

Galaxy Tool Shed

and Changes to the Galaxy Distribution

<http://usegalaxy.org/toolshed>

Greg Von Kuster

The Galaxy main public instance

The screenshot displays the Galaxy web interface. At the top, the navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Cloud', 'Admin', 'Help', 'User', and 'Using'. The left sidebar, titled 'Tools', lists various categories such as 'Get Data', 'Send Data', 'ENCODE Tools', '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', and 'Human Genome Variation'. The main content area features a large card titled 'Managing Data' with the subtitle 'Store, Manage, and Share data with Libraries' and 'An in-depth tutorial'. Below this is a 'Live Quickies' section with two cards: '454 Mapping: Single End' (Galactic quickie # 15) and 'Uploading Data using FTP' (Galactic quickie # 17). At the bottom, a paragraph describes Galaxy as an open, web-based platform for data-intensive biomedical research, mentioning the Galaxy team at Penn State. The right sidebar, titled 'History', shows 'Unnamed history' with '0 bytes' and a message: 'Your history is empty. Click 'Get Data' on the left pane to start'.

The Galaxy main tool shed

The screenshot shows the Galaxy Tool Shed interface. At the top, there are navigation links for 'Repositories', 'Admin', 'Help', and 'User'. Below the navigation bar, the main content area is divided into two columns. The left column contains a search bar and a list of repository-related actions. The right column displays a table of tool categories with columns for Name, Description, and the number of Repositories.

1833 valid tools on Jul 13, 2012

Galaxy Tool Shed Repositories Admin Help User

Search

- [Search for valid tools](#)
- [Search for workflows](#)

Repositories

- [Browse by category](#)
- [Browse my repositories](#)
- [Browse my invalid tools](#)
- [Create new repository](#)

Categories

Name	Description	Repositories
Assembly	Tools for working with assemblies	19
Computational chemistry	Tools for use in computational chemistry	3
Convert Formats	Tools for converting data formats	25
Data Source	Tools for retrieving data from external data sources	8
Fasta Manipulation	Tools for manipulating fasta data	22
Genomic Interval Operations	Tools for operating on genomic intervals	18
Graphics	Tools producing images	14
Metagenomics	Tools enabling the study of metagenomes	5
Next Gen Mappers	Tools for the analysis and handling of Next Gen sequencing data	36
Ontology Manipulation	Tools for manipulating ontologies	5
Proteomics	Tools enabling the study of proteins	1
SAM	Tools for manipulating alignments in the SAM format	18
Sequence Analysis	Tools for performing Protein and DNA/RNA analysis	98

How does the tool shed
complement Galaxy to enrich the
features that it provides?