Introduction to Galaxy

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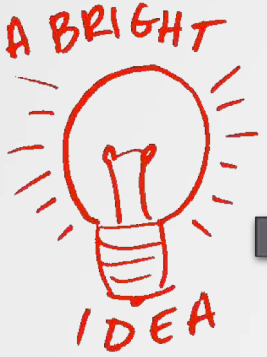
Guidelines

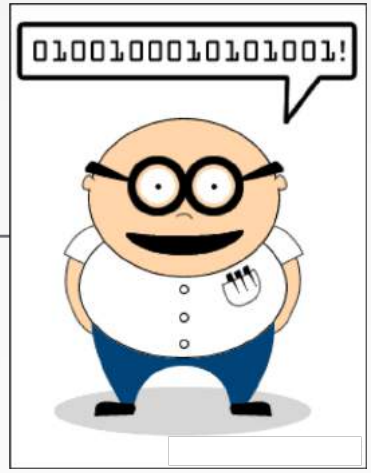
- Analyzing biological data with informatics tools
- Presentation of the Galaxy project
- Description of the main features of the Galaxy platform

Analyzing biological data with informatics tools

Bioinformatics analyses

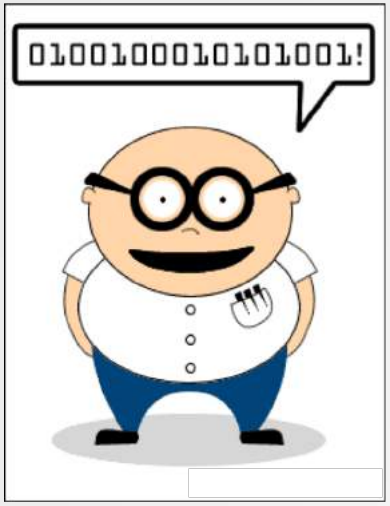


Informatics data



nature

Bioinformatics analyses



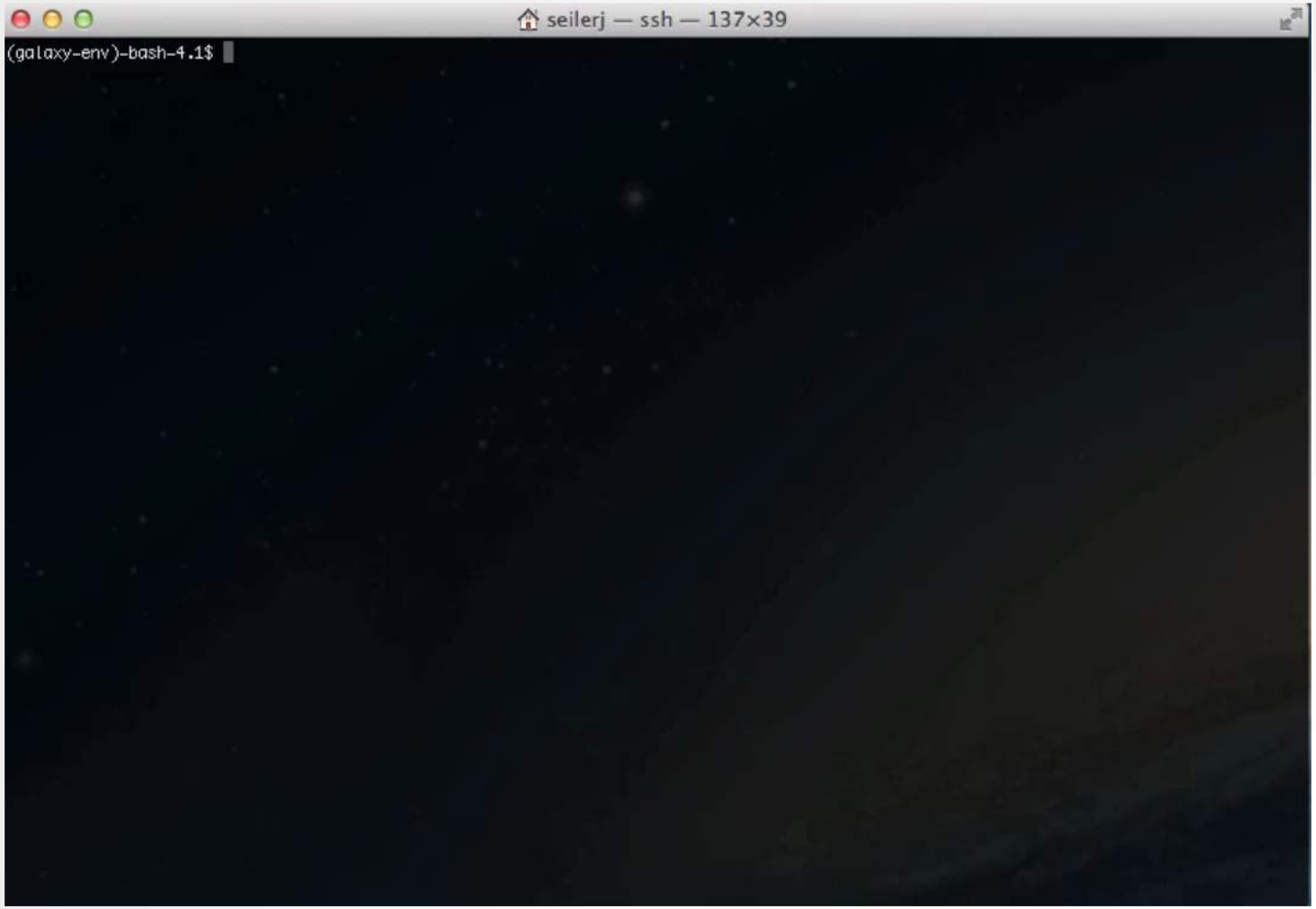
Scripts, softwares

```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.
```

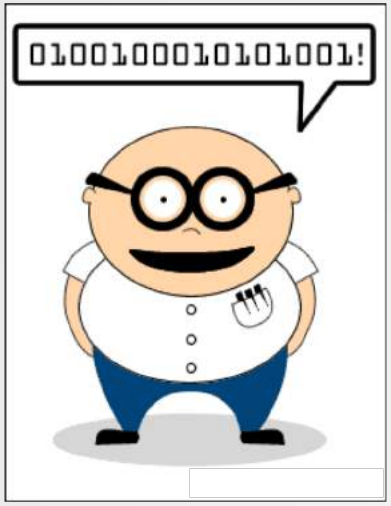
Command line

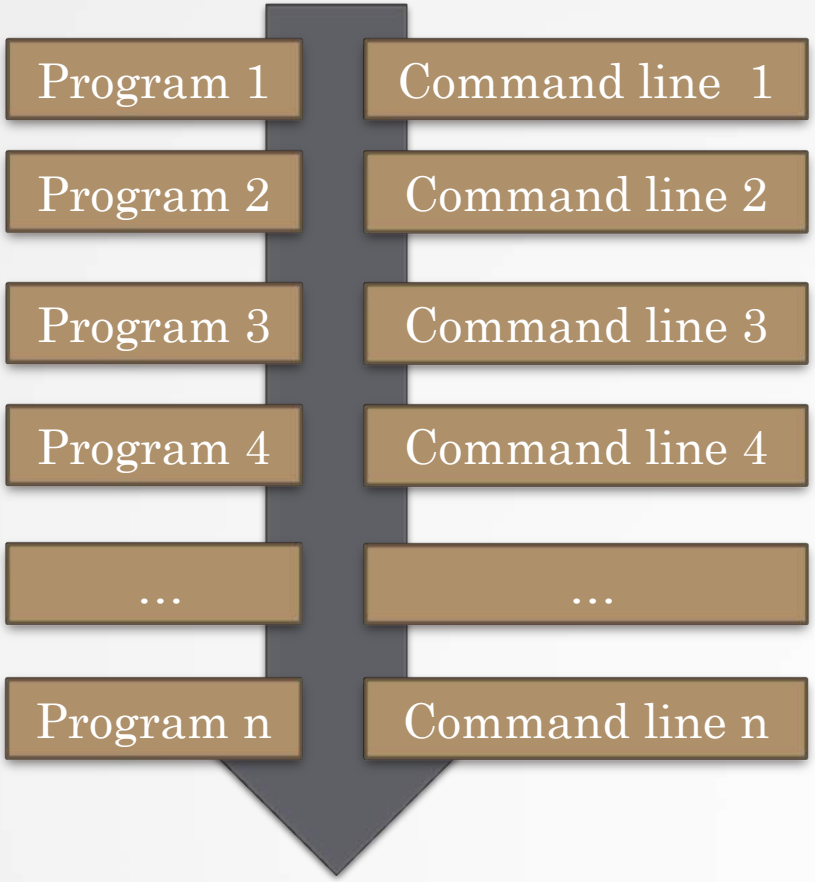
```
macs14 -t treatment.sort.bed -c control.bed -f BED -g mm --name=name1 --llocal=50000
 --slocal=5000 > macs1.nohup 2>&1 &
```

Bioinformatics analyses



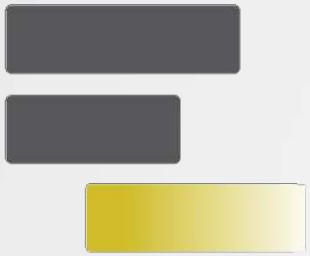
Bioinformatics analyses





PIPELINE/
WORKFLOW

Galaxy ?



Galaxy

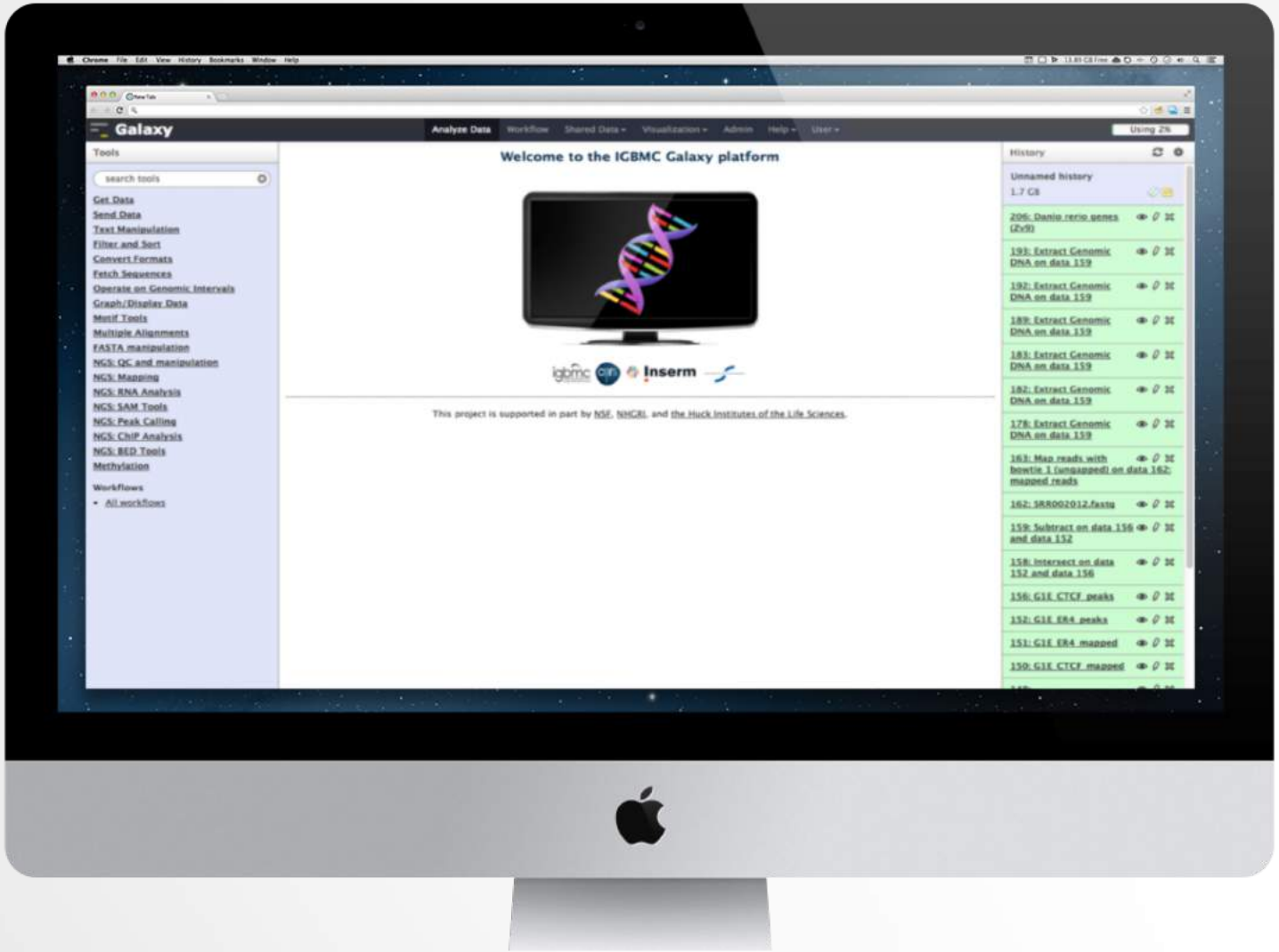
PROJECT

Galaxy project

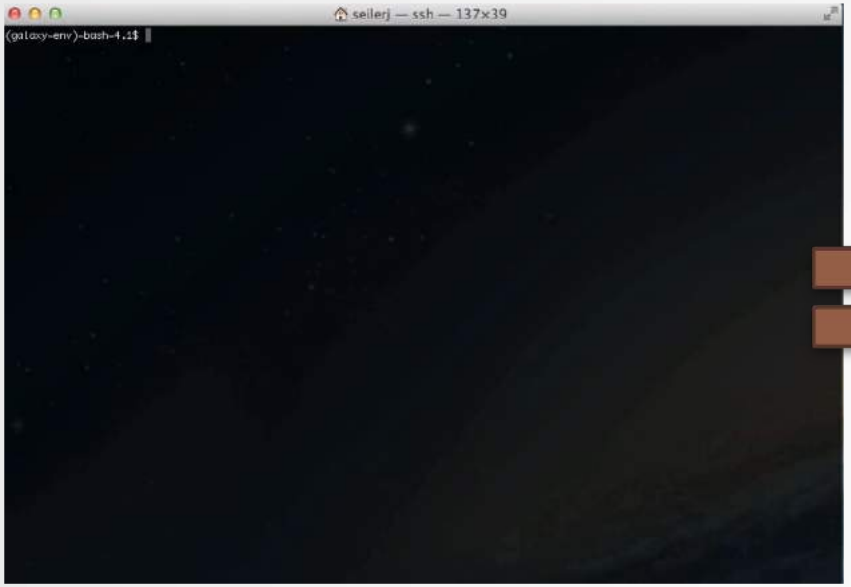
What is Galaxy ?

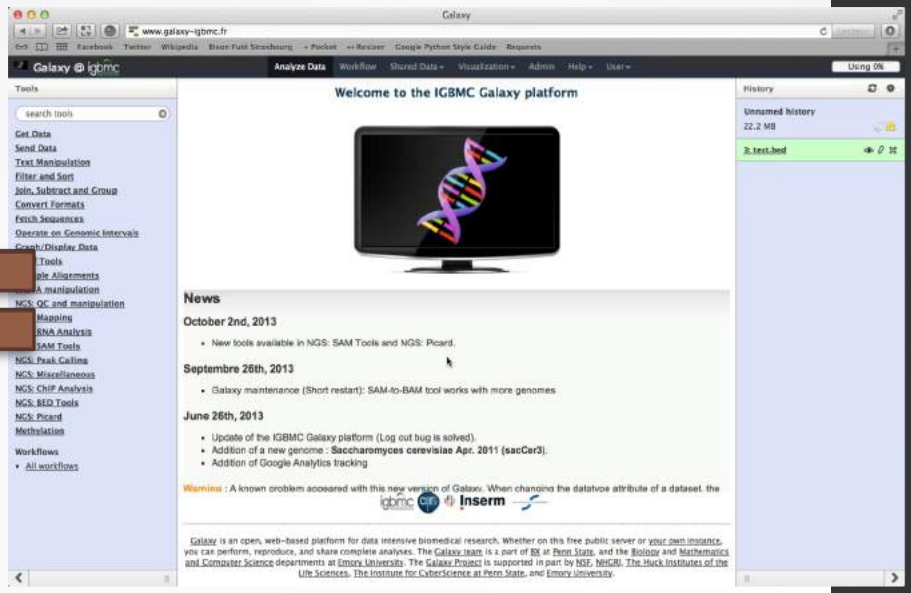
Galaxy is a **computing platform** that enables people to **run complex bioinformatics tools** on a **compute cluster** through a **simple web interface**.

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

- **Public servers**
- **Local servers**
- Clouds (Public, Commercial or Academic)
- Docker
- Virtual Machines

Galaxy **public servers**

- Galaxy Project's public server (https://usegalaxy.org/)
- There are several public remote Galaxy instances worldwide (116)
  - Genomics Servers
  - Domain Servers
  - Tool Publishing Servers

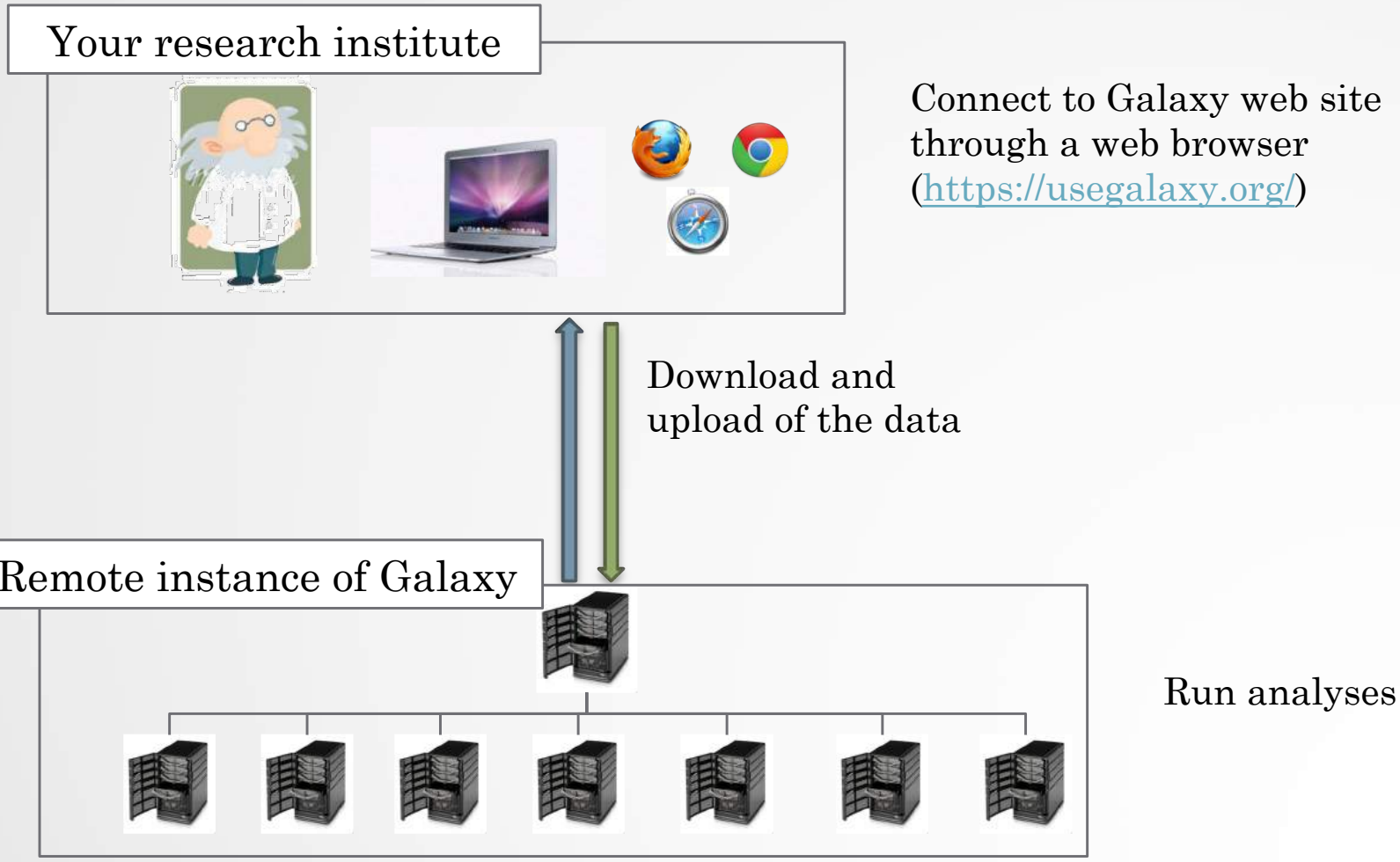
Public Galaxy Servers list :
https://galaxyproject.org/use/
Last Update on: 2019, March 7th

Galaxy **public servers**

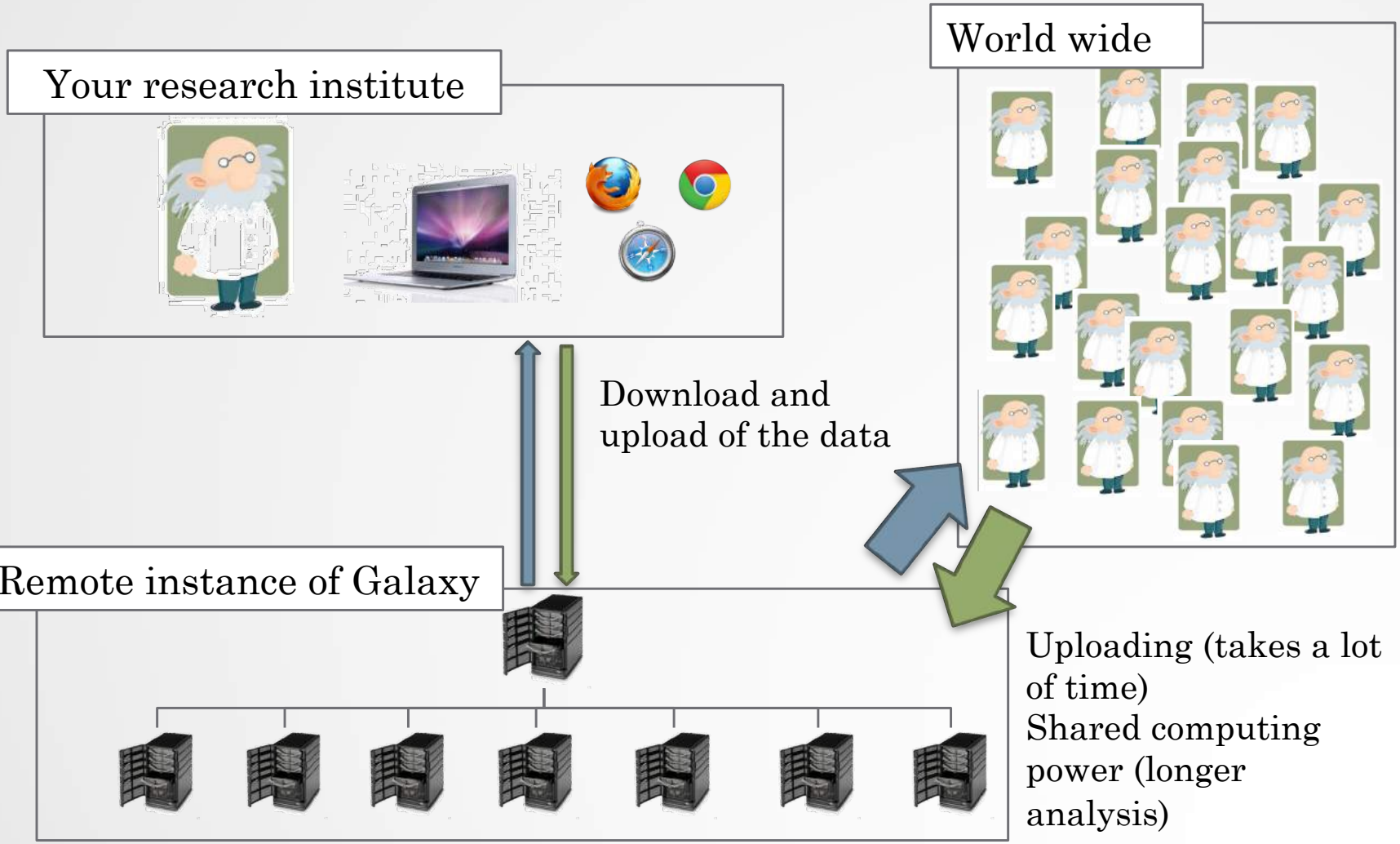
- All analyses are run on remote computing infrastructures
- No need to have a Supercomputer to use Galaxy
- Web browser




Galaxy **public servers**



Galaxy **public servers**

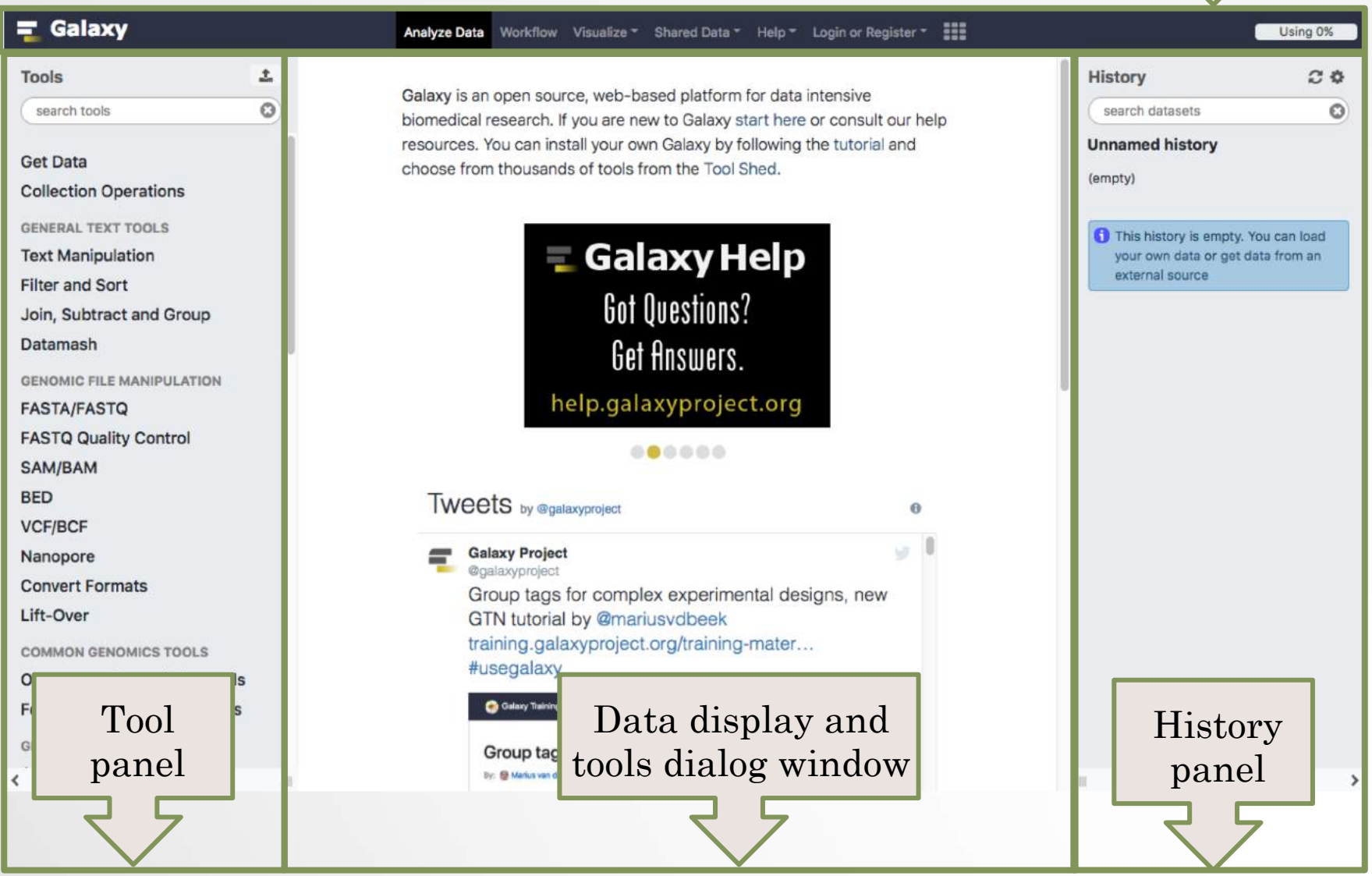


Galaxy **local server**

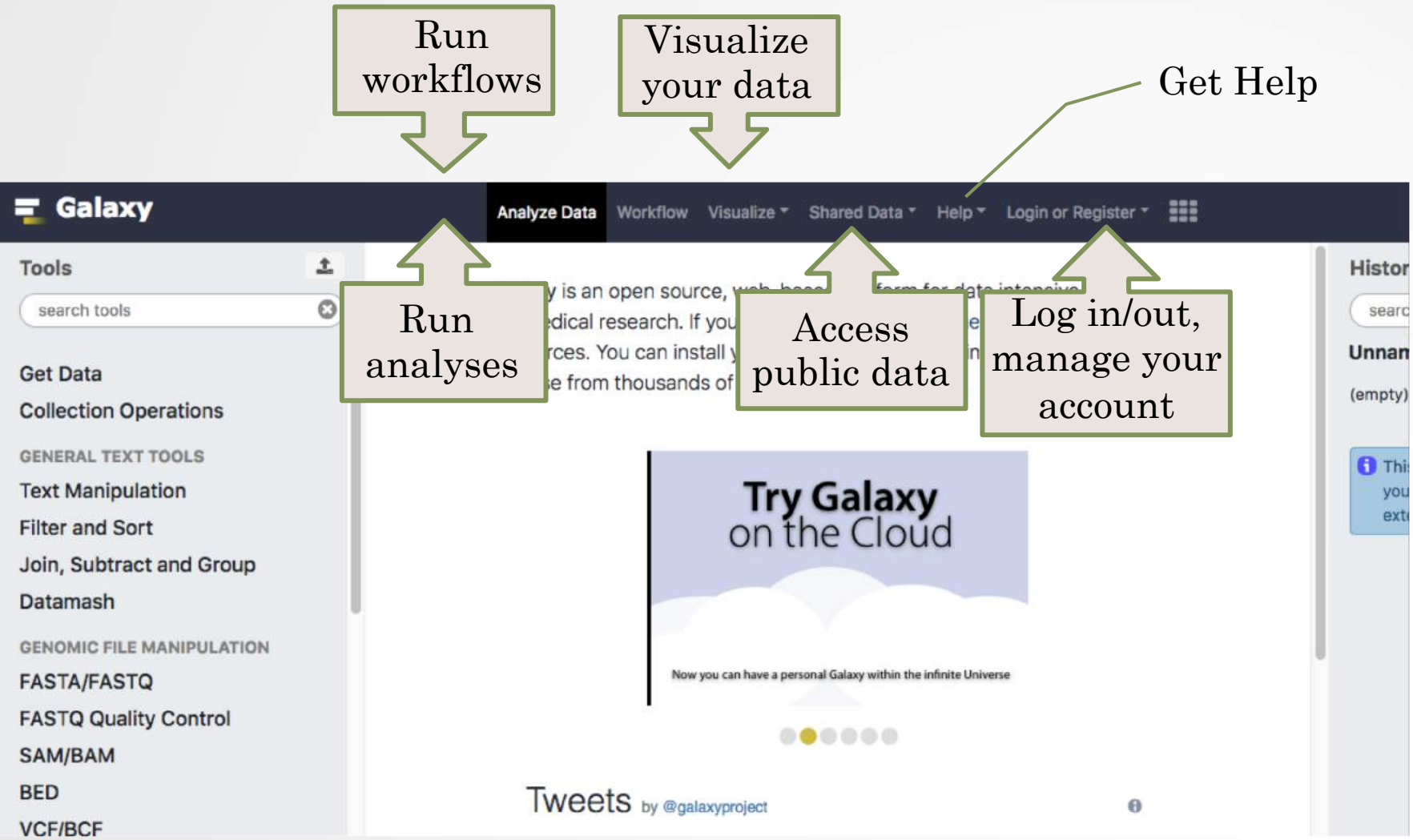
- Run a local production Galaxy because you want to
  - install and use tools unavailable on public Galaxies
  - use sensitive data (e.g. clinical)
  - process large datasets that are too big for public Galaxies
  - plug-in new datasources
  - Develop Galaxy tools
  - Develop Galaxy itself

Description of the main features of Galaxy

Galaxy web interface



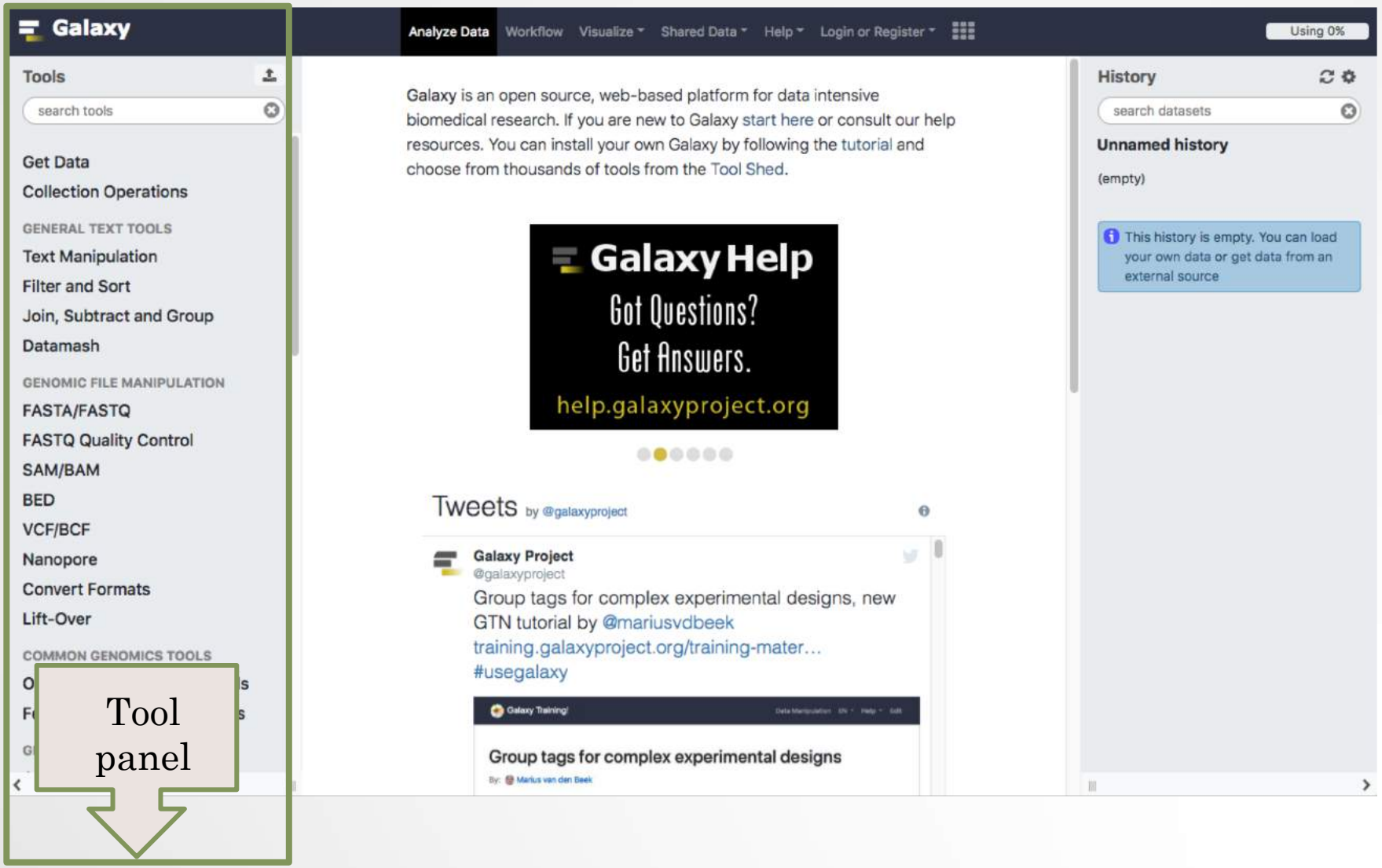
Top menu


Run workflows
Visualize your data
Get Help
Galaxy
Analyze Data
Workflow
Visualize
Shared Data
Help
Login or Register
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
Run analyses
Access public data
Log in/out, manage your account
Try Galaxy on the Cloud
Now you can have a personal Galaxy within the infinite Universe
Tweets by @galaxyproject

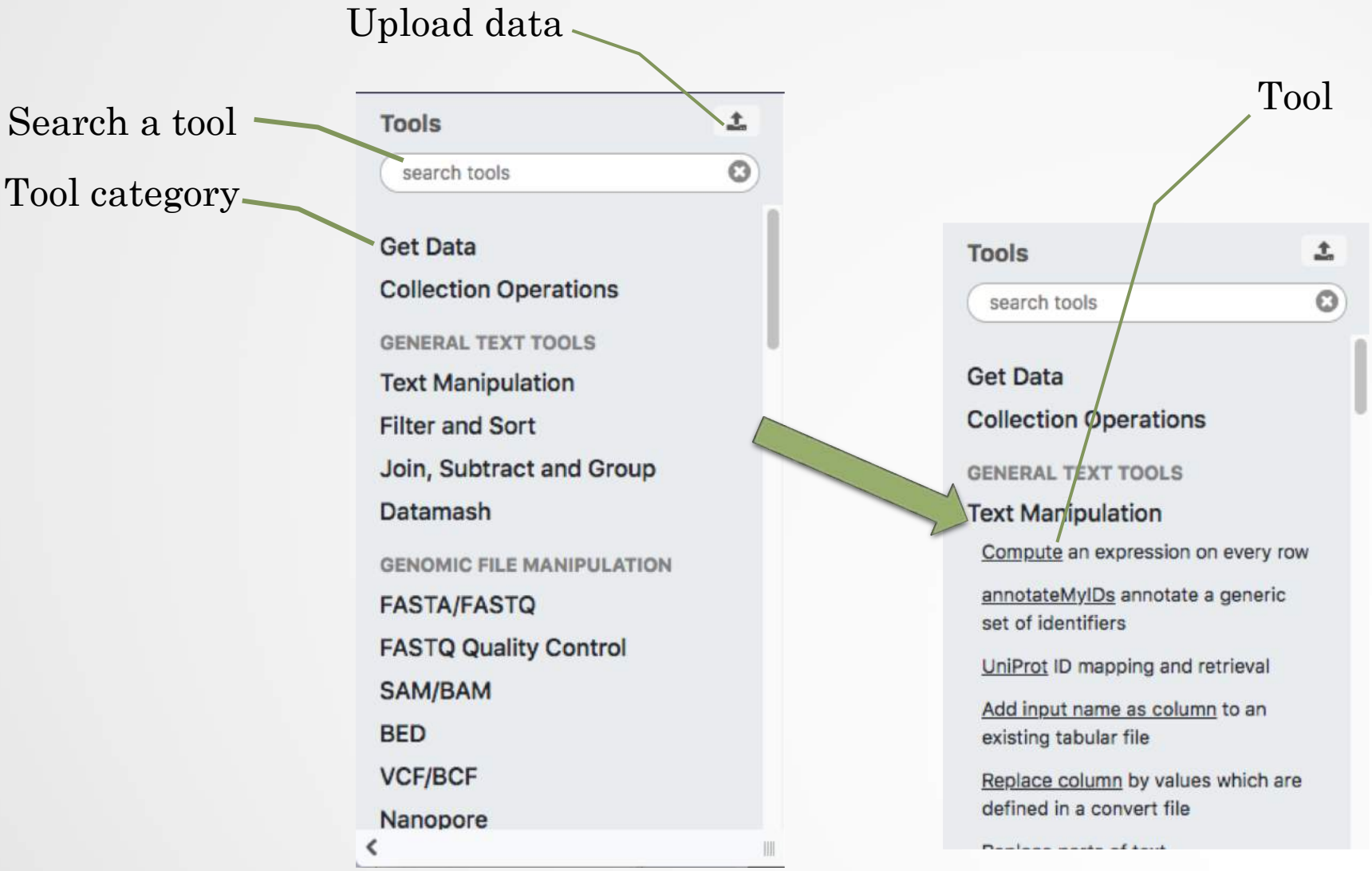
Exercise 1 : Log in

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

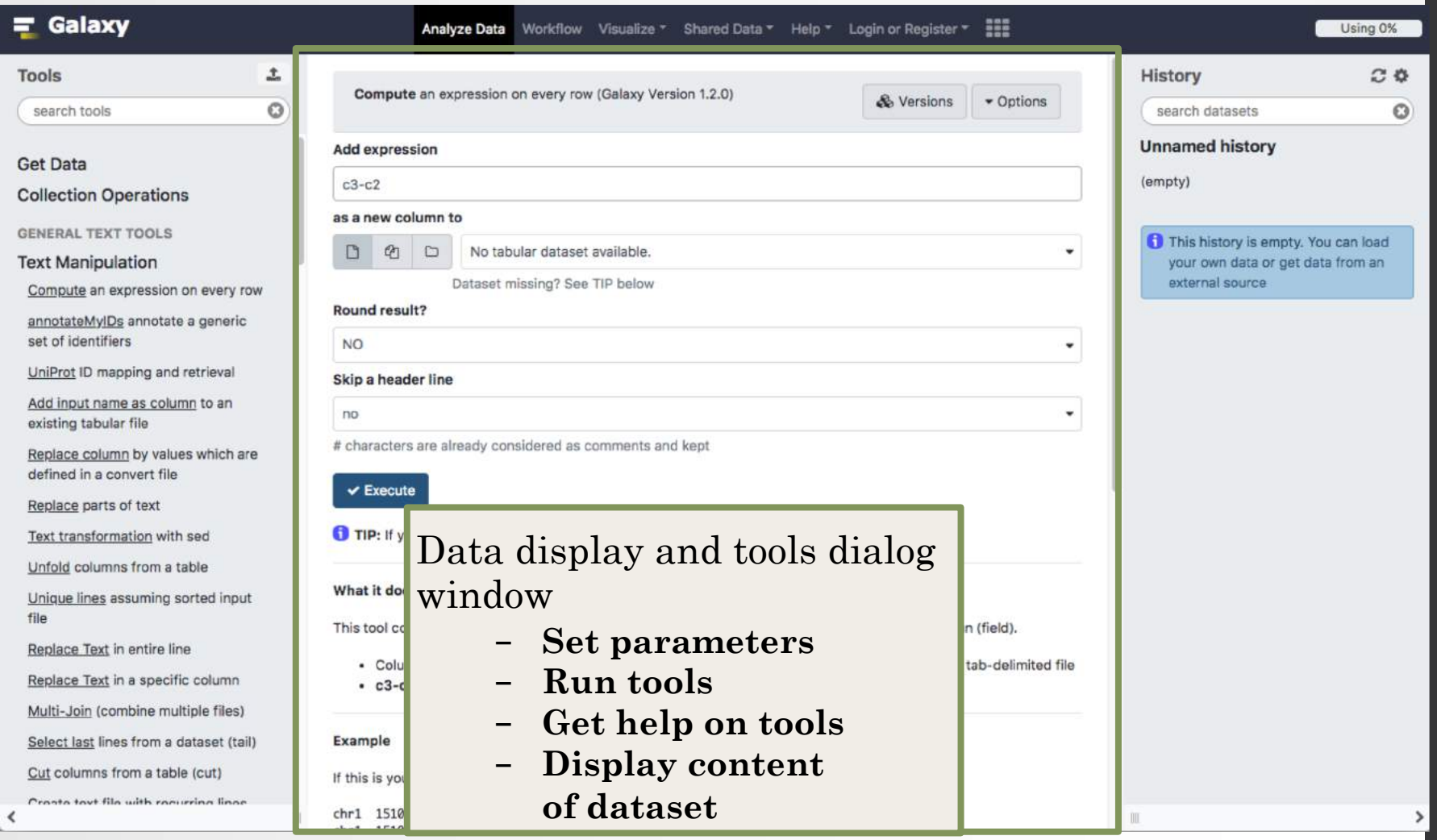
Tool Panel / Run analyses



Tool Panel / Run analyses



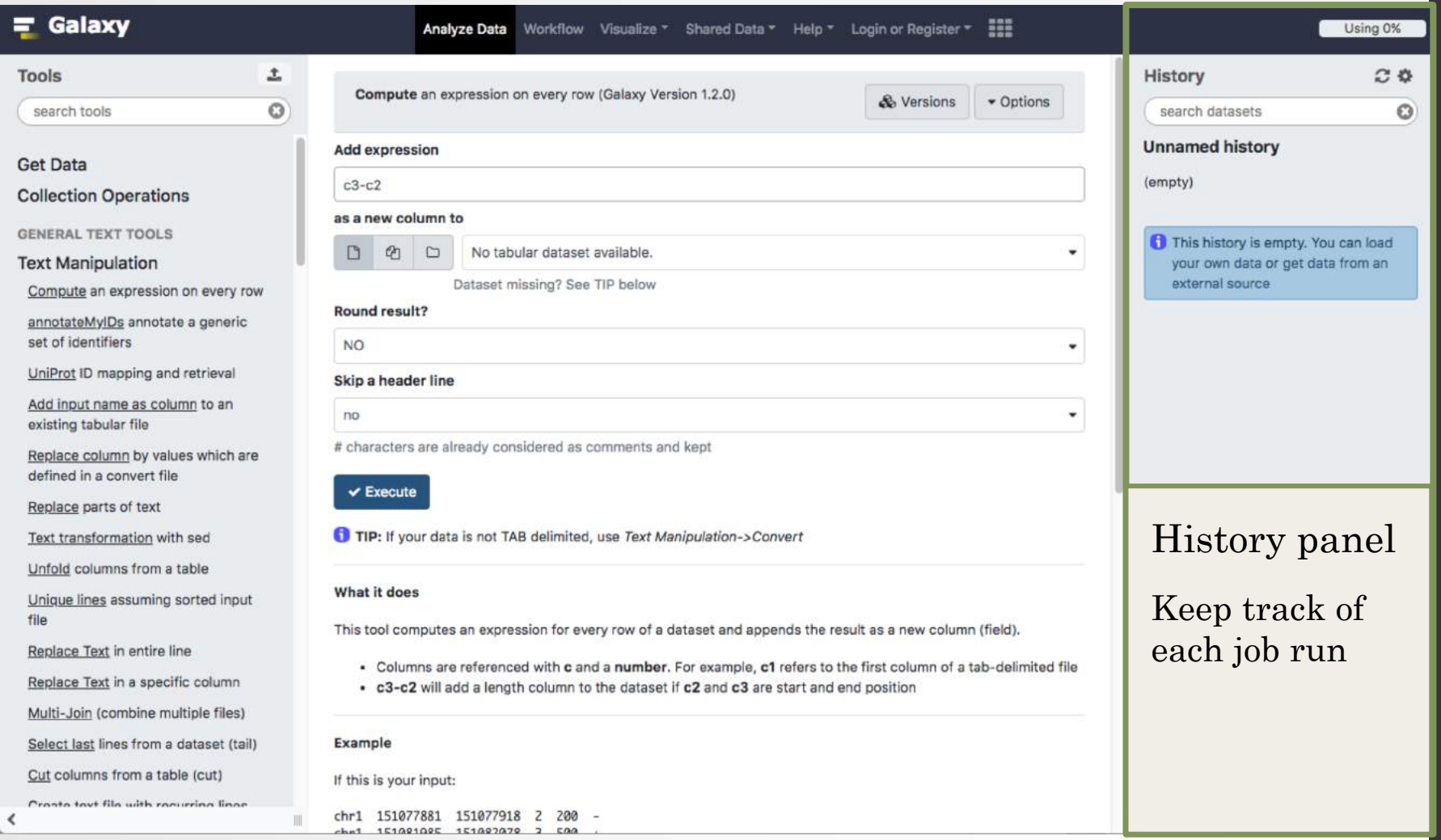
Tools dialog window



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

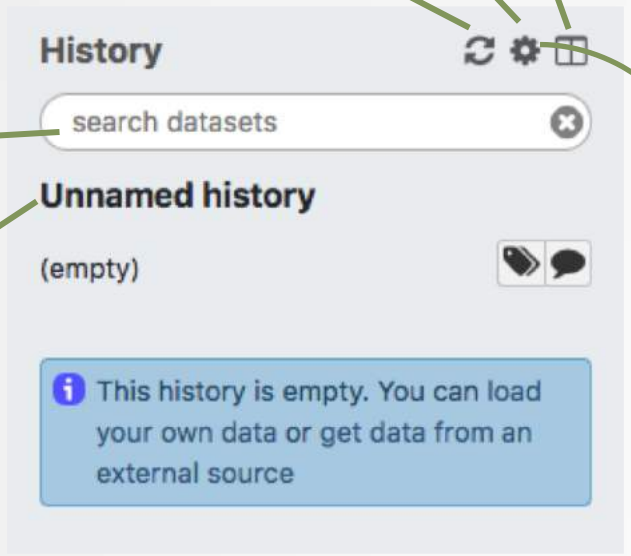
View all histories

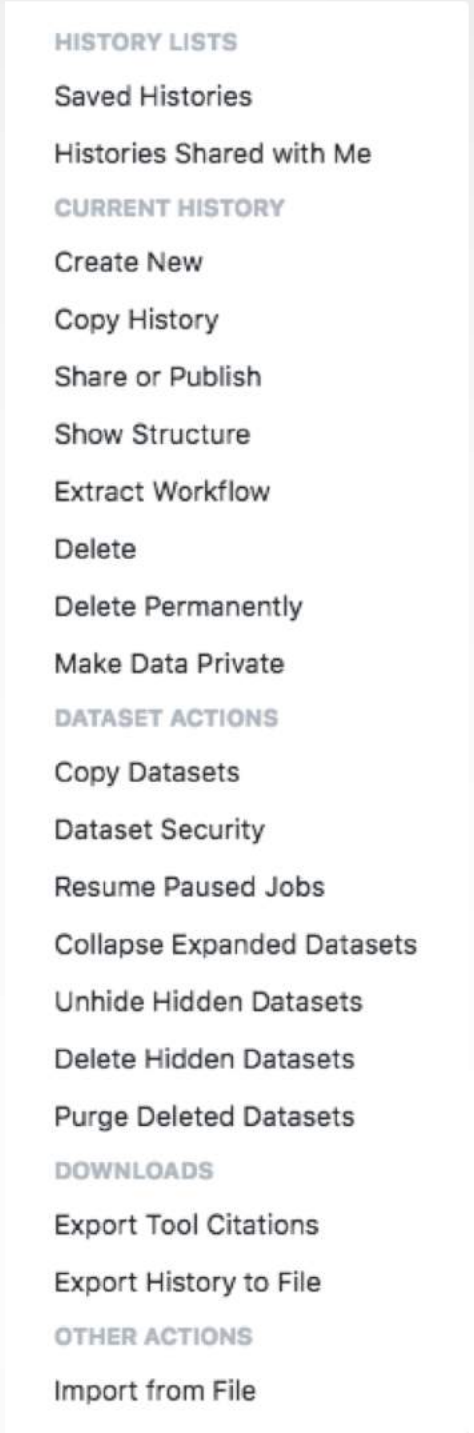
History options

Refresh History

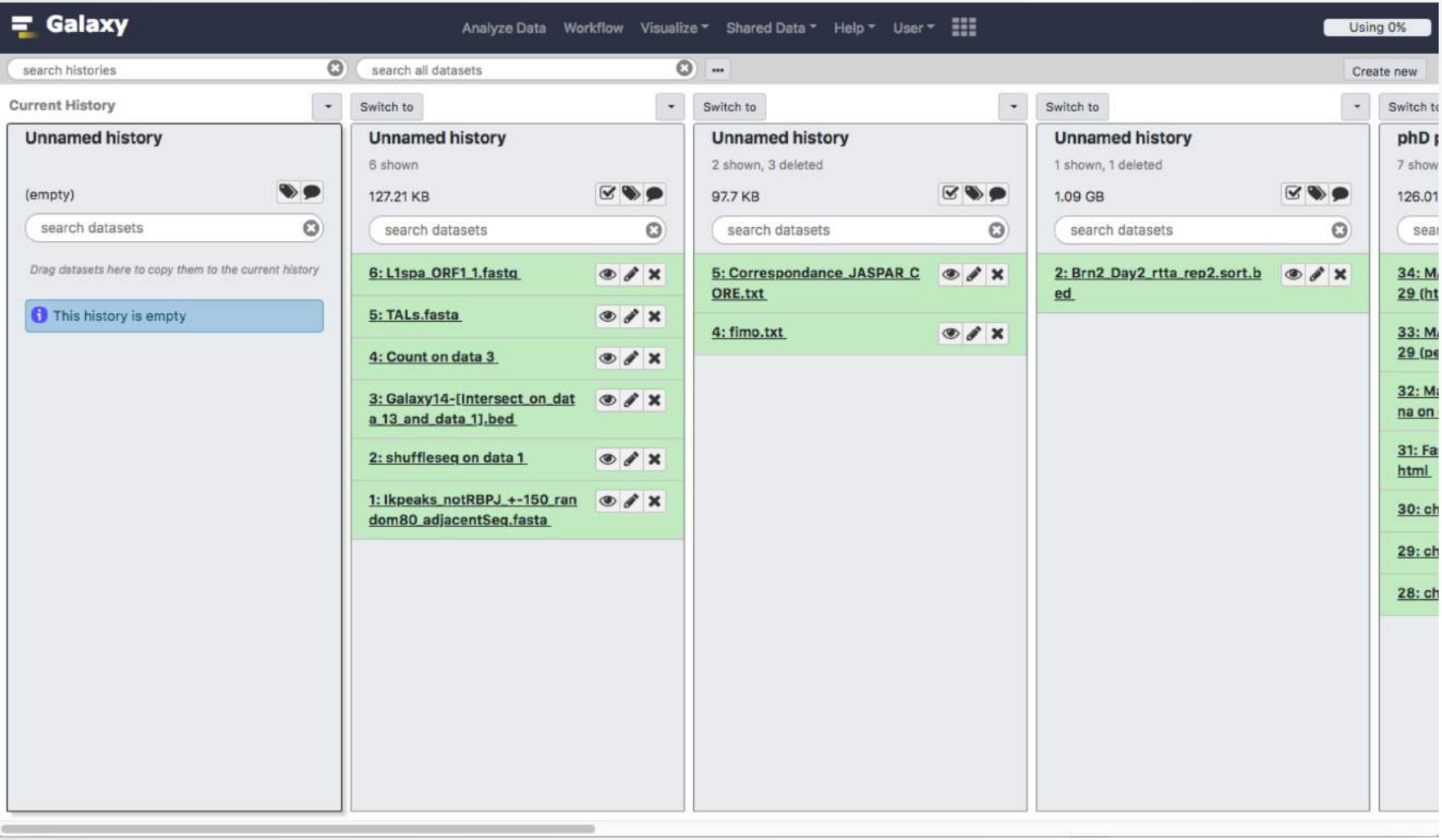
Search datasets

History name





View all histories



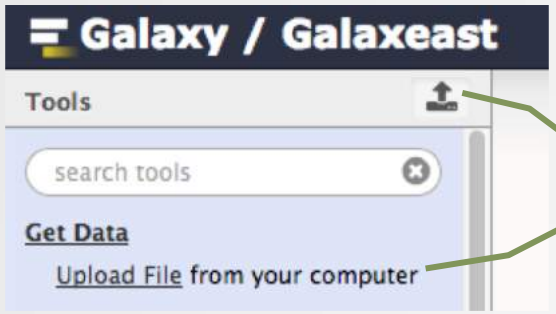
Exercise 2 : History

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

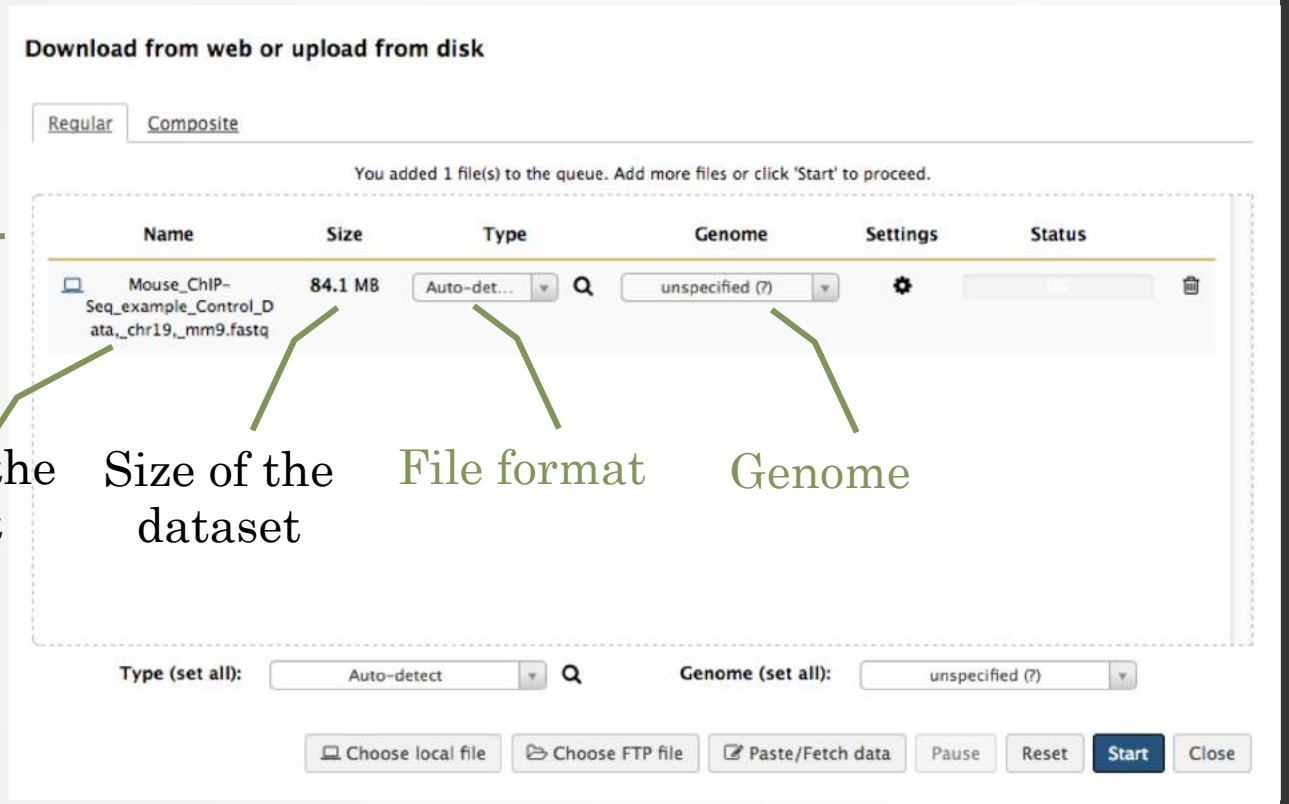
Import data into Galaxy

- 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



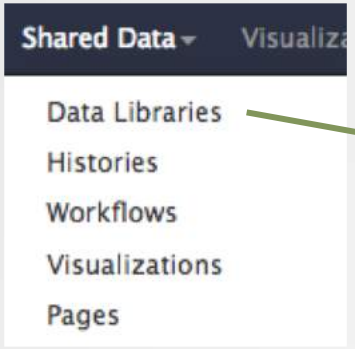
Name of the dataset

Size of the dataset

File format

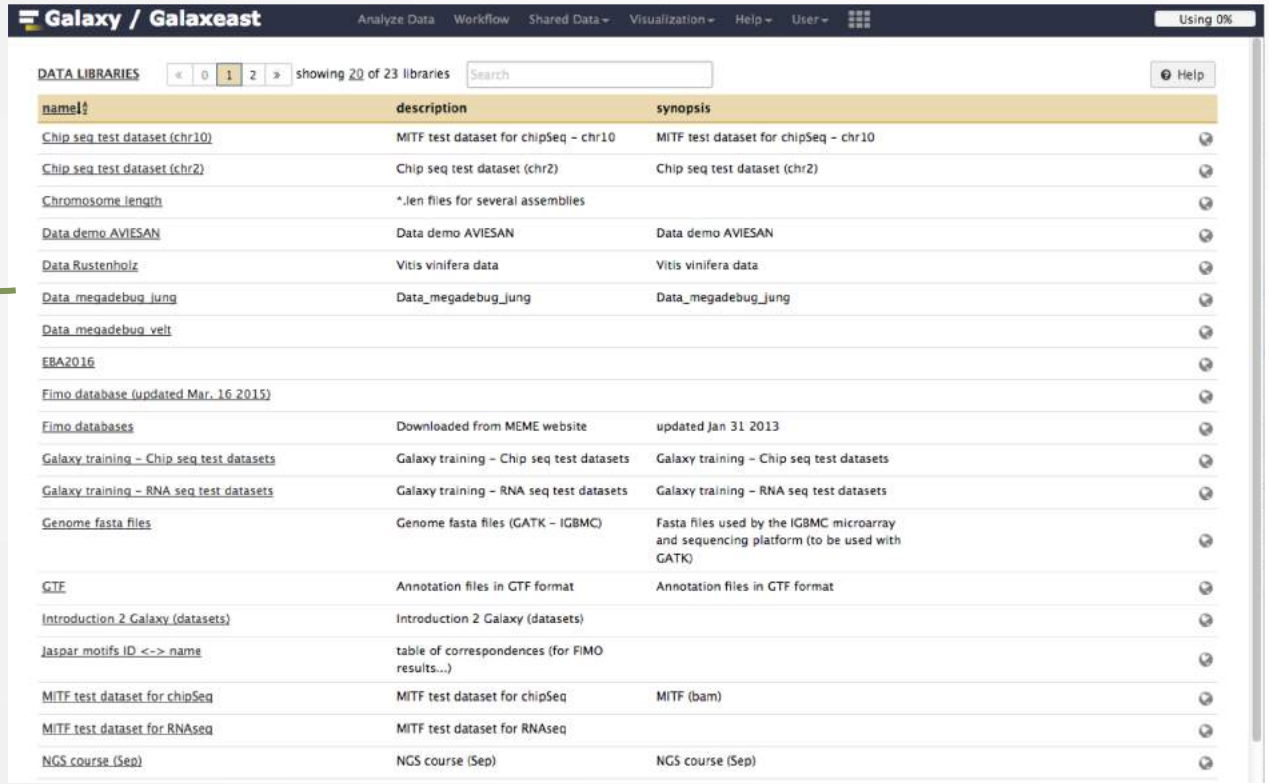
Genome

Import shared data (data libraries)



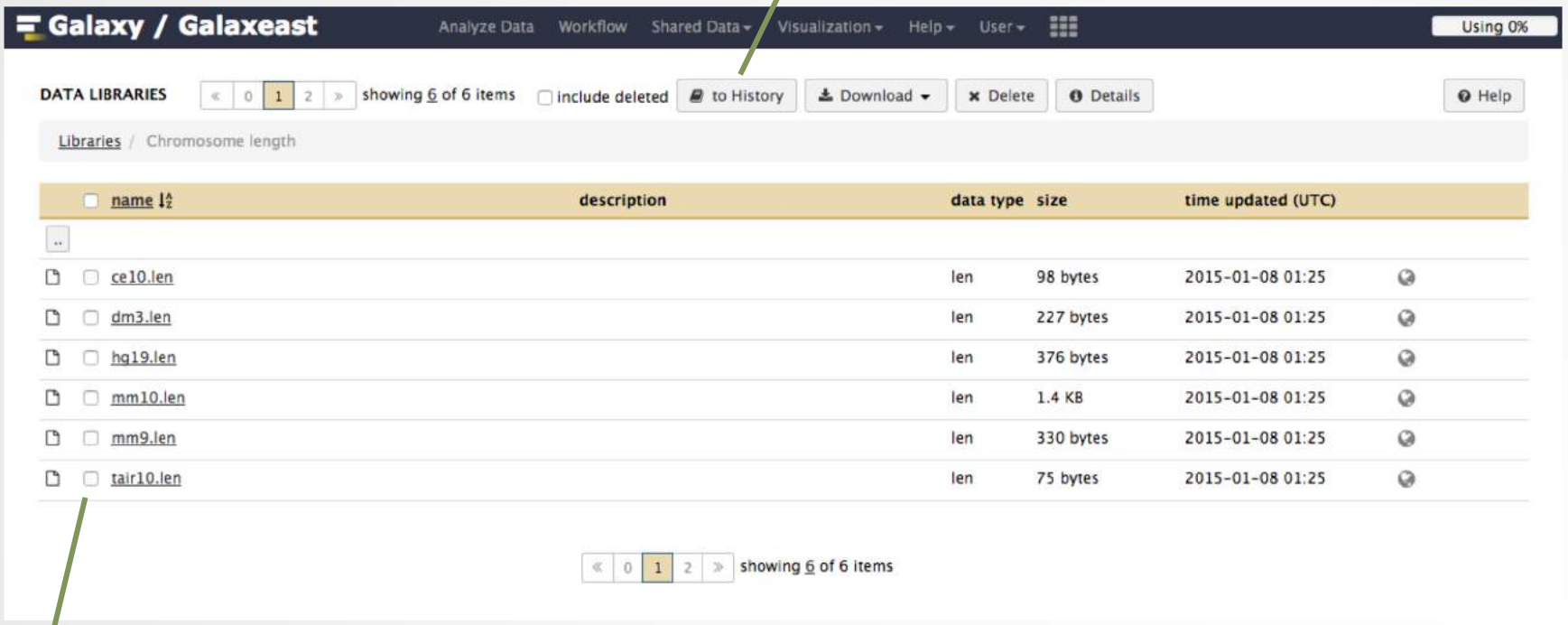
(Top menu)

Data Libraries



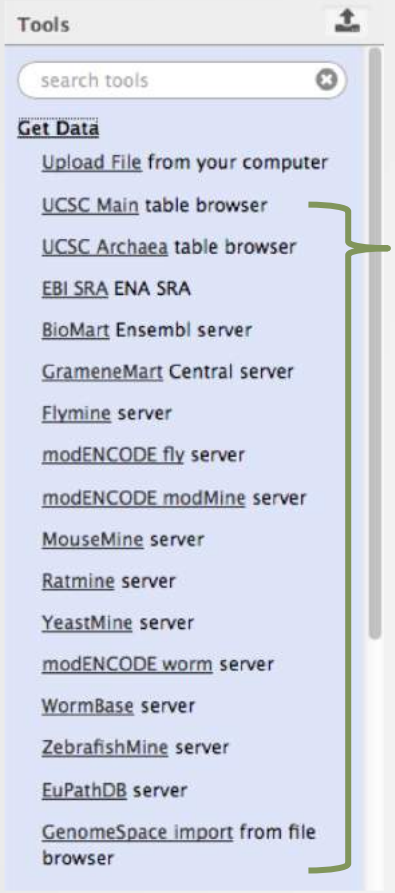
Import shared data (data libraries)

2. Import selected dataset to history

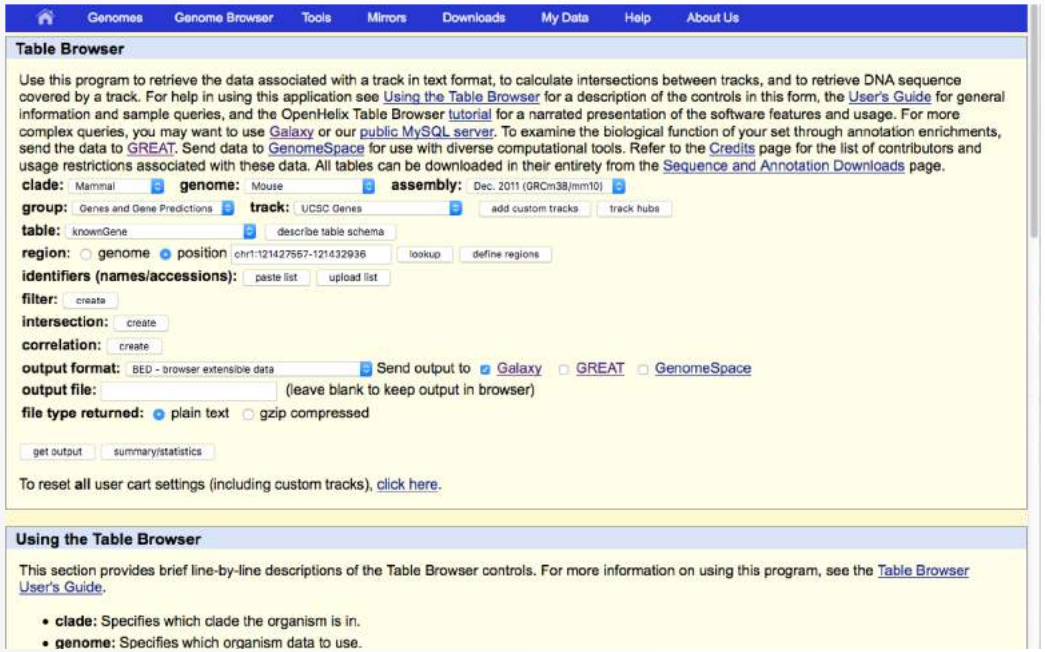


1. Select dataset

Import public data



Browse and import external data from public databases



Exercise 3 : Import data to Galaxy

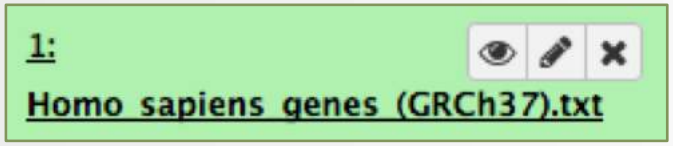
- 1. Import to Galaxy the file siLuc3_S12040.fastq from the “Shared data > Data Libraries > NGS data analysis training > RNAseq > rawdata” to the history called “RNA-seq data analysis”
- 2. You should be in the history “RNA-seq data analysis” (Switch to it if needed)
- 3. Import to Galaxy the file sample.bed.gz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

Datasets/Jobs in the History

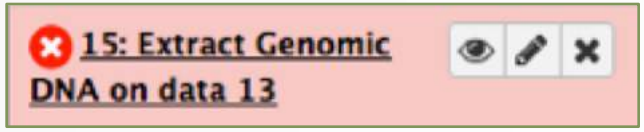
Grey: the job is waiting to run

Yellow: the job is running

Green: the job is successfully done



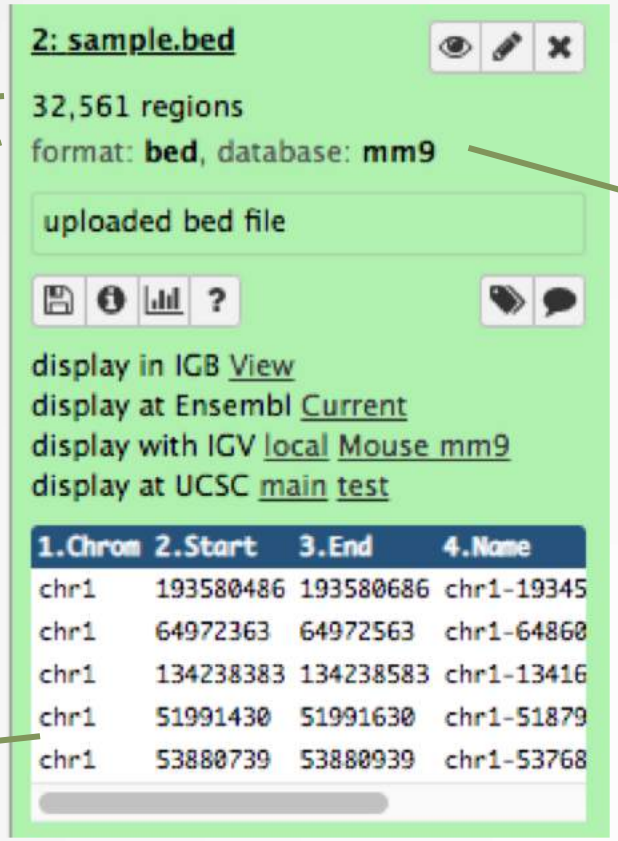
Red: the job encountered a problem



Datasets/Jobs in the History

Number of lines in the file or size of the file

Format



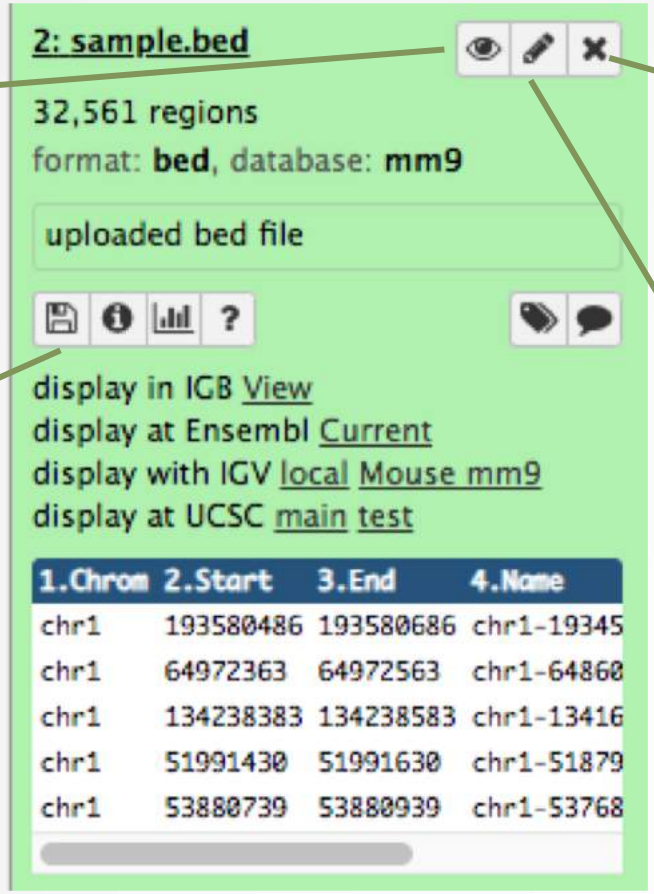
Genome

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

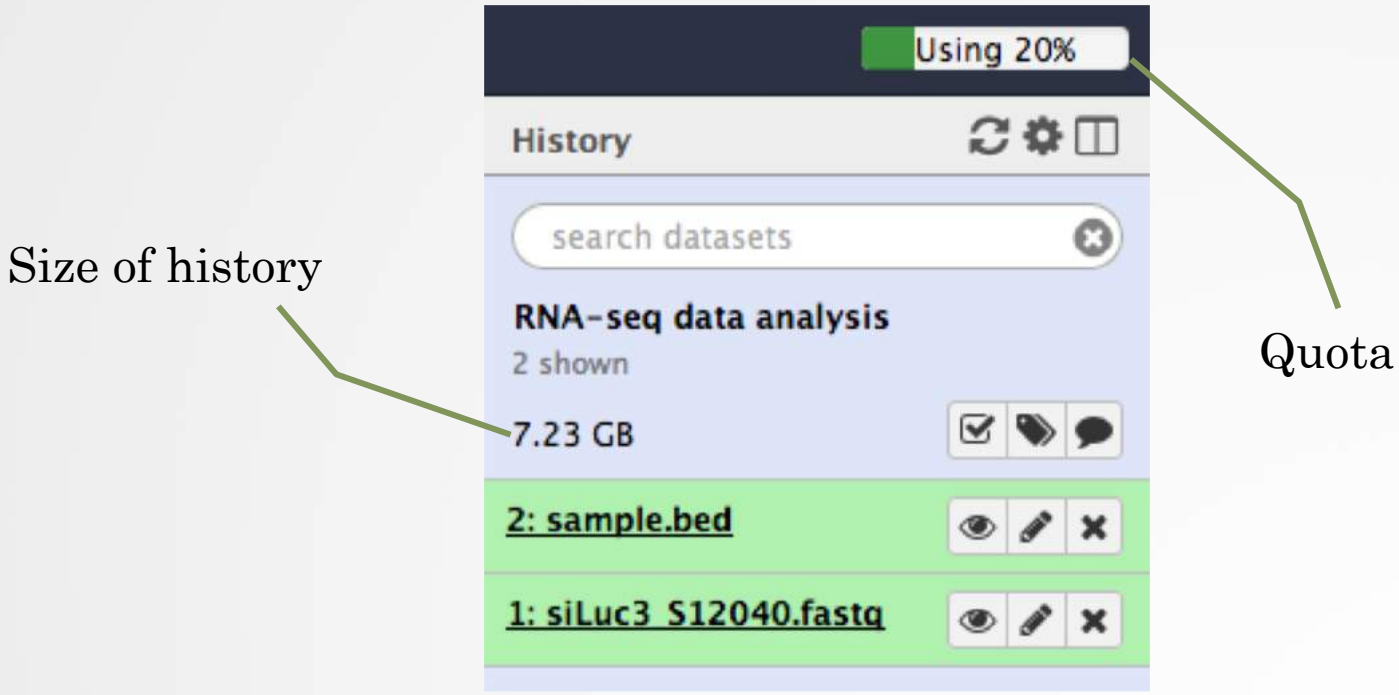
Download dataset



Delete dataset

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

Size of histories and quota



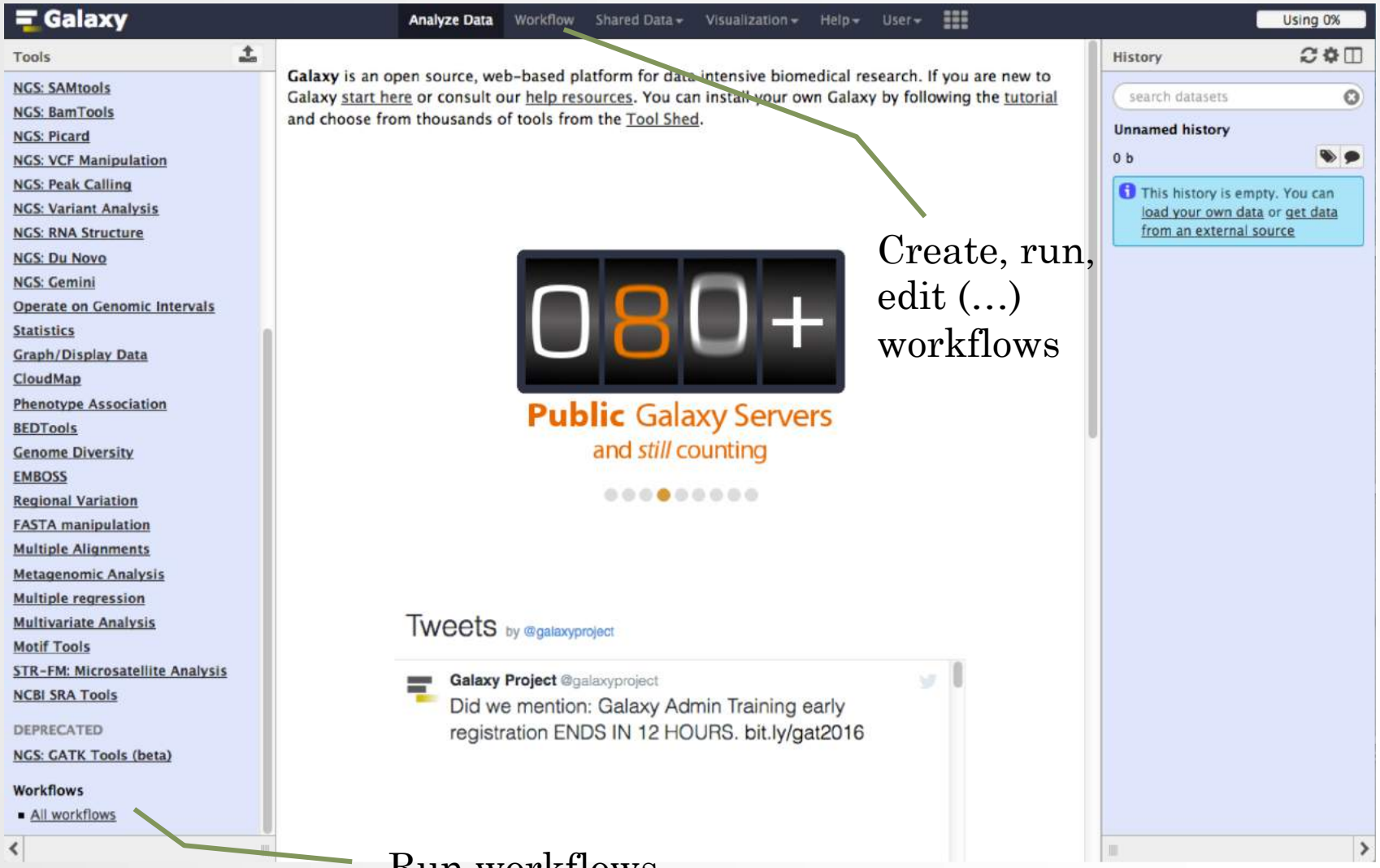
Exercise 4 : remove dataset

- 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



Create, run, edit (…) workflows

Run workflows

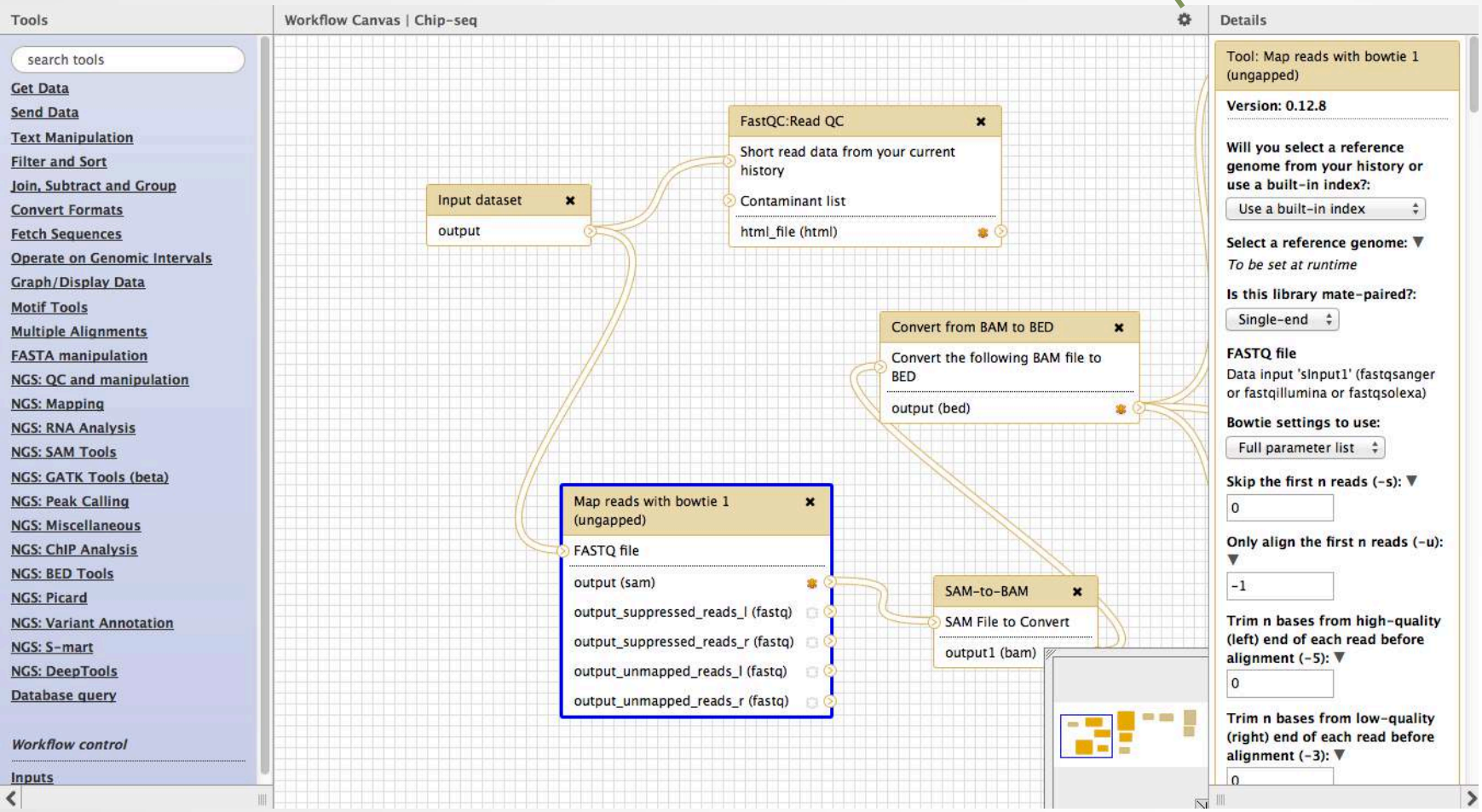
Workflows

Create new workflow

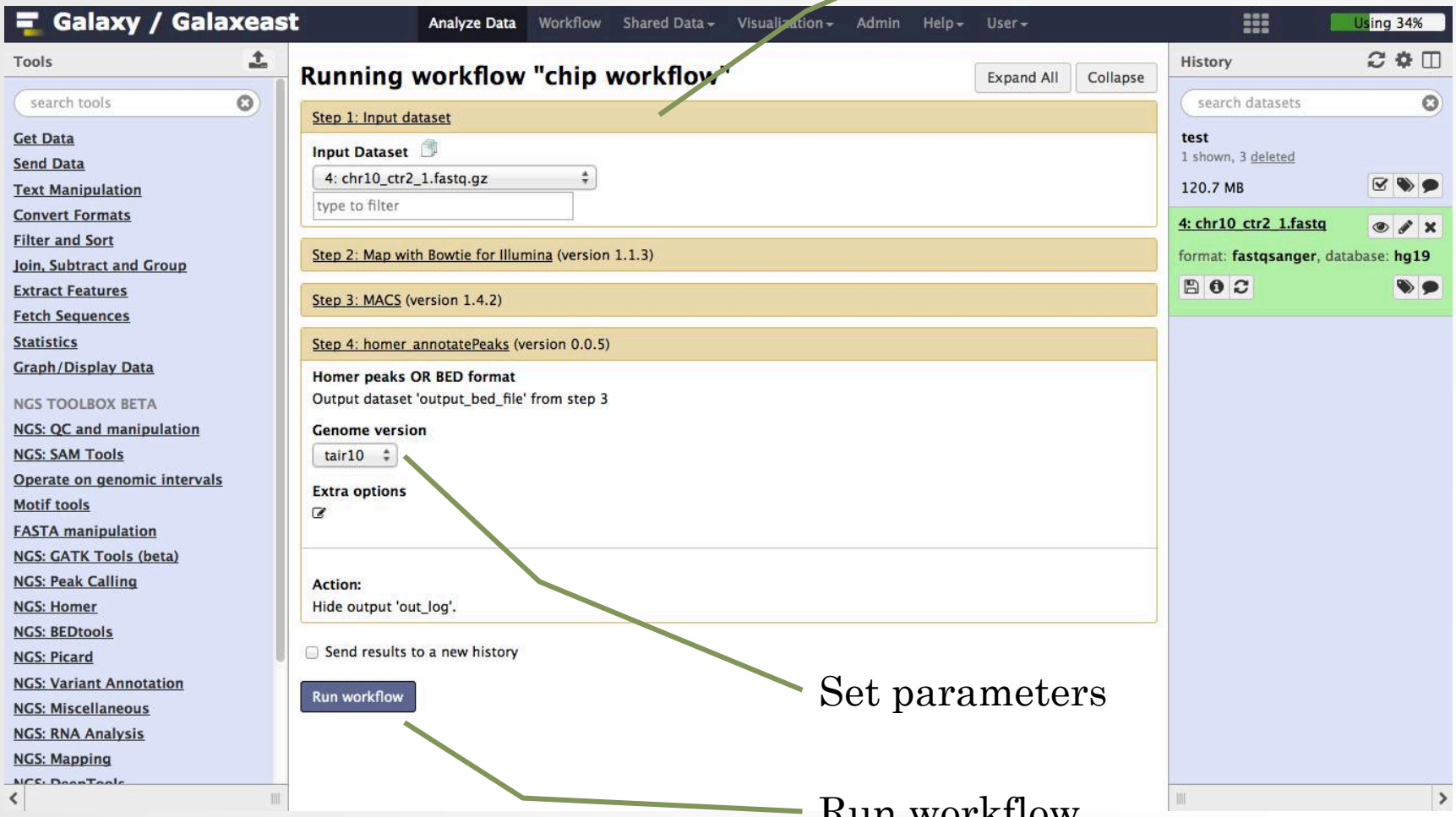
Edit, run, share (…) workflows

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