Community Building, Outreach, and Support in Online Biological Communities

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Galaxy Team
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http://galaxyproject.org

Galaxy Project & Community

Mailing Lists

Wiki

News / Twitter

Social Bookmarking

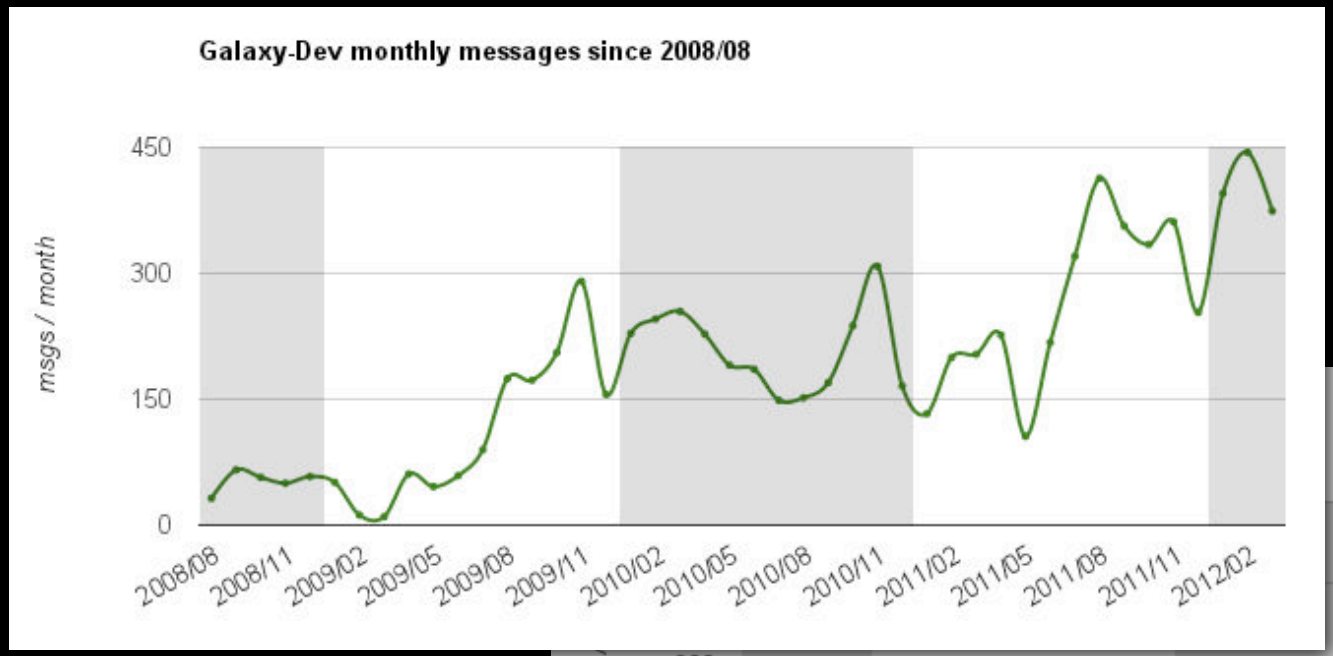
Google Custom Search

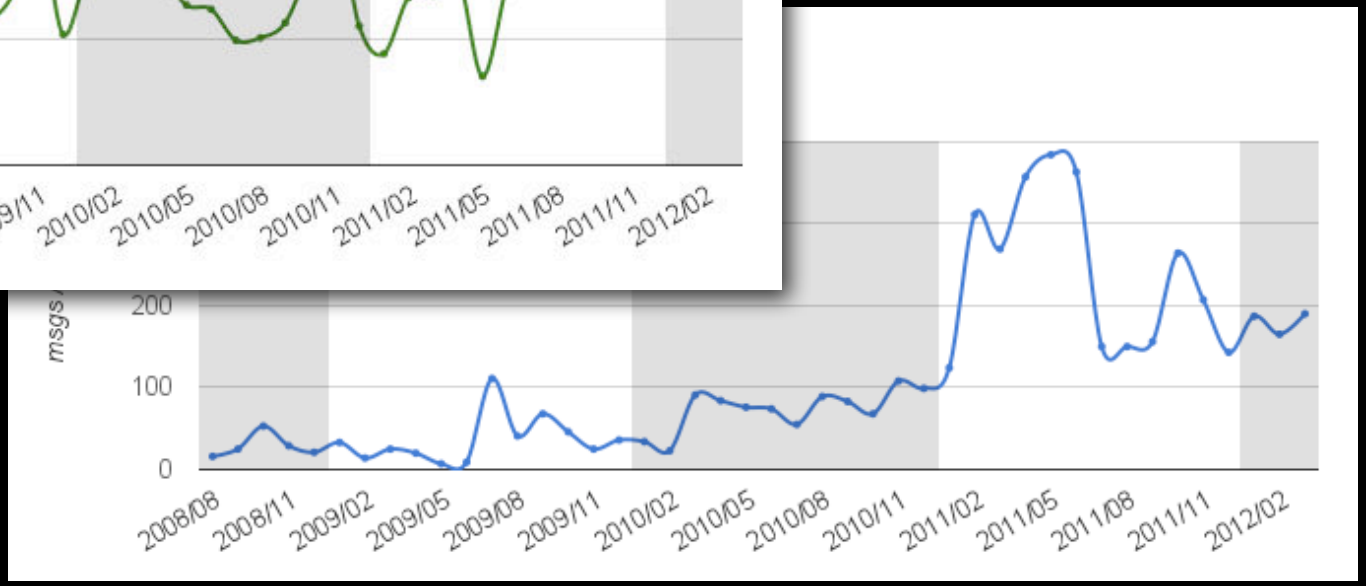
Galaxy Tool Shed

Mailing Lists

Very active galaxy-dev & galaxy-user lists

Led to new low-volume, moderated galaxy-announce List





Mailing Lists

Use Redmine for tracking

- galaxy-dev, galaxy-user threads create an issue
- Automatically assigned to last team member to respond
- Can close issue by BCC a special email address.
- Open issue tracking is done by Jen Jackson
- Redmine-Email bridge by Dannon Baker

http://redmine.org/

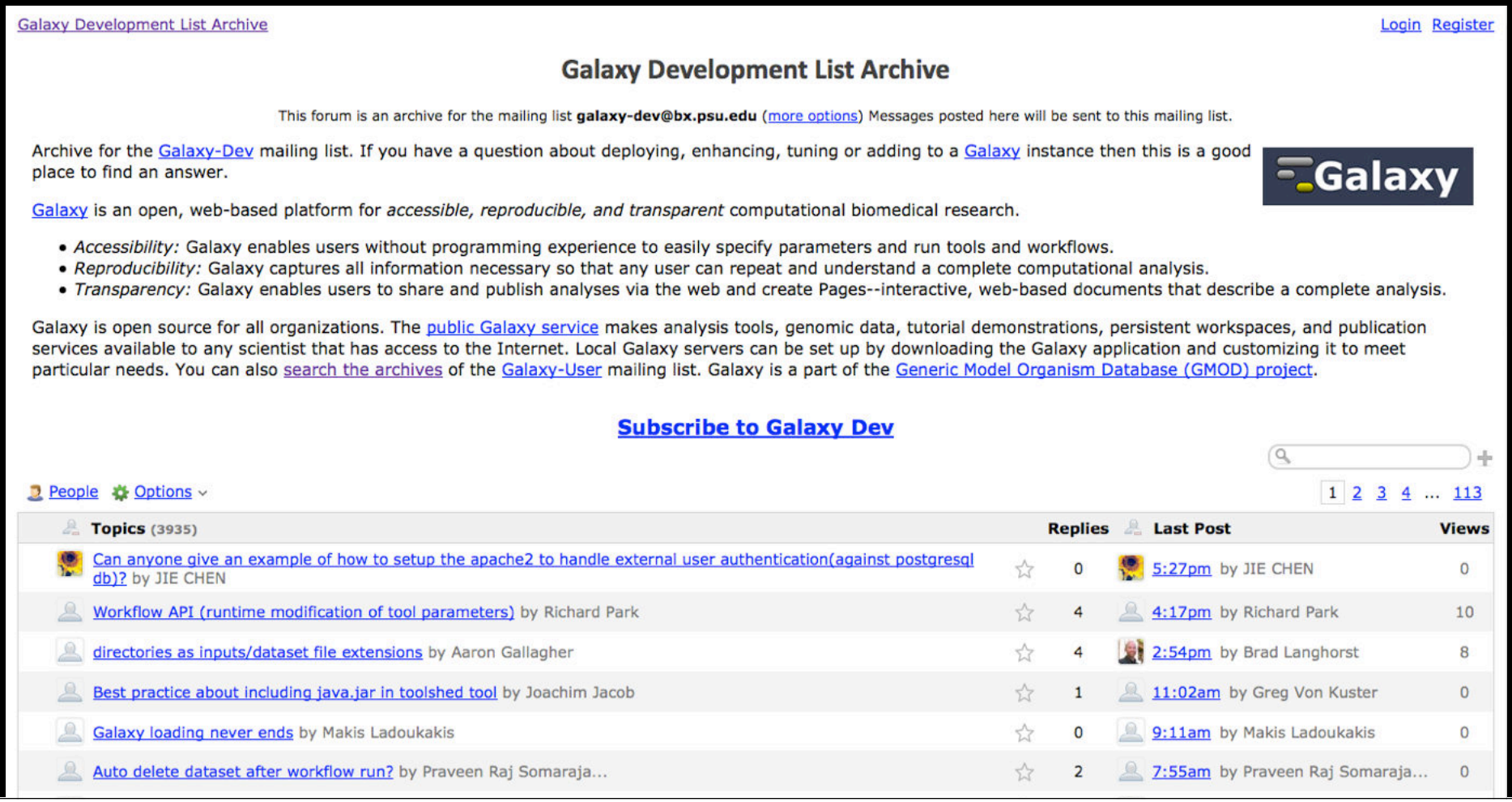
Lists are archived at Nabble.com

Modified to be an archive rather than a forum

Use Nabble's custom domain name support

Way better search interface than Mailman or Sourceforge

http://dev.list.galaxyproject.org/



Galaxy Development List Archive

Login Register

Galaxy Development List Archive

This forum is an archive for the mailing list **galaxy-dev@bx.psu.edu** (more options) Messages posted here will be sent to this mailing list.

Archive for the Galaxy-Dev mailing list. If you have a question about deploying, enhancing, tuning or adding to a Galaxy instance then this is a good place to find an answer.

Galaxy

Galaxy is an open, web-based platform for *accessible, reproducible, and transparent* computational biomedical research.

- *Accessibility:* Galaxy enables users without programming experience to easily specify parameters and run tools and workflows.
- *Reproducibility:* Galaxy captures all information necessary so that any user can repeat and understand a complete computational analysis.
- *Transparency:* Galaxy enables users to share and publish analyses via the web and create Pages--interactive, web-based documents that describe a complete analysis.

Galaxy is open source for all organizations. The public Galaxy service makes analysis tools, genomic data, tutorial demonstrations, persistent workspaces, and publication services available to any scientist that has access to the Internet. Local Galaxy servers can be set up by downloading the Galaxy application and customizing it to meet particular needs. You can also search the archives of the Galaxy-User mailing list. Galaxy is a part of the Generic Model Organism Database (GMOD) project.

Subscribe to Galaxy Dev

People Options

1 2 3 4 ... 113

Topics (3935)	Replies	Last Post	Views
Can anyone give an example of how to setup the apache2 to handle external user authentication(against postgresql db)? by JIE CHEN	0	5:27pm by JIE CHEN	0
Workflow API (runtime modification of tool parameters) by Richard Park	4	4:17pm by Richard Park	10
directories as inputs/dataset file extensions by Aaron Gallagher	4	2:54pm by Brad Langhorst	8
Best practice about including java.jar in toolshed tool by Joachim Jacob	1	11:02am by Greg Von Kuster	0
Galaxy loading never ends by Makis Ladoukakis	0	9:11am by Makis Ladoukakis	0
Auto delete dataset after workflow run? by Praveen Raj Somaraja...	2	7:55am by Praveen Raj Somaraja...	0

Wiki

Moved from Bibucket.org in 2011

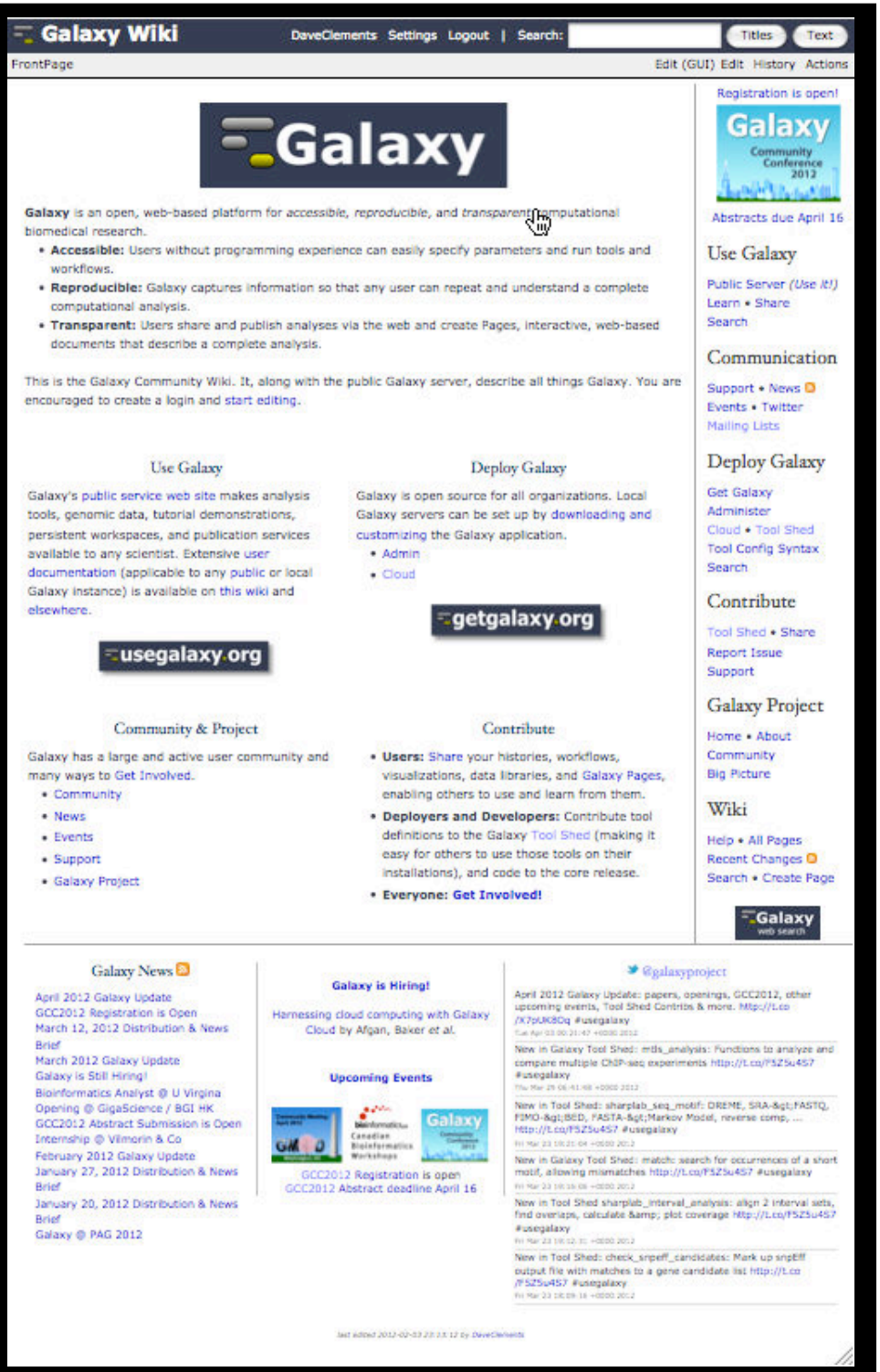
- Now using MoinMoin
- Markup in Creole, native Moin
- It's been a hit

Looked at Mediawiki, others

- We have a strong Python slant
- Mediawiki not built for projects

http://galaxyproject.org/wiki

http://wikimatrix.org/



News

Development News Briefs

- Accompany each release; about releases
- http://galaxyproject.org/wiki/DevNewsBriefs

Galaxy News and Monthly Updates

- Started in 2011 and 2012; web page & RSS feed
- Modeled on GMOD News
- http://galaxyproject.org/wiki/News

Twitter

- Generates a lot of engagement
- Use Bit.ly to track what gets interest
- Appropriate for items that will only interest some
- https://twitter.com/#!/galaxyproject

Social Bookmarking of Papers

Use CiteULike

Mirrored at Mendeley (Stephen Turner @ UVA)

Use tags to classify papers:

- Project: papers about Galaxy
- Shared: papers that use Galaxy's sharing and publishing features
- Howto: detailed tutorials that use Galaxy
- Methods: papers that used Galaxy in methods
- Workflow: papers about workflow
- Other: a very large misc.

http://www.citeulike.org/group/16008

Google Custom Search

Google Custom Search is very useful when

- You have information in several places
- You can identify specific areas of interest and have URLs that go with them

But I can't get Nabble archives to be searched!

http://galaxyproject.org/search/

Galaxy Tool Shed

A Galaxy Tool Shed is a repository for sharing tools, datatypes, and workflows

Once a tool is defined in one Galaxy instance, it is a small step to make it available to others

Built on top of Mercurial (similar to Git)

Moving tools out of distribution and into the Main Tool Shed:

http://toolshed.g2.bx.psu.edu/

What's Coming: Events


Date	Topic/Event	Venue/Location	Contact
April 4-5	**NBIC NGS Exome Sequencing & Variant Calling course** Including a session on *Read Mapping and Variant Calling with Galaxy*	Radboud UMC, Nijmegen	Hailiang "Leon" Mei
April 5-6	**April 2012 GMOD Meeting** Including a Galaxy Workshop on evening of April 5	Washington DC, immediately following Biocuration 2012	Dave Clements
April 24-26	**Leveraging SaaS for Next-Gen Sequencing: Case Study with the Galaxy Community** Pre-Conference Workshop	**Bio-IT World**, Boston, Massachusetts, United States	Ravi Madduri, Elizabeth Bartom
June 6-8	**Dynamically Scalable, Accessible Analysis with Galaxy Cloud**	**Bio-IT World Asia**, Singapore	James Taylor
June 11-12	**Informatics on High Throughput Sequencing Data Workshop**	Toronto, Ontario, Canada	Francis Ouellette
June 11-19	**Next-gen Sequencing in Evolutionary Biology Course**	US National Evolutionary Synthesis Center (NESCent), Durham, North Carolina, United States	Sergei Kosakovsky Pond
July 11	**Reproducible workflows for next generation sequencing analysis**	Nowgen, University of Manchester, United Kingdom	Tom Hancocks
July 13-17	**Bioinformatics Software Interoperability SIG (BSI-SIG)**	**ISMB 2012**, Long Beach, California, United States	Anton Nekrutenko
July 25-27	**2012 Galaxy Community Conference** Early registration and abstract submission are now open.	Chicago, Illinois, United States	Dave Clements
September 27-29	**Beyond the Genome 2012**	Harvard Medical School, Boston, Massachussets	James Taylor
November 6-10	**Galaxy 101: Data Integration, Analysis and Sharing** and **Working with High-Throughput Data and Data Visualization** workshops	**American Society of Human Genetics (ASHG)**, San Francisco, California, United States	Galaxy Outreach

http://galaxyproject.org/wiki/Events

The Galaxy community's annual gathering

A new Training Day added July 25

- 7 topics, 3 parallel tracks, 12 sessions
- 1) Intro, 2) Installing, 3) CloudMan, 4) Integrating Tools & Sources, 5) API, 6) Tool Shed, 7) Ion Torrent SDK

Key Dates

- **April 16: Abstracts due**
- **June 11: Early registration ends (early reg is cheap)**

Thanks

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April 5, 2012
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Galaxy Analysis Workspace