# Introduction to Galaxy
# (answers to questions)

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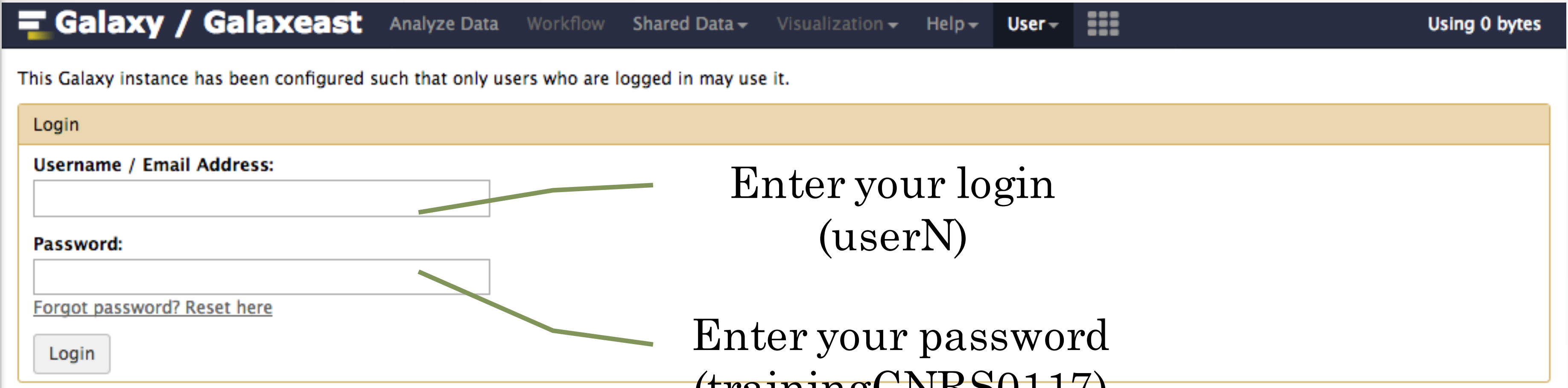
# Answer 1 : Log in

- Go to [http://use.galaxeast.fr](http://use.galaxeast.fr)



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

Login

Username / Email Address:

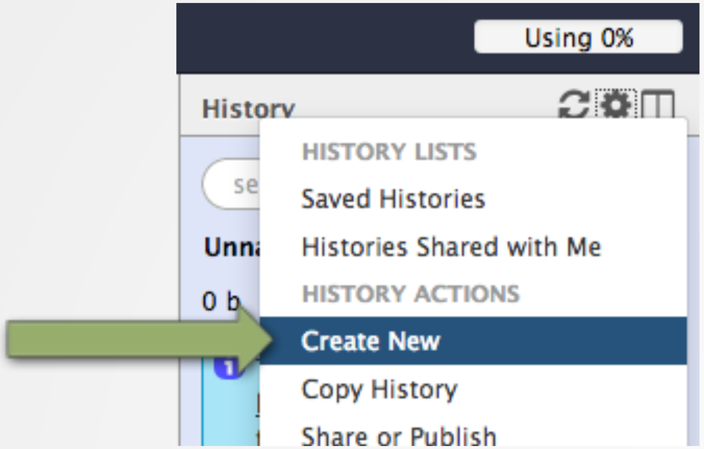
Password:

Enter your login (userN)

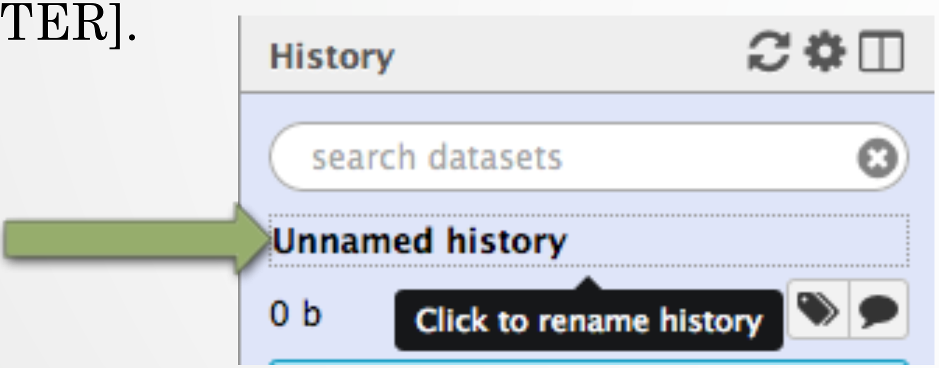
Enter your password (trainingCNRS0117)

# Answer 2 : History

- Create a new history

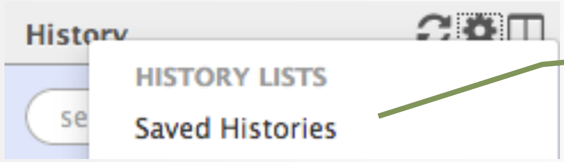


- Change the name of the new history to “RNA-seq data analysis” by clicking on “Unnamed history” on top of the history panel. Then type ” RNA-seq data analysis” and [ENTER].

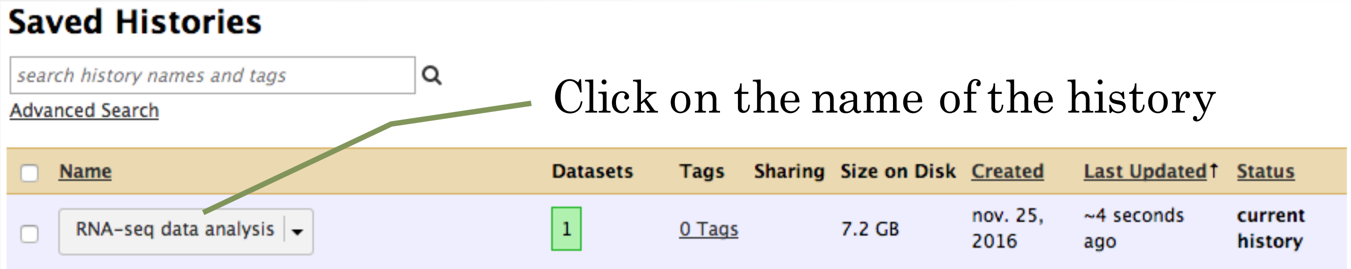


# Answer 3 : Import data to Galaxy

- 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.
  - 

    Go to the saved histories

  - 

    **Saved Histories**

| ☐ | Name | Datasets | Tags | Sharing | Size on Disk | Created | Last Updated↑ | Status |
|---|---|---|---|---|---|---|---|---|
| ☐ | RNA-seq data analysis ▾ | 1 | 0 Tags | | 7.2 GB | nov. 25, 2016 | ~4 seconds ago | current history |

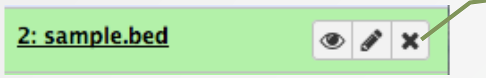
    Click on the name of the history

# 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

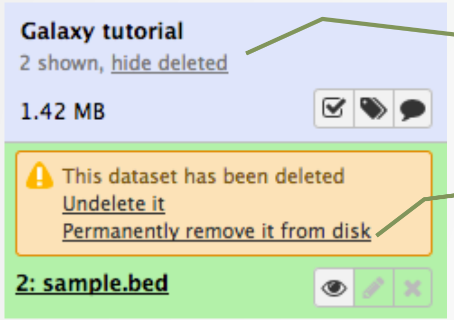
# Answer 4: remove dataset

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



Delete dataset

- 2.
  - A)



This dataset has been deleted
Undelete it
Permanently remove it from disk

Click to hide/display deleted dataset

Click on “permanently remove it from disk”

  - 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”

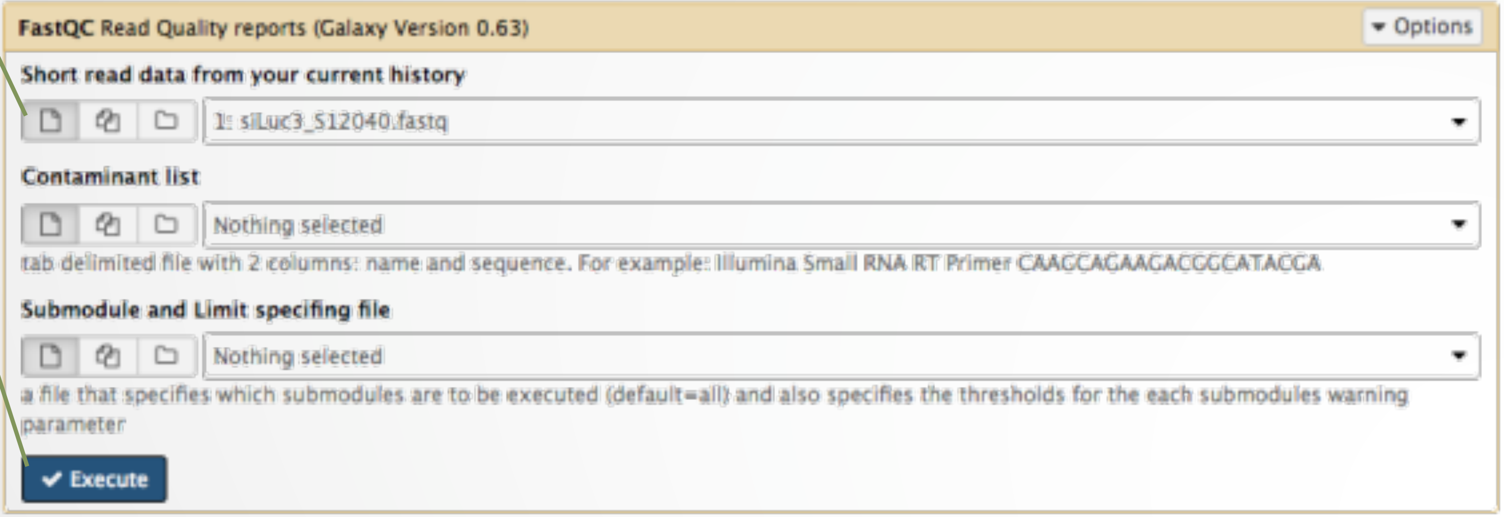
# Answer 5 : Running a tool

- 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”



**FastQC Read Quality reports (Galaxy Version 0.63)**

**Short read data from your current history**

1: siLuc3_S12040.fastq

**Contaminant list**

Nothing selected

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

**Submodule and Limit specifing 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