

Galaxy CloudMan

A Gentle Introduction to Data Analysis on the Cloud

Plant & Animal Genome XXII
San Diego, January 15, 2014

Dave Clements
Johns Hopkins University
<http://galaxyproject.org/>



This talk
complements
yesterday's
workshop →

<http://bit.ly/gxypag2014>



Plant and Animal Genome XXII (PAG 2014)

UCSC Genome Browser

Sat 4:00-6:10, California Room
Robert Kuhn

The Banana Genome Hub

Tues 11:50-12:10, Pacific Salon 6-7
Gaëtan Droc, *et al.*

Galaxy for NGS Analysis A Hands-on Workshop

Tues 4:00-6:10, California Room
Dave Clements, Anushka Brownley

This workshop will introduce the Galaxy platform and walk participants through a multi-step next generation sequencing data analysis, starting with quality control. We will review common choices in NGS data analysis, and demonstrate them within the context of Galaxy, taking advantage of Galaxy's tool set and visualization capabilities.

We will also provide a brief overview of what is needed to set up your own local Galaxy instance. This complements the *Galaxy CloudMan* talk on Wednesday

URGI Plant and Fungi Platform

Distributed Resources Through GMOD Tools
Wed 11:10-11:50, GMOD Workshop Golden West
Joelle Amselem, *et al.*

Galaxy CloudMan

A Gentle Introduction to Data Analysis on the Cloud

Wed 11:50-12:30, GMOD Workshop, Golden West
Dave Clements

Galaxy is open-source and web-based, with over 50 publicly accessible Galaxy servers and hundreds of private installations around the world. Galaxy can also be run on compute clouds using *Galaxy CloudMan*.

This talk will briefly introduce Galaxy, Galaxy CloudMan, and some basic cloud concepts. We'll then show a live demonstration of how to setup a Galaxy server on Amazon Web Services (one of several supported cloud infrastructures) using CloudMan, add a dynamically scalable compute cluster to perform analysis, customize the server by adding new tools, and then shut the server down. All steps can be done through a web browser, without ever using a command line interface.

Poster Sessions

Mon 10:00-11:30

P988: The South Green Bioinformatics Platform,
Mathieu Rouard, *et al.*

**P1050: Integrative System for Gene Family Gathering
and Analysis in a Context of Crops' Stress Response
Study,** Delphine Lavivière, *et al.*

Mon 3:00-4:30

P135: SNP Genotyping to Accelerate Rice Breeding,
Michael Thomson, *et al.*

**P1041: RepeatExplorer: Collection of Tools for
Mining of Repetitive Elements from NGS Data,**
Petr Novak, *et al.*

The Galaxy Project

Galaxy is an open source web-based platform for data integration and analysis in life sciences research.

The Galaxy Project is supported by a large and active community.

<http://galaxyproject.org>

What is Galaxy?

- A web based data integration and analysis framework.
- **Open source software**
- **A free (for everyone) web service**

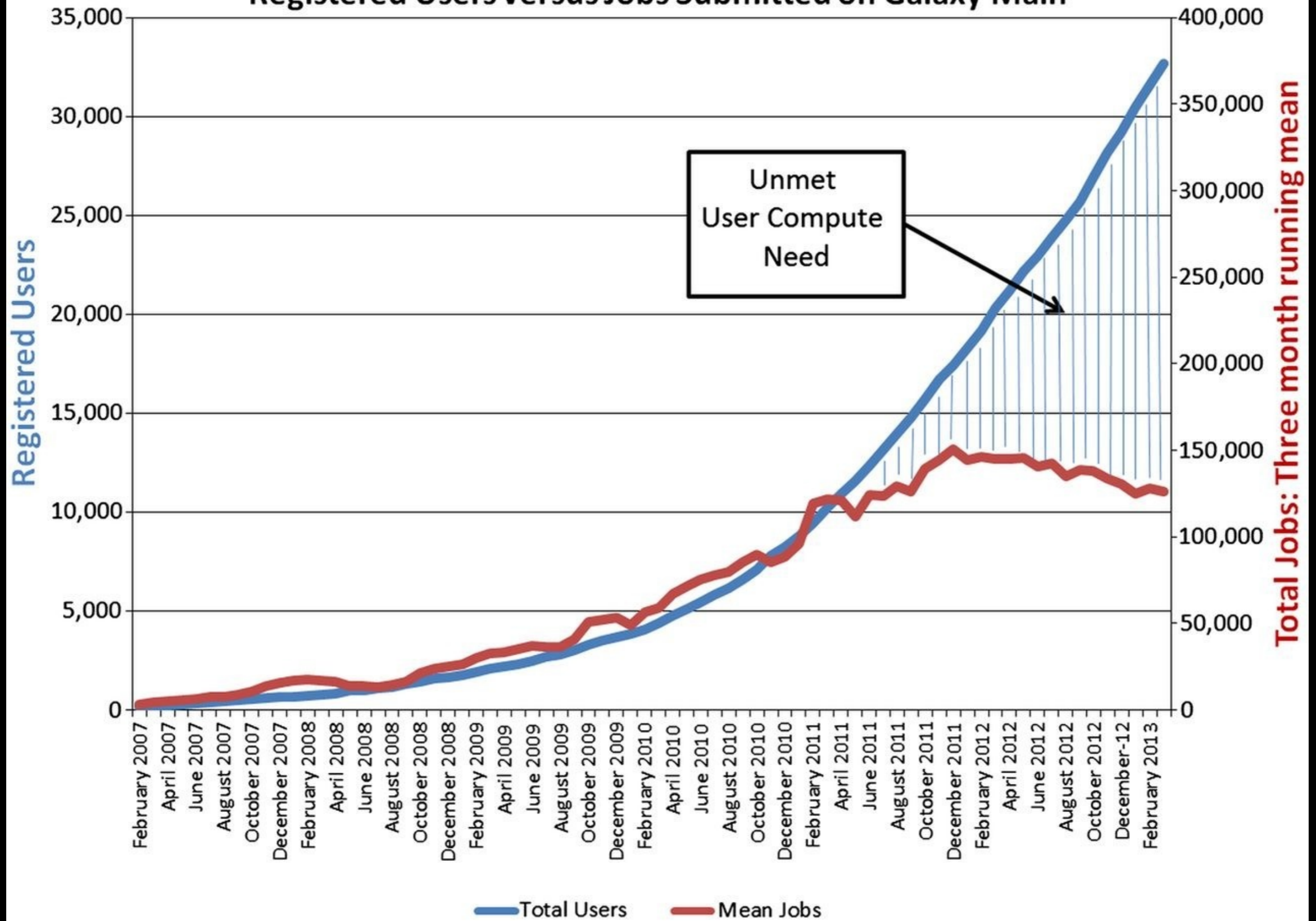
<http://galaxyproject.org>

Galaxy is available ...

As a free for everyone web service (<http://usegalaxy.org>) integrating a wealth of tools, compute resources, terabytes of reference data and permanent storage.

However, *a centralized solution cannot support the different analysis needs of the entire world.*

Registered Users versus Jobs Submitted on Galaxy Main



Leveraging the national cyberinfrastructure for biomedical research
 LeDuc, et al. *J Am Med Inform Assoc* doi:10.1136/amiajnl-2013-002059

Galaxy is available ...

- As a free (for everyone) web service

<http://usegalaxy.org>

- **As open source software** that you can install locally

<http://getgalaxy.org>

See yesterday's slides

Galaxy is available ...

- As a free (for everyone) web service
- As open source software
- ***On the Cloud***



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

AWS in Education Grants Program



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

Galaxy is available ...

- As a free (for everyone) web service
- As open source software
- On the Cloud
- ***With Commercial Support***



A ready-to-use appliance (BioTeam)

Cloud-based solutions (ABgenomica, AIS, Appistry, GenomeCloud)

Consulting & Customization (Arctix, BioTeam, Deena Bioinformatics)

Galaxy Project: Further reading & Resources

<http://galaxyproject.org>

<http://usegalaxy.org>

<http://getgalaxy.org>

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

<http://bit.ly/gxychoices>

What is our path?

Today we will:

- Launch our own Galaxy server on Amazon Web Services
- Make the server dynamically scalable in response to demand.
- Run some basic analysis on it.
- Make it go away.

Full Disclosure

To use AWS you must **create an AWS account with a credit card associated with it.**

You must also have created a key pair.

These have been done prior to this talk.

We will be using an IAM account, a limited AWS account that is useful for teaching with AWS.

CloudLaunch

The screenshot shows the Galaxy web interface. The browser address bar displays <https://usegalaxy.org/root>. The navigation bar includes the Galaxy logo and menu items: Analyze Data, Workflow, Shared Data, Visualization, Cloud (highlighted with a mouse cursor), Help, and User. A left sidebar titled 'Tools' contains a search box and a list of tool categories: 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, and Graph/Display Data. The main content area features a text block: "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](#)." Below this is a slide for "SLIPSTREAM APPLIANCE GALAXY EDITION" with the tagline "Galaxy made easy." and a progress indicator at the bottom.

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](#).

SLIPSTREAM
APPLIANCE GALAXY EDITION
Galaxy made easy.

CloudLaunch

The screenshot shows the Galaxy web interface. The browser address bar displays <https://usegalaxy.org/root>. The main navigation bar includes 'Galaxy' and several menu items: 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Cloud', 'Help', and 'User'. The 'Cloud' menu is expanded, showing a 'New Cloud Cluster' button. The left sidebar contains a 'Tools' section with a search bar and a list of tool categories: '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', and 'Graph/Display Data'. The main content area features a text block: '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](#).' Below this text is a large image of the 'SLIPSTREAM APPLIANCE GALAXY EDITION' logo with the tagline 'Galaxy made easy.' and a progress indicator at the bottom.

← → ↻ 🏠 <https://usegalaxy.org/root>

Galaxy Analyze Data Workflow Shared Data Visualization Cloud Help User

Tools

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](#)

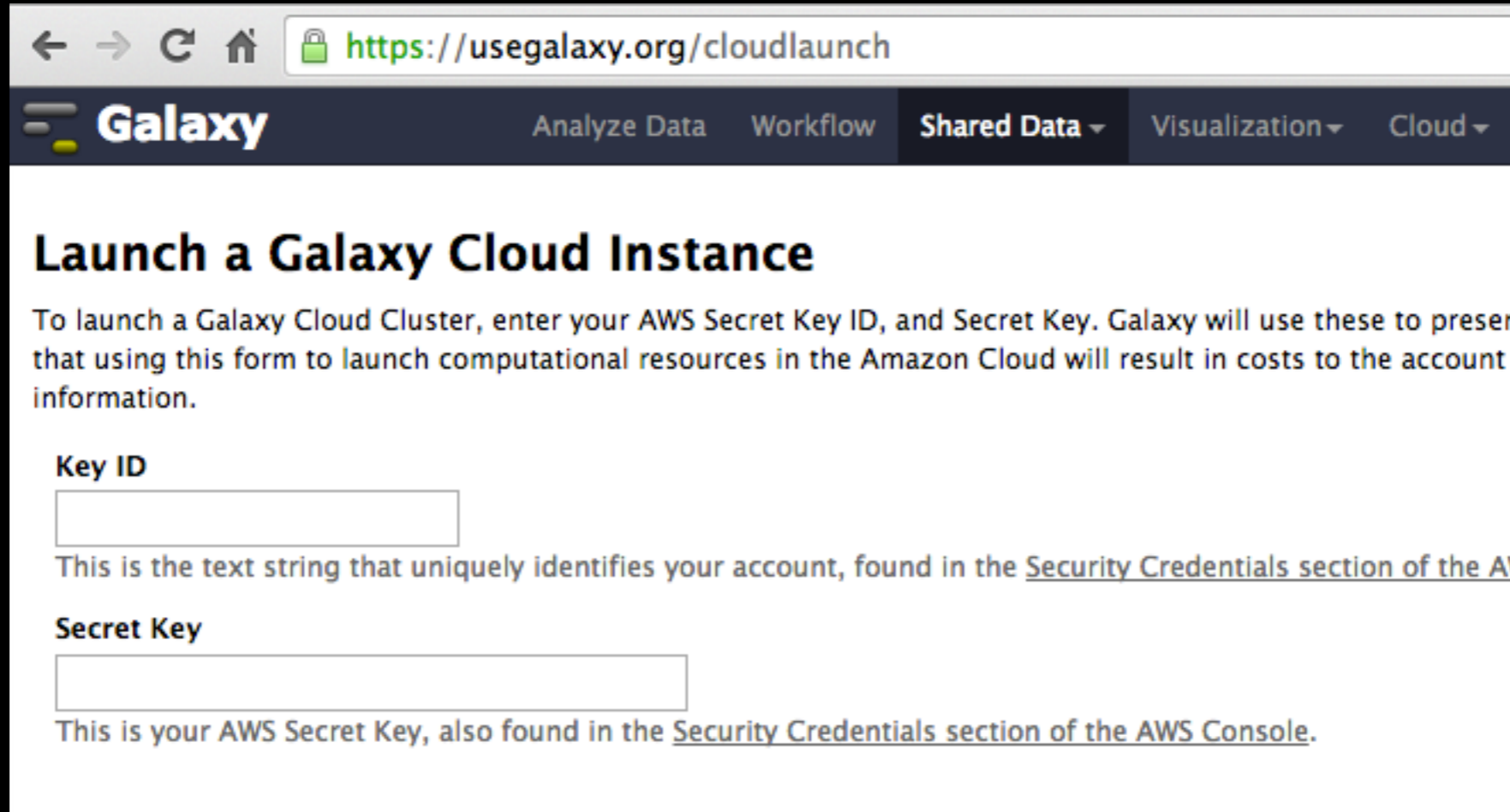
[Graph/Display Data](#)

New Cloud Cluster

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](#).

SLIPSTREAM
APPLIANCE GALAXY EDITION
Galaxy made easy.

CloudLaunch



The screenshot shows a web browser window with the address bar containing `https://usegalaxy.org/cloudlaunch`. The page header features the Galaxy logo and navigation links for 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', and 'Cloud'. The main content area is titled 'Launch a Galaxy Cloud Instance' and includes a warning about costs, followed by input fields for 'Key ID' and 'Secret Key' with their respective instructions.

← → ↻ 🏠 <https://usegalaxy.org/cloudlaunch>

Galaxy Analyze Data Workflow **Shared Data** Visualization Cloud

Launch a Galaxy Cloud Instance

To launch a Galaxy Cloud Cluster, enter your AWS Secret Key ID, and Secret Key. Galaxy will use these to present information that using this form to launch computational resources in the Amazon Cloud will result in costs to the account information.

Key ID

This is the text string that uniquely identifies your account, found in the [Security Credentials](#) section of the AWS Console.

Secret Key

This is your AWS Secret Key, also found in the [Security Credentials](#) section of the AWS Console.

Launch a Galaxy Cloud Instance

To launch a Galaxy Cloud Cluster, enter your AWS Secret Key ID, and Secret Key. Galaxy will use these to present appropriate options for launching your cluster. Note that using this form to launch computational resources in the Amazon Cloud will result in costs to the account indicated above. See [Amazon's pricing](#) for more information.

Key ID

This is the text string that uniquely identifies your account, found in the [Security Credentials](#) section of the AWS Console.

Secret Key

This is your AWS Secret Key, also found in the [Security Credentials](#) section of the AWS Console.

Instances in your account

Cluster Name

This is the name for your cluster. You'll use this when you want to restart.

Cluster Password

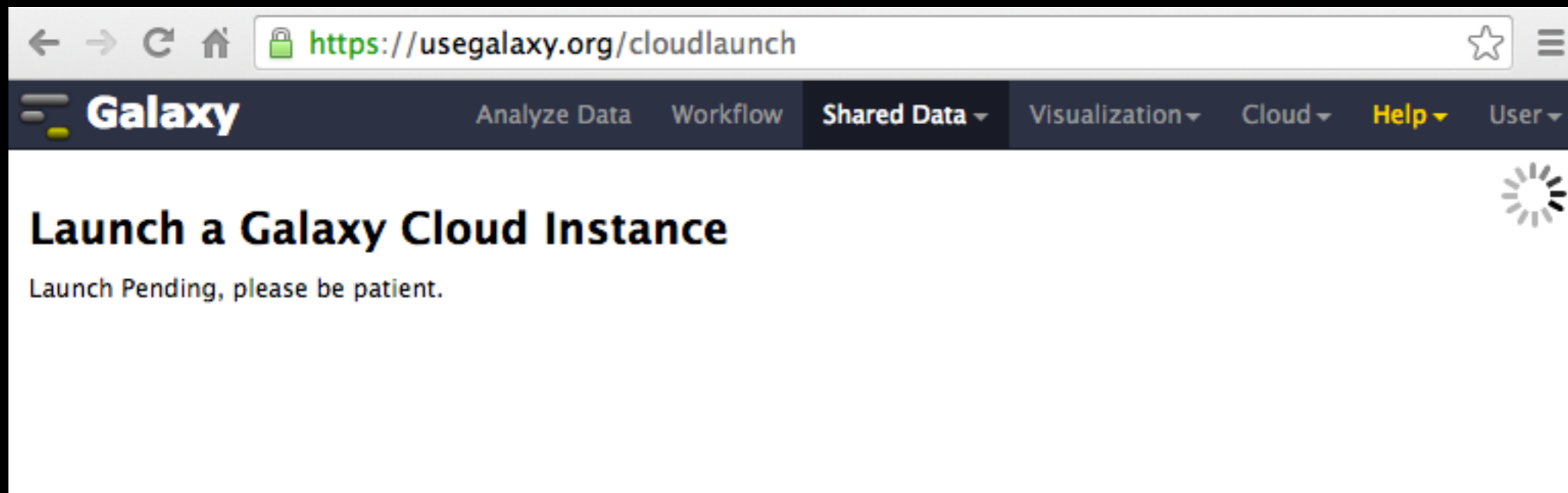
Cluster Password - Confirmation

Key Pair

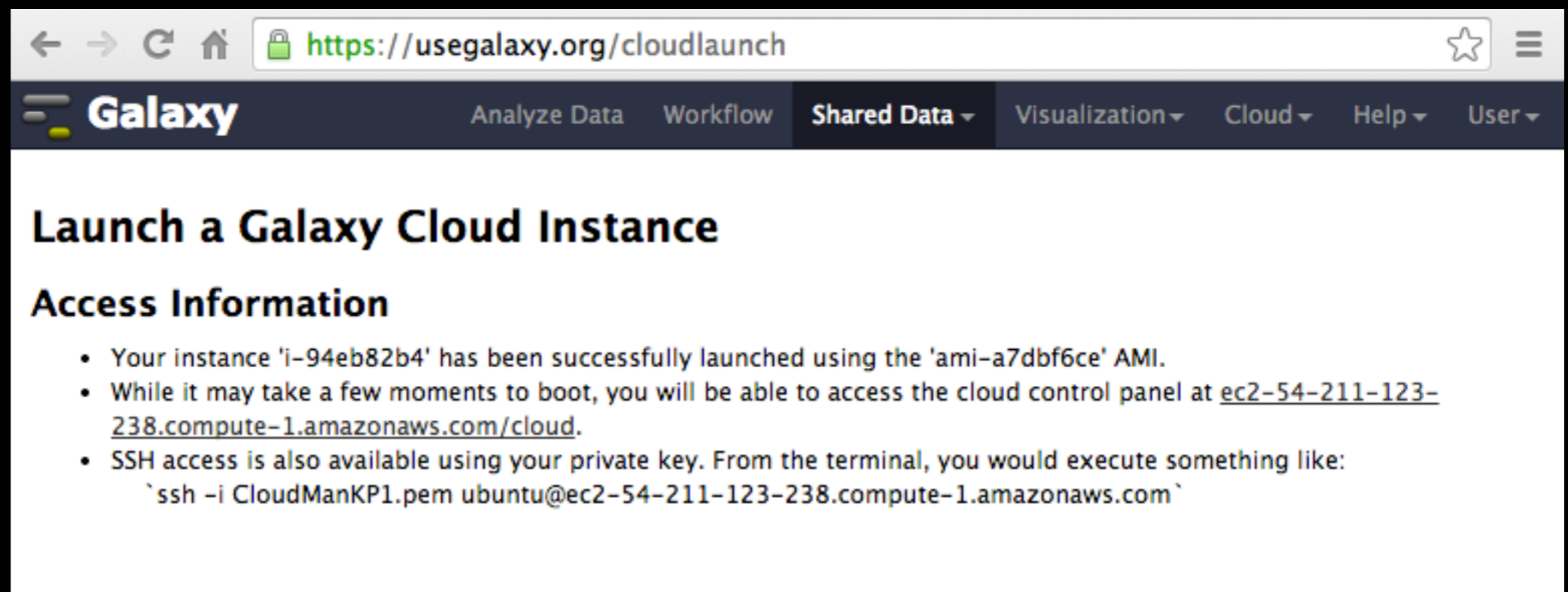
Instance Type

Requesting the instance may take a moment, please be patient. Do not refresh your browser or navigate away from the page

CloudLaunch



A screenshot of a web browser showing the Galaxy CloudLaunch page. The address bar displays <https://usegalaxy.org/cloudlaunch>. The navigation bar includes the Galaxy logo and menu items: Analyze Data, Workflow, Shared Data, Visualization, Cloud, Help, and User. The main content area features the heading "Launch a Galaxy Cloud Instance" and a status message: "Launch Pending, please be patient." A loading spinner icon is visible in the top right corner of the content area.

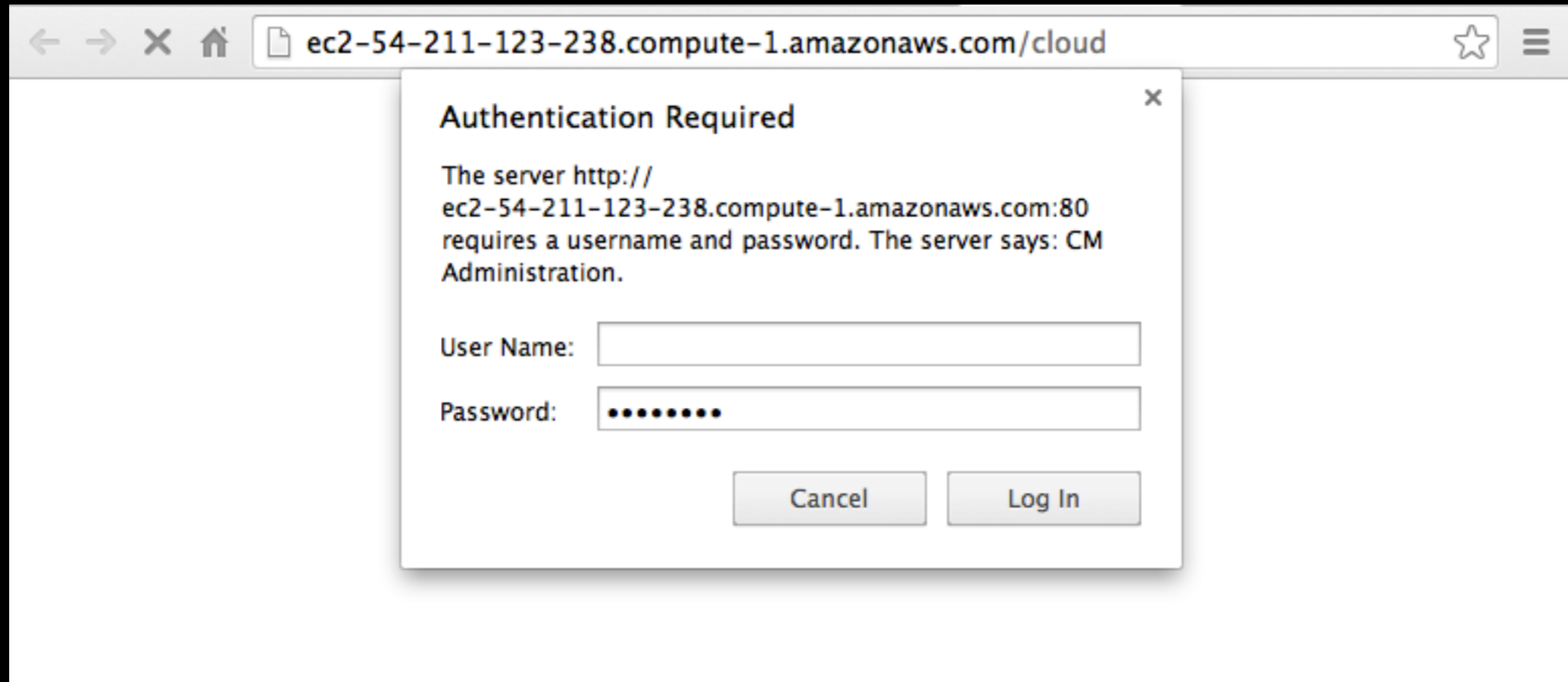


A screenshot of the Galaxy CloudLaunch page showing successful launch information. The address bar displays <https://usegalaxy.org/cloudlaunch>. The navigation bar is identical to the previous screenshot. The main content area features the heading "Launch a Galaxy Cloud Instance" and a sub-heading "Access Information". Below this, there is a list of bullet points providing details about the launched instance and how to access it.

- Your instance 'i-94eb82b4' has been successfully launched using the 'ami-a7dbf6ce' AMI.
- While it may take a few moments to boot, you will be able to access the cloud control panel at ec2-54-211-123-238.compute-1.amazonaws.com/cloud.
- SSH access is also available using your private key. From the terminal, you would execute something like:

```
`ssh -i CloudManKP1.pem ubuntu@ec2-54-211-123-238.compute-1.amazonaws.com`
```

CloudLaunch



CloudLaunch

The screenshot shows a web browser window with the URL `ec2-54-211-123-238.compute-1.amazonaws.com/cloud`. The page title is "CloudMan from Galaxy" and it includes navigation links for "Admin", "Report bugs", "Wiki", and "Screencast". A modal dialog titled "Initial CloudMan Platform Configuration" is displayed in the center. The dialog contains a welcome message and a list of configuration options for the platform type. The "Galaxy Cluster" option is selected, and the "Volume - Default (10 GB)" sub-option is also selected. A "Choose platform type" button is located at the bottom of the dialog. The background of the page is dimmed, showing a sidebar with "Status" information and a main content area with a "Terminal" button.

← → ↻ 🏠 `ec2-54-211-123-238.compute-1.amazonaws.com/cloud` ☆ ☰

CloudMan from Galaxy [Admin](#) | [Report bugs](#) | [Wiki](#) | [Screencast](#)

Initial CloudMan Platform Configuration

Welcome to CloudMan. This application will allow you to manage this cluster platform and the services provided within. To get started, choose the type of platform you'd like to work with and provide the associated value, if any.

- Galaxy Cluster:** Galaxy application, available tools, reference datasets, SGE job manager, and a data volume. Specify the initial storage type:
 - Volume - Default (10 GB)
 - Volume - Custom: GB
 - Transient Storage

[Show more startup options](#)

CloudMan
Welcome to CloudMan. This is your first time using CloudMan. If this is your first time using CloudMan, default settings are configured, default settings are configured, default settings on which jobs are run.

Status

Cluster name:

Disk status:

Worker status:

Service status:

Cluster status:

CloudLaunch

← → ↻ 🏠 ☆ ☰

Messages

Initializing 'Galaxy' cluster type. Please wait... (2014-01-15 06:48:34)

Welcome to [CloudMan](#). This application allows you to manage this cloud cluster and the services provided within. If this is your first time running this cluster, you will need to select an initial data volume size. Once the data store is configured, default services will start and you will be able to add and remove additional services as well as 'worker' nodes on which jobs are run.

[Terminate cluster](#) [Add nodes ▼](#) [Remove nodes](#) [Access Galaxy](#)

Status

Cluster name: PAG_CLOUD_2

Disk status: 0 / 0 (0%)

Worker status: Idle: 0 Available: 0 Requested: 0

Service status: Applications ● Data ●

Autoscaling is **off**.
Turn [on](#)?

[Cluster status log](#) +

Cloud Launched

The screenshot shows a web browser window with the URL `ec2-54-211-123-238.compute-1.amazonaws.com/cloud`. A yellow message box at the top contains the following text:

Messages

Initializing 'Galaxy' cluster type. Please wait... (2014-01-15 06:48:34)

All cluster services started; the cluster is ready for use. (2014-01-15 06:53:24)

is your first time running this cluster, you will need to select an initial data volume size. Once the data store is configured, default services will start and you will be able to add and remove additional services as well as 'worker' nodes on which jobs are run.

Below the message box are four buttons: **Terminate cluster**, **Add nodes ▼**, **Remove nodes**, and **Access Galaxy**.

Status

Cluster name: PAG_CLOUD_2

Disk status: 3.2G / 10G (32%)

Worker status: Idle: 0 Available: 0 Requested: 0

Service status: Applications Data

To the right of the status information is a 4x4 grid of 16 square icons. The top-left icon is green with a white bar, while the others are grey.

Below the grid is a box with the text: **Autoscaling is off.** Turn on?

At the bottom is a grey bar with the text **Cluster status log** and a green plus icon.

Cool things to do

- Create a **login**
- Become an **admin**
- Set up **autoscaling**
- Run **Galaxy 101** (with **Chicken chr1!**)
- **Shut it down**

Community Resources

Galaxy Resources and Community: Mailing Lists

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

Galaxy-Announce

Project announcements, low volume, moderated

Low volume (47 posts in 2013, 3400+ members)

Galaxy-User

Questions about using Galaxy and usegalaxy.org

High volume (1328 posts in 2013, 2600+ members)

Galaxy-Dev

Questions about developing for and deploying Galaxy

High volume (5200 posts in 2013, 900+ members)

Community: Public Galaxy Instances

<http://bit.ly/gxyServers>



ChIP-chip and ChIP-seq?

✓ Cistrome

Statistical Analysis?

✓ Genomic Hyperbrowser

Protein synthesis?

✓ GWIPS-viz

de novo assembly?

✓ CBIIT Galaxy

Reasoning with ontologies?

✓ OPPL Galaxy

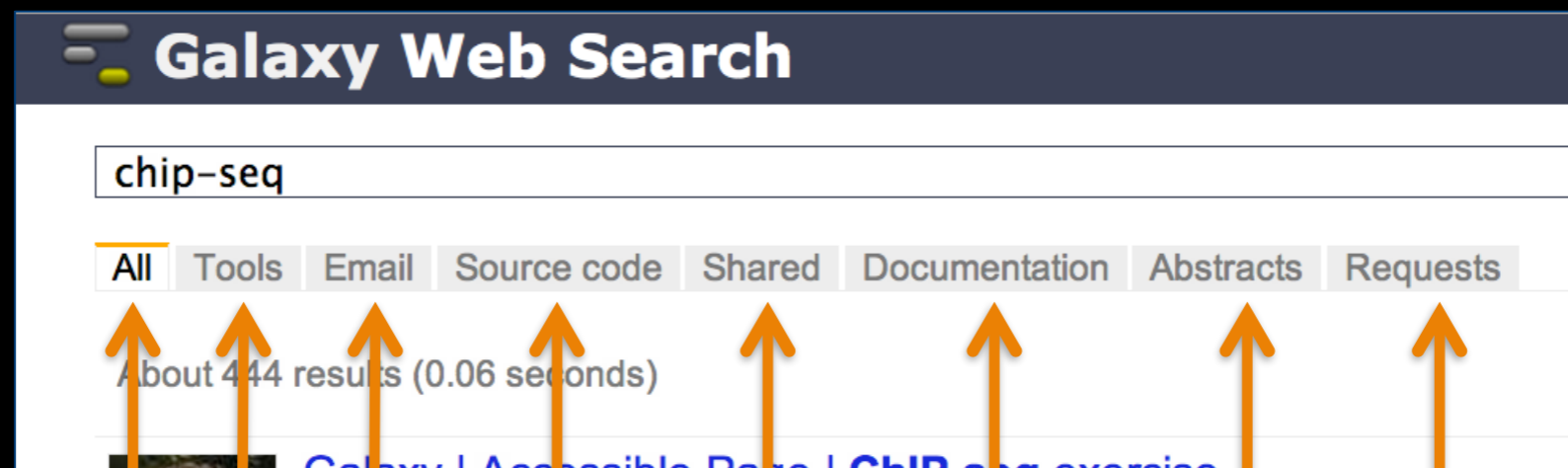
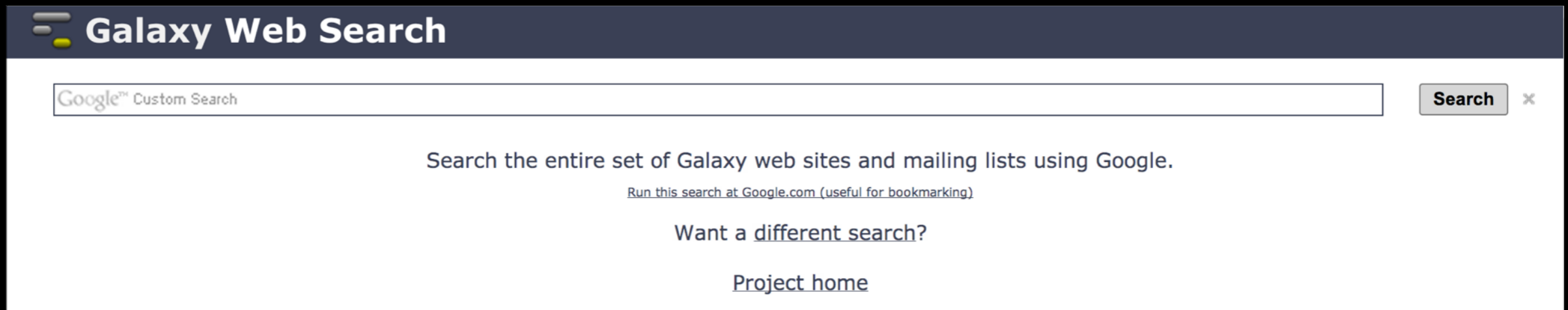
Repeats!

✓ RepeatExplorer

Everything?

✓ Andromeda

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



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

Community can create, vote and comment on issues

The screenshot displays a Trello board for the Galaxy Project, titled "Galaxy: Development Inbox". The board is organized into four main columns: "Inbox", "Developer ideas", "Bug Reports", and "Issues from Bitbucket".

- Inbox:** Contains cards such as "To add cards, use the http://galaxyproject.org/trello" (2 votes, 1 comment), "Filter and Sort: 'Select' tool not dealing with special characters right" (1 comment), "Uploaded fastq file datatype not usable in BWA" (1 comment), "Reference genome request: GATK-ordered hg19" (1 comment), and "Feature request: manually hide datasets" (1 comment).
- Developer ideas:** Contains cards like "Anonymous use of workflows/visualizations" (0/2 votes), "Feature Request: the ability to restart a failed workflow from the point of failure;" (6 votes, 2 comments), "Google Drive / Dropbox / Box / ... integration" (1 vote), "Bug report: always import deleted datasets" (2 comments), "Standalone web application(s) for visualizations", "Enh: Archiving histories" (1 comment), "Modify data library upload completion message" (1 comment), and "Display in UI runtime".
- Bug Reports:** Contains cards such as "Issues with workflow step hiding not persisting" (1 vote, 1 comment), "Workflow View Broken in Toolshed?", "Unable to run jobs when user job limits are set" (1 vote, 4 comments), "Fix tool tip FASTQ Summary Statistics" (1 comment), "Bug when using data_column", "Velvet wrapper broken when real user jobs are used", "apport.fileutils", and "Bug: Running functional tests for migrated or installed tools does not".
- Issues from Bitbucket:** Contains numbered issues: "5: Option to disable automatic history creation" (2 votes, 1 comment), "6: Option to require that histories have names" (1 vote), "8: More flexible output handlers", "10: Allow overriding parameters when running a workflow" (1 vote), "20: Suggestion: new tag in tool's XML file - 12/9/08 email from Assaf Gordon", "21: Real DB key build ontology", and "24: Add ability to password secure tools".

On the right side of the board, there is a "Members" section with a grid of member avatars and an "Add Members..." button. Below that is a "Board" section with "Options", "Add List", and "Filter Cards" buttons. The "Activity" section shows a list of recent actions, including "Dannon Baker added API: Library Contents to Developer ideas and" (sent to the board, joined) and "g2roboto on Feature request: manually hide datasets" (Submitted by @nickstoler, Feb 1 at 4:40 pm).

<http://bit.ly/gxyissues>

http://wiki.galaxyproject.org

Galaxy Wiki Login | Search: Titles Text

FrontPage Locked History Actions



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 service web site](#) 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 on [this wiki](#) and [elsewhere](#).



Deploy Galaxy

Galaxy is open source for all organizations. Local Galaxy servers can be set up by [downloading and customizing](#) the Galaxy application.

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




Community & Project

Galaxy has a large and active user community and many ways to [Get Involved](#).

- [Community](#)
- [News](#)
- [Events](#)
- [Support](#)

Contribute

- **Users:** [Share](#) your histories, workflows, visualizations, data libraries, and [Galaxy Pages](#), enabling others to use and learn from them.
- **Deployers and Developers:** Contribute tool definitions to the [Galaxy Tool Shed](#) (making it easy for others to use those tools on their installations), and code to the core release.



Use Galaxy

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

Communicate

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

Deploy Galaxy

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



Contribute

[Tool Shed](#) • [Share](#)
[Issues & Requests](#)

Events

News

Galaxy Wiki Login | Search:

Events

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 relevant to 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, please add it here or send it to outreach@galaxyproject.org.

Contents

1. [Upcoming Events](#)
2. [Other Calendars](#)
3. [Past Events](#)
 1. [2014](#)
 2. [Archive](#)

Upcoming Events






Date	Topic/Event	Venue/Location	Contact
January 11-15	<i>Galaxy for NGS Data Analysis: A Hands-on Computer Demo</i>	Plant and Animal Genome XXII (PAG 2014) , San Diego, California, United States	Dave Clements, Anushka Brownley
	<i>Galaxy Cloudman: A Gentle Introduction to Data Analysis on the Cloud</i> Part of the GMOD Workshop		Dave Clements, Scott Cain
	<i>Plus 3 more talks and 4 posters</i>		See list
January 16-17	2014 GMOD Meeting	San Diego, California, United States	Dave Clements, Scott Cain
February 5-6	<i>Mosquito Informatics</i>	EBI, Hinxton, United Kingdom	Dan Lawson <lawson AT ebi DOT ac DOT uk>

Galaxy Wiki Login | Search:

News

News

Announcements of interest to the Galaxy Community. These can include items from the Galaxy Team or the Galaxy community and can address anything that is of wide interest to the community.

The Galaxy News is also available as an [RSS feed](#).

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](#).

See also

- [Galaxy News Briefs](#)
- [Galaxy Updates](#)
- [Galaxy on Twitter](#)
- [Events](#)
- [Learn](#)
- [Support](#)
- [About the Galaxy Project](#)

News Items

January 2014 CloudMan Release

We just released an update to Galaxy CloudMan. CloudMan offers an easy way to get a personal and completely functional instance of Galaxy in the cloud in just a few minutes, without any manual configuration.

This update brings a large number of updates and new features, the most prominent ones being:

News Items

- January 2014 CloudMan Release
- GCC2014 Training Day Topics: Vote!
- January 2014 Galaxy Update
- 2013 Galaxy Day Report
- Galaxy Community Log Board
- Galaxy Deployment Catalog
- Nominate 2014 Training Day Topics
- December 2013 Galaxy Update
- Nov 04, 2013 Galaxy Distribution
- November 2013 Galaxy Update
- December Bioinformatics Boot Camps
- GCC2014: Save These Dates!
- Galaxy Day, 4 décembre à Paris

[News Archive](#)





GALAXY

COMMUNITY CONFERENCE

BALTIMORE, MD | JUNE 30 - JULY 2, 2014

<http://bit.ly/gcc2014>



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
- FASTQ Prep - Illumina**
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 MyCiteULike Group: Galaxy Search Logged in as galaxyproject Log Out

Group: Galaxy - library 1347 articles

You are an administrative member of this group.
Invite [other CiteULike users](#) to join, or invite [people who don't use CiteULike yet](#).

Search Unwatch Copy Export Sort Hide Details

- Oqtans: The RNA-seq Workbench in the Cloud for Complete and Reproducible Quantitative Transcriptome Analysis**
Bioinformatics (11 January 2014), doi:10.1093/bioinformatics/btt731
by [Vipin T. Sreedharan](#), [Sebastian J. Schultheiss](#), [Géraldine Jean](#), et al.
posted to [cloud](#) [isgalaxy](#) [shared](#) by [galaxyproject](#) to the group [Galaxy](#) keyed Sreedharan2014Oqtans on 2014-01-12 17:41:09 ★★★★★
Abstract Copy My Copy
- Similar recombination-activating gene (RAG) mutations result in similar immunobiological effects but in different contexts**
Journal of Allergy and Clinical Immunology (January 2014), doi:10.1016/j.jaci.2013.11.028
by [Hanna IJspeert](#), [Gertjan J. Driessen](#), [Michael J. Moorhouse](#), et al.
posted to [methods](#) by [galaxyproject](#) to the group [Galaxy](#) keyed IJspeert2014Similar on 2014-01-11 15:34:30 ★★/
Copy My Copy
- The Demethylase JMJD2C Localizes to H3K4me3 Positive Transcription Start Sites and Is Dispensable for Embryonic Development**
Molecular and Cellular Biology (6 January 2014), doi:10.1128/mcb.00864-13
by [Marianne T. Pedersen](#), [Karl Agger](#), [Anne Laugesen](#), et al.
posted to [methods](#) by [galaxyproject](#) to the group [Galaxy](#) keyed Pedersen2014Demethylase on 2014-01-11 03:54:51 ★★/
Abstract Copy My Copy
- D-Tailor: automated analysis and design of DNA sequences**
Bioinformatics (6 January 2014), doi:10.1093/bioinformatics/btt742
by [Joao C. Guimaraes](#), [Miguel Rocha](#), [Adam P. Arkin](#), [Guillaume Cambray](#)
posted to [workbench](#) by [galaxyproject](#) to the group [Galaxy](#) keyed Guimaraes2014DTailor on 2014-01-11 03:06:40 ★★/
Abstract Copy My Copy
- PAR-CLIP data indicate that Nrd1-Nab3-dependent transcription termination regulates expression of hundreds of protein coding genes in yeast**
Genome Biology, Vol. 15, No. 1. (07 January 2014), R8, doi:10.1186/gb-2014-15-1-r8
by [Shaun Webb](#), [Ralph Hector](#), [Grzegorz Kudla](#), [Sander Granneman](#)
posted to [tools](#) by [galaxyproject](#) to the group [Galaxy](#) keyed Webb2014PARCLIP on 2014-01-11 03:03:36 ★★/ [along with 1 person](#)

Group Tags
All tags in the group Galaxy
Filter:
[\[Display as List\]](#)

cloud howto isgalaxy
methods
other project republic
reproducibility shared tools
unknown usecloud uselocal
usemain usepublic
visualization
workbench

Over
1300
papers

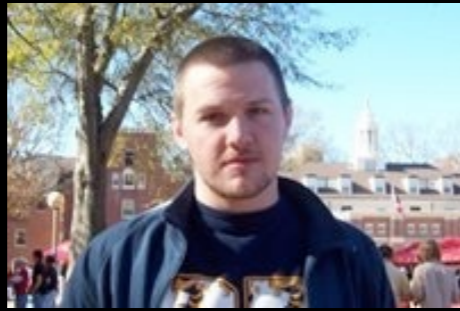
17
different
tags

<http://bit.ly/gxycul>

The Galaxy Team



Enis Afgan



Dannon Baker



Dan Blankenberg



Dave Bouvier



Marten Cech



Dave Clements



Nate Coraor



Carl Eberhard



Dorine Francheteau



Jeremy Goecks



Sam Guerler



Jen Jackson



Greg von Kuster



Ross Lazarus



Nick Stoler



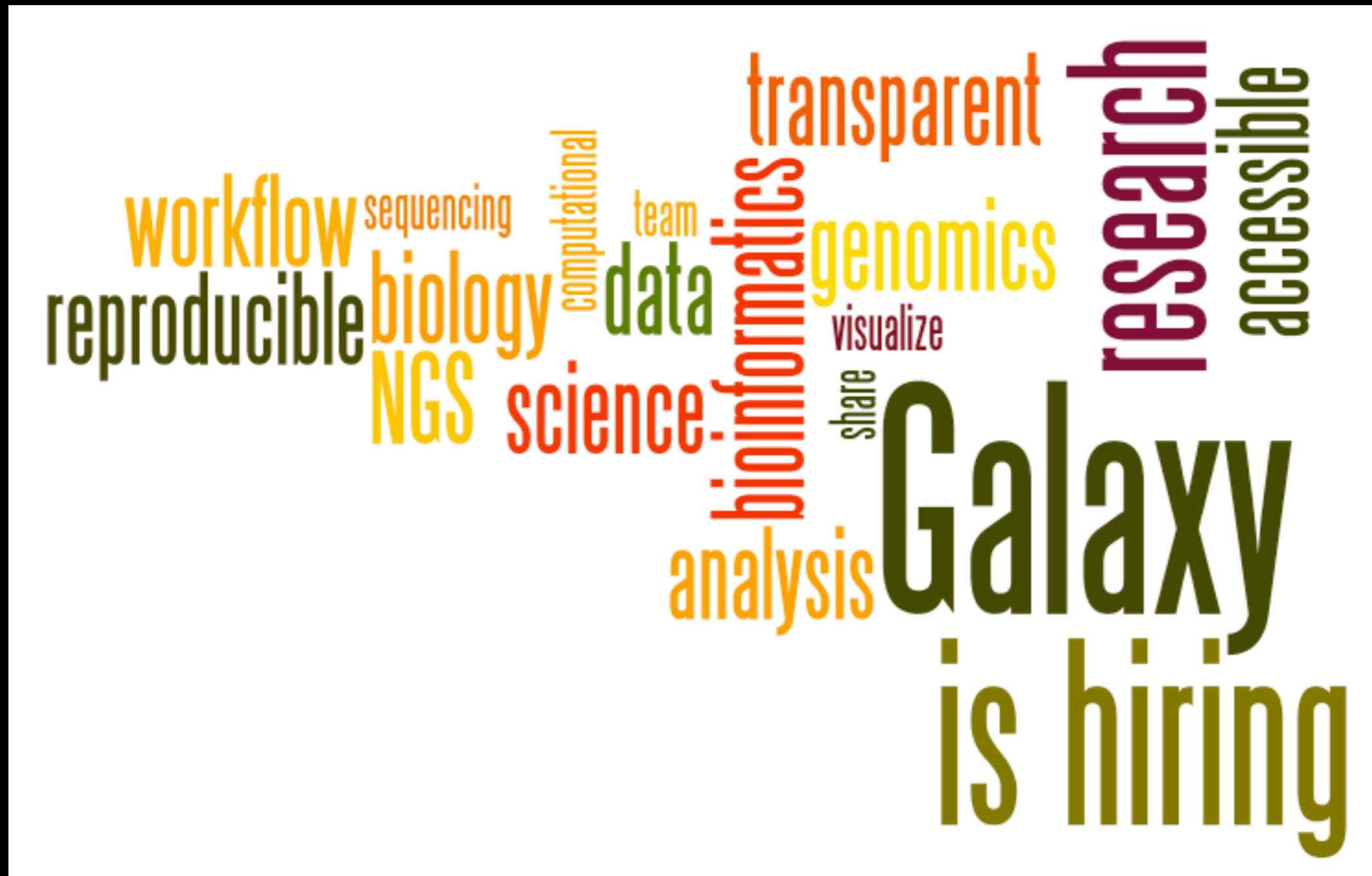
Anton Nekrutenko

James Taylor



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

Galaxy is hiring post-docs and software engineers



Please help.

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

Thanks



Dave Clements

Galaxy Project

Johns Hopkins University

clements@galaxyproject.org