

<http://bit.ly/glaxy2015slides>

Introduction to Galaxy

University of Glasgow
8-9 June 2015

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University
of Glasgow



Galaxy Community Resources

<http://bit.ly/glaxy2015slides>

Galaxy Community Resources: Galaxy **Biostar**

Tens of thousands of users leads to a lot of questions.

Absolutely have to **encourage community support**.

Project traditionally used mailing list

Moved the **user support list** to **Galaxy Biostar**, an online **forum**, that uses the Biostar platform



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

Galaxy Community Resources: Mailing Lists

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

Galaxy-Dev

Questions about developing for and deploying Galaxy
High volume (3246 posts in 2014, 1000+ members)

Galaxy-Announce

Project announcements, low volume, moderated
Low volume (34 posts in 2014, 4400+ members)

Also **Galaxy-UK, -France, -Proteomics, -Training, ...**

Unified Search: <http://galaxyproject.org/search>

Galaxy Web Search

Google™ Custom Search x

Search the entire set of Galaxy web sites and mailing lists using Google.

[Run this search at Google.com \(useful for bookmarking\)](#)

Want a [different search?](#)

[Project home](#)

Galaxy Web Search

chip-seq

All Tools Email Source code Shared Documentation Abstracts Requests

About 444 results (0.06 seconds)

Galaxy | Accessible Page | ChIP-seq exercise

- Find**
- Everything on ...
 - Tools for ...
 - Email about ...
 - Source code for ...
 - Published Histories, Pages, Workflows, about ...
 - Documentation on ...
 - Papers using Galaxy for ...
 - Related feature requests



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.

This is the Galaxy Community Wiki. It describes all things Galaxy.

Use Galaxy

Galaxy's public web server usegalaxy.org makes analysis tools, genomic data, tutorial demonstrations, persistent workspaces, and publication services available to any scientist. Extensive [user documentation](#) applicable to any [public](#) or local Galaxy instance is available.



Community & Project

Galaxy has a large and active user community and many ways to get involved.

- [Community](#)

Deploy Galaxy

Galaxy is a free and open source project available to all. Local Galaxy servers can be set up by [downloading](#) the Galaxy application.

- [Admin](#)
- [Cloud](#)



Contribute

- **Users:** [Share](#) your histories, workflows, visualizations, data libraries, and [Galaxy Pages](#), enabling others to use and learn from them.

Use Galaxy

- [Servers](#) • [Learn](#)
- [Main](#) • [Choices](#)
- [Share](#) • [Search](#)

Communicate

- [Support](#) • [Biostar](#)
- [Events](#) • [Mailing Lists](#)
- [News](#)  • [Twitter](#)

Deploy Galaxy

- [Get Galaxy](#) • [Cloud](#)
- [Admin](#) • [Tool Config](#)
- [Tool Shed](#) • [Search](#)

Contribute

- [Develop](#) • [Tools](#)
- [Issues & Requests](#)
- [Logs](#) • [Deployments](#)
- [Teach](#)

Galaxy Project

- [Home](#) • [About](#) • [Cite](#)
- [Community](#)
- [Big Picture](#)

Events

News

Galaxy Event Horizon

Events with Galaxy-related content are listed here.

Also see the [Galaxy Events Google Calendar](#) for a listing of events and deadlines that are in the Galaxy Community. This is also available as an [RSS feed](#).

If you know of any event that should be added to this page and/or to the Galaxy Event Calendar, send it to outreach@glaxyproject.org.

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

Upcoming Events



Date	Topic/Event	Venue/Location
December 12	Introduction to Galaxy Workshop	Virginia State University, Petersburg, Virginia
December 16-19	RNA-Seq and ChIP-Seq Analysis with Galaxy	UC Davis, California, United States
2015		
January 10-14	Galaxy for SNP and Variant Data Analysis	Plant and Animal Genome XXIII (PAG2014), States
January 19-20	NGS pipelines with Galaxy	e-Infrastructures for Massively Parallel Sequencing, Sweden
February 9-13	Analyse bioinformatique de séquences sous Galaxy	Montpellier, France
February 16-18	Accessible and Reproducible Large-Scale Analysis with Galaxy	Genome and Transcriptome Analysis, Pacific Conference, San Francisco, California
	Large-Scale NGS data Analysis on Amazon Web Services Using Globus Genomic iReport: An Integrative "omics"	Genomics & Sequencing Data Integration, of Molecular Medicine Tri-Conference, San Francisco, California

News Items

Opening at McMaster University

The [McArthur Lab](#) in the [McMaster University Department of Biochemistry & Biomedical Sciences](#) is seeking a Systems Administrator / Information Technologist to help establish a new bioinformatics laboratory at McMaster, plus develop the next generation of the [Comprehensive Antibiotic Resistance Database \(CARD\)](#).



From the [job announcement on EvolDir](#):

The candidate will configure BLADE and other hardware for general bioinformatics analysis, development of a GIT version control system, **construction of an in house Galaxy server (usegalaxy.org)**, and development of a new interface, stand-alone tools, APIs, and algorithms for the CARD (based on [Chado](#)).

See the [full announcement](#) for details.

Posted to the [Galaxy News](#) on 2014-12-05

December 2014 Galaxy Newsletter

As always there's a lot going on in the Galaxy this month. "Like what?" you say. Well, read the dang [December Galaxy Newsletter](#) we say! Highlights include:



- [Galaxy Day! In Paris! This Wednesday!](#)
- Near Richmond, Virginia? There's a [Galaxy Workshop at Virginia State U on December 12](#).
- [GCC2015 needs sponsors!](#)
- Other [upcoming events](#) on two continents
- **96 new papers**, including 6 highlighted papers, referencing, using, extending, and implementing Galaxy.
- [Job openings at 7+ organizations](#)
- A new mailing list: [Galaxy-Training](#)
- [15 new ToolShed repositories from 10 contributors](#)
- And, [10 other juicy](#) (well maybe not *juicy*, but certainly not *crunchy*) [bits of news](#)

Dave Clements and the *crisp* Galaxy Team

Posted to the [Galaxy News](#) on 2014-12-01

Bioinformaticians, Freiburg

[Max Planck Institute of Immunobiology and Epigenetics](#) in Freiburg, Germany has an opening for a Bioinformatician for an initial period of two years. The successful candidate will work at the interface between an in-house deep-sequencing facility (HiSeq-2500) and the various research groups at the institute. Main responsibilities include



primary analysis of deep-sequencing data and quality controls

Cistrome



A Galaxy Server dedicated to ChIP-* analysis

Galaxy / CNIC.DarwinTree

Tools

Workflow: ChIP-Seq Analysis

1. Align reads to the reference genome (BWA-MEM)

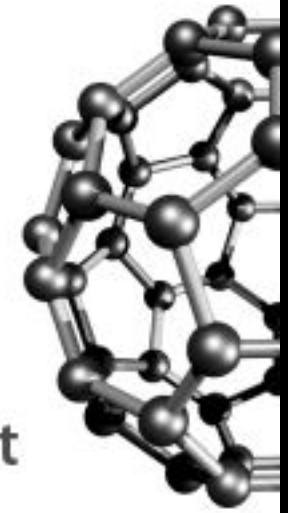
2. Call peaks (MACS2)

3. Annotate peaks (ChIP-Seq Annotation)

4. Visualize enriched elements (IGV)

ballaxy

Powered by the Biochemical Algorithms Library Project



deepTools

bam bigwig

CoSSci

Galaxy for Complex Social Sciences

GENEONTOLOGY

Unifying Biology

galaxy.berkeleybop.org

GWIS: Online exhaustive bivariate GWAS in minutes...

NICTA

Web Service

Timing Data

Processing Pipeline

Welcome to Cloud-based Image Analysis and Processing Toolbox...

CloudBased Image Analysis & Processing Toolbox

More information can be found on the NeCTAR website, and the project blog.

This project is supported in part by NeCTAR, and CSIRO.

Galaxy / Metabiome Portal

The Microbiome Analysis Center

Life on a Smaller Scale

Welcome to the Metabiome Portal @ GMU

bit.ly/gxyServers

Community can create, vote and comment on issues

HOME TOUR GOLD BUSINESS CLASS BLOG Trello Sign Up Log In

Want to subscribe, vote or comment on these cards? [Sign up for free](#) or [learn more about Trello](#)

Galaxy: Development

Public

Inbox

- To add cards, use <http://galaxyproject.org/trello>
4 votes 2 comments
- To request reference genome, comment on this card.
1 vote 5 comments 0/6
- Toolshed installation fails silently
3 votes 1 comment
- Handle cluster job preemption
2 votes 1 comment
- Return code 271 causes traceback for PBS torque
1 vote 2 comments
- BUG: Tool shed repository export to capsule does not always capture all dependencies
1 vote 1 comment
- Remove manual_builds.txt from source control and replace with a .sample version
1 vote 1 comment

Tool Requests

- 595: Add SAMTools "Sort"
4 votes 13 comments
- 601: SAM-to-BAM tool enhancements
2 votes 1 comment
- Tools: Add tool to generate simulated reads to Main
3 votes 1 comment
- default max insert size of Bowtie2 should be increased
2 votes 5 comments
- 307: A tool to produce a set of random intervals.
2 votes 2 comments
- Converter Tool: SAM to BAM enhancements
2 votes
- New Tool: convert IUPAC chars to N
1 vote 7 comments 1 comment

Bug Reports

- Usability: expanding datasets near the bottom of panel
CE
- Bug: SICER on Main dependency issue
2 votes 20 comments 3/5
- Profile Annotations bad values when "select all"
1 vote 5 comments
- Filter pileup tool doesn't recognize pileup output data
1 vote 2 comments
- Bug: Odd Fetch Taxonomy tool behavior
1 vote 1 comment
- Strip message after pause jobs resumed
1 vote 1 comment

Ideas

- 697: Workflow job control functions
10 votes 9 comments
- User Metrics and Analytics
3 votes 3 comments 1/2
CE
- Tuxedo RNA-seq tools: report command-line
2 votes 3 comments
- Tools: Incorporate key Cuffdiff output files for Cumberbund
2 votes 1 comment 0/3
- Moving objects between Galaxy instances, data federation, distributed storage, and data locality
2 votes
- Workflow Editor: Provide explicit access to implicit datatype converter tools
1 vote

Pull Requests

- 665: P issue
2 votes
- Custom
2 votes
- Tools: Reque
3 votes
- add m
downs
2 votes
- Please wrapp
mappi
2 votes
- [galaxy
libxml
1 vote
- Pull Re
manag

Members

Lance Parsons on [Add or update wrappers for SamTools 1.0](#)

I see that @peterjc has a wrapper for idxstats already and that it's listed on this card as "done" but I don't see it in the github repo. Will idxstats become part of this devteam collection or should I just start using the wrapper from @peterjc (Thanks Peter!)

today at 3:52 pm

G g2roboto added Pull Request #606 - [STABLE] Escape instances of message passed in through kwd before pushing them back out to

<http://bit.ly/gxytrello>



GALAXY

COMMUNITY CONFERENCE

BALTIMORE, MD | JUNE 30 - JULY 2, 2014

Slides, posters & videos now online
<http://bit.ly/gcc2014>





GCC 2015

Galaxy Community Conference

4-8th July 2015

The Sainsbury Laboratory
Norwich, UK

gcc2015.tsl.ac.uk



GCUK IS LIVE!

We also support
community
organized efforts
and events.



Galaxy Resources & Community: Videos

vimeo Me Videos Create Watch Tools Upload Search

Galaxy Project PLUS

Joined 1 month ago

54 Videos 0 Likes 0 Following 1 Group 6 Channels 0 Albums

Recently Uploaded + See all 54 videos

- Using Galaxy protocol 3**
Calling Peaks For CHIP-seq Data
CPB Using Galaxy 3
5 days ago
- Using Galaxy protocol 2**
Loading Data and Understanding Datatypes
CPB Using Galaxy 2
5 days ago
- Using Galaxy protocol 1**
Finding Human Coding Exons with Highest SNP Density
CPB Using Galaxy 1
5 days ago
- usegalaxy.org**
FASTQ Prep
Illumina
FASTQ Prep - Illumina
1 week ago

Settings

Galaxy is an open, web-based platform for data intensive biomedical research. Whether on this free public server or your own instance, you can perform, reproduce, and share complete analyses. The Galaxy team is a part of BX at Penn State, and the Biology and Mathematics and Computer Science departments at Emory University. The Galaxy Project is supported in part by NSF, NHGRI, The Huck Institutes of the Life Sciences, The Institute for

“How to”
screencasts on
using and
deploying
Galaxy

Talks from
previous
meetings.

<http://vimeo.com/galaxyproject>

Galaxy Resources & Community: CiteULike Group



CiteULike Group: Galaxy Search Register Log in

Group: Galaxy - library 2336 articles

Search Copy Export Sort Hide Details

✓ Adaptation of the targeted capture Methyl-Seq platform for the mouse genome identifies novel tissue-specific methylation patterns of genes involved in neurodevelopment

Epigenetics (18 May 2015), pp. 00-00, doi:10.1080/15592294.2015.1045179
by Benjamin Hing, Enrique Ramos, Patricia Braun, et al.
posted to methods by galaxyproject to the group Galaxy on 2015-05-28 21:46:38 ★★

■ Abstract

✓ Genomic and experimental evidence for multiple metabolic functions in the *RidA/YjgF/YER057c* locus in *Escherichia coli*

BMC Genomics, Vol. 16, No. 1. (15 May 2015), 382, doi:10.1186/s12864-015-1584-3
by Thomas D. Niehaus, Svetlana Gerdes, Kelsey Hodge-Hanson, et al.
posted to methods usemain by galaxyproject to the group Galaxy on 2015-05-28 21:41:14 ★★

■ Abstract

✓ NetworkAnalyst for statistical, visual and network-based meta-analysis of gene expression data

Nat. Protocols, Vol. 10, No. 6. (07 June 2015), pp. 823-844, doi:10.1038/nprot.2015.052
by Jianguo Xia, Erin E. Gill, Robert E. W. Hancock
posted to visualization by galaxyproject to the group Galaxy on 2015-05-28 21:37:43 ★★ [along with 2 people and](#)

✓ Repression by H-NS of genes required for the biosynthesis of the *Vibrio cholerae* biofilm matrix is mediated by the messenger cyclic diguanylic acid

Molecular Microbiology (1 May 2015), pp. n/a-n/a, doi:10.1111/mmi.13058
by Julio C. Ayala, Hongxia Wang, Anisia J. Silva, Jorge A. Benitez
posted to methods usemain by galaxyproject to the group Galaxy on 2015-05-28 21:30:30 ★★

■ Abstract

✓ A Sleeping Beauty forward genetic screen identifies new genes and pathways driving osteosarcoma development and

Group Tags

All tags in the group Galaxy

Filter:

[\[Display as Cloud\]](#)

<u>methods</u>	1149
<u>workbench</u>	702
<u>usemain</u>	233
<u>tools</u>	169
<u>usepublic</u>	129
<u>isgalaxy</u>	124
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<u>visualization</u>	15
<u>usecloud</u>	4

Now
over
2300
papers

<http://bit.ly/gxycul>

Thanks



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Galaxy Project

Johns Hopkins University

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<http://bit.ly/glaxy2015slides>