

# Reformation of Galaxy for local research

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## Abstract

Galaxy<sup>†</sup> is an open source platform for computational study of biomedical data, in particular the intensive data generated by next generation techniques, without requiring any prior knowledge of computer programming. Galaxy has expanded largely in scale in the past few years to accommodate newly emerged techniques, tools and user's requirements, making it one of the most comprehensive collections of tools for bioinformatics analysis.

Galaxy is currently organized in a task-oriented way, specific and straightforward, it however lacks the strength of systematic consideration of biological background of data, experiment design, and purpose of the study.

In this work, we have reformatted Galaxy into a new layout with improved specificity through emphasizing and extending tools in demand for research *in situ*, apart from keeping the most essential tools already available in Galaxy. The newly formatted BSR/Galaxy has been organized in a project-oriented way by organizing tools into major sections based on the experiment design, data type and purpose of study. In particular, each section has been organized in a way to form a natural flow of work, from data initial processing to result presentation, along with a detailed tutorial covering several standard workflows tailored for the section and the specific types of study. The reformatted BSR/Galaxy has provided a more user-friendly and analysis-efficient interface for computational study of biomedical data.

## Analysis modules

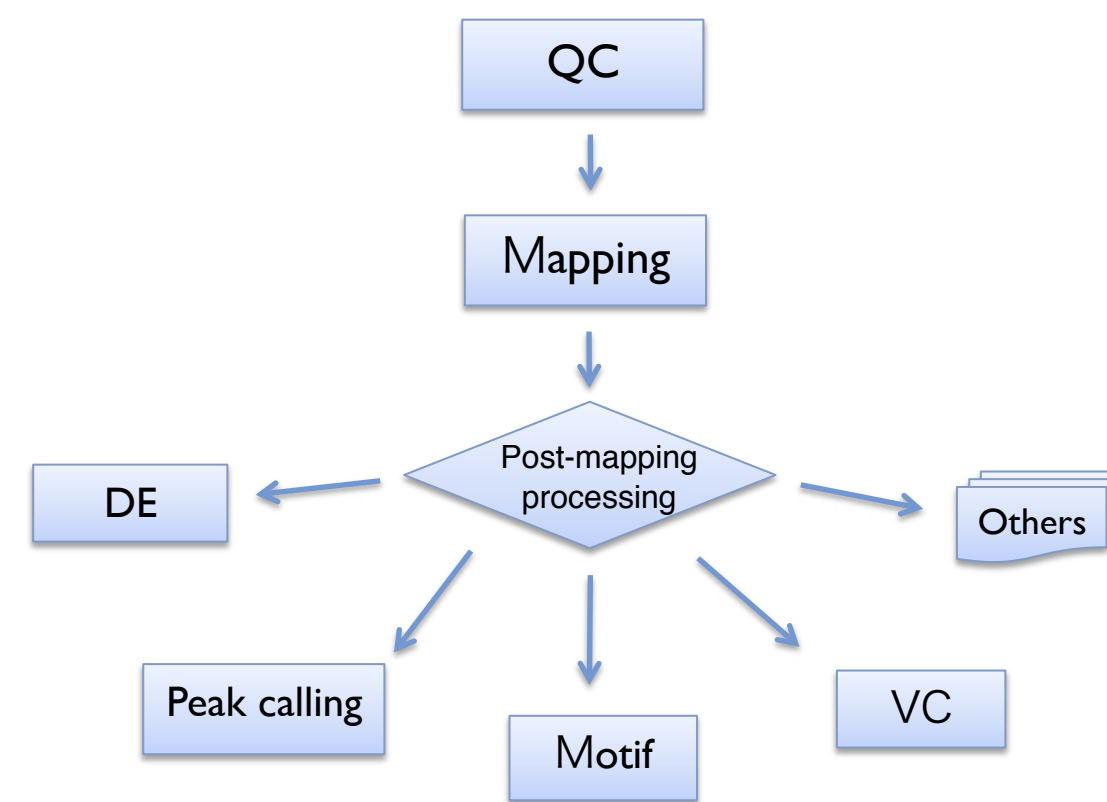
RNA-Seq Analysis

ChIP-Seq Analysis

Variance Calling

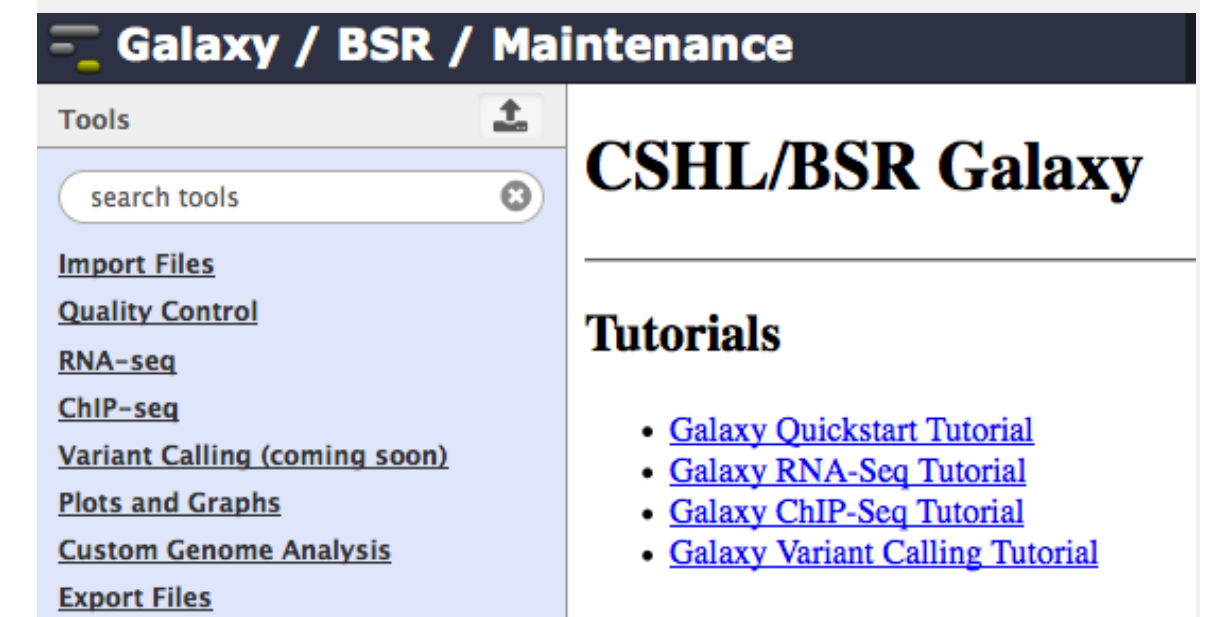
Customized Genome

The BSR/Galaxy has been reformatted into a project-oriented layout with each module contains tools designed only for the project/purpose of study and have been organized in the order to form a complete workflow.



## Support

The BSR/Galaxy has provided documentation and several tutorials on performing NGS analyses



The BSR/Galaxy supports multiple ways of data exchange inside and outside the laboratory

### Import/Export

- Personal computers
- Servers in the laboratory
- Genome browsers

### Sharing

- Data
- Analysis histories
- Customized workflows

Two additional sections provide collections of UNIX style interfaces & toolkits

### Utilities

- Text manipulation
- Table manipulation
- Convert formats
- Statistics
- Genome browsers
- Annotation
- Graphics

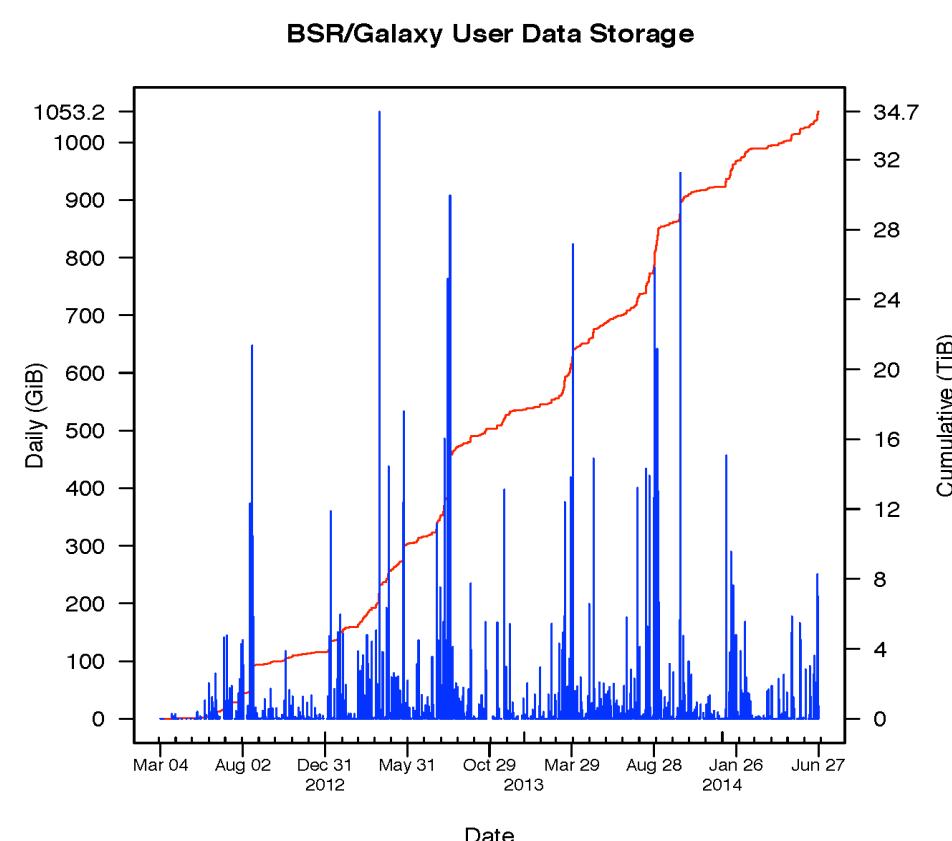
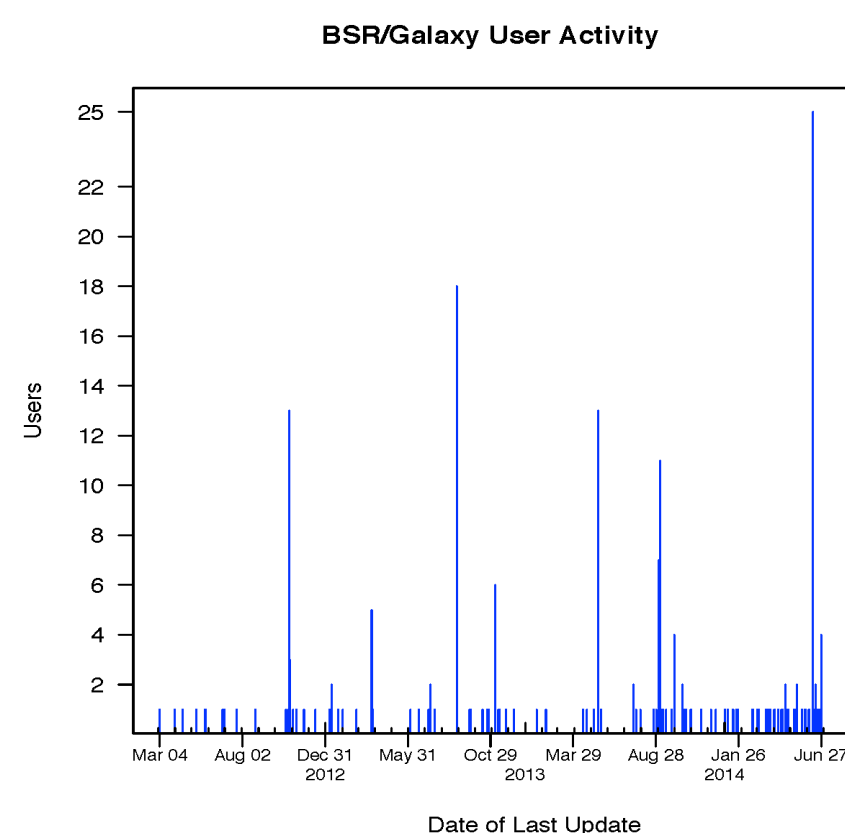
### Toolkits

- BEDTools
- SAMTools
- FASTX Toolkit
- PICARD

### References:

- Giardine B. *et al.* 2005. *Genome Research*. 15:1451  
Goecks J. *et al.* 2010. *Genome Biology*. 11:R86  
Blankenberg D. *et al.* 2010. *Molecular Biol.* Chapter 19: Unit 19.10.1

## BSR/Galaxy usage



NGS related analysis is the major usage of BSR/Galaxy

