

Galaxy

University of Oregon
January 25, 2018

Dave Clements
Johns Hopkins University
Galaxy Community

bit.ly/gxy-bgmp-2018



#usegalaxy @galaxyproject

Agenda

What is Galaxy?

Features / Live demo

Galaxy's audience

Galaxy's availability

Deploying your own Galaxy

Galaxy Project

Galaxy Community

What is Galaxy? The **Project's** definition

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

What is Galaxy? **Kieth Bradnam's** definition

"A web-based platform that provides a simplified interface to many popular bioinformatics tools."

From

"13 Questions You May Have About Galaxy"

<http://bit.ly/13questions>

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Features / Live Demo

usegalaxy.org

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Galaxy for biologists

Clear win.

Galaxy for bioformaticians?

Reproducibility

Sharing and publishing

(and there's an API - you can access Galaxy programmatically)

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As a free for everyone service on the web: usegalaxy.org

The screenshot displays the Galaxy web interface. At the top, the 'Galaxy' logo is on the left, and navigation tabs for 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User' are in the center. A 'Using 0%' indicator is on the right. The left sidebar contains a 'Tools' section with a search bar and a list of tool categories: Get Data, Send Data, Lift-Over, Collection Operations, Text Manipulation, Datamash, Convert Formats, Filter and Sort, Join, Subtract and Group, Fetch Alignments/Sequences, NGS: QC and manipulation, NGS: DeepTools, NGS: Mapping, NGS: RNA Analysis, NGS: SAMtools, NGS: BamTools, NGS: Picard, NGS: VCF Manipulation, NGS: Peak Calling, and NGS: Variant Analysis. The main content area features a tutorial titled 'Running Your Own Understanding how Galaxy works' with the subtitle 'An in-depth tutorial'. The text above the title reads: 'Galaxy is an open source, web-based platform for data intensive biomedical research. If you are new to Galaxy [start here](#) or consult our [help resources](#). You can install your own Galaxy by following the [tutorial](#) and choose from thousands of tools from the [Tool Shed](#).' Below the title is a progress indicator with five dots, the first of which is highlighted. The right sidebar shows a 'History' section with a search bar, a 'View histories' button, and an 'Unnamed history (empty)' entry. A blue information box states: 'This history is empty. You can [load your own data](#) or [get data from an external source](#)'.

Public Galaxy servers

General Purpose / Genomics servers

19 servers as of yesterday

Domain Specific

37 servers

Tool publishing servers

44 servers

Total

100 servers

bit.ly/gxyServers

Galaxy Services



jetstream-cloud.org

Can't use a *service*? Galaxy is available on other Clouds



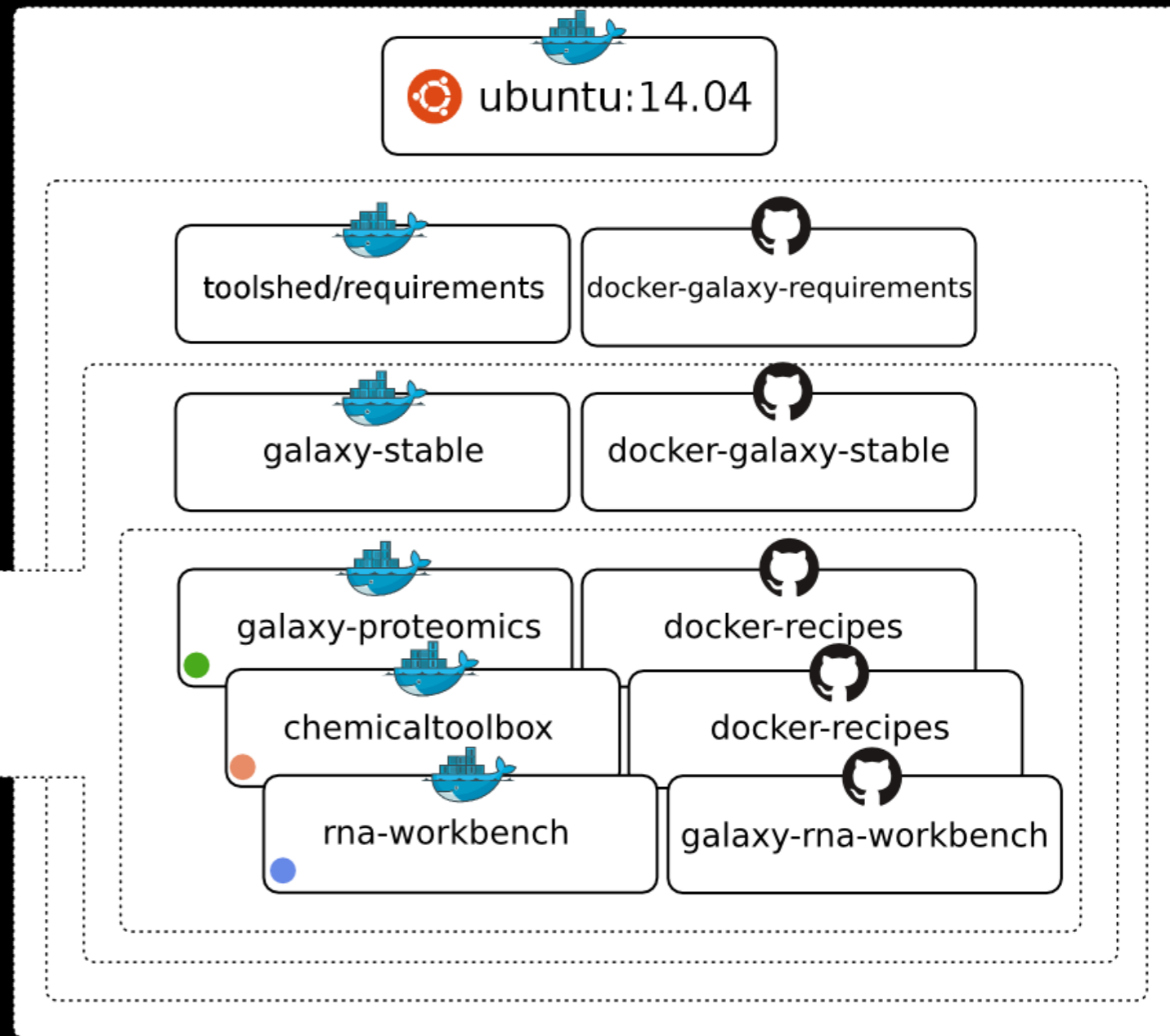
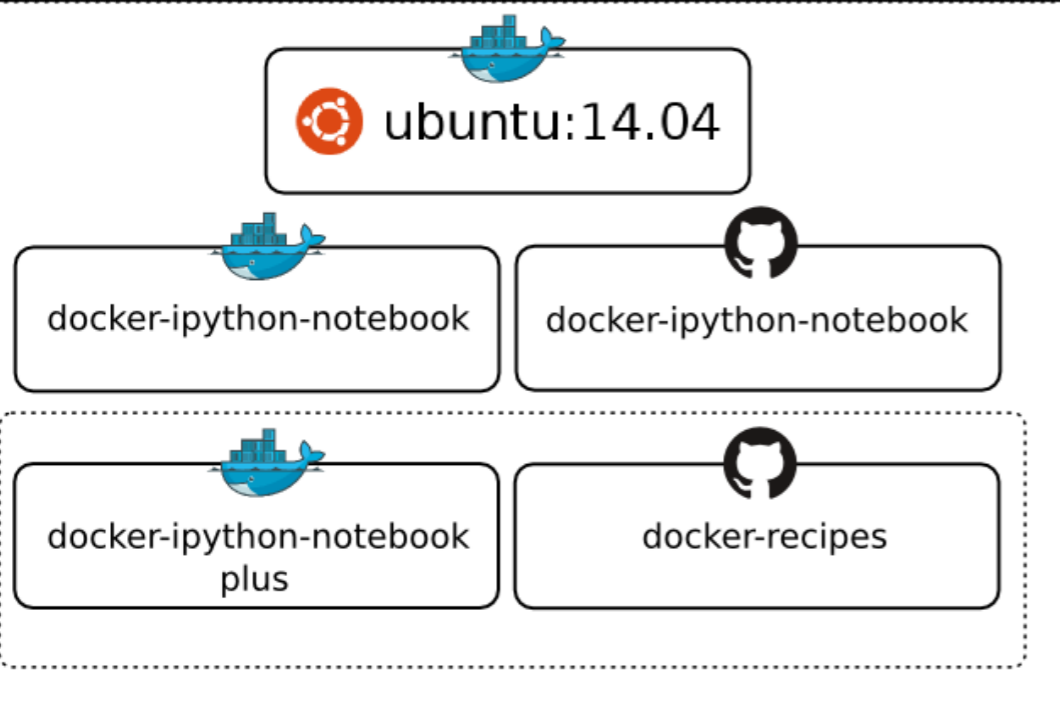
<http://aws.amazon.com/education>

<http://globus.org/>

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

<https://launch.usegalaxy.org/>

Galaxy is available in **Docker**



<https://github.com/bgruening/docker-galaxy-stable>

Galaxy is open source software

getgalaxy.org

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As needed and/or easy options

Galaxy on Docker

Galaxy on AWS

Globus Genomics

Galaxy on Jetstream

getgalaxy.org

Creating a local server

- **Non-trivial**
 - authentication
 - using org's compute & storage infrastructure
- **Less work**
 - Wrapping your own tools
- **Pretty easy**
 - Customizing the tool set from the tool shed.
 - Customizing the genomes
 - Connecting genomes with tools

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Technology

- Python
- JavaScript
- Git & GitHub
- Travis CI
- Ansible

Process

- Releases every 4 months
- Public roadmap on GitHub
- Maximal use of GitHub for issues, etc
- Core team & committers widely dispersed
 - Slack / IRC / Gitter for chat
 - Group video w/ Google or Zoom
- Core team members: daily short status

Core Team, Committers, and Commits

- Core team funded by NIH Galaxy grant
 - Penn State, Johns Hopkins, OHSU, Cleveland Clinic
- **Committers** are a mix of core team and global contributor community
- All changes submitted as pull requests and reviewed by a committer before merging
- **Anyone** can submit a pull request

More than just the core project

BioBlend	a Python library for interacting with CloudMan and Galaxy's API
galaxy-lib	a subset of the Galaxy core code base designed to be used as a library.
Planemo	set of command-line utilities to assist in building tools for the Galaxy project.
StarForge	help build Galaxy things in virtualization
sequence_utils	set of Python modules for reading, analyzing, and converting sequence formats.
Pulsar	Python server application that allows a Galaxy server to run jobs on remote systems (including Windows)

More than just the core project

ephemeris	Python library and set of scripts for managing the bootstrapping of Galaxy plugins - tools, index data, and workflows.
CloudLaunch	New platform for launching multiple appliances on multiple cloud platforms
nebulizer	Command-line utilities for managing users, data libraries and tools in a Galaxy instance
CloudBridge	provides a simple layer of abstraction over different cloud providers
Galaksio	New Galaxy user interface that emphasizes workflows over tools

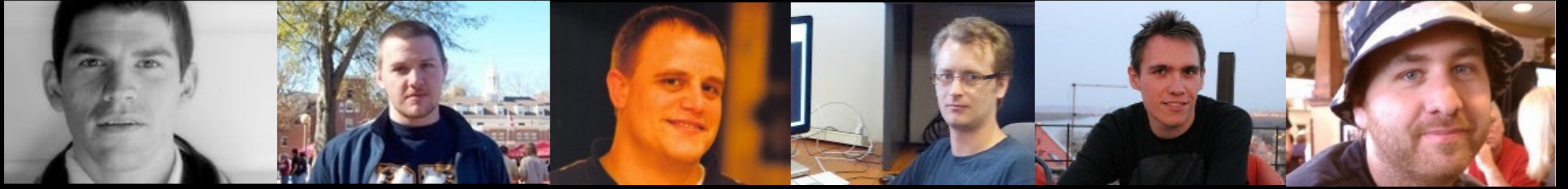
<https://github.com/galaxyproject/>

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We are an open source project

The Core Galaxy Team



Enis Afgan

Dannon Baker

Dan Blankenberg

Dave Bouvier

Marten Cech

John Chilton



Dave Clements

Nate Coraor

Jeremy Goecks

Sam Guerler

Jen Jackson



Vahid Jalili

Delphine Lariviere

Anton Nekrutenko

Nick Stoler

James Taylor

<https://galaxyproject.org/galaxy-team>



Working for the [Galaxy team](#) provides a rare opportunity to perform research and develop software at the leading edge of life sciences, genomics, data-intensive computing, and big data analytics.

We develop [Galaxy](#), a free, open-source platform that (a) enables researchers to store, analyze, visualize and share genomic data and analyses, and (b) provides genomic tool developers with the ability to deploy their tools within a complete analysis framework. Galaxy is well known with [thousands of researchers worldwide](#) using it on a daily basis. Our [team members](#) are well regarded and widely recognized within the biomedical research. With genomics being the pivot of future life sciences and healthcare, joining the Galaxy project will open an immense array of possibilities.

Positions are currently available at

- [Genomic Medicine Institute](#) , [Cleveland Clinic Lerner Research Institute](#) in Cleveland, Ohio in the Blankenberg Lab
- [Johns Hopkins University](#) in Baltimore, Maryland in the [Taylor Lab](#)

Postdoctoral Scholars

At Cleveland Clinic

The [Blankenberg Lab](#) in the [Genomic Medicine Institute](#) at the [Cleveland Clinic Lerner Research Institute](#) has several [Postdoctoral Fellowships](#) available. We utilize high-throughput omics

technologies, such as next generation sequencing, and data-intensive computing to explore biomedical research questions. The



Postdoctoral Scholars

[At Cleveland Clinic](#)

[At Johns Hopkins University](#)

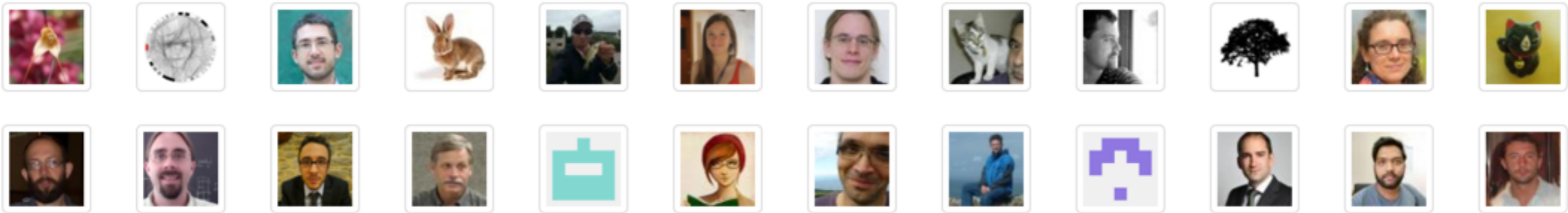
Software Engineers

[At Johns Hopkins University](#)

[Interested?](#)

<https://galaxyproject.org/galaxy-is-hiring/>

Viva contributors!



Thank you for contributing to Galaxy [IUC tools](#).



News

[January 2018 News of the Galaxy!](#) – New events, blog posts, publications, jobs, ...

[All-new CloudLaunch release](#) – Manages your credentials, multiple clouds, multiple apps,...

[GCCBOSC2018 Training Topic Nominations](#) – Choose your own training adventure!

Events

[Plant & Animal Genome XXVI \(PAG 2018\)](#) – Galaxy is for Plants and Animals too...

[Packaging your bioinformatics tool with Bioconda and Galaxy](#) – from Melbourne Bioinformatics

[Developing bioinformatics training materials](#) – from Melbourne Bioinformatics

@galaxyproject



Galaxy Project @galaxyproject



The RepeatExplorer public #usegalaxy server is impressive. Everything you ever wanted to know/learn/discover about repeats. And they have an integrated @usejbrowse as well. [repeatexplorer.org](#) #PAGXXVI



OPEN CHAT

Lots of ways to contribute

- Core code
- Ancillary code
- Support
- Documentation
- Training & Training Materials
- Outreach

Community Hub

Latest Tutorials and Trainings

The Galaxy community maintains a wide variety of trainings at <https://training.galaxyproject.org>. Check out the latest [metagenomics tutorial](#) by [@bebatut](#) and [@shiltemann](#).



News

[Galaxy Cloud embraces the GVL](#) – From Galaxy 17.09, Galaxy cloud instances use the GVL framework

[GCCBOSC 2018 Training Topic Vote!](#) – Voting closes January 31

[January 2018 News of the Galaxy!](#) – New events, blog posts, publications, jobs, ...

Events

[Galaxy-P: an accessible resource for multi-omics analysis](#) – at Lorne Proteomics

[Bioinformatic Analysis of Next Generation Sequencing Data](#) – 4-Day Hands On Workshop

[An Introduction to Integrative Bioinformatics and Novel Tools in Multi-Omics](#) – Galaxy for Clinical & Pharmaceutical Analysis

@galaxyproject

Galaxy Project Retweeted



sciencegateways @sciencegateways

#ScienceGatewaysBootcamp is for leaders of digital offerings (aka #portal, #VRE) offering "a rip-roaring, intensive ride through tested methods that help project leaders define and execute successful projects." Next session is 5/14-5/18 @TACC in Austin: sciencegateways.org/bootcamp

Galaxy Events










Galaxy Event Horizon

Upcoming (and past) events with Galaxy-related content.

The events listed here are also available in the [Galaxy Events Google Calendar](#). The [Galaxy Other Events Google Calendar](#) lists additional events that are relevant to the Galaxy Community, but that are not known to feature significant Galaxy content.

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@galaxyproject.org. For events prior to this year, see the [Events Archive](#).

Upcoming Events

Date	Topic/Event	Venue/Location	Contact
January 13th 2018	Plant & Animal Genome XXVI (PAG 2018)	San Diego, California 	See web page 
January 18th 2018	Packaging your bioinformatics tool with Bioconda and Galaxy	Melbourne Bioinformatics, Carlton, Victoria, Australia 	Saskia Hiltemann, Eric Rasche 
January 22nd 2018	Developing bioinformatics training materials	Melbourne Bioinformatics, Carlton, Victoria, Australia 	Saskia Hiltemann, Eric Rasche 
February 1st 2018	Galaxy-P: an accessible resource for multi-omics analysis	Lorne Proteomics Symposium, Lorne, Victoria, Australia 	Maria Doyle
February 12th 2018	Supporting Highly Scalable Scientific Data Analysis with Galaxy	Converged IT & the Cloud, San Francisco, California, United States 	James Taylor
February 21st 2018	RNA Sequencing and Differential Expression	University of Aberdeen, Scotland, United Kingdom 	Sophie Shaw

OPEN CHAT

<https://galaxyproject.org/events/>



Galaxy Africa

Cape Town, 3-5 April 2018

Data-intensive biology for the African continent





ABOUT US SERVICES PLATFORMS USE CASES **EVENTS**

[Home](#) » [Events](#) »

EVENTS

Past meetings and conferences

Past webinars

Galaxy community kickoff meeting and Galaxy User Conference

 Wed 14 March 2018, 08:00 to Fri 16 March 2018, 18:00

 Lecture Hall, Otto-Krayer-Haus, Albertstraße 25, Freiburg im Breisgau, 79110, Germany

 [Add to calendar](#)

The ELIXIR Galaxy community will have a kickoff meeting in 14-16th March 2018, in Freiburg/Germany. We will combine this with a Galaxy User Conference and the official launch of the usegalaxy.eu server.

This event will also be coordinated with the EMBL in Australia to also launch usegalaxy.au at the same time.

Regional events

GCCBOSC 2018



GCC2018

Galaxy
Community
Conference



Portland 2018



BOSC 2018

Bioinformatics
Open Source
Conference



REED COLLEGE

A bioinformatics

community conference

Galaxy's Community Conference &
OBF's Bioinformatics Open Source Conference
are colocating in 2018

Please join us in **Portland**, Oregon, United States
June 25-30, 2018

<https://gccbosc2018.sched.com/>

Galaxy News Feed

Galaxy News

This page contains announcements of interest to the Galaxy Community. These include items from the Galaxy Team or the Galaxy community and address anything that is of wide interest to the community.

Also see the [Galactic Blog](#) for more.

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](#).

January 5th 2018	January 2018 News of the Galaxy!	New events, blog posts, publications, jobs, ...
January 5th 2018	All-new CloudLaunch release	Manages your credentials, multiple clouds, multiple apps,...
December 14th 2017	GCCBOSC2018 Training Topic Nominations	Choose your own training adventure!
December 7th 2017	December 2017 Galaxy News	New events, blog posts, publications, jobs, ...
November 15th 2017	European Galaxy Administrator Workshop	5 days of admin training in Oslo
November 2nd 2017	Galaxy Release 17.09	Singularity, download collections, switch tool versions in workflows,...
October 31st 2017	November 2017 Galaxy News	Galactic Blog launches, new events, pubs, tools, ...

<https://galaxyproject.org/news/>

January 2018 Galaxy News

Welcome to the January 2018 *Galactic News*, a summary of what is going on in the Galaxy community. If you have anything to add to next month's newsletter, then please send it to outreach@galaxyproject.org.



Events

There are a [plentitude of Galaxy related events coming up](#) in the next few months:

GCCBOSC 2018 Training Nominations Extended to January 12

[Nominate a training topic now.](#)



The joint [2018 Galaxy Community and Bioinformatics Open Source Conferences](#) start with training and **the training topics are determined by you. Topic nominations have been extended January 12.** Any topics of interest to these communities can be nominated.

[GCCBOSC2018](#) will be held 25-30 June in Portland, Oregon, United States. It will feature two days of training: the second of which is multi-track and will feature content for both the BOSC and Galaxy communities.

Nominated topics can cover a wide range. For example:

- How to use open source software using just a web browser (e.g., Intro to Using Galaxy)
- How to use software packages (The Newbie's Guide to BioRuby)
- Advanced applications of software (Genome Assembly with Galaxy, or Proteomics with BioPython)
- Software installation and configuration (Tool Wrapping for Galaxy, or Using CloudLaunch)
- Open source community (Building a Curation Community using Apollo, or Training using the Galaxy Training Network)

These are only examples. If you are looking for ideas, see topics nominated for [GCC2017](#), [GCC2016](#), [GCC2015](#), and the [Galaxy Events page](#), which lists what training the community is offering outside of GCCs. Training is not limited to Galaxy-related

topics. Don't be afraid to think outside the BOSC!

Events

[GCCBOSC 2018 Training Nominations Extended to January 12](#)

[Galaxy \(and GMOD\) at Plant and Animal Genome XXVI](#)

[GMOD @ PAG](#)

[Intro to Galaxy Workshop at CSUSM](#)

[ELIXIR Galaxy Community Kickoff and Meeting](#)

[2018 Big Genomics Data Skills Training course](#)

All Upcoming events

[New Galactic Blog Entries: Galaksio](#)

Publications

[Highlighted Publications](#)

[Publication Topics](#)

Who's Hiring

Public Galaxy Server News

[EuPathDB Galaxy Data Analysis Service](#)

[Langille Lab PICRUST server](#)

[Public Servers in Publications](#)

Commercial Support: Intero Life

<https://galaxyproject.org/news/>

Galactic Blog

The Galactic Blog

Welcome to the *Galactic Blog*, a list of Galaxy related blog posts from community members. This blog contains longer form posts or pointers to longer form posts that are elsewhere on the web.

The Galactic Blog complements the [Galaxy News feed](#).

Add your voice!

See the hub [CONTRIBUTING page](#) in general, and the [blog section](#) in particular for directions on how to add a blog entry.



Here's what people are saying

Date	Author(s)	Topic
2018 Jan 08	Ming Chen <i>from Staton Lab</i>	Galaxy R Markdown Tools Using R Markdown as a framework to develop Galaxy tools
2017 Dec 12	Tomas Klingström <i>from the Galactic Blog</i>	Galaksio: a Galaxy user interface focused on running prepared workflows Make your workflows more accessible to non-bioinformaticians
2017 Dec 11	Tomas Klingström <i>from Freiburg Galaxy Team Blog</i>	Bioinformatic training with the B3Africa project Training using the Galaksio interface
2017 Dec 01	Vimalkumar Velayudhan <i>from Vimalkumar Velayudhan's Blog</i>	Setup your own instance of the Galaxy Bioinformatics platform on DigitalOcean Setup a DigitalOcean droplet with Galaxy, Apache and PostgreSQL

OPEN CHAT

<https://galaxyproject.org/blog/>

Mailing Lists

The lists

Galaxy has several active mailing lists, each for a different purpose in the Galaxy community.

List Link	Description	List Email Address	Archives (see Searching)
galaxy-announce	Announcements of interest to the Galaxy community. <i>Moderated and low volume.</i>		Nabble , Mailman
galaxy-dev	Local installation, configuration, and tool integration help, or to propose new features. <i>High volume.</i>	galaxy-dev AT lists DOT galaxyproject DOT org	Nabble , Mailman
galaxy-proteomics	Proteomics related questions, announcements, and anything else of interest to the Galaxy proteomics community. <i>Low volume.</i>	galaxy-proteomics AT lists DOT galaxyproject DOT org	Nabble , Mailman
galaxy-training	If you have a question about teaching bioinformatics with Galaxy , or about teaching Galaxy itself , then this is a good place to find an answer. This is also the official mailing list of the Galaxy Training Network (GTN) .	galaxy-training AT lists DOT galaxyproject DOT org	Nabble , Mailman
galaxy-france	Cette liste est destinée à l'information (et aux discussions) de la Communauté française Galaxy. (This list is for announcements to (and discussion within) the French Galaxy Community. More information about the French Galaxy Community)	galaxy-france AT lists DOT galaxyproject DOT org	Nabble , Mailman

Support: Galactic Search

Searching the Galaxy

Welcome to the comprehensive Galaxy search interface. This is a Google Custom Search Engine that will search all things Galaxy. This includes all the codebase (Galaxy *and* related projects), the mailing lists, biostars, and more.

If you haven't already, enter your query into the box in the masthead, and results will appear below.

[All results](#) [Use](#) [Hub](#) [Corpus](#) [Code](#) [Admin/Dev](#) [Discussion](#) [Shared](#) [Tools](#) [Requests](#)

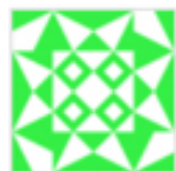
About 87,900 results (0.49 seconds)

[shrnaseq](#)

This tool performs differential representation analysis on either a fastq file of **sgRNA**/shRNA sequencing reads or a table of counts specifying **sgRNA**/shRNA counts. There are options to use exact tests or generalised linear models, the latter allowing for gene set testing. The outputs contain a MDS ...

<https://toolshed.g2.bx.psu.edu/view/shians/shrnaseq>

Labeled [Tools](#)



[CRISPR Screens sequence analysis](#)

Add New Post. Question: CRISPR Screens sequence analysis. 0. gravatar for falaksher2. 15 months ago by. falaksher2 • 0. United States. falaksher2 • 0 has support for CRISPR screens e.g. **sgRNA** sequence analysis pipeline Thanks, Falak. galaxy • 289 views. ADD COMMENT • link • Not following.

<https://biostar.usegalaxy.org/p/19090/>

Labeled [Discussion](#) [Use](#)



[Galaxy | Published Workflow | MAGECK count table to .GCT for IGV](#)

Find pattern. **sgRNA**. Replace with. Name. Step 9: Add column. Add this value. prefix. to Dataset. Output dataset 'output' from step 3. Iterate? NO. Step 10: tabular dataset. Output dataset 'output' from step 7. Step 11: Replace Text. File to process. Output dataset 'outfile' from step 8. in column. 2. Find pattern.

<https://usegalaxy.org/u/ckmah/w/mageck-count-conversion>

Support: Galaxy Biostars Forum

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

Welcome to Galaxy Biostar! User support for Galaxy! [about](#) • [faq](#) • [rss](#)

Community Log In Sign Up Add New Post

Live search: start typing... or Classic search

Limit to: all time <prev • 7,964 results • page 1 of 228 • next > Sort by: update ▾

0 votes **1** answer **8** views **Unable to remove pinned workflows from tools panel after deleting**
pin workflow tool panel delete
written 7 hours ago by TWV • 10 • updated 3 minutes ago by Jennifer Hillman Jackson ♦ 23k

1 vote **0** answers **13** views **Workflow jobs not running/queueing on a local Galaxy**
local job workflow queue
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0 votes **1** answer **18** views **Depth of coverage in one nucleotide**
galaxy
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2 votes **1** answer **26** views **Out Of Disk Space with Picard's FastqtoSam Tools from Galaxy**
picard galaxy samtools
written 2 days ago by mainulhossain • 10 • updated 1 hour ago by Jennifer Hillman Jackson ♦ 23k

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Problems with Trinity

Traffic: 117 users visited in the last hour

Recent Votes

- Workflow jobs not running/queueing on a local Galaxy
- Out Of Disk Space with Picard's FastqtoSam Tools from Galaxy
- C: Out Of Disk Space with Picard's FastqtoSam Tools from Galaxy
- File loading error in local galaxy
- Problems with Trinity
- BWA-MEM Fatal error: Matched on ERROR
- A: Galaxy storage problem

Recent Locations • All »

- United States, 3 minutes ago
- United States, 24 minutes ago
- Germany, 1 hour ago

Recent Awards • All »

- Scholar 🏆 to Jennifer Hillman Jackson ♦ 23k
- Teacher 😊 to Devon Ryan • 1.9k
- Scholar 🏆 to Devon Ryan • 1.9k
- Appreciated ❤️ to Jennifer Hillman Jackson ♦ 23k
- Scholar 🏆 to Jennifer Hillman Jackson ♦ 23k
- Scholar 🏆 to Jennifer Hillman Jackson ♦

<https://biostar.usegalaxy.org/>

Support: Galaxy Biostars Forum

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

Welcome to Galaxy Biostar! User support for Galaxy! [about](#) • [faq](#) • [rss](#)

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Support: Gitter Chat

The screenshot shows the Galaxy Community Hub website. At the top, there is a navigation bar with the Galaxy logo and menu items: Use, Community, Education, Deploy & Develop, and Support. A search bar and an 'Edit' button are also visible. The main content area features a large heading 'Viva contributors!' followed by a grid of contributor avatars. A tweet from the Galaxy Project (@galaxyproject) is highlighted, containing the text: 'The RepeatExplorer public #usegalaxy server is impressive. Everything you ever wanted to know/learn/discover about repeats. And they have an integrated @usejbrowse as well. repeatexplorer.org #PAGXXVI'. Below the tweet is a green 'OPEN CHAT' button. An orange arrow points from this button to another 'OPEN CHAT' button located at the bottom right of the page, which is also linked to the tweet's content.

<https://gitter.im/galaxyproject/Lobby>

Support: Gitter Chat

GITTER

Where communities thrive

FREE FOR COMMUNITIES

JOIN OVER 800K+ PEOPLE

JOIN OVER 90K+ COMMUNITIES

CREATE YOUR OWN COMMUNITY

EXPLORE MORE COMMUNITIES

Browser, Desktop and Mobile Apps.



galaxyproject/Lobby Data intensive science for everyone. <http://galaxyproject.org> | Use now! <http://u...>



Thanks guys! Ping [@nekrut](#) - just copying those columns directly from the SRA data with either the Mac's Numbers or Google Charts seems to work when just pasting the data into Galaxy.



Yvan Le Bras [@yvanlebras](#)
Groooovy!

Jan 12 12:21



galaxybot [@galaxybot](#)
[jxtx] Awesome.

Jan 12 13:24



Martin Cech [@martenson](#)
[@jmchilton](#) cool beans! The table is live, right?

Jan 12 13:50

because once we get this in, it would be awesome to extend it to csv-like dataset editing 😊



John Chilton [@jmchilton](#)

Jan 12 13:52

It is reactive - as you add rules (columns, filters, swap things, sorting rules, etc...) it redraws in real time.

Yeah - the rules backend is a little JSON language I'm building up with the widget - it is meant to be portable and executable on the backend. It would be cool to a tool that would apply the rules to datasets in addition to uploads like this (also to apply to existing collections in the middle of a workflow - this could serve as the most expressive collection operation I think).

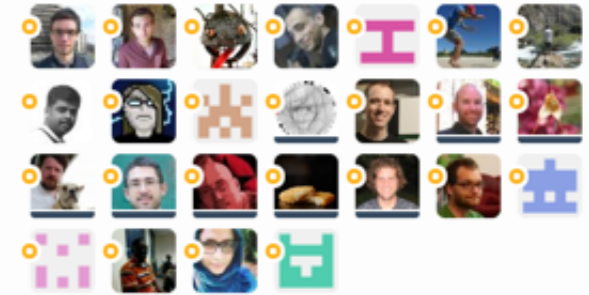


Martin Cech [@martenson](#)

Jan 12 14:01

The library also supports direct edit it seems.

PEOPLE



[SEE ALL \(343 PEOPLE\)](#)

SIGN IN TO START TALKING



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Galaxy Training Network

Galaxy Trainer Directory



Trainers

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OPEN CHAT

The *Galaxy Trainer Directory* is a service of the [Galaxy Training Network](#) which aims to make it easy to share and find [Galaxy training resources](#). This directory lists individuals and groups that do Galaxy training. The contacts listed here are willing to present Galaxy at meetings and workshops. The directory includes particular areas of expertise and how far the instructors are willing to travel.

Do you or your organization do Galaxy training? Then please tell the Galaxy Community! You can

<https://galaxyproject.org/teach/trainers/>

Galaxy Training Network

Welcome to Galaxy Training!

Collection of tutorials developed and maintained by the worldwide Galaxy community.

Galaxy for Scientists

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Epigenetics	1
Metagenomics	2
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Galaxy for Developers and Admins

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<http://galaxyproject.github.io/training-material/>

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You! UO BGMP

The Galaxy Community

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Cleveland Clinic



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Thanks