

Introduction to Galaxy

(answers to questions)

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Answer 1 : Log in

- Go to <http://use.galaxeast.fr>

Galaxy / Galaxeast Analyze Data Workflow Shared Data Visualization Help User Using 0 bytes

This Galaxy instance has been configured such that only users who are logged in may use it.

Login

Username / Email Address:

Password:

[Forgot password? Reset here](#)

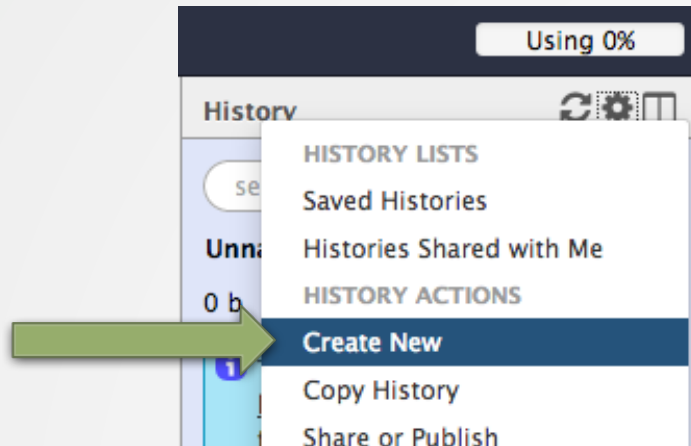
Login

Enter your login
(userN)

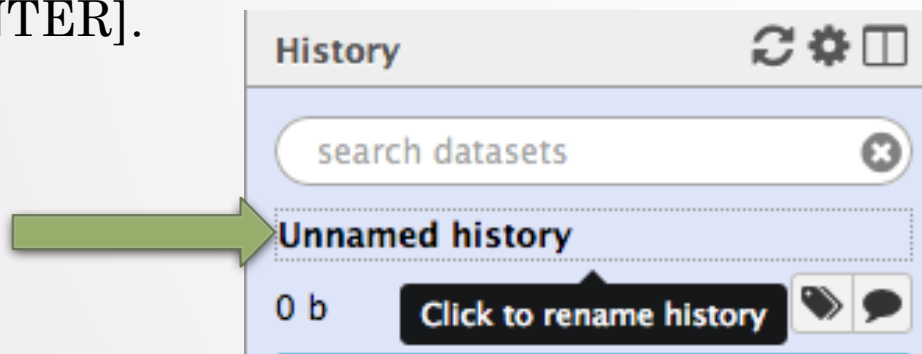
Enter your password
(trainingCNRS0917)

Answer 2 : History

- Create a new history



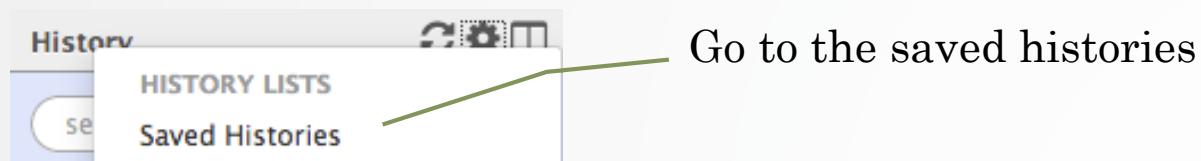
- Change the name of the new history to “RNA-seq data analysis” by clicking on “Unnamed history” on top of the history panel. Then type ” RNA-seq data analysis” and [ENTER].



Answer 3 : Import data to Galaxy

- 1.
 - Go to Shared data (top menu) > Data libraries.
 - Go to CNRS training > RNAseq > rawdata.
 - Tick the box beside the sample name “siLuc3_S12040.fastq”.
 - Click on the button “to History”.
 - The history “RNAseq data analysis” is selected. Click on import.
 - Click on “Analyze Data” (top menu) to go back to the main Galaxy page.

- 2.



Saved Histories


search history names and tags

[Advanced Search](#)

<input type="checkbox"/> Name	Datasets	Tags	Sharing	Size on Disk	Created	Last Updated ↑	Status
<input type="checkbox"/> RNA-seq data analysis	1	0 Tags		7.2 GB	nov. 25, 2016	~4 seconds ago	current history

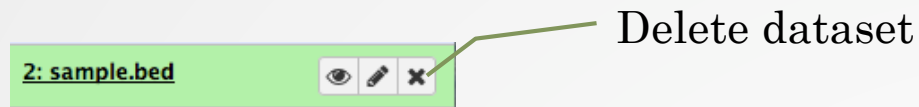
Click on the name of the history

Answer 3 : Import data to Galaxy

- 3
 - Click on the button to display the drag and drop utility 
 - Drag and drop the file sample.bed.gz into the opened window.
 - Select Type: bed
 - Select Genome: Mouse July 2007 (NCBI37/mm9) (mm9)
 - Click on Start
 - Click on Close to close the upload utility

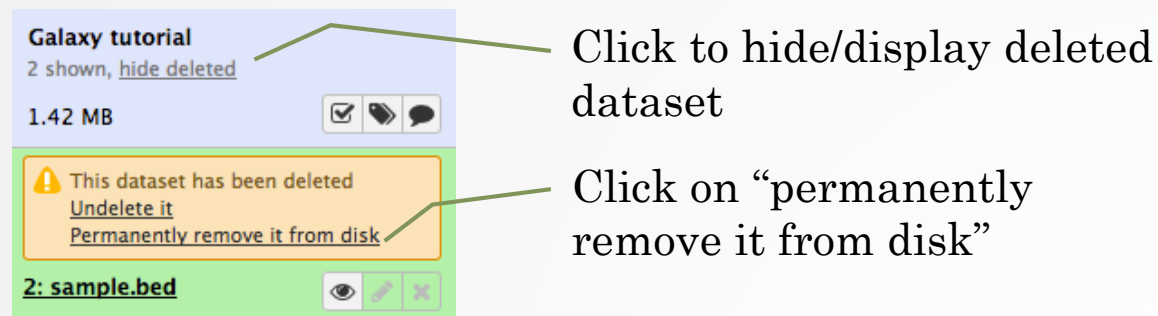
Answer 4: remove dataset

- 1. Click on the cross of the dataset box 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”

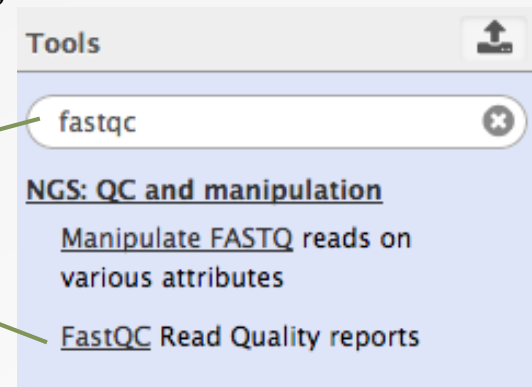


Answer 5 : Running a tool

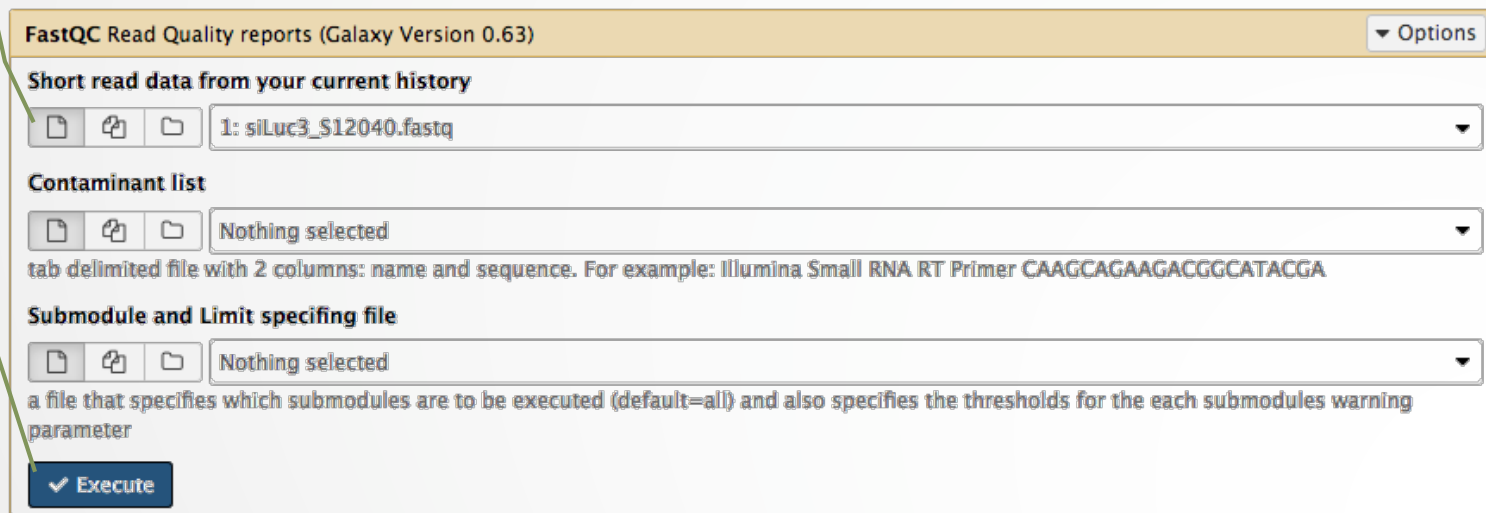
- Search “fastqc” in the list or using the search field of the tool panel.

Enter: “fastqc”

Click on the tool name



- Select the file to analyze and click on “Execute”

A screenshot of the FastQC tool configuration interface in Galaxy. The title bar reads "FastQC Read Quality reports (Galaxy Version 0.63)" with an "Options" dropdown on the right. The main area contains three input fields, each with a file icon, a copy icon, and a folder icon. The first field is labeled "Short read data from your current history" and contains the file "1: siLuc3_S12040.fastq". The second field is labeled "Contaminant list" and contains "Nothing selected". The third field is labeled "Submodule and Limit specifying file" and also contains "Nothing selected". Below these fields is a blue button with a checkmark and the text "Execute". A green line points from the text "Select the file to analyze and click on 'Execute'" to the "Execute" button.