

Galaxy: An Open Platform for Data Analysis and Integration

Plant & Animal Genome XXVI (PAG 2018)

January 16, 2018

San Diego, California,
United States



#usegalaxy @galaxyproject

Agenda

4:00 Galaxy: Introduction and Ecosystem
Dave Clements, Johns Hopkins University

4:20 G-OnRamp: Visualizing and Annotating
Eukaryotic Genomes with Galaxy
Jeremy Goecks, OHSU

5:30 South Green, a Hitchhiker's Guide to
Galaxy
Marilyne Summo, CIRAD

5:50 Building a Bridge from the Tripal
Community Database to Galaxy
Margaret Staton, University of Tennessee, Knoxville

Galaxy: Introduction and Ecosystem

Plant & Animal Genome XXVI (PAG 2018)

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Dave Clements

Johns Hopkins University

Galaxy Team / Galaxy Community



#usegalaxy @galaxyproject

bit.ly/gxy-pag2018-eco

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>

Galaxy User Interface

usegalaxy.org

Galaxy is available several ways ...

<http://galaxyproject.org>

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

The screenshot displays the Galaxy web interface. The top navigation bar includes the Galaxy logo and links for Analyze Data, Workflow, Shared Data, Visualization, Help, and User. A status bar on the right indicates 'Using 0%'. The left sidebar, titled 'Tools', contains 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 paragraph about Galaxy's purpose, a large heading 'Running Your Own Understanding how Galaxy works', and a subtitle 'An in-depth tutorial'. Below the text is a progress indicator with five dots, the first of which is highlighted. The right sidebar, titled 'History', shows a search bar, a 'View histories' button, and an 'Unnamed history' section which is currently empty. A blue information box in the history panel states: 'This history is empty. You can load your own data or get data from an external source'.

Galaxy

Analyze Data Workflow Shared Data Visualization Help User Using 0%

Tools

search tools

[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](#)

[NGS: Variant Analysis](#)

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](#).

Running Your Own

Understanding how Galaxy works

An in-depth tutorial

History

search datasets View histories

Unnamed history

(empty)

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 last week

Domain Specific

36 servers

Tool publishing servers

44 servers

Total

99 servers

bit.ly/gxyServers

Galaxy Services



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



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

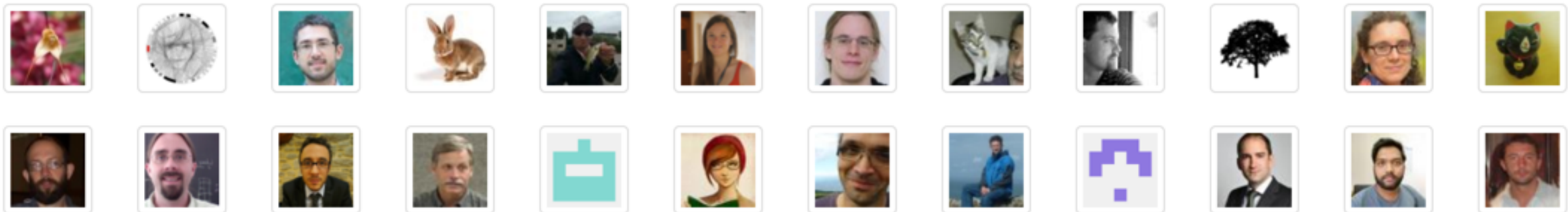
<http://globus.org/>

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

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

Community and Ecosystem

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

galaxyproject.org

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](#)

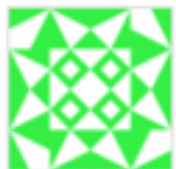
About 87,900 results (0.49 seconds)

[shrnaeq](#)

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/shrnaeq>

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: Add column. Add this value. prefix. to Dataset. Output dataset 'output' from step 3. Iterate? NO. 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

LATESTOPENRNA-SEQCHIP-SEQSNPASSEMBLYFORUMPLANETALL »



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

CommunityLog InSign UpAdd New Post

Live search: start typing...or Q Classic search

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

0 votes1 answer8 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 vote0 answers13 views

Workflow jobs not running/queueing on a local Galaxy

local job workflow queue

written 7 hours ago by TWV • 10 • updated 32 minutes ago by Jennifer Hillman Jackson ♦ 23k

0 votes1 answer18 views

Depth of coverage in one nucleotide

galaxy

written 1 day ago by samira.kalayinia • 0 • updated 1 hour ago by Jennifer Hillman Jackson ♦ 23k

2 votes1 answer26 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

0 votes1 answer11 views

Converting transcript data from Salmon to gene level TPM

rna-seq deseq2 galaxy salmon tpm

written 2 hours ago by dw2p • 0 • updated 1 hour ago by Jennifer Hillman Jackson ♦ 23k

1 vote1 answer30 views

File loading error in local galaxy

conda local ftp upload admin

written 2 days ago by michael.flower.14 • 10 • updated 2 hours ago by Jennifer Hillman Jackson ♦ 23k

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](#)

[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](#)

written 7 hours ago by [TWV](#) • 10 • updated 32 minutes ago by [Jennifer Hillman Jackson](#) ♦ 23k

0 votes 1 answer 18 views

[Depth of coverage in one nucleotide](#)

[galaxy](#)

written 1 day ago by [samira.kelavina](#) • 0 • updated 1 hour ago by [Jennifer Hillman Jackson](#) ♦ 23k

2 votes 1 answer 26 views

[Out Of Disk Space with Picard](#)

[picard](#) [galaxy](#) [samtools](#)

written 2 days ago by [mainulhossain](#) • 10 • updated 1 hour ago by [Jennifer Hillman Jackson](#) ♦ 23k

0 votes 1 answer 11 views

[Converting transcript data from Salmon to gene level TPM](#)

[rna-seq](#) [deseq2](#) [galaxy](#) [salmon](#) [tpm](#)

written 2 hours ago by [dw2p](#) • 0 • updated 1 hour ago by [Jennifer Hillman Jackson](#) ♦ 23k

1 vote 1 answer 30 views

[File loading error in local galaxy](#)

[conda](#) [local](#) [ftp](#) [upload](#) [admin](#)

written 2 days ago by [michael.flower.14](#) • 10 • updated 2 hours ago by [Jennifer Hillman Jackson](#) ♦ 23k

0 votes 0 answers 0 views

[Problems with Trinity](#)

written 2 days ago by [michael.flower.14](#) • 10 • updated 2 hours ago by [Jennifer Hillman Jackson](#) ♦ 23k

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Recent Awards • All »

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- [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](#) ♦ 23k

Support: Gitter Chat

The screenshot shows the Galaxy Community Hub website. At the top, there is a navigation bar with links: Use, Community, Education, Deploy & Develop, and Support. A search bar labeled 'Search Galaxy' and an 'Edit' link are also present. The main heading reads 'Viva contributors!'. Below this, a grid of contributor avatars is displayed. A white Gitter chat window is overlaid on the page, containing the following 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'. The chat window includes a green 'OPEN CHAT' button. An orange arrow points from the bottom right of the chat window to a tweet on the right side of the page. The tweet is from @galaxyproject and contains the same text as the chat window. Below the chat window, there are sections for 'News', 'Events', and a tweet from @galaxyproject. The 'News' section lists 'January 2018 News of the Galaxy!', 'All-new CloudLaunch release', and 'GCCBOSC2018 Training Topic Nominations'. The 'Events' section lists 'Plant & Animal Genome XXVI (PAG 2018)', 'Packaging your bioinformatics tool with Bioconda and Galaxy', and 'Developing bioinformatics training materials'. The tweet from @galaxyproject is identical to the one in the chat window. A green 'OPEN CHAT' button is also visible at the bottom right of the tweet.

Galaxy
COMMUNITY HUB

Use Community Education Deploy & Develop Support

Search Galaxy

Edit

Viva contributors!

Thank you for contributing to the Galaxy Project

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

News

January 2018 News of the Galaxy! – New events, blog posts, publications, jobs, ...

All-new CloudLaunch release – Manages your credentials, multiple clouds, multiple apps,...

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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

<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
[jtxt] 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).

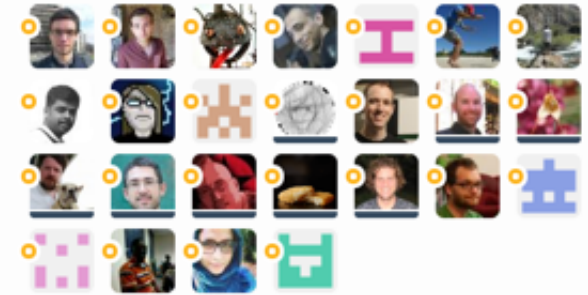


Martin Cech @martenson

Jan 12 14:01

The library also supports direct edit it seems.

PEOPLE



SEE ALL (343 PEOPLE)

SIGN IN TO START TALKING



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

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. Most likely, it will be in French.) Full description	galaxy-france AT lists DOT galaxyproject DOT org	Nabble , Mailman

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/>

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 [Galxy 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/>

Galaxy Training Network



[Fork me on GitHub](#) [Help](#) ▾

Welcome to Galaxy Training!

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

Galaxy for Scientists


Topic	Tutorials
Introduction to Galaxy	10
Assembly	3
ChIP-Seq data analysis	2
Epigenetics	1
Metagenomics	2
Proteomics	8
Sequence analysis	6

Galaxy for Developers and Admins

Topic	Tutorials
Galaxy Server administration	8
Development in Galaxy	13
Train the trainers	6

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

Galaxy Training Network



The map displays the global distribution of Galaxy training trainers. Trainers are marked with colored dots across various continents: Europe (blue, orange, red), Africa (red), Asia (blue), North America (blue, red), South America (red), Oceania (blue), and Australia (red). Specific labels on the map include: University of Aberdeen, FMI Bioinformatics and..., Noor Biotechnologies Ltd., Stingray@Galaxy, QFAB Bioinformatics, MMG@IICT, and Texas A&M University/C... The map is titled 'Galaxy Training Network: Trainer Locations' and includes a Google My Maps logo and a 2,000 mi scale bar.

Trainers

Global

- [The Centre for Bioinformatics and Computational Biology](#)
- [The FMI Bioinformatics Core Facility](#)
- [Freiburger Galaxy Project](#)
- [Galaxy Project](#)
- [GalaxyP Project](#)
- [Geneclat Technologies](#)
- [Memorial Sloan Kettering Cancer Center, Rätsch Laboratory](#)
- [MMG@IICT](#)
- [Noor Biotechnologies Ltd.](#)
- [OpenHelix](#)
- [QFAB Bioinformatics](#)
- [Stingray@Galaxy](#)
- [University of Bradford School of Me Sciences, Kr](#)

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

[OPEN CHAT](#)

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

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/>

GCCBOSC 2018



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/>



Just
announced
today

galaxyafrika
.sanbi.ac.za

Cape Town, 3-5 April 2018


Data-intensive biology for the African continent




National
Research
Foundation




3 more events, tomorrow

 Galaxy
COMMUNITY HUB

Use ▾ Community ▾ Education ▾ Deploy & Develop ▾ Support ▾

Search Galaxy 

 Ed

Plant & Animal Genome XXVI (PAG 2018)

Galaxy is for Plants and Animals too...

Date: January 13th 2018- January 17th 2018
Location: [San Diego, California](#)
Contact: See web page

Galaxy will be at [Plant and Animal Genome XXVI \(PAG 2018\)](#), being held in San Diego, California, United States, January 13-17. There will also be pre-conference events this year as well.

Galaxy. January. PAG XXVI. San Diego.

That about covers it.



Wednesday, January 17	10:30- 10:45	C25: PiRATE: A Pipeline to Retrieve and Annotate Transposable Elements of Non-Model Organisms	Digital Tools and Resources Session 4 , California Room	Jérémy Berthelier
	11:05- 11:25	Galaxy Community Update	Workshop: GMOD , Pacific Salon 4-5	Dave Clements
	11:25- 11:45	G-OnRamp: Collaborative Eukaryotic Genome Annotations with Galaxy and Apollo	Workshop: GMOD , Pacific Salon 4-5	Luke Sargent

<https://galaxyproject.org/events/2018-pag/>

The 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>

Acknowledgements

You! PAG

Jeremy Goecks Marilynne Summo Meg Staton

The Galaxy Community

NIH

Johns Hopkins University

Penn State University

Oregon Health & Science University

Cleveland Clinic



Dave Clements

Galaxy Project

Johns Hopkins University

clements@galaxyproject.org

Thanks