Introduction à Galaxy

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Introduction

- « Big data » problem : a small facet of a much bigger challenge
- Meaningful **interpretation** of sequencing data has become particularly important
- Big data intrepretation constrains : c.f. « Travailler avec les données NGS »
- Galaxy Project : « **democratization** of biomedical computation so that even the smallest research units with modest budgets are capable of carrying out analyses using appropriate tools in a reproducible fashion »

Democratization

- developing **best practices**
- removing obstacles associated with using heterogenous software on complex high performance computing infrastructure : **accessibility**
- promoting the concept of **transparency** and **reproductibility**

Best Practices : emergency !

- 1000 Genomes Project : a serie of accepted practices for variant discovery
- Galaxy P.I survey (Anton Nekrutenko and James Taylor)
- 2011 : 299 articles that explicitly cite the 1000 genomes project :
  - 10/299 : used tools recommended by the consortium for mapping and variant discovery
  - 4/299 : used the whole workflow

=> The difficulty of reproductibility

Reproductibilty : is it so easy ?

- NGS analysis is constant flux
- Not only ONE best practice
- Apply to non-model organisms
- Researchers choose to use more straightforward approaches
- Best pratices, accessibility, transparency, reproductibility : the solution with **integrative ressources** ?

Integrative ressources

- Integratives ressources, integrative frameworks : bring together diverse tools under the umbrella of unified interface
- BioExtract, GenePattern, GeneProf, Mobyle
- Galaxy

Galaxy and « meaningfull interpretation »

- a.k.a how Galaxy embrace accessibility, reproductibility and best practices ?
- **Accessibility** : use computational approaches without programming or informatics expertise
- **Reproductibility** : reproduce experimental results
- **Transparency** : analysis can easily be communicated or understood

Accessibility

Provide a unified, web based interface for bioinformatics analysis

Galaxy Items (1 /2)

tools

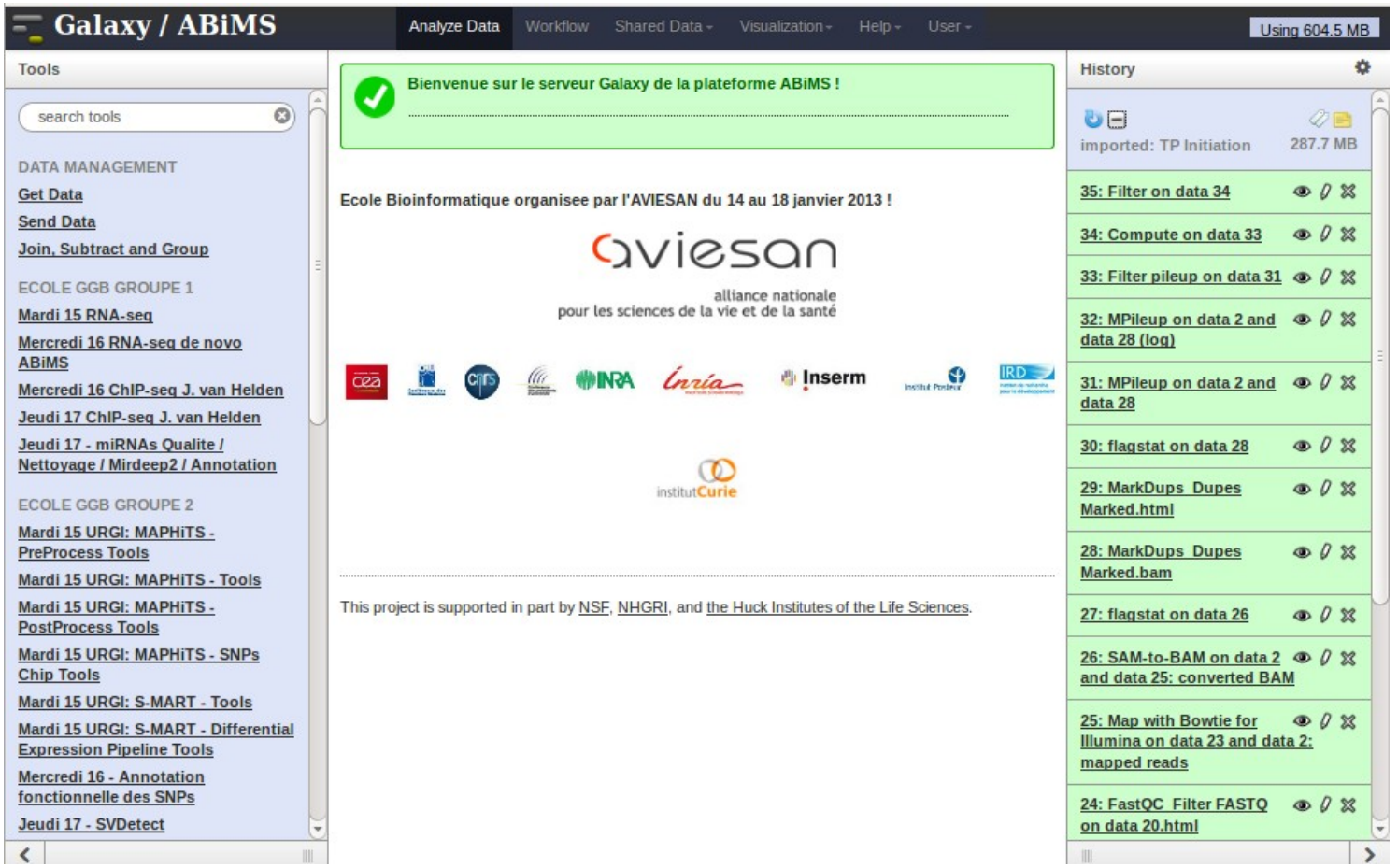
Dataset

history

2 distributions

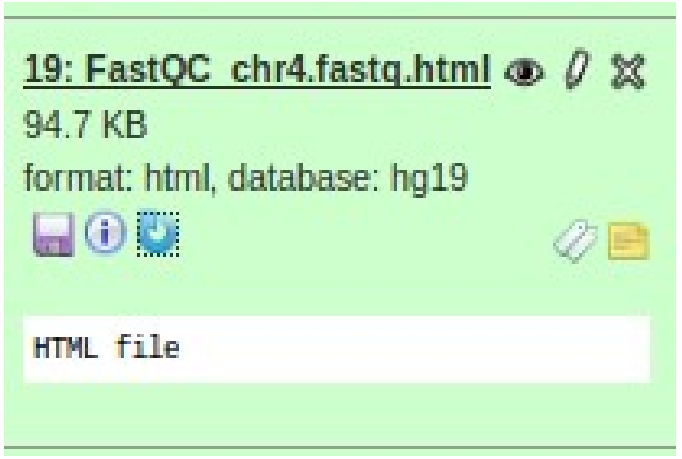
- 2 distribituions : central (https://main.g2.bx.psu.edu/) and « dist »
- Dist : create your own analysis environment
  - Follow the model Galaxy use for integrating tools
  - A tool = a simple piece of software (cmd line)
  - A developper write a config file (how to run the tool, input and output param)
  - And … Galaxy works with the tool abstractly : automatic generating web interfaces

Your own analysis env, example



Reproductibility

- Galaxy captures **metadata**
- For each step in an analysis : input dataset, tools used, parameters values and output dataset
- With these metadata users can reproduce the analysis



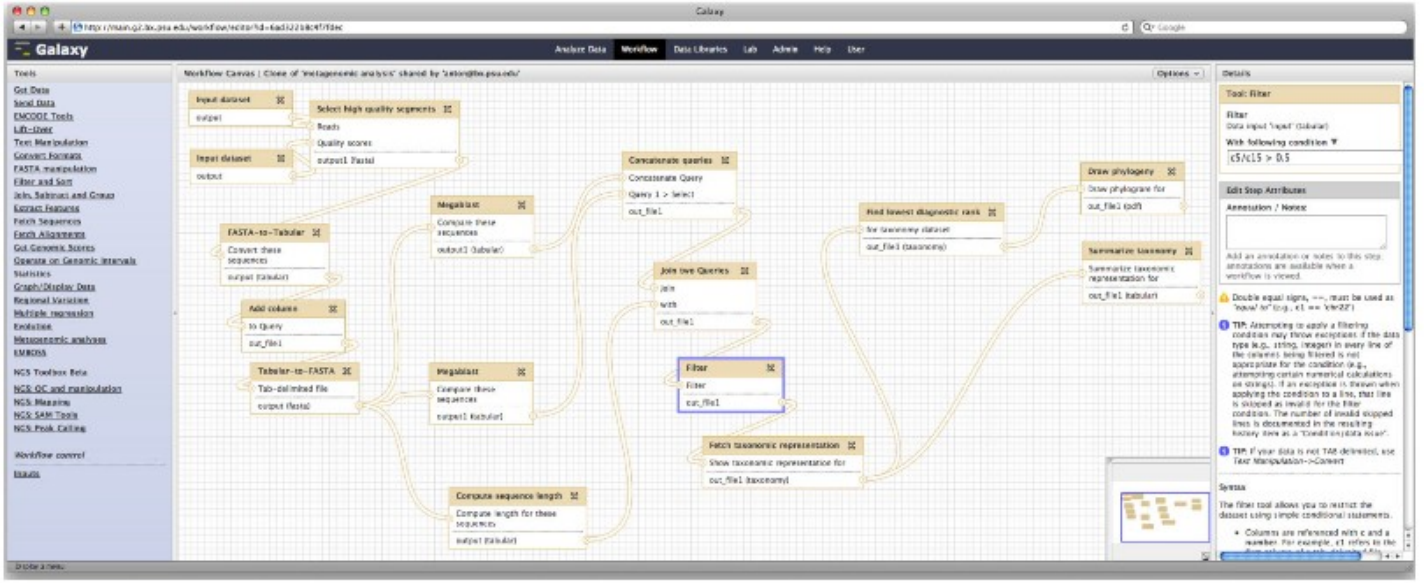
Reproductibility

- But what about the **intent** of the analysis ?
- Use **annotations** and **tags** (c.f. web practices) to express the intent
- Annotations and tags = user metadata

Galaxy Items (2/2)

- And … if I want to reproduce the whole analysis ?
- Galaxy use **workflows**
- Create workflows from scratch, or create from history of your analysis

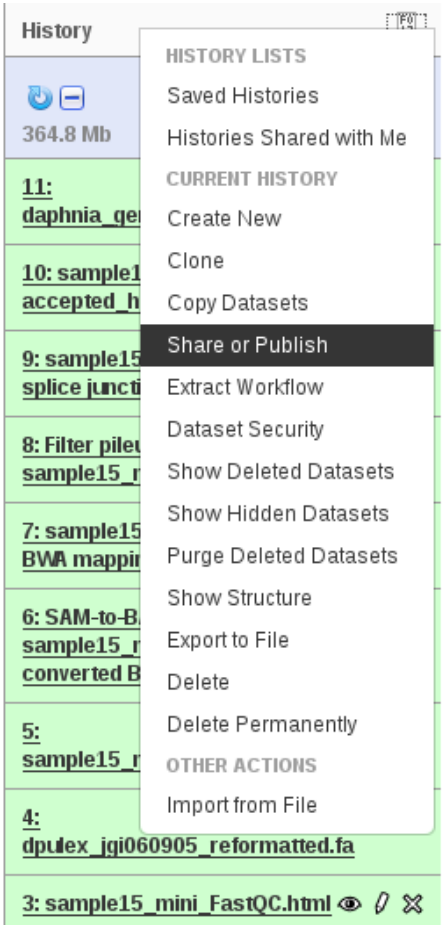
Workflow (example)



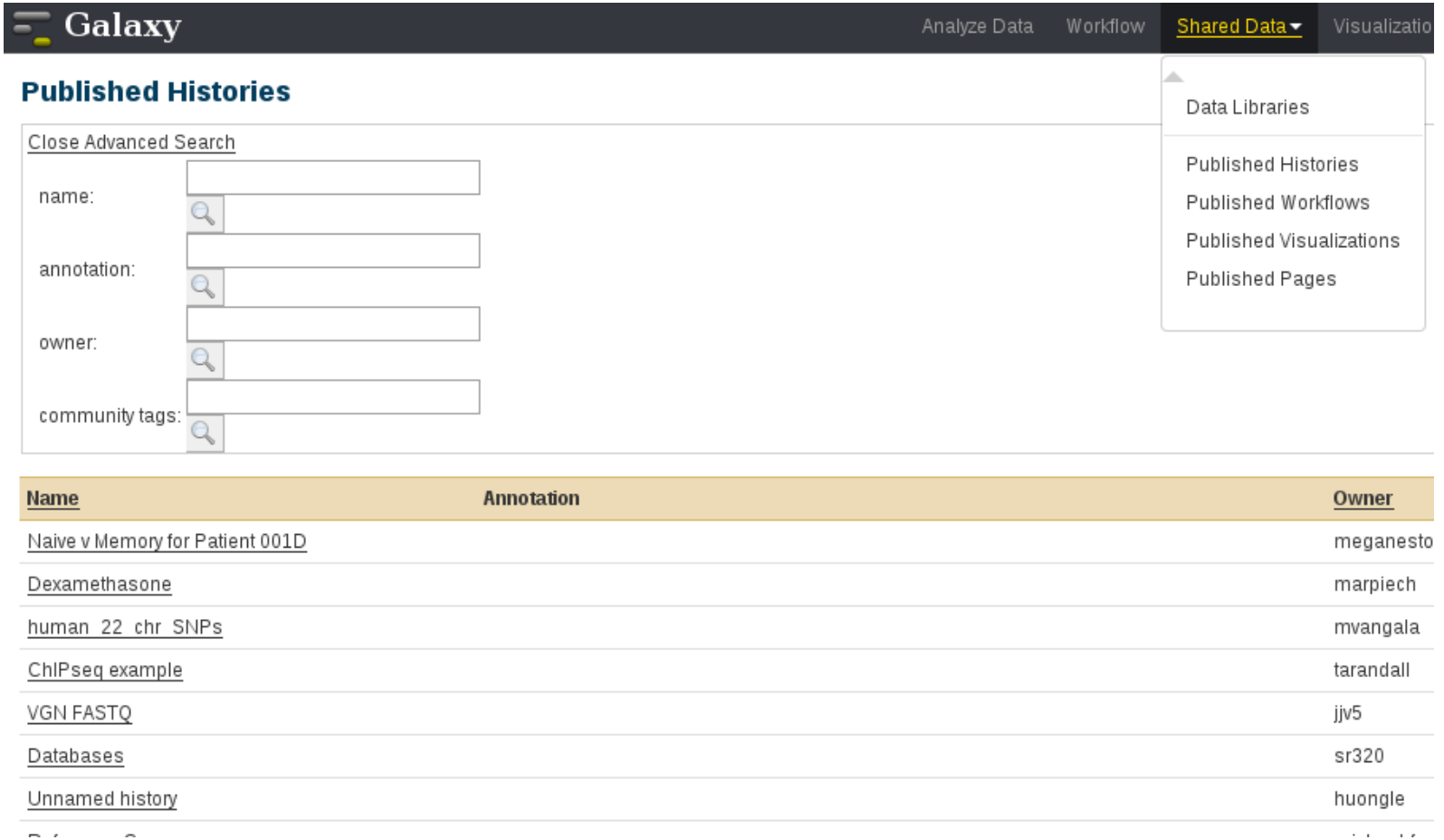
Transparency

- Transparency : enable user to share and communicate their experimental results and output
- **3** elements for Galaxy transparency
- 1 : Galaxy **sharing model** = sharing a Galaxy item* : dataset, histories, visualisation and workflows
- 2 : search shared item from **Galaxy Web Based framework**

Sharing model : example



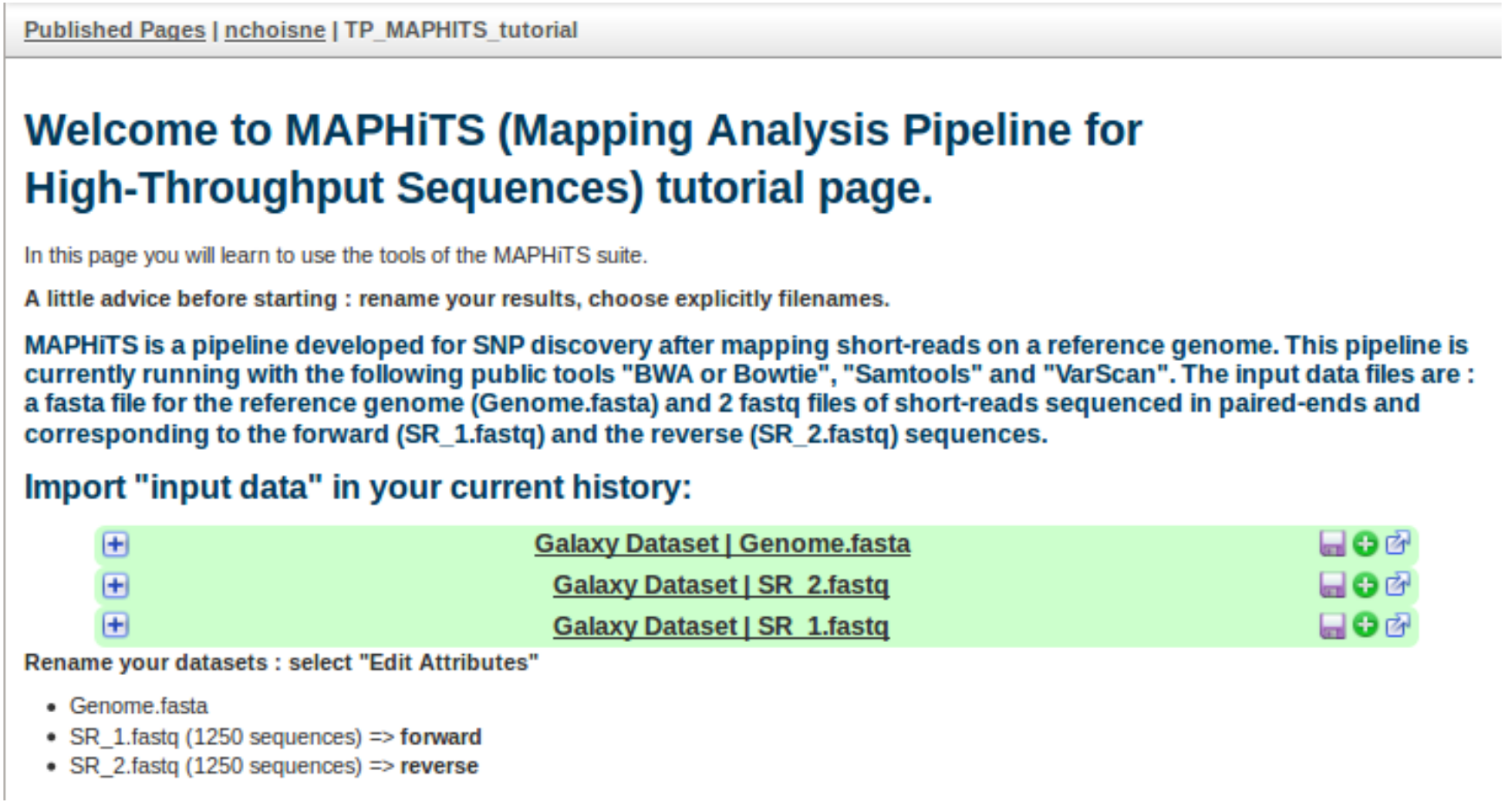
Search shared item : example



Transparency

- 3 : Galaxy **pages**
- Web based document that enable user to communicate their experiement
- A mix of text and graph describing the experiment analysis
- embedded Galaxy items in the page used for the experiment
- Pages and Galaxy sharing model

Page (example)



Published Pages | nchoisne | TP_MAPHITS_tutorial

Welcome to MAPHiTS (Mapping Analysis Pipeline for High-Throughput Sequences) tutorial page.

In this page you will learn to use the tools of the MAPHiTS suite.

A little advice before starting : rename your results, choose explicitly filenames.

MAPHiTS is a pipeline developed for SNP discovery after mapping short-reads on a reference genome. This pipeline is currently running with the following public tools "BWA or Bowtie", "Samtools" and "VarScan". The input data files are : a fasta file for the reference genome (Genome.fasta) and 2 fastq files of short-reads sequenced in paired-ends and corresponding to the forward (SR_1.fastq) and the reverse (SR_2.fastq) sequences.

Import "input data" in your current history:

Galaxy Dataset | Genome.fasta

Galaxy Dataset | SR_2.fastq

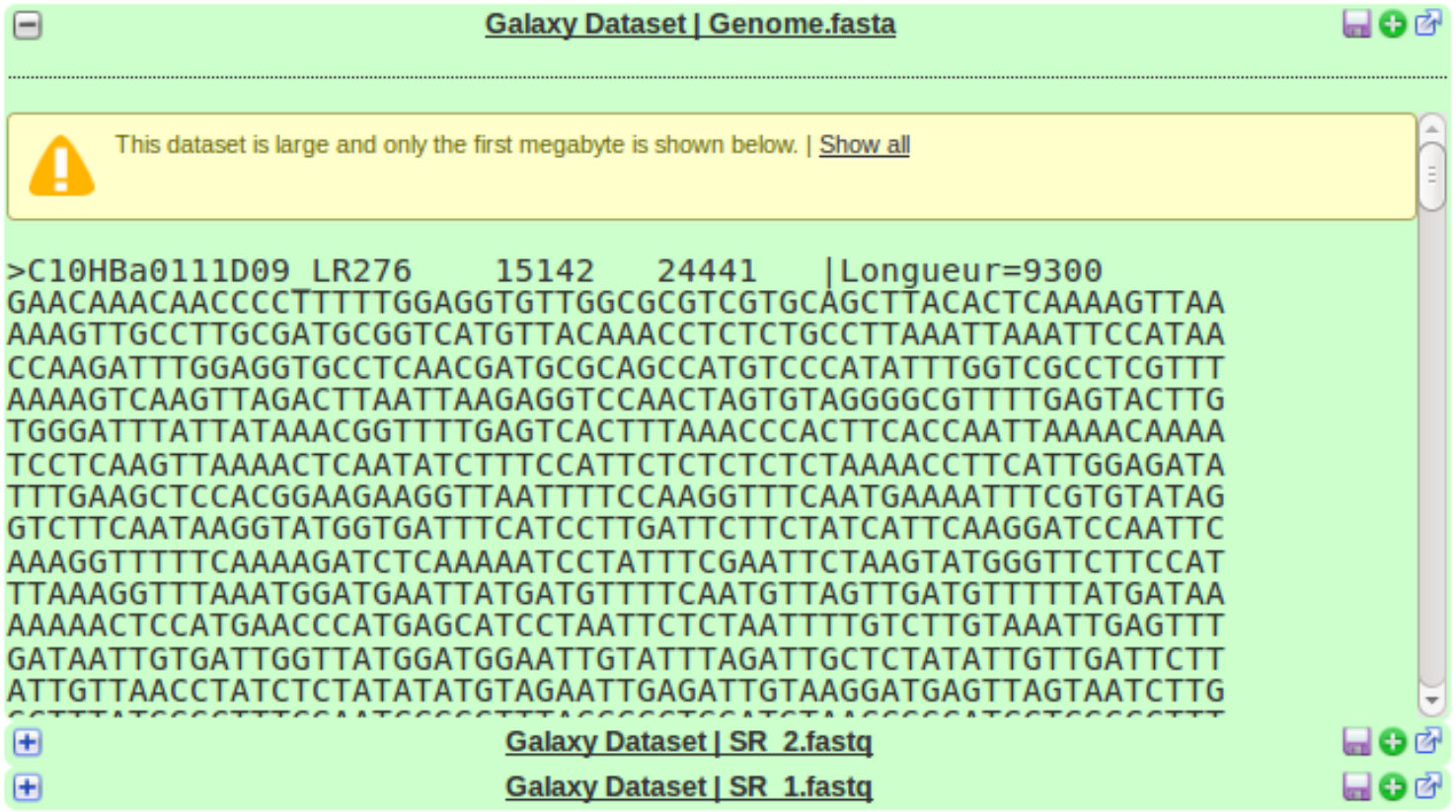
Galaxy Dataset | SR_1.fastq

Rename your datasets : select "Edit Attributes"

- Genome.fasta
- SR_1.fastq (1250 sequences) => **forward**
- SR_2.fastq (1250 sequences) => **reverse**

Embedded Galaxy item (example)

Import "input data" in your current history:



Rename your datasets : select "Edit Attributes"

References and links

- Galaxy Project home page : http://galaxyproject.org/
  - Use galaxy : galaxy-central, a free public server
  - Get a galaxy distribution
  - Learn galaxy : tutorials, screencast
  - Get involved : mailing lists and wiki
- Next-generation sequencing and data interpretation : enhancing reproductibility and accessibility. Anton Nekrutenko ; James Taylor – 2012 – Nature Review Genetics.
- Galaxy : a comprehensive approach for supporting accessible, reproductible and transparent computational research in life science. Jeremy Goecks *et al.* - 2010 – Genome Biology