Galaxy Project Update

5th Edinburgh Bioinformatics
Meeting
University of Edinburgh
12 May 2014

Dave Clements
Johns Hopkins University

http://galaxyproject.org

Agenda

- Project Introduction (brief)
- Project Update

What is Galaxy?

- A web based data integration and analysis framework.
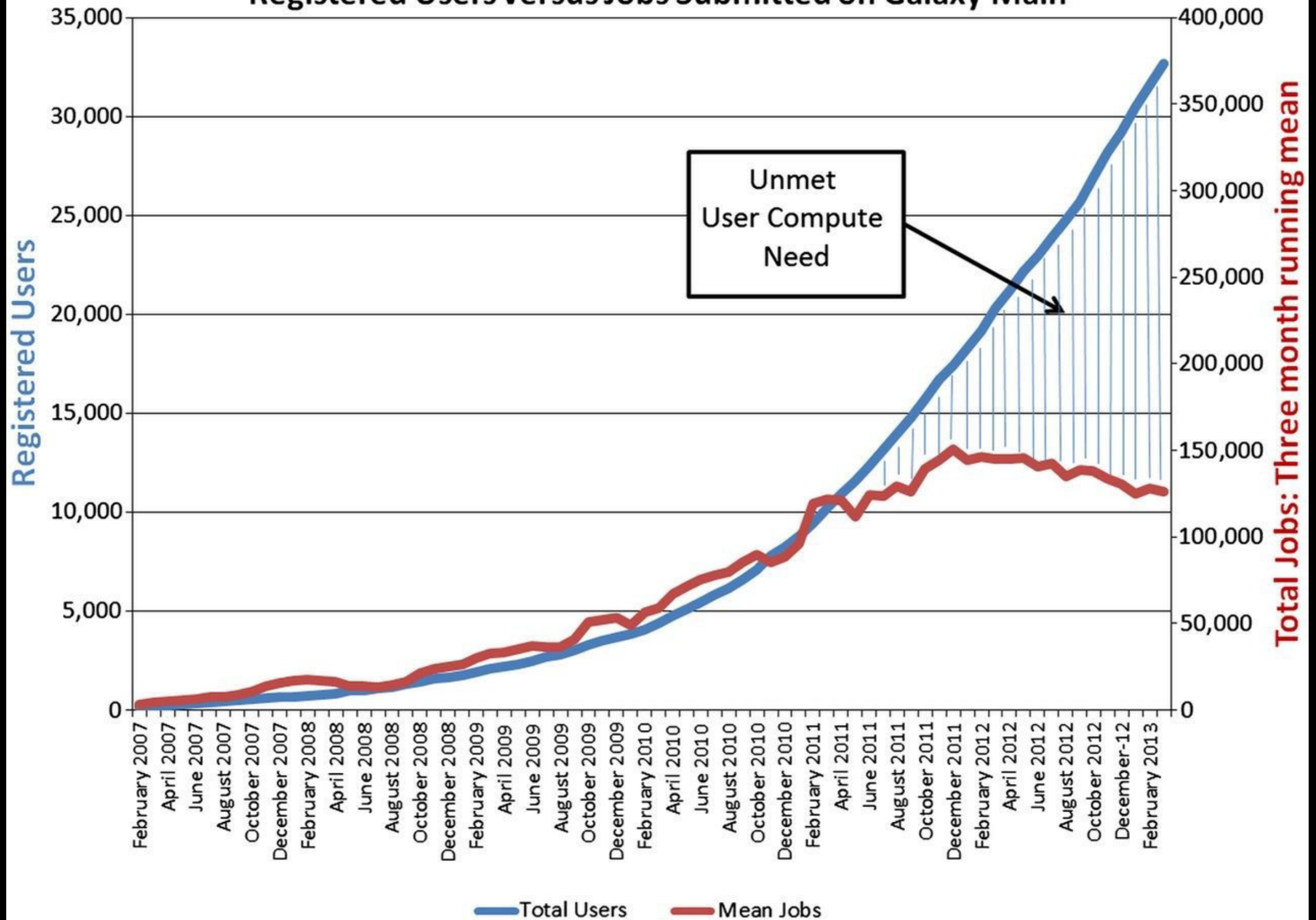
- **Open source software**

http://galaxyproject.org

Galaxy is available as: usegalxy.org

The Galaxy Project's free for everyone web server integrating a wealth of tools, compute resources, terabytes of reference data and permanent storage.

However, *a centralized solution cannot support the different analysis needs of the entire world.*

Leveraging the national cyberinfrastructure for biomedical research
LeDuc, *et al. J Am Med Inform Assoc doi:10.1136/amiajnl-2013-002059*

Galaxy is available as

- As a free (for everyone) web service

  http://usegalaxy.org

- **As open source software**

  http://getgalaxy.org

  It is installed at locations around the world

Galaxy is available: With Commercial Support

A ready-to-use appliance
(BioTeam)

Cloud-based solutions
(ABgenomica, AIS, Appistry, GenomeCloud)

Consulting & Customization
(Arctix, BioTeam, Deena Bioinformatics)

Agenda

- Project Introduction
- Project Update

New Development

- Tool Shed Work

  - Lots of enhancements to handle dependencies.

  - Continue moving tools out of source distribution and into Tool Shed

New Development

- User Management

  - Disk quotas added a few years ago

  - Limited execution concurrency before that

    - Led to widespread abuse w/ multiple accounts

  - Put effort into ending that on Main

    - Email verification and duplicate detection

    - Added supporting code into distribution

Release Cycle: Galaxy

Experimented with 2-3 week release cycle
Less than popular

Aiming for every 2 months or so
2013/04/01 Release
2013/06/03 Release
2013/08/12 Release
2013/11/04 Release
2014/02/10 Release
2014/04/14 Release

Releases

Project now makes extensive use of Trello cards for tracking work. This is reflected in release notes:

Core

1. Explicitly set TEMP dir in Local Runner, when a temp dir value is not already set.
   https://trello.com/c/HbFeoWRI
2. Tool element return_code (under stdio) now functions from_work_dir or when setting metadata externally. https://trello.com/c/JfB2w1Br
3. Using Auto-detect and a cluster job runner now sets metadata only once.
   https://trello.com/c/Kc3NDGyN
4. Upgrades to HierarchicalObjectStore, more planned. https://trello.com/c/k4tovlFd
5. New Plugin Framework lib/galaxy/web/base/pluginframework.py. https://trello.com/c/lrfWbtw3
6. Plugins define hook functions called by a Galaxy app when certain events/situations happen.
   https://trello.com/c/c2AzV3Xf

Releases
Doing a much better job of incorporating pull requests from community into dist:

Pull Requests Merged

1. Björn Grüning contributed a method to implement the ability to change the tool-panel as user preference (Dynamic Toolbox Filtering). #179. This was a frequently requested feature by the community and full documentation on this can be found here UserDefinedToolboxFilters. https://trello.com/c/Xl7CZFMd

2. Björn Grüning also contributed several extensions allowing developers to utilize new actions simplifying various tool shed dependency definition idioms:
   - make_install action. #217
   - autoconf action. #218
   - setup_r_environment action. #219 Further extensions enhancing this last tag and a corresponding setup_ruby_environment tag from Björn will be forthcoming in the next release.

3. Additionally, Björn Grüning contributed other tool shed and tool related enhancements enhancements: #205, #216, and #239

4. Andrew Warren contributed an API method allowing coping datasets between histories as well as support for more secure e-mail settings. #199 and #198.

5. Nicola Soranzo contributed small fixes for various tools as well as enhancements for customizing and localizing data and time display in various parts of Galaxy. #222 and #211.

6. Kyle Ellrott contributed many enhancements for the API and the Galaxy search engine. #187, #241, and #234.

7. Lance Peterson contributed two enhancements to management scripts. #196 and #158. https://trello.com/c/qzjBuljp

8. Google Summer of Code Intern Saket Choudhary contributed enhancements for VCF 4.1 compatibility. #184.

9. Matthew Shirley contributed grammar fixes to the tool shed interface. #210.

10. Stephen Mcmahon contributed fixes to the PBS job runner's staging functionality. #194

11. Rémy Dernat contributed enhancements to the administrative interface allowing for management of user API keys. #134

12. Adam Brenner contributed an enhancement making it easier to deploy the histogram2 tool. #215.

13. A. Rretaud contributed extensions enabling data source tool developers to utilize the tool runners login e-mail address when implementing such tools. #206

14. John Chilton fixed job splitting to rewrite references in config files in addition to command-line. #169. https://trello.com/c/FMPydE8L

15. John Chilton and Simon Guest implemented configurable plugins for tool dependency resolution. #228. https://trello.com/c/cP3tGSJv

16. John Chilton implement GALAXY_SLOTS allowing tools to uniformly obtain allocated thread count. #236. https://trello.com/c/cfOlSfdP

17. Kyle Ellrott contributed enhancements that allow API tool's POST to define history for tool state. #193. https://trello.com/c/hpFanyx0

Release Cycle: CloudMan

After a lull, now doing semi-annually
2013/07 Release
2014/01 Release

Where are we going?

Dataset Collections

Support dataset collections as 1st class objects.
Run tools once on each dataset in the collection.
Run tools on the collection as a whole.
Tools become much more dynamic, flexible and responsive to input.
Support map/reduce paradigm.

Makes it possible to build workflows that can reason about paired datasets, technical replicates, multiple biological samples, ...

Big Data: Plans

## Rewrite default workflow engine

Histories will be able to contain pending workflows, dataset groups, other entities - not just datasets

Rather than scheduling all at once, monitor workflow progress, allow pausing in response to failure or user intervention, decision nodes, streaming data and intermediate datasets, ...

Make workflow scheduling engine pluggable

Once it is a background process, can afford the time to delegate

Visual Analytics
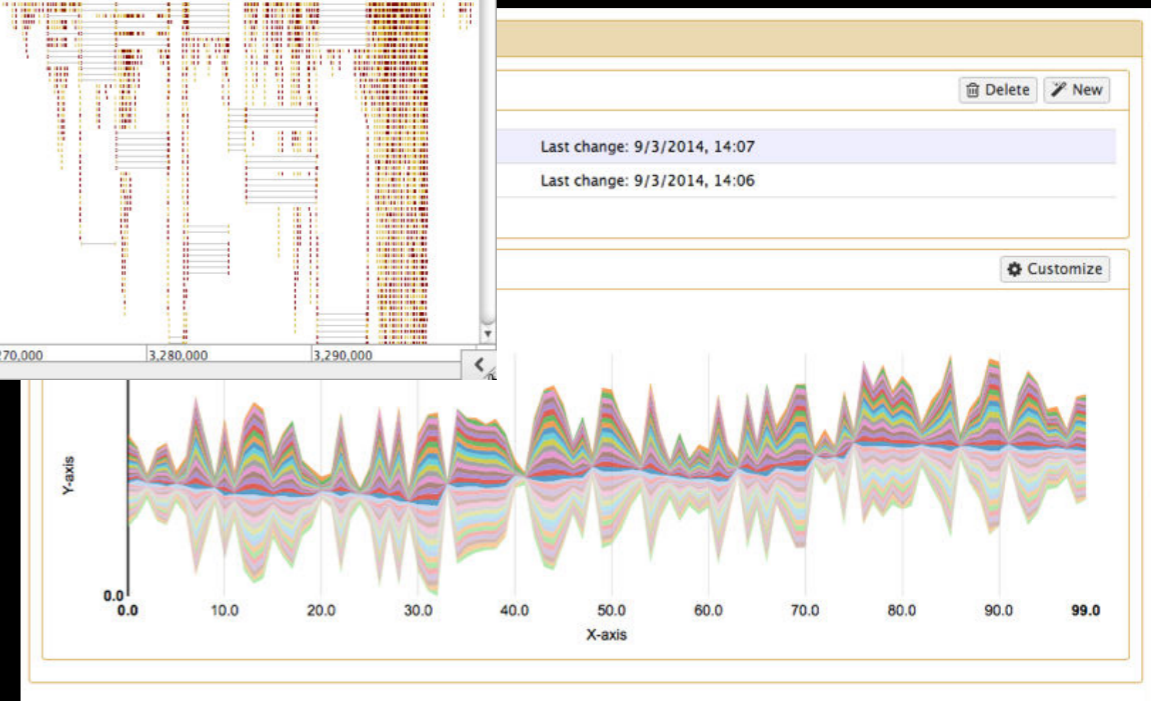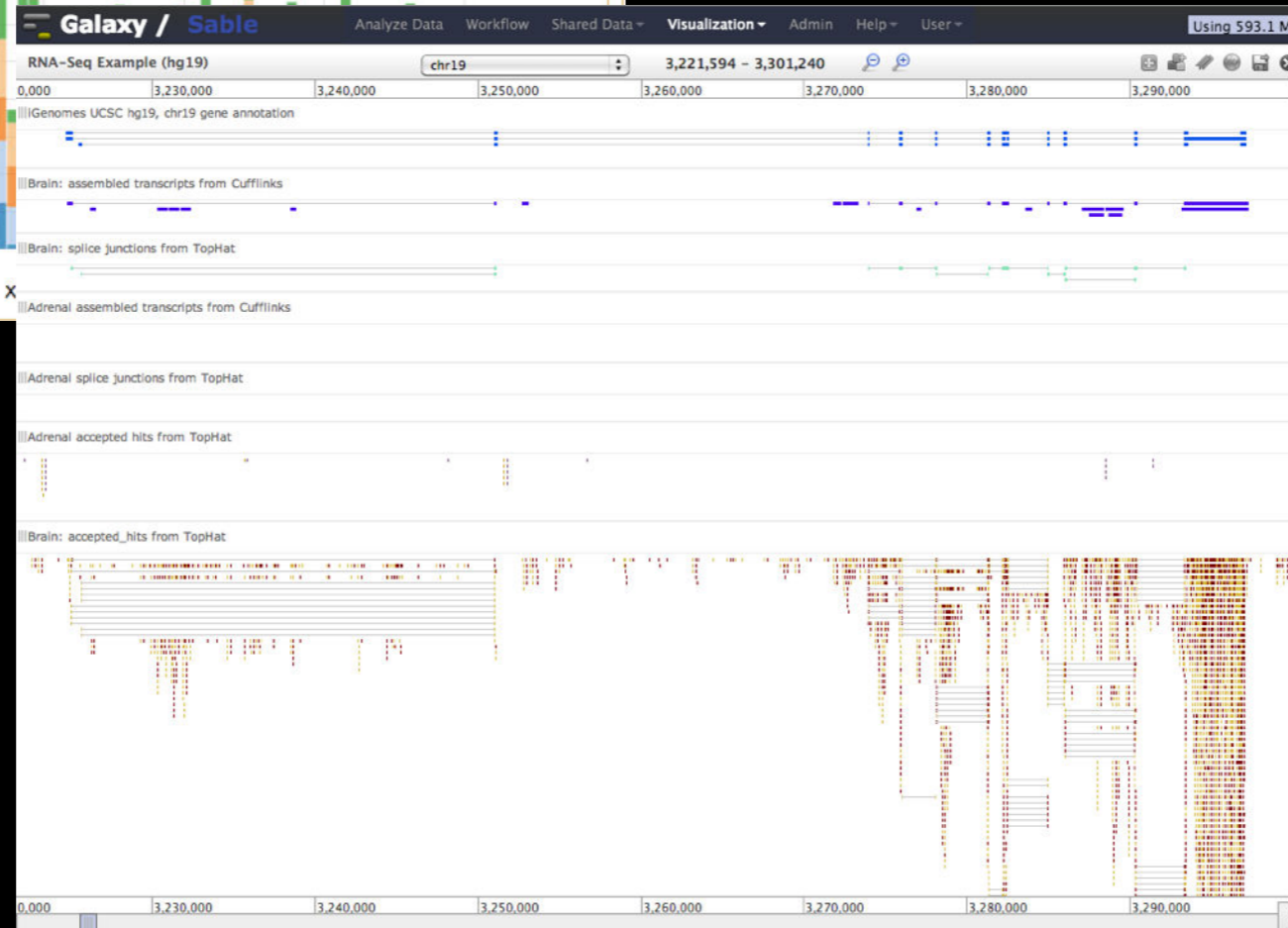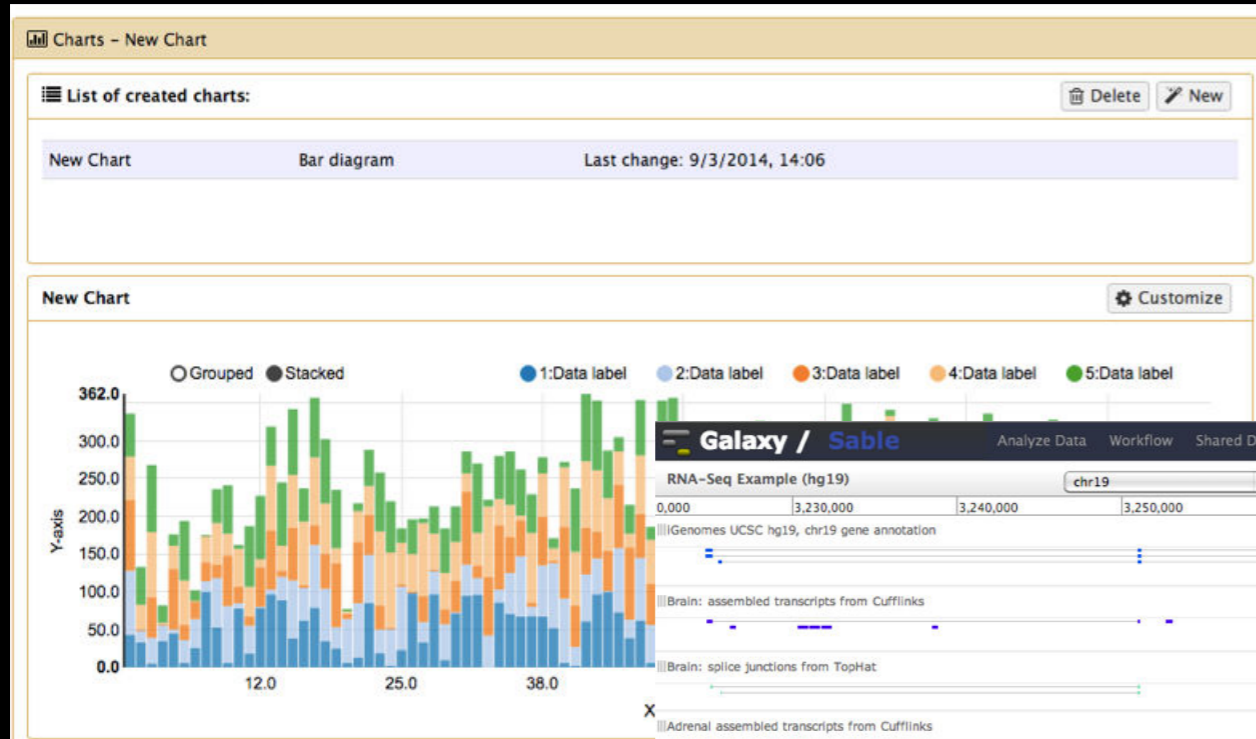
Pluggability / Extensibility / APIs

- Workflow rewrite

- Visualization framework

- ObjectStore storage api

- Galaxy API

- ...

- Make everything pluggable; start using those interfaces internally.

Galaxy toolshed vision

- Allow users to share "suites" containing tools, datatypes, workflows, sample data, and automated installation scripts for tool dependencies

- Version controlled

- Community annotation, rating, comments, review

- Dependency resolution

- Integration with Galaxy instances to automate tool installation and updates

- A key to intergalactic federation

- Intergalactic Utilities Commission
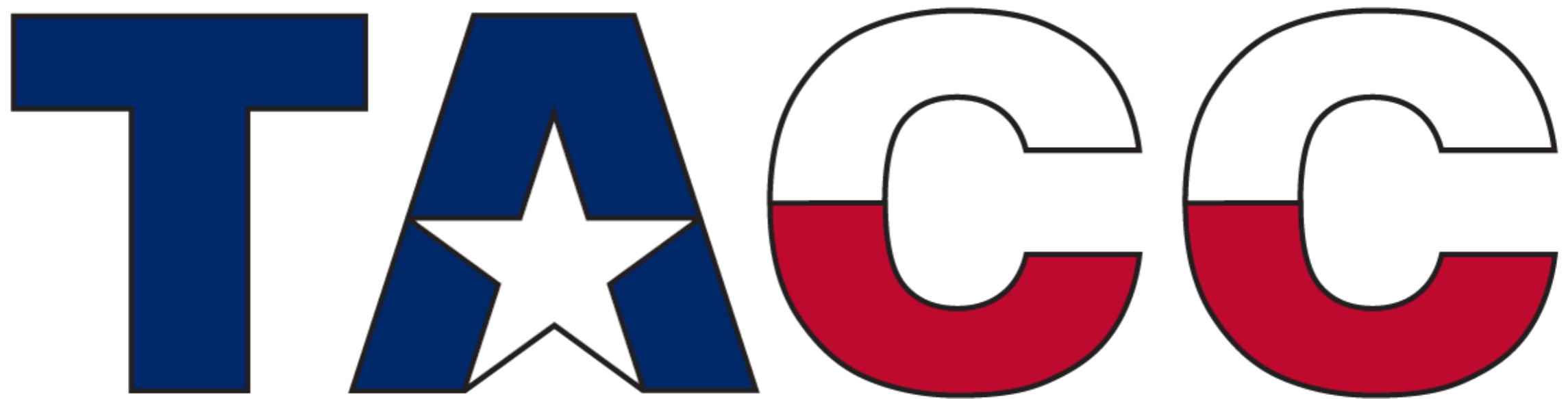
usegalaxy.org moved to the Texas Advanced Computing Center on October 8

But it is still not enough to
meet the analysis needs of the world.

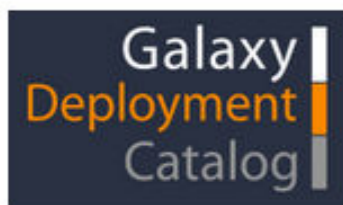The Galaxy Project continues to emphasize

Cloud Installs
Local Installs
Public Servers

Community

Community Hubs

Galaxy Deployment Catalog

Welcome to the *Galaxy Deployment Catalog*. This catalog describes the details of how Galaxy is installed at different institutions. Details include infrastructure information as well as user community and domain information for each deployment.

You are strongly encouraged to add your local Galaxy deployment to this catalog so that the Galaxy Community can benefit from your experience.

Contents

1. Deployments: User and Domain Information
2. Deployments: Implementation
3. Add Your Galaxy Deployment
   1. Using the Wiki
   2. Using the Google Form

GALAXY COMMUNITY CONFERENCE

BALTIMORE, MD | JUNE 30 - JULY 2, 2014

Training Day voting closes Friday

Use Galaxy

Servers • Learn
Main • Share • Search

Communicate

Support • News
Events • Twitter
Mailing Lists (search)

Deploy Galaxy

Get Galaxy • Cloud
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SLIPSTREAM APPLIANCE
Galaxy made easy.

Contribute

Tool Shed • Share
Issues & Requests
Teach • Support

Galaxy Project

Home • About
Community

Deployments: User and Domain Information

Deployment	Domain	Owners	User Base	Audience
CSIRO Galaxy Service	NGS analysis: RNAseq, Genomics, metagenomics, custom tools.	CSIRO	209 registered users and 30 active users	
Galaxy server at the FMI	NGS analysis, MA analysis, custom tools.	Friedrich Miescher Institute for Biomedical Research		wet lab scientists
GalaxyAtUIowa	Local instance at the U of Iowa	IIHG		Human geneticists, biologists
Idaho State University MRCF	Bioinformatics, biology, next generation sequencing. Custom tools.	Idaho State University Molecular Research Core Facility (MRCF)		Idaho State University and Molecular Research Core Facility (MRCF) customers.
Sigenae Bioinfo-Genotoul	Genomics, esp. read alignment, SNP calling and annotation, RNA-Seq, and sRNAseq	Sigenae Team, GenoToul Bioinfo		bioinfo gentoul and INRA researchers and collaborators
URGI	Genomics	INRA	~ 30	researchers at the institution, lab members
UAB Galaxy	NGS analysis: Genomics (reference and de novo), RNAseq, metagenomics, custom tools.	Collaboration between Center for Clinical and Translational Science and Research Computing	currently ~200	Informatics core, sequencing core, researchers and students at the institution
ZBIT	Bioinformatics: SBML tools,	Center for Bioinformatics Tuebingen		

Community Hubs

Community/Deployment/GalaxyAtUIowa   Locked History Action

THE UNIVERSITY
OF IOWA

GalaxyAtUIowa

This is a local installation of Galaxy at the University of Iowa.

Domain

Human genetics, biology. Custom tools and reports.

Community

The University of Iowa community and members of the Iowa Institute of Human Genetics.

Compute Infrastructure

This instances of Galaxy runs on a local HPC cluster.

Compute

3600 cores, SGE DRM.

Storage

Deployment
GalaxyAtUIowa

Domain
Local instance at the U of Iowa

Owners
IIHG

Audience
Human geneticists, biologists

User Base

Server Topology
SGE cluster

Compute

Memory

Storage
NFS

Disk Space

User Management
University or IIHG affiliation
required

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BALTIMORE, MD | JUNE 30 – JULY 2, 20

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APPLIANCE
Galaxy made easy.

Contribute

Tool Shed • Share
Issues & Requests

Community Hubs

The *Galaxy Community Log Board* is a place to share how you addressed a particular task in your Galaxy deployment. Log entries describe specific solutions to particular tasks, such as the details of what steps were taken to deploy Galaxy on particular platforms, or with particular software. It's an easy way to help others (and learn from others) by sharing what you've already done.

So, if you have figured out how to do something, and it took you a while, then this is the ideal forum for sharing that information with the community.

Logs

2014

Date	Topic	Resolution	Who
2014/03/20	**Basic Galaxy Puppet Module**	A puppet module for a very basic galaxy server (use for development)	Olivier Inizan, Mikael Loaec
2014/01/27	**Problem with logout when using LDAP for authentication with remoteUser enabled.**	Make changes to 4 Galaxy configuration files	Tim Booth

2013

Date	Topic	Resolution	Who
2013/12/05	**Tool Integration Short Tutorial**	Documents best tool integration practices from Institut Français de Bioinformatique Galaxy working group	Contributors
2013/11/13	**VelvetG error on CloudMan instance: cannot find 'cov_cutoff'**	Fixed XML wrapper	Dave Clements
2013/10/27	**IGV Integration**	How to set up IGV-Galaxy integration in Apache and Galaxy, including adding custom genomes.	Sarah Maman, Nabihoudine Ibou

Passed ~~50~~ 60 this year
OSDD
CoSSci
Galaxy-P
GO Galaxy
Orione

Public Tool Sheds
GenOuest
DTL

050+
Public Galaxy Servers
and counting

Upcoming Events

In the next 60 days: Norway, France, online, Italy, Croatia, the Netherlands.

Date	Topic/Event	Venue/Location	Contact
May 6-7	Scaling Galaxy for Big Data	NGS Data after the Gold Rush, TGAC, Norwich, United Kingdom	Dave Clements
May 9	Introduction to Galaxy Workshop	The Genome Analysis Centre (TGAC), Norwich, United Kingdom	
May 12	Galaxy Workshop	University of Edinburgh, Edinburgh, UK	
May 12	Galaxy Project Update	5th Edinburgh Bioinformatics Meeting, University of Edinburgh, Edinburgh, UK	
May 13	Galaxy Workshop	Institute of Genetics and Molecular Medicine (IGMM), Edinburgh, UK	
May 12-14	Short course on RNA-seq and ChIP-seq	University of Bergen, Bergen, Norway	✉ David Fredman
May 16	Galaxy Initiation	Formation en Bioinformatique Plateforme ABiMS, Station Biologique de Roscoff, France	✉ Christophe Caron
May 19	Initiation au traitement et à l'analyse des données métabolomiques sur la plateforme scientifique web Galaxy IFB-MetaboHUB	8e Journées Scientifiques du RFMF, Lyon, France	✉ Réseau Français de Métabolomique et Fluxomique

http://wiki.galaxyproject.org/Events

GALAXY
COMMUNITY
CONFERENCE

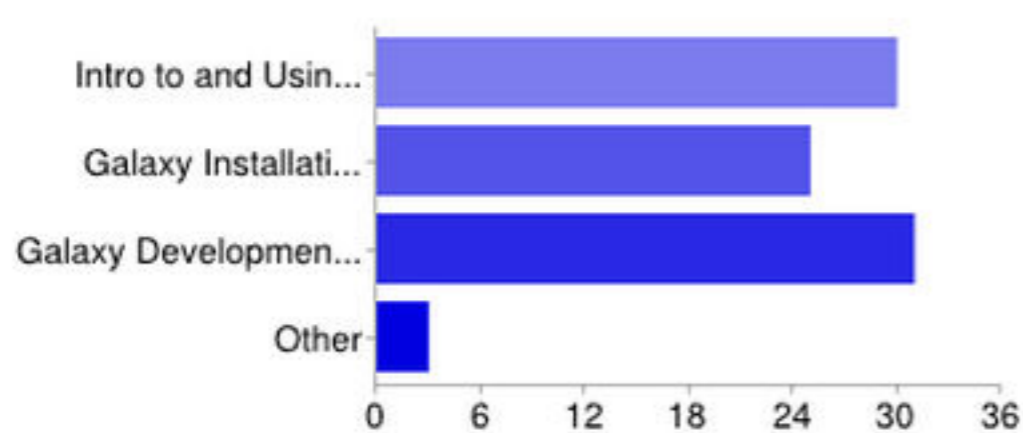BALTIMORE, MD | JUNE 30 - JULY 2, 2014

Training Day: 15 sessions, 2.5 hrs each
Poster sessions, BoFs
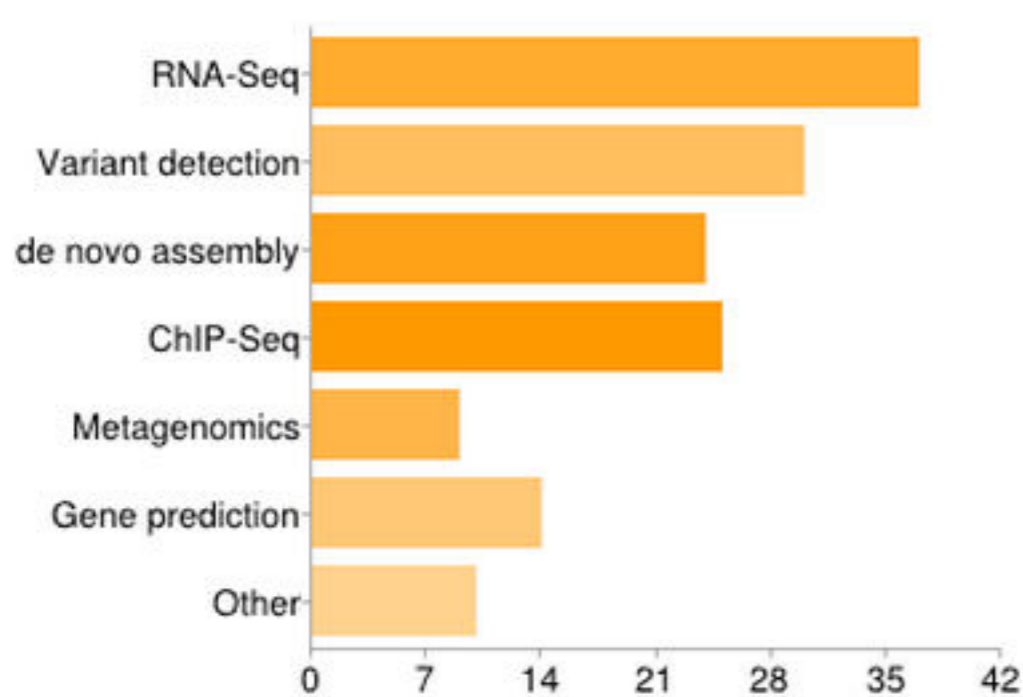Hackathon
Early registration ends 23 May

Training: Survey

What type of training are you most interested in?

Intro to and Using Galaxy	**30**	34%
Galaxy Installation and Administraton	**25**	28%
Galaxy Development and Tool Integration	**31**	35%
Other	**3**	3%

What type of data analysis are you interested in?

RNA-Seq	**37**	25%
Variant detection	**30**	20%
de novo assembly	**24**	16%
ChIP-Seq	**25**	17%
Metagenomics	**9**	6%
Gene prediction	**14**	9%
Other	**10**	7%

Training in 2014: Scalability

Create a Training Network
Make it easy to find and use workshop materials created by anyone.
Training AMIs, VMs
Look seriously at MOOCs and Screencasts

Project

Core Team is at 18 people.

1 in Croatia
1 in Australia
10 with Penn State University
5 with Johns Hopkins University
1 with George Washington University

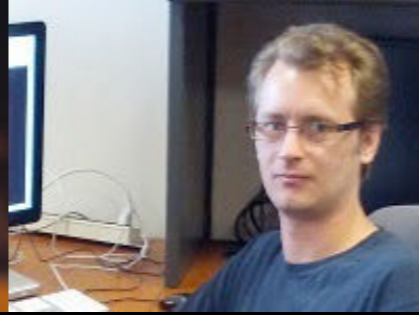# The Galaxy Team

Enis Afgan   Dannon Baker   Dan Blankenberg   Dave Bouvier   Marten Cech   John Chilton

Dave Clements   Nate Coraor   Carl Eberhard   Dorine Francheteau   Jeremy Goecks   Sam Guerler

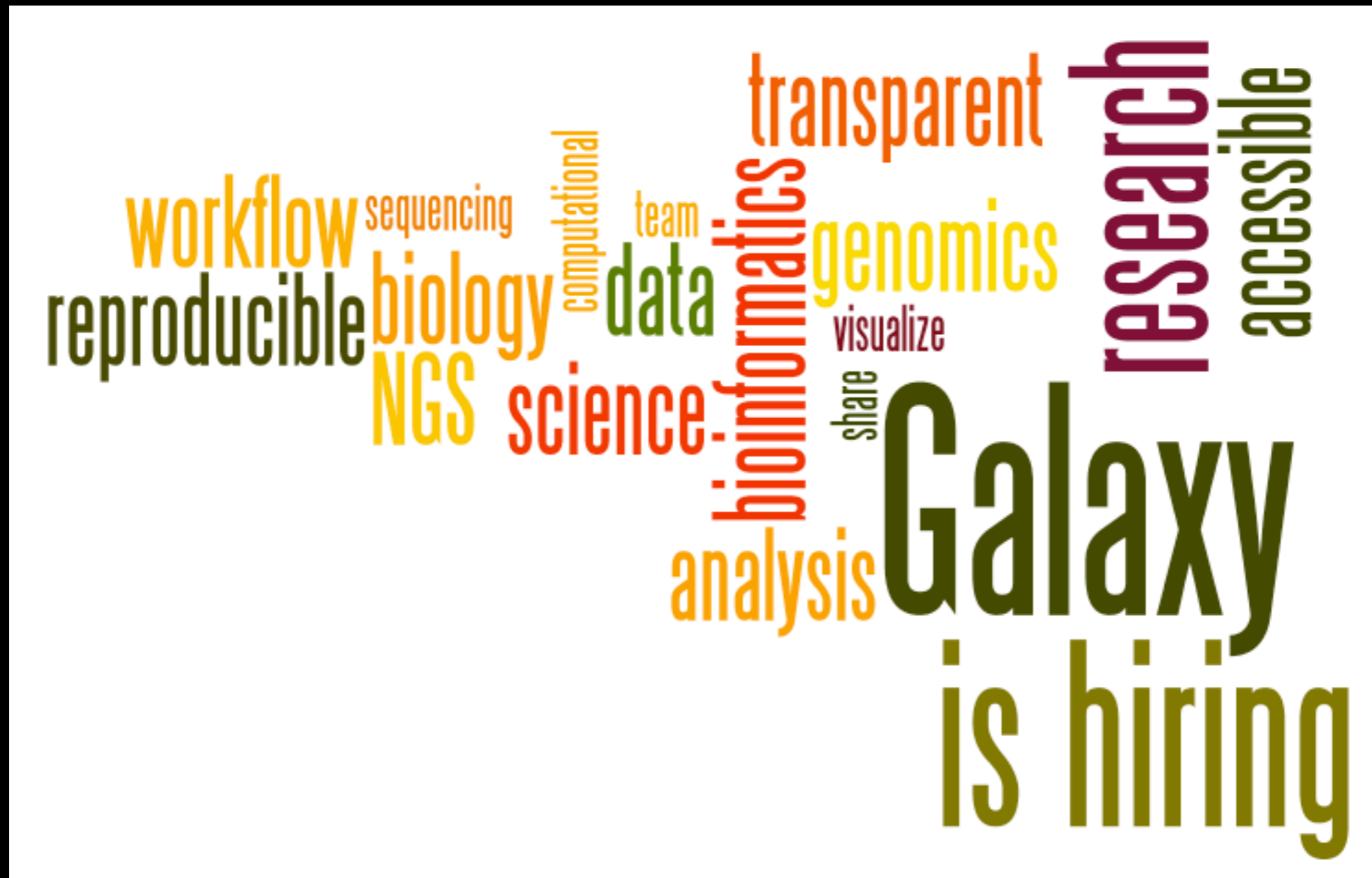Jen Jackson   Ross Lazarus   Anton Nekrutenko   Nick Stoler   James Taylor   Greg von Kuster

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

Acknowledgements

Edinburgh

Alastair Kerr   Graeme Grimes
Mick Watson   Shaun Webb
James Prendergast   Bert Overduin

Norwich

Matt Drew
Vicky Schneider-Gricar

Thank You!

Events: 2013

200+ Talks, workshops, tutorials, ...

90+ Events

80% With archived slides, video, exercises, ...

75% Presented by the Galaxy Community

GCC2013

Added Poster sessions
Longer training sessions (2 hrs)
Breakout reformed into BoFs
2nd year with sponsors
Had a pub onsite!

GCC attendance over time

250?

219

201

148

69

2010   2011   2012   2013   2014