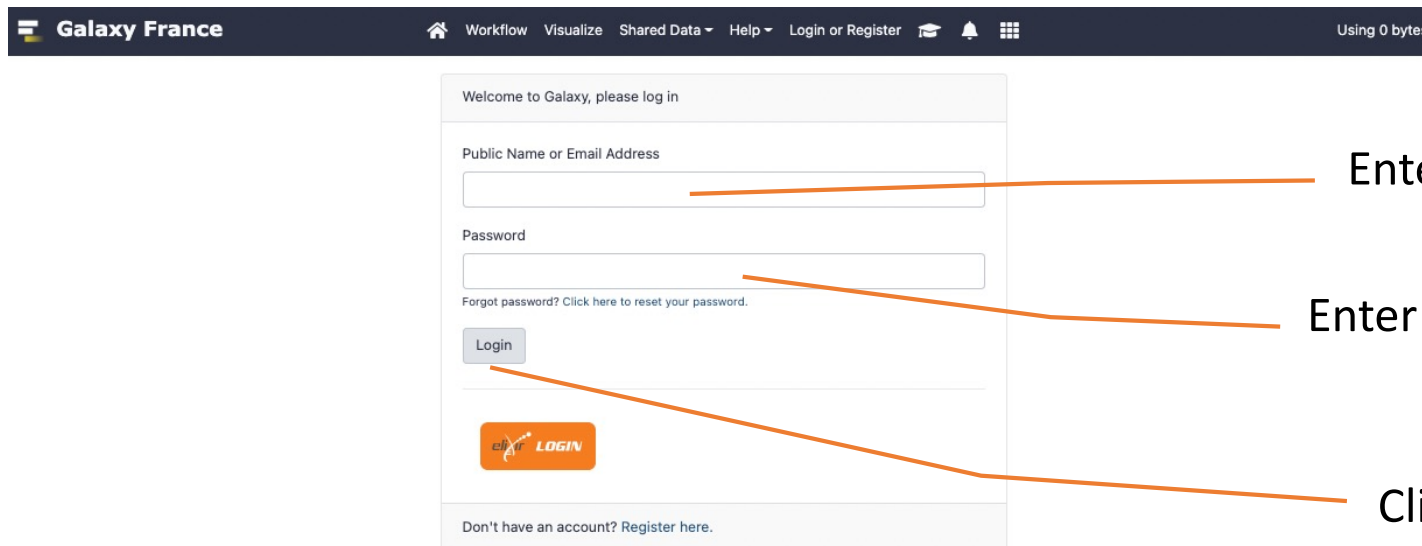


# Introduction to Galaxy (answers to questions)

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# 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 Galaxy France logo, a home icon, and menu items: Workflow, Visualize, Shared Data, Help, Login or Register, a graduation cap icon, a bell icon, and a grid icon. On the right side of the navigation bar, it says "Using 0 bytes". Below the navigation bar is a white login form. The form has a header "Welcome to Galaxy, please log in". It contains two input fields: "Public Name or Email Address" and "Password". Below the password field is a link: "Forgot password? Click here to reset your password." There is a "Login" button and a larger orange "LOGIN" button with the Galaxy logo. At the bottom of the form, there is a link: "Don't have an account? Register here." Three orange arrows point from text labels on the right to the form elements: "Enter your login" points to the first input field, "Enter your password" points to the second input field, and "Click on Login" points to the "Login" button.

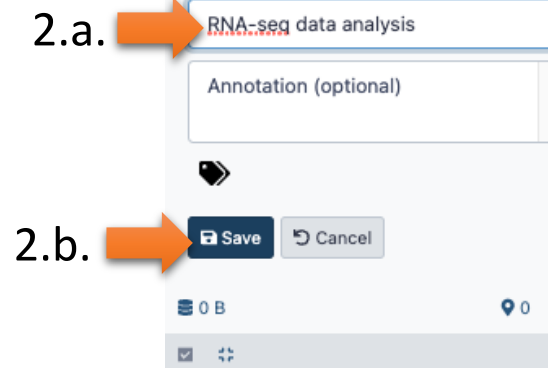
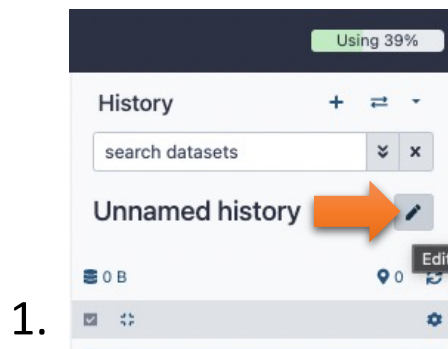
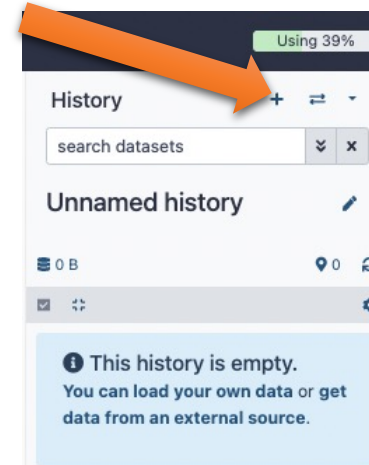
Enter your login

Enter your password

Click on Login

# Answer 2 : History

- Create a new history by clicking on the [+ button]
- Change the name of the new history to “RNA-seq data analysis” by clicking on [the pencil button] (1.) on top of the history panel. Then, type “RNA-seq data analysis” (2.a.) and click on “Save” (2.b.).



# Answer 3 : Import data to Galaxy

- 1.
  - Go to Shared data (top menu) (1.a) > Histories (1.b.).
  - You can enter “Strasbourg” in the search field (2). Click « NGS data analysis training Strasbourg » (3).

1.a.

1.b.

2.

3.

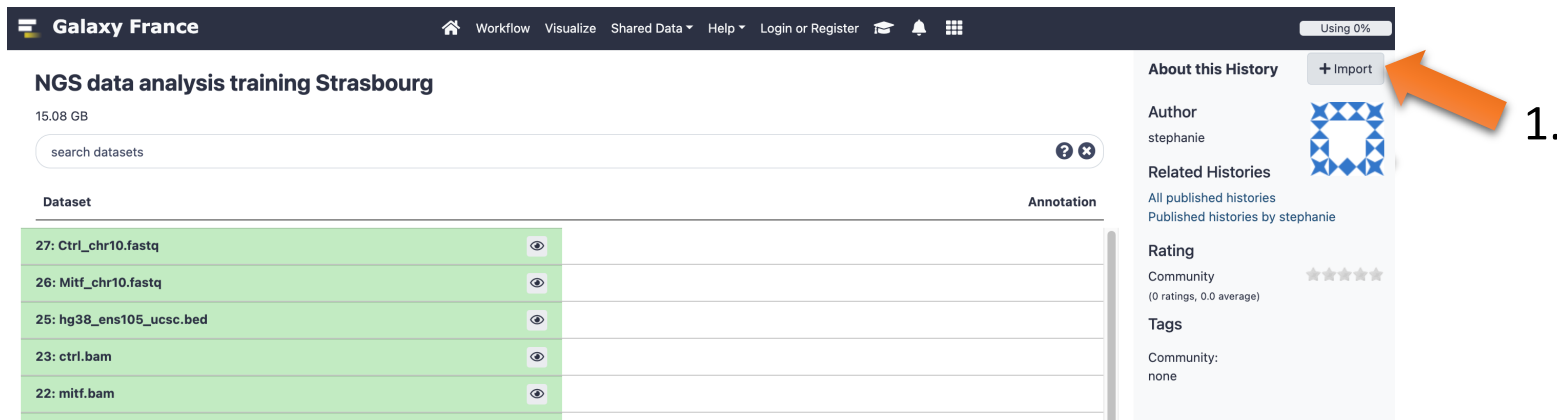
The screenshot shows the Galaxy France interface. The top navigation bar includes 'Workflow', 'Visualize', 'Shared Data', 'Help', 'User', and a 'Using 39%' indicator. The 'Shared Data' menu is open, showing options like 'Data Libraries', 'Histories', 'Workflows', 'Visualizations', and 'Pages'. The 'Histories' option is selected, and a search for 'strasbourg' is performed. The search results table shows one entry: 'NGS data analysis training Strasbourg' by 'stephanie' with a 5-star rating and last updated on 'Apr 05, 2023'. The 'Send Data' button is highlighted in the left sidebar. A message on the right indicates 'This history is empty. You can load your own data or get data from an external source.'

Name	Annotation	Rating	Community Tags	Last Updated
NGS data analysis training Strasbourg		stephanie ★★★★★		Apr 05, 2023

https://usegalaxy.fr/histories/list\_published

# Answer 3 : Import data to Galaxy

- Click on [+ Import] (1.)

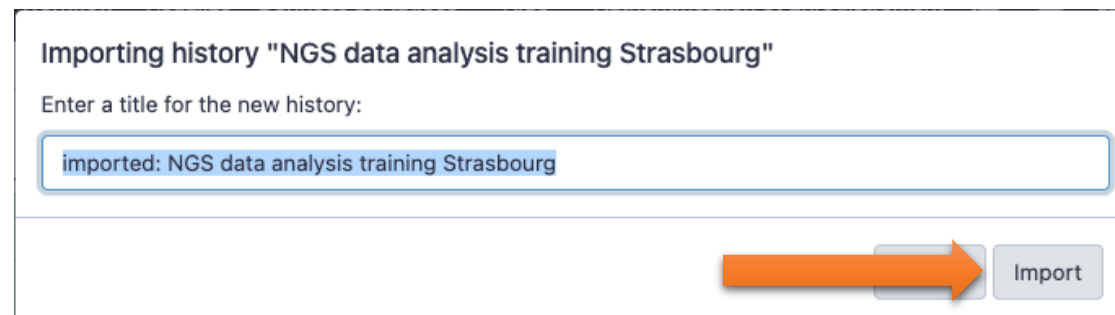


The screenshot shows the Galaxy France interface. The main content area displays the history 'NGS data analysis training Strasbourg' with a size of 15.08 GB. Below this is a search bar for datasets and a table of datasets:

Dataset	Annotation
27: Ctrl_chr10.fastq	
26: Mitf_chr10.fastq	
25: hg38_ens105_ucsc.bed	
23: ctrl.bam	
22: mitf.bam	

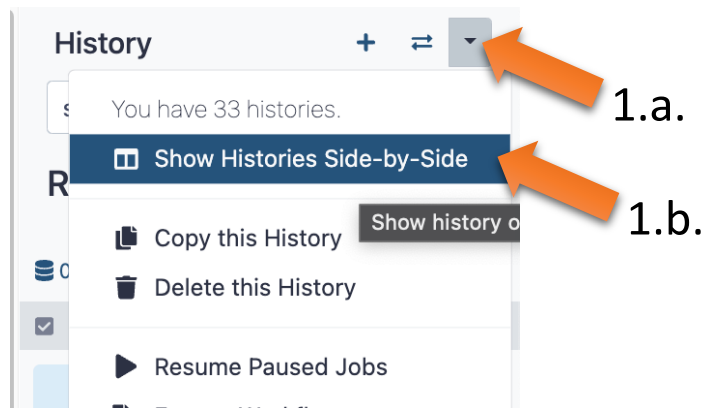
On the right side, the 'About this History' panel is visible, featuring a '+ Import' button at the top right, which is highlighted by an orange arrow and the number '1.'. Other details in the panel include the author 'stephanie', related histories, a rating of 0 stars, and no tags.

- You can leave the name as it is. Click on Import

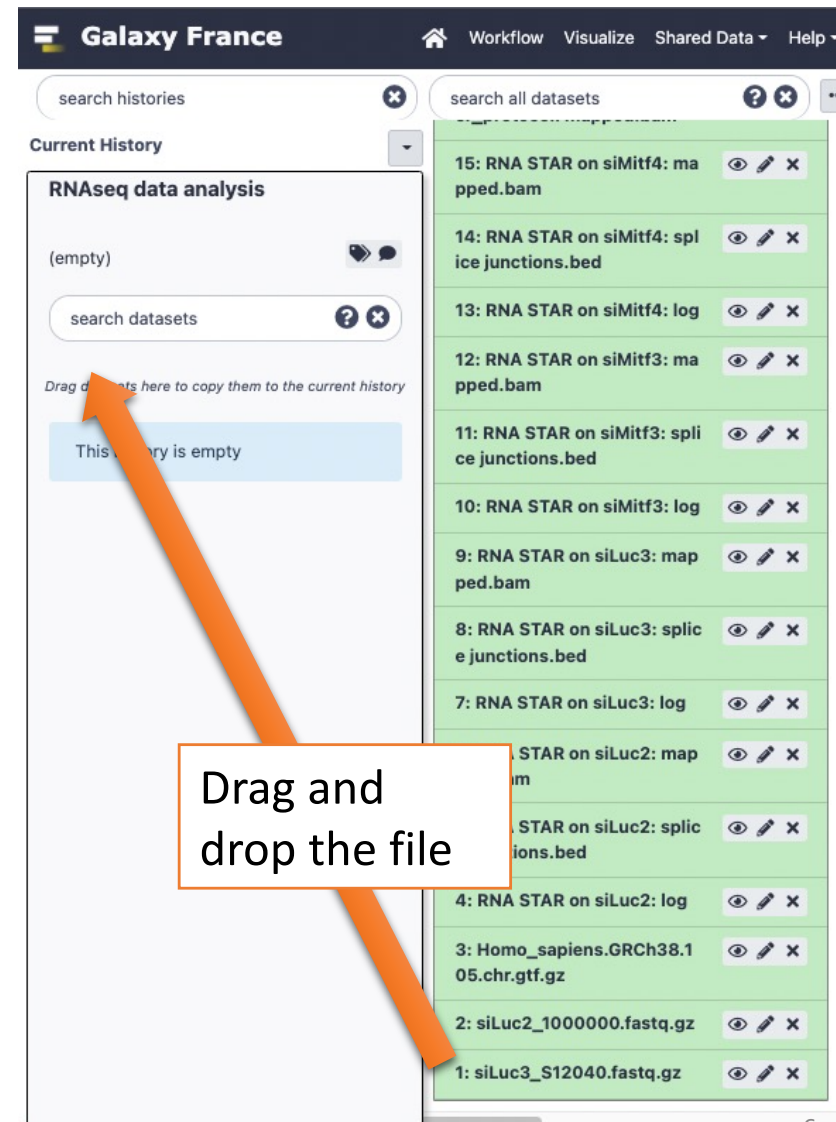


The screenshot shows the 'Importing history' dialog box. The title is 'Importing history "NGS data analysis training Strasbourg"'. Below the title, there is a prompt 'Enter a title for the new history:' followed by a text input field containing the text 'imported: NGS data analysis training Strasbourg'. At the bottom right of the dialog, there is an 'Import' button, which is highlighted by an orange arrow.

# Answer 3 : Import data to Galaxy



- Go to ▼ (1.a.) in the history panel and select “Show Histories Side-by-side” (1.b.)




Drag and drop the file

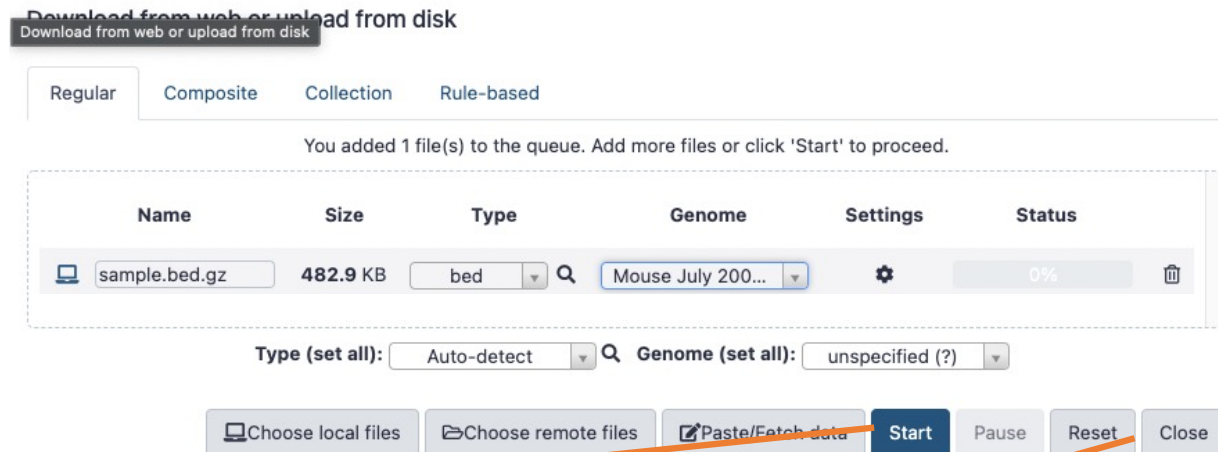
# Answer 3 : Import data to Galaxy

- 2

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

A grey rectangular button with a white upward-pointing arrow icon and the text "Upload Data" in bold black font.

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

The screenshot shows the Galaxy upload utility interface. At the top, there are two tabs: "Download from web or upload from disk" (selected) and "Upload from disk". Below the tabs are four filter buttons: "Regular", "Composite", "Collection", and "Rule-based". A message states: "You added 1 file(s) to the queue. Add more files or click 'Start' to proceed." Below this is a table with columns: Name, Size, Type, Genome, Settings, and Status. The table contains one row for "sample.bed.gz" with a size of "482.9 KB", type "bed", genome "Mouse July 200...", and status "0%". Below the table are two dropdown menus: "Type (set all): Auto-detect" and "Genome (set all): unspecified (?)". At the bottom, there are six buttons: "Choose local files", "Choose remote files", "Paste/Fetch data", "Start" (highlighted in dark blue), "Pause", "Reset", and "Close".

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

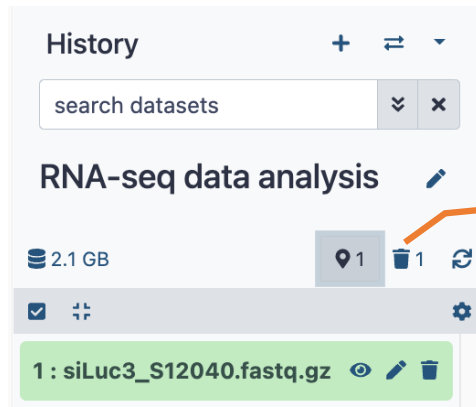
- Click on Start
- Click on Close to close the upload utility

# Answer 4: remove dataset

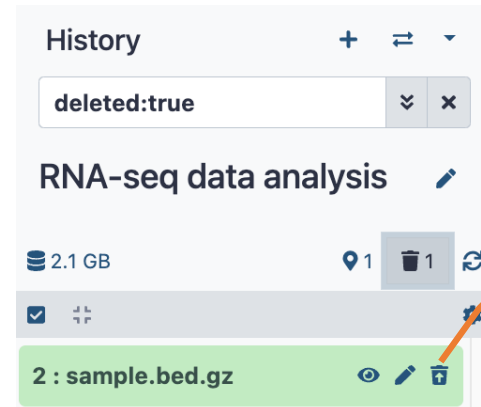
- 1. Click on the  of the dataset in the history



- 2.A.

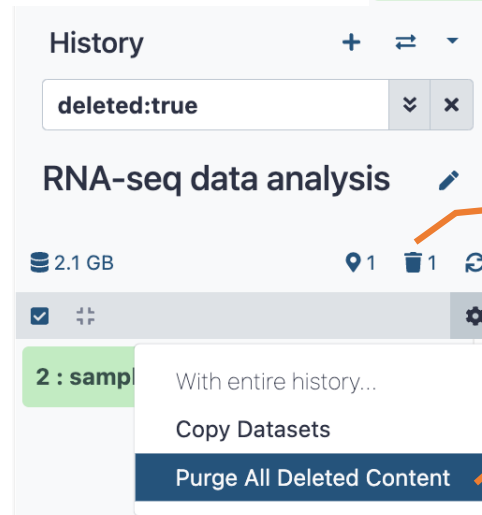


- 1. Click to display deleted dataset



- 2. Restore the dataset

- 2.B. Do 1. again and :



- 1. Click to display deleted dataset

- 2. Remove data permanently

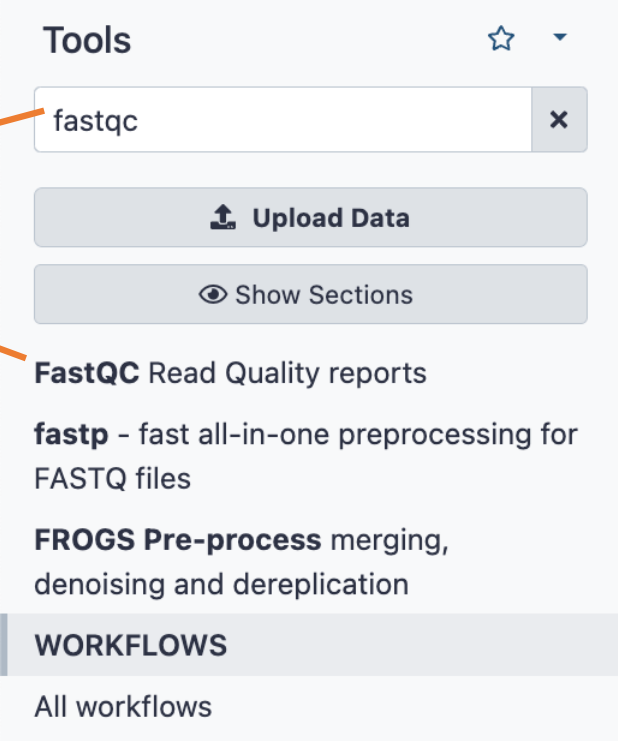


# Answer 5 : Running a tool

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

Enter: “fastqc”

Click on the tool name



The screenshot shows a 'Tools' panel with a search bar containing 'fastqc'. Below the search bar are two buttons: 'Upload Data' and 'Show Sections'. The search results are displayed below, including 'FastQC Read Quality reports', 'fastp - fast all-in-one preprocessing for FASTQ files', and 'FROGS Pre-process merging, denoising and dereplication'. A 'WORKFLOWS' section is also visible, containing 'All workflows'.

Tools ☆ ▾

fastqc ×

⬆️ Upload Data

👁 Show Sections

**FastQC** Read Quality reports

**fastp** - fast all-in-one preprocessing for FASTQ files


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

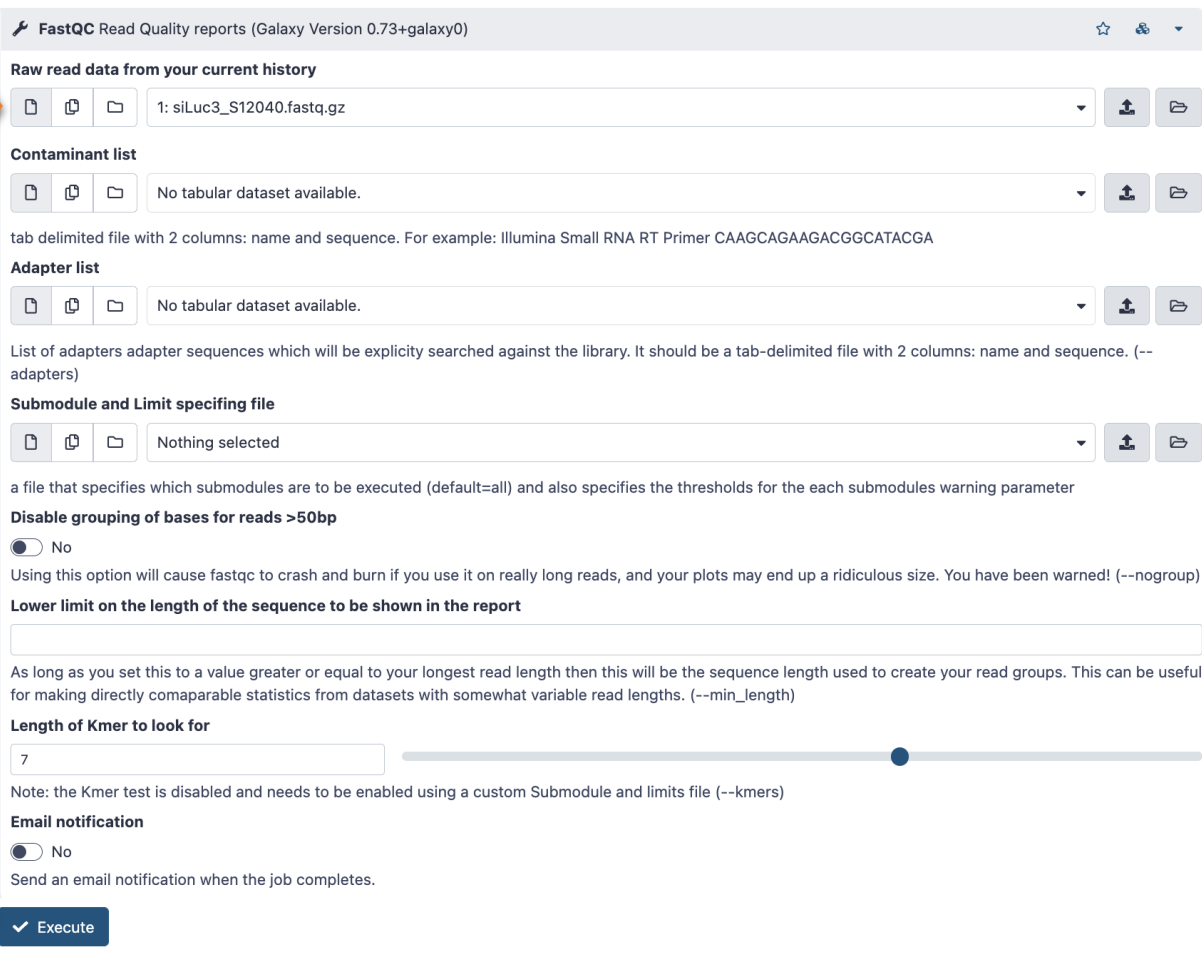
**WORKFLOWS**

All workflows

# 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**

No

Send an email notification when the job completes.

2. 