Galaxy

https://galaxy.rcc.fsu.edu/

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Galaxy

FSU researchers now have access to an instance of Galaxy at the Research Computing Center. Galaxy is a web-based framework for accessible, reproducible and transparent biological computing.

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Importing data into Galaxy

Small files can be added to a Galaxy history using the upload tool.

Larger files that reside on our Panfs file system can be linked to in Galaxy and added to your history.

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Running jobs in Galaxy

Galaxy allows local jobs and jobs submitted to the HPC cluster.

HPC jobs are submitted as the logged in user. Condor jobs will always be submitted as the user galaxy.

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What is Galaxy?

"Integrated tool management system with a user-friendly interface"

- Variety of tools
  - same tools as stand-alone version
  - mostly aimed at NGS analysis
- Graphical interface
  - no command line
  - easy navigation through tools options
- Integration

  easy data management throughout pipeline (input -> output -> input -> ...)

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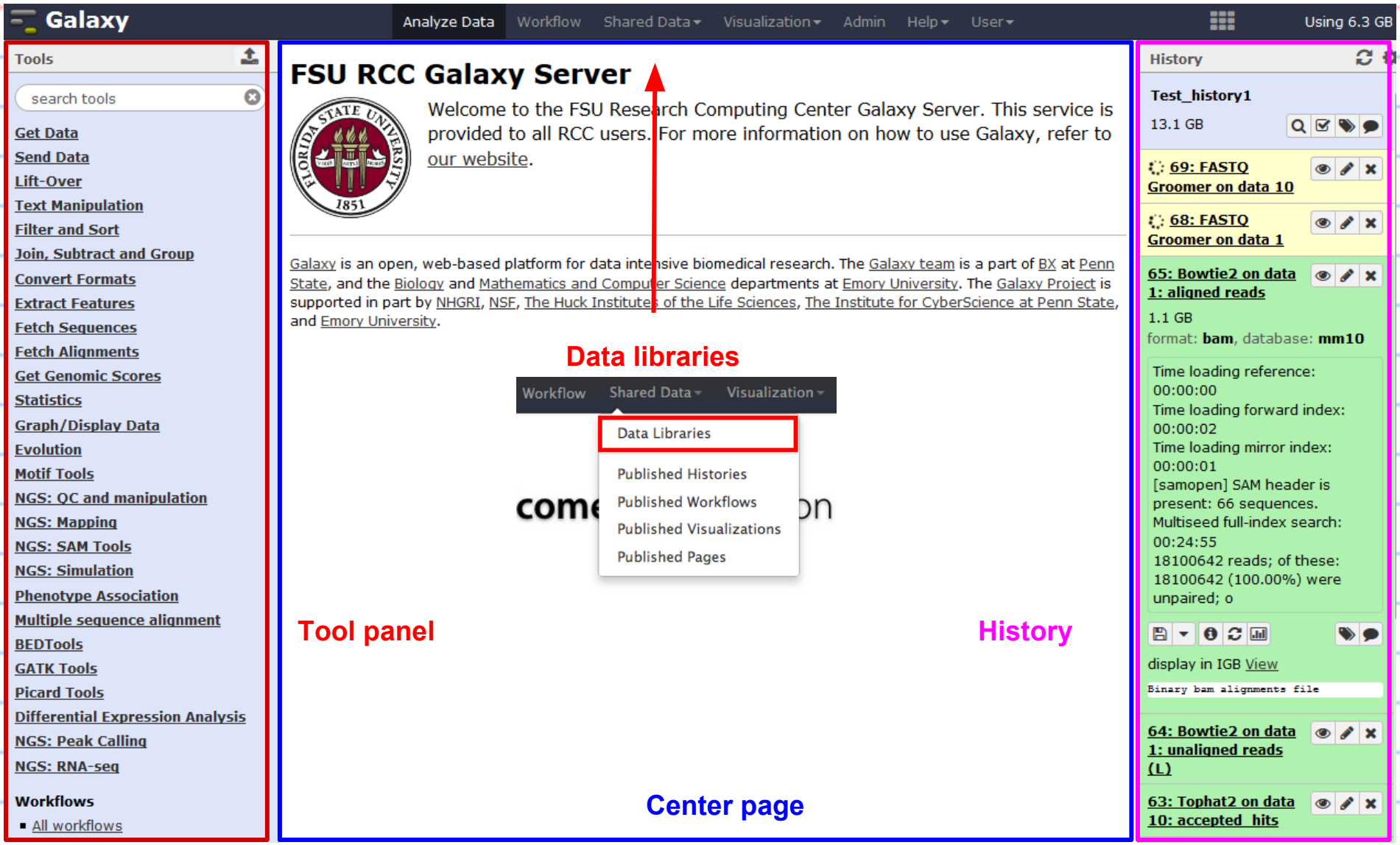

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Tools?

- Data preprocessing:
  - FastQC (v0.10.1)
  - FastX Toolkit
  - Trimmomatic (v0.32)
  - FastA/Q manipulation tools

  - TrimGalore/CutAdapt?

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Tools?

- Data Mapping:
  - BWA(v0.5.9)
  - Bowtie2 (v2.1.0)
  - Tophat2(v2.0.9)

  - Bowtie/Tophat v1?

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Genomes?

(all UCSC, so far)

- Human
  - hg19
- Mouse
  - mm10
- Rat
  - rn4
  - rn5
  - rn6
- Custom genomes

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Tools?

- Post-Mapping processing:
  - Samtools suite
  - Picard_Tools (v1.106)
  - BedTools (v2.20.1)
  - ChIP-seq peak calling

  - GATK/Variant calling?

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Tools?

- RNA-seq / Statistics / Others
  - Cufflinks suite (v2.1.1)
  - HTSeq
  - DESeq2
  - DEXSeq
  - EdgeR

  - Various plotting tools

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Demo?