

# Community Building and Support

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2013 GMOD Meeting  
Cambridge, UK



Dave Clements  
Emory University



# Agenda

- What?
- How?

# What: Communities?

- End Users
- Deployers
- Contributors

# What: Goals?

- **Grow** your community
- A **well-informed** community
- A community that is **connected** to your project and each other
- A community that **contributes**:
  - Curation and data
  - Support
  - Outreach and training

# How?

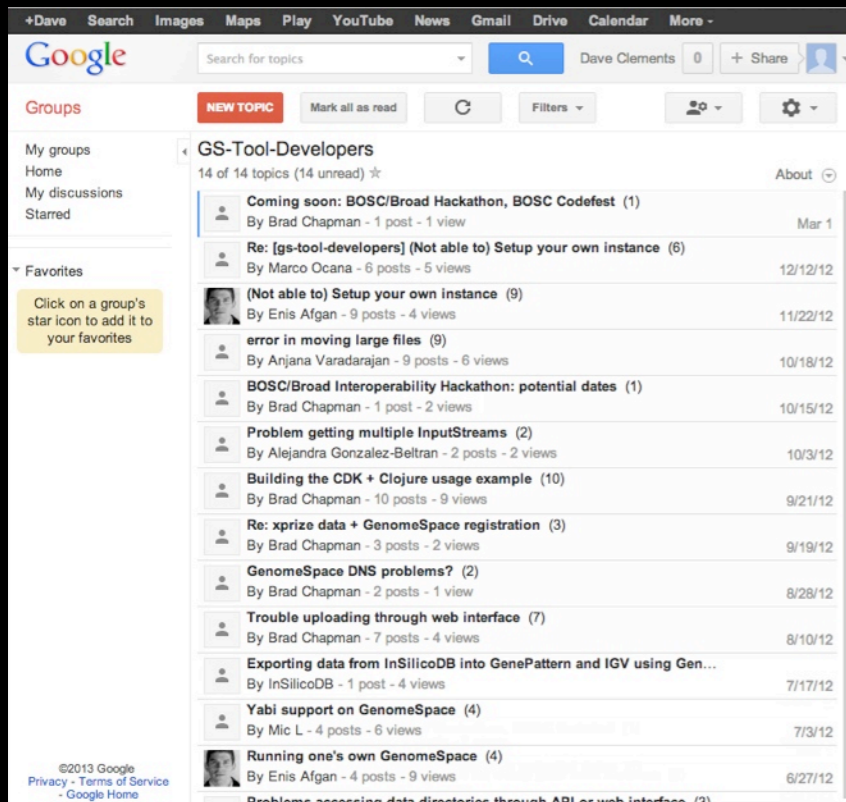
**Enable** your community

**Communicate** with your community

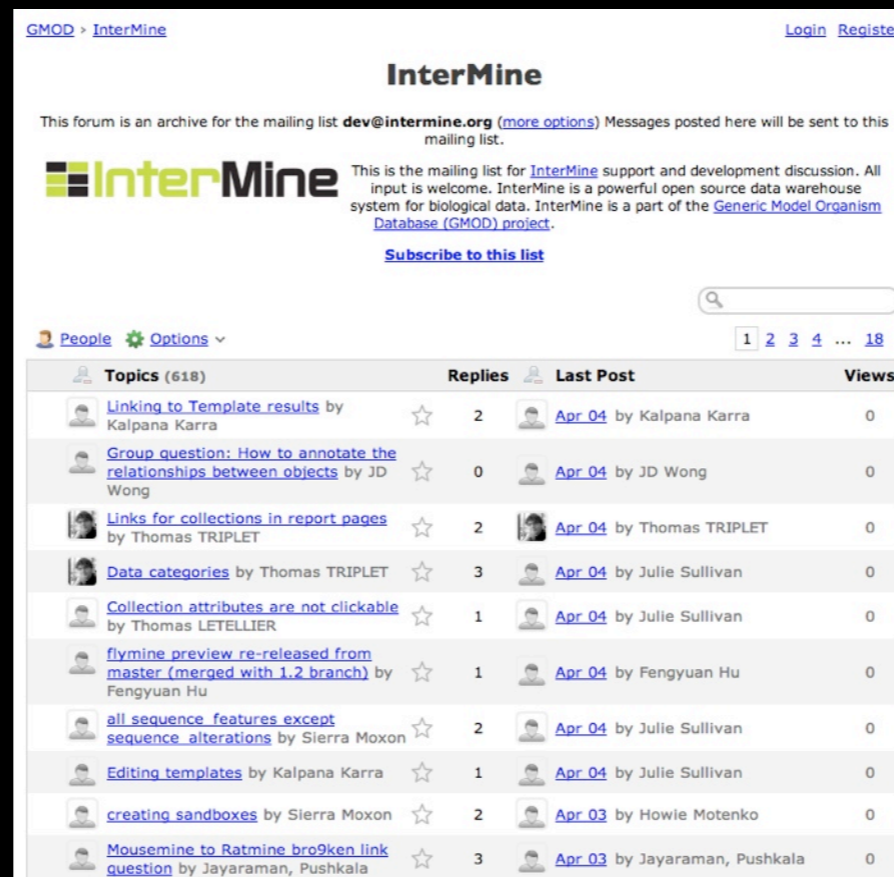
**Reward** your community

# Provide **Open** Support Channels

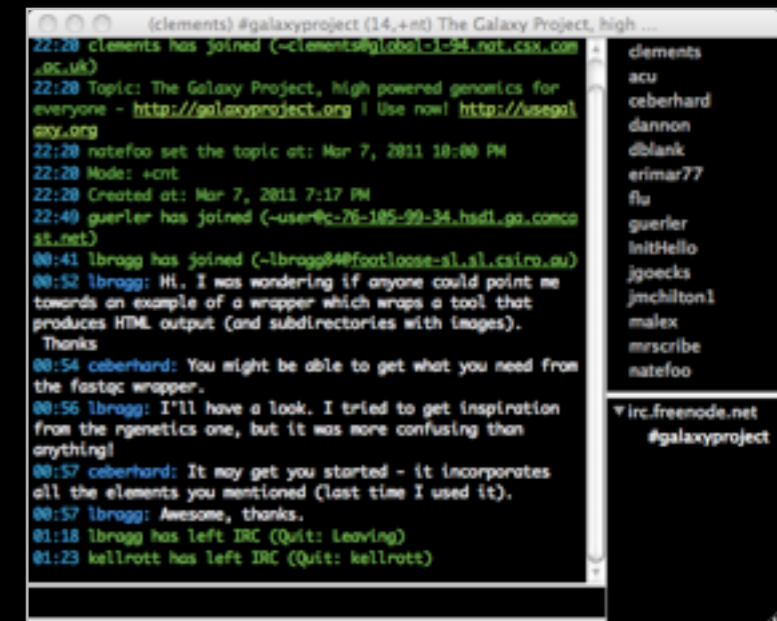
## Forums, mailing lists, IRC, ..



GenomeSpace Tool developer forum @ Google



InterMine Dev mailing list, archived @ Nabble



GalaxyProject IRC channel

Open channels support anyone posting questions *and answers*



# Archives accessible and searchable

## The dev Archives

You can get [more information about this list](#).

Archive	View by:	Downloadable version
April 2013:	<a href="#">[ Thread ]</a> <a href="#">[ Subject ]</a> <a href="#">[ Author ]</a> <a href="#">[ Date ]</a>	<a href="#">[ Gzip'd Text 14 KB ]</a>
March 2013:	<a href="#">[ Thread ]</a> <a href="#">[ Subject ]</a> <a href="#">[ Author ]</a> <a href="#">[ Date ]</a>	<a href="#">[ Gzip'd Text 39 KB ]</a>
February 2013:	<a href="#">[ Thread ]</a> <a href="#">[ Subject ]</a> <a href="#">[ Author ]</a> <a href="#">[ Date ]</a>	<a href="#">[ Gzip'd Text 32 KB ]</a>
January 2013:	<a href="#">[ Thread ]</a> <a href="#">[ Subject ]</a> <a href="#">[ Author ]</a> <a href="#">[ Date ]</a>	<a href="#">[ Gzip'd Text 27 KB ]</a>
December 2012:	<a href="#">[ Thread ]</a> <a href="#">[ Subject ]</a> <a href="#">[ Author ]</a> <a href="#">[ Date ]</a>	<a href="#">[ Gzip'd Text 13 KB ]</a>
November 2012:	<a href="#">[ Thread ]</a> <a href="#">[ Subject ]</a> <a href="#">[ Author ]</a> <a href="#">[ Date ]</a>	<a href="#">[ Gzip'd Text 38 KB ]</a>
October 2012:	<a href="#">[ Thread ]</a> <a href="#">[ Subject ]</a> <a href="#">[ Author ]</a> <a href="#">[ Date ]</a>	<a href="#">[ Gzip'd Text 27 KB ]</a>
September 2012:	<a href="#">[ Thread ]</a> <a href="#">[ Subject ]</a> <a href="#">[ Author ]</a> <a href="#">[ Date ]</a>	<a href="#">[ Gzip'd Text 64 KB ]</a>
August 2012:	<a href="#">[ Thread ]</a> <a href="#">[ Subject ]</a> <a href="#">[ Author ]</a> <a href="#">[ Date ]</a>	<a href="#">[ Gzip'd Text 26 KB ]</a>
July 2012:	<a href="#">[ Thread ]</a> <a href="#">[ Subject ]</a> <a href="#">[ Author ]</a> <a href="#">[ Date ]</a>	<a href="#">[ Gzip'd Text 65 KB ]</a>
June 2012:	<a href="#">[ Thread ]</a> <a href="#">[ Subject ]</a> <a href="#">[ Author ]</a> <a href="#">[ Date ]</a>	<a href="#">[ Gzip'd Text 6 KB ]</a>
May 2012:	<a href="#">[ Thread ]</a> <a href="#">[ Subject ]</a> <a href="#">[ Author ]</a> <a href="#">[ Date ]</a>	<a href="#">[ Gzip'd Text 14 KB ]</a>
April 2012:	<a href="#">[ Thread ]</a> <a href="#">[ Subject ]</a> <a href="#">[ Author ]</a> <a href="#">[ Date ]</a>	<a href="#">[ Gzip'd Text 8 KB ]</a>
March 2012:	<a href="#">[ Thread ]</a> <a href="#">[ Subject ]</a> <a href="#">[ Author ]</a> <a href="#">[ Date ]</a>	<a href="#">[ Gzip'd Text 44 KB ]</a>
February 2012:	<a href="#">[ Thread ]</a> <a href="#">[ Subject ]</a> <a href="#">[ Author ]</a> <a href="#">[ Date ]</a>	<a href="#">[ Gzip'd Text 25 KB ]</a>
January 2012:	<a href="#">[ Thread ]</a> <a href="#">[ Subject ]</a> <a href="#">[ Author ]</a> <a href="#">[ Date ]</a>	<a href="#">[ Gzip'd Text 24 KB ]</a>
December 2011:	<a href="#">[ Thread ]</a> <a href="#">[ Subject ]</a> <a href="#">[ Author ]</a> <a href="#">[ Date ]</a>	<a href="#">[ Gzip'd Text 14 KB ]</a>

## Mailman search interface

### Getting Help

Questions about TopHat should be sent to [tophat.cufflinks@gmail.com](mailto:tophat.cufflinks@gmail.com). Please do not email technical questions to TopHat contributors directly.

But still way better than no search interface

## Galaxy Mailing List Search

chip-seq peak calling

All User Dev Announce France

About 10 results (0.14 seconds)

### Galaxy Users List Archive - Chip-seq

Sep 20, 2011 ... Can I analyze two bed files from **Chip seq** experimnt in Galaxy? I have one file ... Is there any **peak calling** done with ChIP v are the ...

[user.list.galaxyproject.org/Chip-seq-td4137093.html](http://user.list.galaxyproject.org/Chip-seq-td4137093.html)

Labeled [User](#)

### MA2C peak calling or nimbelgen chip on chip analysis

Nov 11, 2011 ... MA2C **peak calling** or nimbelgen chip on chip analysis. Do we have ... And a tutorial covering **ChIP-seq** analysis using MACS "Shared ...

[user.list.galaxyproject.org/MA2C-peak-calling-or-nimbelgen-chip-on-chip-analysis-td4138014.html](http://user.list.galaxyproject.org/MA2C-peak-calling-or-nimbelgen-chip-on-chip-analysis-td4138014.html)

Labeled [User](#)

### Galaxy Users List Archive - Peak-calling with MACS from .bowtie file

Sep 11, 2012 ... Hi, I have **ChIP-seq** alignment files in .bowtie format and would like to perform **peak-calling** using MACS. However, .bowtie for seem ...

[user.list.galaxyproject.org/Peak-calling-with-MACS-from-bowtie-file-td4654582.html](http://user.list.galaxyproject.org/Peak-calling-with-MACS-from-bowtie-file-td4654582.html)

Labeled [User](#)

### Galaxy Development List Archive - input security validation

Jun 20, 2011 ... I am developing a Galaxy wrapper for our **ChIP-seq peak-calling** program BELT ( PMID: 21138948), and I have a question abo [dev.list.galaxyproject.org/input-security-validation-td4140582.html](http://dev.list.galaxyproject.org/input-security-validation-td4140582.html)

Labeled [Dev](#)

### Galaxy Users List Archive - Unable to run SICER or Find Peaks

Nov 23, 2011 ... Unable to run SICER or Find Peaks. Hi, I want to use SICER or Find Peaks for peak calling on GALAXY. I am using my align

Help 'em out with something like a Google custom search or a Nabble archive

Searchable archives encourage community support, and make those efforts publicly visible.

# Unified Search: <http://galaxyproject.org/search>

**Galaxy Web Search**

Google™ Custom Search   x

Search the entire set of Galaxy web sites and mailing lists using Google.

[Run this search at Google.com \(useful for bookmarking\)](#)

Want a [different search?](#)

[Project home](#)

**Galaxy Web Search**

chip-seq

All Tools Email Source code Shared Documentation Abstracts Requests

About 444 results (0.06 seconds)

Galaxy | Accessible Page | ChIP-seq exercise

## Find

Everything on ...

Tools for ...

Email about ...

Source code for ...

Published Histories, Pages, Workflows, about ...

Documentation on ...

Papers using Galaxy for ...

Related feature requests



# Incentivize contributions

BioStar is a **gamified** online forum.  
Points, badges, voting, ...

**Question: Is there a list of public Galaxy servers?**

We've been looking into setting up a local Galaxy installation for our bioinformatics core facility and in the process of doing so I've stumbled across several Galaxy mirrors and instances that have been customized in various ways. Before we go re-inventing the wheel I was wondering if there are any other known Galaxy servers out there that we could use to borrow design ideas or code from.

Here is the list I've put together thus far, others would be most welcome....

Main Galaxy Server: <http://main.g2.bx.psu.edu/>

Test Galaxy Server: <http://test.g2.bx.psu.edu/>

GeneNetwork Galaxy Mirror: <http://galaxy.genenetwork.org:8080/>

NBIC Galaxy Server: <http://galaxy.nbic.nl/> (includes proteomics tools)

Galaxy/Rätsch Lab Server: <http://galaxy.fml.mpg.de/> (includes machine learning based tools for sequence and tiling array data analysis)

Cistrome Galaxy Server: <http://cistrome.org/ap/root> (dry-lab workbench for integrative analysis of CHIP-chip/seq and gene expression data)

created 21 months ago by Casey Bergman ♦ 13,700 • 2 • 13 • 37 updated 16 months ago by tnabtaf

**Editor: Casey Bergman ♦**

Userid: 314  
Website: <http://bergmanlab.smith.man.ac.uk/>  
Location: Manchester, UK  
Member for: 2 years, 10 months  
Last seen: 10 hours, 56 minutes ago

Molecular Evolutionist turned Genome Annotator, Genomics Work Blog: <http://bergmanlab.smith.man.ac.uk/>  
Work Twitter: <http://twitter.com/caseybergman>  
Personal Blog: <http://caseybergmanlab.com/>  
Personal Twitter: <http://twitter.com/caseybergman>

13,700 • 2 • 13 • 37

[Send Message](#)

Status  
Casey Bergman has contributed 647 posts: 15 questions, 287 answers and 340 comments. User has voted 12

Notifications (25) Content Created Bookmarks (35) Upvoted Posts Supporters Badges (52) Moderator Actions

• Popular Question 9 weeks ago	• Popular Question 10 weeks ago	• Popular Question 11 weeks ago	• Popular Question 11 weeks ago	• Notable Question 3 months ago
• Notable Question 3 months ago	• Popular Question 3 months ago	• Popular Question 5 months ago	• Famous Question 12 months ago	• Nice Question 12 months ago
• Necromancer 12 months ago	• Nice Answer 12 months ago	• Popular Question 12 months ago	• Nice Answer 14 months ago	• Necromancer 14 months ago
• Necromancer 15 months ago	• Good Question 16 months ago	• Nice Answer 16 months ago	• Nice Question 16 months ago	• Nice Answer 17 months ago
• Nice Question 17 months ago	• Enlightened 17 months ago	• Nice Answer 17 months ago	• Nice Answer 17 months ago	• Nice Answer 17 months ago
• Nice Question 19 months ago	• Nice Answer 19 months ago	• Self-Learner 20 months ago	• Nice Answer 21 months ago	• Popular Question 21 months ago



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Location: Manchester, UK  
Member for: 2 years, 10 months  
Last seen: 10 hours, 56 minutes ago

Molecular Evolutionist turned Genome Annotation, Genomics  
Work Blog: <http://bergmanlab.org/>  
Work Twitter: <http://twitter.com/bergmanlab>  
Personal Blog: <http://caseybergman.com/>  
Personal Twitter: <http://twitter.com/caseybergman>

13,700 • 2 • 13 • 37

Send Message

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- Popular Question 3 months ago
- Famous Question 12 months ago
- Nice Question 12 months ago
- Necromancer 12 months ago
- Nice Answer 12 months ago
- Popular Question 12 months ago
- Nice Answer 14 months ago
- Necromancer 14 months ago
- Necromancer 15 months ago
- Good Question 16 months ago
- Nice Answer 16 months ago
- Nice Question 16 months ago
- Nice Answer 17 months ago
- Nice Answer 17 months ago
- Nice Question 17 months ago
- Nice Answer 17 months ago
- Nice Answer 17 months ago
- Nice Answer 17 months ago
- Nice Question 19 months ago
- Nice Answer 19 months ago
- Self-Learner 20 months ago
- Nice Answer 21 months ago
- Popular Question 21 months ago

Casey Bergman has  
**52 badges!**  
*He's a Necromancer  
4 times over!*  
*He's Enlightened too!*

# Mailing Lists vs Forums?

We are **replacing** Galaxy-User mailing list with a **forum**.

We will be using Biostar (<http://biostars.org>) directly





# Create Community Resources and Hubs

The screenshot shows the GMOD website homepage. At the top left is the GMOD logo. Below it is a navigation menu with links to Home, Software, Categories/Tags, and View of pages. A main content area features a large banner for the "2013 GMOD Community Meeting" in Cambridge, UK, held on 5-6 April 2013. The banner includes a circular logo with the text "2013 GMOD COMMUNITY MEETING CAMBRIDGE, UK 5-6 APRIL 2013". To the right of the logo, text describes the meeting and lists guest speakers: Dr Kentaro Yoshida on the Open Ash Dieback Project, Dr Jane Lomax on the Gene Ontology, and Dr Manuel Corpas on BioJS. A "Register now" link is provided. Below the banner are sections for "How do I Get Started?", "How do I Get Support?", and "How do I Get Involved?". A sidebar on the left contains a search bar and a "toolbox" with links to What links here, Related changes, Special pages, and Printable version.

The screenshot shows a LinkedIn group page for the "Galaxy Project". The page header includes the LinkedIn logo, account type "Basic | Upgrade", and the user name "Dave Clements" with an "Add Connections" button. The group name "Galaxy Project" is prominently displayed. Below the name are tabs for "Discussions", "Members", "Promotions", "Jobs", "Search", "Manage", and "More...". A "Start" section offers options for "Discussion" and "Poll". A "Your Activity" section shows a recent discussion titled "GalaxyAdmins Web Meetup: 10 am US Central, March 20" by Dave Clements, posted 17 days ago. The discussion content mentions a meeting on March 20, 2013, and a migration to a HPC cloud. Below the discussion are "Like", "Comment", and "Unfollow" buttons. A "Latest Discussions" section shows another discussion titled "2013 Galaxy Community Conference (GCC2013), 30 June - 2 July, Oslo, Norway". A "Latest Updates" sidebar on the right lists recent group members: Courtney Reveal, Ratnamala Dam Manna, and Samuel Lampa. At the bottom, there are advertisements for "You a Web/App Developer?" and "Perfect Online Training".

Wikis and social sites:  
communicate, enable,  
reward.

# Enable sharing, contributing

**Galaxy Tool Shed** Repositories Help User

2543 valid tools on Apr 03, 2013

**Search**

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

**Valid Galaxy Utilities**

- [Tools](#)
- [Custom datatypes](#)
- [Repository dependency definitions](#)
- [Tool dependency definitions](#)

**All Repositories**

- [Browse by category](#)

**Available Actions**

- [Login to create a repository](#)

## Categories

<u>Name</u>	<u>Description</u>	<u>Repositories</u>
<a href="#">Assembly</a>	Tools for working with assemblies	18
<a href="#">Computational chemistry</a>	Tools for use in computational chemistry	4
<a href="#">Convert Formats</a>	Tools for converting data formats	25
<a href="#">Data Source</a>	Tools for retrieving data from external data sources	14
<a href="#">Fasta Manipulation</a>	Tools for manipulating fasta data	20
<a href="#">Genomic Interval Operations</a>	Tools for operating on genomic intervals	21
<a href="#">Graphics</a>	Tools producing images	10
<a href="#">Metagenomics</a>	Tools enabling the study of metagenomes	7
<a href="#">Micro-array Analysis</a>	Tools for performing micro-array analysis	4
<a href="#">Next Gen Mappers</a>	Tools for the analysis and handling of Next Gen sequencing data	44
<a href="#">Ontology Manipulation</a>	Tools for manipulating ontologies	6
<a href="#">Phylogenetics</a>	Tools for performing phylogenetic analysis	4
<a href="#">Proteomics</a>	Tools enabling the study of proteins	21




# Communicate!

**Galaxy Wiki** DaveClements Settings Logout | Search:

News

## News

Announcements of interest to the Galaxy Community. These can include items from the Galaxy Team or the Galaxy community and can address anything that is of wide interest to the community.

The Galaxy News is also available as an [RSS feed](#) .

See [Add a News Item](#) below for how to get an item on this page, and the [RSS feed](#). Older news items are available in the [Galaxy News Archive](#).

### See also

- Galaxy News Briefs
- Galaxy Updates
- Galaxy on Twitter
- Events
- Learn
- Support
- About the Galaxy Project

## News Items


[GCC2013 & Galaxy GigaScience Series](#)  
[April 2013 Galaxy Update](#)  
[April 1, 2013 Galaxy Distribution](#)  
[Galaxy LinkedIn Group](#)  
[March 2013 GalaxyAdmins Meetup](#)  
[Main & Test ServerDowntime: 3/14](#)  
[March 2013 Galaxy Update](#)  
[GCC2013 Abstract Submission & Registration](#)  
[Galaxy, GMOD2013 & Biocuration 2013](#)  
[Feb 8, 2013 Galaxy Distribution & News Brief](#)  
[February 2013 Galaxy Update](#)  
[GCC2013 Training Day Topics: Vote!](#)  
[Galaxy Project Openings](#)

[News Archive](#)

## News Items

[GCC2013 & Galaxy GigaScience Series](#)

The 2013 Galaxy Community Conference (GCC2013) and BioMed Central are announcing a special thematic series in *GigaScience*, a new journal co-published in collaboration between BGI Shenzhen and BioMed Central focused on studies utilizing large-scale datasets and workflows. Galaxy is an open, web-based platform for data intensive biomedical research allowing their growing community of users to reproduce and share analyses. All accepted oral presentations from the meeting will be eligible for consideration in the series, and working with the [scientific committee](#), peer review will be coordinated,



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The Galaxy News is also available via RSS.

See [Add a News Item](#) on this page, and the RSS feeds available in the Galaxy Wiki.

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- [Galaxy Updates](#)
- [Galaxy on Twitter](#)
- [Events](#)
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## News Items

[GCC2013 & Galaxy](#)

The 2013 Galaxy Community Meeting is announcing a special track published in collaboration with the Galaxy community focused on studies utilizing Galaxy. This track will feature an open, web-based presentation format for users to reproduce analyses and for consideration in the Galaxy community.

## News Items

[GCC2013 & Galaxy GigaScience Series](#)



338 TWEETS

89 FOLLOWING

133 FOLLOWERS

[Follow](#)

## Tweets

 **The Tweet Of GMOD** @gmodproject 2 Apr  
Email [help@gmod.org](mailto:help@gmod.org) if you want to attend all (or part) of #GMOD2013 remotely. Streaming video+audio: all you need is a browser!  
[Expand](#)

 **The Tweet Of GMOD** @gmodproject 1 Apr  
Don't be an April fool and miss the GMOD conference: email [help@gmod.org](mailto:help@gmod.org) to attend online, or attend in person: [tinyurl.com/bvd7it7](http://tinyurl.com/bvd7it7)  
[View summary](#)

 **The Tweet Of GMOD** @gmodproject 30 Mar  
SGD and ENCODE DCC Jobs [dlvr.it/38vvGH](http://dlvr.it/38vvGH)  
[Expand](#)

 **The Tweet Of GMOD** @gmodproject 29 Mar  
New NGDx Group at Novartis [dlvr.it/38kS9Z](http://dlvr.it/38kS9Z)  
[Expand](#)







# Communicate!

News

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338 TWEETS 89 FOLLOWING 133 FOLLOWERS

### Tweets

**The Tweet Of GMOD** @gmodproject  
Email [help@gmod.org](mailto:help@gmod.org) if you want to attend [#GMOD2013](#) remotely. Streaming video+audio browser!  
Expand

**The Tweet Of GMOD** @gmodproject  
Don't be an April fool and miss the GMOD [help@gmod.org](mailto:help@gmod.org) to attend online, or attend [tinyurl.com/bvd7it7](http://tinyurl.com/bvd7it7)  
View summary

**The Tweet Of GMOD** @gmodproject  
SGD and ENCODE DCC Jobs [divr.it/38vvg](http://divr.it/38vvg)  
Expand

**The Tweet Of GMOD** @gmodproject  
New NGDx Group at Novartis [divr.it/38kS9Z](http://divr.it/38kS9Z)  
Expand

### April 2013 Galaxy Update

The April 2013 Galaxy Update is now available.

#### Highlights:

- the GCC2013 **oral presentation abstract deadline is 12 April**, which is less than 2 weeks away. Early registration, and poster abstract submission are also open.
- Two new public Galaxy servers are featured
- The slides and screencast for the March Galaxy Community Meeting
  - And, please help determine what the Galaxy Team will be presenting
- 32 new papers and 5 new tags
- Open Positions at six different institutions
- Other Upcoming Events
- Galaxy Distributions
- Tool Shed Contributions
- Other News

If you have anything you would like to see in the next update, please contact Dave Clements and the Galaxy Team

Dave Clements and the Galaxy Team

Posted to

### April 1, 2013 Galaxy Distribution

#### Complete News Brief

#### Highlights:

- Job running configuration changes and refactored runner plugins
- Required reset of the metadata on your instance repositories plus Changes required to your instance if you are hosting a local Tool Shed
- Basic Data Manager Functionality now present
- Tool Shed, Trackster, Cloudman, Workflows and new Pull Request updates.
- New bug fixes and improvements.

<http://getgalaxy.org>

<http://bitbucket.org/galaxy/galaxy-dist>

<http://galaxy-dist.readthedocs.org>

new: hg clone <http://www.bx.psu.edu/hg/galaxy>

upgrade: hg pull  
hg update release\_2013.04.01

Thanks for using Galaxy,

The Galaxy Team

Posted to



Events

## Galaxy Event Horizon

Events with Galaxy-related content are listed here.



Also see the [Galaxy Events Google Calendar](#) for a listing of events and deadlines that are relevant to the Galaxy Community. This is also available as an RSS feed

If you know of any event that should be added to this page and/or to the Galaxy Event Calendar, please add it here or send it to [outreach@galaxyproject.org](mailto:outreach@galaxyproject.org).

#### Contents

- Upcoming Events
- Other Calendars
- Past Events
  - 2013
  - Archive

## Upcoming Events



Date	Topic/Event	Venue/Location	Contact
April 5-6	2013 GMOD Meeting	Cambridge, United Kingdom, immediately prior to Biocuration 2013	Dave Clements
April 7-10	GO Galaxy Workshop	Biocuration 2013, Cambridge, United Kingdom	Dave Clements, Suzanna Lewis
April 7-8	BOSC/Broad Interoperability Hackathon	Cambridge, Massachusetts, United States	Brad Chapman
April 9-11	Workshop: <i>Integrated Research Data Management for Next Gen Sequencing Analysis Using Galaxy and Globus Online Software-as-a-Service</i>	BioIT World, Boston, Massachusetts, United States	Ravi K. Madduri, Alex R. Paciorkowski, Vas Vasiliadis
	Talk: <i>Integrated Research Data management and Analysis in NGS using Globus Online Software-as-a-Service</i>		Ravi K. Madduri

# Listen!

The screenshot shows the GitHub interface for the repository `GMOD/jbrowse`. The top navigation bar includes the GitHub logo, links for 'Explore GitHub', 'Search', 'Features', and 'Blog', along with 'Sign up for free' and 'Sign in' buttons. The repository name 'GMOD/jbrowse' is displayed with '90' stars and '41' forks. Below this, there are tabs for 'Code', 'Network', 'Pull Requests' (0), 'Issues' (61), 'Wiki', and 'Graphs'. The 'Issues' tab is active, showing a search bar and a 'New Issue' button. On the left, there are filters for 'Everyone's Issues' (61) and a list of labels: 'big task' (10), 'bug' (4), 'feature' (50), 'from-lighthouse' (12), 'important' (22), 'in progress' (1), 'small task' (3), 'documentation' (0), 'needs-IE' (0), 'needs-review' (0), 'urgent' (0), and 'user support' (0). The main content area displays a list of 61 open issues, sorted by 'Newest'. The first few issues are: '#232 merge and update @a8wright GBrowse conf converter' (feature, important), '#231 allow scrolling further left than 0' (feature), '#230 display VCF genotypes as subtracks' (feature, important), '#228 more canvas glyphs' (feature, important), '#226 sortable table of genotypes in VCF details' (feature), '#225 drag to adjust track height' (feature), '#224 cytoband/ideogram tracks' (feature), and '#221 add a 6-frame translation track' (feature).

The screenshot shows a survey titled '2012 Galaxy Community Conference Evaluation'. The survey asks for feedback on the 2012 Galaxy Community Conference. The first question is 'Would you recommend future Galaxy events to others?' with radio button options: 'Yes', 'Yes, but ...', and 'No'. Below this is a text box for providing reasons if the answer is 'no' or 'Yes, but ...'. The survey then asks 'How useful was the Training Day?' with a 5-point scale from 'Not at all' to 'Exceptional'. The next question is 'Was the Training Day well run and organized?' with a similar 5-point scale. The final question is 'Did the Training Day meet your expectations?' with a 3-point scale from 'Fell short' to 'Exceeded'. At the bottom, there is a section for 'Additional comments on Training Day usefulness, organization and expectations:' with a note that general comments and specific comments on particular workshops are encouraged, followed by a text box for comments.

*Just appearing* to listen is not enough



# Sing your community's efforts

**MENDELEY**

Generic Model Organism Database (GMOD) project

Group activity

- Amelia Ireland added a document to this group: Visualizing next-generation sequencing data with JBrowse.
- Amelia Ireland added documents to this group: G-DOC: a systems medicine platform for personalized genomics; An online database for genome information of agricultural plants.
- Amelia Ireland added documents to this group: New insights into the Tyrolean Isomarm's origin and evolution as inferred by whole-genome sequencing; Chado controller: advanced annotation management community annotation system.
- Amelia Ireland added documents to this group: JBrowse: a next-generation genome browser; WebJBrowse-a web server for JBrowse; Using WebJBrowse to visualize genome annotations.

**madduri** 2 days  
 Looking forward to #BioIT13. Please join us in our pre-conference workshop on NGS analysis using @globusonline and @galaxyproject @awscloud  
 by galaxyproject

**CiteULike** MyCiteULike Group: Galaxy

Group: Galaxy - library 926 articles

Group Tags: methods (450), workbench (231), other (111), isogalaxy (45), tools (31), unknown (30), shared, project, howto, reproducibility, usemain, usepublic, cloud, usecloud, uselocal

- Acidobacterial community responses to agricultural management of soils
- Parallelization in Scientific Workflow Management Systems
- Ecology of Subglacial Lake Vostok (Antarctica), Based on Metagenomic Analyses of Accretion Ice
- The Role of the Arabidopsis Exosome in siRNA-Independent Silencing of Heterochromatin
- The challenges of delivering bioinformatics training in the analysis of high-throughput data
- Diagnostic Cancer Genome Sequencing and the Contribution of Germline Variants

**Swiss Galaxy Workshop**  
 Bern, 3 October 2012  
<http://bit.ly/gxyswiss>

## Publicly Accessible Galaxy Servers

Galaxy's public server (UseGalaxy.org, Main) can meet many needs, but it is not suitable for everything (see Big Picture/Choices for why) and cannot possibly scale to meet the entire world's needs.

Fortunately the Galaxy Community is helping out by installing Galaxy at their institutions and then making those installations either publicly available or open to their organizations or community.

This page lists such public or semi-public Galaxy servers.

To add your public Galaxy server to this list, please either just add it (hey, it's a wiki), or contact Galaxy Outreach

### Andromeda

- Link: [Andromeda](#)
- Domain/Purpose: This is a fully populated Galaxy instance.
- Comments:



is hosted at the SURFsara High Performance Computing (HPC) cloud. The installation is supported by Enis (the Dutch GridMan project) and Mattias de Hollander (NIOO).

users: 10GB; Anonymous users: 10MB

is Bioinformatics Centre (NBIC) and BiG Grid SURFsara

- Domain/Purpose: Hosts the BALL (Biochemical Algorithms Library) Project tools, i.e. computer aided drug design and molecular modelling based on protein and ligand structure data.
- Comments:

ballaxy is a workflow framework for structure based computational biology based on the Galaxy workflow engine and the BALL (Biochemical Algorithms Library) application framework. It is tailored to handle structural molecular data



lightShift" or optimal bond order assignment of ligands "BOA Constructor".

login, but there is no guarantee how long any data will be preserved.

University, Saarbrücken, Germany), Oliver Kohlbacher (University of Tübingen, Germany), and many).

- Link: [Cistrome Analysis Pipeline](#)
- Domain/Purpose: ChIP-chip/seq and gene expression data
- Comments: The Cistrome Analysis Pipeline has the standard Galaxy tools, plus 29 additional ChIP-chip and ChIP-seq specific tools, including preliminary peak calling and correlation analyses, downstream genome feature association, gene expression analyses, and motif discovery.

### Contents

- Andromeda
- ballaxy
- Cistrome Analysis Pipeline
- DBCLS Galaxy
- Galaxy Main
- Galaxy Test
- GeneNetwork
- Genboree
- Genomic Hyperbrowser
- Gene Ontology (GO)
- GigaGalaxy
- GWIPS-viz
- Huttenhower Lab
- IBDsite
- INRA-URGI
- MGTAXA
- Nebula
- NELLY
- Netherlands Metabolomics
- OPPL Galaxy
- Oqtans
- Pathogen Portal
- PopGenIE
- Regulatory Genomics
- RepeatExplorer
- Stem Cell Discovery Engine
- South Green
- SymD
- Wageningen University
- Yeoman

## Cistrome

A Galaxy Server dedicated to ChIP-\* analysis



# Gather!



# Encourage Sub-Communities

## GalaxyAdmins

Administrators of large Galaxy Instances  
Started by Ulowa in 2012

## Galaxy-France

French language and France-centric Galaxy community mailing list  
Launched after Galaxy Tour de France in 2012

## Galaxy-Public-Servers

Mailing list for those hosting public Galaxy servers  
Just launched

# Acknowledgements

GMOD:

Scott Cain

Amelia Ireland



# The Galaxy Team



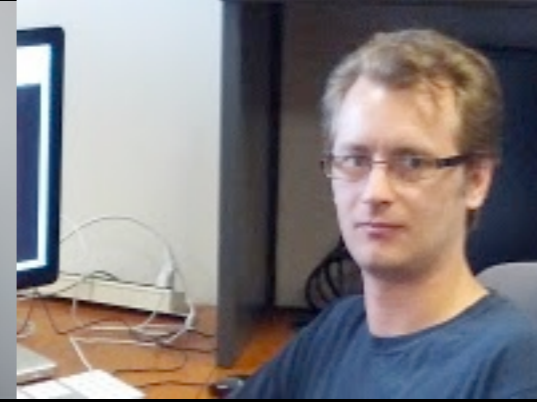
Enis Afgan



Dannon Baker



Dan Blankenberg



Dave Bouvier



Dave Clements



Nate Coraor



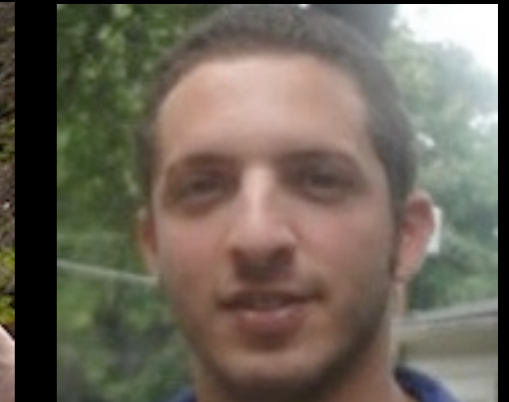
Carl Eberhard



Dorine Francheteau



Jeremy Goecks



Sam Guerler



Jen Jackson



Greg von Kuster



Ross Lazarus



Anton Nekrutenko



James Taylor

<http://wiki.galaxyproject.org/GalaxyTeam>



Galaxy is hiring post-docs and software engineers  
at both Emory and Penn State.



Please help.

<http://wiki.galaxyproject.org/GalaxyIsHiring>



***Thank You!***