a value greater or equal to your longest read length then this will be the sequence length used to create your read groups. This can be useful for making directly comparable statistics from datasets with somewhat variable read lengths. (--min_length)

Length of Kmer to look for

7

Note: the Kmer test is disabled and needs to be enabled using a custom Submodule and limits file (--kmers)

Email notification

Send an email notification when the job completes.

2. 