NGS Data Analysis With GenomeSpace & Galaxy, Part 2

FGED 15th International Conference

Seattle, Washington
June 22, 2013

Dave Clements, Emory University
http://galaxyproject.org/

Agenda

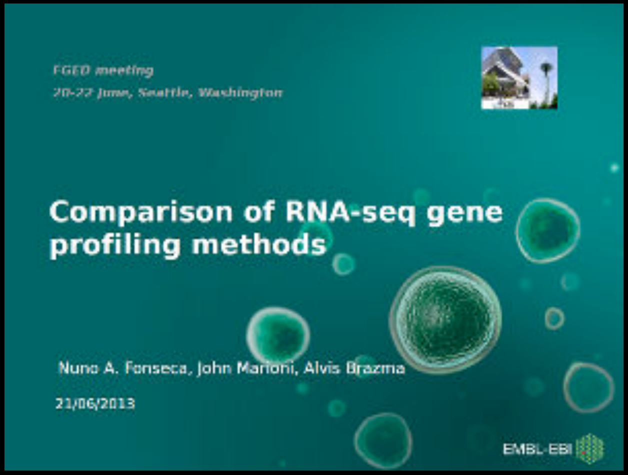
9:00	Welcome
9:15	GenomeSpace
10:15	Galaxy: First Steps and Data Quality
11:00	Break
11:30	RNA-Seq Analysis and Galaxy Project
12:30	Done

Link to slides on http://bit.ly/gxyEvents

Goals

1. Introduce Galaxy
2. Introduce bioinformatics concepts and formats
3. Hands-on experience

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



FGED meeting
20-22 June, Seattle, Washington

Comparison of RNA-seq gene profiling methods

Nuno A. Fonseca, John Marioni, Alvis Brazma

21/06/2013

EMBL-EBI

What we actually cover depends on participants' interests.

What is Galaxy?

- **A free (for everyone) web service** integrating a wealth of tools, compute resources, terabytes of reference data and permanent storage
- **Open source software** that makes integrating your own tools and data and customizing for your own site simple
- These options result in several **ways to use Galaxy**

http://galaxyproject.org

Galaxy: First Impressions

http://cloud1.galaxyproject.org/

http://cloud2.galaxyproject.org/

http://cloud3.galaxyproject.org/

RNA-seq Exercise

http://cloud1.galaxyproject.org/
http://cloud2.galaxyproject.org/
http://cloud3.galaxyproject.org/

Shared Data → Published Pages

→ RNA-Seq Analysis Exercise

RNA-seq Exercise: A Plan

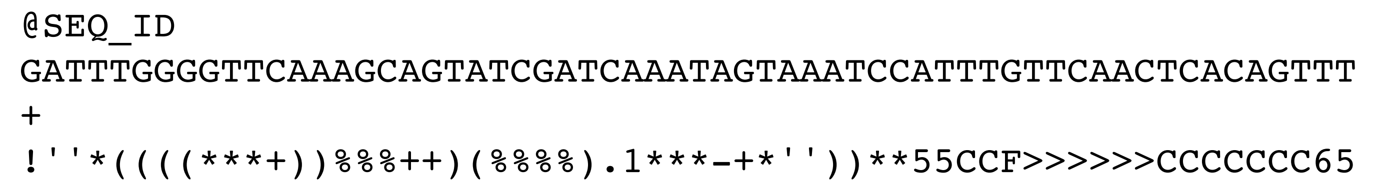
- Get input datasets; will mostly map to chr19
- Look at quality
- Trim as we see fit.
- Map the reads to the human reference (hg19) using Tophat
- Run Cufflinks on Tophat output to assemble reads into transcripts
- Visualize it

RNA-seq Exercise: A Plan

- Get input datasets; will mostly map to chr19
    - All datasets are FASTQ and from the Body Map 2.0 project
        - Shared Data → Published Pages → RNA-Seq Analysis Exercise
        - or Shared Data → Data Libraries → RNA-Seq Example

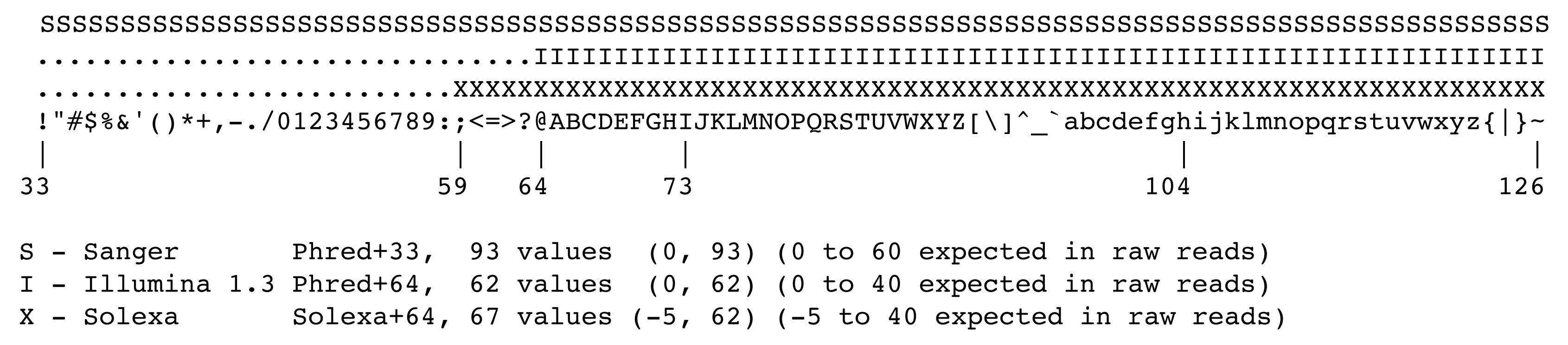
What is FASTQ?

- Specifies sequence (FASTA) and quality scores (PHRED)
- Text format, 4 lines per entry



```
@SEQ_ID
GATTTGGGGTTCAAAGCAGTATCGATCAAATAGTAAATCCATTTGTTCAACTCACAGTTT
+
!''*((((***+))%%%++)(%%%%).1***-+*''))**55CCF>>>>>>CCCCCCC65
```

- FASTQ is such a cool standard, there are 3 (or 5) of them!



```
 SSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS
 ...............................IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
 ..........................XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
 !"#$%&'()*+,-./0123456789:;<=>?@ABCDEFGHIJKLMNOPQRSTUVWXYZ[\]^_`abcdefghijklmnopqrstuvwxyz{|}~
 |                         |    |        |                              |                     |
33                        59   64       73                            104                   126

S - Sanger        Phred+33,  93 values  (0, 93) (0 to 60 expected in raw reads)
I - Illumina 1.3 Phred+64,  62 values  (0, 62) (0 to 40 expected in raw reads)
X - Solexa        Solexa+64, 67 values (-5, 62) (-5 to 40 expected in raw reads)
```

http://en.wikipedia.org/wiki/FASTQ_format

RNA-seq Exercise: A Plan

Look at quality Options 1 & 2:

1. NGS QC and Manipulation → Compute Quality Statistics

   NGS QC and Manipulation → Draw quality score boxplot

   No control over how it is calculated or presented.

2. NGS QC and Manipulation → FastQ Summary Statistics,

   Graph / Display Data → Boxplot of quality statistics

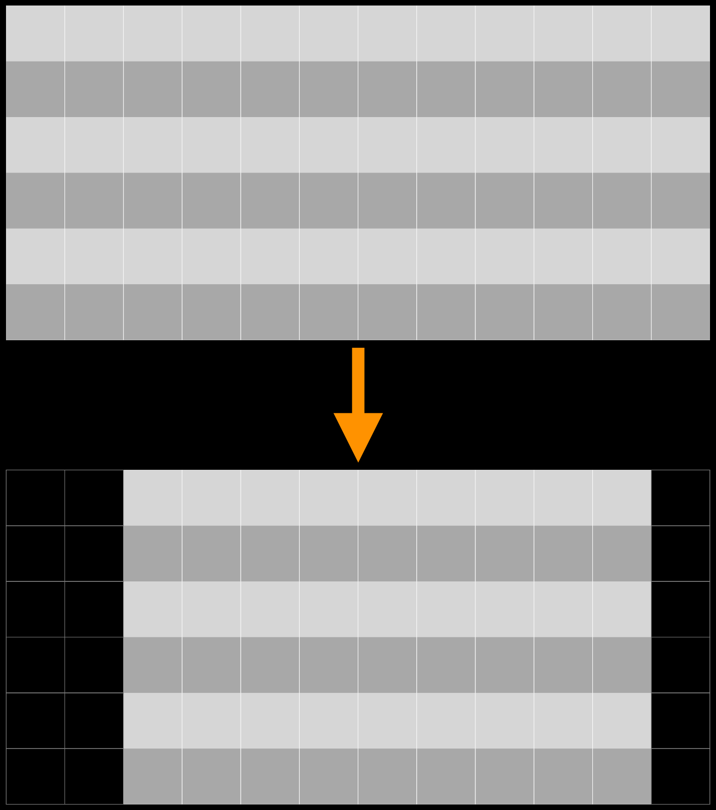
   Lots of control over what the box plot looks like,
   Stats in text and graphic formats

RNA-seq Exercise: A Plan

- Get input datasets; will mostly map to chr19
- Look at quality: Option 3
  - NGS QC and Manipulation → **FastQC**
  - Gives you a lot a lot more information but little control over how it is calculated or presented.

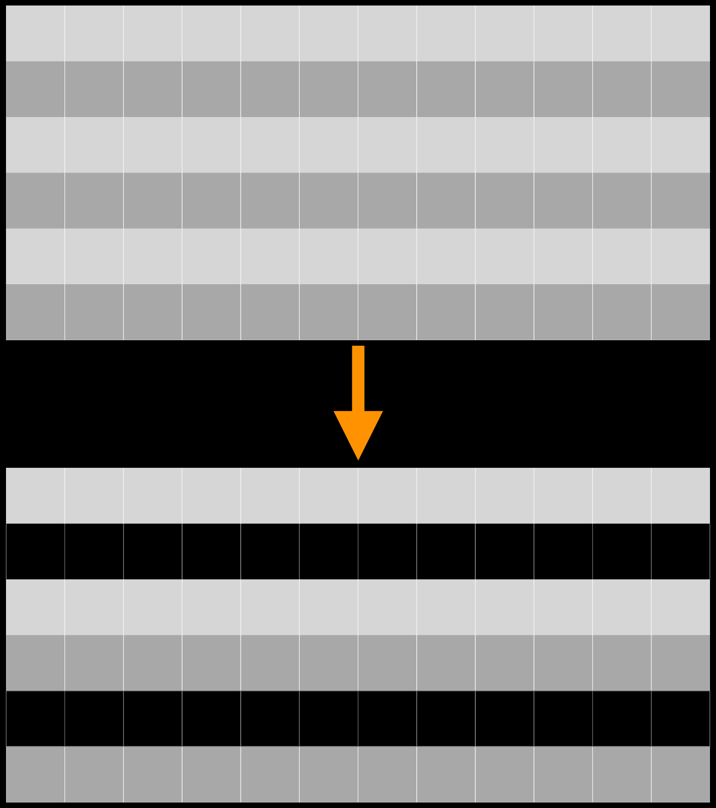
RNA-seq Exercise: A Plan

- Look at quality
- Trim as we see fit: Option 1
  - **NGS QC and Manipulation → FASTQ Trimmer by column**
  - Trim same number of columns from every record
  - Can specify different trim for 5′ and 3′ ends



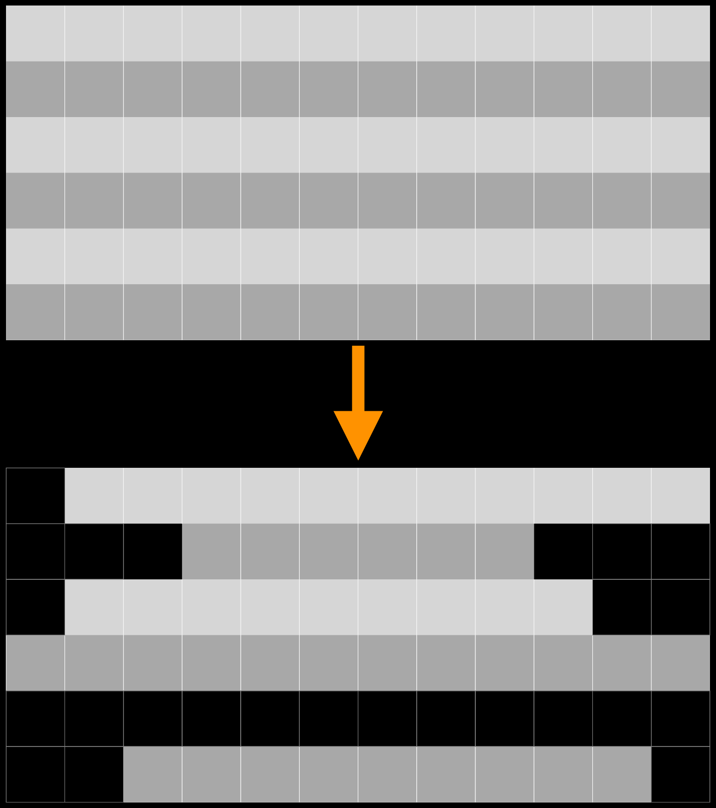
RNA-seq Exercise: A Plan

- Look at quality
- ~~Trim~~ Filter as we see fit: Option 2
  - NGS QC and Manipulation → **Filter FASTQ reads by quality score and length**
  - Keep or discard whole reads
  - Can have different thresholds for different regions of the reads.
  - Keeps original read length.

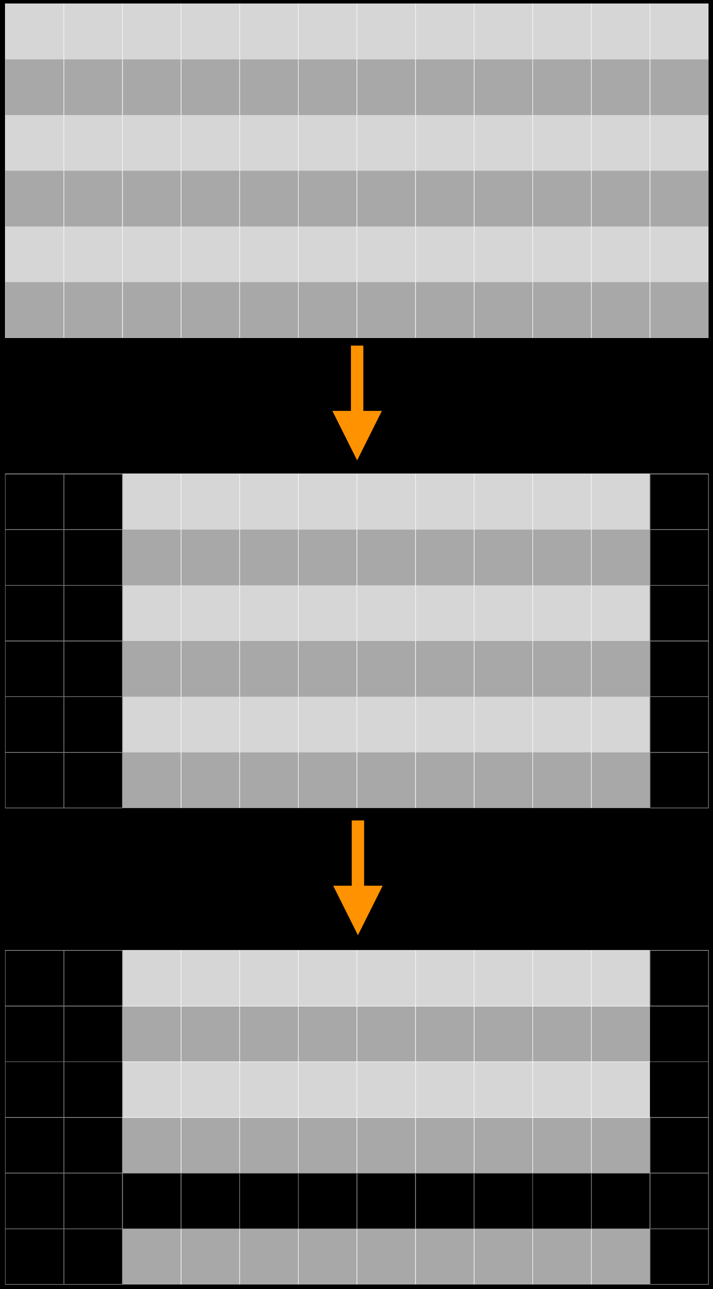


RNA-seq Exercise: A Plan

- Look at quality
- Trim as we see fit: Option 3
  - NGS QC and Manipulation → **FASTQ Quality Trimmer by sliding window**
  - Trim from both ends, using sliding windows, until you hit a high-quality section.
  - Produces variable length reads



Options are not mutually exclusive



Option 1

+

Option 2

Trim? *As we see fit?*

- Introduced 3 options
  - One preserves original read length, two don't
  - One preserves number of reads, two don't
  - Two keep/make every read the same length, one does not
  - One preserves pairings, two don't

Trim? *As we see fit?*

- Choice depends on downstream tools
- Find out assumptions & requirements for downstream tools and make appropriate choice(s) now.
- How to do that?
    - http://biostars.org/
    - http://seqanswers.com/
    - http://galaxyproject.org/search

SEQanswers
the next generation sequencing community

Biostar
BIOINFORMATICS EXPLAINED

Agenda

9:00 Welcome
9:15 GenomeSpace
10:15 Galaxy: First Steps and Data Quality
11:00 Break
11:30 RNA-Seq Analysis and Galaxy Project
12:30 Done

GMOD.org: purveyors of fine
genomics software

Agenda

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RNA-seq Exercise: A Plan

- Get input datasets; hg19, will mostly map to chr19
- Look at quality
- Trim as we see fit.
- Map the reads to the human reference using Tophat
  - *Imagine pages and pages of discussion on the intricacies and pitfalls of RNA-seq mapping here.*

RNA-seq Exercise: A Plan

- ...
- Trim as we see fit.
- Map the reads to the human reference using Tophat
- Run Cufflinks on Tophat output to assemble reads into transcripts
  - *Imagine pages and pages of discussion on the intricacies and pitfalls of RNA-seq transcript prediction here.*

RNA-seq Exercise: A Plan

- ...
- Map the reads to the human reference using Tophat
- Run Cufflinks on Tophat output to assemble reads into transcripts
  - *Imagine pages and pages of discussion on the intricacies and pitfalls of RNA-seq transcript prediction here.*
  - Visualize it

Visualizing Genomics

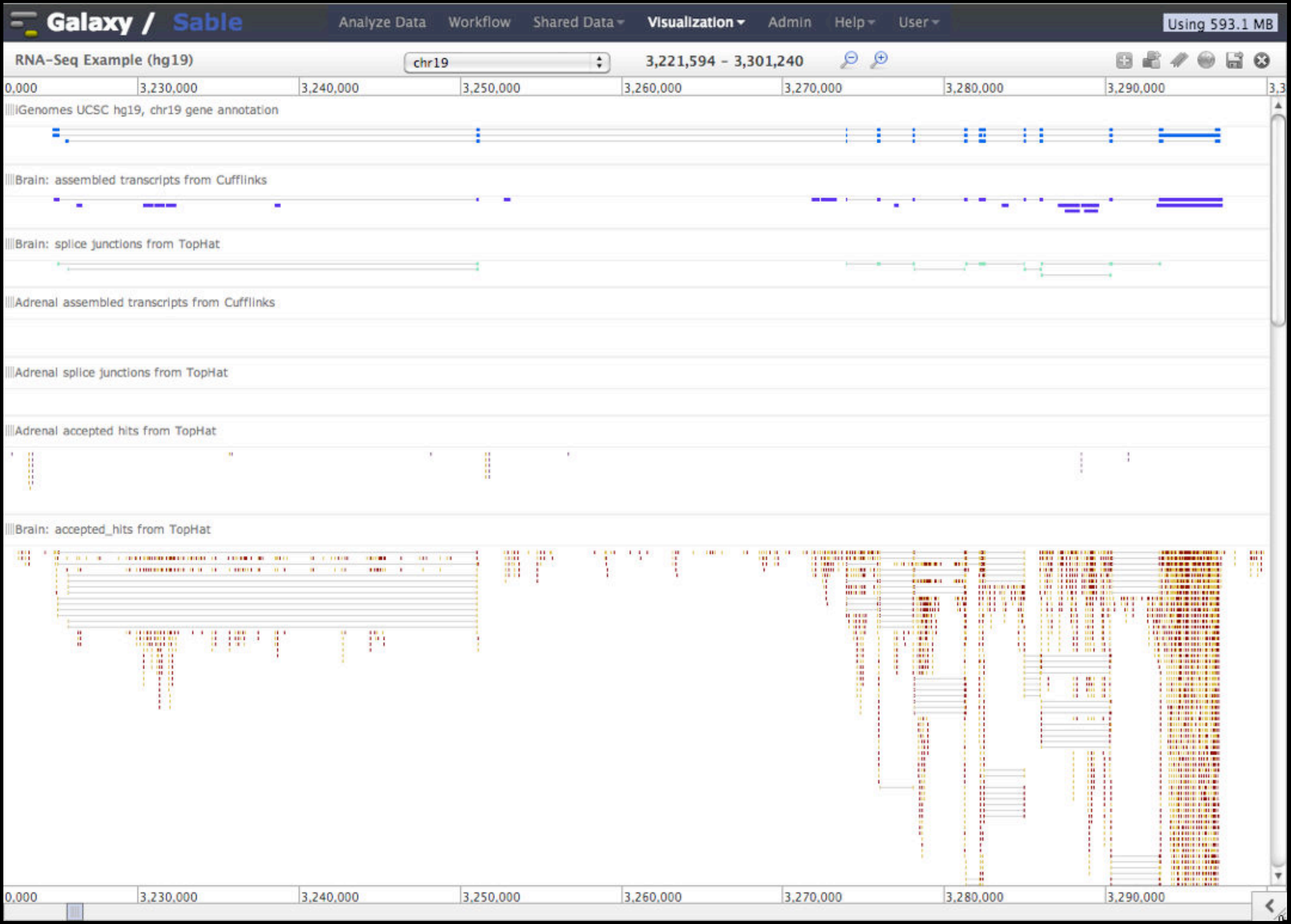
Supported external browsers

- UCSC
- Ensembl
- GBrowse
- IGB
- IGV

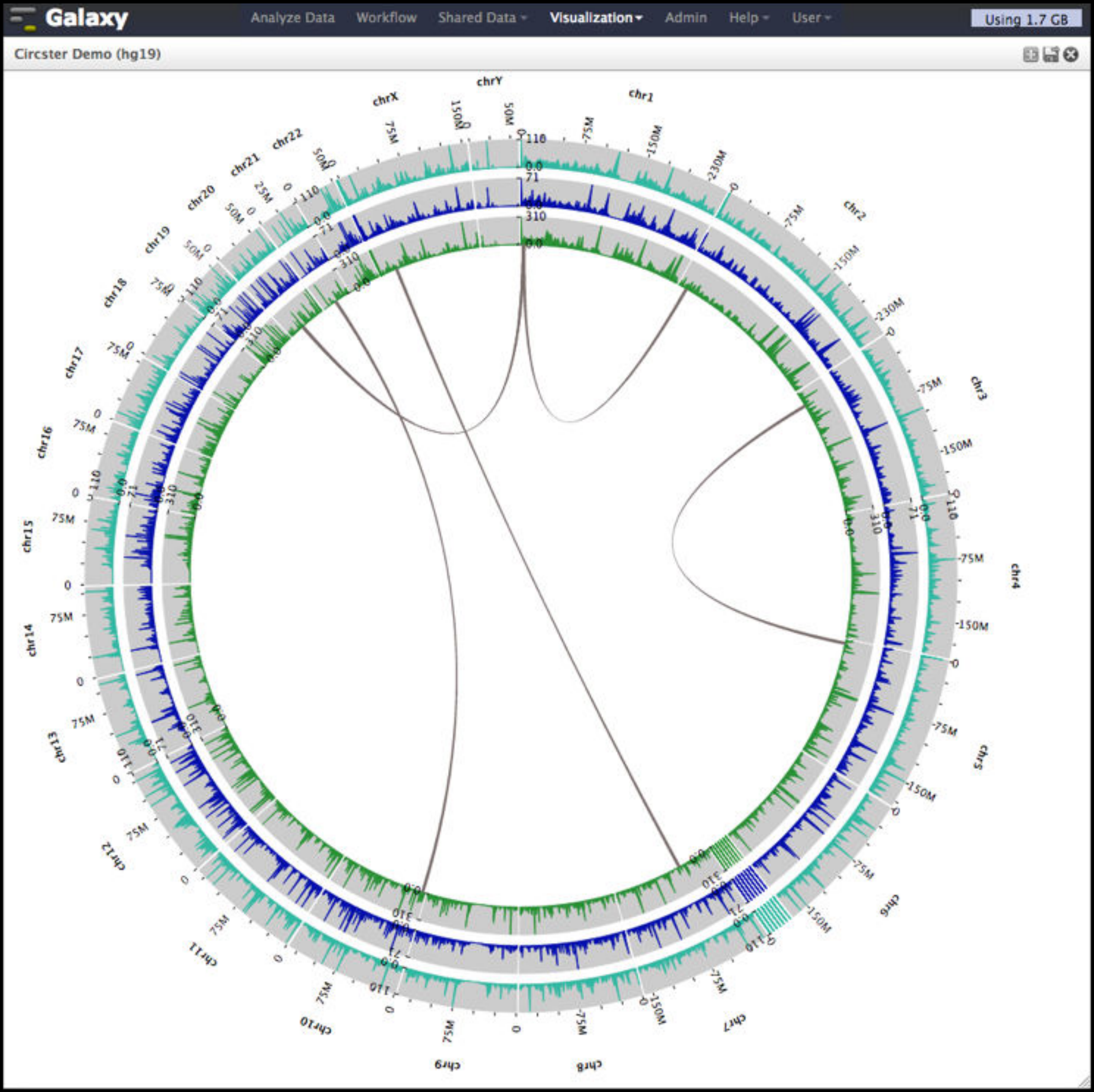
Traditional browser strengths:

- Showing what is nearby
- what else is happening here
- highlighting correlations
- integrating many datasets

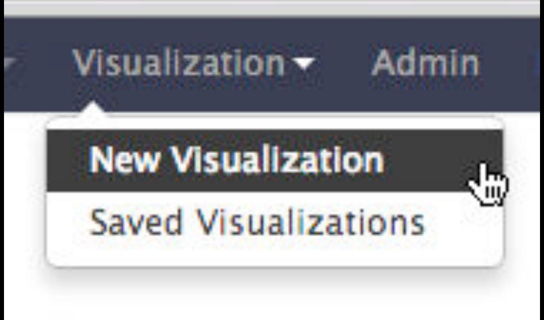
Trackster: Galaxy's embedded track browser



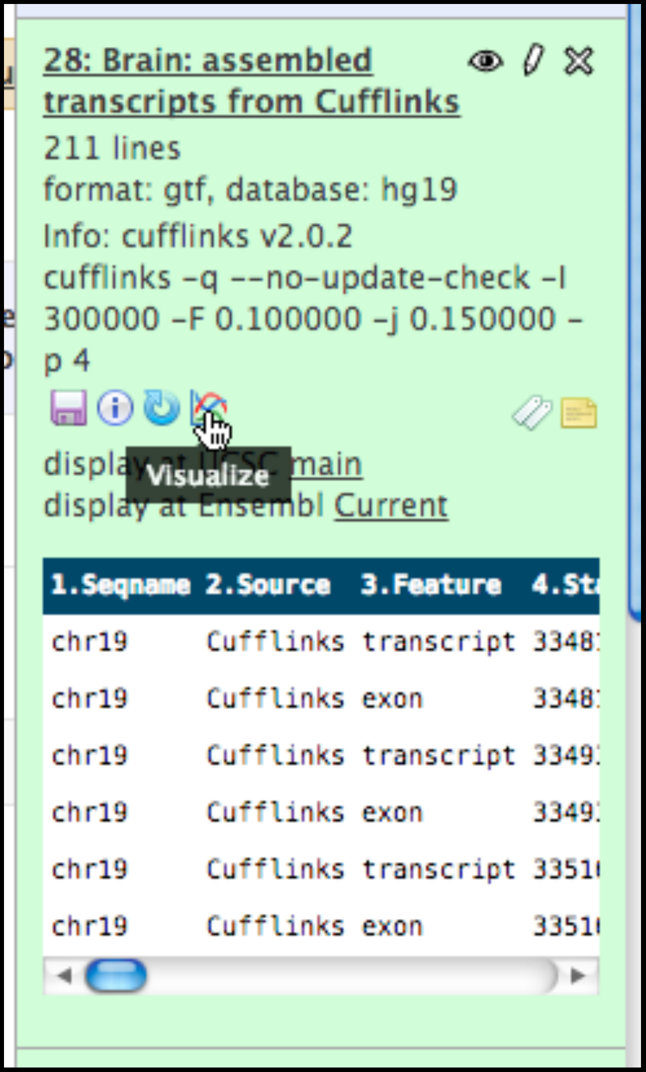
Circster


Galaxy
Analyze Data
Workflow
Shared Data
Visualization
Admin
Help
User
Using 1.7 GB
Circster Demo (hg19)
chr1
chr2
chr3
chr4
chr5
chr6
chr7
chr8
chr9
chr10
chr11
chr12
chr13
chr14
chr15
chr16
chr17
chr18
chr19
chr20
chr21
chr22
chrX
chrY
75M
150M
230M
110
0.0
71
310

Create a visualization in Galaxy



or



28: Brain: assembled transcripts from Cufflinks

211 lines

format: gtf, database: hg19

Info: cufflinks v2.0.2 cufflinks -q --no-update-check -I 300000 -F 0.100000 -j 0.150000 -p 4

display at UCSC main

display at Ensembl Current

1.Seqname	2.Source	3.Feature	4.St
chr19	Cufflinks	transcript	3348
chr19	Cufflinks	exon	3348
chr19	Cufflinks	transcript	3349
chr19	Cufflinks	exon	3349
chr19	Cufflinks	transcript	3351
chr19	Cufflinks	exon	3351

Vizualization inside Galaxy

- Levarges visualization to evaluate and refine analyses
- Exposes basic analyses in visualization to make it more informative
- Makes the analyze-visualize-refine loop seamless and fast
- Enables learning tools and exploring their parameter space
- Supports custom genome browsers, without a predefined reference genome

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What is Galaxy?

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- **Open source software** that makes integrating your own tools and data and customizing for your own site simple
- These options result in several **ways to use Galaxy**

http://galaxyproject.org

Galaxy is available ...

As a free (for everyone) web service

http://usegalaxy.org

However, ***a centralized solution cannot scale to meet the analysis needs of the entire world.***

Galaxy is available ...

- As a free (for everyone) web service

  http://usegalaxy.org

- As open source software

  http://getgalaxy.org

As Open Source Software: Local Galaxy Instances

- Galaxy is designed for local installation and customization
  - Easily integrate new tools
  - Easy to deploy and manage on nearly any (unix) system
  - Run jobs on existing compute clusters
- Requires a computational resource on which to be deployed

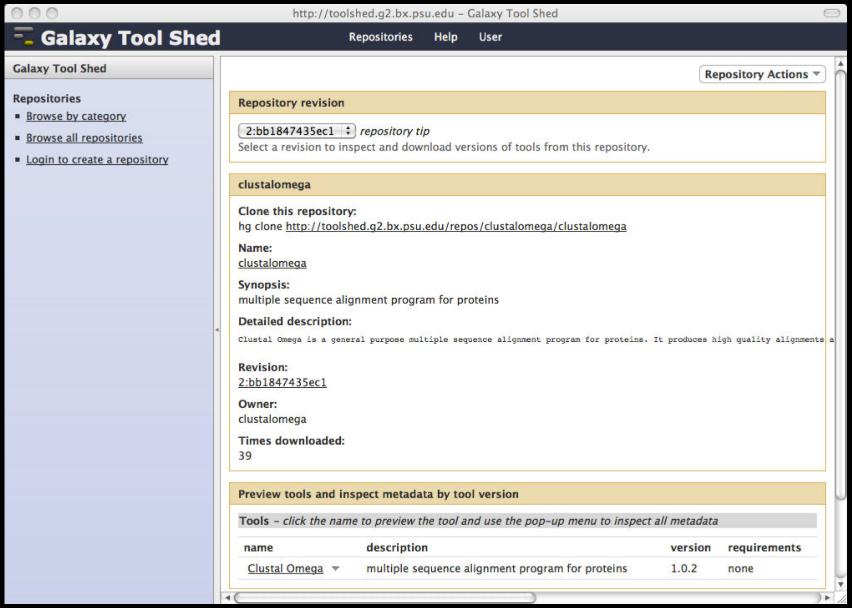
http://getgalaxy.org

Encourage Local Galaxy Instances

- Encourage and support Local Galaxy Instances
  - Support increasingly decentralized model and improve access to existing resources
  - Focus on building infrastructure to enable the community to integrate and share tools, workflows, and best practices

Galaxy Tool Shed

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



Repository revision

2:bb1847435ec1 *repository tip*

Select a revision to inspect and download versions of tools from this repository.

clustalomega

Clone this repository:
hg clone http://toolshed.g2.bx.psu.edu/repos/clustalomega/clustalomega

Name:
clustalomega

Synopsis:
multiple sequence alignment program for proteins

Detailed description:
`Clustal Omega is a general purpose multiple sequence alignment program for proteins. It produces high quality alignments a`

Revision:
2:bb1847435ec1

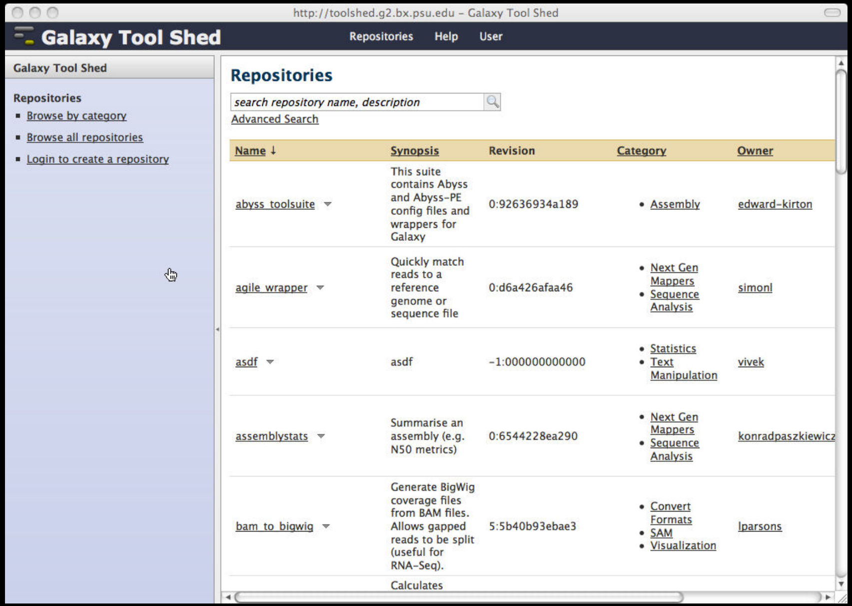
Owner:
clustalomega

Times downloaded:
39

Preview tools and inspect metadata by tool version

Tools – *click the name to preview the tool and use the pop-up menu to inspect all metadata*

name	description	version	requirements
Clustal Omega	multiple sequence alignment program for proteins	1.0.2	none



Repositories

Name ↓	Synopsis	Revision	Category	Owner
abyss_toolsuite	This suite contains Abyss and Abyss-PE config files and wrappers for Galaxy	0:92636934a189	• Assembly	edward-kirton
agile_wrapper	Quickly match reads to a reference genome or sequence file	0:d6a426afaa46	• Next Gen Mappers • Sequence Analysis	simonl
asdf	asdf	-1:000000000000	• Statistics • Text Manipulation	vivek
assemblystats	Summarise an assembly (e.g. N50 metrics)	0:6544228ea290	• Next Gen Mappers • Sequence Analysis	konradpaszkiewicz
bam_to_bigwig	Generate BigWig coverage files from BAM files. Allows gapped reads to be split (useful for RNA-Seq).	5:5b40b93ebae3	• Convert Formats • SAM • Visualization	lparsons
	Calculates			

Encourage **Public** Galaxy Instances

http://bit.ly/gxyServers

Interested in:

ChIP-chip and ChIP-seq?

- ✓ Cistrome

Statistical Analysis?

- ✓ Genomic Hyperbrowser

Protein synthesis?

- ✓ GWIPS-viz

de novo assembly?

- ✓ CBIIT Galaxy

Reasoning with ontologies?

- ✓ OPPL Galaxy

Repeats!

- ✓ RepeatExplorer

Everything?

- ✓ Andromeda

Plus many more

As Open Source Software: Local Galaxy Instances

- Galaxy is designed for local installation and customization
  - Easily integrate new tools
  - Easy to deploy and manage on nearly any (unix) system
  - Run jobs on existing compute clusters
- Requires a **computational resource** on which to be deployed

http://getgalaxy.org

Got your own cluster?

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

CLUSTER RESOURCES
TORQUE

GRID ENGINE

Platform Computing

DRMAA
Distributed Resource Management Application API — www.drmaa.org

Galaxy is available ...

- As a free (for everyone) web service

  http://usegalaxy.org

- As open source software

  http://getgalaxy.org

- *On the Cloud*

  http://usegalaxy.org/cloud

  We are using this right now

http://aws.amazon.com/education

Sharing and Publishing

Share:

Make something available to someone else

Publish:

Make something available to everyone

Galaxy Page:

Analysis documentation within Galaxy; easy to embed any Galaxy object

Sharing & Publishing enables Reproducibility

Reproducibility: Everybody talks about it, but ...

Galaxy aims to push the goal of reproducibility from the bench to the bioinformatics realm

All analysis in Galaxy is recorded without any extra effort from the user.

Histories, workflows, visualizations and *pages* can be shared with others or published to the world.

Sharing & Publishing enables Reproducibility

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]

OPEN ACCESS ARTICLE

This Article

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

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- » Abstract *Free*
- Full Text (PDF)

Current Issue

October 2010, 20 (10)

Sharing & Publishing enables Reproducibility

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]

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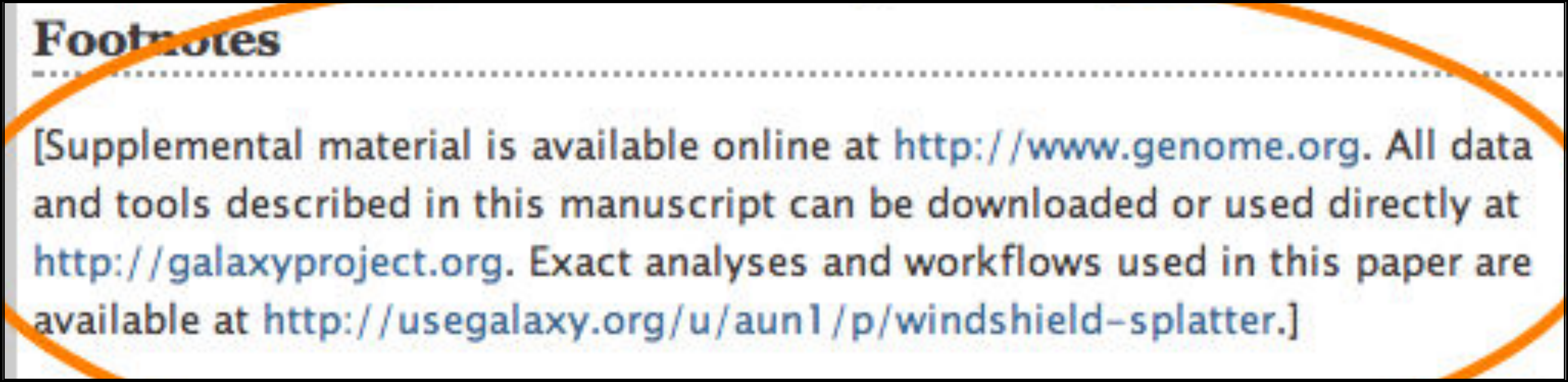
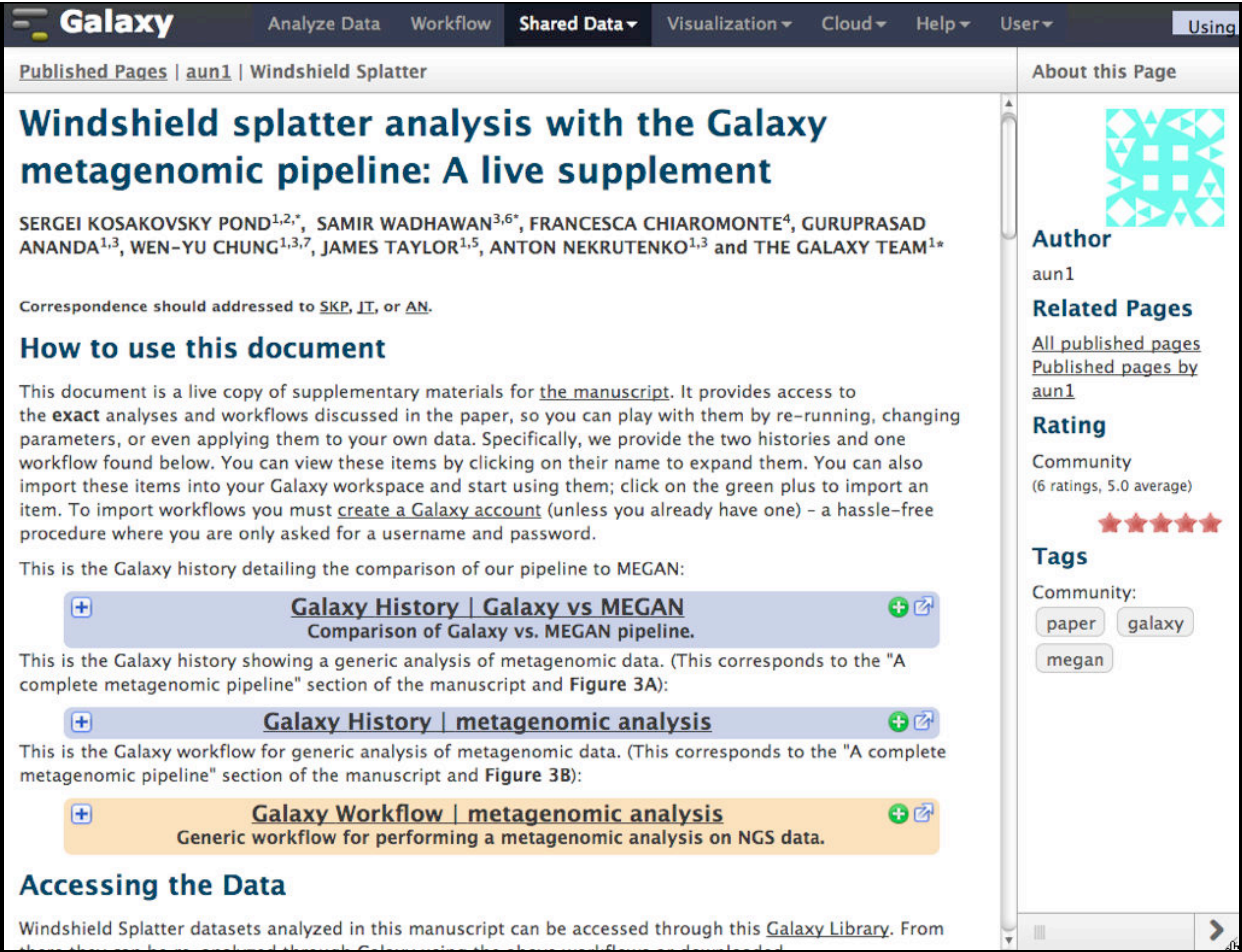


Footnotes

[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.]



Windshield splatter analysis with the Galaxy metagenomic pipeline: A live supplement

SERGEI KOSAKOVSKY POND[1,2,*], SAMIR WADHAWAN[3,6*], FRANCESCA CHIAROMONTE[4], GURUPRASAD ANANDA[1,3], WEN-YU CHUNG[1,3,7], JAMES TAYLOR[1,5], ANTON NEKRUTENKO[1,3] and THE GALAXY TEAM[1*]

Correspondence should addressed to SKP, JT, or AN.

How to use this document

This document is a live copy of supplementary materials for the manuscript. It provides access to the **exact** analyses and workflows discussed in the paper, so you can play with them by re-running, changing parameters, or even applying them to your own data. Specifically, we provide the two histories and one workflow found below. You can view these items by clicking on their name to expand them. You can also import these items into your Galaxy workspace and start using them; click on the green plus to import an item. To import workflows you must create a Galaxy account (unless you already have one) - a hassle-free procedure where you are only asked for a username and password.

This is the Galaxy history detailing the comparison of our pipeline to MEGAN:

Galaxy History | Galaxy vs MEGAN
Comparison of Galaxy vs. MEGAN pipeline.

This is the Galaxy history showing a generic analysis of metagenomic data. (This corresponds to the "A complete metagenomic pipeline" section of the manuscript and **Figure 3A**):

Galaxy History | metagenomic analysis

This is the Galaxy workflow for generic analysis of metagenomic data. (This corresponds to the "A complete metagenomic pipeline" section of the manuscript and **Figure 3B**):

Galaxy Workflow | metagenomic analysis
Generic workflow for performing a metagenomic analysis on NGS data.

Accessing the Data

Windshield Splatter datasets analyzed in this manuscript can be accessed through this Galaxy Library. From

Author

aun1

Related Pages

All published pages
Published pages by aun1

Rating

Community
(6 ratings, 5.0 average)
★★★★★

Tags

Community:
paper
galaxy
megan

http://usegalaxy.org/u/aun1/p/windshield-splatter

Sharing for Galaxy Administrators Too

Data Libraries

Make data easy to find

Genome Builds

Care about a particular subset of life?

Galaxy Tool Shed

Wrapping tools and datatypes

Galaxy Resources and Community

Mailing Lists (very active)
Unified Search
Issues Board
Events Calendar, News Feed
Community Wiki
GalaxyAdmins
Screencasts
Tool Shed
Public Installs
CiteULike group, Mendeley mirror
Annual Community Meting

http://wiki.galaxyproject.org

Galaxy Resources and Community: Mailing Lists

http://wiki.galaxyproject.org/MailingLists

Galaxy-Announce

Project announcements, low volume, moderated

Low volume (42 posts in 2012, 2100+ members)

Galaxy-User

Questions about using Galaxy and usegalaxy.org

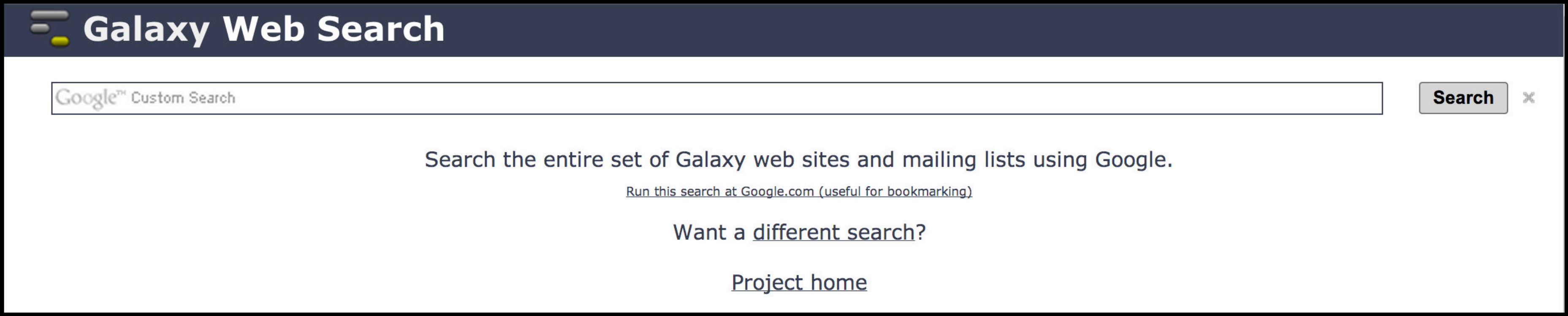
High volume (2900 posts in 2012, 2700+ members)

Galaxy-Dev

Questions about developing for and deploying Galaxy

High volume (4500 posts in 2012, 900+ members)

Unified Search: http://galaxyproject.org/search

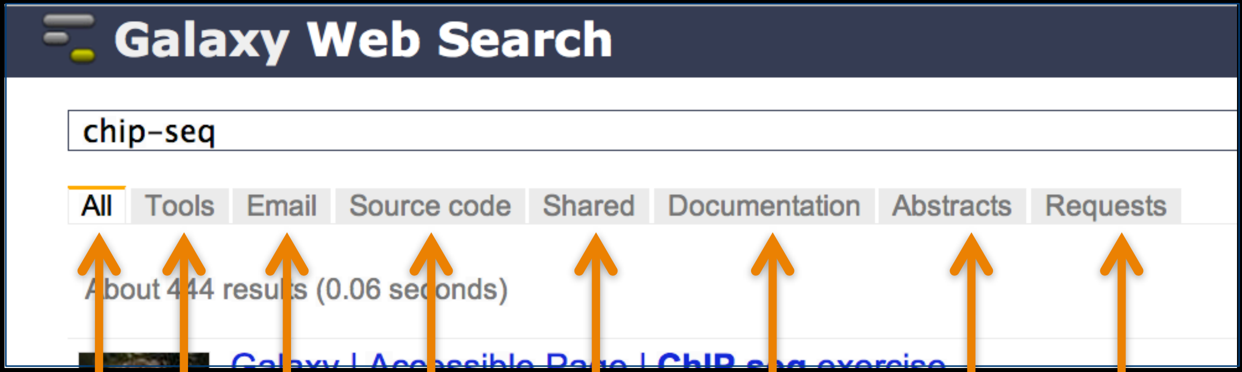


Search the entire set of Galaxy web sites and mailing lists using Google.

Run this search at Google.com (useful for bookmarking)

Want a different search?

Project home



About 444 results (0.06 seconds)

Galaxy | Accessible Page | ChIP-seq exercise

Find

Everything on …

Tools for …

Email about …

Source code for …

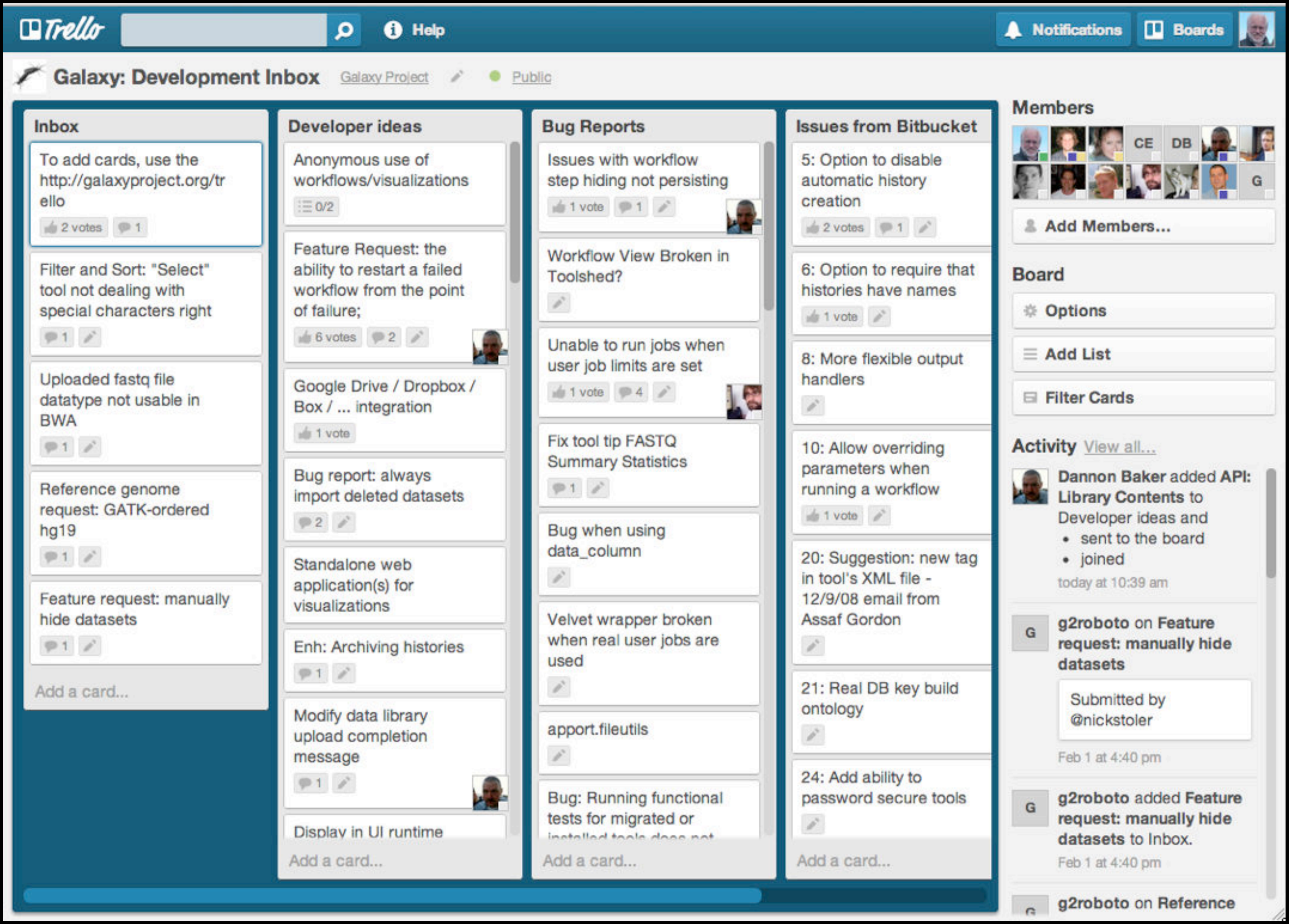
Published Histories, Pages, Workflows, about …

Documentation on …

Papers using Galaxy for …

Related feature requests

Community can create, vote and comment on issues



Galaxy: Development Inbox Galaxy Project Public

Inbox

- To add cards, use the http://galaxyproject.org/trello — 2 votes, 1
- Filter and Sort: "Select" tool not dealing with special characters right — 1
- Uploaded fastq file datatype not usable in BWA — 1
- Reference genome request: GATK-ordered hg19 — 1
- Feature request: manually hide datasets — 1

Add a card...

Developer ideas

- Anonymous use of workflows/visualizations — 0/2
- Feature Request: the ability to restart a failed workflow from the point of failure; — 6 votes, 2
- Google Drive / Dropbox / Box / ... integration — 1 vote
- Bug report: always import deleted datasets — 2
- Standalone web application(s) for visualizations
- Enh: Archiving histories — 1
- Modify data library upload completion message — 1
- Display in UI runtime

Add a card...

Bug Reports

- Issues with workflow step hiding not persisting — 1 vote, 1
- Workflow View Broken in Toolshed?
- Unable to run jobs when user job limits are set — 1 vote, 4
- Fix tool tip FASTQ Summary Statistics — 1
- Bug when using data_column
- Velvet wrapper broken when real user jobs are used
- apport.fileutils
- Bug: Running functional tests for migrated or

Add a card...

Issues from Bitbucket

- 5: Option to disable automatic history creation — 2 votes, 1
- 6: Option to require that histories have names — 1 vote
- 8: More flexible output handlers
- 10: Allow overriding parameters when running a workflow — 1 vote
- 20: Suggestion: new tag in tool's XML file - 12/9/08 email from Assaf Gordon
- 21: Real DB key build ontology
- 24: Add ability to password secure tools

Add a card...

Members

Add Members...

Board

Options

Add List

Filter Cards

Activity View all...

Dannon Baker added **API: Library Contents** to Developer ideas and
- sent to the board
- joined

today at 10:39 am

g2roboto on **Feature request: manually hide datasets**

Submitted by @nickstoler

Feb 1 at 4:40 pm

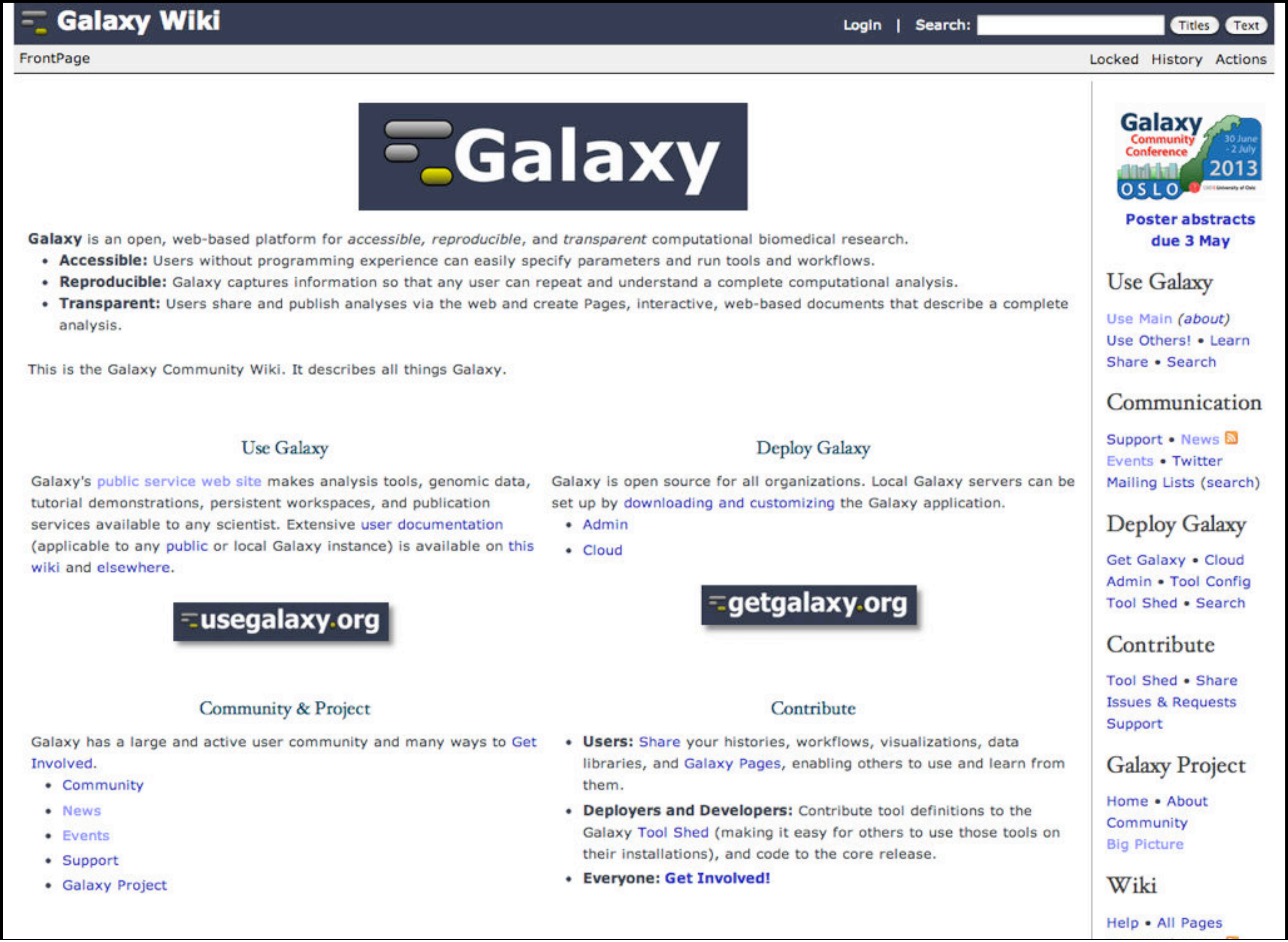
g2roboto added **Feature request: manually hide datasets** to Inbox.

Feb 1 at 4:40 pm

g2roboto on **Reference**

http://bit.ly/gxyissues

http://wiki.galaxyproject.org



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

- **Accessible:** Users without programming experience can easily specify parameters and run tools and workflows.
- **Reproducible:** Galaxy captures information so that any user can repeat and understand a complete computational analysis.
- **Transparent:** Users share and publish analyses via the web and create Pages, interactive, web-based documents that describe a complete analysis.

This is the Galaxy Community Wiki. It describes all things Galaxy.

Use Galaxy

Galaxy's public service web site makes analysis tools, genomic data, tutorial demonstrations, persistent workspaces, and publication services available to any scientist. Extensive user documentation (applicable to any public or local Galaxy instance) is available on this wiki and elsewhere.

Deploy Galaxy

Galaxy is open source for all organizations. Local Galaxy servers can be set up by downloading and customizing the Galaxy application.

- Admin
- Cloud

Community & Project

Galaxy has a large and active user community and many ways to Get Involved.

- Community
- News
- Events
- Support
- Galaxy Project

Contribute

- **Users:** Share your histories, workflows, visualizations, data libraries, and Galaxy Pages, enabling others to use and learn from them.
- **Deployers and Developers:** Contribute tool definitions to the Galaxy Tool Shed (making it easy for others to use those tools on their installations), and code to the core release.
- **Everyone: Get Involved!**

Poster abstracts due 3 May

Use Galaxy

Use Main *(about)*
Use Others! • Learn
Share • Search

Communication

Support • News
Events • Twitter
Mailing Lists (search)

Deploy Galaxy

Get Galaxy • Cloud
Admin • Tool Config
Tool Shed • Search

Contribute

Tool Shed • Share
Issues & Requests
Support

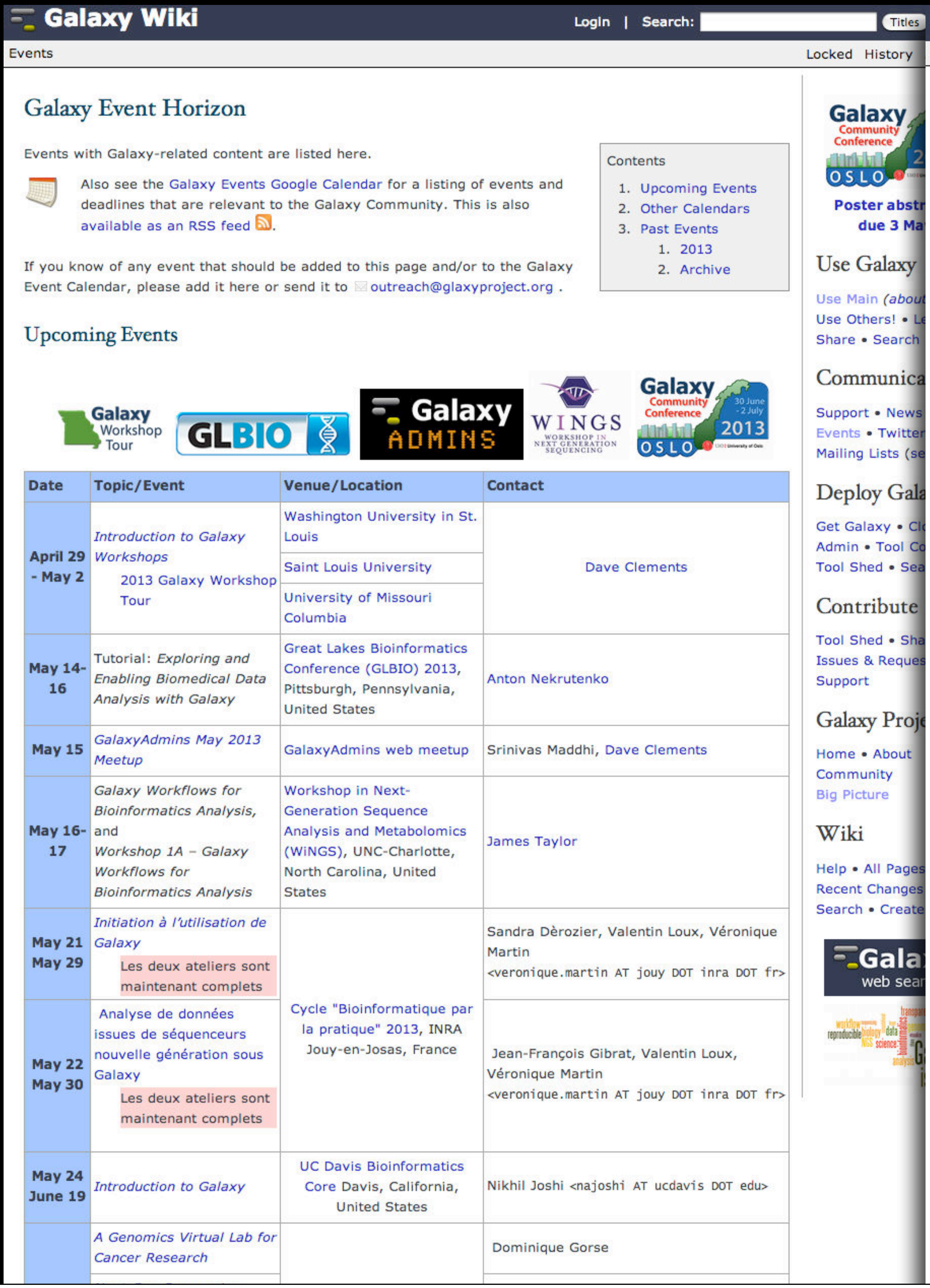
Galaxy Project

Home • About
Community
Big Picture

Wiki

Help • All Pages

Events



Galaxy Event Horizon

Events with Galaxy-related content are listed here.

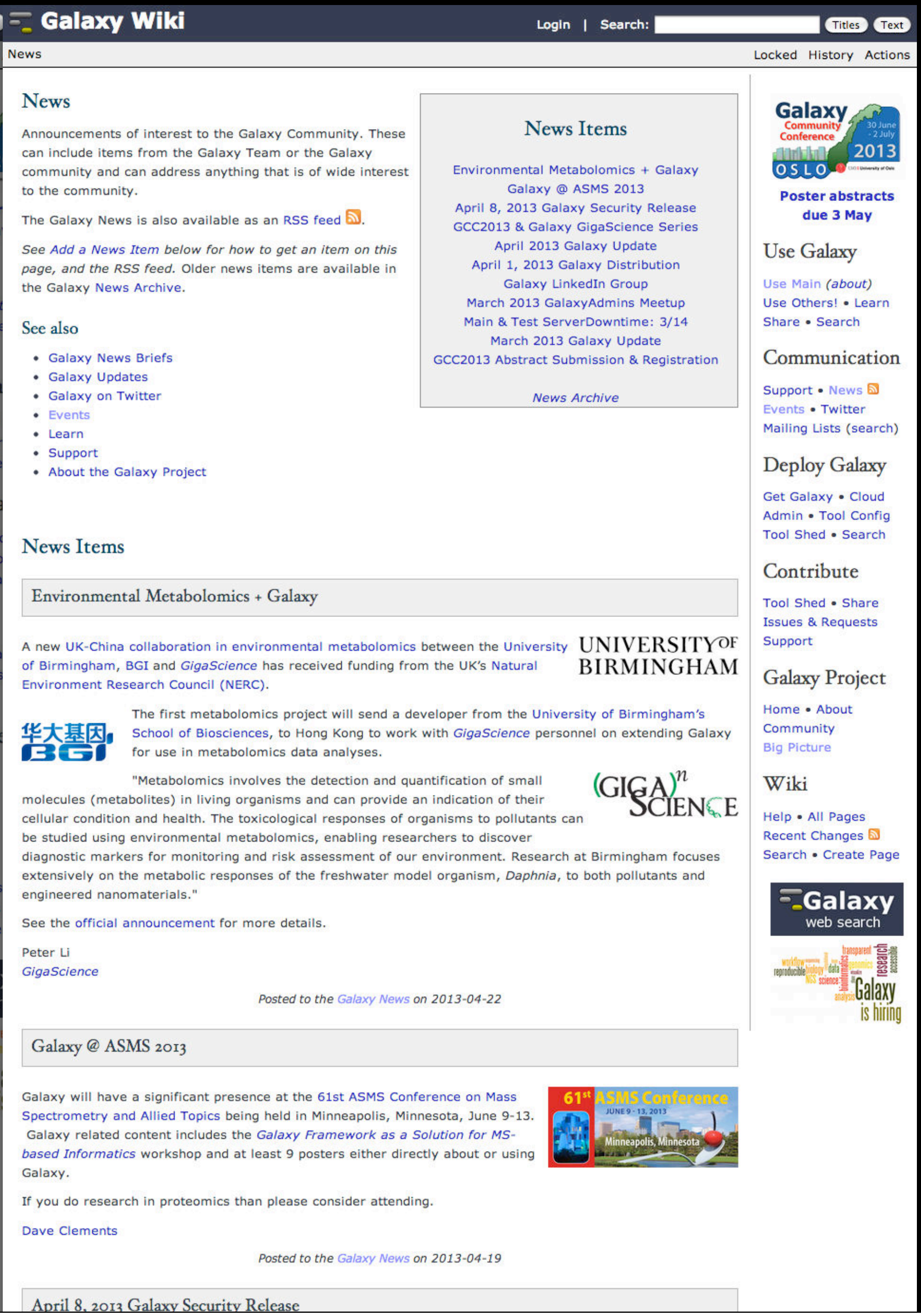
Also see the Galaxy Events Google Calendar for a listing of events and deadlines that are relevant to the Galaxy Community. This is also available as an RSS feed.

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@glaxyproject.org .

Upcoming Events

Date	Topic/Event	Venue/Location	Contact
April 29 - May 2	*Introduction to Galaxy Workshops* 2013 Galaxy Workshop Tour	Washington University in St. Louis Saint Louis University University of Missouri Columbia	Dave Clements
May 14-16	Tutorial: *Exploring and Enabling Biomedical Data Analysis with Galaxy*	Great Lakes Bioinformatics Conference (GLBIO) 2013, Pittsburgh, Pennsylvania, United States	Anton Nekrutenko
May 15	*GalaxyAdmins May 2013 Meetup*	GalaxyAdmins web meetup	Srinivas Maddhi, Dave Clements
May 16-17	*Galaxy Workflows for Bioinformatics Analysis*, and *Workshop 1A – Galaxy Workflows for Bioinformatics Analysis*	Workshop in Next-Generation Sequence Analysis and Metabolomics (WiNGS), UNC-Charlotte, North Carolina, United States	James Taylor
May 21 May 29	*Initiation à l'utilisation de Galaxy* Les deux ateliers sont maintenant complets	Cycle "Bioinformatique par la pratique" 2013, INRA Jouy-en-Josas, France	Sandra Dèrozier, Valentin Loux, Véronique Martin <veronique.martin AT jouy DOT inra DOT fr>
May 22 May 30	Analyse de données issues de séquenceurs nouvelle génération sous Galaxy Les deux ateliers sont maintenant complets		Jean-François Gibrat, Valentin Loux, Véronique Martin <veronique.martin AT jouy DOT inra DOT fr>
May 24 June 19	*Introduction to Galaxy*	UC Davis Bioinformatics Core Davis, California, United States	Nikhil Joshi <najoshi AT ucdavis DOT edu>
	A Genomics Virtual Lab for Cancer Research		Dominique Gorse

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

Environmental Metabolomics + Galaxy

A new UK-China collaboration in environmental metabolomics between the University of Birmingham, BGI and *GigaScience* has received funding from the UK's Natural Environment Research Council (NERC).

The first metabolomics project will send a developer from the University of Birmingham's School of Biosciences, to Hong Kong to work with *GigaScience* personnel on extending Galaxy for use in metabolomics data analyses.

"Metabolomics involves the detection and quantification of small molecules (metabolites) in living organisms and can provide an indication of their cellular condition and health. The toxicological responses of organisms to pollutants can be studied using environmental metabolomics, enabling researchers to discover diagnostic markers for monitoring and risk assessment of our environment. Research at Birmingham focuses extensively on the metabolic responses of the freshwater model organism, *Daphnia*, to both pollutants and engineered nanomaterials."

See the official announcement for more details.

Peter Li
GigaScience

Posted to the Galaxy News on 2013-04-22

Galaxy @ ASMS 2013

Galaxy will have a significant presence at the 61st ASMS Conference on Mass Spectrometry and Allied Topics being held in Minneapolis, Minnesota, June 9-13. Galaxy related content includes the *Galaxy Framework as a Solution for MS-based Informatics* workshop and at least 9 posters either directly about or using Galaxy.

If you do research in proteomics than please consider attending.

Dave Clements

Posted to the Galaxy News on 2013-04-19

April 8, 2013 Galaxy Security Release

galaxyproject.org/GCC2013

(GIGA)^n SCIENCE

GCC2013 Training Day

galaxyproject.org/GCC2013

Late registration ends Wednesday

(GIGA)^n SCIENCE

The Galaxy Team


Enis Afgan


Dannon Baker


Dan Blankenberg


Dave Bouvier


Dave Clements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Carl Eberhard


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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

Agenda

9:00	Welcome
9:15	GenomeSpace
10:15	Galaxy: First Steps and Data Quality
11:00	Break
11:30	RNA-Seq Analysis and Galaxy Project
12:30	Done, almost

Feedback, *please*: http://bit.ly/fged13w1

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