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# 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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**Galaxy** Analyze Data Workflow Shared Data Visualization Admin Help User Using 6.3 GB

## FSU RCC Galaxy Server

Welcome to the FSU Research Computing Center Galaxy Server. This service is provided to all RCC users. For more information on how to use Galaxy, refer to our [website](#).

Galaxy is an open, web-based platform for data intensive biomedical research. The [Galaxy team](#) is a part of [BX](#) at [Penn State](#), and the [Biology](#) and [Mathematics and Computer Science](#) departments at [Emory University](#). The [Galaxy Project](#) is supported in part by [NHGRI](#), [NSE](#), [The Huck Institutes of the Life Sciences](#), [The Institute for CyberScience at Penn State](#), and [Emory University](#).

**Data Libraries**

- Workflow
- Shared Data
- Visualization
- Data Libraries**
- Published Histories
- Published Workflows
- Published Visualizations
- Published Pages

**Tools panel**

- Tools
- search tools
- Get Data
- Send Data
- Lift-Over
- Text Manipulation
- Filter and Sort
- Join, Subtract and Group
- Convert Formats
- Extract Features
- Fetch Sequences
- Fetch Alignments
- Get Genomic Scores
- Statistics
- Graph/Display Data
- Evolution
- Motif Tools
- NGS: QC and manipulation
- NGS: Mapping
- NGS: SAM Tools
- NGS: Simulation
- Phenotype Association
- Multiple sequence alignment
- BEDTools
- GATK Tools
- Picard Tools
- Differential Expression Analysis
- NGS: Peak Calling
- NGS: RNA-seq
- Workflows
  - All workflows

**History**

Test\_history1  
13.1 GB

69: FASTQ  
Groomer on data 10

68: FASTQ  
Groomer on data 1

65: Bowtie2 on data 1: aligned reads  
1.1 GB  
format: bam, database: mm10

Time loading reference: 00:00:00  
Time loading forward index: 00:00:02  
Time loading mirror index: 00:00:01  
[samopen] SAM header is present: 66 sequences.  
Multiseed full-index search: 00:24:55  
18100642 reads; of these: 18100642 (100.00%) were unpaired; o

64: Bowtie2 on data 1: unaligned reads (L)

63: Tophat2 on data 10: accepted hits

**Center page**

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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?