

Galaxy Community Update

PAG XXV

January 18, 2017

San Diego, California, United States

Dave Clements

Johns Hopkins University

Galaxy Team / Galaxy Community



#usegalaxy @galaxyproject



What is Galaxy?

Keith 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 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. On the left is a navigation menu with categories like 'Get Data', 'Text Manipulation', and 'NGS: DeepTools'. The main content area features a text block about Galaxy's open-source nature and a 'GAME 2017 Melbourne 3-9 February' announcement with a red globe logo and a deadline for abstracts. Below this is a horizontal progress indicator. On the right, a 'Tweets by @galaxyproject' section shows two tweets, one retweeted by the Galaxy Project and another from Pratik Jagtap. The footer contains logos for Penn State, Johns Hopkins, TACC, and Cyverse.


Galaxy Analyze Data Workflow Shared Data Visualization Help User Using 0%

Tools

search tools

- Get Data
- Lift-Over
- 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
- NGS: RNA Structure
- NGS: Du Novo
- NGS: Gemini
- NGS: Assembly
- Operate on Genomic Intervals
- Statistics
- Graph/Display Data
- Phenotype Association


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](#).

 **GAME**
2017
Melbourne
3-9 February

Talk abstracts due 30 November

Tweets by @galaxyproject

Galaxy Project Retweeted

 **Pratik Jagtap** @pratikomics
z.umn.edu/hayahym 'How are you - and How's your Microbiome?' an article in @tAnaSci Issue#1116 #microbiome #metaproteomics #usegalaxyp

Galaxy Project @galaxyproject
28-30 Nov: Analyse avancée de séquences, Bordeaux
cnrsformation.cnrs.fr/stage-16148-An...
#usegalaxy @cgfbordeaux

PENNSSTATE
JOHNS HOPKINS
TACC
CYVERSE

usegalaxy.org: What's new?

Fetch Alignments/Sequences

NGS: QC and manipulation

- [FastQC](#) Read Quality reports
- [Trim Galore!](#) adaptive quality and adapter trimmer
- [FASTQ joiner](#) on paired end reads **updated**
- [Pear](#) Paired-End read merger **new**
- [Trimmomatic](#) flexible read trimming tool for Illumina NGS data **new**
- [Select high quality segments](#)
- [Build base quality distribution](#)

Lots of new and updated tools

Interactive tours

Workflow run forms

Trinity

Help User

- Galaxy Biostar
- Ask a question
- Support
- Search
- Mailing Lists
- Videos
- Wiki
- How to Cite Galaxy
- Interactive Tours**
- Terms and Conditions

Tweet Of GMOD @gmodproject
@ianholmes JBLAST is a plugin

NGS: Assembly

Trinity (Beta) De novo assembly of RNA-Seq data Using Trinity on PSC's Bridges

Public Galaxy servers

General Purpose (3 new, 17 total)

Galaxy@Pasteur

Galaxy Sigenae / BioInfo Genotoul

Insitut Curie

Domain (4 new, 33 total)

Alveo

Galaxy-CEFAP

ImmPort Galaxy

PhenoMeNal

19 new servers in past year

Now 90 public servers

Tool Servers (12 new, 40 total)

Apostl

ARGs-AOP

Bistro

BitLAB

Chemical Annotation Retrieval

Toolkit (CART)

Halogen Bonding

IBERS @ Aberystwyth

Koslicki Lab

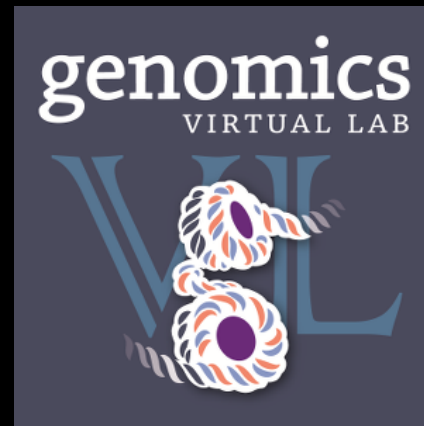
MGEScan

MiModD NacreousMap

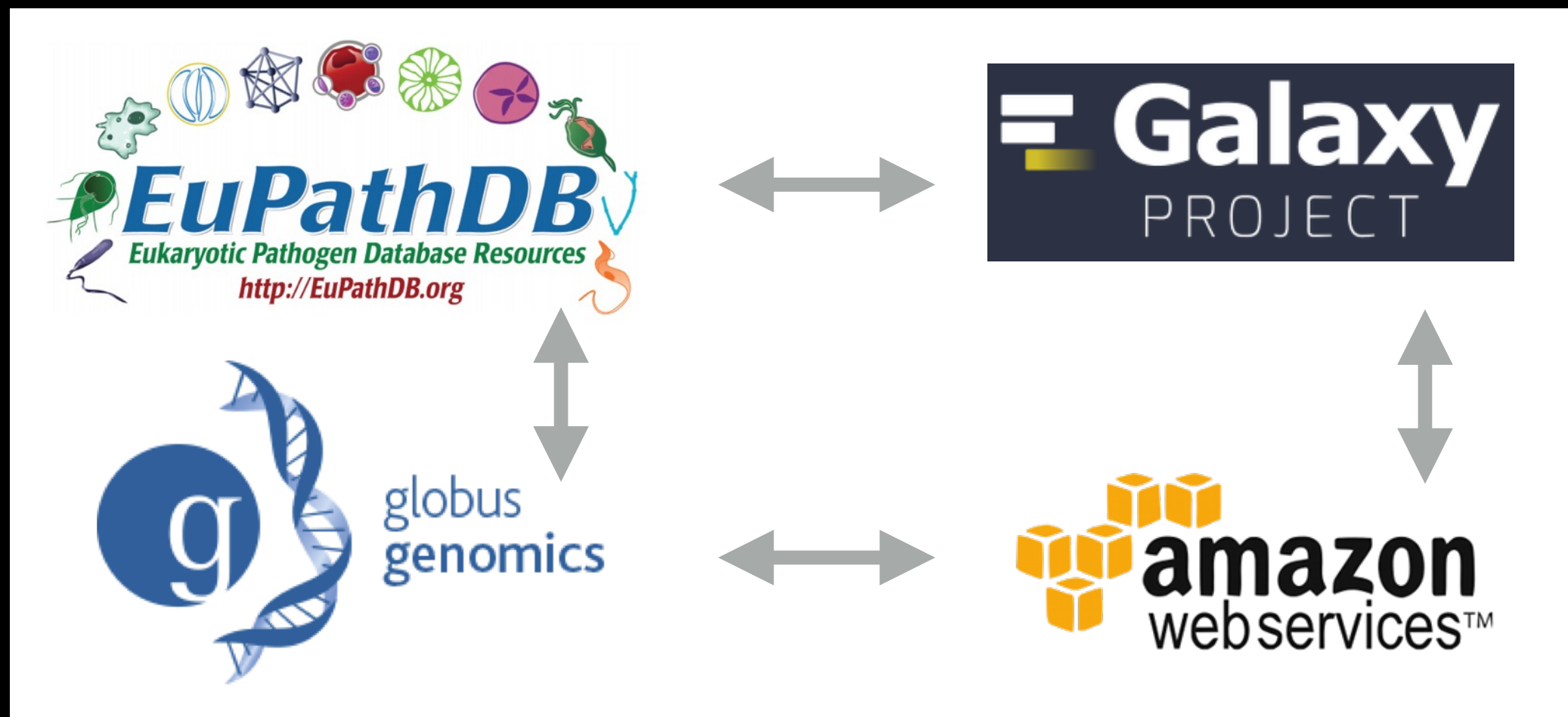
Palfinder

VarCap

Galaxy Services



Galaxy Services: Just added



Developed in partnership with Globus Genomics (11), workspaces offer a private analysis platform with published workflows and pre-loaded annotated genomes for the organisms we support. The workspace is accessed through the 'Analyze My Experiment' ...

EuPathDB: the eukaryotic pathogen genomics database resource Aurrecoechea et al., *Nucleic Acids Research* (29 November 2016), gkw1105, doi:10.1093/nar/gkw1105

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



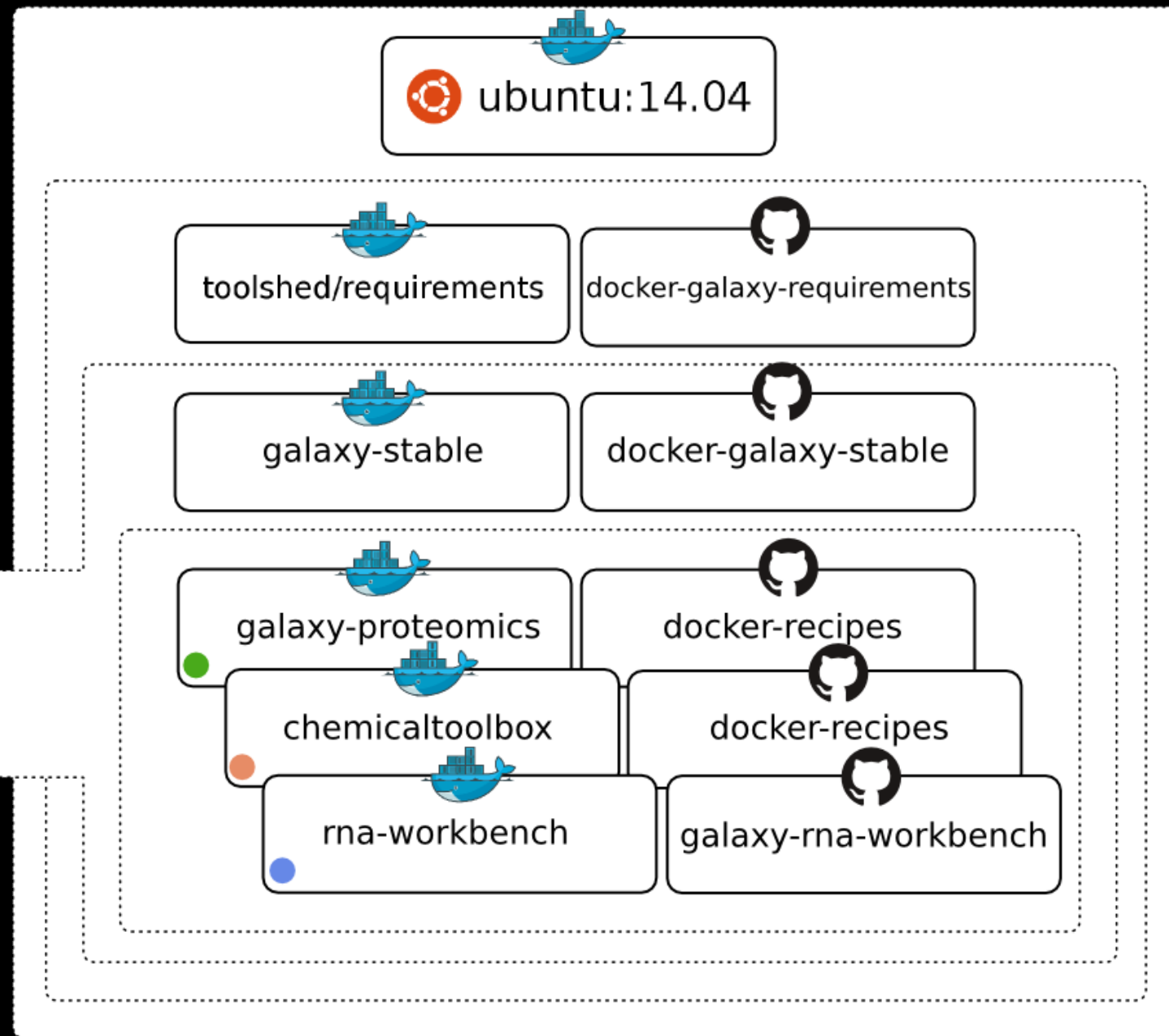
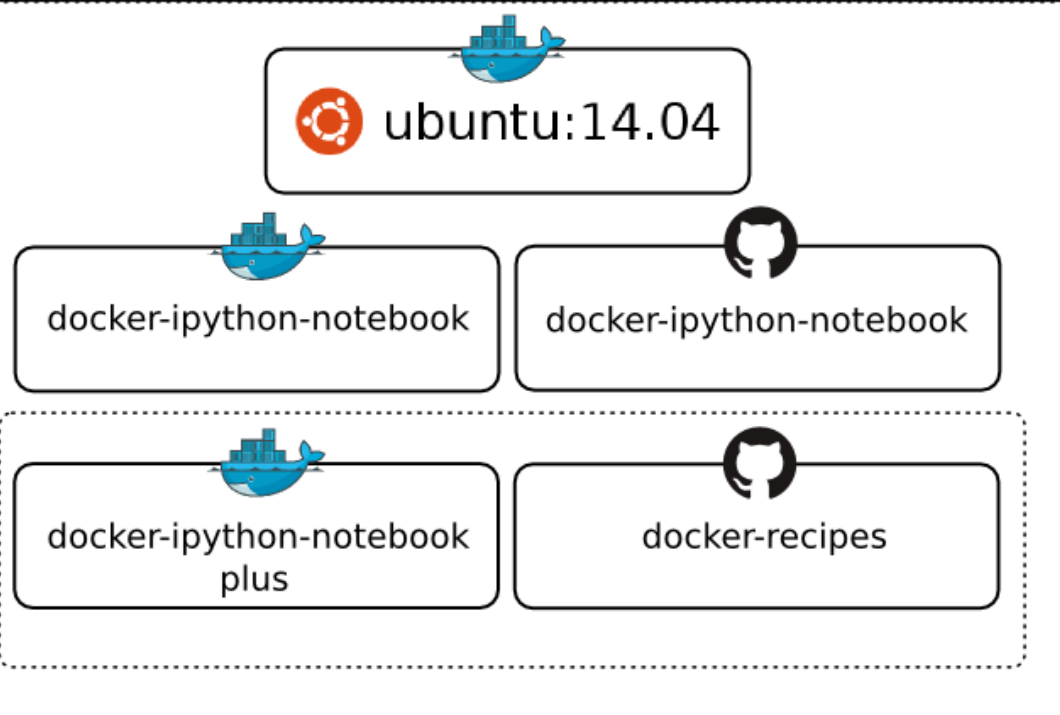
<http://aws.amazon.com/education>

<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 available in Docker

Docker Cancer Genomics Galaxy flavor

<https://github.com/morinlab/tools-morinlab/blob/master/docker/Readme.md>

Galaxy tools for Constructive Solid Geometry flavor

<https://github.com/gregvonkuster/galaxy-csg>

Enhancing pre-defined workflows with ad hoc analytics using Galaxy, Docker and Jupyter

Björn Grüning, Eric Rasche, Boris Rebolledo-Jaramillo, Carl Eberhard, Torsten Houwaart, John Chilton, Nathan Coraor, Rolf Backofen, James Taylor, Anton Nekrutenko. *bioRxiv* (16 September 2016), 075457, doi:10.1101/075457

Galaxy is available as Open Source Software

<http://getgalaxy.org>

New Features in past year

We have (more or less) quarterly releases:

16.01, 16.04, 16.07, 16.10

17.01 is in the pipe

Interactive Tours (16.01)

As seen at PAG XXV!

Wheels (16.01)

Went from Eggs to PIP and Wheels for Galaxy core dependencies.

Nested Workflows (16.01)

Workflows can run other workflows as a single abstract step in the parent workflow.

New Features in past year

Tool Profile Versions (16.04)

Tools can declare which version of Galaxy they require.
Tools requiring 16.04 or newer will have new default behaviors.

Dynamic tool Destinations (16.07)

Dynamic mapping of tools to destinations based on finer grained admin-specified rules.

From Canada's National Microbiology Laboratory

New Features in past year

Galaxy chat (16.07)

Admins can add the included communication server to enable users of their instance to use real-time chat within the Galaxy interface.

Conda for tool dependencies (all)

Galaxy is switching to using the Conda package manager to handle tool dependencies.

Bioconda Contribution Fest, November 2-3

Galaxy-P Conda Contribution Fest September 27-28

Conda Dependencies Codefest, April 4

New Features in past year

Webhooks (16.10)

A simple way of inserting icons, links, or other HTML elements into predefined locations.

Work from [@bgruening](#), [@anatskiy](#), and [@joachimwolff](#)

<https://docs.galaxyproject.org/en/master/admin/webhooks.html>

Webhooks (16.10)

The screenshot displays the Galaxy web interface. At the top, the browser address bar shows the URL `127.0.0.1:8080`. The Galaxy logo and navigation menu are visible, including 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User'. The interface is divided into three main sections:

- Tools Panel (Left):** Contains a search bar and a list of tool categories: 'Get Data', 'Send Data', 'Collection Operations', and 'Text Manipulation'. Under 'Text Manipulation', various tools are listed, such as 'Add column to an existing dataset', 'Concatenate datasets tail-to-head', 'Cut columns from a table', 'Merge Columns together', 'Convert delimiters to TAB', 'Create single interval as a new dataset', 'Change Case of selected columns', 'Paste two files side by side', 'Remove beginning of a file', 'Select random lines from a file', 'Select first lines from a dataset', 'Select last lines from a dataset', 'Trim leading or trailing characters', 'Line/Word/Character count of a dataset', and 'Secure Hash / Message Digest on a dataset'.
- Central Panel:** Features a green notification box with a checkmark icon, stating: '1 job has been successfully added to the queue - resulting in the following datasets: 145: Cut on data 3'. Below this, it provides instructions: 'You can check the status of queued jobs and view the resulting data by refreshing the History pane. When the job has been run the status will change from 'running' to 'finished' if completed successfully or 'error' if problems were encountered.' Below the notification is a 'PHD Comics' section with a 'Random' button and a four-panel comic strip. The comic depicts a character in a red shirt who is nervous about asking a question in public, eventually asking 'CAN I TAKE THE LEFT OVER COOKIES HOME?'.
- History Panel (Right):** Shows a search bar for datasets and a 'Main History' section. It indicates '2 shown, 143 deleted' and shows a total size of '29.54 KB'. Two dataset entries are listed: '145: Cut on data 3' and '3: cut test.txt', each with icons for viewing, editing, and deleting.

Other Software

Nebulizer

Command line utility for managing users, tools and libraries

From Peter Briggs

<https://pypi.python.org/pypi/nebulizer>

CloudBridge

Simple abstraction layer over different cloud providers.

<http://cloudbridge.readthedocs.org/>

CloudBridge: a Simple Cross-Cloud Python Library

Nuwan Goonasekera, Andrew Lonie, James Taylor, Enis Afgan. XSEDE16.

Other Software

blend4php

The blend4php package, a PHP wrapper for the Galaxy API.
Used in Tripal-Galaxy connection

<https://github.com/galaxyproject/blend4php>



blend4php: a PHP API for galaxy. Connor Wytko, Brian Soto, Stephen P. Ficklin, *Database* (2017) baw154. DOI: <https://doi.org/10.1093/database/baw154>

Banner year for cool publications

SparkGalaxy: Workflow-based Big Data Processing

Sara Riazi
Department of Computer and Information Science
University of Oregon



Università degli Studi di Cagliari
Dottorato di Ricerca in Ingegneria Biomedica
Ciclo XXVII

Omicron: a Galaxy for reproducible proteogenomics

By
Matthew Chase Chambers

Thesis

Unlocking Large-Scale Genomics

Presentata da: Luca Pireddu
Coordinatore dottorato: Prof. Giacomo Cao
Tutor: Prof. Riccardo Scateni e
Prof. Giacomo Cao


Settore scientifico-disciplinare di afferenza: ING-INF/06
Esame finale anno accademico 2014-2015

Banner year for cool publications

J Grid Computing (2016) 14:533–543
DOI 10.1007/s10723-016-9379-6



The Essential Components of a Successful Galaxy Service

Annette McGrath  · Steve McMahon · Sean Li ·
Joel Ludbey · Tim Ho

Bioinformatics, 32(11), 2016, 1743–1745

doi: 10.1093/bioinformatics/btw042

Advance Access Publication Date: 27 January 2016

Applications Note

OXFORD

Genome analysis

Galaxy Portal: interacting with the galaxy platform through mobile devices

Claus Børnich¹, Ivar Grytten¹, Eivind Hovig^{1,2,3} Jonas Paulsen¹
Martin Čech⁴ and Geir Kjetil Sandve^{1,*}

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SOFTWARE TOOL ARTICLE

A guide and best practices for R/Bioconductor tool integration in Galaxy [version 1; referees: 1 approved, 1 approved with reservations]

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²Department of Biochemistry and Molecular Biology, Pennsylvania State University, University Park, USA

Published online 2 May 2016

*Nucleic Acids Research, 2016, Vol. 44, Web Server issue W3–W10
doi: 10.1093/nar/gkw343*

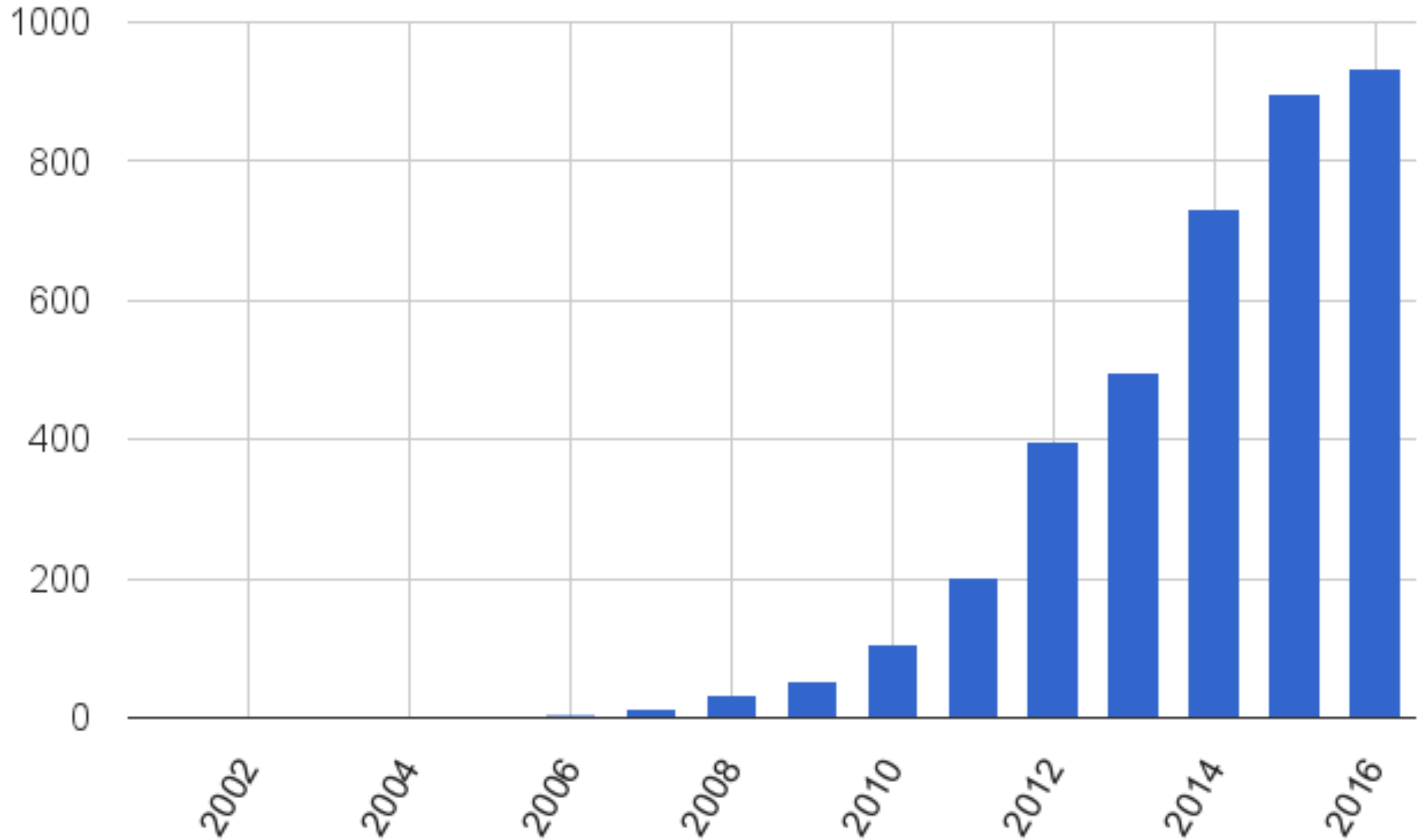
The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2016 update

Enis Afgan¹, Dannon Baker¹, Marius van den Beek², Daniel Blankenberg³, Dave Bouvier³, Martin Čech³, John Chilton³, Dave Clements¹, Nate Coraor³, Carl Eberhard¹, Björn Grüning^{4,5}, Aysam Guerler¹, Jennifer Hillman-Jackson³, Greg Von Kuster⁶, Eric Rasche⁷, Nicola Soranzo⁸, Nitesh Turaga¹, James Taylor^{1,*}, Anton Nekrutenko^{3,*} and Jeremy Goecks^{9,*}

¹Department of Biology, Johns Hopkins University, Baltimore, MD USA, ²Institut de Biologie Paris-Seine, Université Pierre et Marie Curie, Paris, France, ³Department of Biochemistry and Molecular Biology, Penn State University, University Park, PA, USA, ⁴Department of Computer Science, Albert-Ludwigs-University, Freiburg, Freiburg, Germany, ⁵Center for Biological Systems Analysis (ZBSA), University of Freiburg, Freiburg, Germany, ⁶Academic Computing Services, Penn State University, University Park, PA, USA, ⁷Department of Biochemistry and Biophysics, Texas A&M University, College Station, TX, USA, ⁸The Genome Analysis Centre, Norwich, United Kingdom and ⁹The Computational Biology Institute, George Washington University, Washington DC, USA

Received March 1, 2016; Revised April 9, 2016; Accepted April 18, 2016

Pubs per year topped 900 in 2016



Now 3909 papers in Galaxy CiteULike group

F1000 Research Galaxy Channel

Galaxy



Browse Channel

🔍 Search channel

📌 SUBMIT TO THIS CHANNEL

Articles

Posters

Slides

61 SLIDES

SHOW FILTERS

1 - 20 of 61

ABOUT THIS CHANNEL



Galaxy is an open web based platform for scientific data integration and analysis. The Galaxy Project was developed to support life science research but the platform is domain agnostic and is now used in fields as diverse as climate change and social sciences. Galaxy is an open source project with vibrant developer and user communities. This channel brings together in one place presentations and posters about the Galaxy framework, including presentations from Galaxy events such as the annual Galaxy Community Conference.

MORE ABOUT THIS CHANNEL

Channel Advisor



Galaxy Architecture



Setting up a Galaxy instance as a service

Resources and Communities

New Directories

Commercial Support Directory



[Communicate](#) ▾

[Using Galaxy](#) ▾

[Galaxy Project](#) ▾

[Deploy Galaxy](#) ▾

[Contribute](#) ▾

[Edit on GitHub](#)

Commercial Galaxy Support

Galaxy [servers](#) and [support](#) are available in a wide variety of different ways, including commercial solutions. This lists the commercial providers that we are aware of

Consulting



Deena Bioinformatics

[Deena Bioinformatics](#) can help you to setup your own Galaxy Server. Give your your researchers an easy to use web interface to the command-line utilities they need to work with.

Noor Biotechnologies

Galaxy is a powerful and open, web-based platform, which is accessible to all scientists. For the beginner, it can be difficult to know how to select from the thousands of available tools, which ones are right for your data analysis.



Consulting

[Deena Bioinformatics](#)

[Noor Biotechnologies](#)

Servers

[BioTeam Appliance:
Galaxy Edition](#)

Hosting and Commercial Cloud Solutions

[Galaxy Specific
Commercial Cloud
Solutions](#)

[GenomeCloud](#)

Training

New Directories: Galaxy Tours

<https://github.com/galaxyproject/galaxy-tours>

galaxyproject / galaxy-tours

Watch 12

Star 5

Fork 4

Code

Issues 2

Pull requests 0

Projects 0

Pulse

Graphs

Collection of Galaxy-tours

16 commits

2 branches

0 releases

5 contributors

MIT

Branch: master

New pull request

Find file

Clone or download

dannon committed on GitHub Merge pull request #6 from galaxyproject/data-upload

Latest commit bc906da on Oct 20, 2016

advanced-galaxy-introduction	Improvements on the Galaxy introduction tour	10 months ago
exom-seq	adopt to latest Galaxy changes	6 months ago
multiqc	adopt to latest Galaxy changes	6 months ago
rad-seq	adopt to latest Galaxy changes	6 months ago
.gitignore	Initial commit	10 months ago
LICENSE	Initial commit	10 months ago
README.md	Update README.md	10 months ago

README.md

New Communities: Galaxy Arabic

Galaxy Arabic Community



أرشيف للقائمة البريدية جالاكسي بالعربية يحتوي على الاخبار والمناقشات والاعلانات الخاصة بمستخدمي جالاكسي من البلاد الناطقة بالعربية نرحب بانضمام أي شخص مهتم بالجالاكسي بلاتفورم جالاكسي هي بلاتفورم لتحليل المعلومات الحيوية باستخدام أدوات برمجة أونلاين مجاناً تتميز بأنها متاحة للجميع ونتائجها تتميز بالشفافية وبالقدرة على الحصول على نفس النتائج عند إجراء التحليل مرات عديدة.

السهولة : يمكن لأي شخص استخدام جالاكسي حتى لو لم تكن لديه خبرة كافية بتحليل المعلومات الحيوية

النتائج : تحصل على نفس النتائج مهما أجريت التجربة مرات عديدة وهذا يميز جالاكسي عن العديد من الأدوات الأخرى .

الشفافية : يمكنك أن تشارك ما توصلت إليه مع زملائك والعالم كله ويمكنك النشر أيضاً

جالاكسي مفتوحة لكل المنظمات والسرفر الرئيسي يمكنك من إجراء تحليل على المعلومات الجينية وإيضاً توجد مواد تعليمية للتدريب وأماكن العمل وخدمات النشر يمكنك استخدام جالاكسي أونلاين ويمكنك أيضاً تنزيلها على الكمبيوتر الخاص بك واستخدامها

We are pleased to announce the launch of the **Galaxy Arabic community**. Galaxy Arabic supports and promotes Galaxy activity for the Arabic speaking community and in Arabic speaking regions of the world.

If you are interested in joining the community, please

- Follow [@Galaxy_Arabic](#) on Twitter
- Join the [Galaxy Arabic mailing list](#). Regional Galaxy news will be posted here, and you can also ask fellow Arabic speakers support questions.
- Join the [Galaxy Arabic Facebook group](#)

We look forward to connecting and growing the Arabic speaking Galaxy community.

Thanks,

Abdelazeem Abdelhameed <abdelazeem_abdelhameed2015505@yahoo.com> and [Dave Clements](#)

New Communities, **New Events**: Galaxy Australia



GAME 2017

Galaxy Australasia Meeting

3 - 9 February, Melbourne, Australia

New Communities: Galaxy Australia, GAMe 2017



3 Feb // Researcher Training Day

for analysis-focussed biologists & biomedical researchers with limited Galaxy experience



4 Feb // BIO Conference Day

for Galaxy users including biologists & bioinformaticians



5 Feb // INFO Conference Day

for technical users of Galaxy including bioinformaticians, tool & software developers & research infrastructure providers



6-9 Feb // Galaxy Admin Training

intensive sessions for those installing & maintaining Galaxy servers

<https://www.embl-abr.org.au/game2017/>

New Events: Admin Training



This was fantastic. It was a huge help toward the goals that we're trying to accomplish in our group and we were grateful that the training was offered. Kudos.

I learned a lot!

It was very interesting and at a perfect level for me. I learned a lot that I will be able to implement very soon.

Extremely happy with the knowledge transfer.

I also liked the fact we were a small group, this was easier to follow all the exercises and to ask questions.

Huge THANK YOU

This training session was exactly what I needed as far as skills-training



6-9 Feb // Galaxy Admin Training

intensive sessions for those installing & maintaining Galaxy servers

Strasbourg
16-19 Jan



European Galaxy Developers Workshop





26 - 30 June France

GCC 2017

Montpellier

Marilyne Summo
Jean-François Dufayard
Olivier Inizan
Christophe Caron

For the **French Institute of Bioinformatics**

 **Galaxy**
PROJECT

<https://gcc2017.sciencesconf.org/>



Galaxy Wiki Migration: URLs

From

wiki.galaxyproject.org

to

new.galaxyproject.org

(work in progress)

to

galaxyproject.org

Wiki migration Technology

From

MoinMoin 1.9.x

to

Markdown

Content in GitHub

Rendering / Serving done with Metalsmith

Automatically propagate GitHub updates

<http://www.metalsmith.io/>

<https://github.com/galaxyproject/galaxy-hub>

Why?

Increasingly frustrated by inability to create/manage/
reuse semi-structured data.

This is only going to get more challenging over time.

<https://wiki.galaxyproject.org/Community/Logs>

<https://wiki.galaxyproject.org/Community/Deployments>

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

<https://wiki.galaxyproject.org/Teach/Trainers>

Metalsmith on GitHub

Hope is that **more people will contribute** if they can

- **directly edit wiki content on GitHub**, a platform that many are already on and familiar with
- **using Markdown**, a markup language that many already know.

GitHub infrastructure also makes site-wide changes easier.

Advanced users can also install Metalsmith and perform edits locally.

Training Material Paradigm Shift

galaxyproject / training-material

Watch 28

Star 27

Fork 49

Code

Issues 40

Pull requests 9

Projects 10

Pulse

Graphs

A collection of training material from offered Galaxy courses <http://galaxyproject.github.io/traini...>

1,160 commits

15 branches

0 releases

32 contributors

Branch: master

New pull request

Find file

Clone or download

bebatut committed on GitHub Merge pull request #196 from galaxyproject/interactive_tour_intro_rem... Latest commit ee47a9a 3 hours ago

Admin-Corner	Update Docker slides (#186)	a day ago
ChIP-Seq	Replace bgruening by galaxyproject in ChIP-Seq	8 days ago
Dev-Corner	Remove any `intro` mention	3 hours ago
Exome-Seq	Replace bgruening by galaxyproject in Exome-Seq	8 days ago
Genome-Annotation	Add genome annotation to template	a month ago
Introduction	Replace bgruening by galaxyproject in Introduction	8 days ago
MethylC-Seq	Replace bgruening by galaxyproject for MethylC-seq	8 days ago
NGS-CC	Replace bgruening by galaxyproject for NGS-CC	8 days ago

<https://github.com/galaxyproject/training-material>

https://bebatut-slides.github.io/swiss_german_galaxy_days_10_16/#/

The Galaxy Team



Enis Afgan



Dannon Baker



Dan Blankenberg



Dave Bouvier



Marten Cech



John Chilton



Dave Clements



Nate Coraor



Jeremy Goecks



Sam Guerler



Mo Heydarian



Jen Jackson



Vahid Jalili



Delphine Lariviere



Ross Lazarus



Anton Nekrutenko



Nick Stoler



James Taylor

<https://new.galaxyproject.org/GalaxyTeam>

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You

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Björn Grüning

Bérénice Batut

NIH NSF

Johns Hopkins University

Penn State University

Oregon Health Sciences University



Dave Clements

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Thanks