Introduction to Galaxy (answers to questions)

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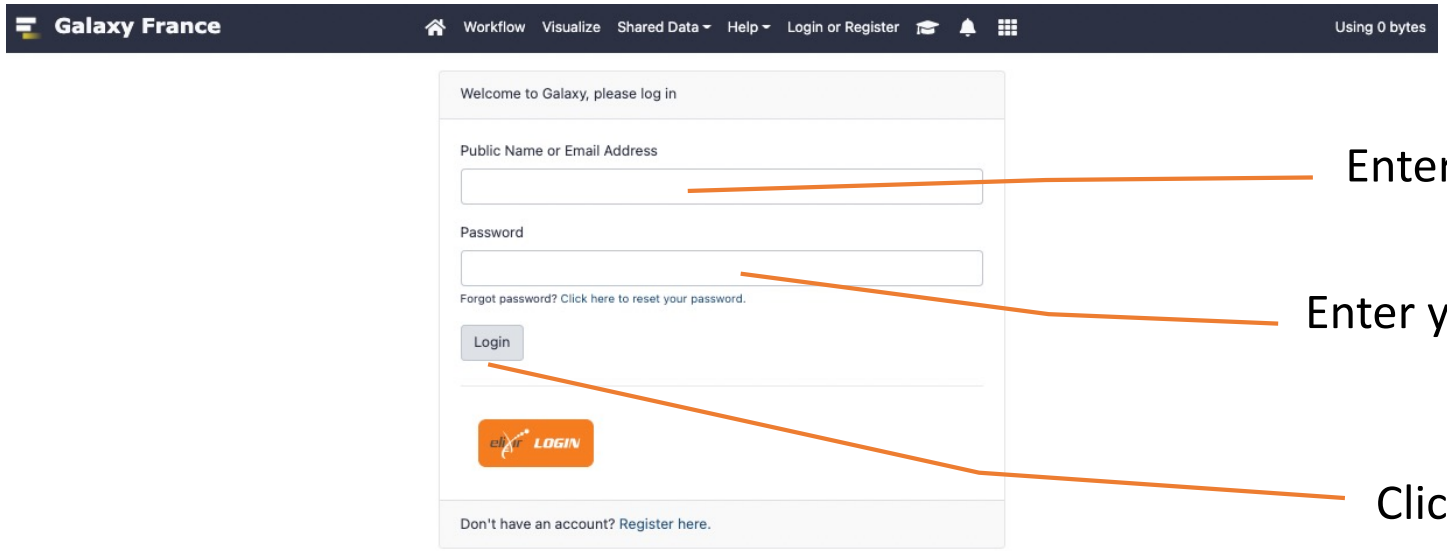
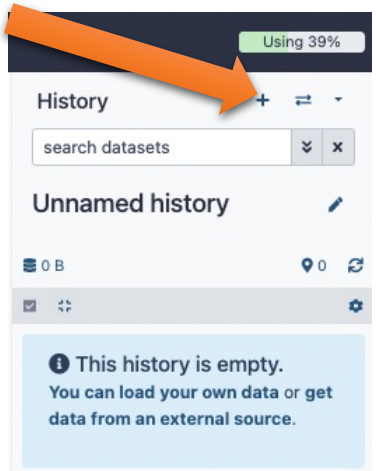
Answer 1 : Log in

- Go to https://usegalaxy.fr/



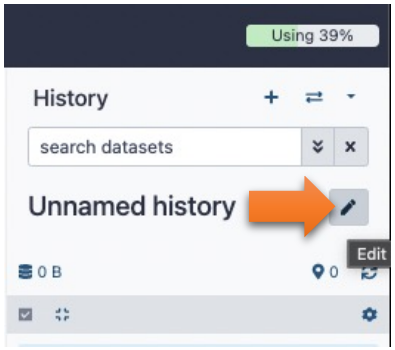
Answer 2 : History

- Create a new history by clicking on the [+ button]



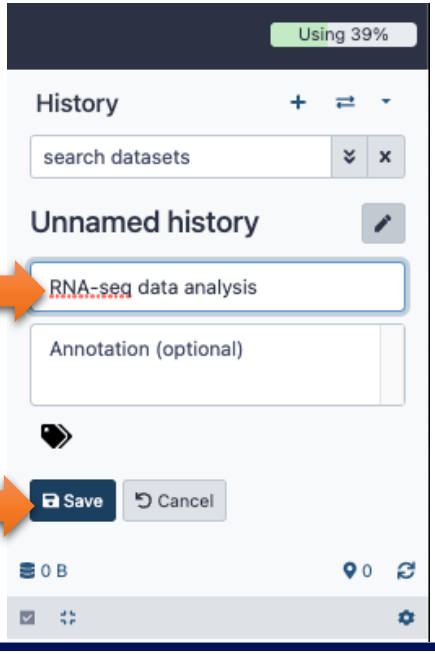
- Change the name of the new history to “RNA-seq data analysis” by clicking on [the pencil button] (1.) on top of the history panel. Then, type “RNA-seq data analysis” (2.a.) and click on ”Save” (2.b.).

1.



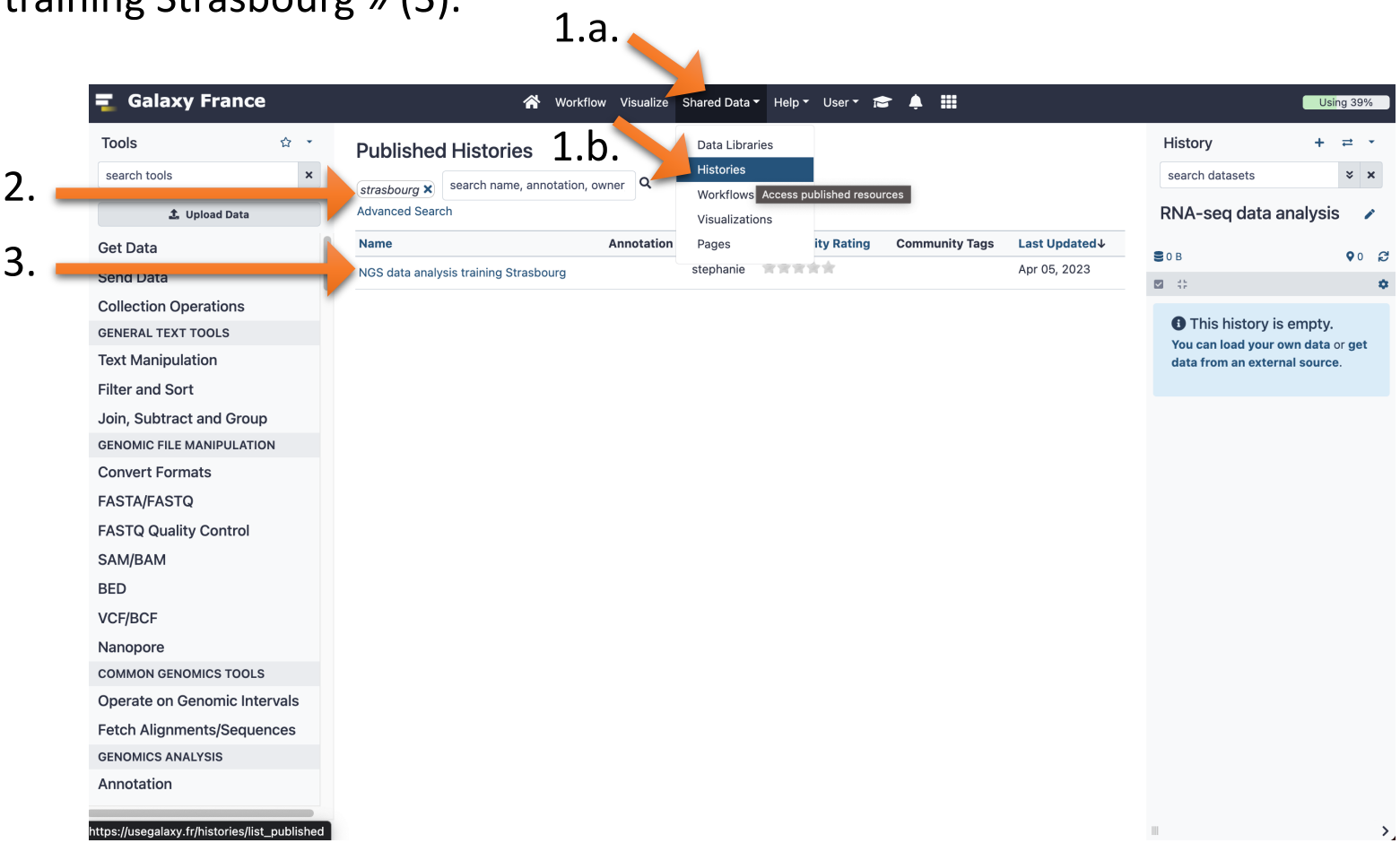
2.a.

2.b.



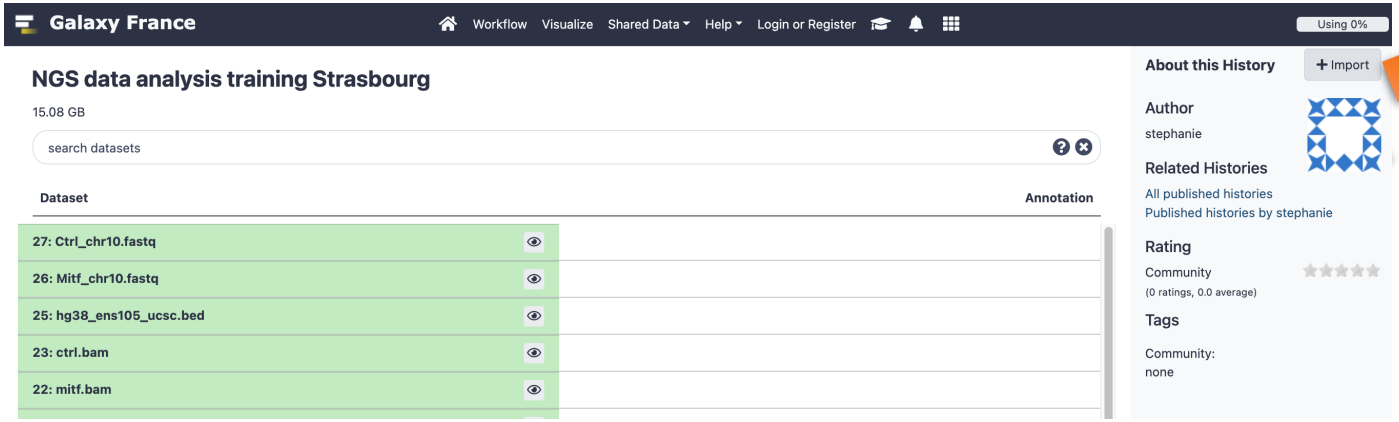
Answer 3 : Import data to Galaxy

- 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).



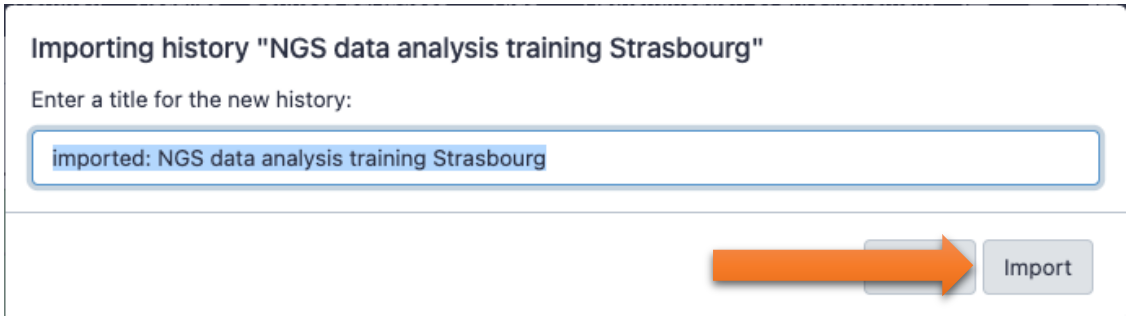
Answer 3 : Import data to Galaxy

- Click on [+ Import] (1.)

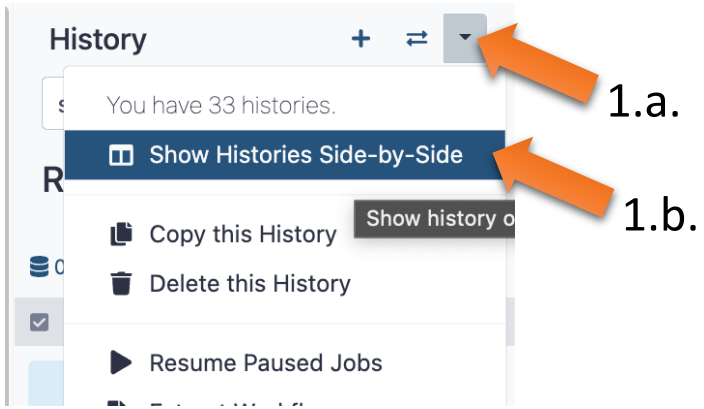


1.

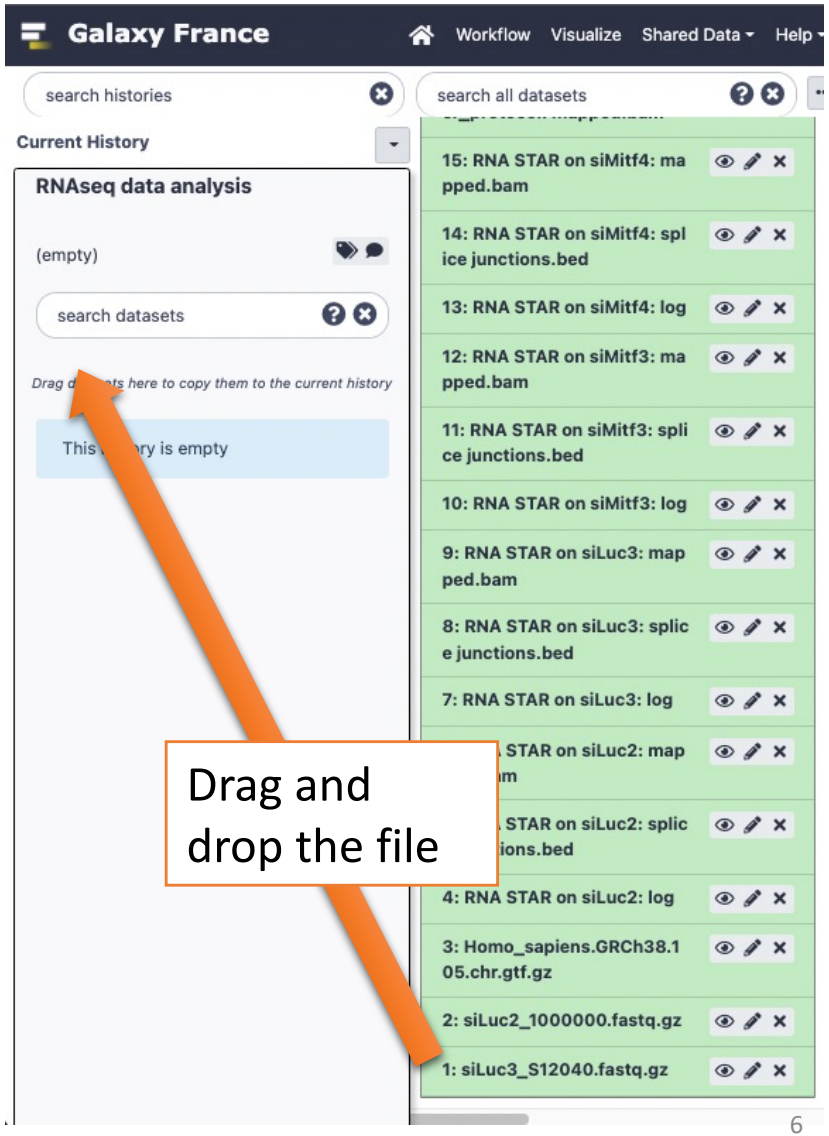
- You can leave the name as it is. Click on Import



Answer 3 : Import data to Galaxy



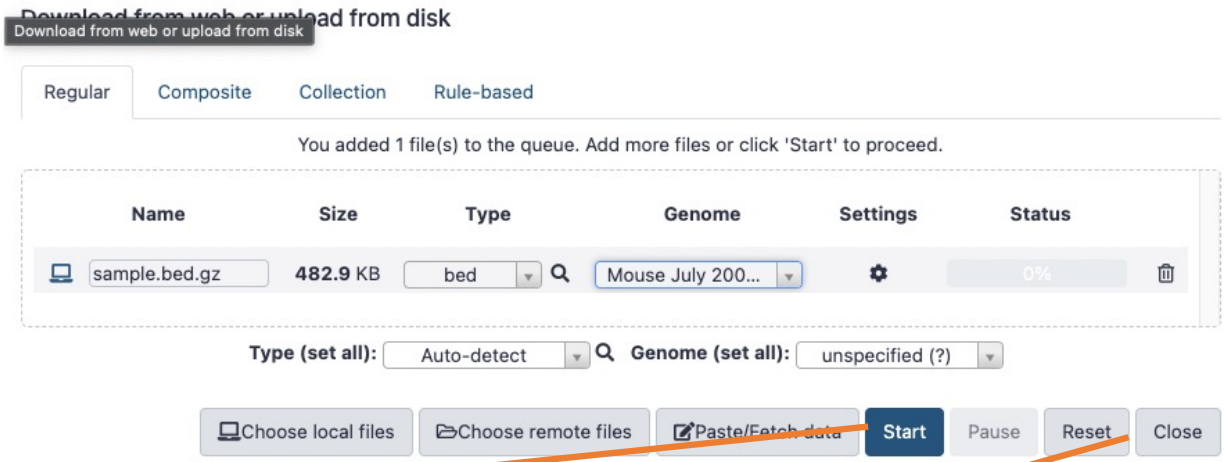
- Go to ▼ (1.a.) in the history panel and select “Show Histories Side-by-side” (1.b.)



Answer 3 : Import data to Galaxy

- 2
  - Click on the button to display the drag and drop utility

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

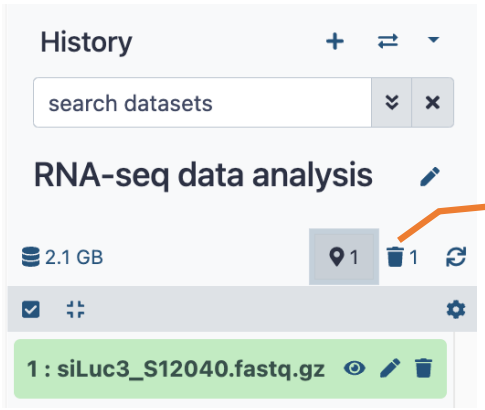


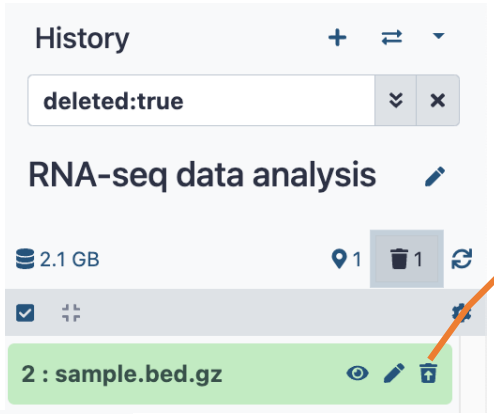
  - Click on Start
  - Click on Close to close the upload utility

Answer 4: remove dataset

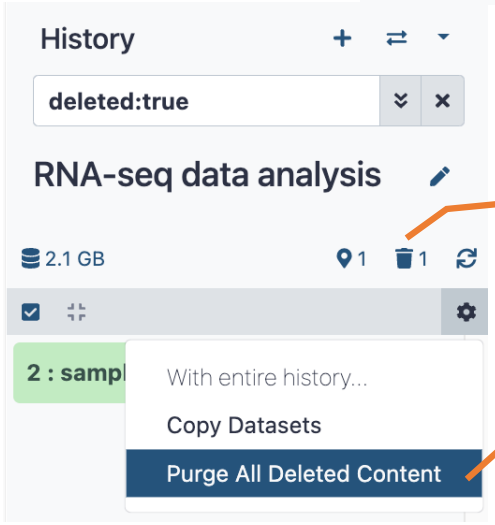
- 1. Click on the 🗑 of the dataset in the history

- 2.A.





- 2.B. Do 1. again and :

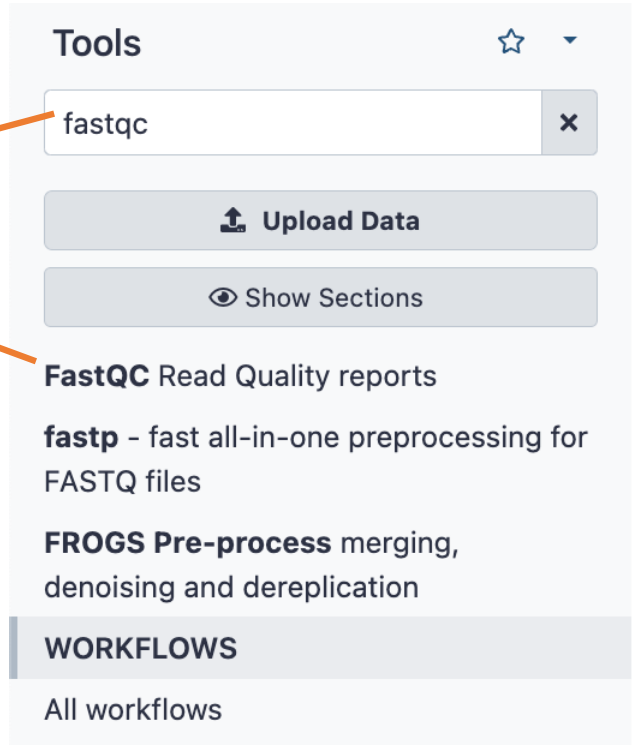


Answer 5 : Running a tool

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

Enter: “fastqc”

Click on the tool name



Answer 5 : Running a tool

2. Select the file to analyze and click on Execute