

# Enhancing the Galaxy Experience through Community Involvement

Daniel Blankenberg

Postdoctoral Research Associate

**The Galaxy Team | Nekrutenko Lab@Penn State**

<http://UseGalaxy.org>

# The Galaxy Team



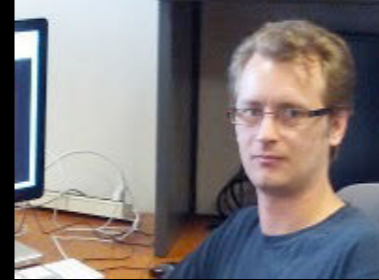
Enis Afgan



Dannon Baker



Dan Blankenberg



Dave Bouvier



Marten Čech



John Chilton



Dave Clements



Nate Coraor



Carl Eberhard



Jeremy Goecks



Sam Guerler



Jen Jackson



Ross Lazarus



Anton Nekrutenko



Nick Stoler



James Taylor



Greg Von Kuster

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

# Overview

**What is Galaxy?**

**Usage / Contributions**

**Virtual Interactions**

**ToolShed**

**Events and Outreach**

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**What is Galaxy?**

**Usage / Contributions**

**Virtual Interactions**

**ToolShed**

**Events and Outreach**

# Galaxy Project Mission

**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.

# What is Galaxy?

A **data analysis and integration** tool

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

There are several **ways to use Galaxy**

# Using Galaxy - 4 ways

- Public Main Galaxy web instance: [usegalaxy.org](https://usegalaxy.org)
- Local instance: [getgalaxy.org](https://getgalaxy.org)
- Cloud instance: [usegalaxy.org/cloud](https://usegalaxy.org/cloud)
- Other Public Galaxy web instances hosted by various groups:  
[wiki.galaxyproject.org/PublicGalaxyServers](https://wiki.galaxyproject.org/PublicGalaxyServers)



# Galaxy as a *Genomics WorkBench*

## Dataset:

Any input, output or intermediate set of data + metadata.  
A record of a specific data or analysis step.

## History:

A series of inputs, analysis steps, intermediate datasets, and outputs. A record of a group of data and analysis steps.

## Tool:

An operation within Galaxy that acts upon dataset(s) as an analysis step. May be developed by Galaxy team or a 3rd party program that has been “wrapped” for Galaxy.

## Workflow:

A series of analysis steps executed as a unit.



# More Galaxy Terminology

## Share:

Make something available to someone else

## Publish:

Make something available to everyone

## Galaxy Page:

Analysis documentation within Galaxy; easy to embed and link to any Galaxy object (histories, datasets, workflows, visualization) or external resource (video, graphics, publications).

## Visualize:

External resources. [Trackster](#). Galaxy Charts (D3/NVD3).

# Galaxy Analysis Workspace

The screenshot displays the Galaxy Analysis Workspace interface. At the top, the navigation bar includes the Galaxy logo, a menu with options like 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Cloud', 'Admin', 'Help', and 'User', and a user profile icon with the text 'Using 10.0 TB'.

The main workspace is divided into three vertical panels:

- Tools Panel (Left):** A sidebar with a search bar and a list of tool categories including 'Get Data', 'Send Data', 'Lift-Over', 'Text Manipulation', 'Convert Formats', 'FASTA manipulation', 'Filter and Sort', 'Join, Subtract and Group', 'Extract Features', 'Fetch Sequences', 'Fetch Alignments', 'Get Genomic Scores', 'Operate on Genomic Intervals', 'Statistics', 'Graph/Display Data', 'Regional Variation', 'Multiple regression', 'Multivariate Analysis', 'Evolution', 'Motif Tools', 'Multiple Alignments', 'Metagenomic analyses', 'Genome Diversity', 'NGS TOOLBOX BETA', 'Phenotype Association', and 'NGS: QC and manipulation'. A 'Load Data' button is at the top.
- Tool Configuration Panel (Center):** The 'Map with BWA for Illumina (version 1.2.3)' tool interface. It contains several sections:
  - Reference Genome:** A dropdown menu set to 'Human (Homo sapiens) (hg19 with mtDNA replaced with rCRS): Homo\_sapiens\_nuHg19\_mtrCRS'.
  - Library Type:** A dropdown menu set to 'Paired-end'.
  - FASTQ Files:** Two input fields for 'Forward FASTQ file' (1: raw\_child-ds-1.fq) and 'Reverse FASTQ file' (2: raw\_child-ds-2.fq).
  - BWA Settings:** A dropdown menu set to 'Commonly Used'.
  - Header Suppression:** A checkbox for 'Suppress the header in the output SAM file' which is currently unchecked.A blue 'Execute' button is located at the bottom of the configuration area.
- History Panel (Right):** A list of previous jobs. The top job is 'Galaxy 101 NGS Variant' (313.4 MB). Below it are several jobs related to filtering and variant calling, such as '21: Filter on data 20', '20: Filter on data 19', '19: Variant Annotator on data 17', '18: FreeBayes on data 15 (variants)', '17: Naive Variant Caller on data 15', '16: child-mother Merge BAM Files.log', '15: child-mother.bam', '14: Add or Replace Groups on data 12: bam with read groups replaced', '13: Add or Replace Groups on data 11: bam with read groups replaced', '12: SAM-to-BAM on data 10: converted BAM', '11: SAM-to-BAM on data 9: converted BAM', and '10: Filter SAM on data 8'. Each job entry includes an eye icon, a pencil icon, and a close icon.

At the bottom of the interface, there is a navigation bar with a back arrow, a search bar containing the text 'Know what you are doing', and a forward arrow.



# Galaxy Analysis Workspace

The screenshot displays the Galaxy Analysis Workspace interface. The main panel shows the configuration for the 'Map with BWA for Illumina (version 1.2.3)' tool. The 'Forward FASTQ file' is set to '1: raw\_child-ds-1.fq' and the 'Reverse FASTQ file' is '2: raw\_child-ds-2.fq'. The 'BWA settings to use' are set to 'Commonly Used'. An 'Execute' button is visible at the bottom of the tool configuration.

On the right side, the 'History' panel lists several jobs, including 'Galaxy 101 NGS Variant' (313.4 MB) and various filtering and annotation jobs.

A central window displays a workflow execution error. The error message is '8: A job that will surely fail'. Below the error, a preview window shows the output of job '5: Sort on data 4', which contains 15,310 lines of tabular data. The first line of the output is highlighted in blue:

```
1 uc003qqn.2_cds_0_0_chr6_157099238_f 1
```

The preview window also shows the format 'tabular, database: hg19' and a scrollable list of genomic coordinates and identifiers.



# Workflow Editor

Galaxy Analyze Data **Workflow** Shared Data Visualization Cloud Help User Using 3%

Tools Workflow Canvas | metagenomic analysis Details

search tools

- Get Data
- Send Data
- ENCODE Tools
- Lift-Over
- Text Manipulation
- Convert Formats
- FASTA manipulation
- Filter and Sort
- Join, Subtract and Group
- Extract Features
- Fetch Sequences
- Fetch Alignments
- Get Genomic Scores
- Operate on Genomic Intervals
- Statistics
- Graph/Display Data
- Regional Variation
- Multiple regression
- Multivariate Analysis
- Evolution
- Motif Tools
- Multiple Alignments
- Metagenomic analyses
- Genome Diversity
- Phenotype Association
- EMBOSS
- NGS TOOLBOX BETA
- NGS: QC and manipulation
- NGS: Mapping
- NGS: SAM Tools
- NGS: GATK Tools (beta)
- NGS: Variant Detection
- NGS: Indel Analysis
- NGS: Peak Calling
- NGS: RNA Analysis
- NGS: Picard (beta)
- BEDTools
- snpEff
- RGENETICS
- SNP/WGA: Data: Filters
- SNP/WGA: QC: LD: Plots
- SNP/WGA: Statistical Models
- Workflow control
- Inputs

```
graph LR; I1[Input dataset] --> S[Select high quality segments]; I2[Input dataset] --> S; S --> M1[Megablast]; I1 --> F[FASTA-to-Tabular]; F --> A[Add column]; A --> T[Tabular-to-FASTA]; T --> M2[Megablast]; M1 --> C[Concatenate datasets]; M2 --> C; C --> J[Join two Datasets]; J --> F2[Filter]; F2 --> R[Find lowest diagnostic rank]; R --> P[Draw phylogeny]; R --> S2[Summarize taxonomy]; P --> D[Draw phylogram for]; S2 --> S3[Summarize taxonomic representation for];
```

Tool: Megablast  
Version: 1.2.0

Compare these sequences  
Data input 'input\_query' (fasta)

against target database: ▼  
 htgs 28-Jan-2013  
 nt 28-Jan-2013  
 wgs 28-Jan-2013  
 phiX174

using word size: ▼  
28

report hits above this identity (-perc\_identity): ▼  
80.0

set expectation value cutoff (-evalue): ▼  
0.0001

Filter out low complexity regions? (-dust): ▼  
Yes

Edit Step Actions  
Rename Dataset  
output1 Create

Add actions to this step; actions are applied when this workflow step completes.

Edit Step Attributes  
Annotation / Notes:  
Add an annotation or notes to this step; annotations are available when a workflow is viewed.  
⚠ Note. Database searches may take substantial amount of time. For large input datasets it is advisable to allow overnight processing.

What it does  
This tool runs megablast function of BLAST+ blastn tool – a high performance nucleotide local aligner developed by Webb Miller and colleagues.

Output format  
Output of this tool contains 13 columns delimited by Tabs:  
1. Id of your sequence

# Create Workflow Automatically

## Extract Workflow from History

Create a workflow from a History that you created interactively.

Run it

**Running workflow "metagenomic analysis"** Expand All Collapse

Generic workflow for performing a metagenomic analysis on NGS data.

**Step 1: Input dataset**  
454 Reads

reads

1: 454 reads

type to filter

**Step 2: Input dataset**  
454 Quality Dataset

qualities

2: 454 qualities

type to filter

**Step 3: Select high quality segments** (version 1.0.0)  
Here we select segments of reads with contiguous high quality bases above threshold phred score of 20

**Step 4: FASTA-to-Tabular** (version 1.1.0)  
Convert to tabular format so that column for additional metadata can be added

**Step 5: Add color**

**Step 6: Tabulate**

**Step 7: Make**

**Step 8: Make**

**Step 14: Find lowest diagnostic rank** (version 1.0.1)  
Get reads specific to ranks below Kingdom level

**Step 15: Summarize taxonomy** (version 1.0.0)  
Tabulate list of taxonomic groups contained in reads from dataset 14

**Step 16: Draw phylogeny** (version 1.0.0)  
Build and draw phylogenetic tree from ranks in dataset 14

Send results to a new history

**Run workflow**

History

**HISTORY LISTS**

- Saved Histories
- Histories Shared with Me

**CURRENT HISTORY**

- Create New
- Copy History
- Copy Datasets
- Share or Publish
- Extract Workflow**
- Dataset Security
- Resume Paused Jobs
- Collapse Expanded Datasets
- Include Deleted Datasets
- Include Hidden Datasets
- Unhide Hidden Datasets
- Purge Deleted Datasets
- Show Structure
- Export to File
- Delete
- Delete Permanently

**OTHER ACTIONS**

- Import from File



# Sharing and Publishing Your Work

The screenshot shows the top of a Genome Research article page. At the top left is the CSH PRESS logo and the 'GENOME RESEARCH' title. To the right is an advertisement for Illumina's Cancer GWAS Grant. Below the header is a navigation menu with links: HOME | ABOUT | ARCHIVE | SUBMIT | SUBSCRIBE | ADVERTISE | AUTHOR INFO | CONTACT | HELP. A blue bar below the menu contains the text 'Institution: PENN STATE UNIV Sign In via User Name/Password' and a search box with 'Search for Keyword: Go' and 'Advanced Search' options. The main article title is 'Windshield splatter analysis with the Galaxy metagenomic pipeline' by Sergei Kosakovsky Pond and Samir Wadhawan. A section titled 'OPEN ACCESS ARTICLE' contains publication details: 'This Article', 'Published in Advance October 9, 2009, doi: 10.1101/gr.094508.109', and 'Copyright © 2009 by Cold'. To the right is a 'Current Issue' section for October 2010, 20 (10). A 'Footnotes' section is highlighted with an orange oval, containing a paragraph about supplemental material availability.

CSH PRESS GENOME RESEARCH

EXPRESSION ANALYSIS<sup>®</sup> illumina<sup>®</sup> Apply today for the Cancer GWAS Grant.

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Institution: PENN STATE UNIV Sign In via User Name/Password

Search for Keyword:  Go  
Advanced Search

## Windshield splatter analysis with the Galaxy metagenomic pipeline

Sergei Kosakovsky Pond<sup>1,2,6,9</sup>, Samir Wadhawan<sup>3,6,7</sup>,  
Fran  
Jame

### OPEN ACCESS ARTICLE

#### This Article

Published in Advance October 9, 2009, doi: 10.1101/gr.094508.109  
Copyright © 2009 by Cold

#### Current Issue

October 2010, 20 (10)

### 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>.]

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

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



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

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

Correspondence should be 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** [+](#) [↗](#)

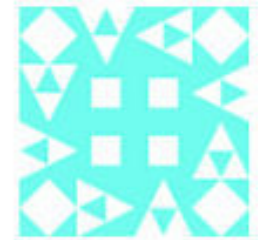
This is the Galaxy workflow for generic analysis of metagenomic data. (This corresponds to the "A complete metagenomic pipeline" section of the manuscript and **Figure 3B**):

[+](#) **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 there, they can be re-analyzed through Galaxy using the shared workflows or downloaded.

## About this Page



### Author

aun1

### Related Pages

[All published pages](#)  
[Published pages by aun1](#)

### Rating

Community  
(6 ratings, 5.0 average)



### Tags

Community:

- paper
- galaxy
- megan

# Overview

**What is Galaxy?**

**Usage / Contributions**

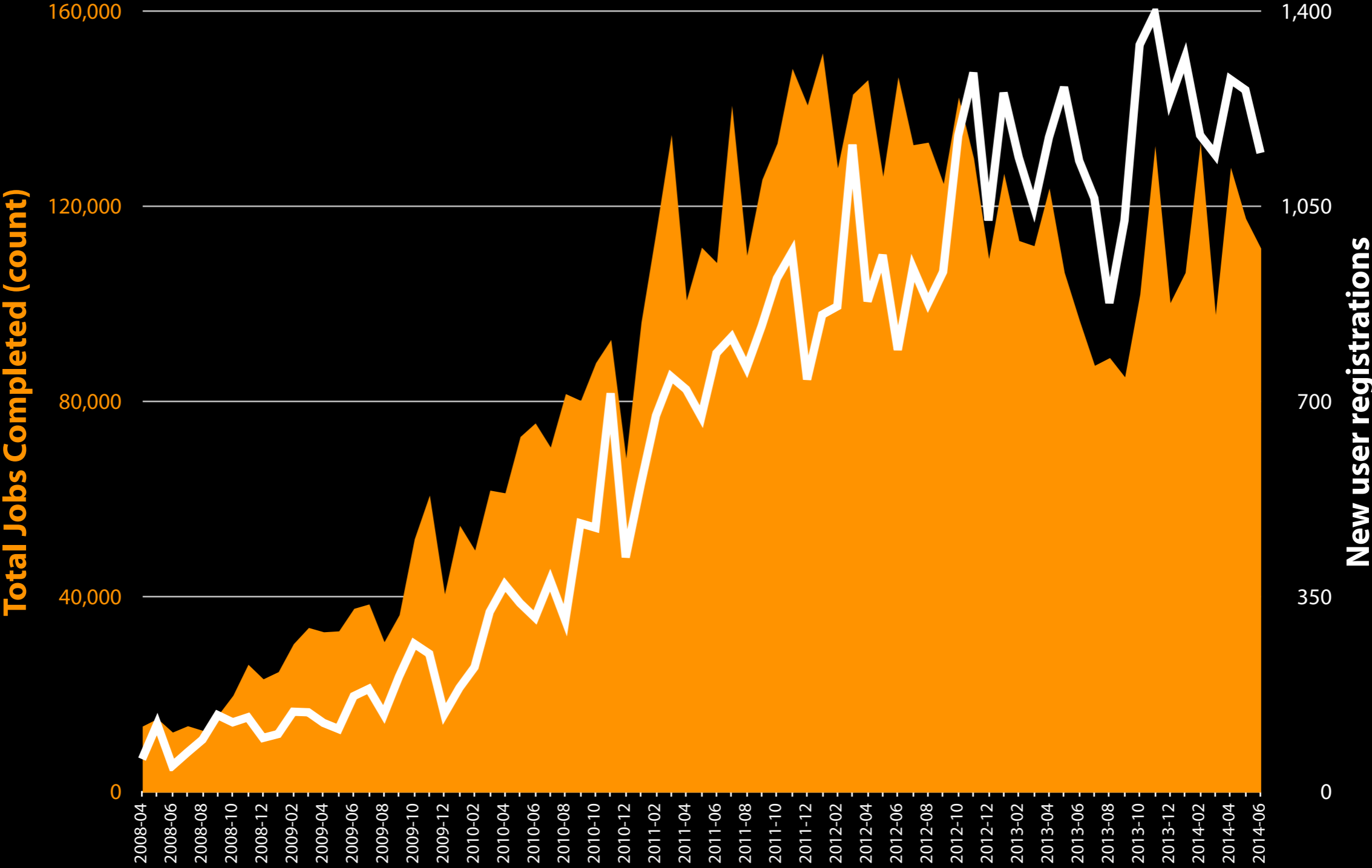
**Virtual Interactions**

**ToolShed**

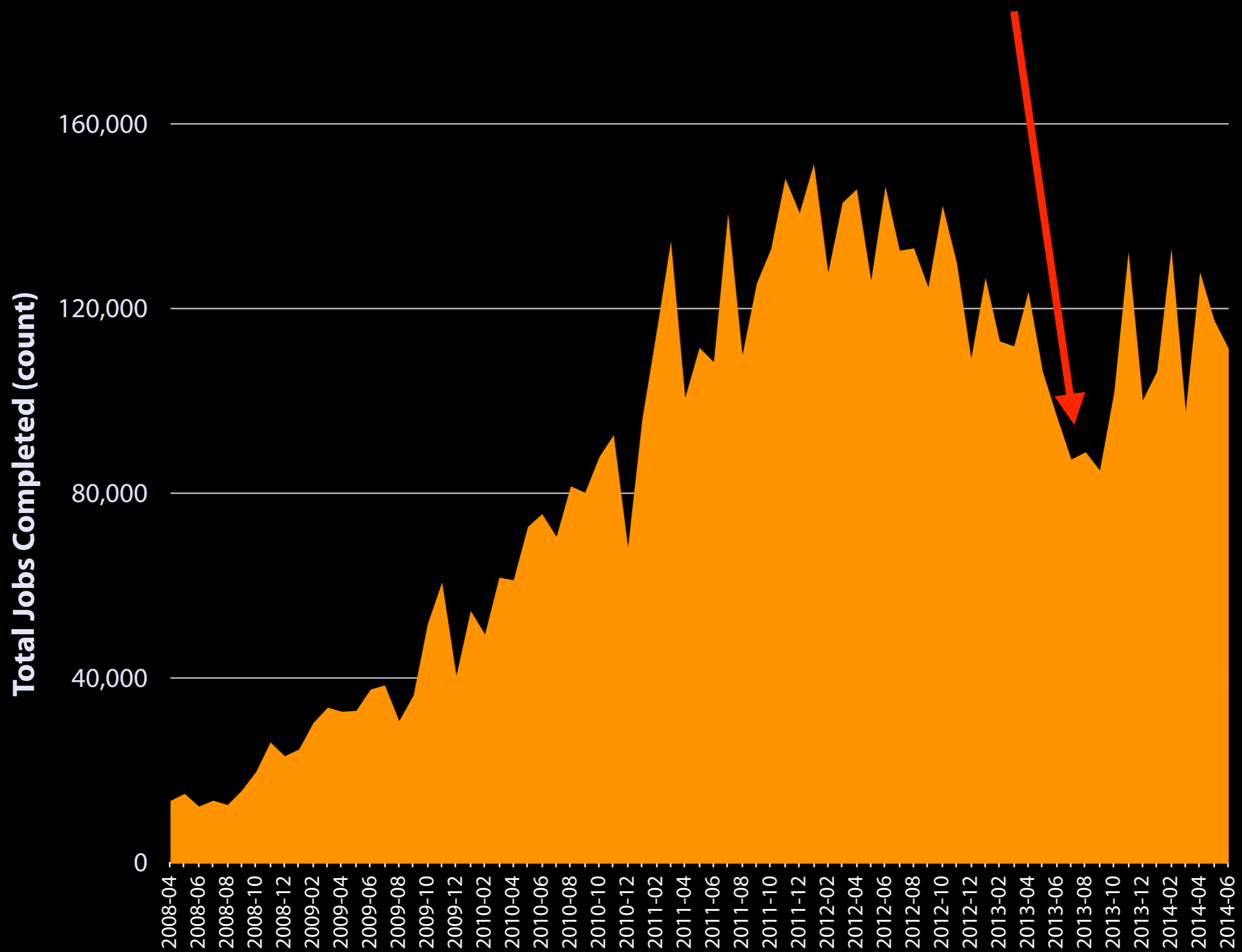
**Events and Outreach**



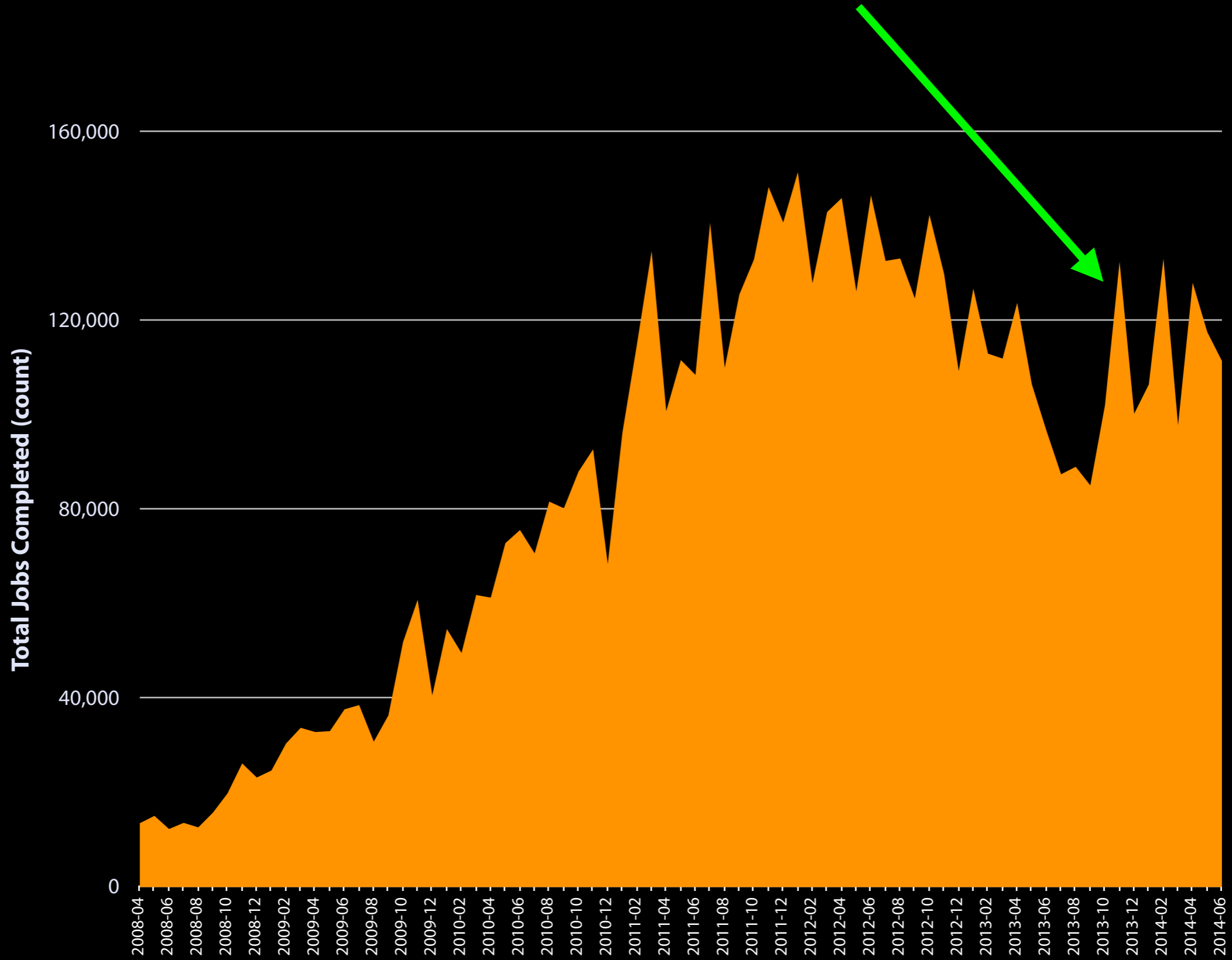
# user dynamics at usegalaxy.org



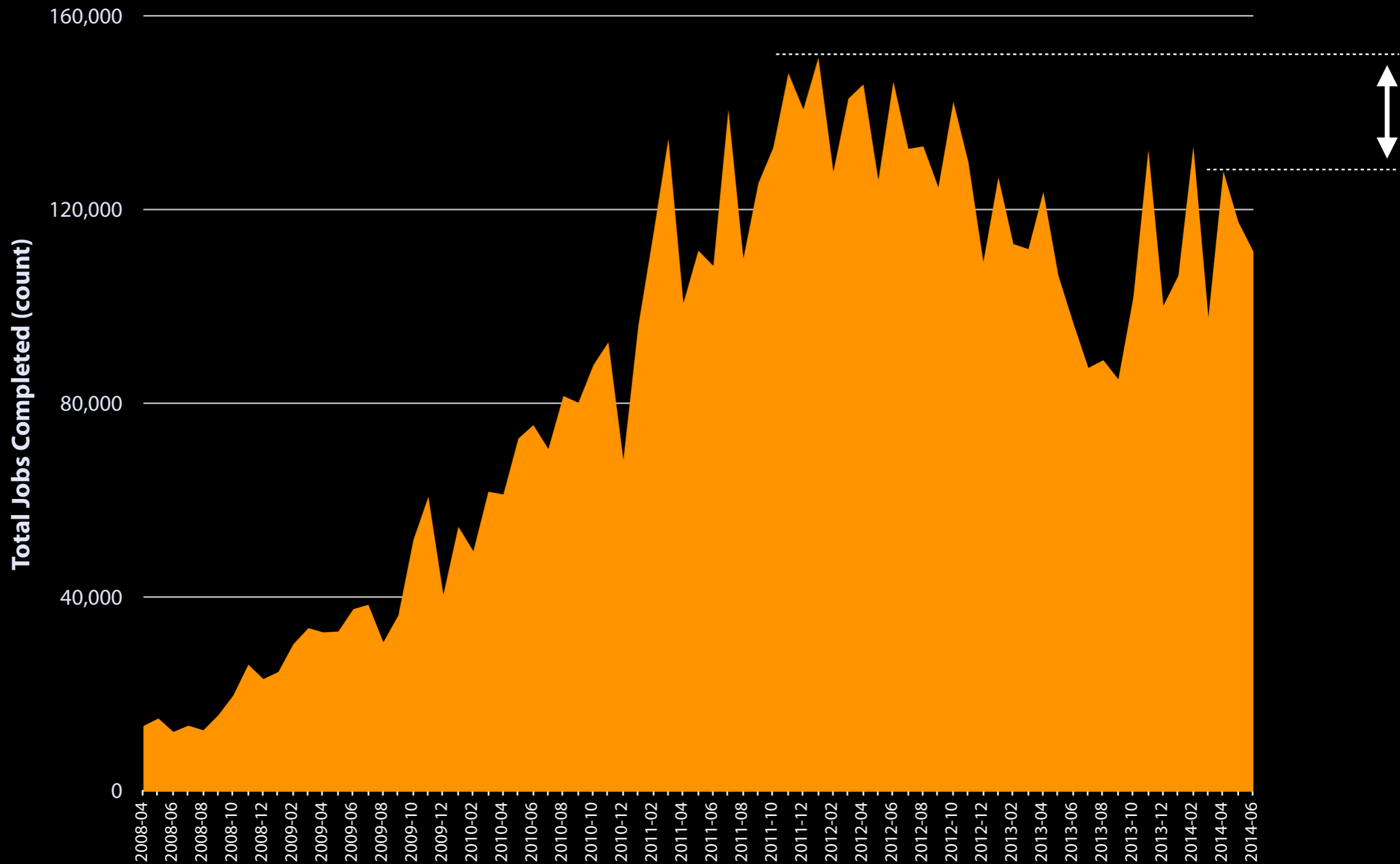
# severe resource bottleneck



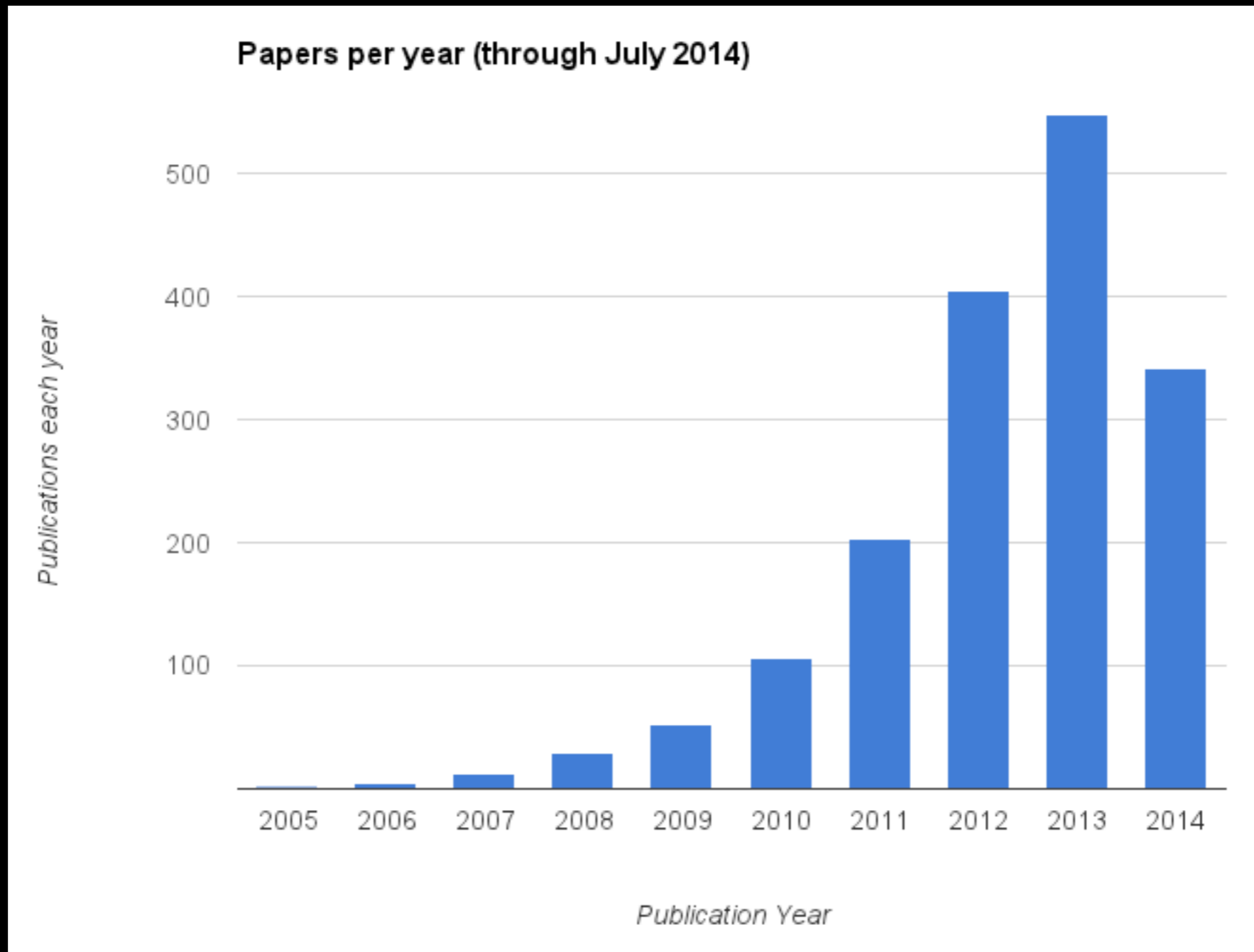
# move to TACC



# data is bigger = jobs are longer



# Citations / Publications





# Community Code Contributions

## 12 Month Summary

*Jun 30 2013 — Jun 30 2014*

**3738 Commits**

Up **+840 (28%)** from previous 12 months

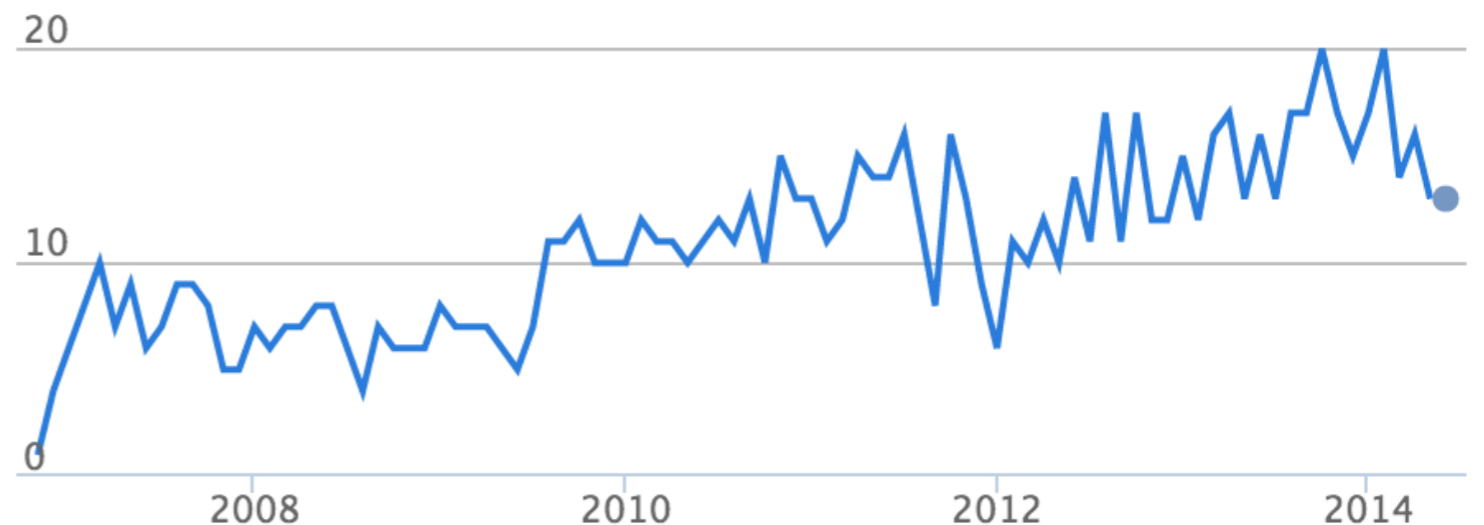
**51 Contributors**

Up **+6 (13%)** from previous 12 months

### Commits per Month



### Contributors per Month



# Overview

**What is Galaxy?**

**Usage / Contributions**

**Virtual Interactions**

**ToolShed**

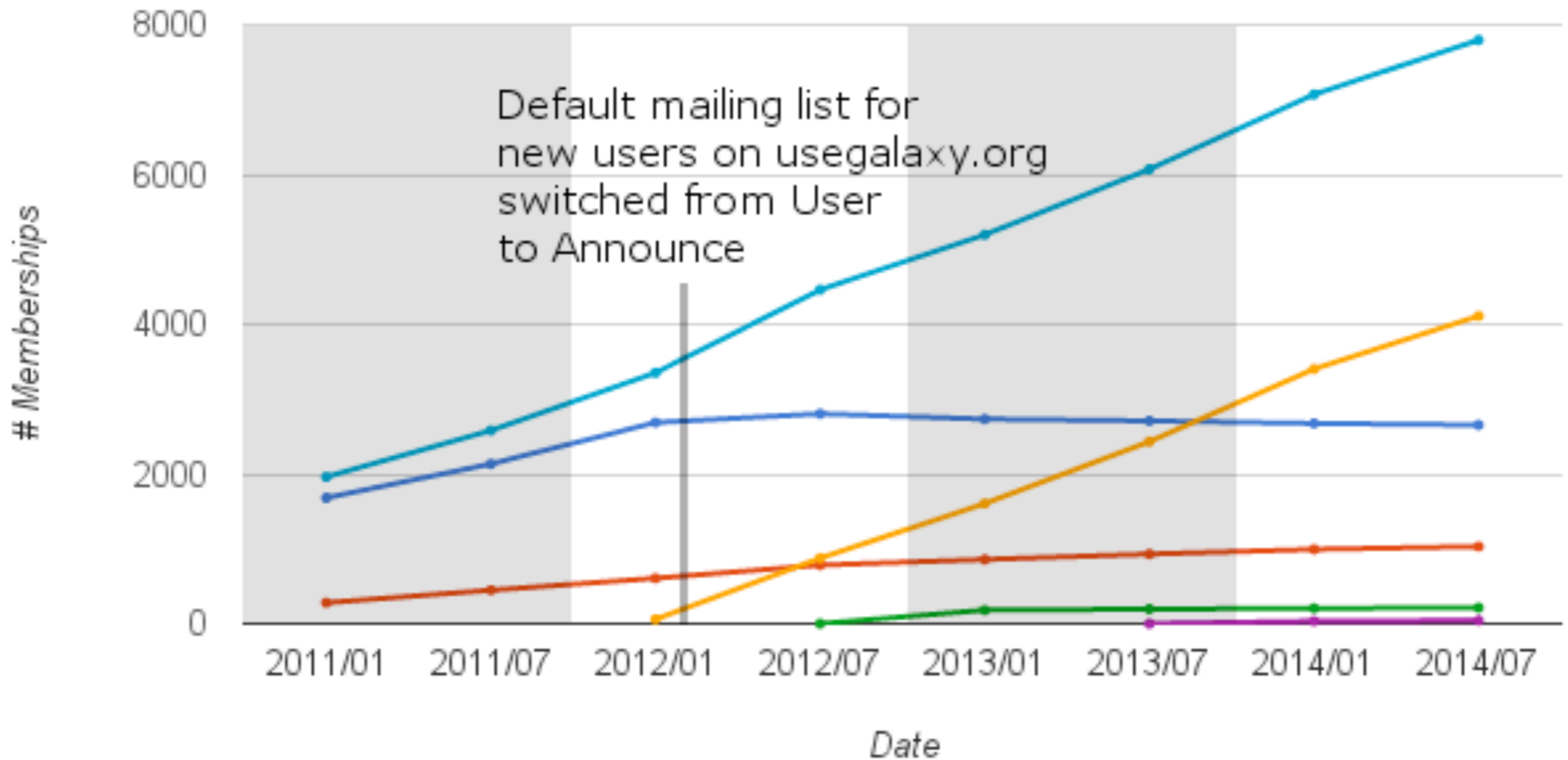
**Events and Outreach**



# Mailing Lists

## Galaxy Mailing List Memberships

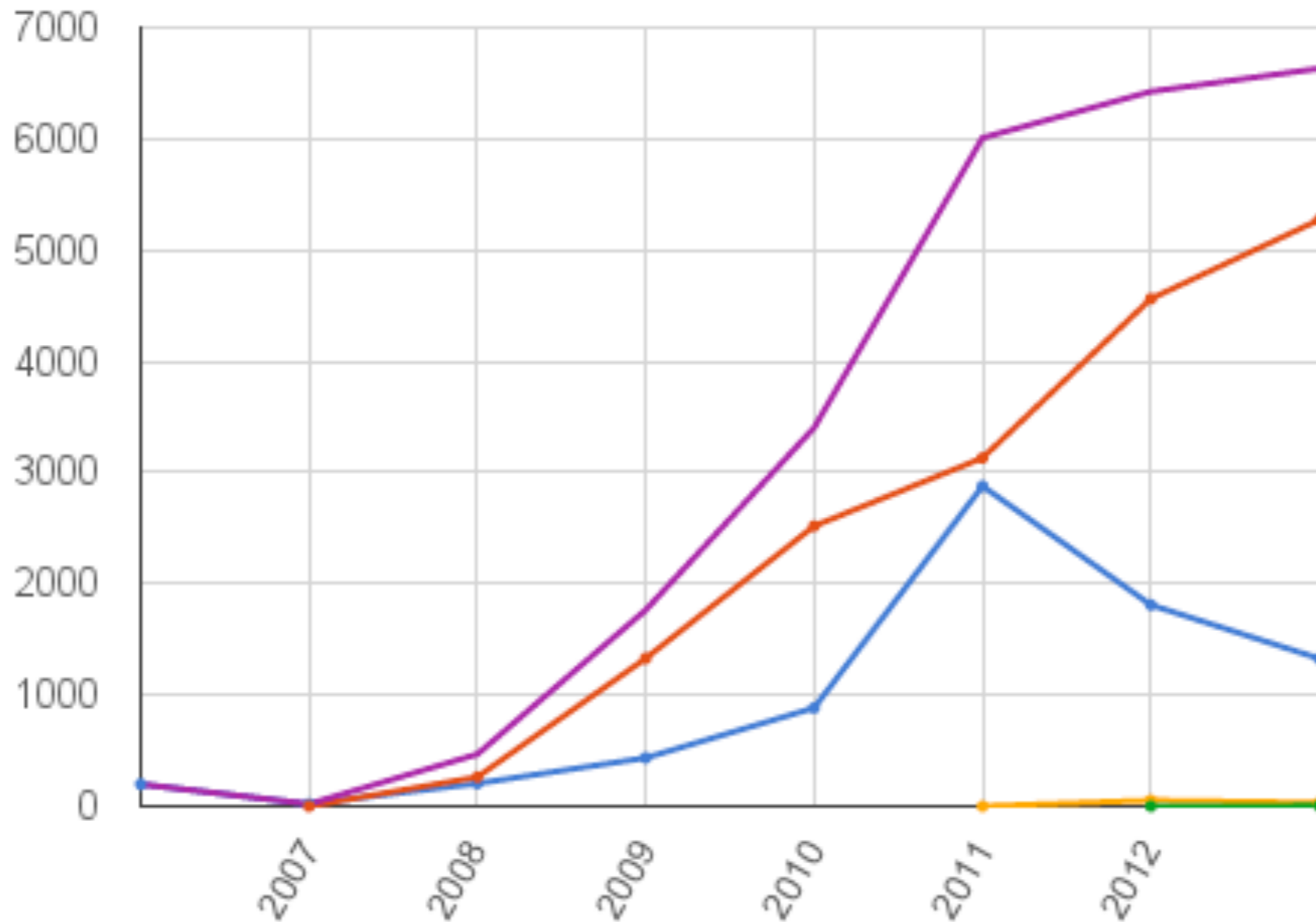
User Dev Announce France Proteomics Us+Dv+An\*



# Mailing Lists

**Yearly Message Counts**

■ User   ■ Dev   ■ France   ■ Proteomics   ■ Total\*



# Biostar: Software for building Scientific Communities

Detailed documentation: <http://docs.biostars.org/>

BioStar is a [Python](#) and [Django](#) based Q&A software. It is a simple, generic, flexible and extensible Q&A framework.

The site has been developed by **scientists and for scientists**. It aims to address the requirements and needs that scientific communities have.

Biostar is the software that runs several science oriented Q&A sites:

- Biostars Bioinformatics Q&A at: <https://www.biostars.org>
- Galaxy User support site: <https://biostar.usegalaxy.org>
- Metabolomics Q&A: <http://www.metastars.org>
- Neurostars: <http://www.neurostars.org>



**Istvan Albert**

## Features

- Standard Q&A: post questions, answers, comments, user moderation, voting, badges, threaded discussions
- Email integration: import previous posts from mailing lists, reply to posts via email
- RSS Planet: feed aggregation from different sources
- External authentication: authenticate users with a different web service
- Low resource utilization and easy deployment



# Biostar

LATEST 19 OPEN 11 RNA-SEQ 5 CHIP-SEQ 1 SNP ASSEMBLY 1 FORUM PLANET 12 ALL »



Daniel Blankenberg ♦♦ 980 | Logout

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- Community
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- Following
- Bookmarks
- New Post

Live search: start typing...

or  Classic search

Limit to: all time ▾

<prev • 2,985 results • page 1 of 86 • next >

Sort by: update ▾

- 0 votes 0 answers 7 views **waiting on Cufflinks and Tophat in Galaxy for longer than usual**  
galaxy rna-seq written 13 hours ago by willschachterle • 0
- 1 vote 2 answers 22 views **How do I automagically make informative dataset names at different workflow stages?**  
renaming datasets workflow written 1 day ago by cgibas • 10
- 0 votes 0 answers 8 views **Need help with "Convert genome coordinates" tool**  
convert-genome-coordinates written 16 hours ago by hjs2121 • 0
- 1 vote 0 answers 17 views **Cluster manager for Galaxy: which one ?**  
cluster written 22 hours ago by plindenbaum • 30
- 1 vote 0 answers 14 views **Empty Cuffdiff Output**  
rna-seq written 1 day ago by wzaky • 10
- 0 votes 0 answers 15 views **Visualize gff3 file**  
gff written 1 day ago by s.saha • 0
- 0 votes 0 answers 14 views **input file types to DESeq on the cloud**  
rna-seq written 1 day ago by anna.gordon • 0
- 1 vote 1 answer 32 views **Can't connect to FTP server**  
galaxy written 2 days ago by ashmchu • 0

## Recent Votes

- Cluster manager for Galaxy: which one ?
- A: Can't connect to FTP server
- How do I automagically make informative dataset names at different workflow stages?
- A: Adding custom tools: resolving (external) XML entities
- Adding custom tools: resolving (external) XML entities
- A: Adding custom tools: resolving (external) XML entities
- Empty Cuffdiff Output

## Recent Locations • All »

- Australia, 7 hours ago
- United States, 10 hours ago
- Germany, 10 hours ago

## Recent Awards • All »

- Teacher 😊 to Bjoern Gruening • 890
- Teacher 😊 to Jennifer Hillman Jackson ♦ 15k
- Voter 🗳️ to Martin Čech ♦♦ 290
- Centurion ⚡ to Bjoern Gruening • 890
- Supporter 👍 to Bjoern Gruening • 890
- Scholar 🎓 to Bjoern Gruening • 890

## Question: sum all but first 500 lines



I'd like to make a genome coverage distribution plot using the X-Y plotting tool

X = coverage depth

0

Y = fraction of reads at coverage depth.



I'd like to sum up all the coverage beyond 500X and consider that 500X+ to avoid a very wide X axis.

I can cut off the first 500 lines in galaxy, but I don't see how to retain the remaining lines for me to operate on.

Any ideas?

I could do this with a little script, but I'm wondering about how to do this with the galaxy native tools.

galaxy

[ADD COMMENT](#) • [link](#) • [edit](#) • [moderate](#) • [Follow via email](#) ▾

modified 9 weeks ago by [Bjoern Gruening](#) • 890 • written 9 weeks ago by [Brad Langhorst](#) • 50



Nice! Thanks for sharing!

[ADD REPLY](#) • [link](#) • [edit](#) • [moderate](#)

written 9 weeks ago by [Bjoern Gruening](#) • 890



Hi Brad,

the tool "[Remove beginning of a file](#)" can remove the first 500 lines for you. Is that what you are searching?

1

Cheers,

Bjoern



[ADD COMMENT](#) • [link](#) • [edit](#) • [moderate](#)

written 9 weeks ago by [Bjoern Gruening](#) • 890



Perfect!

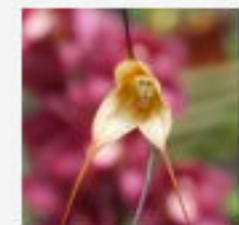
1 I've published the [workflow](#) in case anyone has a similar itch.

[ADD REPLY](#) • [link](#) • [edit](#) • [moderate](#)

written 9 weeks ago by [Brad Langhorst](#) • 50



9 weeks ago by  
[Brad Langhorst](#) • 50  
United States



9 weeks ago by  
[Bjoern Gruening](#) • 890  
Germany



# Gamification

LATEST OPEN RNA-SEQ CHIP-SEQ SNP ASSEMBLY FORUM PLANET ALL »



Daniel Blankenberg ♦♦ 980 | Logout

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Community

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New Post

Enter name

Search user

Limit to: all time ▾

<prev • 2,538 users • page 1 of 43 • next >

Sort by: reputation ▾



Jennifer Hillman Jackson ♦ 15k  
joined 4.1 years ago  
United States



Nate Coraor ♦ 2.3k  
joined 8.0 years ago  
United States



Jeremy Goecks • 2.2k  
joined 4.5 years ago



Anton Nekrutenko ♦ 1.5k  
joined 8.5 years ago



Dannon Baker ♦ 1.5k  
joined 4.1 years ago  
United States



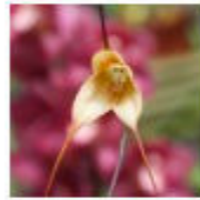
Peter Cock • 1.3k  
joined 3.4 years ago  
European Union



Dave Clements ♦♦ 1.2k  
joined 3.4 years ago  
United States



Daniel Blankenberg ♦♦ 980  
joined 6.2 years ago  
United States



Bjoern Gruening • 890  
joined 11 months ago  
Germany



mailing list • 840  
joined 2.6 years ago



Greg Von Kuster • 840  
joined 6.1 years ago



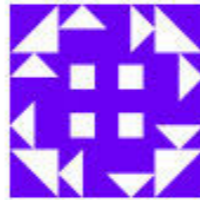
Greg Von Kuster ♦ 790  
joined 4.7 years ago  
Penn State University



Enis Afgan • 680  
joined 3.6 years ago



fubar ♦ 640  
joined 5.9 years ago  
Australia



David Matthews • 630  
joined 3.7 years ago



shamsheer jagat • 580  
joined 3.2 years ago



Erick Antezana • 570  
joined 5.0 years ago



James Taylor ♦ 410  
joined 3.9 years ago  
United States

## Badge list

Teacher 😊 × 20

created an answer with at least 3 up-votes

Scholar 🎓 × 19

created an answer that has been accepted

Centurion ⚡ × 6

created 100 posts

Supporter 👍 × 4

voted at least 25 times

Autobiographer 🗣️ × 3

has more than 80 characters in the information field of the user's profile

Appreciated ❤️ × 3

created a post with more than 5 votes

Oracle ⚙️ × 1

created more than 1,000 posts (questions + answers + comments)

Voter 👍 × 1

voted more than 100 times

Good Answer ✍️ × 0

created an answer that was upvoted at least 5 times

Good Question ? × 0

asked a question that was upvoted at least 5 times

Prophet 🌿 × 0

created a post with more than 20 followers

Student 🎓 × 0

asked a question with at least 3 up-votes

Great Question 🔥 × 0

created a question with more than 5,000 views

Gold Standard 🏆 × 0

created a post with more than 25 bookmarks

Librarian 📖 × 0

created a post with more than 10 bookmarks

Commentator 💬 × 0

created a comment with at least 3 up-votes

Cylon 🚀 × 0

received 1,000 up votes

Rising Star ★ × 0

created 50 posts within first three months of joining

Guru 🙏 × 0

received more than 100 upvotes

Popular Question 👁️ × 0

created a question with more than 1,000 views

Epic Question 🎯 × 0

created a question with more than 10,000 views

Pundit 🗨️ × 0

created a comment with more than 10 votes



# Accessing Biostar through Galaxy

The screenshot shows the Galaxy web interface. The top navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Cloud', 'Admin', and 'Help'. The left sidebar contains a 'Tools' section with a search bar and a list of tool categories: 'Get Data', 'BEDtools', 'SNP Eff', 'Send Data', 'Lift-Over', 'Text Manipulation', 'Filter and Sort', 'Join, Subtract and Group', and 'Convert Formats'. The main content area displays the configuration for the 'Map with BWA for Illumina (version 1.2.3)' tool. It includes a 'Will you select a reference genome from your history or use a built-in index?' dropdown set to 'Use a built-in index', a 'Select a reference genome:' dropdown set to 'Arabidopsis lyrata: Araly1', an 'Is this library mate-paired?' dropdown set to 'Single-end', and a 'FASTQ file:' dropdown set to '56: F41-M51C2-BL.R1.fq'. A tooltip 'Search for this tool' is visible over the 'Help from Biostar' link. Below the FASTQ file dropdown, there is a note: 'FASTQ with either Sanger-scaled quality values (fastqsanger) or Illumina-scaled quality values (fastqillumina)'.

Registered Galaxy Users are automatically logged in

The screenshot shows the 'Help' dropdown menu in the Galaxy interface. The menu is open, showing the following options: 'Galaxy Q&A Site', 'Ask a question', 'Support', 'Search', 'Mailing Lists', 'Videos', 'Wiki', 'How to Cite Galaxy', and 'Terms and Conditions'. The 'Help' and 'User' tabs are visible at the top of the dropdown.



## Galaxy BioStar

The [Galaxy Biostar forum](#) was launched on April 23, 2014. Every thread that existed in the Galaxy-User mailing list was copied to Galaxy Biostar at that time, and people were strongly advised to post future questions to Galaxy Biostar. On June 6, 2014, all posting to Galaxy-User was suspended.

The statistics here don't reflect just what's happened since the switch, but also what happened (sort of) on Galaxy-User before the switch. As more time passes, result, and especially the recent numbers will more accurately reflect what's happening on Galaxy Biostar.

All date ranges here are from Biostar. For example, the "last 12 months" means anything that Biostar identifies as having happened between now and "12 months ago", inclusive.

### Active Users

Active here means "visited", as defined by Biostar.

Date	Last 12 Weeks	Last 6 Months	Last 12 Months
2014/07/09	1190	1274	1424

### Active Threads

Date	Last 12 Weeks	Last 6 Months	Last 12 Months
2014/07/09	268	383	654

### All Time Totals

Date	Posts	Threads	Questions	Answers	Comments	Users
2014/07/09	8223	2978	2959	2908	2337	2517

# Biostar is a success, but...

Users haven't quite mastered the Q&A format

Reuse a post for multiple questions

Not accepting Answers

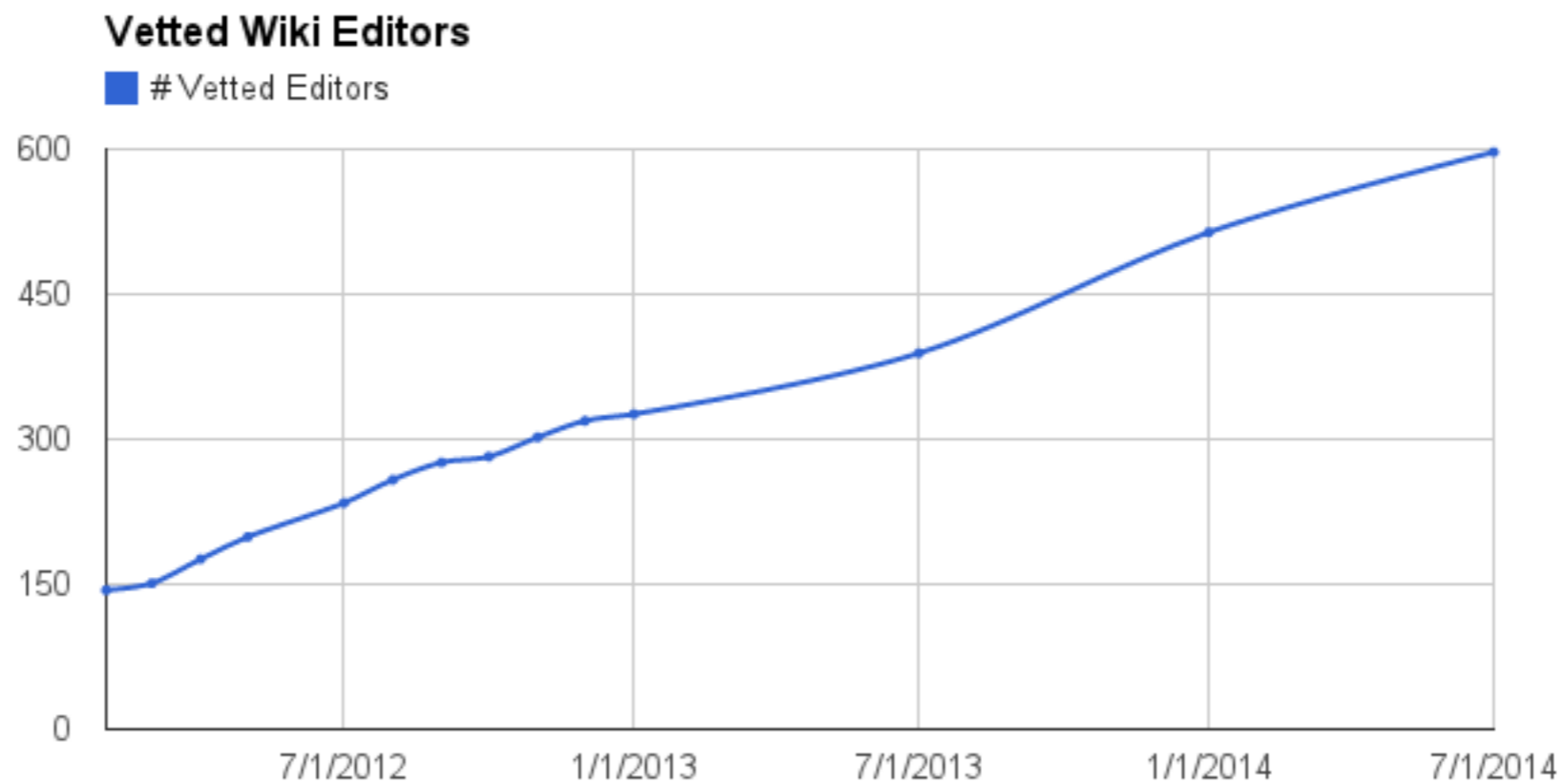
Comments are being Posted as Answers

# wiki.galaxyproject.org

## Wiki

### Vetted Editors

*Vetted Editors* are wiki logins that have been verified as belonging to Galaxy community members. Vetted editors can update the wiki without having to answer Captchas. You don't need a login to read the wiki, only to update it. The number of vetted editors is a measure of interest in maintaining this wiki.

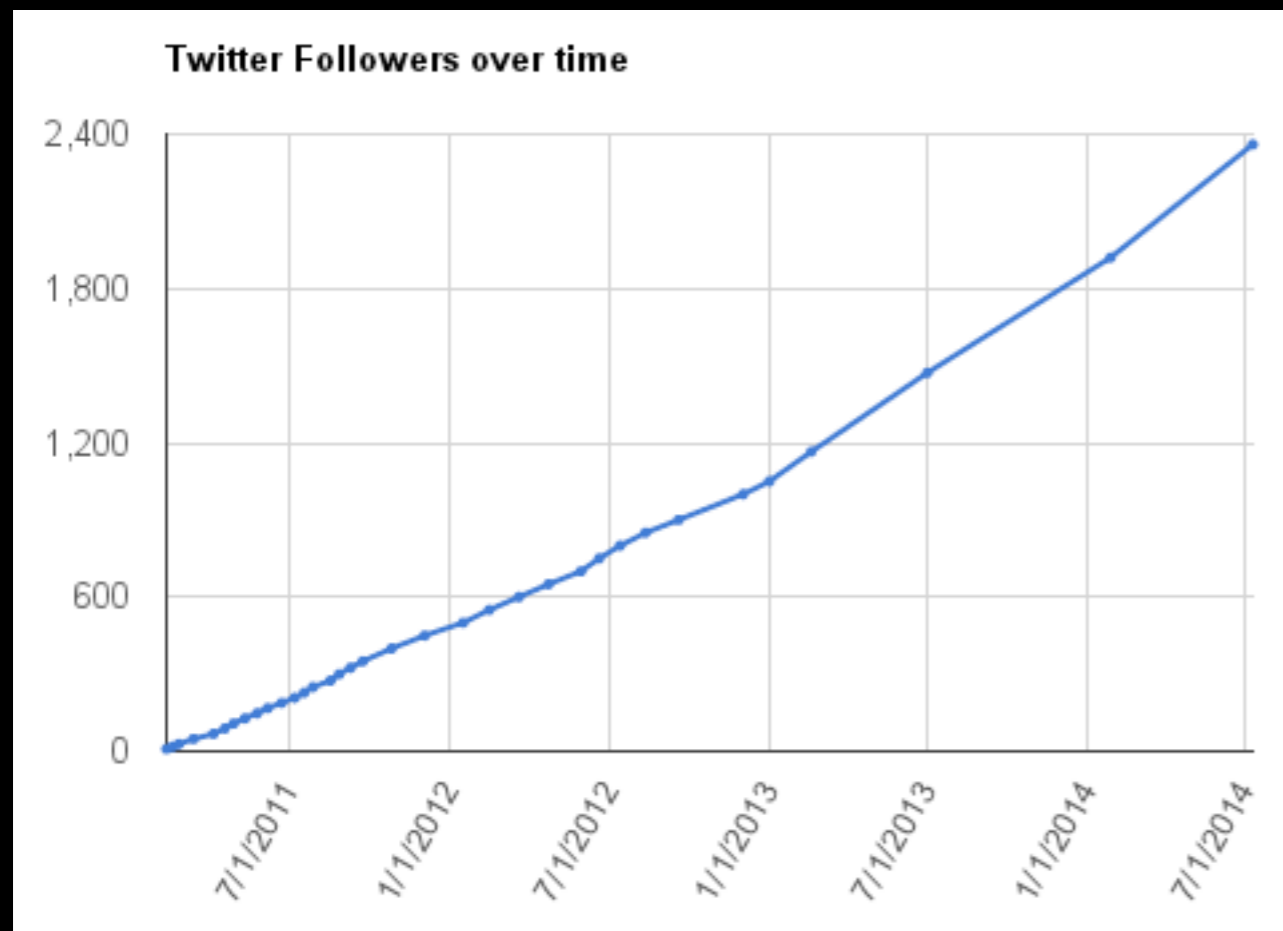


This is an undercount of registered community members as not all logins can be verified. The process of vetting was semi-automated on 2012/04/08, thanks to help from [ToriR](#).

# Additional Channels

<https://wiki.galaxyproject.org/GetInvolved>

@galaxyproject #usegalaxy



**IRC Channel**

**Server:** irc.freenode.net

**Channel** #galaxyproject

<https://twitter.com/galaxyproject>

# Overview

**What is Galaxy?**

**Usage / Contributions**

**Virtual Interactions**

**ToolShed**

**Events and Outreach**



Enables sharing of Galaxy **Utilities**:  
tools  
proprietary datatypes  
exported Galaxy workflows

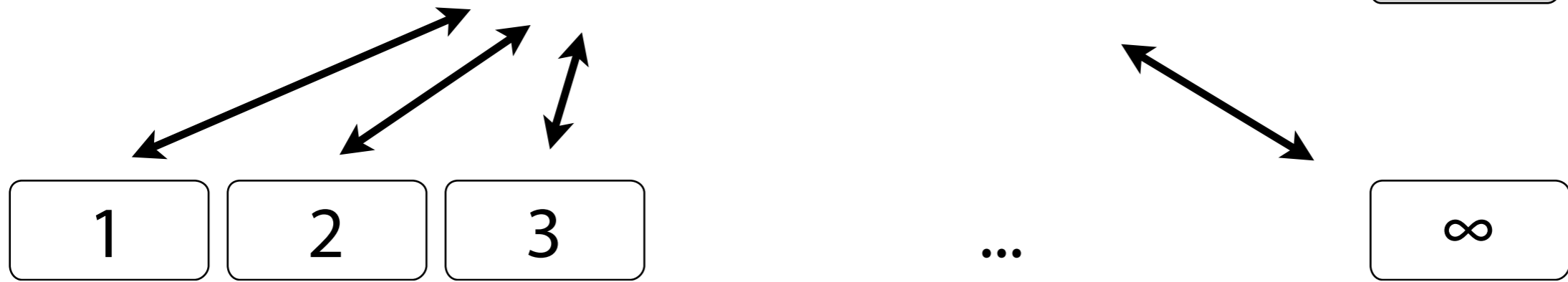
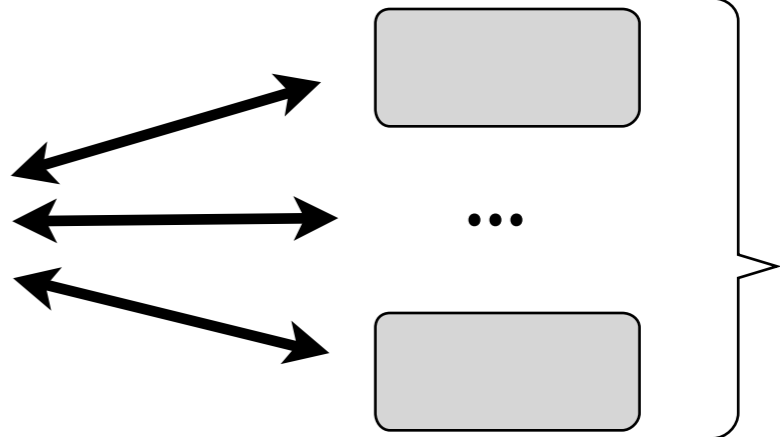
**Automatically install** tools and **tool suites**, and their **dependencies**, into a Galaxy instance

Galaxy Utilities can be created and shared by any member of the **community**

<https://wiki.galaxyproject.org/ToolShed>



<http://usegalaxy.org>



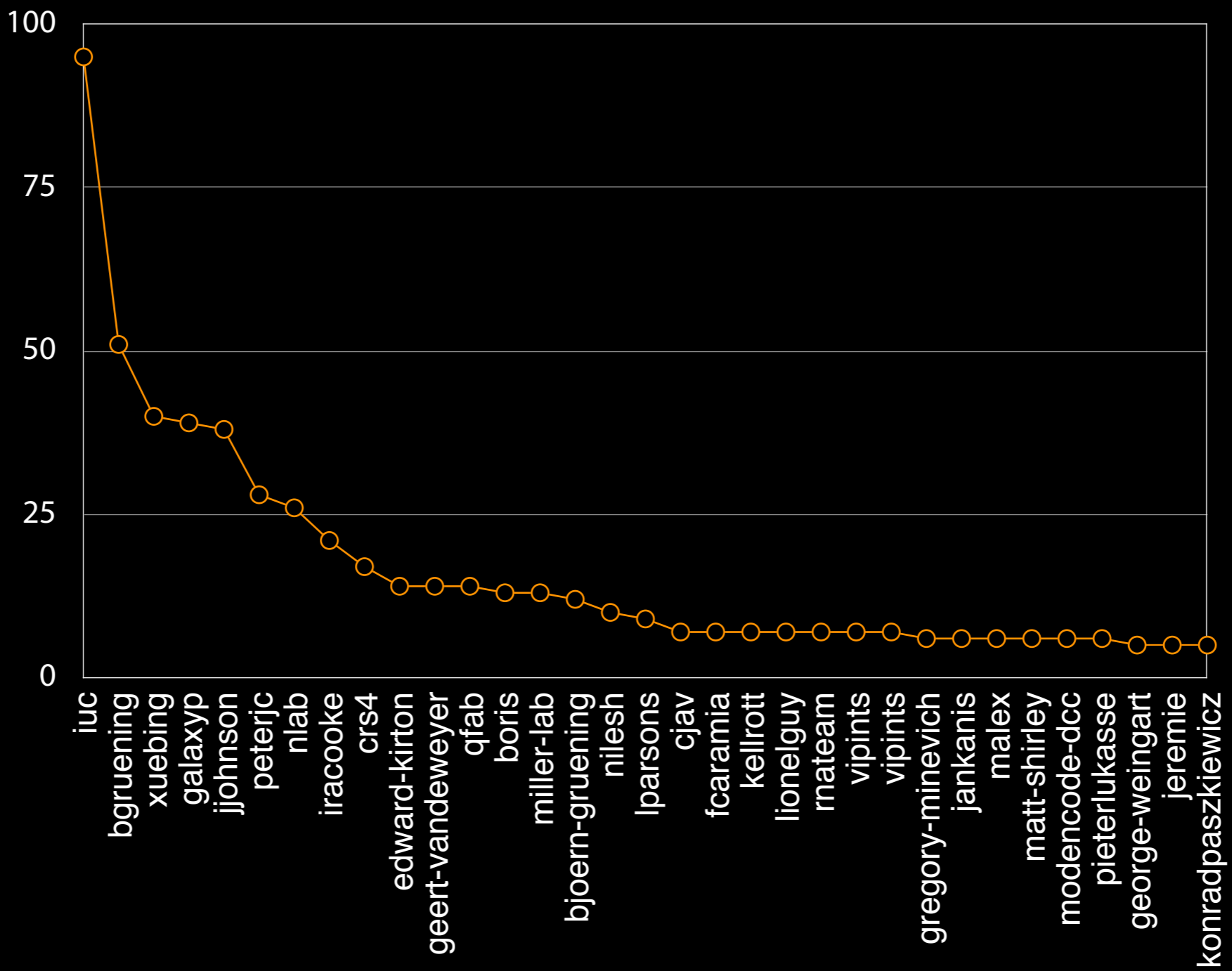
**private Galaxy installations**

# toolshed statistics

- 897 repositories
- 222 unique owners
- 176 Tool dependency package installation recipes
- 2,330 valid tools
- 3,420 valid versions of tools
- 54 exported Galaxy workflows
- 455 custom datatypes
- 62,021 total repository installations



# toolshed contributions



# Overview

**What is Galaxy?**

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## Upcoming Events



Date	Topic/Event	Venue/Location	Contact
July 7-9	<i>NBIC/BioSB RNA- seq data analysis course</i>	Leiden, the Netherlands	✉ NBIC/BioSB
July 10	<i>An Introduction to Galaxy with the Genomics Virtual Lab</i>	Post-GSA 2014 Workshop, Sydney, Australia	Mark Crowe
July 11-15	<b>ISMB and BOSC 2014</b> At least six talks and five posters	Boston, Massachusetts, United States	See <a href="#">presenter list</a>
July 18	<i>Workshop: RNA-Seq analysis using Galaxy</i>	Brisbane, Australia	Mark Crowe
July 28 - August 1	<i>Workshop: DNA Sequence Bioinformatics Analysis with the Galaxy Platform</i>	University of São Paulo (USP), São Paulo, Brazil	Dave Clements
August 25-27	<i>Análise e anotação funcional de seqüências NGS usando Stingray@Galaxy</i>	Fiocruz, Rio de Janeiro, Brasil	✉ Plataforma de Bioinformática do IOC
September 6-10	<i>T07 - Scientific Workflows for Analysing, Integrating and Scaling Bioinformatics Data: a Practical Introduction to Galaxy, Taverna and WS-PGRADE</i>	European Conference on Computational Biology (ECCB'14), Strasbourg, France	Hailiang (Leon) Mei
September 30 - October 2	<i>RNA-Seq &amp; ChIP-Seq analysis course using Galaxy</i>	PRABI, Lyon, France	✉ Navratil V., ✉ Oger C., ✉ Veber P., ✉ Deschamps C., ✉ Perriere G.
September 30 - October 2	Galaxy Training and Demo Day	Bern (Switzerland)	Hans-Rudolf Hotz and Bjoern Gruening
	<i>(second Swiss) Galaxy Workshop</i>	SyBIT Tech Day, Bern (Switzerland)	
	<i>German Galaxy Developers Day</i>	Freiburg (Germany)	



Fifth Annual Conference

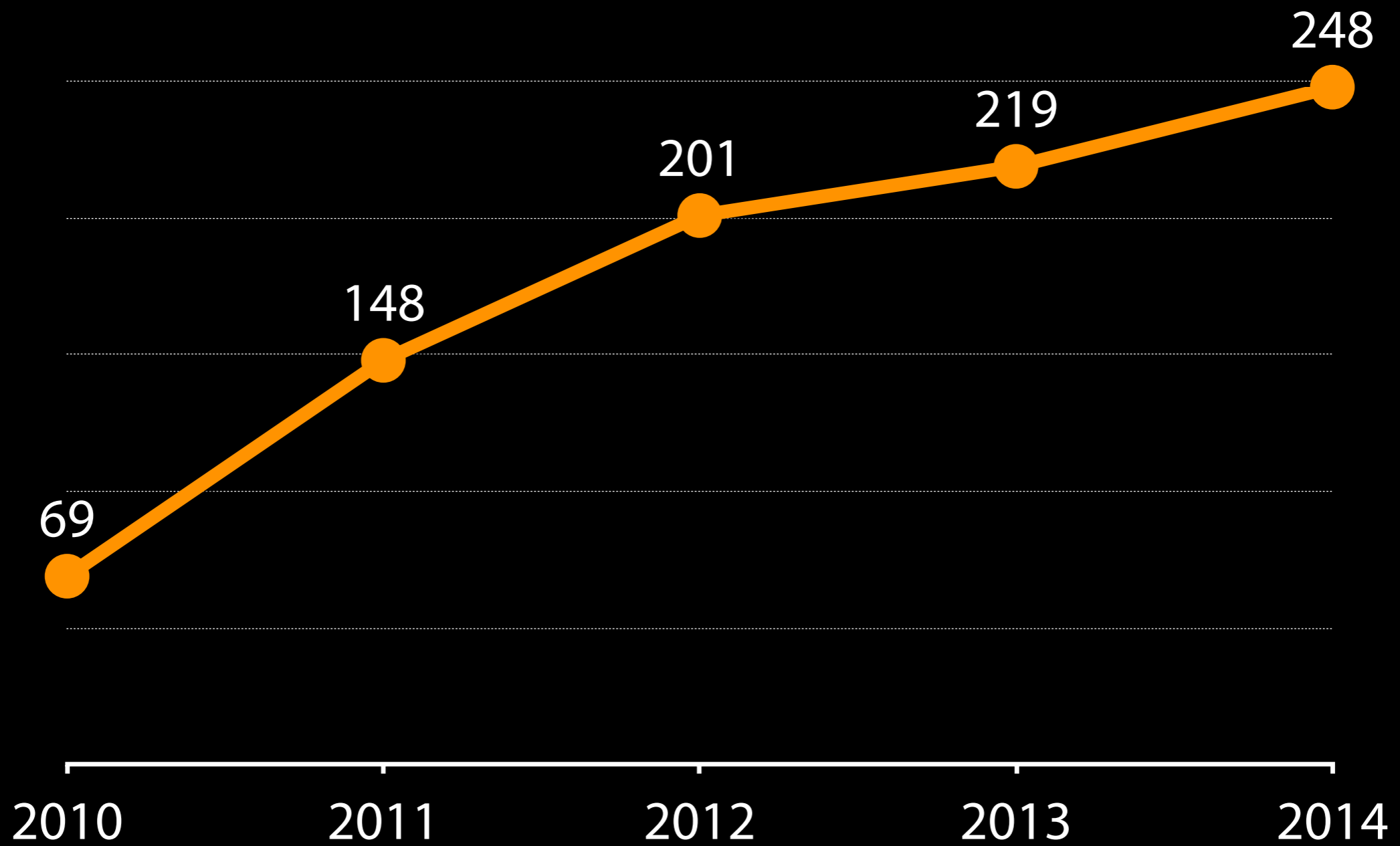
Two day Hackathon

One full day of Training Workshops

Two full days of presentations, posters, lightning talks, Birds of a Feather



# GCC participation



# GCC2015

2015 Galaxy Community Conference will be held in  
Norwich, United Kingdom, at The Sainsbury Lab,  
6-8th July



# The Galaxy Team



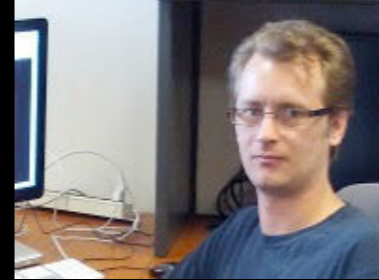
Enis Afgan



Dannon Baker



Dan Blankenberg



Dave Bouvier



Marten Čech



John Chilton



Dave Clements



Nate Coraor



Carl Eberhard



Jeremy Goecks



Sam Guerler



Jen Jackson



Ross Lazarus



Anton Nekrutenko



Nick Stoler



James Taylor



Greg Von Kuster

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