Community Building, Outreach, and Support in Online Biological Communities

Dave Clements

Galaxy Team

April 6, 2012

http://galaxyproject.org
Galaxy Project & Community

Mailing Lists
Wiki
News / Twitter
Social Bookmarks
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

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/](http://dev.list.galaxyproject.org/)
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 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/
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

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

April 5, 2012
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