

# Galaxy Tool Shed

and Changes to the Galaxy Distribution

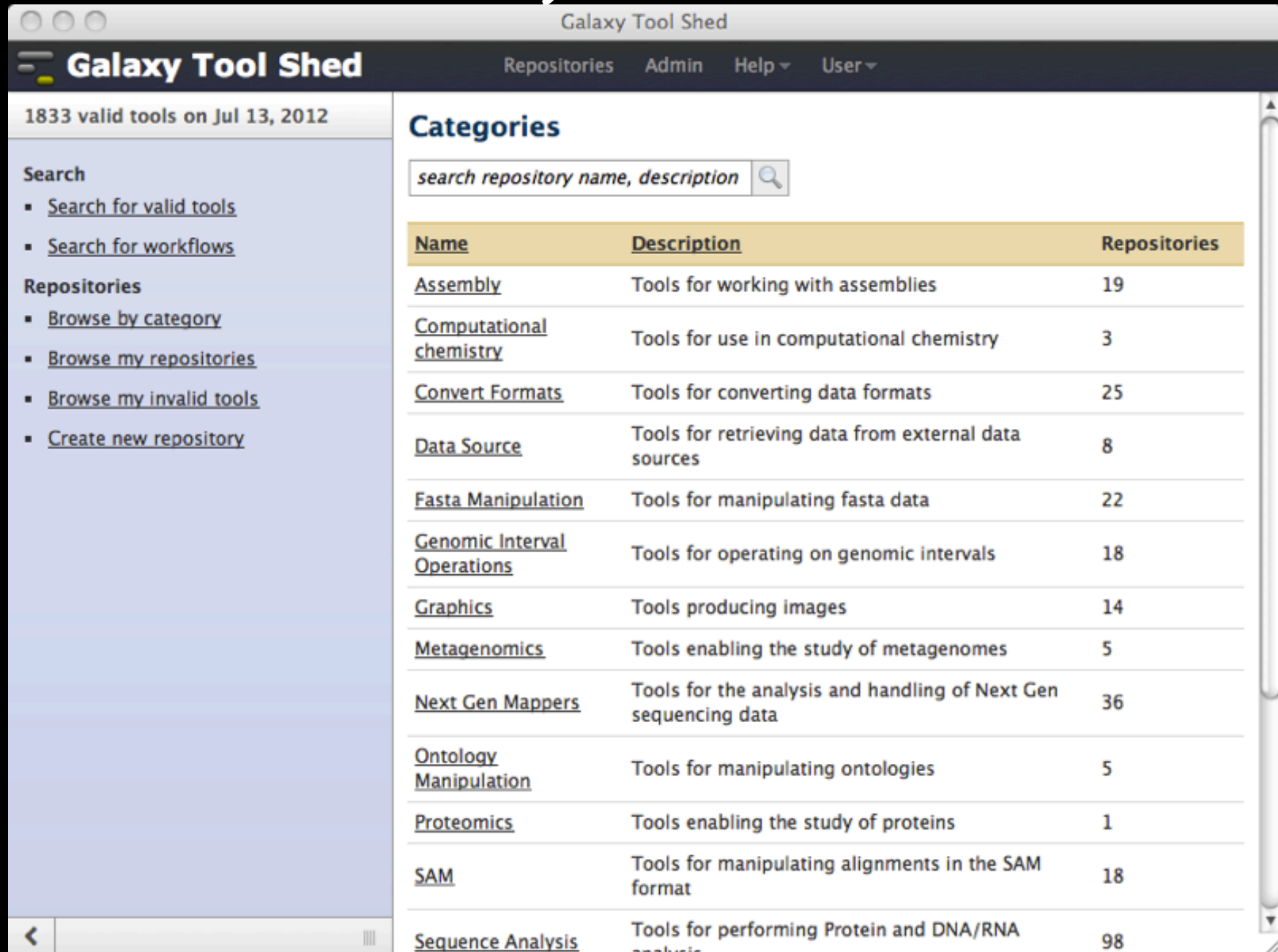
<http://usegalaxy.org/toolshed>

Greg Von Kuster

# The Galaxy main public instance

The screenshot displays the Galaxy web interface. At the top, the navigation bar includes the 'Galaxy' logo and menu items: 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Cloud', 'Admin', 'Help', 'User', and 'Using'. The left sidebar contains a 'Tools' menu with 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). A message box on the right states: 'Your history is empty. Click 'Get Data' on the left pane to start'. The bottom of the interface shows a navigation bar with back and forward arrows.

# The Galaxy main tool shed



The screenshot shows the Galaxy Tool Shed interface. At the top, the title bar reads "Galaxy Tool Shed". Below it, a navigation bar contains "Repositories", "Admin", "Help", and "User". The main content area is divided into two columns. The left column, titled "Galaxy Tool Shed", displays "1833 valid tools on Jul 13, 2012" and a search section with links for "Search for valid tools" and "Search for workflows". Below this is a "Repositories" section with links for "Browse by category", "Browse my repositories", "Browse my invalid tools", and "Create new repository". The right column, titled "Categories", features a search box for "search repository name, description" and a table listing various tool 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 does the tool shed  
complement Galaxy to enrich the  
features that it provides?