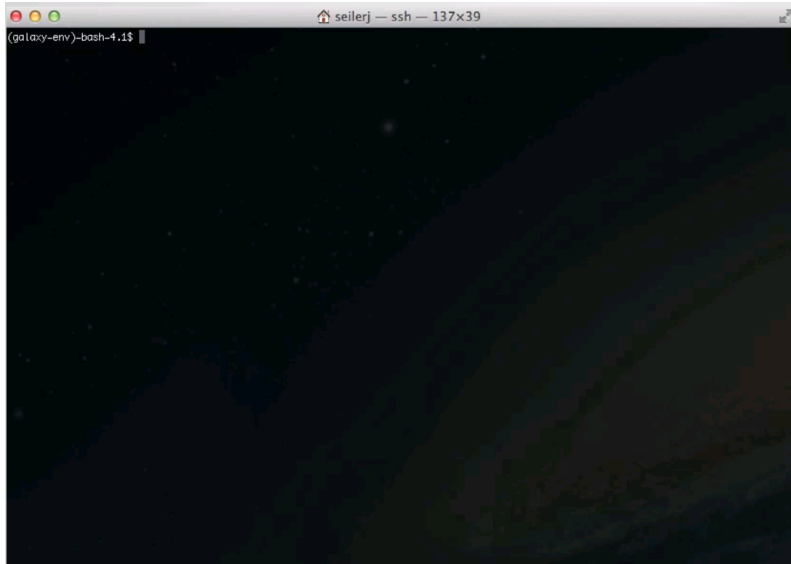


Your Bioinformatic Analyses with Galaxy

Sarah Maman – Maria Bernard
Montpellier 2016



Classical bioinformatic



```
#!/usr/bin/perl
use strict;
use warnings;
use Getopt::Long;

## Date : 22 fev 2011
## Author : Stephanie Le Gras

## Objectives :

my $num_arg = scalar @ARGV;
my $programe = "ExtractID.pl";
my $input;
my $out;
my $id;

my $result = GetOptions(
    "id=s" => \$id,
    "out=s" => \$out,
    "input=s" => \$input,
);

my $usage = <<END;

Usage: $programe --id=FILENAME --out=FILENAME --input=FILENAME

END
```

Bioinformatic with Galaxy

Galaxy Analyze Data Workflow Shared Data Visualization Help User Using 58.5 GB

Tools search tools

MANAGE YOUR DATA
FILES
[Get Data](#)
[Jobs statistics](#)

FILES MANIPULATION
[Text Manipulation](#)
[Filter and Sort](#)
[Join, Subtract and Group](#)
[GFF](#)
[BED Tools](#)
[Convert Formats](#)
[Fetch Sequences](#)
[Statistics](#)
[Graph/Display Data](#)

SEQUENCES
MANIPULATION
[FASTA manipulation](#)
[FastQC: fastq/sam/bam](#)
[Illumina fastq](#)
[Generic FASTQ manipulation](#)
[FASTX-Toolkit for FASTQ data](#)

SAM/BAM MANIPULATION
: [PICARD \(BETA\)](#)
[Conversion](#)
[QC/Metrics for sam/bam](#)
[BAM/SAM Cleaning](#)
[SAM/BAM manipulation: SAMtools](#)
[Sequences Queries](#)
[YCF Tools](#)

SGS MAPPING
[BWA - Bowtie](#)
[Indel Analysis](#)
[Variant calling](#)
[SNP annotation](#)
[RNAseq Alignment](#)

FastQC Report

jeu. 17 nov. 2016
SRR1425152-chr25_1.fastq

Summary

- Basic Statistics
- Per base sequence quality**
- Per sequence quality scores
- Per base sequence content
- Per base GC content
- Per sequence GC content
- Per base N content
- Sequence Length Distribution
- Sequence Duplication Levels
- Overrepresented sequences
- Kmer Content

Per base sequence quality

Quality scores across all bases (Sanger / Illumina 1.9 encoding)

Position in read (bp)

Per sequence quality scores

Quality score distribution over all sequences

Produced by [FastQC](#) (version 0.10.0)

History search datasets

imported:
TP_SNP_OCT2016
11 shown
8.48 GB

- 12: [FastQC_SRR1425152-chr25_1.fastq.html](#)
- 11: [Bos taurus incl consequences-chr25.vcf](#)
- 10: [dbSNP_BosTaurus.vcf](#)
- 9: [variants_BosTaurus.vcf](#)
- 7: [SRR1425152-chr25_1.fastq](#)
- 6: [SRR1425152-chr25_2.fastq](#)
- 5: [SRR1425153-chr25_1.fastq](#)
- 4: [SRR1425153-chr25_2.fastq](#)
- 3: [SRR1425154-chr25_1.fastq](#)
- 2: [SRR1425154-chr25_2.fastq](#)
- 1: [ensembl_bos_taurus_genome-chr25.fa](#)

Galaxy

Initial Galaxy Project team (<https://www.galaxyproject.org/>) :

- ▶ The Center for Comparative Genomics and Bioinformatics of the University of Penn State,
- ▶ Departments of Biology and Mathematics and Computer Science of the University of Emory.



EMORY
UNIVERSITY



Anton Nekrutenko
Penn State



Nate Coraor
Penn State



James Taylor
Emory

Galaxy

► Galaxy Philosophy

Useless to know:

Command lines

Programming in perl, python, shell ...

To launch a script

To Allow:

Automatisation of analyses,

Reproduce them,

Share them,

Publish then in a **transparency** way

Galaxy, that's:

An **intuitive** way to do bioinformatic,

Open source,

In **constant evolution** thanks to a very
**large community of (bio)informatic
scientists**



A Galaxy among others

- ▶ Galaxy is a web server with more and more instances across the world (+ 91 public servers and + 5 public tool repositories)

Public server (<https://main.g2.bx.psu.edu/>):

Free

Limited quota

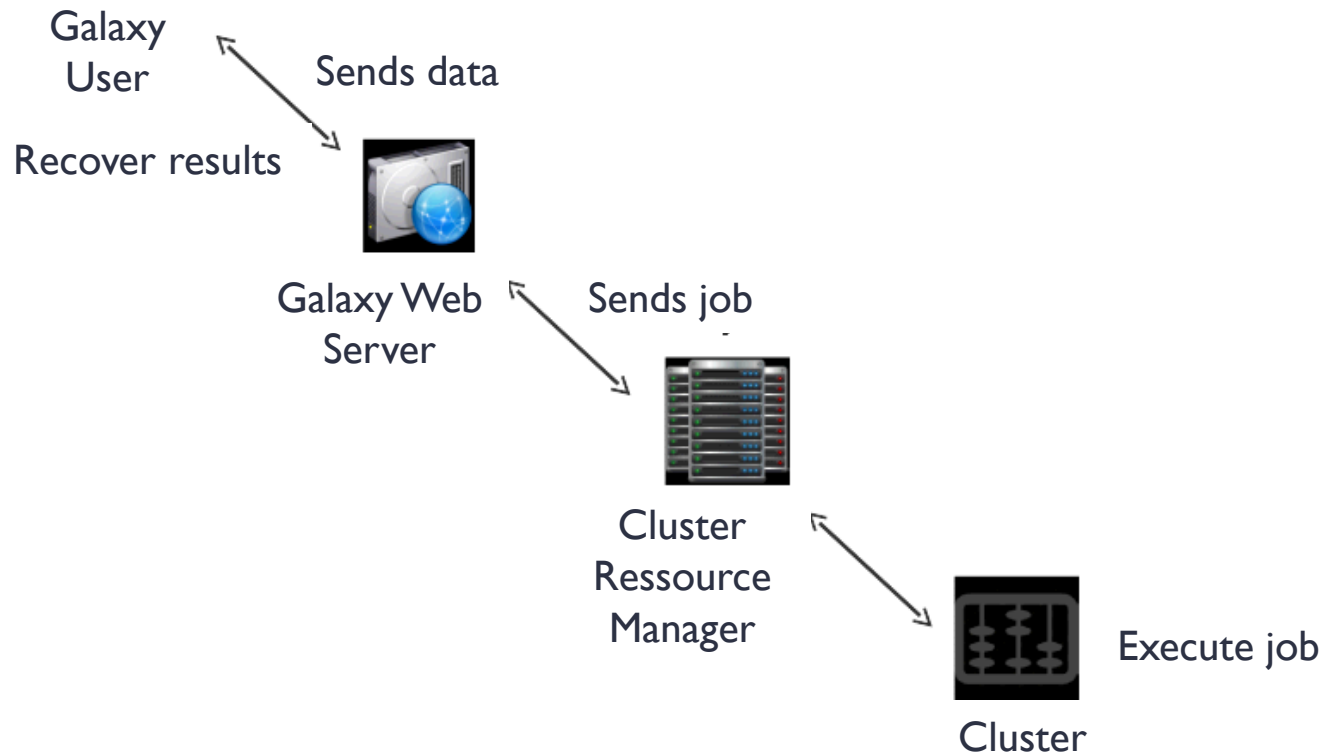
Unprotected data

→ useful to familiarise yourself on common tools on small datasets

In France : in particular <http://www.france-bioinformatique.fr/fr/groupe-de-travail/galaxy>



How Galaxy works ?



Useless to wait the end of a treatment:

Possible to **launch multiple jobs** in parallel

Go away, ..**close the Internet !**

See the results later



<http://sigenae-workbench.toulouse.inra.fr>

Galaxy

Administration Menu

Galaxy Analyze Data Workflow Shared Data Visualization Help User Using 98.8 GB

Tools search tools

Tool Menu

MANAGE YOUR FILES
Get Data
Jobs statistics

FILES MANIPULATION
Text Manipulation
Filter and Sort
Join, Subtract and Group
GFF
BED Tools
Convert Formats
Fetch Sequences
Statistics
Graph/Display Data

SEQUENCES MANIPULATION
FASTA manipulation
FastQC: fastq/sam/bam
Illumina fastq
Generic FASTQ manipulation
FASTX-Toolkit for FASTQ data

SAM/BAM MANIPULATION : PICARD (BETA)
Conversion
QC/Metrics for sam/bam
BAM/SAM Cleaning
SAM/BAM manipulation: SAMtools

WELCOME TO GALAXY WORKBENCH

galaxy logo | genotoul bioinfo | EUROPEAN UNION | REGION OCCITANIE

Galaxy is a workbench available for biologists from Sigenae Platform. Galaxy objectives are:

- Make bioinfo Linux tools accessible to biologists
- Hide the complexity of the infrastructure
- Allow creation, execution and sharing of workflows.

ACCESS TO OLD GALAXY VERSION (2015) : [ICI](#)

Warnings :

- All jobs running on galaxy are sent to BioInfo Genotoul cluster.
- Your data are stored in work/ directory. Consequently, BioInfo Genotoul platform reserves the right to purge all files not accessed since 120 days on work/ disk space.
- Contact your support : sigenae-support@listes.inra.fr

Results Visualization and Tool Parameter Space

History search datasets

Unnamed history
0 b

Current History

History Message: This history is empty. You can load your own data or get data from an external source

History

Galaxy Analyze Data Workflow Shared Data Visualization Help User Using 98.8 GB

Tools search tools

MANAGE YOUR DATA FILES
[Get Data](#)
[Jobs statistics](#)

FILES MANIPULATION
[Text Manipulation](#)
[Filter and Sort](#)
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SEQUENCES MANIPULATION
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SAM/BAM MANIPULATION : PICARD (BETA)
[Conversion](#)
[QC/Metrics for sam/bam](#)
[BAM/SAM Cleaning](#)
[SAM/BAM manipulation: SAMtools](#)

WELCOME TO GALAXY WORKBENCH

Make bioinfo Linux tools accessible to biogists.
Hide the complexity of the infrastructure.
Allow creation, execution and sharing of workflows.

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Warnings :

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- Contact your support : sigenae-support@listes.inra.fr

History search datasets

Unnamed history

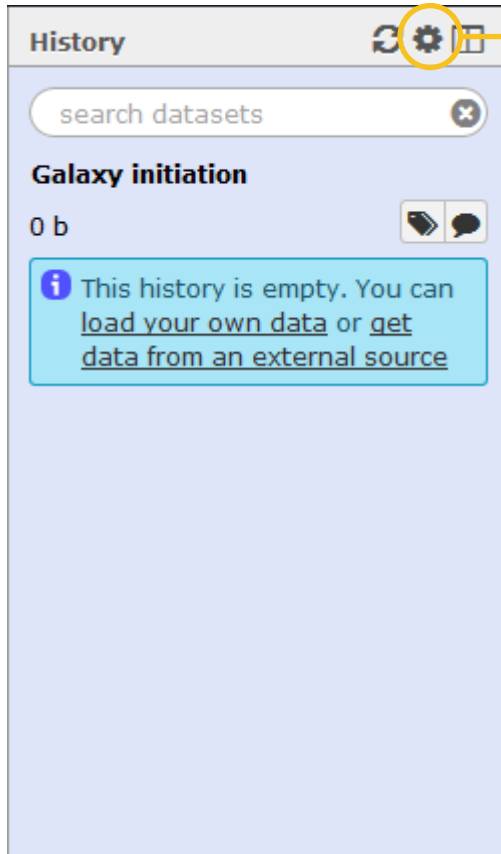
0 b

This history is empty. You can [load your own data](#) or [get data from an external source](#)

Rename your history:
«Galaxy initiation »

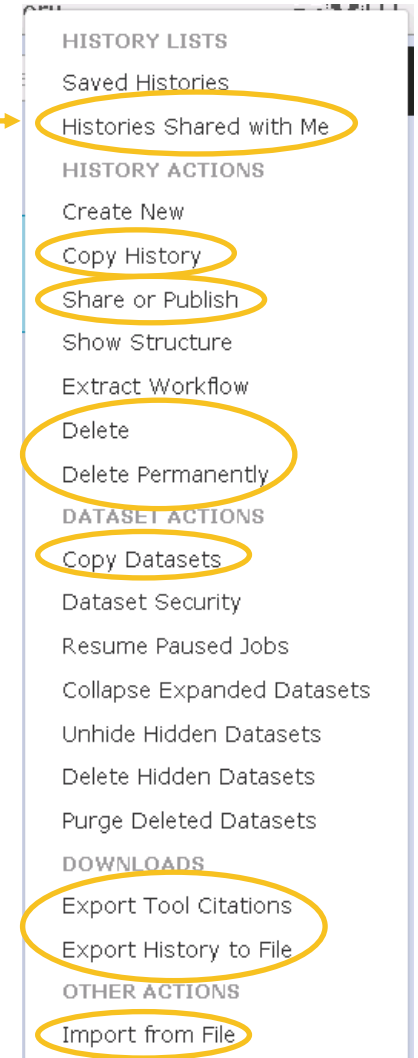
History

▶ Explore the history Menu



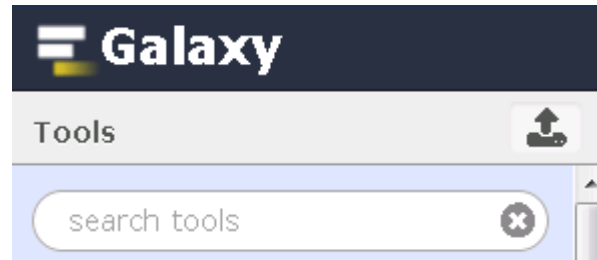
▶ You may:

- ▶ **Publish** your History
→ Share or Publish
- ▶ **Access** to shared histories
→ Histories Shared With Me
- ▶ **Copy** ou **Export/Import**, or **delete**



Tools and Datasets

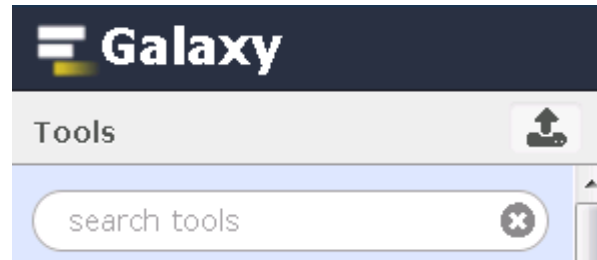
- ▶ How to find a tool in Galaxy ?



How much tools do you find for « FROGS » ?

Tools and Datasets

- ▶ How to find a tool in Galaxy ?



How much tools are linked with the fastq format ?

Tools and Datasets

- ▶ How to find a tool in Galaxy ?



Which section may you use for uploading data ?

Tools and Datasets

- ▶ How to upload Data in Galaxy ? ⇒ section **Get Data**
- ▶ For files **smaller than 2Go** use the tool: **Upload File from your computer**

Download from web or upload from disk

Regular Composite

File on your computer

Drop files here

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

Tools and Datasets

- ▶ How to upload Data in Galaxy ? ⇒ section **Get Data**
- ▶ For files **smaller than 2Go** use the tool: **Upload File from your computer**

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
New File	-	Auto-det...	unspecified (?)		0%

You can tell Galaxy to download data from web by entering URL in this box (one per line). You can also directly paste the contents of a file.

A file on the Internet, or by writing yourself some text

Type (set all): Auto-detect Genome (set all): unspecified (?)

Choose local file Paste/Fetch data Pause Reset Start Close

Tools and Datasets




- ▶ How to upload Data in Galaxy ? ⇒ section **Get Data**
- ▶ **Go to :** http://genoweb.toulouse.inra.fr/~formation/15_FROGS/FROGS_ini/DATA/
- ▶ **Upload file 454.fastq by « copying link adress »**

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
 New File	76 b	fastq	unspecified (?)		0% 


You can tell Galaxy to download data from web by entering URL in this box (one per line). You can also directly paste the contents of a file.


```
http://genoweb.toulouse.inra.fr/~formation/15_FROGS/FROGS_ini/DATA/454.fastq
```

Do not forget to precise the type of data.
You may copying multiple links of same data type, one link by line.

Type (set all): Auto-detect

Genome (set all): unspecified (?)

 Choose local file

 Paste/Fetch data

Pause

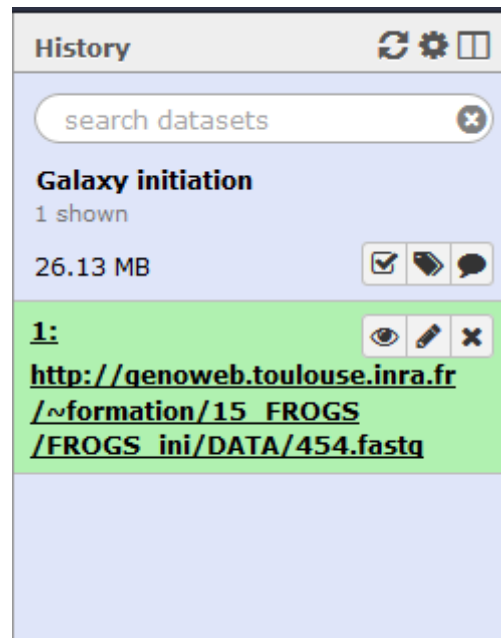
Reset

Start

Close

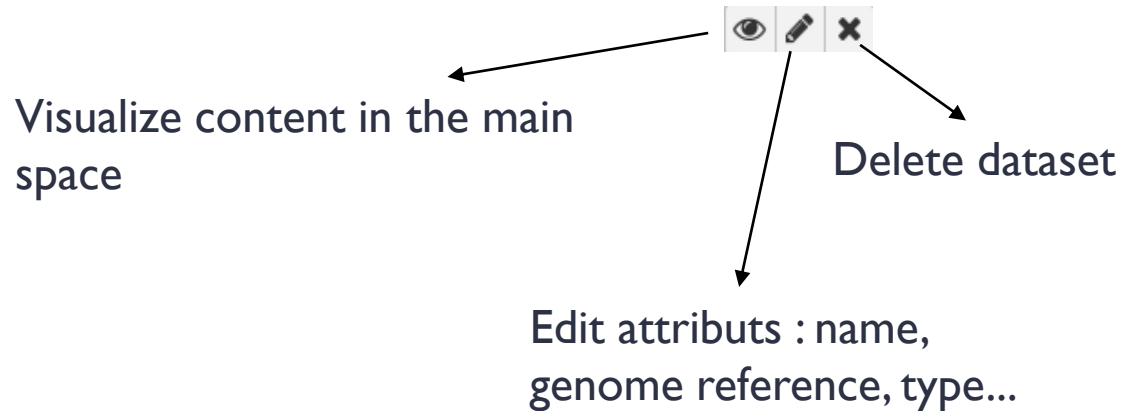
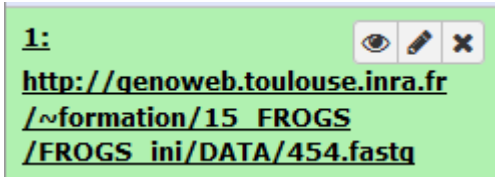
Tools and Datasets

- ▶ How to upload Data in Galaxy ? ⇒ section **Get Data**
- ▶ Go to : http://genoweb.toulouse.inra.fr/~formation/15_FROGS/FROGS_ini/DATA/
- ▶ Upload file 454.fastq by « copying link adress »



Tools and Datasets

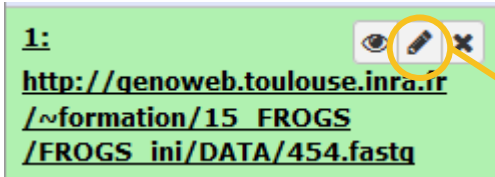
- ▶ To what corresponds each icon : « eye », « pen », « cross », « diskette »



Download the dataset

Tools and Datasets

► Rename your dataset.



Attributes Convert Format Datatype Permissions

Edit Attributes

Name:
454.fastq

Info:
uploaded fastq file

Annotation / Notes:

Add an annotation or notes to a dataset; annotations are available when a history is viewed.

Database/Build:
unspecified (?)

Save

Auto-detect

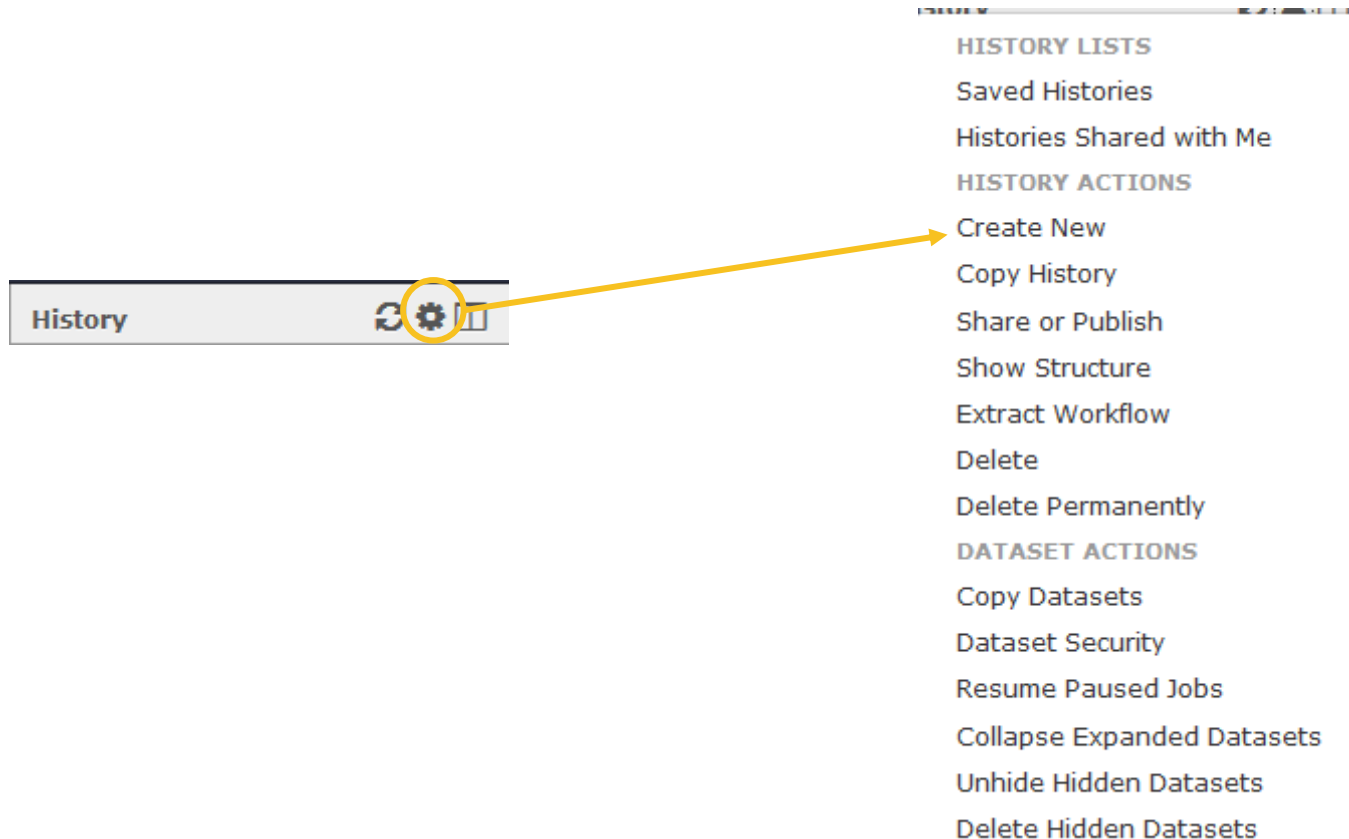
This will inspect the dataset and attempt to correct the above column values if they are not accurate.

This screenshot shows the 'Edit Attributes' panel for a dataset. The 'Name' field is highlighted with a yellow circle and contains the text '454.fastq'. Below the 'Name' field is the 'Info' field, which contains the text 'uploaded fastq file'. Below the 'Info' field is the 'Annotation / Notes' field, which is empty. Below the 'Annotation / Notes' field is a dropdown menu for 'Database/Build' with the value 'unspecified (?)'. Below the dropdown menu is a 'Save' button, which is highlighted with a yellow circle. Below the 'Save' button is an 'Auto-detect' button. Below the 'Auto-detect' button is a note: 'This will inspect the dataset and attempt to correct the above column values if they are not accurate.'



Tools and Datasets

- ▶ How to upload Data in Galaxy ? ⇒ section **Get Data**
- ▶ For files **bigger than 2Go** use the tool: **Upload File from Genotoul**
- ▶ **Create a new history, named « Hantagulumic training »**



Tools and Datasets

- ▶ How to upload Data in Galaxy ? ⇒ section **Get Data**
- ▶ For Files bigger than 2Go use the tool: **Upload File from Genotoul**
- ▶ Create a new history, name « Hantagulumic training »
- ▶ **Upload the tar.gz archive available on Genotoul thanks to « Upload File from Genotoul »:**

/work/project/frogs/Formation/100spec_90000seq_9samples_Hantagulumic.tar.gz

Upload File from Genotoul (Galaxy Version 1.0.0) Options

Path to file

/work/project/frogs/Formation/100spec_90000seq_9samples_Hantagulumic.tar.gz

Path must be like : /work/USERNAME/somewhere/afile

File type

tar.gz

Execute

Do not forget to precise, the data type

Tools and Datasets

- ▶ How to upload Data in Galaxy ? ⇒ section **Get Data**
- ▶ For Files bigger than 2Go use the tool: **Upload File from Genotoul**
- ▶ Create a new history, name « Hantagulumic training »
- ▶ Upload the tar.gz archive available on Genotoul:
`/work/project/frogs/Formation/100spec_90000seq_9samples_Hantagulumic.tar.gz`
- ▶ **May you visualize the content of this dataset?**
- ▶ **How to change data type, if you forget to change it during upload?**

1: /work/project
/frogs/Formation
/100spec_90000seq_9samples
Hantagulumic.tar.gz

Attributes Convert Format **Datatype** Permissions

Change data type

New Type:

ab1

tar|

tar

ing dataset but *not* modify its contents. Use this if Galaxy has incorrectly guessed the

Tools and Datasets

- ▶ How to upload Data in Galaxy ? ⇒ section **Get Data**
- ▶ For Files bigger than 2Go use the tool: **Upload File from Genotoul**
- ▶ Create a new history, name « Hantagulumic training »
- ▶ Upload the tar.gz archive available on Genotoul:

`/work/project/frogs/Formation/100spec_90000seq_9samples_Hantagulumic.tar.gz`

- ▶ **May you visualize the content of this dataset?**
- ▶ **How to change data type, if you forget to change it during upload?**

Datatype are important. Each tool will take as input a precise type of data.

- ▶ **Do not forget to rename dataset**

History, Tools and Dataset

UPLOAD YOUR DATA

[Get Data](#)

[Upload File](#)

Left menu lists the **TOOLS**.

A **TOOL**

generates

A/some **DATASET(S)**

1: **GM.fastqsanger**
17.4 Mb
format: fastqsanger, database:
2

```
@HWUSI-EAS627_1:8:1:17:202
TGGTTGGAGACCCCGAGATGGTCTTTCAGCTCC
+
BB@=A<9@?AB??=?B?B?B33>?A@?><1:9=A
@HWUSI-EAS627_1:8:1:66:1050
CAGAAGTAGAGCAGAAGAAGAAGCGGACCTCCG
```

Each green bloc, a **DATASET**, represents an input or output data file of a tool

Which together forms

A **HISTORY**

History Options ▾

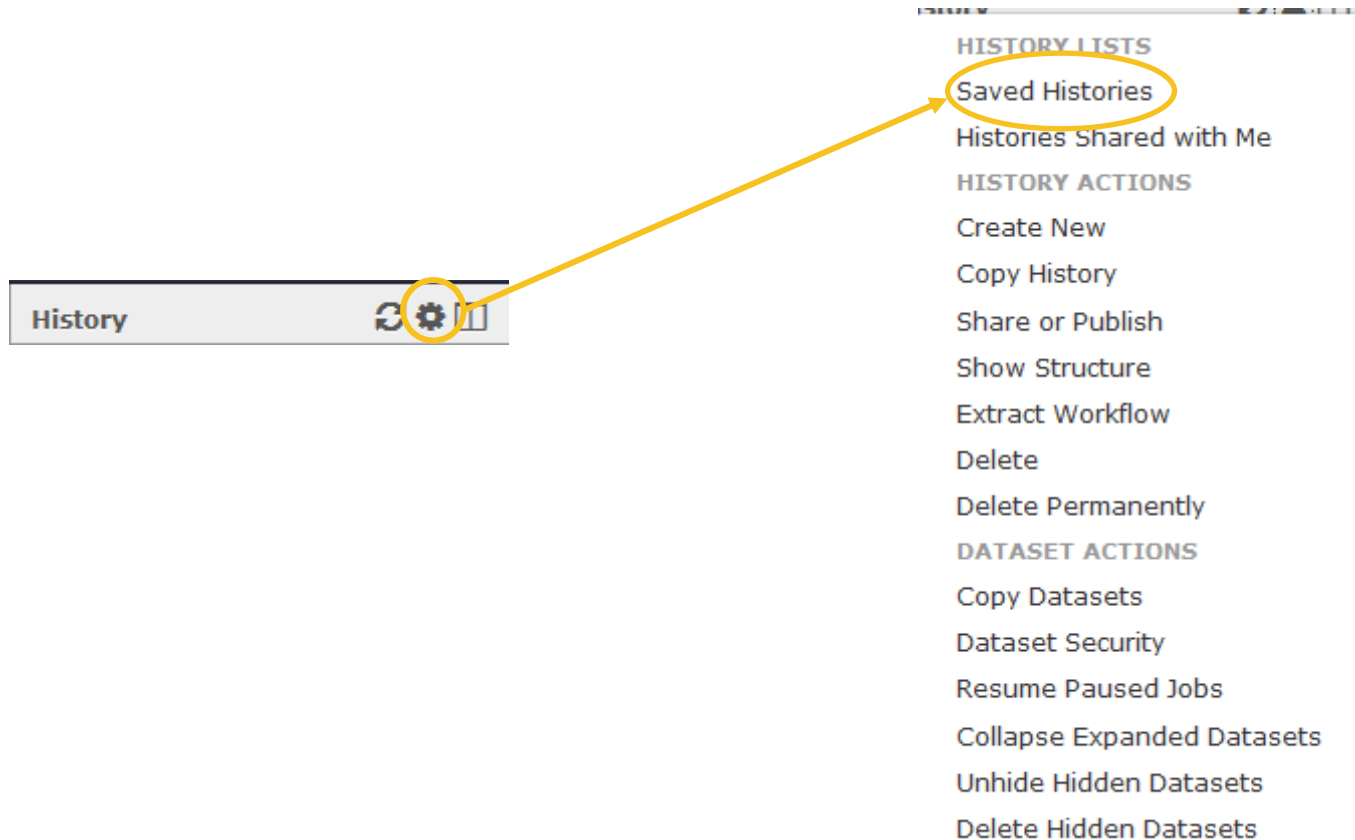
TP FastQC 54.0 Mb

- 8: **FastQC_data 5.html**
- 6: **GM.fastqsanger**
- 5: **h1.fastqsanger**
- 4: **FastQC_data 18.html**

All together forms a **HISTORY**, that finally represents a complete analysis

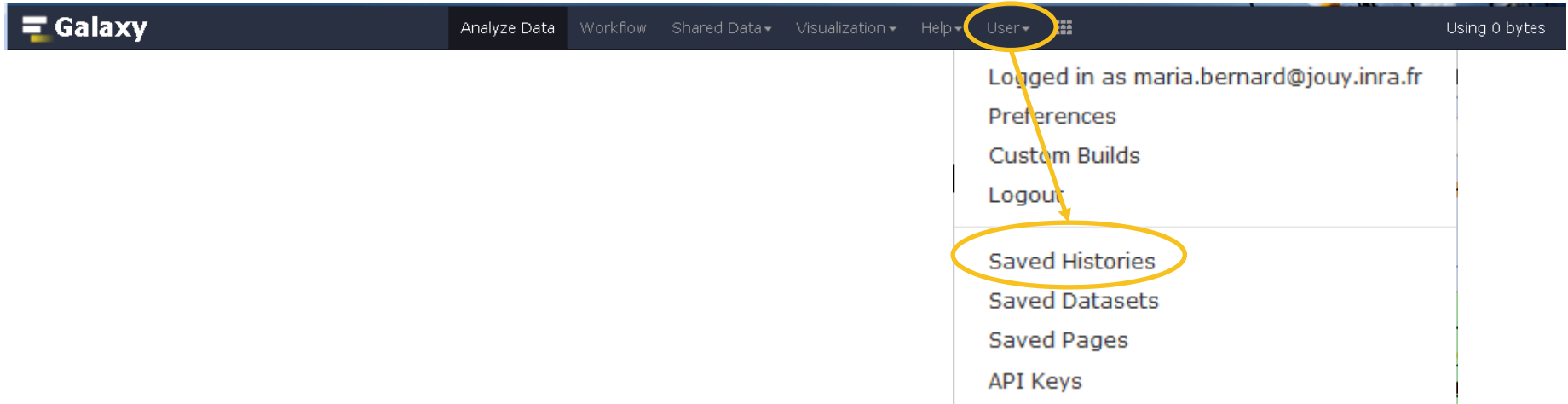
Back to History

- ▶ How to list all histories ?



Back to History

- ▶ How to list all histories ?



Back to History

- ▶ How to list all histories ?

Saved Histories

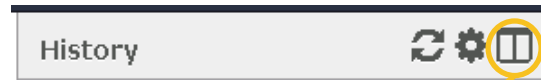


[Advanced Search](#)

<input type="checkbox"/>	<u>Name</u>	<u>Datasets</u>	<u>Tags</u>	<u>Sharing</u>	<u>Size on Disk</u>	<u>Created</u>	<u>Last Updated</u> ↑	<u>Status</u>
<input type="checkbox"/>	Hantagulumic training ▾	1	0 Tags		4.3 MB	~27 minutes ago	~20 minutes ago	current history
<input type="checkbox"/>	Galaxy initiation ▾	1	0 Tags		26.1 MB	~9 hours ago	~1 hour ago	
<input type="checkbox"/>	imported: CLIMAPIG_Rectum_5 mois ▾	33	2	0 Tags	971.8 MB	~2 hours ago	~2 hours ago	
<input type="checkbox"/>	imported: marine ▾	24	4	0 Tags	2.3 GB	~4 days ago	~4 days ago	
<input type="checkbox"/>	Unnamed history ▾		0 Tags		0 bytes	~5 days ago	~5 days ago	

Back to History

- ▶ How to list all histories ?



A screenshot of the Galaxy web interface. The top navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', 'User', and 'Using 99.8'. Below the navigation bar are search bars for 'search histories' and 'search all datasets'. The main area is divided into three history panels, each with a 'Switch to' dropdown. The left panel is titled 'Hantagulumic training' (1 shown, 4.31 MB) and contains a dataset named '1: 100spec_90000seq_9samples_Hantaqu... mic.tar.gz'. The middle panel is titled 'Galaxy initiation' (1 shown, 26.13 MB) and contains a dataset named '1: 454.fastq'. The right panel is titled 'imported: CLIMAPIG_Rectum_5 mois' (35 shown, 971.82 MB) and contains several datasets, including '80: FROGS TSV to BIOM: abundance.biom', '79: FROGS TSV to BIOM: abundance.biom', '78: Galaxy55- (FROGS BIOM to TSV multi hits.tsv) .tabular apres gestion multiaffiliations test1 apres notepad fichierOK.txt', and '70: Galaxy54-'. Each dataset entry has icons for visibility, edit, and delete.

Back to History

- ▶ How to list all histories ?
- ▶ Meaning of color code:

Saved Histories

search history names and tags

[Advanced Search](#)

<input type="checkbox"/> Name	Datasets	Tags	Sharing	Status
<input type="checkbox"/> Contiged	20 2 5 5	0 Tags		37.9 MB ~ 2 hours ago 2 minutes ago current history
<input type="checkbox"/> MiSeq contiged	11 9 12	0 Tags Shared		175.9 MB ~ 7 hours ago ~ 3 hours ago
<input type="checkbox"/> barcode_formation	5	0 Tags		4.5

Analyse OK




Analyse in waiting

Analyse in progress




Analyse not OK

How to debug?

- ▶ What to do when something goes wrong ?

✖ 4: Extract Genomic DNA on data 2   

error
An error occurred with this dataset:
No sequences are available for '?', request them by reporting this error.

no peek

Tool: Extract Genomic DNA

Name:	Extract Genomic DNA on data 2
Created:	Thu Sep 17 15:20:08 2015 (UTC)
Filesize:	0 bytes
Dbkey:	?
Format:	fasta
Galaxy Tool ID:	Extract genomic DNA 1
Galaxy Tool Version:	2.2.3
Tool Version:	
Tool Standard Output:	stdout
Tool Standard Error:	stderr
Tool Exit Code:	0
API ID:	f09437b8822035f7
History ID:	5a1cff6882ddb5b2
UUID:	4bb33045-5f78-41f7-96e5-854c09711c06

Input Parameter	Value	Note for rerun
Fetch sequences for intervals in	2: mes_positions.txt	
Interpret features when possible	Yes	
Source for Genomic Data	cached	
Output data type	FASTA	

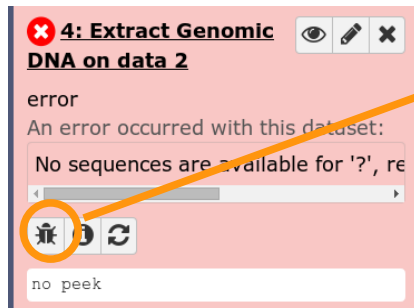
Inheritance Chain

Extract Genomic DNA on data 2

No sequences are available for '?', request them by reporting this error.

How to debug?

- ▶ What to do when something goes wrong ?



Dataset generation errors

Dataset 4: Extract Genomic DNA on data 1

Tool execution generated the following error message:

No sequences are available for '?', request them by reporting this error.

Report this error to the local Galaxy administrators

Usually the local Galaxy administrators regularly review errors that occur on the server. However, if you would like to provide additional information (such as what you were trying to do when the error occurred) and a contact e-mail address, we will be better able to investigate your problem and get back to you.

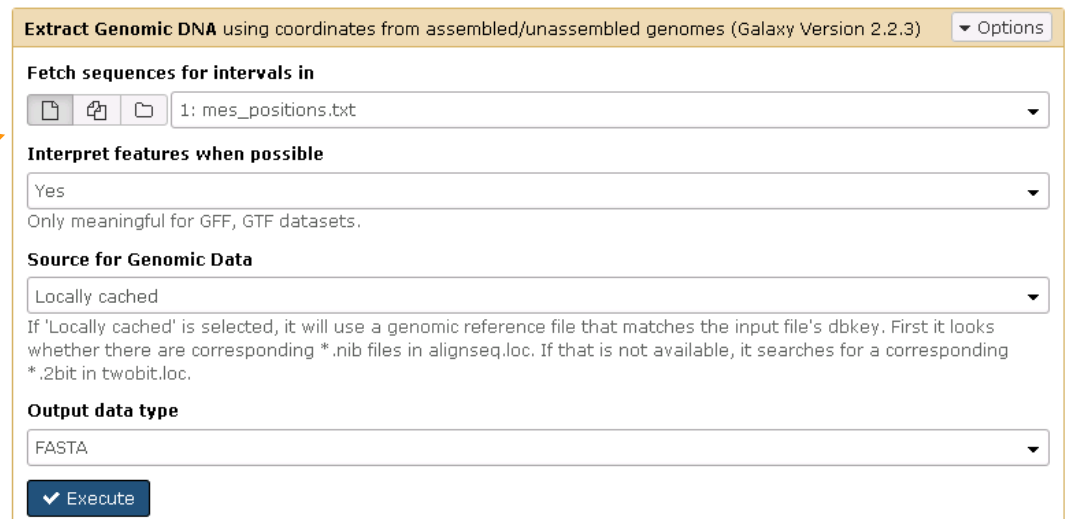
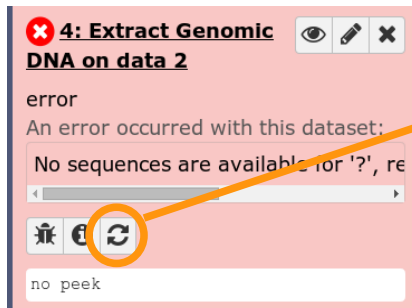
Error Report

Your email

Message

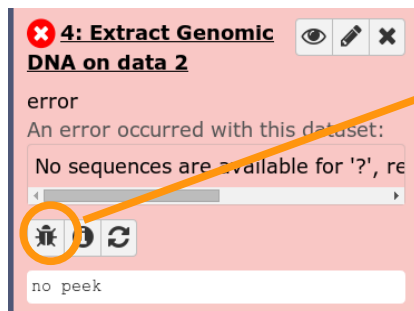
How to debug?

- ▶ What to do when something goes wrong ?
- ▶ Use « double arrow » to reload the tool with the previous parameters. Correct them and Execute



How to debug?

- ▶ What to do when something goes wrong ?
- ▶ Use « double arrow » to reload the tool with the previous parameters. Correct them and Execute
- ▶ What to do when the job still crash ?



Dataset generation errors

Dataset 4: Extract Genomic DNA on data 1

Tool execution generated the following error message:

No sequences are available for '?', request them by reporting this error.

Report this error to the local Galaxy administrators

Usually the local Galaxy administrators regularly review errors that occur on the server. However, if you would like to provide additional information (such as what you were trying to do when the error occurred) and a contact e-mail address, we will be better able to investigate your problem and get back to you.

Error Report

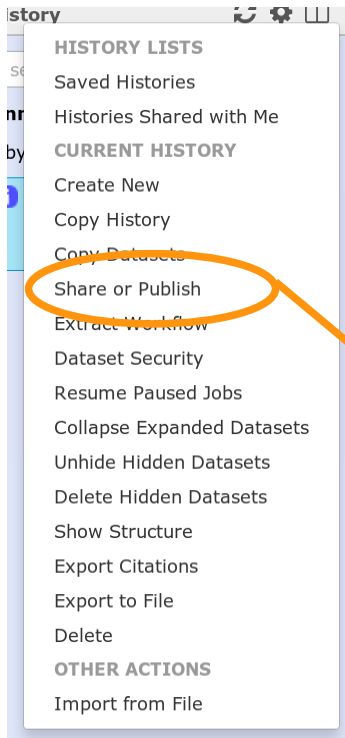
Your email

Send a message to the support.
He will probably ask you to share
your history!

Message

How to debug?

- ▶ What to do when something goes wrong ?
- ▶ Use « double arrow » to reload the tool with the previous parameters. Correct them and Execute
- ▶ What to do when the job still crashed ?
- ▶ How to share your history ?



Share or Publish History 'How To Galaxy'

Make History Accessible via Link and Publish It

This history is currently restricted so that only you and the users listed below can access it. You can:

Generates a web link that you can share with other people so that they can view and import the history.

Makes the history accessible via link (see above) and publishes the history to Galaxy's [Published Histories](#) section, where it is publicly listed and searchable.

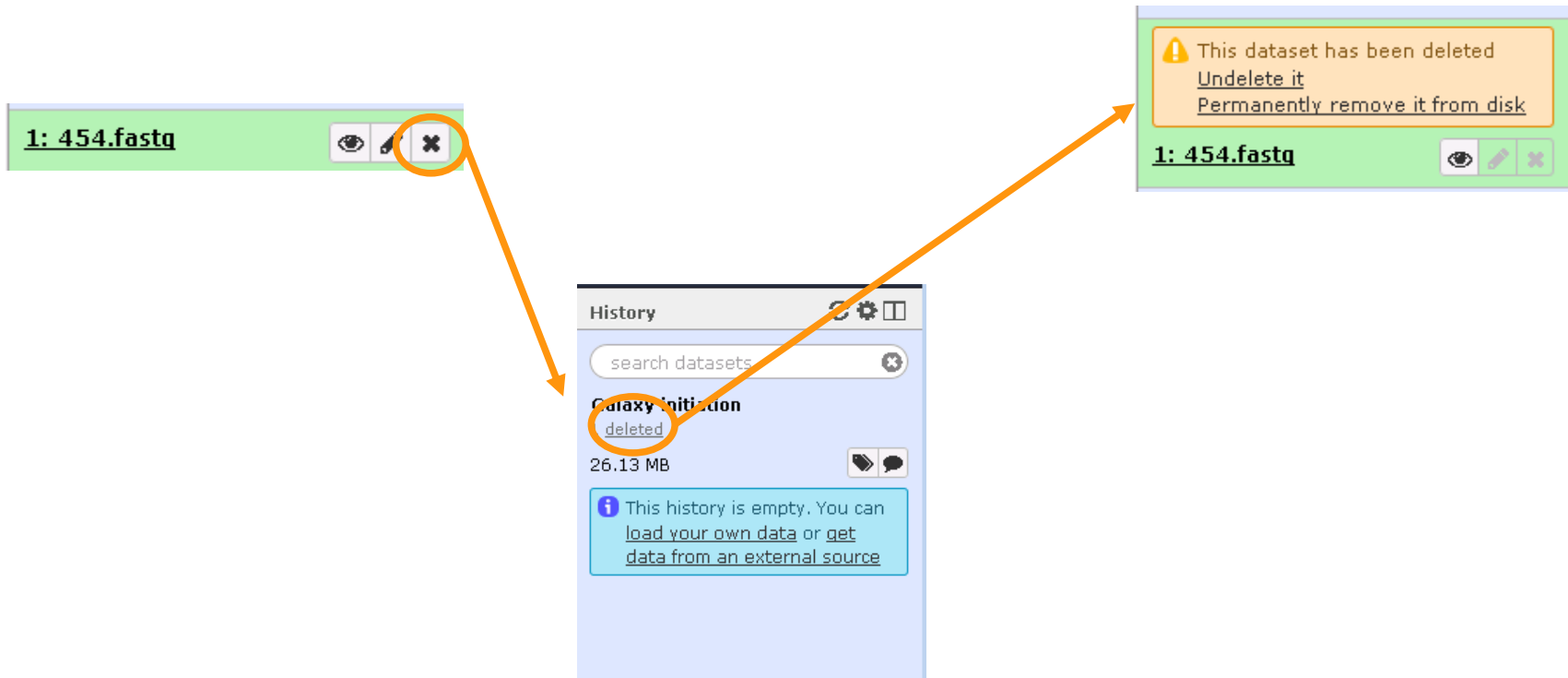
Share History with Individual Users

You have not shared this history with any users.

[Back to Histories List](#)

How to clean?

- ▶ Very often, there is a space disk quota on your Galaxy account. So you need to clean your histories.
- ▶ How to delete dataset ?
 - ▶ Go back to your « Galaxy initiation » history.
 - ▶ Delete your dataset.



How to clean?

- ▶ Very often, there is a space disk quota on your Galaxy account. So you need to clean your histories.
- ▶ How to delete history ?
 - ▶ **Delete your history.**

How to undelete history ?

Saved Histories

Close [Advanced Search](#)

name: Q

tags: Q

sharing: [accessible](#) | [shared](#) | **all** | [private](#) | [published](#)

status: [active](#) | **deleted** | [all](#)

<input type="checkbox"/>	Name	Datasets	Tags	Sharing	Size on Disk	Created	Last Updated	Status
<input type="checkbox"/>	Galaxy initiation	1	0 Tags		26.1 MB	~1 day ago	~11 seconds ago	current history

View

Delete Permanently

Undelete

Use « delete permanently » to save space

HISTORY LISTS

- Saved Histories
- Histories Shared with Me

HISTORY ACTIONS

- Create New
- Copy History
- Share or Publish
- Show Structure
- Extract Workflow
- Delete
- Delete Permanently

DATASET ACTIONS

- Copy Datasets
- Dataset Security
- Resume Paused Jobs
- Collapse Expanded Datasets
- Unhide Hidden Datasets
- Delete Hidden Datasets
- Purge Deleted Datasets

DOWNLOADS

- Export Tool Citations
- Export History to File

OTHER ACTIONS

- Import from File

Workflow

- ▶ A workflow chains automatically all steps you want.
- ▶ How to create a workflow ?
- ▶ I) Based on a **history** created manually

HISTORY LISTS

Saved Histories

Histories Shared with Me

HISTORY ACTIONS

Create New

Copy History

Share or Publish

Show Structure

Extract Workflow

Delete

Delete Permanently

DATASET ACTIONS

Copy Datasets

Dataset Security

Resume Paused Jobs

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Unhide Hidden Datasets

Delete Hidden Datasets

Purge Deleted Datasets

DOWNLOADS

Workflow

- ▶ A workflow chains automatically all steps you want.
- ▶ How to create a workflow ?
- ▶ 2) Thanks to the **Workflow tab**:

The screenshot displays the Galaxy/ABiMS interface. At the top, a navigation bar includes 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User'. Below this, the 'Your workflows' section shows a table with columns for 'Name' and '# of Steps'. A 'Create new workflow' button is highlighted with an orange arrow. A context menu is open over the 'mon_workflow' entry, listing actions like 'Edit', 'Run', 'Share or Publish', 'Download or Export', 'Copy', 'Rename', 'View', and 'Delete'. The main area is the 'Workflow Canvas' for 'mon_workflow', showing a sequence of steps: 'Filter FASTQ', 'Map with BWA for Illumina', 'FastQC:Read QC', 'SAM-to-BAM', and 'SAM/BAM Alignment Summary Metrics'. A 'Details' panel on the right shows the configuration for the 'SAM-to-BAM' step, including tool version, reference list, and input/output options. The bottom left corner features the text 'Montpellier 2016 – Galaxy Initiative'.

Citations

- ▶ Cite used tools and their version (see the « info » icône and stdout output)
- ▶ Cite Galaxy publication:

Enis Afgan, Dannon Baker, Marius van den Beek, Daniel Blankenberg, Dave Bouvier, Martin Čech, John Chilton, Dave Clements, Nate Coraor, Carl Eberhard, Björn Grüning, Aysam Guerler, Jennifer Hillman-Jackson, Greg Von Kuster, Eric Rasche, Nicola Soranzo, Nitesh Turaga, James Taylor, Anton Nekrutenko, and Jeremy Goecks. The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2016 update. *Nucleic Acids Research* (2016) doi: 10.1093/nar/gkw343

- ▶ Cite which instance you used.