Introduction to Galaxy

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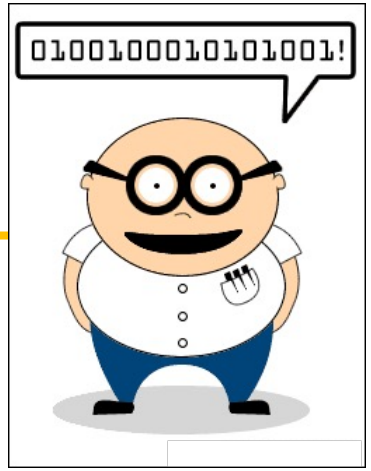
Guidelines

- Analyzing biological data with informatics tools
- Presentation of the Galaxy project
- Description of the main features of the Galaxy platform

Analyzing biological data with informatics tools

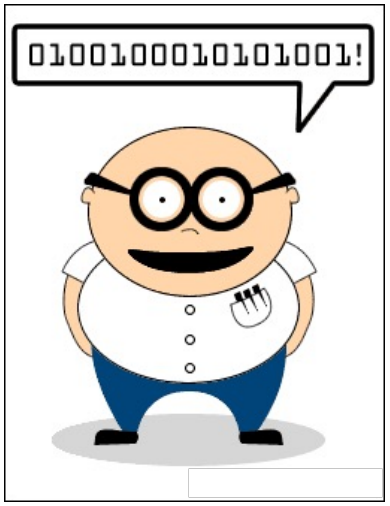
Bioinformatics analyses

Informatics data



nature

Bioinformatics analyses



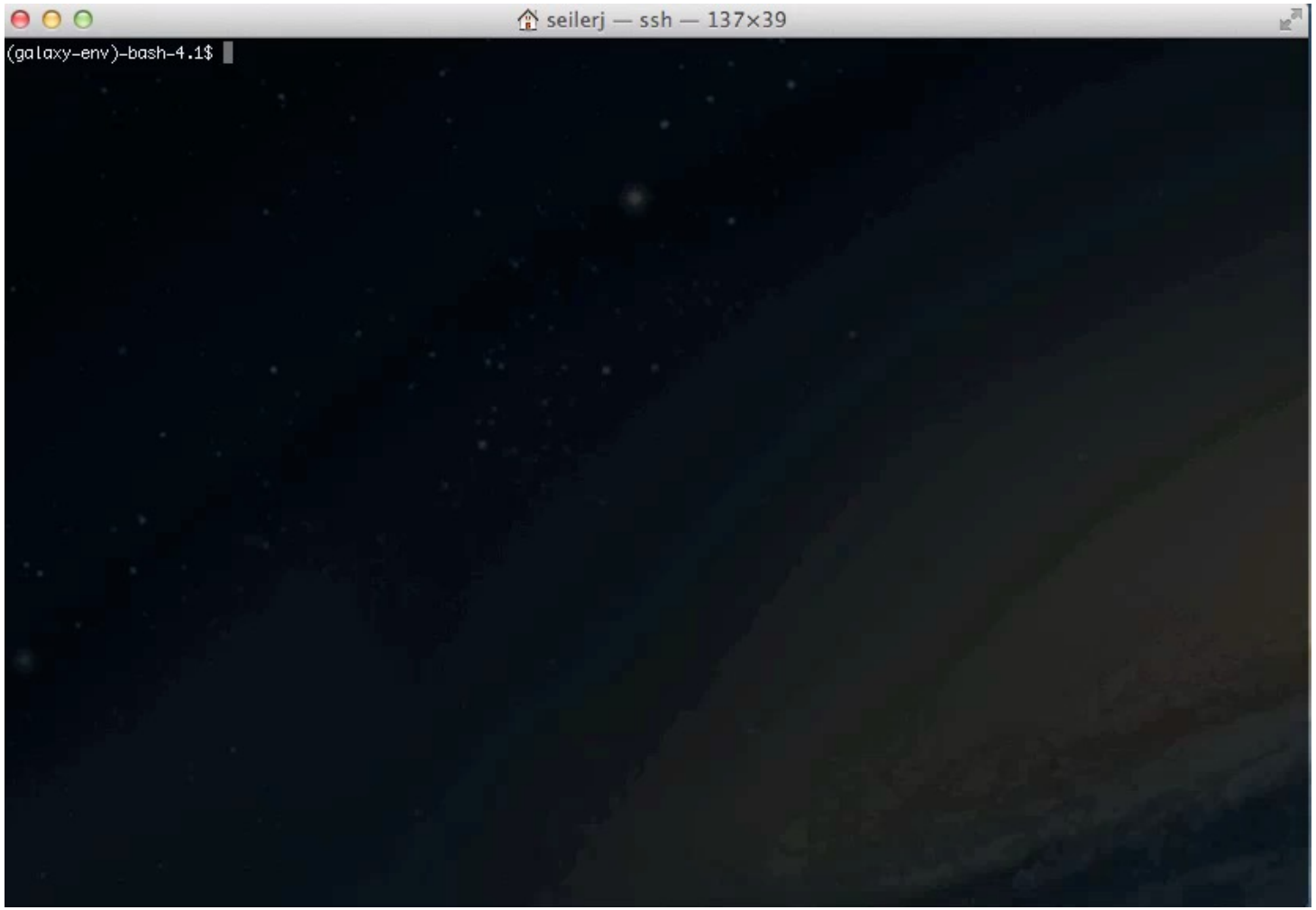
Scripts, softwares

```perl
#! /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 $progname = "ExtractID.pl";
my $input;
my $out;
my $id;

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

my $usage = <<END;

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

END

die $usage unless ($result);
my @files = @ARGV;
die "Enter at least two files\n$usage" if ( $num_arg < 2 );
die $usage if ( $num_arg == 0 );

my %ids;
$out = ( defined $out ) ? $out : "results.txt";

## first, every lines of each files are put in the hash table ids. Variant ids are used as keys of the
## hash table and it contains a table.
```

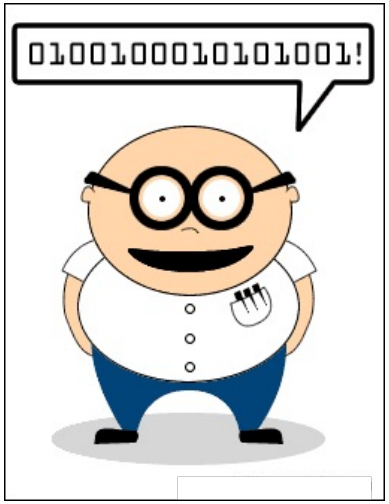
Command line

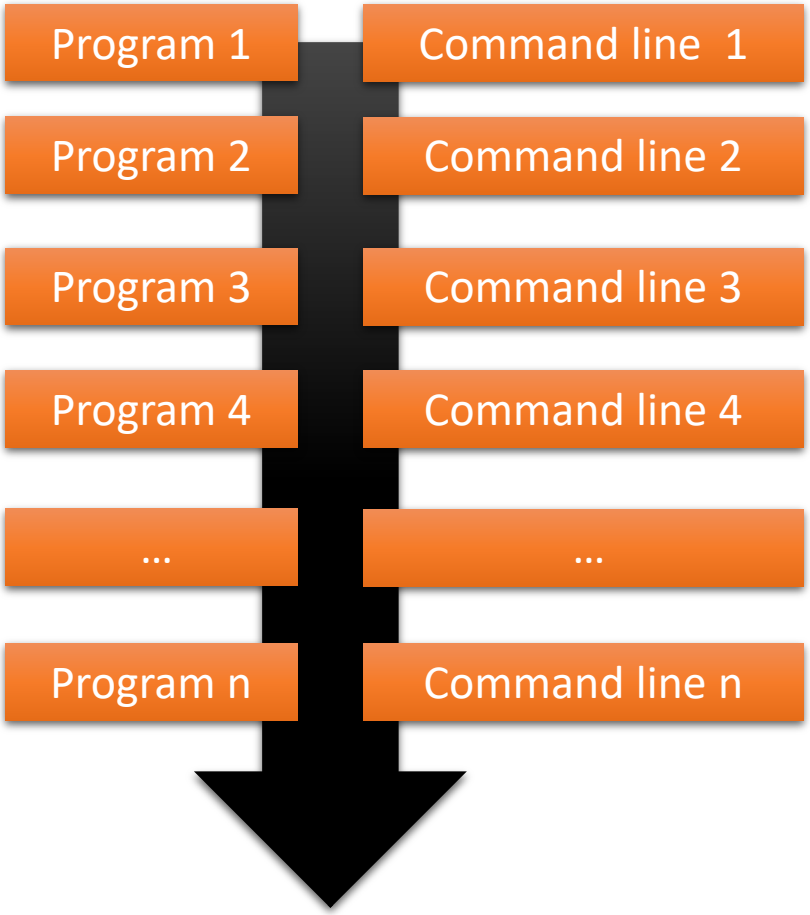
```
macs14 -t treatment.sort.bed -c control.bed -f BED -g mm --name=name1 --llocal=50000
 --slocal=5000 > macs1.nohup 2>&1 &
```

Bioinformatics analyses



Bioinformatics analyses





PIPELINE / WORKFLOW

Galaxy ?


Galaxy
PROJECT

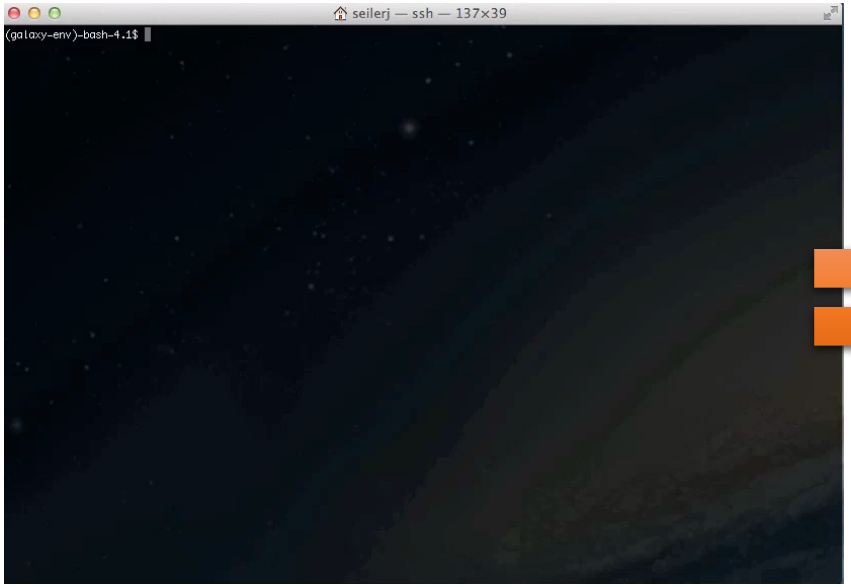
Galaxy project

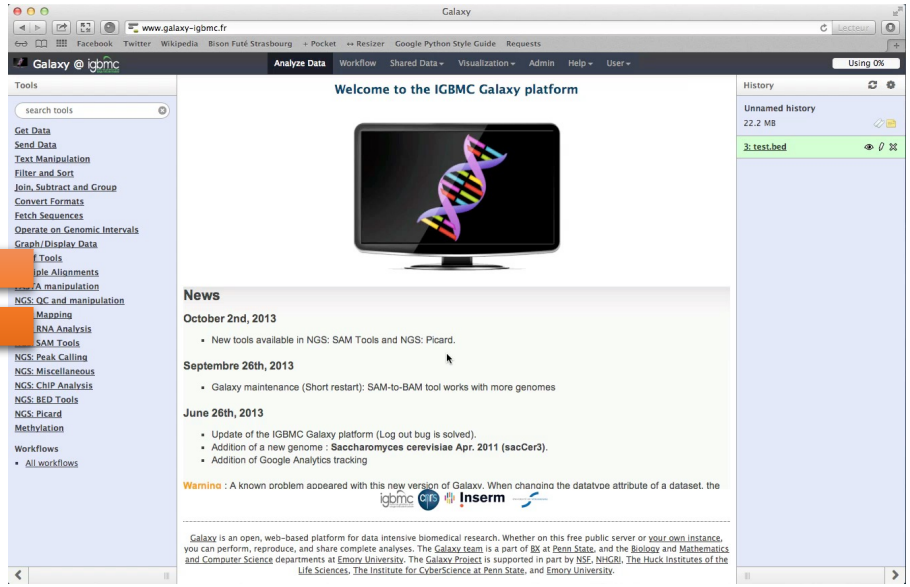
What is Galaxy ?

Galaxy is a **computing platform** that enables people to **run complex bioinformatics tools** on a **compute cluster** through a **simple web interface**.


This is Galaxy

Running analyses with tools





Galaxy philosophy

- **Perform**, and **share** complete analysis
- **No programming skills** required
- **Open source** and **free** solution
- **Very large** and **active** community
- **Reproducibility/Usability/Transparency**

How to use Galaxy

Use Galaxy

- All analyses are run on remote computing infrastructures
- No need to have a Supercomputer to use Galaxy
- Web browser




Use Galaxy

	UseGalaxy Servers	Public Servers	TIaaS	Academic Clouds	Commercial Clouds	Containers	VMs	Local
Free to use	Yes	Yes	Yes	Yes[1]	No	Yes	Yes	Yes
Uses your local compute infrastructure	No	No	No	No	No	Yes[2]	Yes[2]	Yes
Datasets (including intermediate) total > 250GB	No	?[5]	Yes	Yes	Yes	Yes[3]	Yes[3]	Yes
Computational requirements are similarly large	No	?[5]	Yes	Yes	Yes	Yes[3]	Yes[3]	Yes
Share Galaxy objects outside your organization	Yes	Yes	Yes	Yes	Yes	Yes[4]	Yes[4]	Yes[5]
Install custom tools and reference genomces	No	No	No	Yes[5]	Yes	Yes	Yes	Yes
Have absolute data security requirements	No	No	No	?[5]	?[5]	?[5]	?[5]	Yes

* TIaaS: Training Infrastructure as a Service

- https://galaxyproject.org/use/
  - 171 resources for using Galaxy (Last Update on: 2021, June 7th)

Galaxy public servers

Your research institute

Connect to Galaxy web site through a web browser (https://usegalaxy.org/)

Download and upload of the data

Remote instance of Galaxy

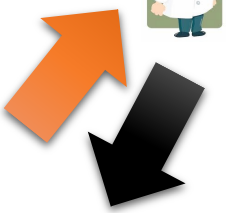
Run analyses

Galaxy **public servers**

Your research institute

World wide

Download and
upload of the data



Remote instance of Galaxy

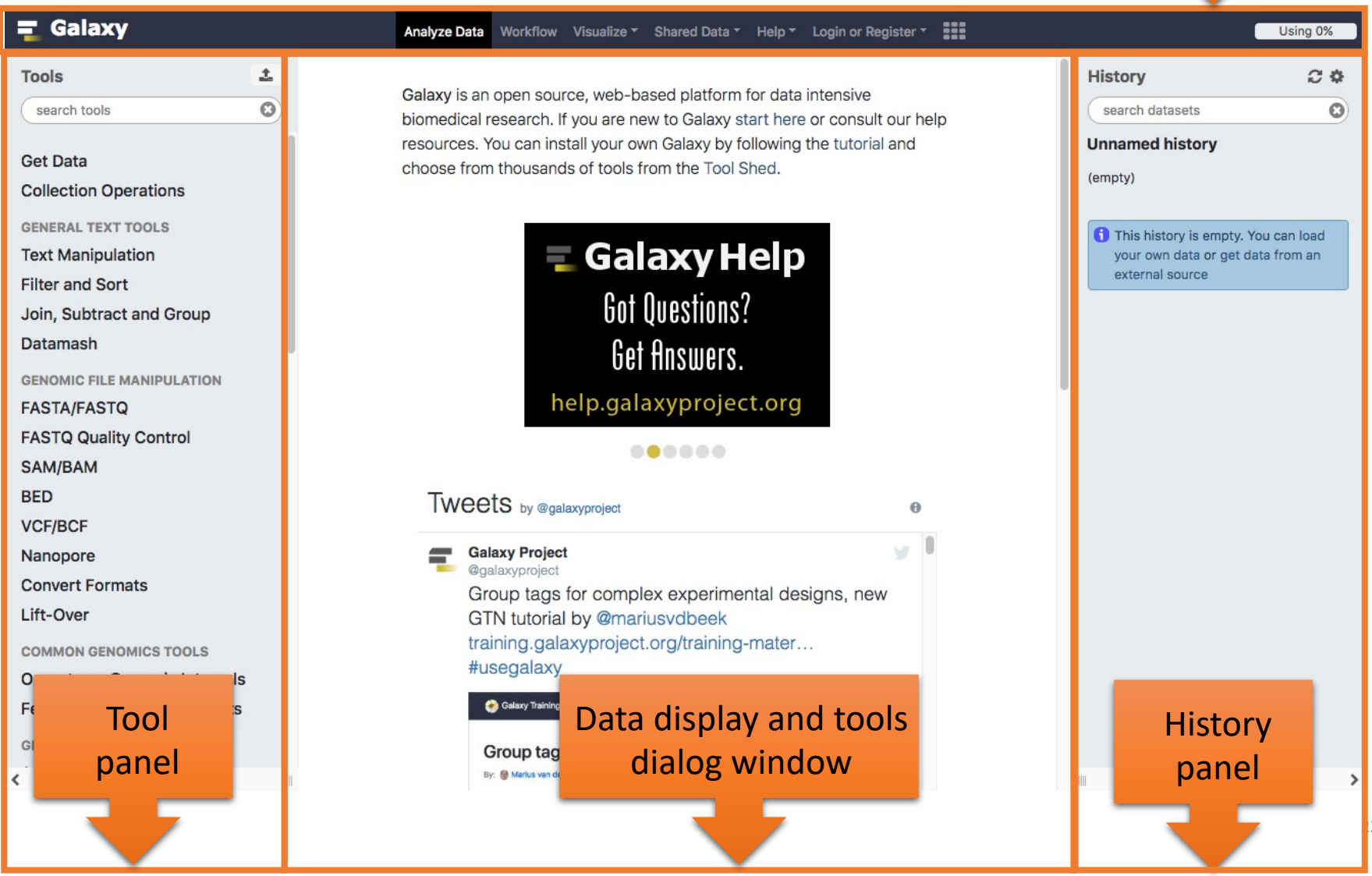
Uploading (takes a lot of time)
Shared computing power (longer analysis)

Galaxy local server

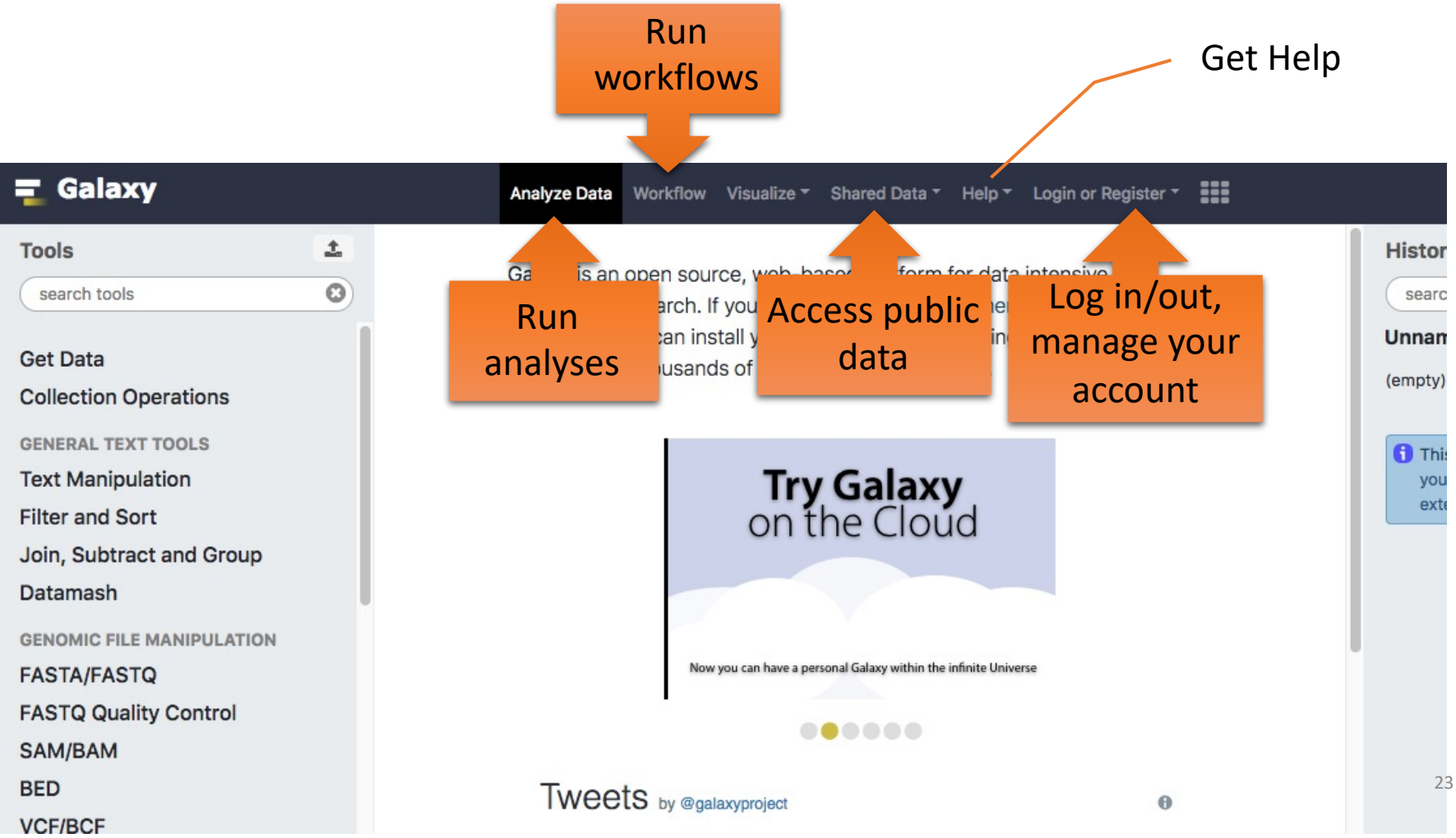
- Run a local production Galaxy because you want to
  - install and use tools unavailable on public Galaxies
  - use sensitive data (e.g. clinical)
  - process large datasets that are too big for public Galaxies
  - Develop Galaxy tools
  - Develop Galaxy itself

Description of the main features of Galaxy

Galaxy web interface



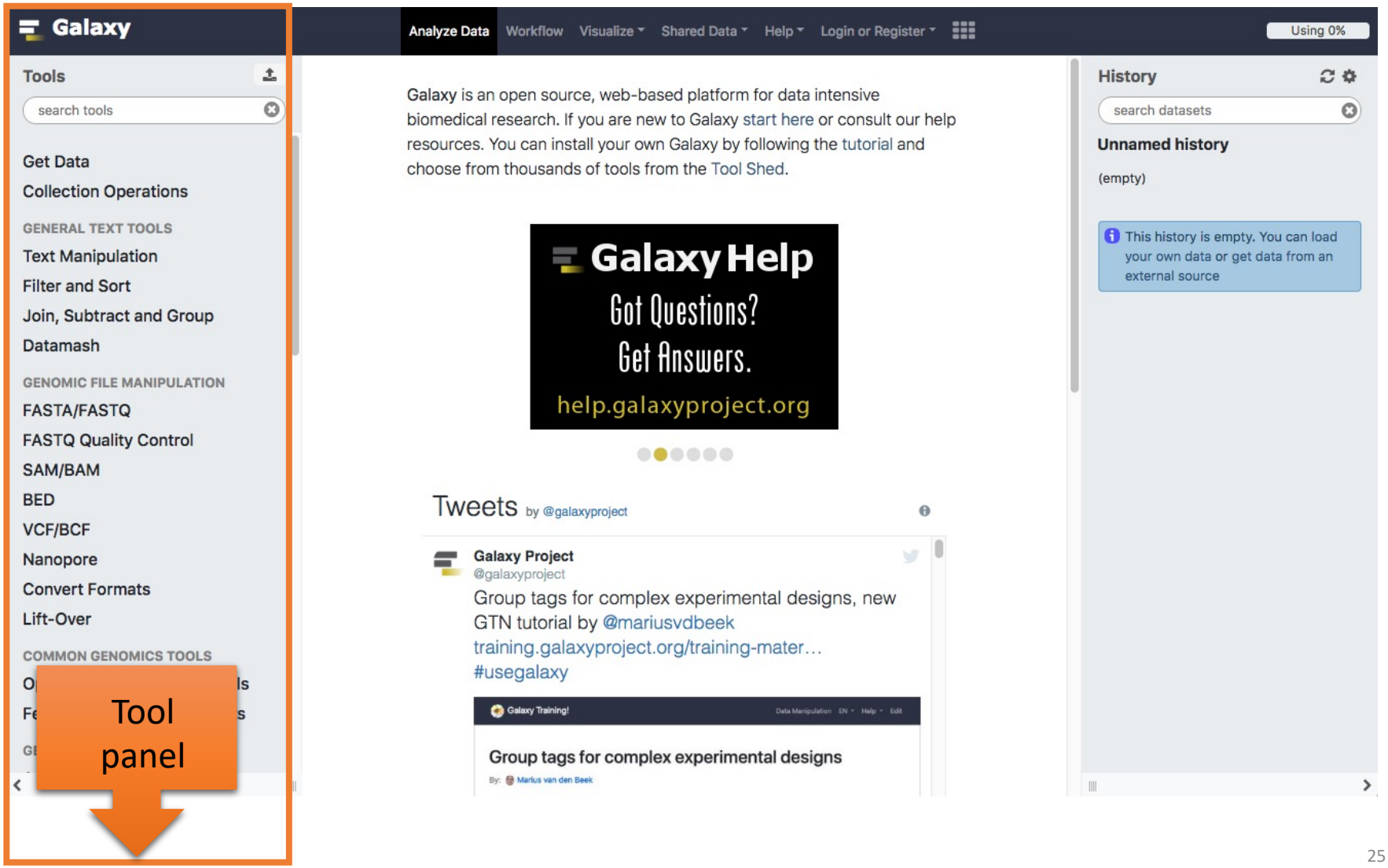
Top menu


Run workflows
Get Help
Galaxy
Analyze Data
Workflow
Visualize
Shared Data
Help
Login or Register
Run analyses
Access public data
Log in/out, manage your account
Tools
search tools
Get Data
Collection Operations
GENERAL TEXT TOOLS
Text Manipulation
Filter and Sort
Join, Subtract and Group
Datamash
GENOMIC FILE MANIPULATION
FASTA/FASTQ
FASTQ Quality Control
SAM/BAM
BED
VCF/BCF
Try Galaxy on the Cloud
Now you can have a personal Galaxy within the infinite Universe
Tweets by @galaxyproject
Histor
Unnam
(empty)

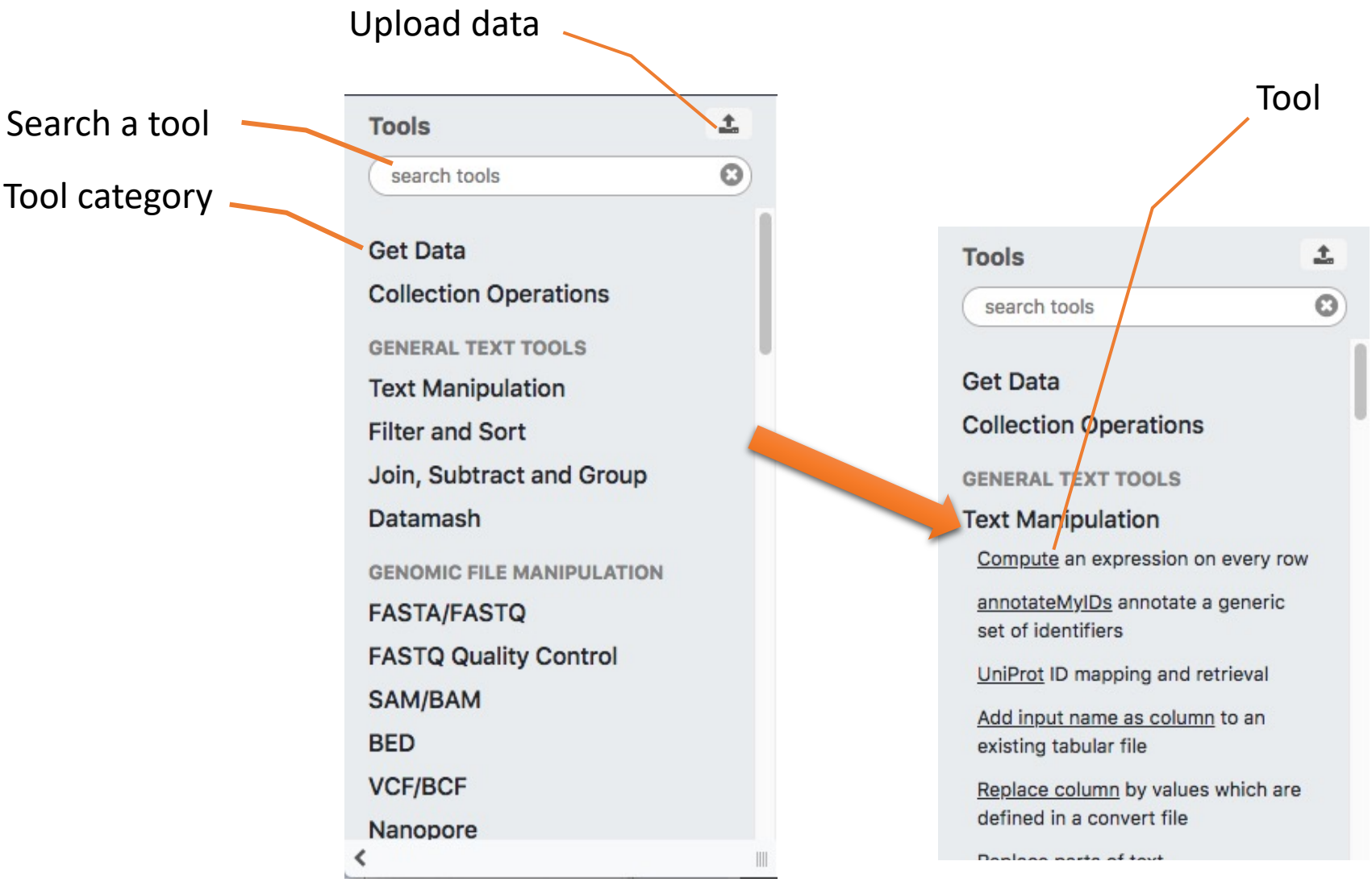
Exercise 1 : Log in

- Go to http://use.galaxeast.fr
- Log in with your training account (look to the post-it).

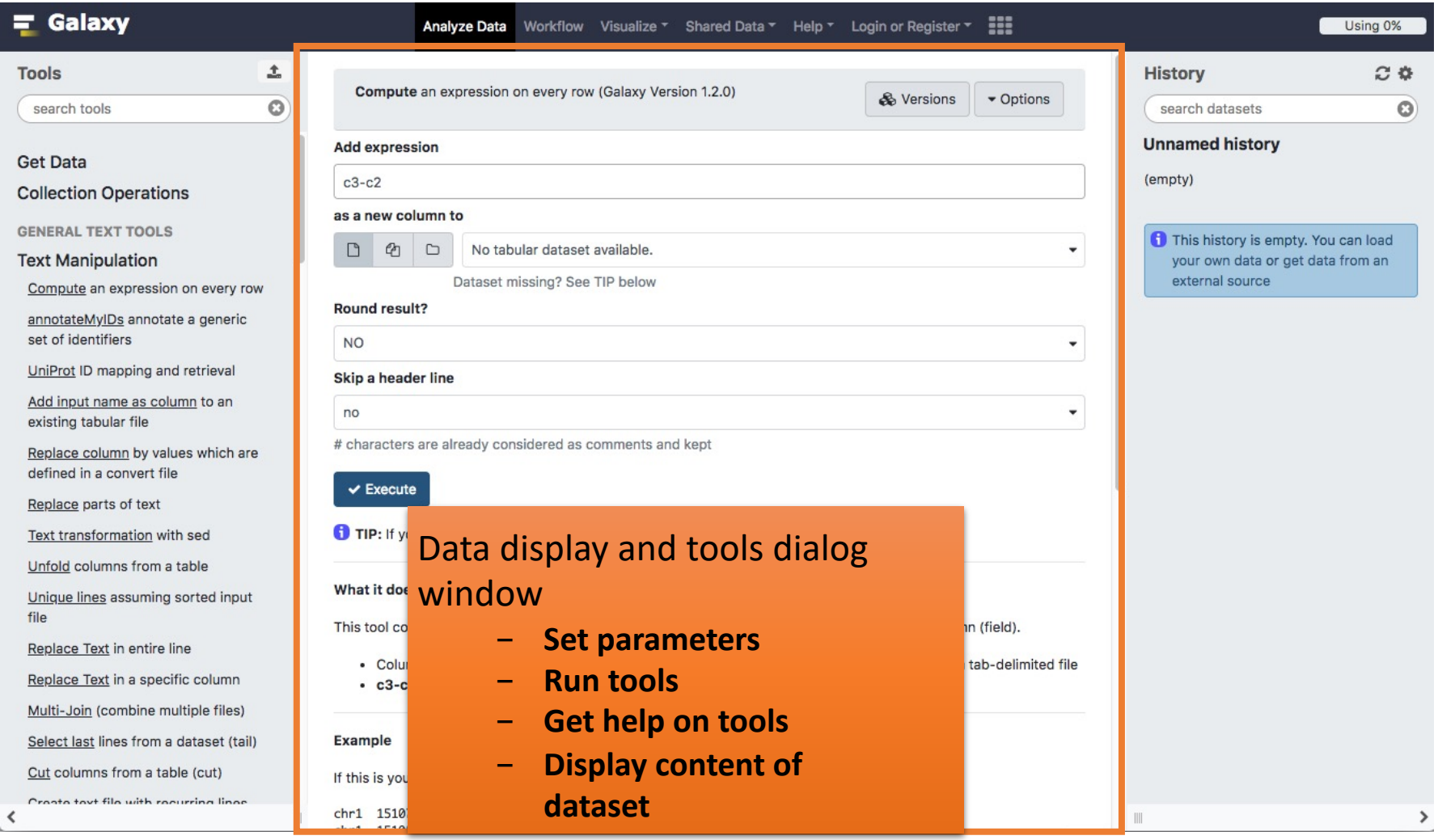
Tool Panel / Run analyses



Tool Panel / Run analyses



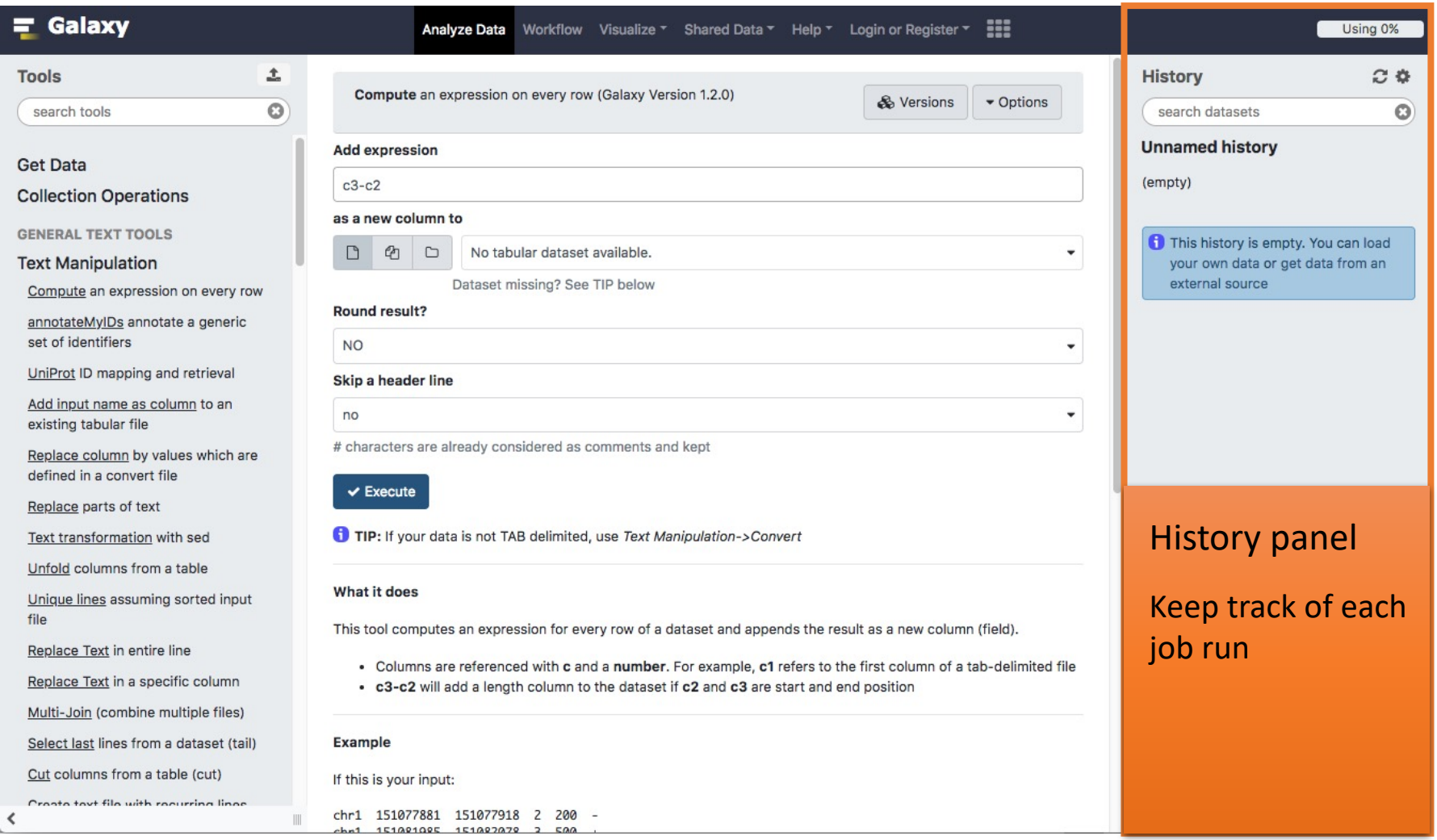
Tools dialog window



Data display and tools dialog window

- **Set parameters**
- **Run tools**
- **Get help on tools**
- **Display content of dataset**

History



History panel

Keep track of each job run

History

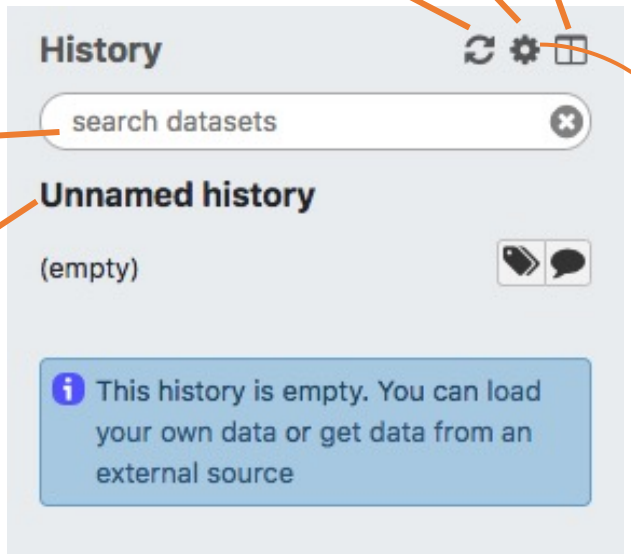
View all histories

History options

Refresh History

Search datasets

History name



HISTORY LISTS

Saved Histories

Histories Shared with Me

CURRENT HISTORY

Create New

Copy History

Share or Publish

Show Structure

Extract Workflow

Delete

Delete Permanently

Make Data Private

DATASET ACTIONS

Copy Datasets

Dataset Security

Resume Paused Jobs

Collapse Expanded Datasets

Unhide Hidden Datasets

Delete Hidden Datasets

Purge Deleted Datasets

DOWNLOADS

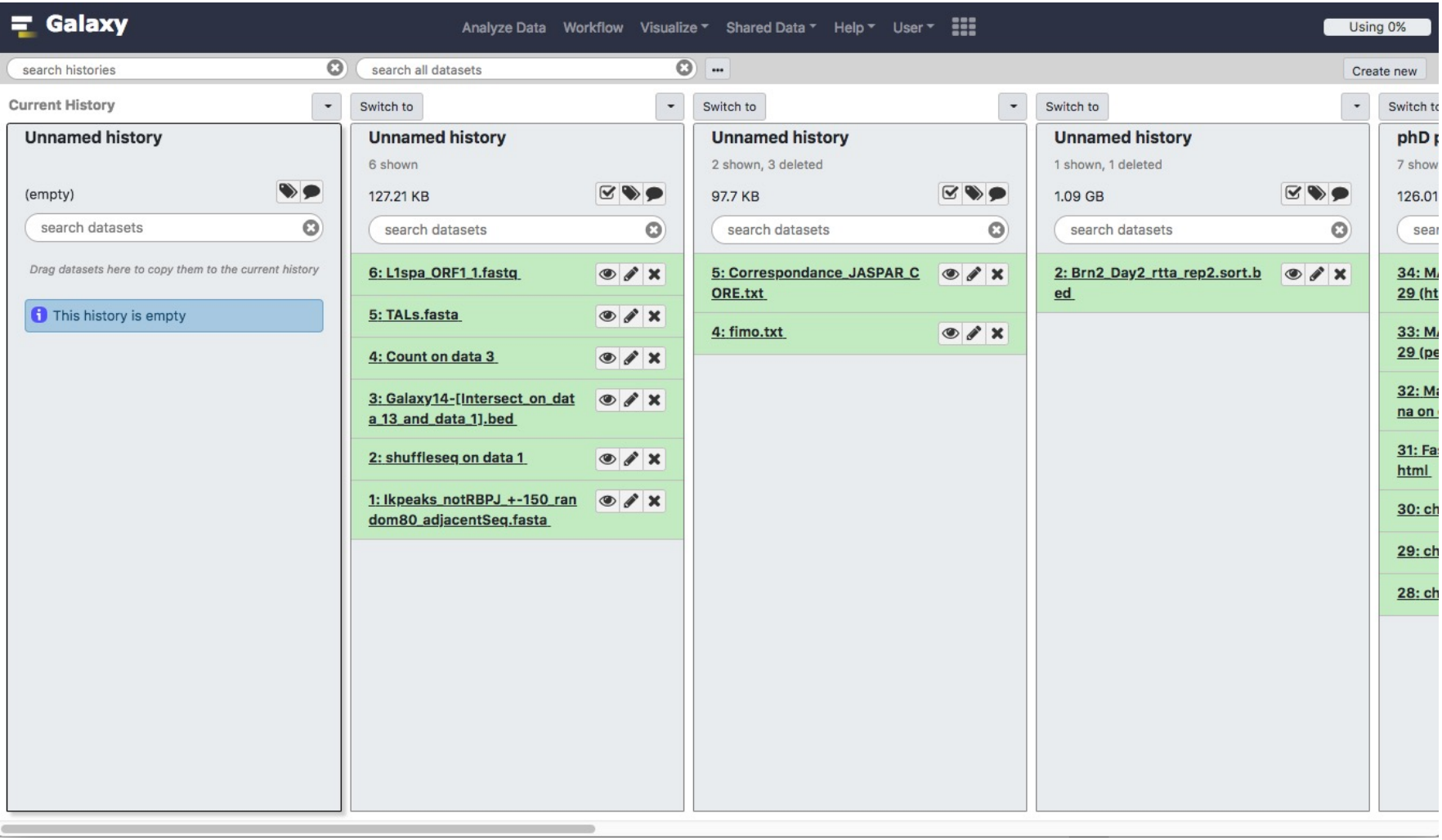
Export Tool Citations

Export History to File

OTHER ACTIONS

Import from File

View all histories



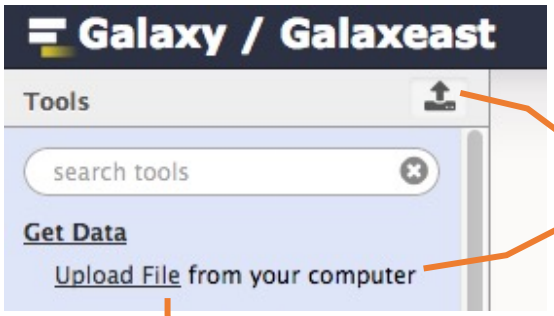
Exercise 2 : History

- Create a new history
- Change the name of the history to “RNA-seq data analysis”

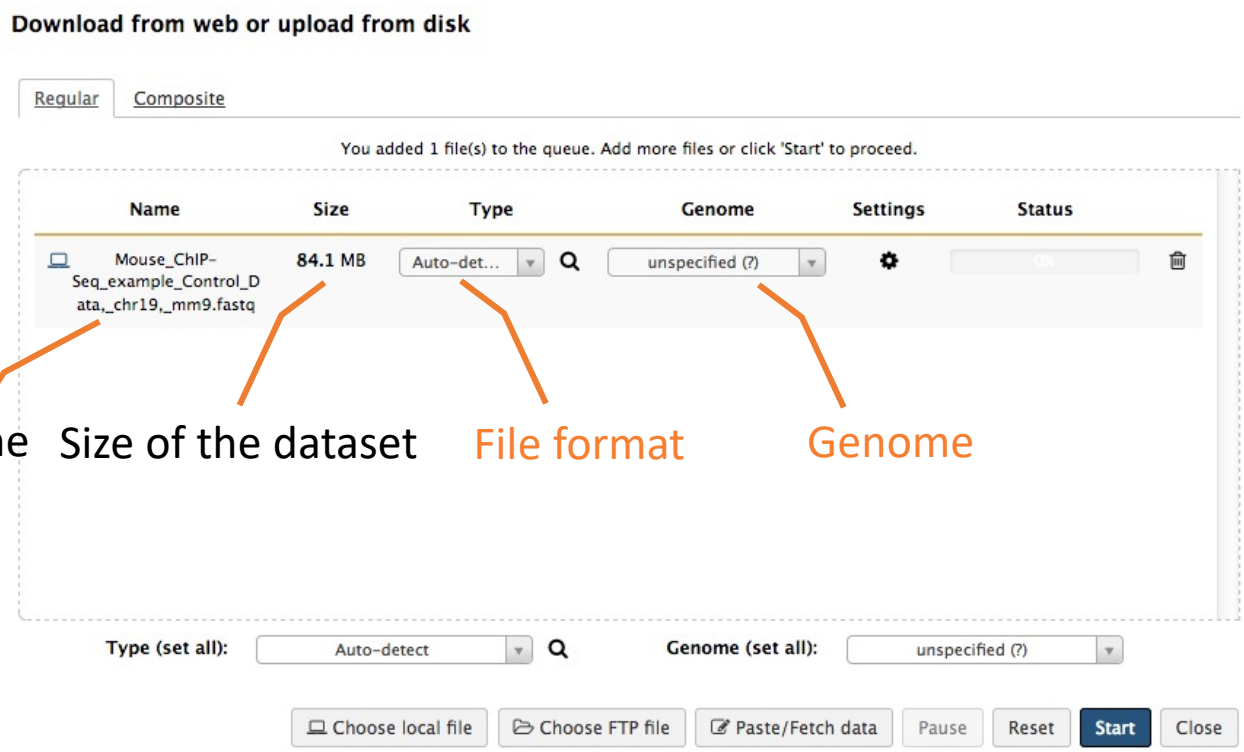
Import data into Galaxy

- Your own data (from your computer)
- Shared data
- Data from external sources

Import your own data to Galaxy



Display the drag and drop utility used to upload local files



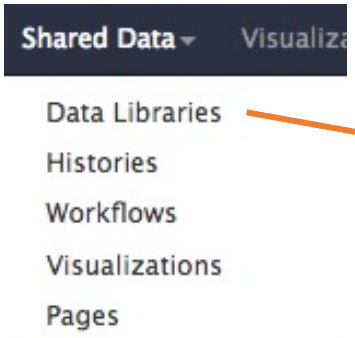
Name of the dataset

Size of the dataset

File format

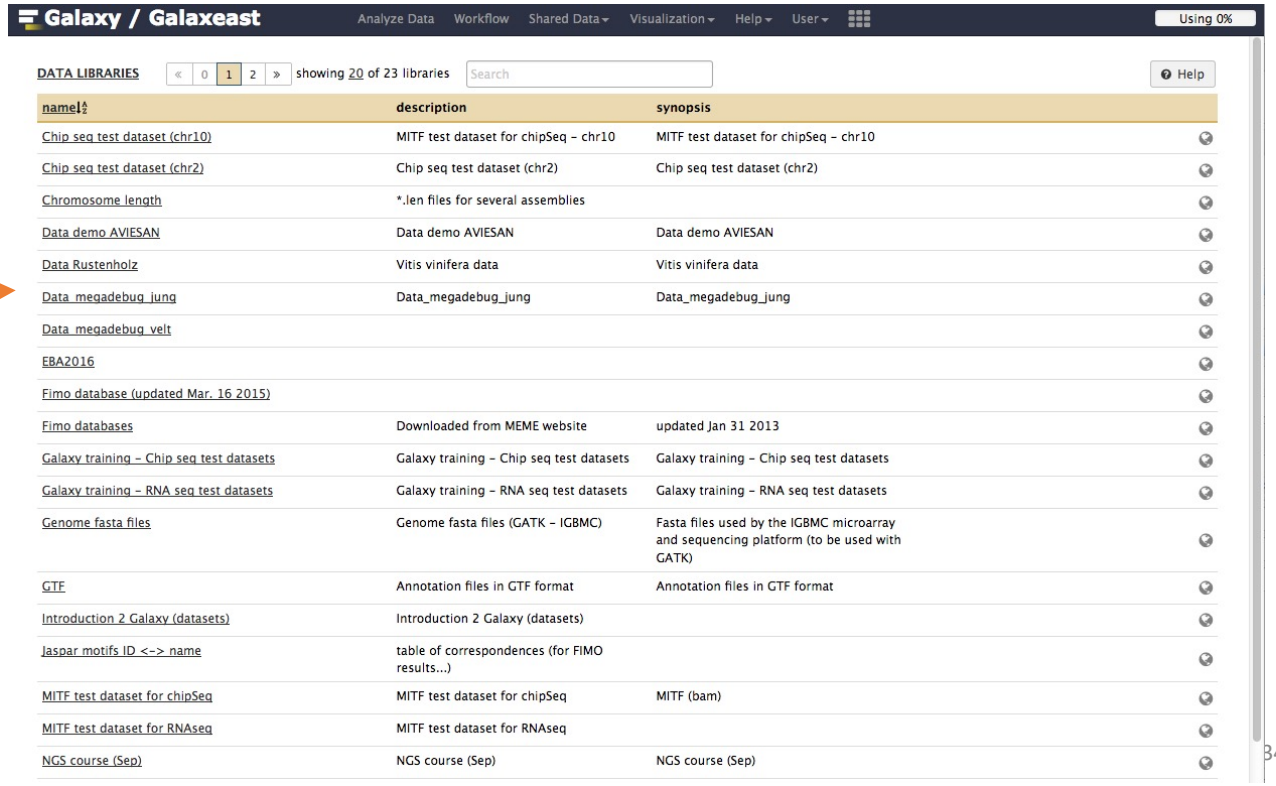
Genome

Import shared data (data libraries)



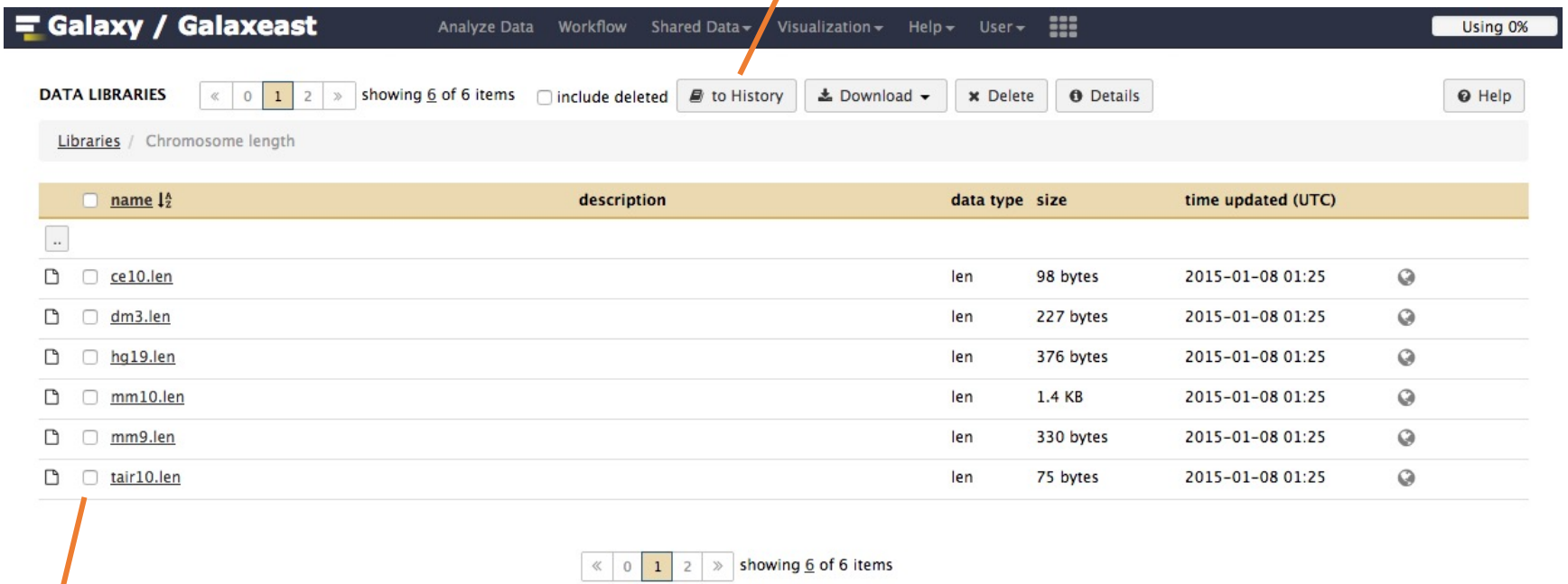
(Top menu)

Data Libraries



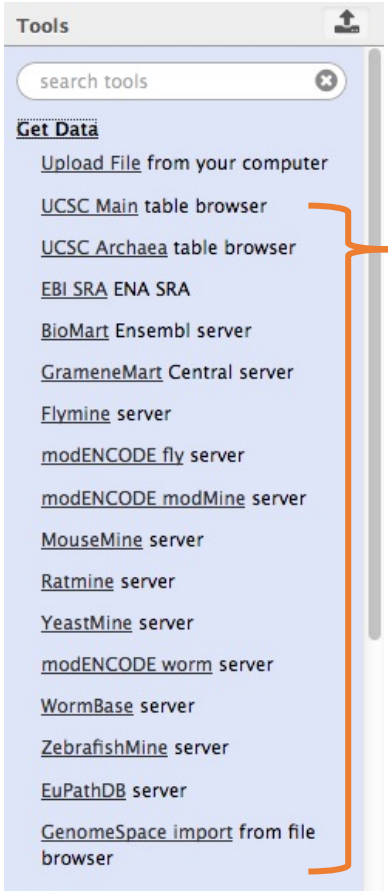
Import shared data (data libraries)

2. Import selected dataset to history

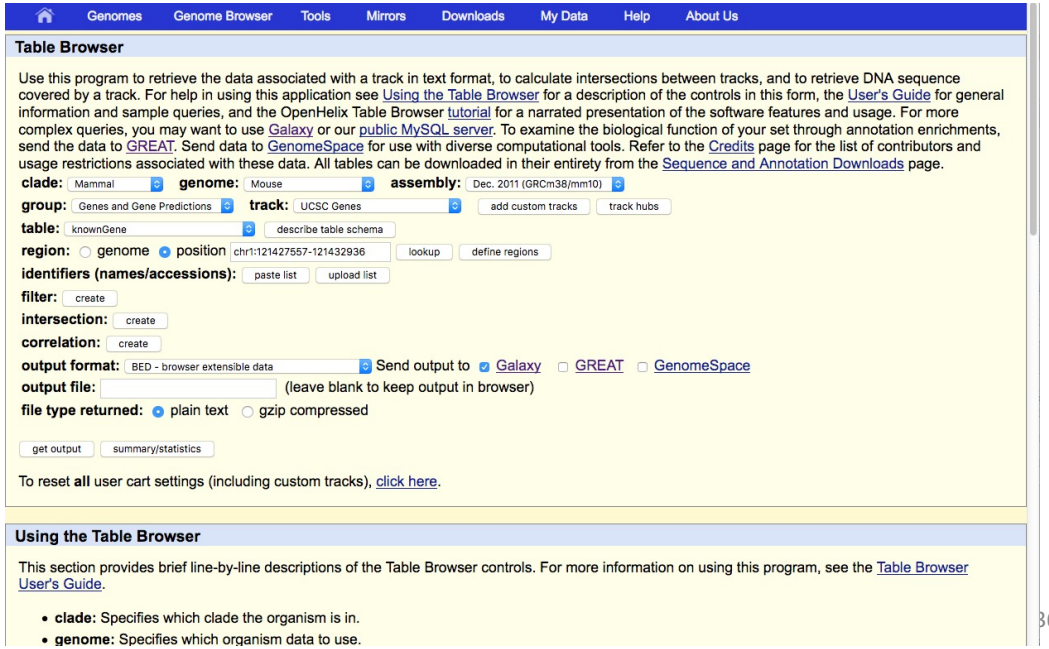


1. Select dataset

Import public data



Browse and import external data from public databases



Exercise 3 : Import data to Galaxy

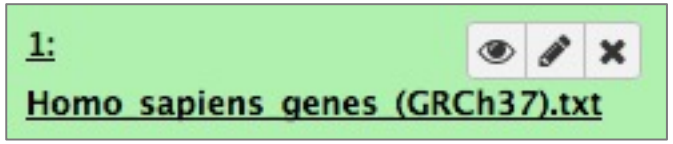
- 1. Import to Galaxy the file siLuc3_S12040.fastq from the “Shared data > Data Libraries > NGS data analysis training > RNAseq > rawdata” to the history called “RNA-seq data analysis”
- 2. You should be in the history “RNA-seq data analysis” (Switch to it if needed)
- 3. Import to Galaxy the file sample.bed.gz located in the directory galaxy.
    - Type : bed
    - Genome : Mouse July 2007 (NCBI37/mm9) (mm9)

Datasets/Jobs in the History

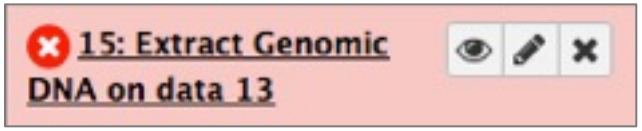
Grey: the job is waiting to run

Yellow: the job is running

Green: the job is successfully done



Red: the job encountered a problem



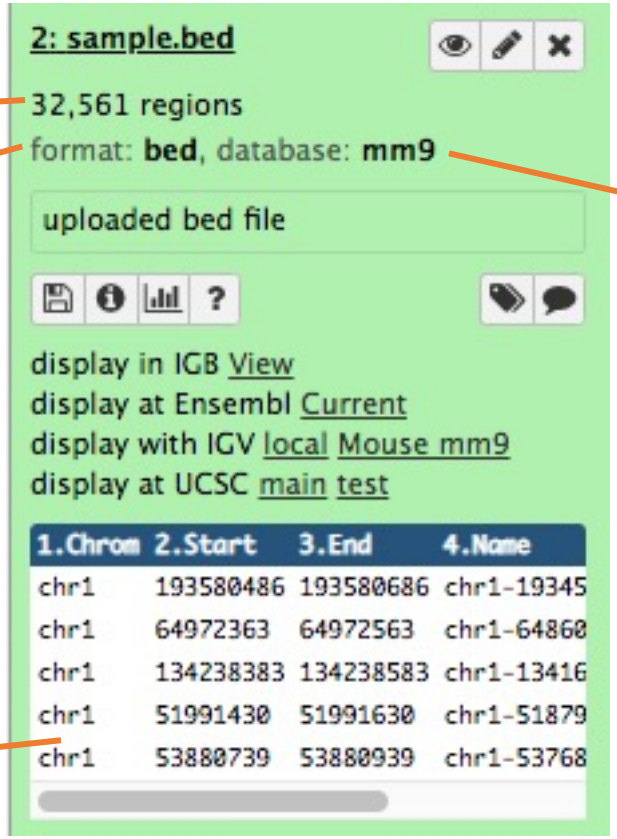
Datasets/Jobs in the History

Number of lines in the file or size of the file

Format

Genome

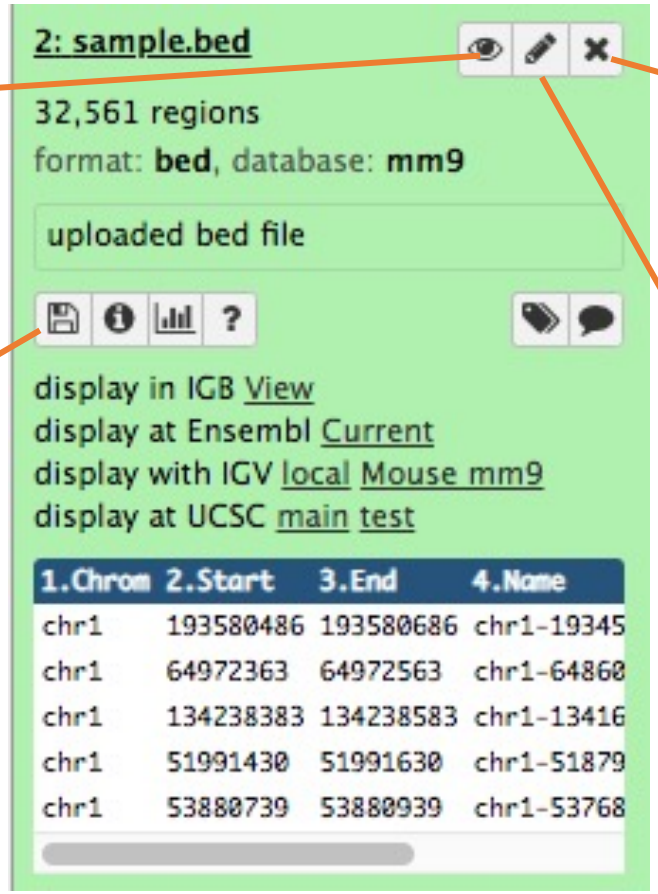
If the dataset is a text file, the first lines of the file are displayed



Datasets/Jobs in the History

View dataset (if possible) in the middle panel of Galaxy

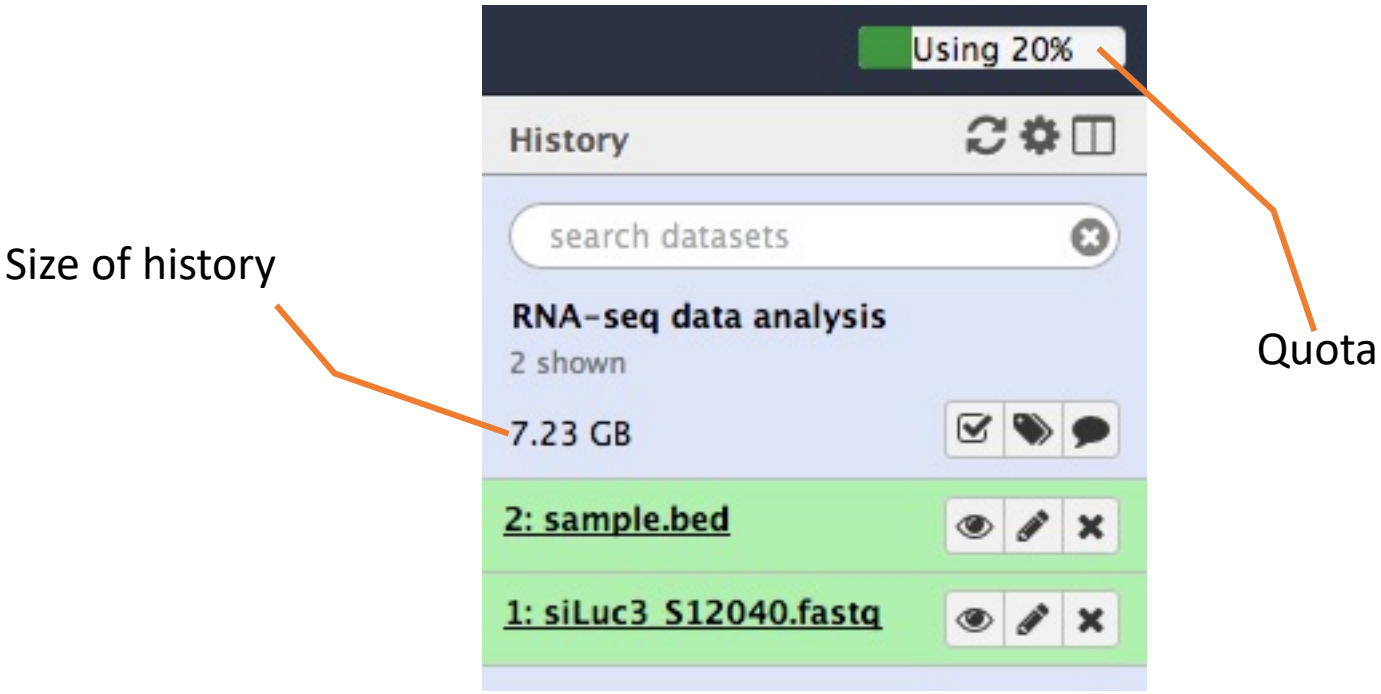
Download dataset



Delete dataset

Edit attributes of the dataset (change name, format, genome, permission)

Size of histories and quota



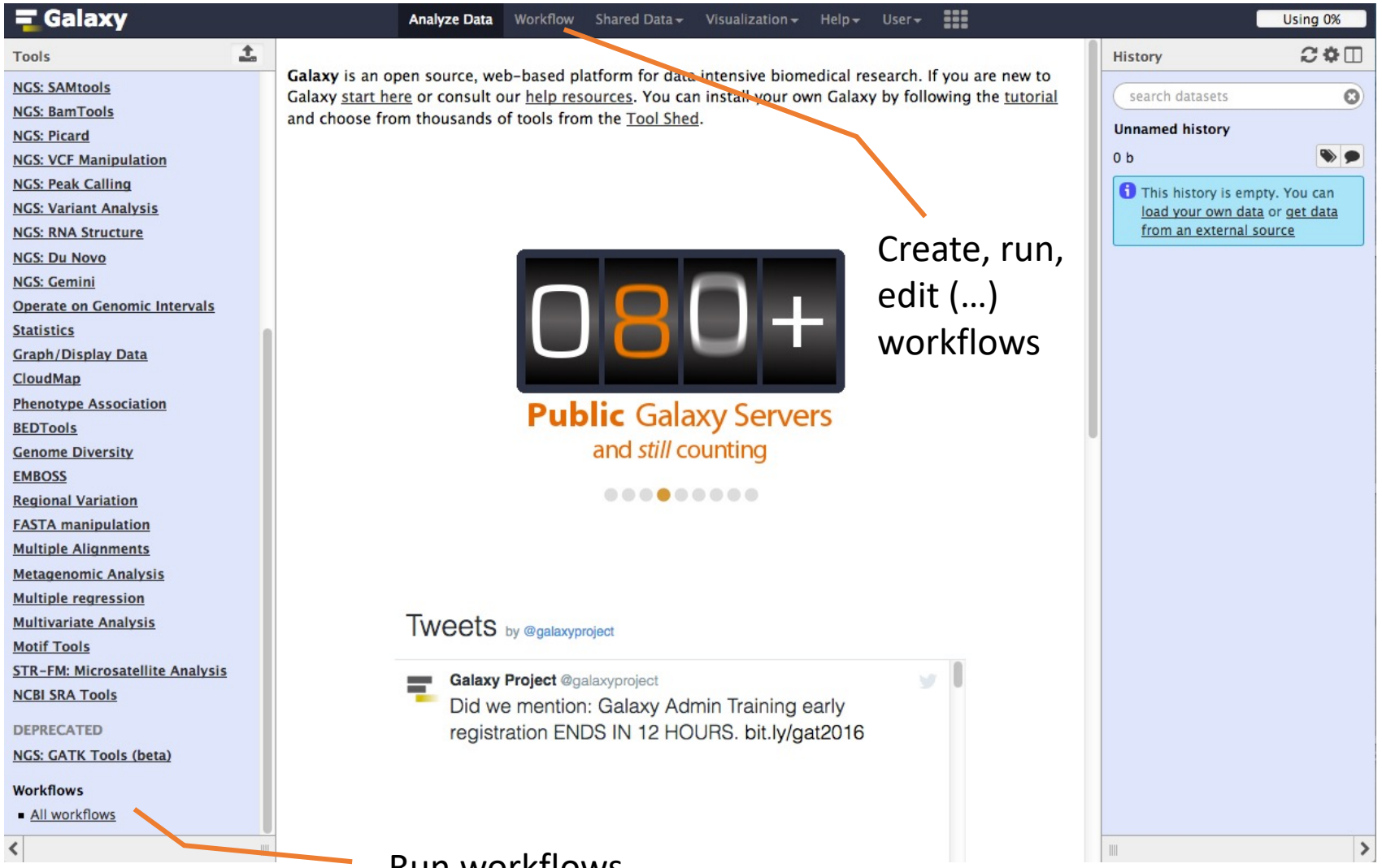
Exercise 4 : remove dataset

- 1. Remove the dataset sample.bed from your history by clicking on the button 
- 2.
  - A. Click on “deleted” in the top of the history panel (below the history name). Remove definitely the file from the disk by clicking on ” Permanently remove it from disk”.
  - B. Click on “hide deleted”

Exercise 5 : Running a tool

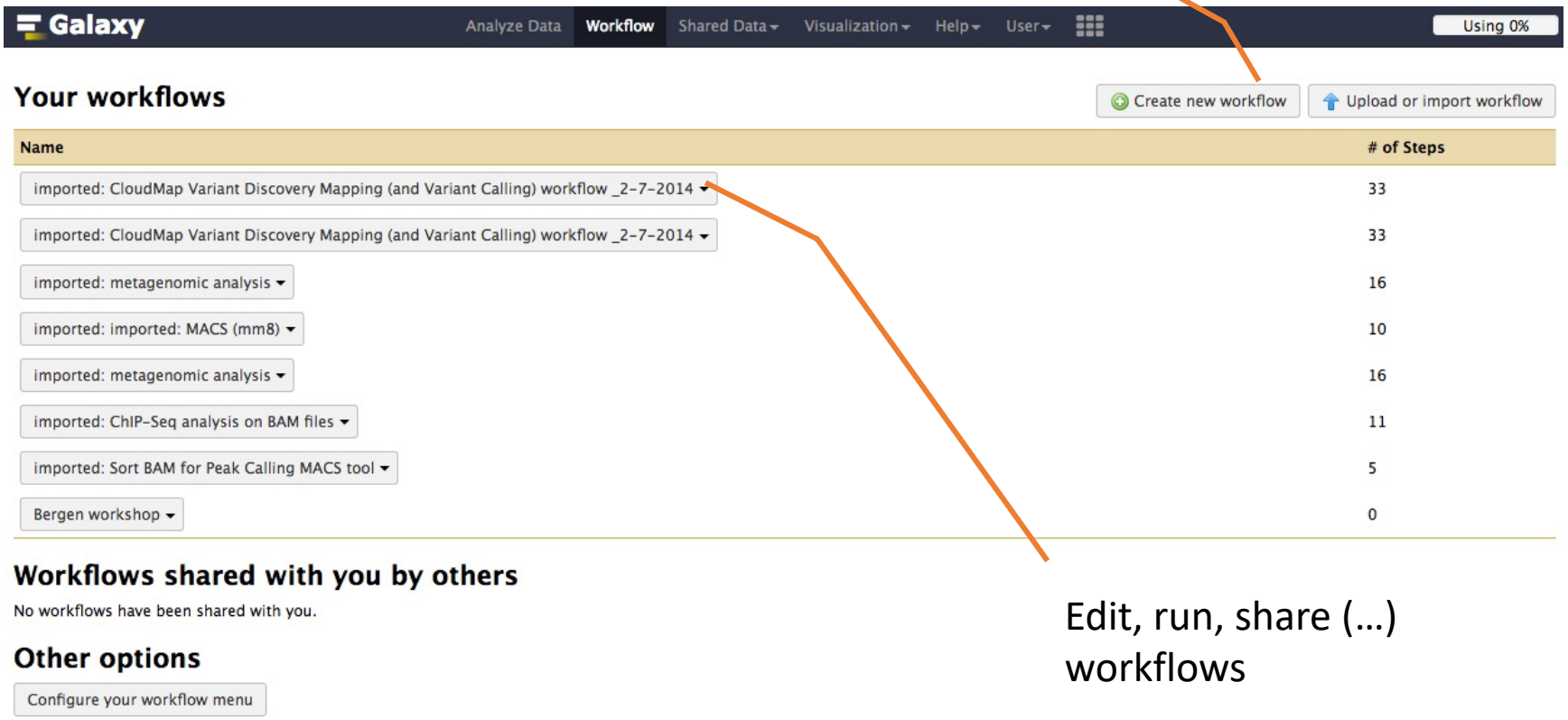
- 1. Use the tool “FastQC Read Quality reports” to compute quality analysis on the dataset “siLuc3_S12040.fastq”
  - Use default parameters.

Workflows


Galaxy
Analyze Data
Workflow
Shared Data
Visualization
Help
User
Using 0%
Tools
NGS: SAMtools
NGS: BamTools
NGS: Picard
NGS: VCF Manipulation
NGS: Peak Calling
NGS: Variant Analysis
NGS: RNA Structure
NGS: Du Novo
NGS: Gemini
Operate on Genomic Intervals
Statistics
Graph/Display Data
CloudMap
Phenotype Association
BEDTools
Genome Diversity
EMBOSS
Regional Variation
FASTA manipulation
Multiple Alignments
Metagenomic Analysis
Multiple regression
Multivariate Analysis
Motif Tools
STR-FM: Microsatellite Analysis
NCBI SRA Tools
DEPRECATED
NGS: GATK Tools (beta)
Workflows
All workflows
Galaxy is an open source, web-based platform for data intensive biomedical research. If you are new to Galaxy start here or consult our help resources. You can install your own Galaxy by following the tutorial and choose from thousands of tools from the Tool Shed.
080+
Public Galaxy Servers
and still counting
Tweets by @galaxyproject
Galaxy Project @galaxyproject
Did we mention: Galaxy Admin Training early registration ENDS IN 12 HOURS. bit.ly/gat2016
History
search datasets
Unnamed history
0 b
This history is empty. You can load your own data or get data from an external source
Create, run, edit (…) workflows
Run workflows

Workflows

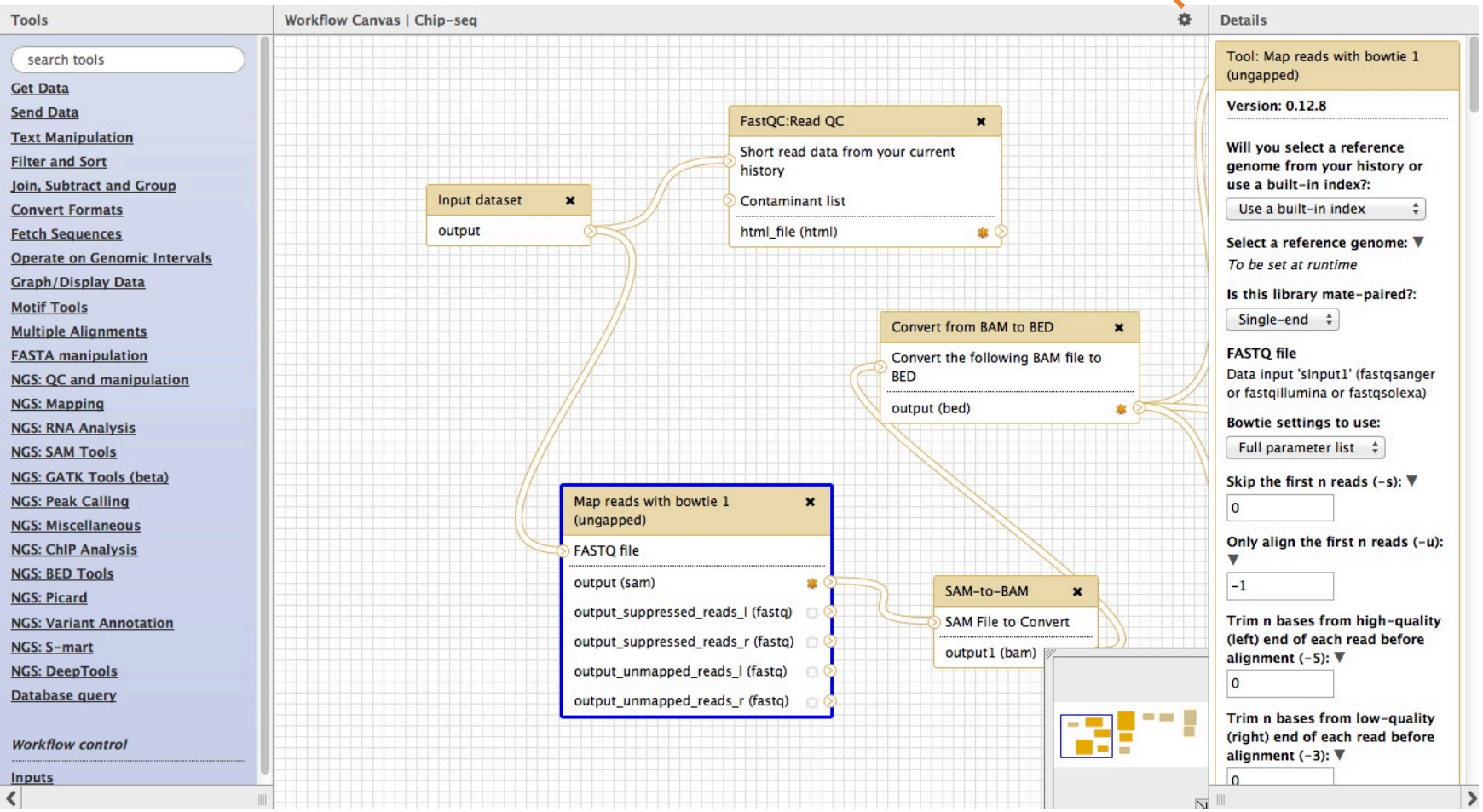
Create new workflow



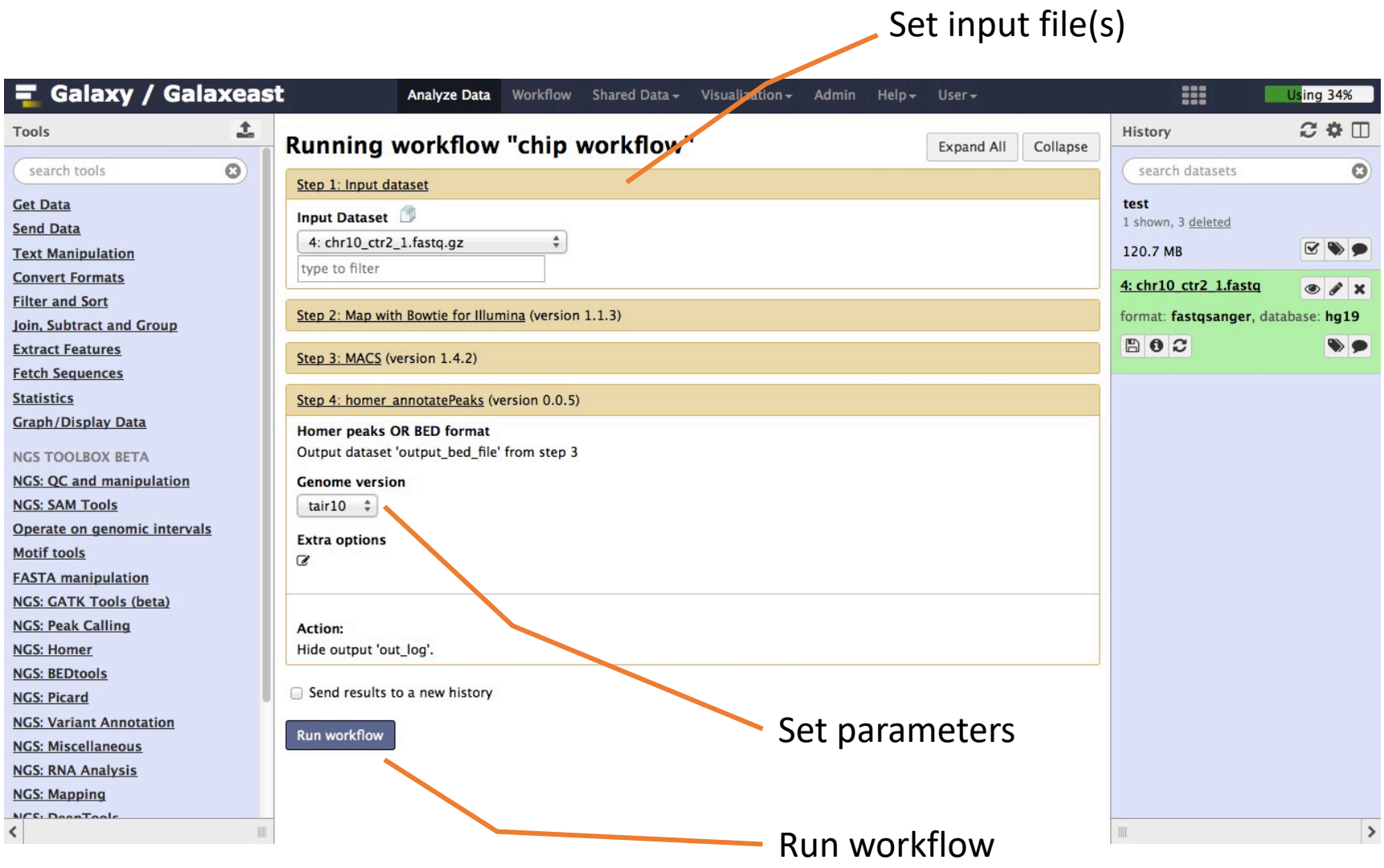
Edit, run, share (…) workflows

Workflows

Save, run (…) workflows



Workflows


Set input file(s)
Galaxy / Galaxeast
Analyze Data
Workflow
Shared Data
Visualization
Admin
Help
User
Using 34%
Tools
search tools
Get Data
Send Data
Text Manipulation
Convert Formats
Filter and Sort
Join, Subtract and Group
Extract Features
Fetch Sequences
Statistics
Graph/Display Data
NGS TOOLBOX BETA
NGS: QC and manipulation
NGS: SAM Tools
Operate on genomic intervals
Motif tools
FASTA manipulation
NGS: GATK Tools (beta)
NGS: Peak Calling
NGS: Homer
NGS: BEDtools
NGS: Picard
NGS: Variant Annotation
NGS: Miscellaneous
NGS: RNA Analysis
NGS: Mapping
Running workflow "chip workflow"
Expand All
Collapse
Step 1: Input dataset
Input Dataset
4: chr10_ctr2_1.fastq.gz
type to filter
Step 2: Map with Bowtie for Illumina (version 1.1.3)
Step 3: MACS (version 1.4.2)
Step 4: homer_annotatePeaks (version 0.0.5)
Homer peaks OR BED format
Output dataset 'output_bed_file' from step 3
Genome version
tair10
Extra options
Action:
Hide output 'out_log'.
Send results to a new history
Run workflow
History
search datasets
test
1 shown, 3 deleted
120.7 MB
4: chr10_ctr2_1.fastq
format: fastqsanger, database: hg19
Set parameters
Run workflow

Privacy

- By default datasets, workflows, histories are private to the user that generated/uploaded them.
- They can be shared across Galaxy users (of the same Galaxy instance) or via links