

Science Support @ Becker

supporting science from the bench to the clinic

GALAXY

Supporting genomics research and education using Galaxy (two collaborative projects):

- Genomics research - supporting use as a genomics research data analysis tool
- Genomics education - experimenting with use as a clinical genomics teaching tool

GALAXY OVERVIEW

- Free web-based tool (<http://usegalaxy.org/>)
- Enables users without programming experience to run jobs on large genomic datasets
- Easy to share workflows with others and reproduce analyses

GALAXY OVERVIEW

The screenshot displays the Galaxy web interface. At the top, a navigation bar includes 'Galaxy' and menu items: 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Cloud', 'Help', and 'User'. The right side of the top bar shows 'Using 0 bytes'.

Tools Panel (Left): A sidebar with a search bar and a list of tool categories: Get Data, Lift-Over, Text Manipulation, Convert Formats, FASTA manipulation, Filter and Sort, Join, Subtract and Group, Extract Features, Fetch Sequences, Fetch Alignments, Get Genomic Scores, Operate on Genomic Intervals, Statistics, Graph/Display Data, Regional Variation, Multiple regression, Multivariate Analysis, Evolution, Motif Tools, Multiple Alignments, Metagenomic analyses, Genome Diversity, NGS TOOLBOX BETA, Phenotype Association, NGS: QC and manipulation, NGS: Mapping, and NGS: SAM Tools.

Main Content Area: A central panel titled 'Galaxy 101 Start small' with the subtitle 'The very first tutorial you need'. Below the text is a progress indicator with 10 dots, the first of which is filled. To the right, a 'Tweets' section shows two tweets: one from the Galaxy Project (@galaxyproject) and another from BF Francis Ouellette (@bfo).

History Panel (Right): A panel titled 'History' showing 'Unnamed history' with '0 bytes'. A message states: 'This history is empty. You can load your own data or get data from an external source'.

Footer (Red Box): A row of logos for Penn State, Johns Hopkins University, TACC, and iPlant Collaborative.

<http://usegalaxy.org/>

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MEDICAL LIBRARY

GALAXY OVERVIEW

- Central (Main) servers can't accommodate analysis needs of growing number of users
- Open source software (in addition to being a web platform) – allows users to implement a local instance

GALAXY – RESEARCH TOOL

- Onsite Galaxy training workshop feedback – it would be great if we had a WUSTL Galaxy instance
- Finding a partner – Genome Technology Access Center, Center for Biomedical Informatics, Center for High Performance Computing (CHPC)
- Local WUSTL Galaxy instance - collaboration between Becker Library and the CHPC – run jobs on CHPC cluster

GALAXY – RESEARCH TOOL

Galaxy / WUSTL Analyze Data Workflow Shared Data Visualization Admin Help User Using -28%

Tools

search tools

- [Get Data](#)
- [Send Data](#)
- [ENCODE Tools](#)
- [Lift-Over](#)
- [Text Manipulation](#)
- [Filter and Sort](#)
- [Join, Subtract and Group](#)
- [Convert Formats](#)
- [Extract Features](#)
- [Fetch Sequences](#)
- [Fetch Alignments](#)
- [Get Genomic Scores](#)
- [Operate on Genomic Intervals](#)
- [Statistics](#)
- [Wavelet Analysis](#)
- [Graph/Display Data](#)
- [Regional Variation](#)
- [Multiple regression](#)
- [Multivariate Analysis](#)
- [Evolution](#)
- [Motif Tools](#)
- [Multiple Alignments](#)
- [Metagenomic analyses](#)
- [FASTA manipulation](#)
- [NGS: QC and manipulation](#)
- [NGS: Mapping](#)
- [NGS: Indel Analysis](#)
- [NGS: RNA Analysis](#)
- [NGS: SAM Tools](#)

Welcome to the WUSTL Galaxy instance!

A collaboration between WUSTL's Bernard Becker Medical Library and the Center for High Performance Computing.

BERNARDBECKER MEDICAL LIBRARY
CHPC
Center for High Performance Computing

For instructions on running Galaxy, and our local policies see:
<https://becker.wustl.edu/services/software/wustl-chpc-galaxy>

We also maintain a local mailing list for Wash U Galaxy users on the cluster:
<http://management.wustl.edu/mailman/listinfo/galaxy>
Feel free to register for this low-traffic list to post questions or problems.

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](#), [NSF](#), [The Huck Institutes of the Life Sciences](#), [The Institute for CyberScience at Penn State](#), and [Emory University](#).

History

Unnamed history
0 bytes

Your history is empty. Click 'Get Data' on the left pane to start

GALAXY – RESEARCH TOOL

- General installation that can be customized over time based on feedback from WUSTL users (Galaxy Tool Shed)
- WUSTL CHPC Galaxy mailing list – use list to post questions, suggest enhancements, and/or report problems

GALAXY – TEACHING TOOL

- Clinical next-generation sequencing (NGS) at WUSTL through Genomics and Pathology Services – GPS@WUSTL (<http://gps.wustl.edu/>)
- Faculty in Pathology and Immunology, Laboratory and Genomic Medicine looking for a way to introduce clinical NGS data analysis pipeline used by GPS@WUSTL to their residents and fellows
- Can we use Galaxy as a teaching tool?

GALAXY – TEACHING TOOL

- Hands-on experience using sample clinical sequencing data – run sequencing data through analysis pipeline in Galaxy (using default tool settings)
- Interest from other departments as well
- Use Pathology and Immunology, Laboratory and Genomic Medicine as a pilot and go from there.....

COLLABORATORS

- Kristi Holmes, PhD – Bioinformaticist, Becker Library (now Director, Galter Health Sciences Library and Associate Professor, Preventive Medicine-Health and Biomedical Informatics, Northwestern University)
- Malcolm Tobias, PhD – Systems Manager, CHPC

COLLABORATORS

- Jackie Payton, MD, PhD – Assistant Professor, Pathology and Immunology, Laboratory and Genomic Medicine
- Eric Duncavage, MD – Assistant Professor, Pathology and Immunology, Laboratory and Genomic Medicine