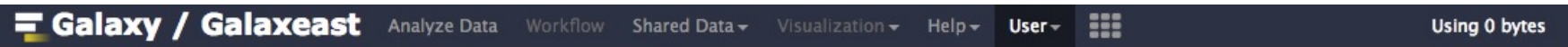


# Introduction to Galaxy (answers to questions)

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# Answer 1 : Log in

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



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

The image shows a login form with two input fields and a button. The first field is labeled 'Username / Email Address:' and the second is labeled 'Password:'. Below the password field, there is a link that says 'Forgot password? Reset here'. A 'Login' button is located at the bottom left of the form. Two lines with arrows point from the text on the right to the input fields. The first line points to the username field and is accompanied by the text 'Enter your login (userN@galaxeast.fr)'. The second line points to the password field and is accompanied by the text 'Enter your password (training2106)'.

Username / Email Address:

Password:

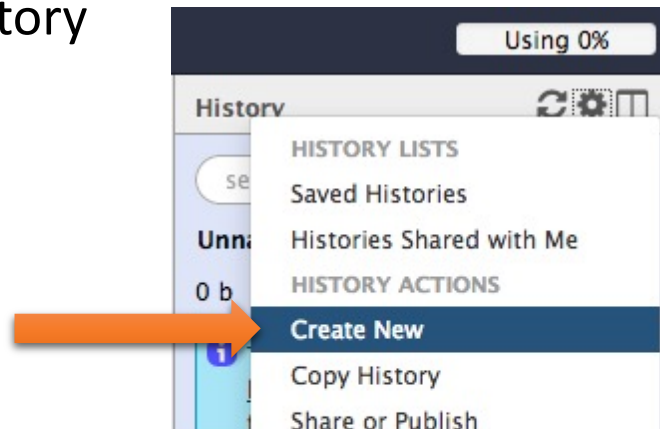
[Forgot password? Reset here](#)

Enter your login  
(userN@galaxeast.fr)

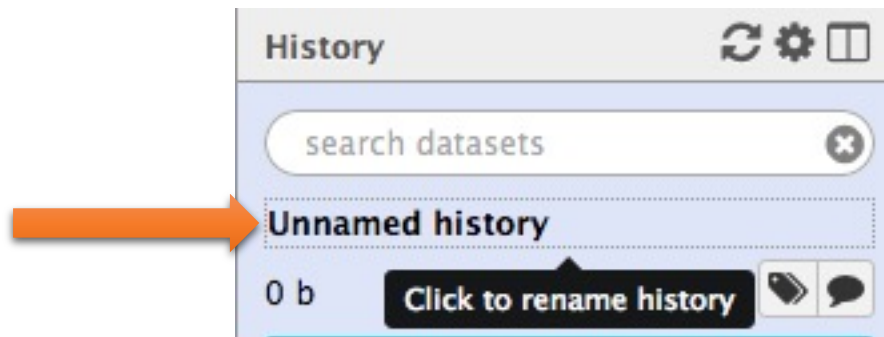
Enter your password  
(training2106)

# 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


[Advanced Search](#)

Click on the name of the history

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

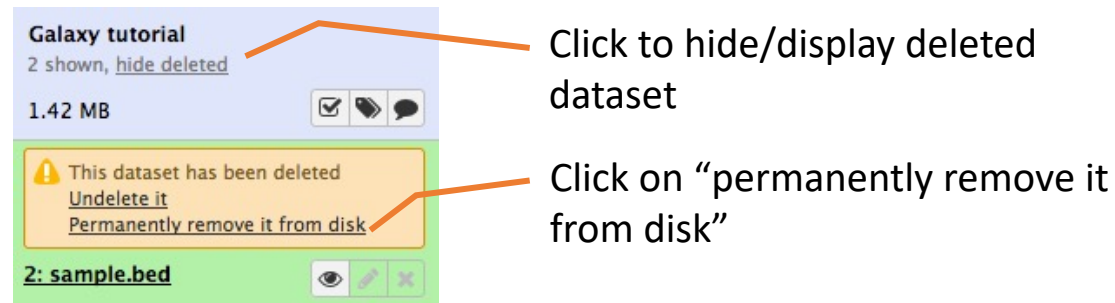
# Answer 4: remove dataset

- 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”

