

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](#)

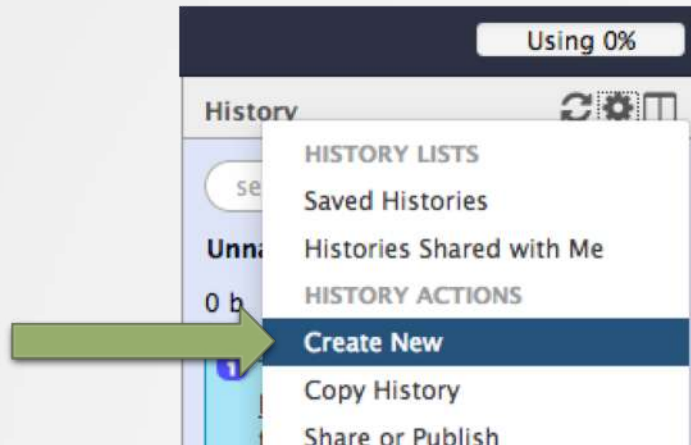
Login

Enter your login
(userN)

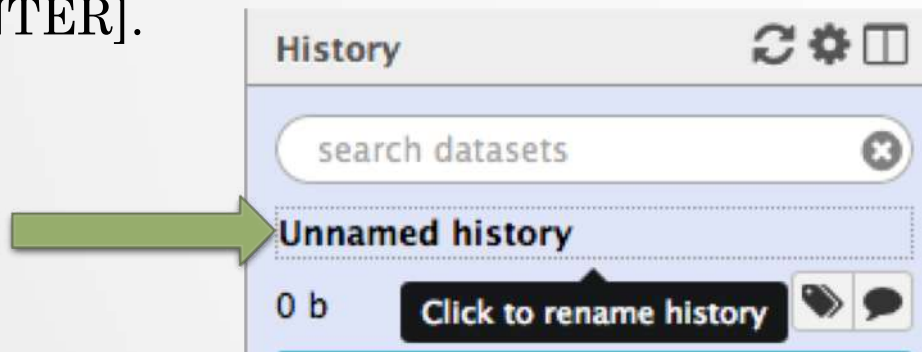
Enter your password
(NGStraining0319)

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 NGS data analysis 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.



Go to the saved histories

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)

Download from web or upload from disk

Regular Composite

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 2007 (...)		

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

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

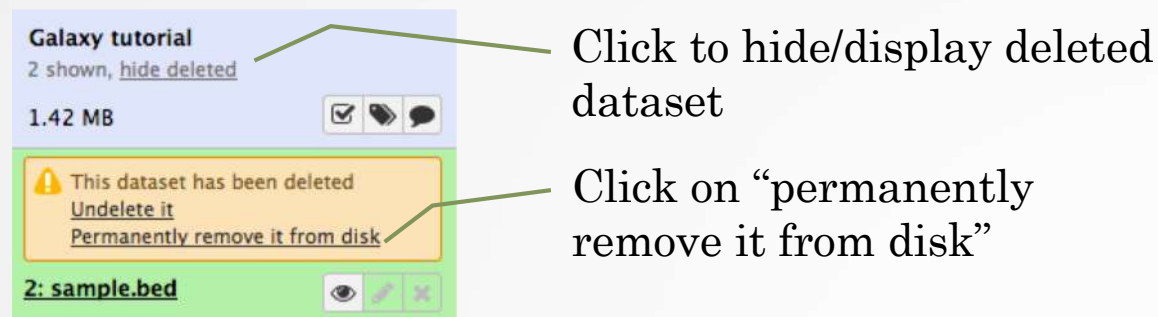
Answer 4: remove dataset

- 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

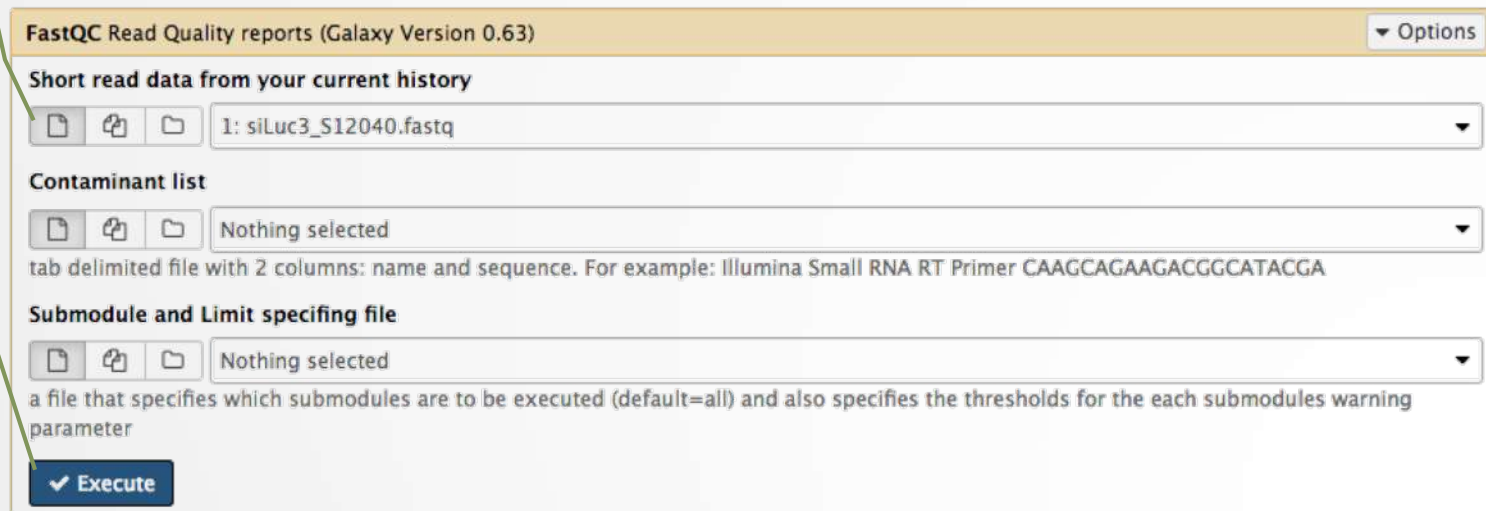
- Search “fastqc” in the list or using the search field of the tool panel.

Enter: “fastqc”

Click on the tool name



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

A screenshot of the "FastQC Read Quality reports (Galaxy Version 0.63)" tool interface. The interface has a yellow header bar with the title and a "Options" dropdown. Below the header, there are 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.