

# The first biomedical AppStore: the Galaxy Tool Shed

<http://usegalaxy.org/toolshed>

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# The Galaxy main public instance

The screenshot displays the Galaxy web interface. At the top, the navigation bar includes the Galaxy logo and menu items: Analyze Data, Workflow, Shared Data, Visualization, Cloud, Admin, Help, and User. The left sidebar, titled 'Tools', lists various tool 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 of the main content area, there is a paragraph describing Galaxy as an open, web-based platform for data-intensive biomedical research. The right sidebar, titled 'History', shows an 'Unnamed history' entry 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 sections. On the left is a sidebar with navigation options, and on the right is a main content area displaying a list of tool categories.

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

How can the Galaxy tool shed be integrated with Galaxy to enrich the features that Galaxy provides?

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