Galaxy

GMOD Workshop
Plant and Animal Genome XX
18 January 2012

Dave Clements, Emory University

http://galaxyproject.org/
http://gmod.org

Agenda

Introduction

Worked example

Deployment Options

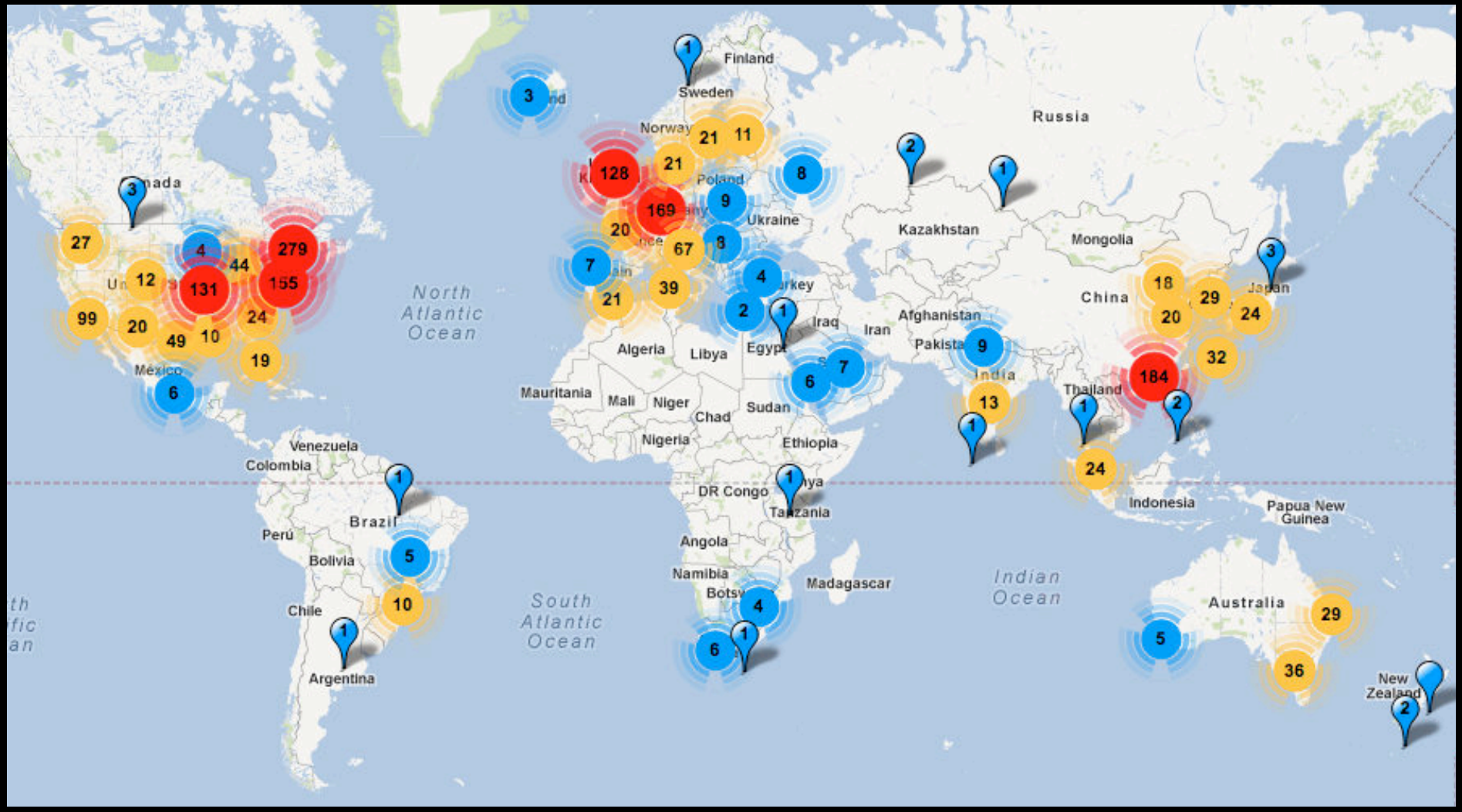
Community

Goals for this workshop

1. Introduce the Galaxy platform.
2. Demonstrate how to:
   - Load and integrate data from popular online resources
   - Perform bioinformatics analysis with Galaxy
   - Save, share, describe and publish your analysis and generated datasets

This workshop will not cover details of how the tools are implemented or new algorithm designs or which assembler or mapper or ... is best for you.

The Motivation Slide



Next Generation Genomics: World Map of High-throughput Sequencers
Nick Loman, James Hadfield

http://pathogenomics.bham.ac.uk/hts/

What is Galaxy?

- **A free (for everyone) web service** integrating a wealth of tools, compute resources, terabytes of reference data and permanent storage
- An **analysis and data integration** tool
- **Open source software** that makes integrating your own tools and data and customizing for your own site simple
- A part of **GMOD**

http://galaxyproject.org

Galaxy URLs to Remember

http://galaxyproject.org

http://usegalaxy.org

http://getgalaxy.org

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Galaxy aims to

Enable
accessible,
reproducible,
and
transparent
computational biomedical research.

Demo: Accessibility

On pig chromosome 18,
which coding exons have the most
repeats in them?

http://usegalaxy.org

Galaxy: A Rough Plan

- Get some data
  - Coding exons on chromosome 18
  - Repeats on chromosome 18
- Mess with it
  - Identify which exons have repeats
  - Count repeats per exon
  - Save, download, visualize, ... exons with most repeats.

(~ http://usegalaxy.org/galaxy101)

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Demo: Reproducibility and Transparency

http://usegalaxy.org

CSH PRESS GENOME RESEARCH

Windshield splatter analysis with the Galaxy metagenomic pipeline

Sergei Kosakovsky Pond[1,2,6,9], Samir Wadhawan[3,6,7], Francesca Chiaromonte[4], Guruprasad Ananda[1,3], Wen-Yu Chung[1,3,8], James Taylor[1,5,9], Anton Nekrutenko[1,3,9] and The Galaxy Team[1]

[+] Author Affiliations

Abstract

How colle has subje repre colle dema comp

Footnotes

[Supplemental material is available online at http://www.genome.org. All data and tools described in this manuscript can be downloaded or used directly at http://galaxyproject.org. Exact analyses and workflows used in this paper are available at http://usegalaxy.org/u/aun1/p/windshield-splatter.]

Article published online before print. Article and publication date are at http://www.genome.org/cgi/doi/10.1101/gr.094508.109.

OPEN ACCESS ARTICLE

This Article

Published in Advance October 9, 2009, doi: 10.1101/gr.094508.109

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Galaxy main site
http://usegalaxy.org

- Public web site, **anybody can use**
- Hundreds of tools
- **Persistent**
- ~500 new users per month, ~100 TB of user data, ~135,000 analysis jobs per month

But, it's a big world

Main has lots of tools, storage, processor, users, ...

- But **not all tools** - there are thousands and adding new tools is not taken lightly
- But **not infinite storage and processors** - main will continue to be maintained and enhanced, but with use limits and storage quotas

A centralized solution cannot scale to meet data analysis demands of the whole world

Scaling Galaxy

- Encourage local Galaxy instances and Galaxy on the cloud. Support increasingly decentralized model and *improve access to existing resources*
- Focus on building infrastructure to allow community to integrate and share tools, workflows, and best practices

Local Galaxy Instances
http://getgalaxy.org

Galaxy is designed for local installation and customization

- Easily integrate new tools
- Easy to deploy and manage on nearly any (Unix) system
- ***Just download and run, completely self-contained!*** *

* Some assembly required. †
† But not much. ‡
‡ And help is on the way.

Public Galaxy Servers

http://galaxyproject.org/wiki/PublicGalaxyServers

Interested in:

ChIP-chip and ChIP-seq?

✓ Cistrome

Statistical Analysis?

✓ Genomic Hyperbrowser

Sequence and tiling arrays?

✓ Oqtans

Text Mining?

✓ DBCLS Galaxy

Reasoning with ontologies?

✓ GO Galaxy

Internally symmetric protein structures?

✓ SymD

Got your own cluster?

- Move tool execution to other systems
- Galaxy works with any DRMAA compliant cluster job scheduler (which is most of them).
- Galaxy is just another client to your scheduler.

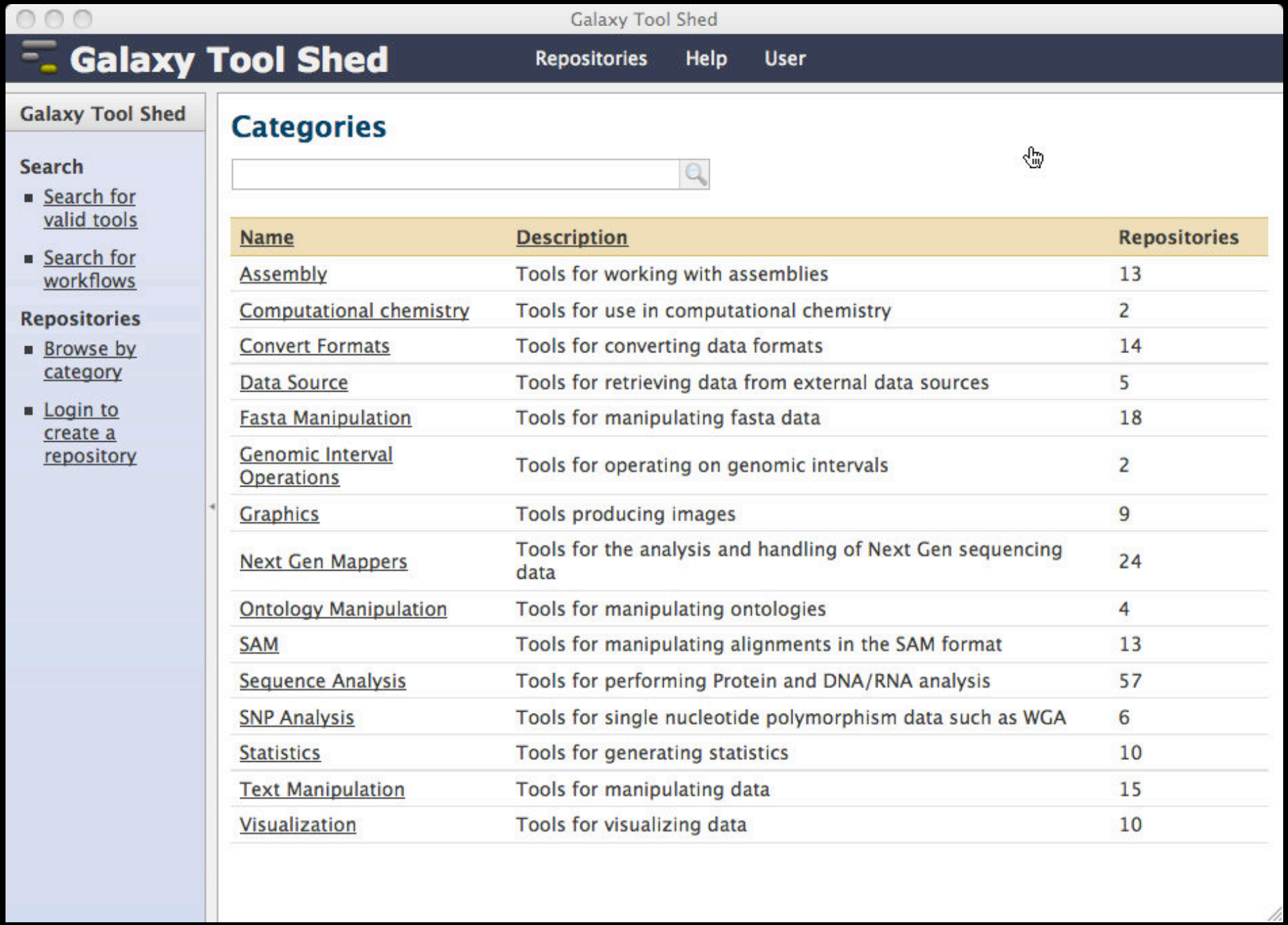
Galaxy CloudMan
http://usegalaxy.org/cloud

- Start with a fully configured and populated (tools and data) Galaxy instance.
- Allows you to scale up and down your compute assets as needed.
- Someone else manages the data center.
- Dannon Baker demonstrated this on Monday:
  - In 30 minutes, using only a web browser, Dannon:
  - Setup an elastic compute cluster, fully pre-populated with data and tools, ran some ChIP-Seq analysis, and then shut it down, *and* gave a talk and answered questions.

Galaxy Tool Shed

- Allow users to share "suites" containing tools, datatypes, workflows, sample data, and automated installation scripts for tool dependencies
- Integration with Galaxy instances to automate tool installation and updates

http://usegalaxy.org/community


Galaxy Tool Shed
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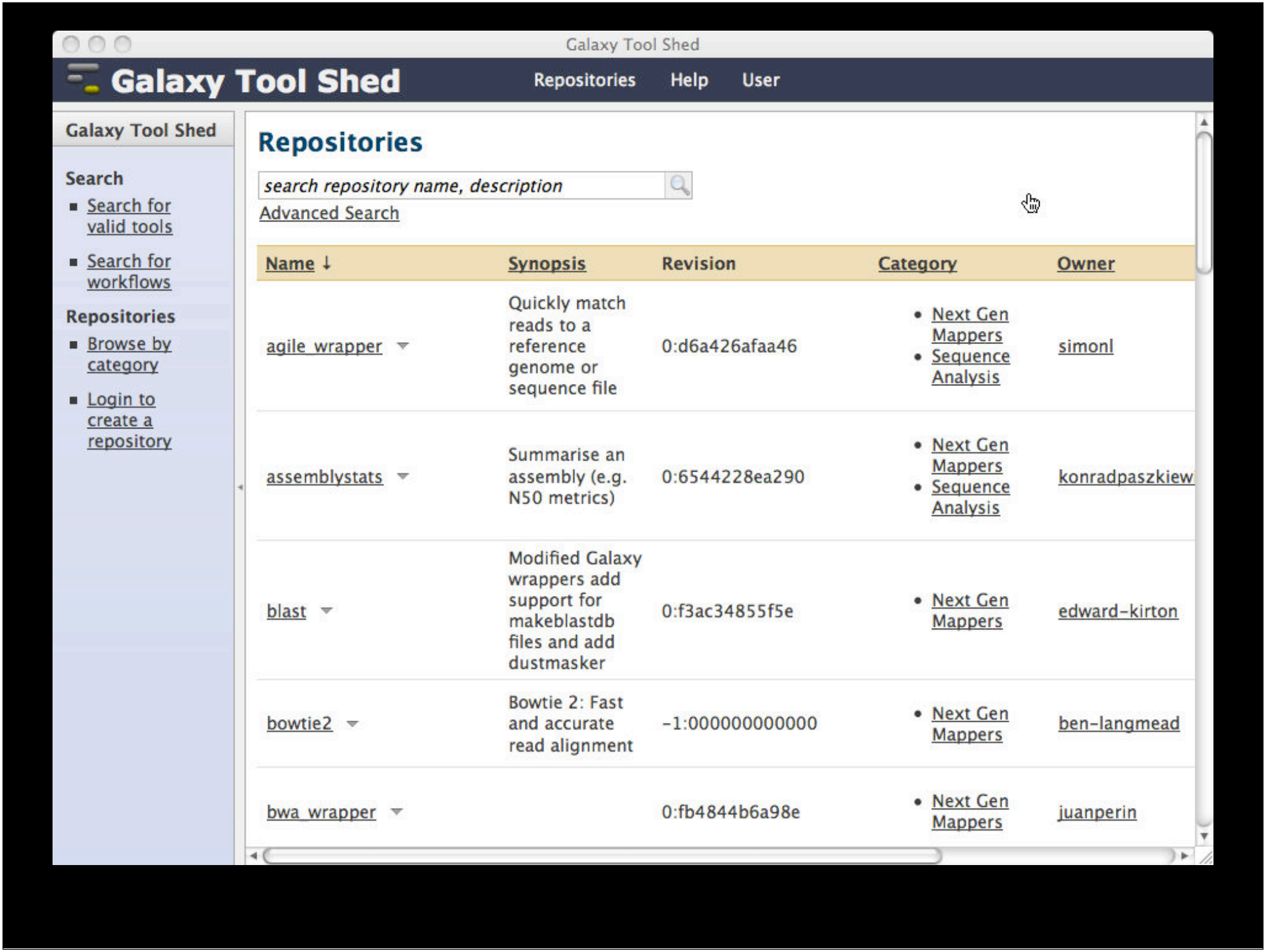
Repositories
Help
User
Galaxy Tool Shed
Search
Search for valid tools
Search for workflows
Repositories
Browse by category
Login to create a repository
Categories
Name
Description
Repositories
Assembly
Tools for working with assemblies
13
Computational chemistry
Tools for use in computational chemistry
2
Convert Formats
Tools for converting data formats
14
Data Source
Tools for retrieving data from external data sources
5
Fasta Manipulation
Tools for manipulating fasta data
18
Genomic Interval Operations
Tools for operating on genomic intervals
2
Graphics
Tools producing images
9
Next Gen Mappers
Tools for the analysis and handling of Next Gen sequencing data
24
Ontology Manipulation
Tools for manipulating ontologies
4
SAM
Tools for manipulating alignments in the SAM format
13
Sequence Analysis
Tools for performing Protein and DNA/RNA analysis
57
SNP Analysis
Tools for single nucleotide polymorphism data such as WGA
6
Statistics
Tools for generating statistics
10
Text Manipulation
Tools for manipulating data
15
Visualization
Tools for visualizing data
10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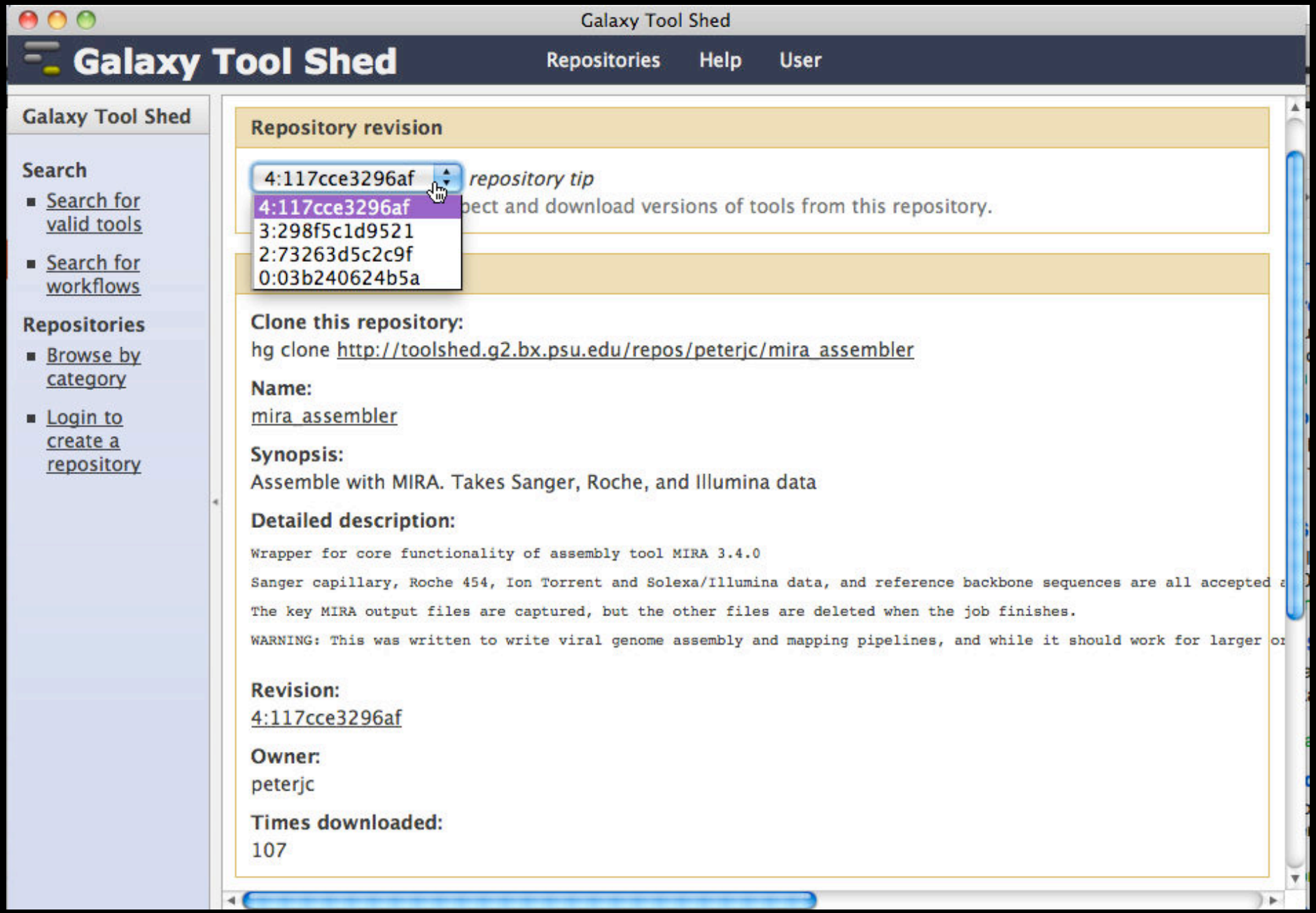
Login to create a repository
Repositories
search repository name, description
Advanced Search
Name ↓
Synopsis
Revision
Category
Owner
agile_wrapper
Quickly match reads to a reference genome or sequence file
0:d6a426afaa46
Next Gen Mappers
Sequence Analysis
simonl
assemblystats
Summarise an assembly (e.g. N50 metrics)
0:6544228ea290
Next Gen Mappers
Sequence Analysis
konradpaszkiew
blast
Modified Galaxy wrappers add support for makeblastdb files and add dustmasker
0:f3ac34855f5e
Next Gen Mappers
edward-kirton
bowtie2
Bowtie 2: Fast and accurate read alignment
-1:000000000000
Next Gen Mappers
ben-langmead
bwa_wrapper
0:fb4844b6a98e
Next Gen Mappers
juanperin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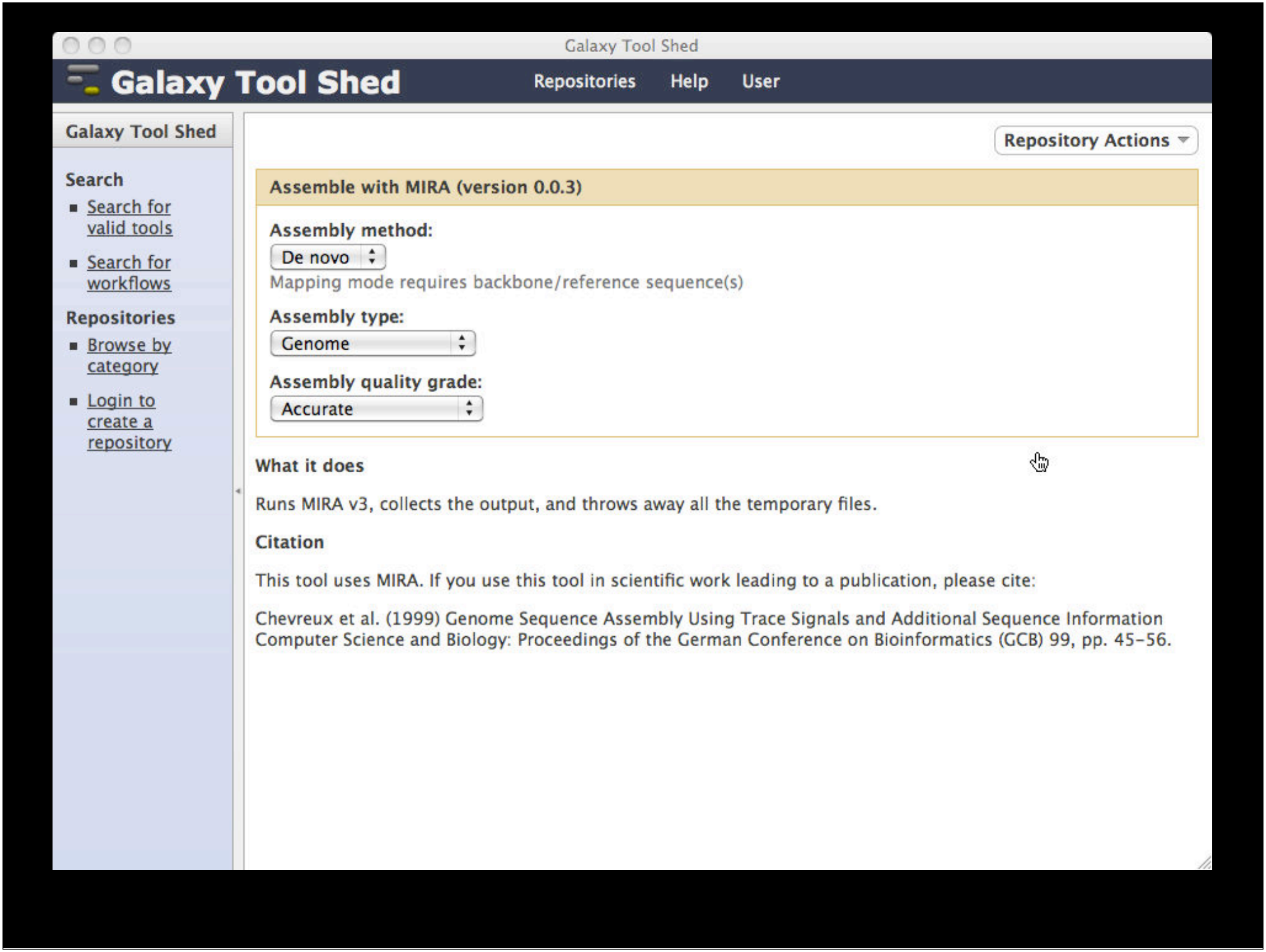
Browse by category
Login to create a repository
Repository revision
4:117cce3296af
repository tip
4:117cce3296af
3:298f5c1d9521
2:73263d5c2c9f
0:03b240624b5a
Clone this repository:
hg clone http://toolshed.g2.bx.psu.edu/repos/peterjc/mira_assembler
Name:
mira_assembler
Synopsis:
Assemble with MIRA. Takes Sanger, Roche, and Illumina data
Detailed description:
Wrapper for core functionality of assembly tool MIRA 3.4.0
Sanger capillary, Roche 454, Ion Torrent and Solexa/Illumina data, and reference backbone sequences are all accepted
The key MIRA output files are captured, but the other files are deleted when the job finishes.
WARNING: This was written to write viral genome assembly and mapping pipelines, and while it should work for larger
Revision:
4:117cce3296af
Owner:
peterjc
Times downloaded:
107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Search for valid tools
Search for workflows
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Browse by category
Login to create a repository
Repository Actions
Assemble with MIRA (version 0.0.3)
Assembly method:
De novo
Mapping mode requires backbone/reference sequence(s)
Assembly type:
Genome
Assembly quality grade:
Accurate
What it does
Runs MIRA v3, collects the output, and throws away all the temporary files.
Citation
This tool uses MIRA. If you use this tool in scientific work leading to a publication, please cite:
Chevreux et al. (1999) Genome Sequence Assembly Using Trace Signals and Additional Sequence Information Computer Science and Biology: Proceedings of the German Conference on Bioinformatics (GCB) 99, pp. 45-56.

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Galaxy Community

Galaxy

Data intensive biology
for everyone

Galaxy is *an open, web-based platform for data intensive biological research*. Whether on the free public server, or your own instance you can perform, share, and reproduce complete bioinformatic analyses.

To learn more about how Galaxy can help you gain insight from your data, please attend one of these Galaxy related presentations at PAG 2012:

Sunday	**The Galaxy Platform: Running analysis in the cloud** 1:40-2:10, Town and Country, Dannon Baker Need high-end computation, but lack the infrastructure? This session (part of the *Cloud Computing* workshop) will show you how to use Galaxy on the cloud to run your analysis.	
Monday	**Poster Sessions** Grand Exhibit Hall Even: 10:00-11:30 Odd: 3:00- 4:30	**P698: Developing Tools for Genomic Analysis in a Wide Bulb Onion (*Allium Capa L.*),** John A. McCallum Galaxy pipelines were developed to enable large-scale design of PCR-based markers for validation and mapping of polymorphisms identified between transcriptomes of parent lines.
		P936: DDBJ Sequence Read Archive and cloud-computing based annotation tool for new-generation sequencing data, Hideki Nagasaki This DDBJ resource provides analysis support using Galaxy.
		P87: GMOD in the Cloud, Scott Cain Galaxy is a part of the GMOD consortium and is just one of many GMOD components that are cloud enabled.
Wednesday	**Galaxy** 10:30-11:30, Golden West, Dave Clements *Want to learn about Galaxy, and how to use it? This is the session for you.* This is the first session of a workshop on GMOD components that also covers tools for genome annotation (MAKER), visualization (JBrowse, GBrowse_syn), and online database construction (Tripal).	
	MAPHiTS: an efficient workflow for SNP detection 11:35-11:50, California Room, Marc Bras MAPHiTS has been integrated into INRA URGI's local Galaxy instance, allowing biologists without Unix skills to easily analyse short-reads sequences with a user-friendly interface.	

http://galaxyproject.org

Annual Community Meting
Tool Shed
Mailing Lists (very active)
Screencasts
Events Calendar, News Feed
Community Wiki
Local Public Installs

http://galaxyproject.org/wiki

Try it now:
http://UseGalaxy.org

Develop and deploy:
http://GetGalaxy.org

EMORY

PENNSTATE. 1855

Dannon Baker

Jeremy Goecks

Dan Blankenberg

Nate Coraor

James Taylor

Enis Afgan
(IRB)

Ross Lazarus
(Baker IDI, Harvard)

Jennifer Jackson

Greg von Kuster

Anton Nekrutenko

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http://GalaxyProject.org

Thanks

GMOD

Dr. Scott Cain

PAG Organizers