

Introduction to Galaxy

The Genome Analysis Centre (TGAC)

Norwich, UK

11 April 2013

Dave Clements, Emory University

<http://galaxyproject.org/>



Agenda

- 9:00 **Welcome**
- 9:20 Basic Analysis with Galaxy
- 10:20 Basic Analysis into Reusable Workflows
- 10:40 Break
- 11:00 RNA-Seq Example Part I
- 12:00 Galaxy Project Overview
- 12:20 Lunch
- 13:05 RNA-Seq Example Part II
 - Cufflinks, Visualization and Visual Analytics
- 13:55 Sharing, Publishing and Reproducibility
- 14:15 Break
- 14:35 Setting up your own Galaxy Cluster on AWS
- 16:30 Done

Introductions

In 60 seconds or less tell us

- your name
- your affiliation(s)
- something about your research
- something about what you want to learn

Goals

1. Introduce Galaxy
2. Introduce bioinformatics concepts and formats
3. Hands-on experience
 - Load and integrate data
 - Perform bioinformatic analysis with Galaxy
 - Save, share describe and publish your analyses
 - Visualize your results
 - Set up your own Galaxy server in the cloud

This workshop will not cover details of how tools are implemented, or new algorithm designs, or which assembler or mapper or ... is best for you.

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Basic Analysis

On human chromosome 22,
which coding exons have the most
repeats in them?

<http://bit.ly/gxytgac1>

<http://bit.ly/gxytgac2>

(~ <http://usegalaxy.org/galaxy101>)

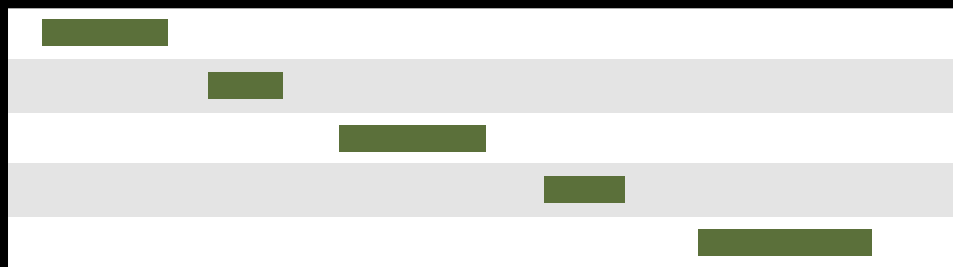
Exons & Repeats: A General Plan

- Get some data
 - Coding exons on chromosome 22
 - Repeats on chromosome 22
- Mess with it
 - Identify which exons have repeats
 - Count repeats per exon
 - Save, download, ... exons with most repeats

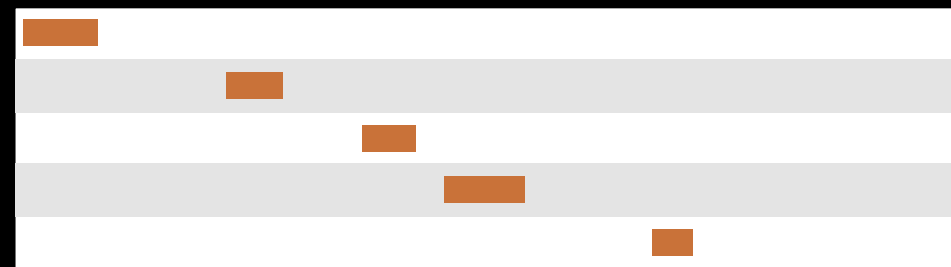
<http://bit.ly/gxytgac1>

<http://bit.ly/gxytgac2>

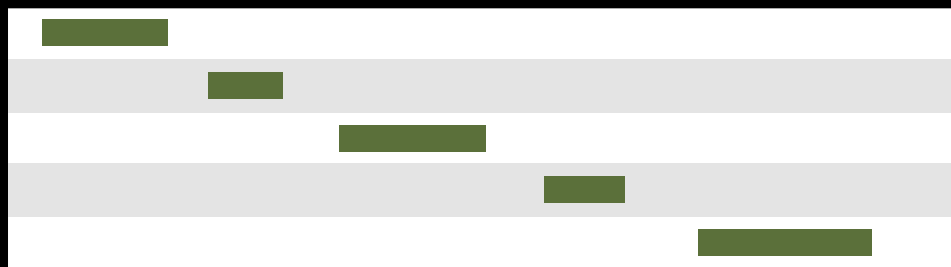
(~ <http://usegalaxy.org/galaxy101>)



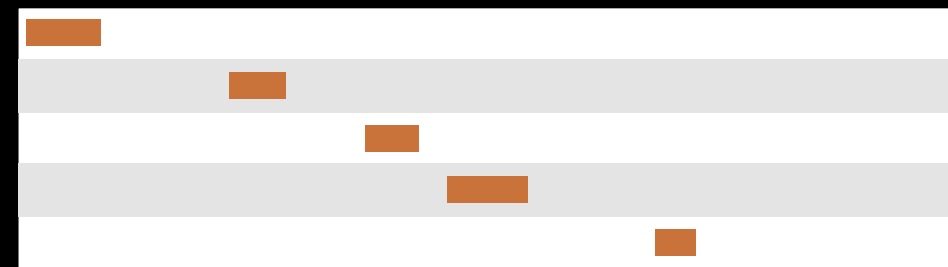
Exons, from UCSC



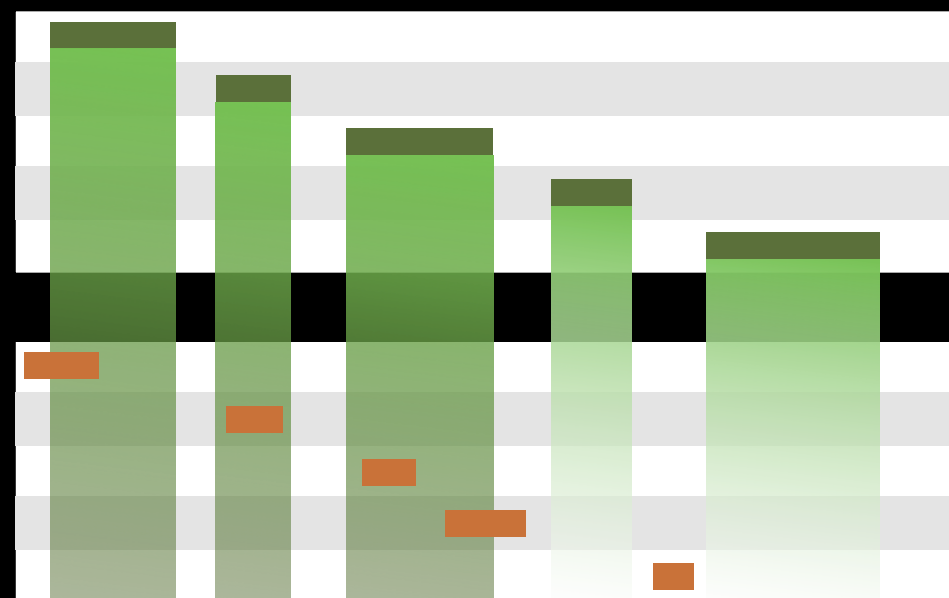
Repeats, from UCSC



Exons, from UCSC



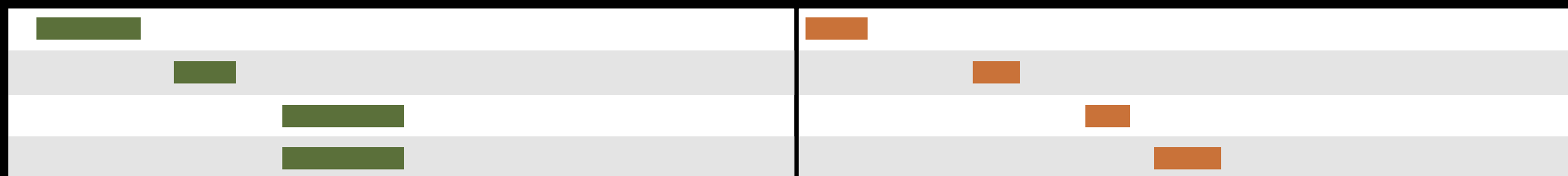
Repeats, from UCSC

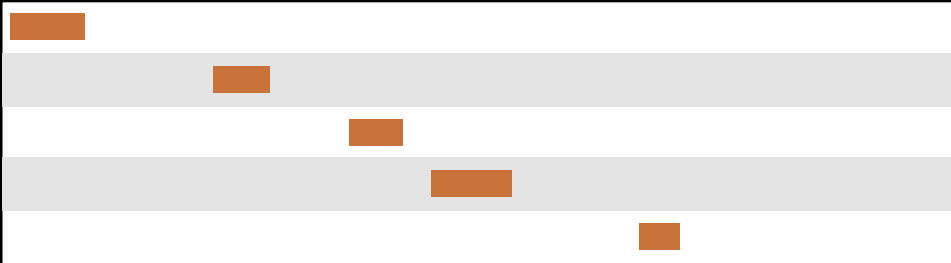
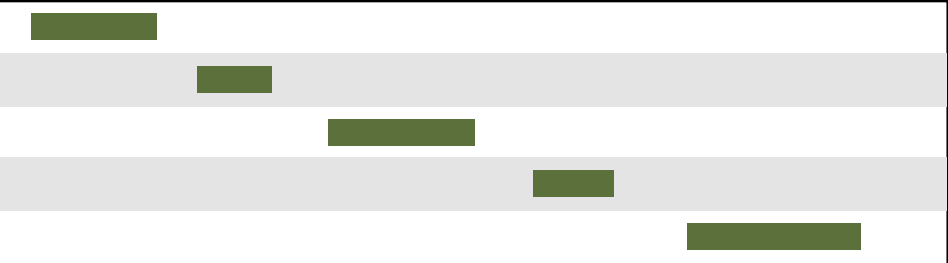


Exons, from UCSC

Repeats, from UCSC

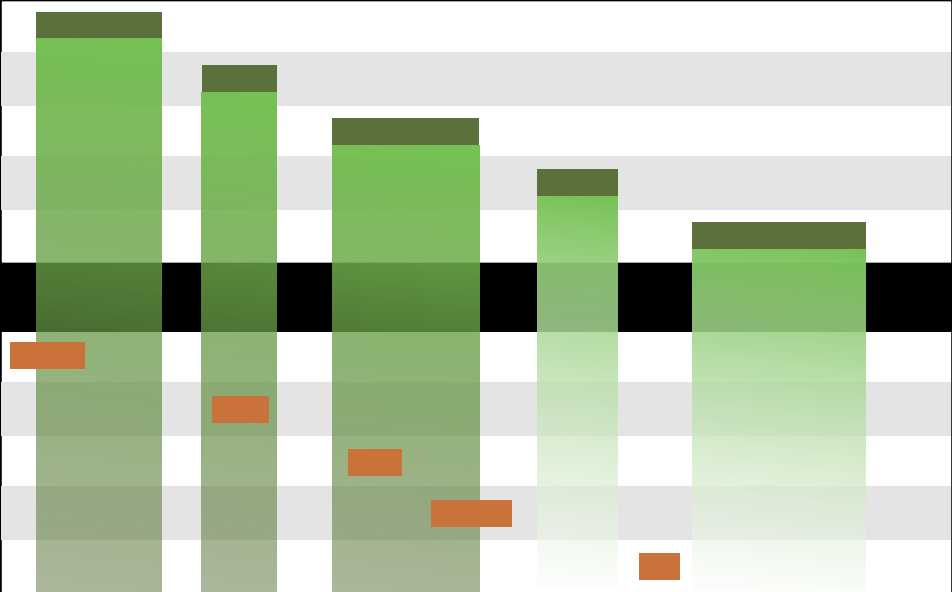
Overlap pairings





Exons, from UCSC

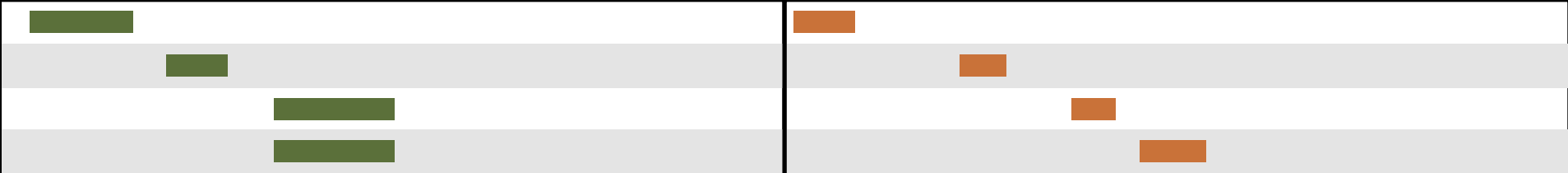
Repeats, from UCSC



Exons, from UCSC

Repeats, from UCSC

Overlap pairings

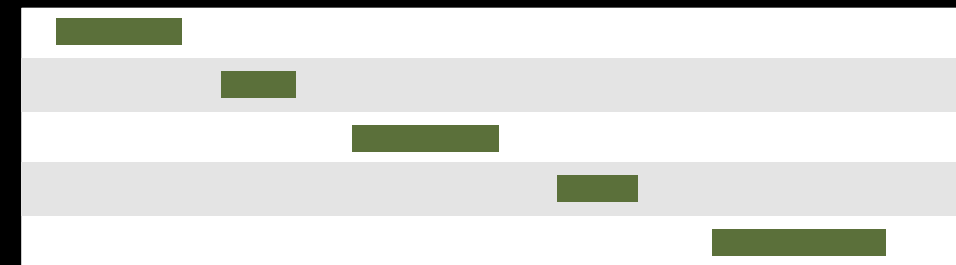


	1
	1
	2

Exon overlap counts



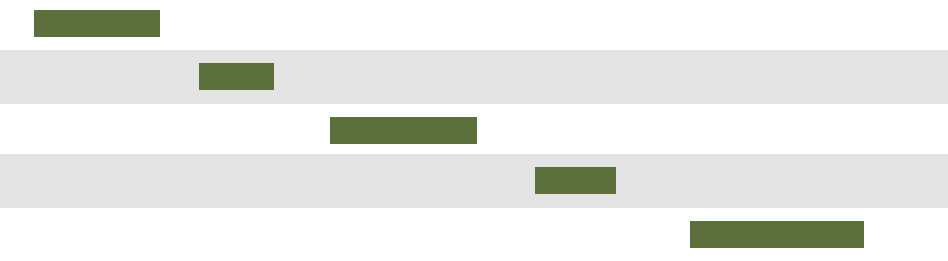
Exon overlap counts



Exons, from UCSC

	1
	1
	2

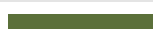
Exon overlap counts



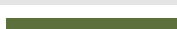
Exons, from UCSC

	1		0
	1		0
	2		0

Join on exon name

	1
	1
	2

Exon overlap counts

Exons, from UCSC

	1		0
	1		0
	2		0

Join on exon name

	1
	1
	2

Rearrange columns w/
cut

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Some Galaxy Terminology

Dataset:

Any input, output or intermediate set of data + metadata

History:

A series of inputs, analysis steps, intermediate datasets, and outputs

Workflow:

A series of analysis steps

Can be repeated with different data

Exons and Repeats *History* → Reusable *Workflow*?

- The analysis we just finished was about
 - Human chromosome 22
 - Overlap between exons and repeats
- But, ...
 - there is **nothing inherently** in the analysis **about humans, chromosomes, exons or repeats**
 - It is a series of steps that **sets the score of one set of features to the number of overlaps from another set of features.**

Create a generic *Overlap* Workflow

Extract Workflow from history

Create a workflow from this history.
Edit it to make some things clearer.

Run / test it

Guided: rerun with same inputs

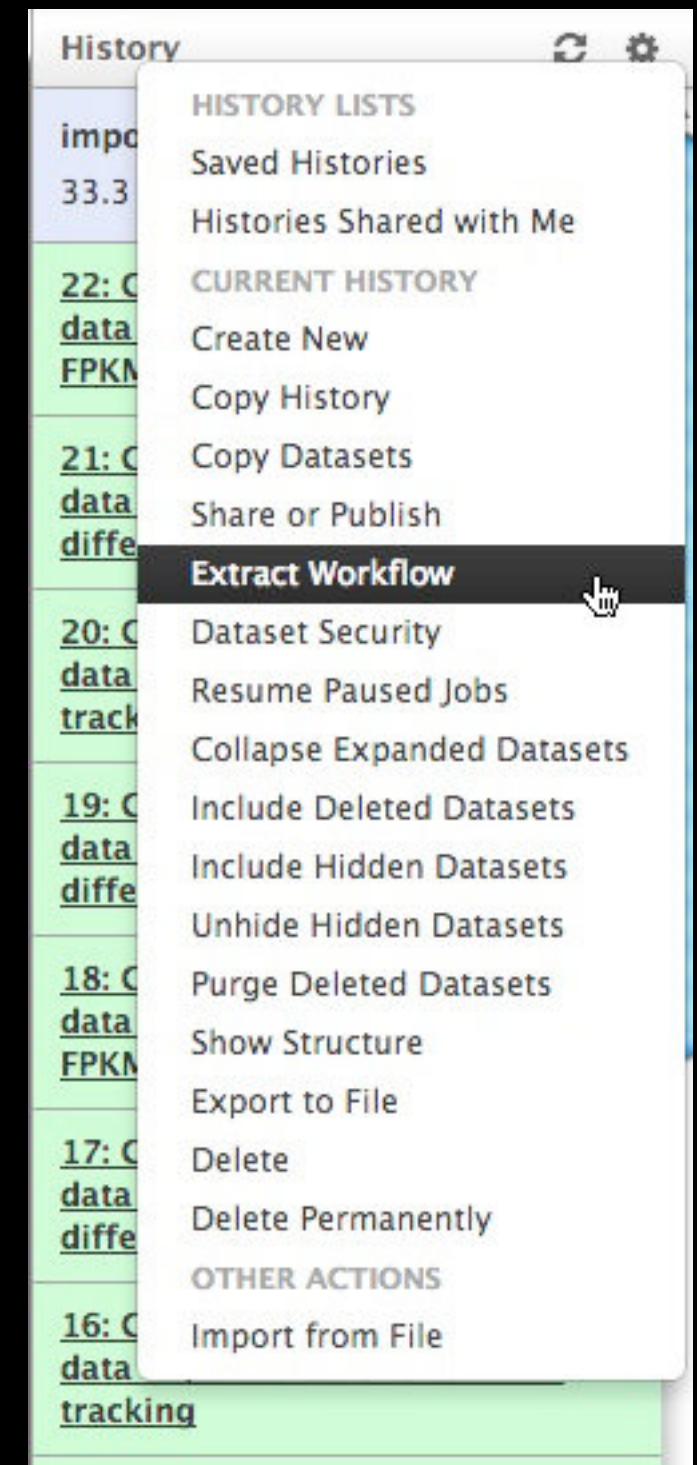
On your own:

Count # CpG islands in each exon
Did that work?

On your own:

Count # of exons in each repeat
Did that work? *Why not?*

Edit workflow: doc assumptions



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RNA-seq Exercise

<http://usegalaxy.org/u/jeremy/p/galaxy-rna-seq-analysis-exercise>

<http://bit.ly/GxyRNASeqEx>

<http://bit.ly/gxytgac1>

<http://bit.ly/gxytgac2>

RNA-seq Exercise: A Plan

- Get input datasets; hg19, will mostly map to chr19
- Look at quality
- Trim as we see fit.
- Map the reads to the human reference using Tophat
- Run Cufflinks on Tophat output to assemble reads into transcripts
- Visualize it

<http://bit.ly/GxyRNASeqEx>

RNA-seq Exercise: A Plan

- Get input datasets; hg19, will mostly map to chr19
- All datasets are FASTQ and from the Body Map 2.0 project

<http://bit.ly/GxyRNASeqEx>

What is FASTQ?

- Specifies sequence (FASTA) and quality scores (PHRED)
- Text format, 4 lines per entry

```
@SEQ_ID
GATTTGGGGTTCAAAGCAGTATCGATCAAATAGTAAATCCATTTGTTCAACTCACAGTTT
+
! ' ' * ( ( ( ( * * * + ) ) % % % + + ) ( % % % % ) . 1 * * * - + * ' ' ) ) * * 55CCF>>>>>CCCCCCC65
```

- FASTQ is such a cool standard, there are 3 (or 5) of them!

[illegible]

http://en.wikipedia.org/wiki/FASTQ_format

RNA-seq Exercise: A Plan

- Get input datasets; hg19, will mostly map to chr19
- Look at quality: Option 1
 - NGS QC and Manipulation → **Compute Quality Statistics**
 - NGS QC and Manipulation → **Draw quality score boxplot**
 - Gives you no control over how it is calculated or presented.

<http://bit.ly/GxyRNASeqEx>

RNA-seq Exercise: A Plan

- Get input datasets; hg19, will mostly map to chr19
- Look at quality: Option 2
 - NGS QC and Manipulation → **FastQ Summary Statistics**
 - Graph / Display Data → **Boxplot of quality statistics**
 - Gives you a lot of control over what the box plot looks like, but no additional information

<http://bit.ly/GxyRNASeqEx>

RNA-seq Exercise: A Plan

- Get input datasets; hg19, will mostly map to chr19
- Look at quality: Option 3
 - NGS QC and Manipulation → **Fastqc**
 - Gives you a lot a lot more information but little control over how it is calculated or presented.

<http://bit.ly/GxyRNASeqEx>

RNA-seq Exercise: A Plan

- Get input datasets; hg19, will mostly map to chr19
- Look at quality
- Trim as we see fit: Option 1
 - **NGS QC and Manipulation** → **FASTQ Trimmer by column**
 - Trim same number of columns from every record
 - Can specify different trim for 5' and 3' ends

<http://bit.ly/GxyRNASeqEx>

RNA-seq Exercise: A Plan

- Get input datasets; hg19, will mostly map to chr19
- Look at quality
- ~~Trim~~ Filter as we see fit: Option 2
 - NGS QC and Manipulation → **Filter FASTQ reads by quality score and length**
 - **Keep or discard whole reads at a time**
 - Can have different thresholds for different regions of the reads.
 - **Keeps original read length.**

<http://bit.ly/GxyRNASeqEx>

RNA-seq Exercise: A Plan

- Get input datasets; hg19, will mostly map to chr19
- Look at quality
- Trim as we see fit: Option 3
 - NGS QC and Manipulation → **FASTQ Quality Trimmer by sliding window**
 - Trim from both ends, using sliding windows, until you hit a high-quality section.
 - **Produces variable length reads**

<http://bit.ly/GxyRNASeqEx>

RNA-seq Exercise: A Plan

- Get input datasets; hg19, will mostly map to chr19
- Look at quality
- Trim as we see fit.
- Map the reads to the human reference using Tophat
- *Imagine pages and pages of discussion on the intricacies and pitfalls of RNA-seq mapping here.*

<http://bit.ly/GxyRNASeqEx>

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What is Galaxy?

- **A free (for everyone) web service** integrating a wealth of tools, compute resources, terabytes of reference data and permanent storage
- **Open source software** that makes integrating your own tools and data and customizing for your own site simple
- These options result in several **ways to use Galaxy**

<http://galaxyproject.org>

Galaxy is available ...

- As a free (for everyone) web service

<http://usegalaxy.org>

However, *a centralized solution cannot scale to meet the analysis needs of the entire world.*

Galaxy is available ...

- As a free (for everyone) web service

<http://usegalaxy.org>

- As open source software

<http://getgalaxy.org>

As Open Source Software: Local Galaxy Instances

- Galaxy is designed for local installation and customization
- Easily integrate new tools
- Easy to deploy and manage on nearly any (unix) system
- Run jobs on existing compute clusters
- Requires a computational resource on which to be deployed

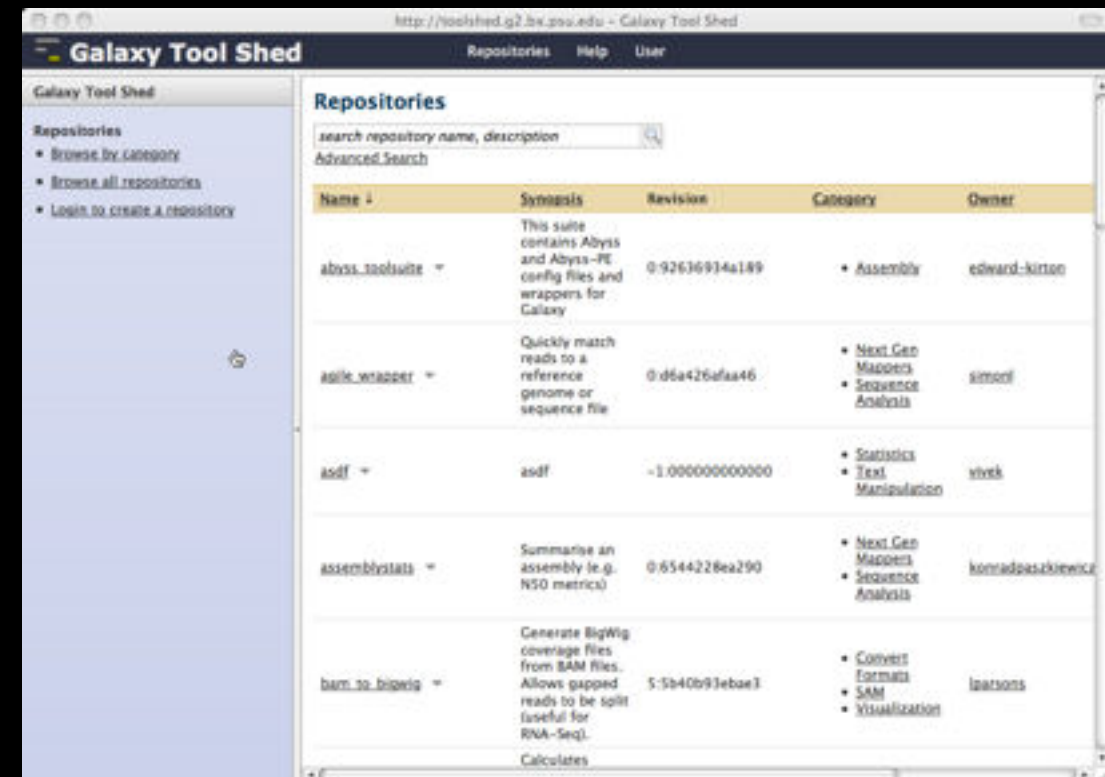
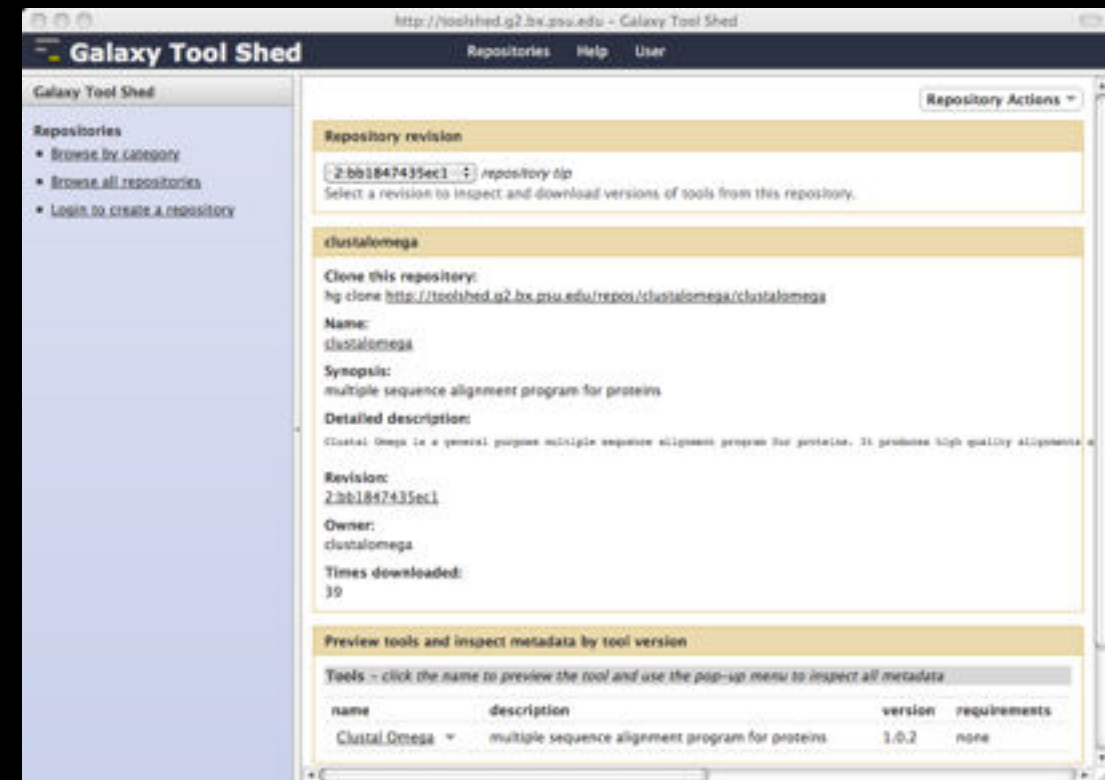
<http://getgalaxy.org>

Encourage **Local** Galaxy Instances

- Encourage and support Local Galaxy Instances
- Support **increasingly decentralized model** and improve access to existing resources
- Focus on building **infrastructure to enable the community to integrate and share** tools, workflows, and best practices

Galaxy Tool Shed

<http://toolshed.g2.bx.psu.edu>



Encourage **Public** Galaxy Instances

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

Interested in:

Plus many more

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

As Open Source Software: Local Galaxy Instances

- Galaxy is designed for local installation and customization
- Easily integrate new tools
- Easy to deploy and manage on nearly any (unix) system
- Run jobs on existing compute clusters
- Requires a **computational resource** on which to be deployed

<http://getgalaxy.org>

Got your own cluster?

- Galaxy **works with any DRMAA** compliant cluster job scheduler (which is most of them).
- Galaxy is **just another client** to your scheduler.



Galaxy is available ...

- As a free (for everyone) web service

<http://usegalaxy.org>

- As open source software

<http://getgalaxy.org>



- *On the Cloud*

<http://usegalaxy.org/cloud>

We are using this right now, and you will set up your own instance today

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

Galaxy Resources and Community

Mailing Lists (very active)

Unified Search

Issues Board

Events Calendar, News Feed

Community Wiki

GalaxyAdmins

Screencasts

Tool Shed

Public Installs

CiteULike group, Mendeley mirror

Annual Community Meeting

<http://wiki.galaxyproject.org>

Galaxy Resources and Community: Mailing Lists

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

Galaxy-Announce

Project announcements, low volume, moderated

Low volume (42 posts, 1600 members in 2012)

Galaxy-User

Questions about using Galaxy and usegalaxy.org

High volume (2900 posts, 2700 members in 2012)

Galaxy-Dev

Questions about developing for and deploying Galaxy

High volume (4500 posts, 850 members in 2012)

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

 **Galaxy Web Search**



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](#)

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 shows a Trello board titled "Galaxy: Development Inbox" with a "Public" status. The board is organized into four main columns: "Inbox", "Developer ideas", "Bug Reports", and "Issues from Bitbucket".

- Inbox:** Contains cards for adding cards, filtering and sorting, uploaded fastq file datatype, reference genome request, and feature request to manually hide datasets.
- Developer ideas:** Includes cards for anonymous use of workflows, feature request to restart failed workflows, Google Drive/Dropbox/Box integration, bug report for dataset import, standalone web applications, archiving histories, and data library upload messages.
- Bug Reports:** Lists issues such as workflow step hiding, broken workflow views, job limits, FASTQ summary statistics, data column bugs, broken Velvet wrappers, and functional tests for migrated tools.
- Issues from Bitbucket:** Features numbered issues (5, 6, 8, 10, 20, 21, 24) related to automatic history creation, history naming, output handlers, parameter overriding, XML tags, DB key build ontology, and password security.

On the right side, there is a "Members" section with a grid of user avatars, an "Add Members..." button, and a "Board" section with "Options", "Add List", and "Filter Cards" buttons. Below these is an "Activity" feed showing recent actions like "Dannon Baker added API: Library Contents" and "g2roboto" adding feature requests.

<http://bit.ly/gxyissues>

http://wiki.galaxyproject.org

Galaxy Wiki

DaveClements Settings Logout | Search:

Titles Text

FrontPage

Edit 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](#)



Community & Project

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

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

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.
- **Everyone:** [Get Involved!](#)



Topic voting now open!



Use Galaxy

[Project Server](#) (*Use it!*)
[Other Servers](#) • [Learn](#)
[Share](#) • [Search](#)

Communication

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

Deploy Galaxy

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

Contribute

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

Galaxy Project

[Home](#) • [About](#)
[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 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.

Upcoming Events



Date	Topic/Event	Venue/Location
February 4	Introduction to Galaxy Boot Camp	UC Davis Bioinformatics Core Davis, California, United States
March 2-5	Accessible, Transparent and Reproducible Analysis With Galaxy, part of SW1: Application of NGS Platforms for Whole Transcriptome and Genome Analysis Galaxy for Core Facilities, part of "W6: Community Resource Solutions to Analyzing Large Genomic Data Sets"	ABRF 2013 Palm Springs, California, United States
March 26-28	RNA Technologies and Analysis Workshop	DOE JGI User Meeting
April 5-6	2013 GMOD Meeting	Cambridge, United Kingdom, immediately prior to Biocuration 2013
April 7-10	GO Galaxy Workshop	Biocuration 2013, Cambridge, United Kingdom
April 9-11	Workshop: Integrated Research Data Management for Next Gen Sequencing Analysis Using Galaxy and Globus Online Software-as-a-Service Talk: Integrated Research Data management and Analysis in NGS using Globus Online, Galaxy and Amazon Web Services	BioIT World, Boston, Massachusetts, United States
May 14-16	Tutorial: Exploring and Enabling Biomedical Data Analysis with Galaxy	Great Lakes Bioinformatics Conference (GLBIO) 2013, Pittsburgh, Pennsylvania, United States
May 21 May 29	Initiation à l'utilisation de Galaxy Les deux ateliers sont maintenant complets	Cycle "Bioinformatique par la pratique" 2013, INRA Jouy-en-Josas, France
May 22 May 30	Analyse de données issues de séquenceurs nouvelle génération sous Galaxy Les deux ateliers sont maintenant complets	
June 6-7	Informatics on High Throughput Sequencing Data Workshop	Toronto, Ontario, Canada

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

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

News Items

February 2013 Galaxy Update

The February 2013 Galaxy Update is now available.

Highlights:

- Three new public Galaxy servers
- New papers
- Open Positions at five different institutions
- GCC2013 Training Day Topic voting, Registration, and Sponsorships
- January GalaxyAdmins Web Meetup slides and screencast
- Other Upcoming Events and Deadlines
- Galaxy Distributions
- Tool Shed Contributions
- Other News

If you have anything you would like to see in the March *Galaxy Update*, please let us know.

Dave Clements and the Galaxy Team

Posted to the Galaxy News on 2013-02-01

GCC2013 Training Day Topics: Vote!

A list of possible topics for the GCC2013 Training Day is now available. Please take a few minutes to review these possibilities and then vote for your favorite three topics.*

Your votes will determine not only the topics that are offered, but also which topics should be offered more than once, assigned to which rooms, and which ones should not be scheduled at the same time. Your vote matters.

News Items

February 2013 Galaxy Update
GCC2013 Training Day Topics: Vote!
Galaxy Project Openings
Jan 11, 2013 Distribution & News Brief
January 2013 GalaxyAdmins
January 2013 Galaxy Update
Dec 20, 2012 Distribution & News Brief
Galaxy Internships @ EMBL
Nominate GCC2013 Training Topics
Dec 3, 2012 Distribution & News Brief
December 2012 Galaxy Update
Nov 14, 2012 Distribution & News Brief
NGS Analysis by Viz. with Trackster
November 2012 GalaxyAdmins

[News Archive](#)



galaxyproject.org/GCC2013



STARTING @ €95

galaxyproject.org/GCC2013



Talk abstracts due **12 April**



STARTING

@

€95

The Galaxy Team



Enis Afgan



Dannon Baker



Dan Blankenberg



Dave Bouvier



Dave Clements



Nate Coraor



Carl Eberhard



Dorine Francheteau



Jeremy Goecks



Sam Guerler



Jen Jackson



Greg von Kuster



Ross Lazarus



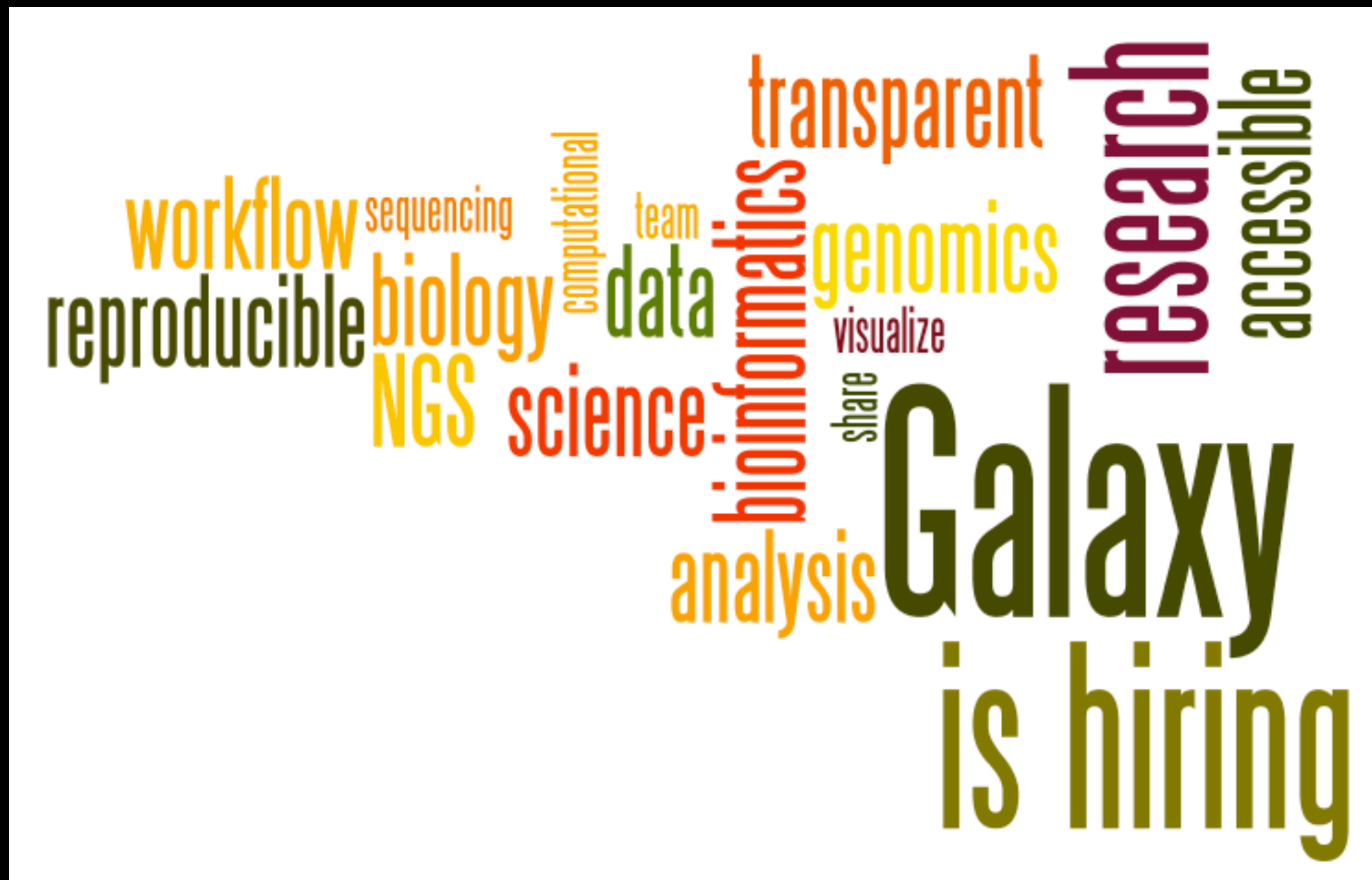
Anton Nekrutenko



James Taylor

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

Galaxy is hiring post-docs and software engineers
at both Emory and Penn State.



Please help.

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

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<http://bit.ly/GxyRNASeqEx>

RNA-seq Exercise: A Plan

- ...
- Map the reads to the human reference using Tophat
- Run Cufflinks on Tophat output to assemble reads into transcripts
- *Imagine pages and pages of discussion on the intricacies and pitfalls of RNA-seq transcript prediction here.*
- Visualize it

<http://bit.ly/GxyRNASeqEx>

Visualizing Genomics

Supported external browsers

- UCSC
- Ensembl
- GBrowse
- IGB
- IGV

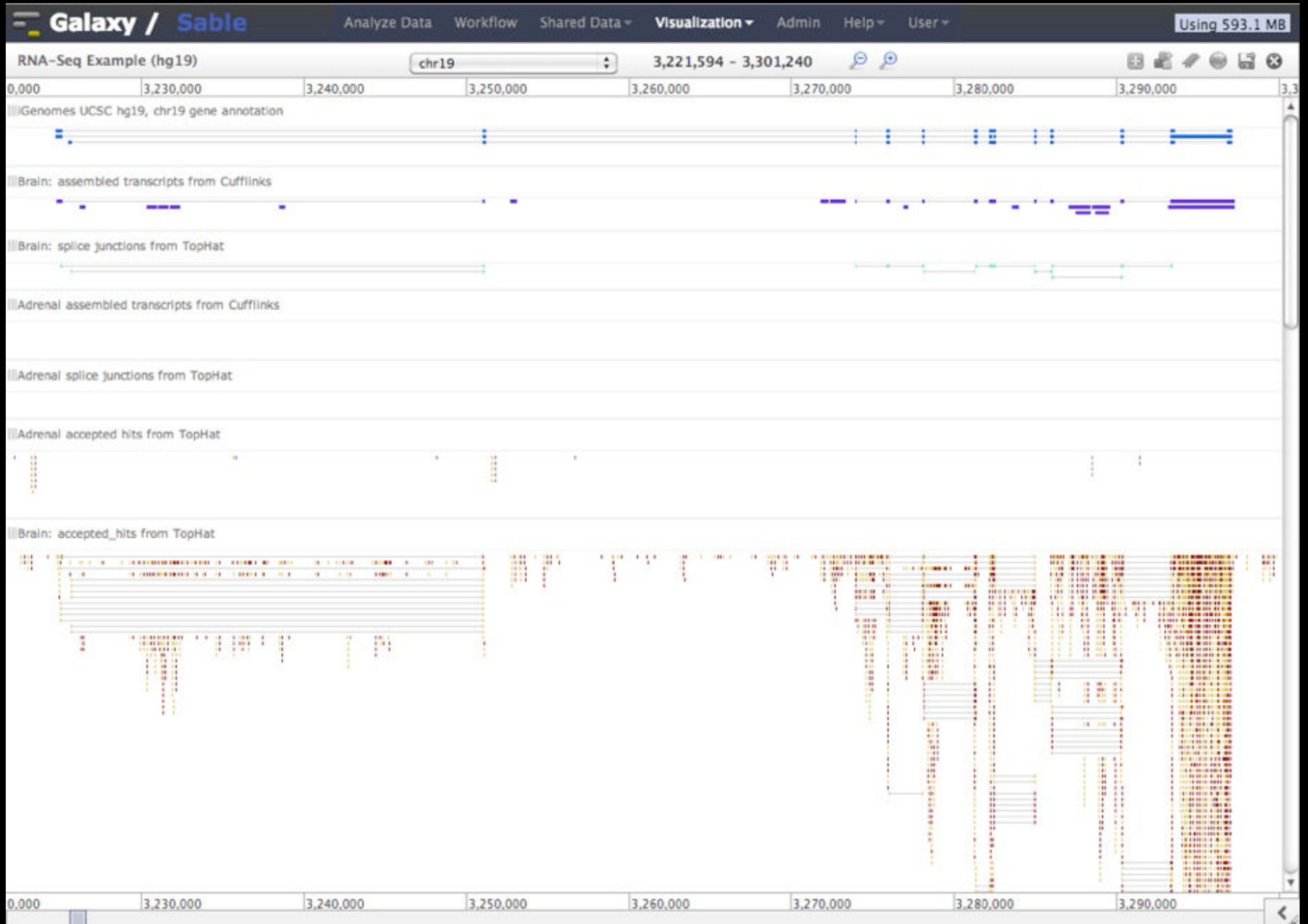
Traditional browser strengths:

- Showing what is nearby
- what else is happening here
- highlighting correlations
- integrating many datasets

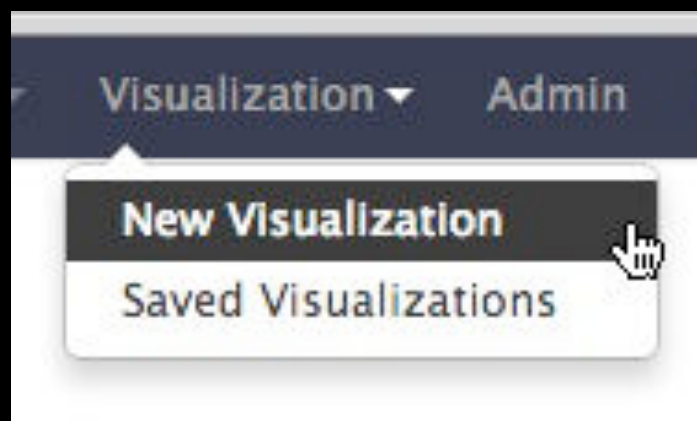
But, *wouldn't it be nice to*

- Use visualization to **evaluate and refine analyses?**
- **Expose** some **basic analyses in visualization** to make it more informative?
- Make that **analyze-visualize-refine** loop seamless and **fast?** That is, integrate the two?
- Use visualization to **learn tools and explore their parameter space?**
- Not be tied to a **predefined reference genome?**

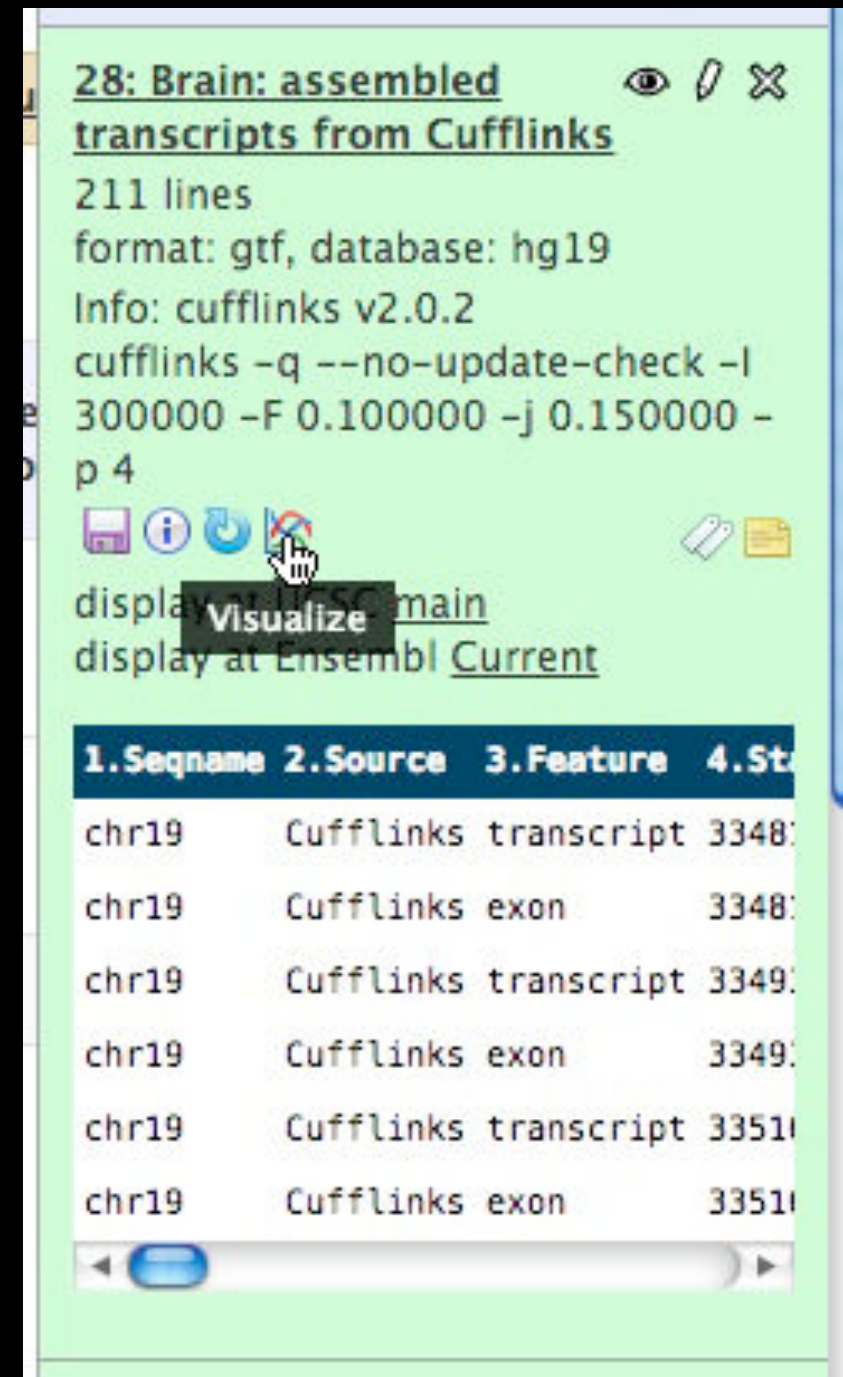
Trackster: Galaxy's embedded track browser



Create a visualization in Galaxy



or



A screenshot of a Galaxy visualization panel. The panel title is '28: Brain: assembled transcripts from Cufflinks'. It shows 211 lines of data in gtf format for the hg19 database, generated by cufflinks v2.0.2. The command used is 'cufflinks -q --no-update-check -l 300000 -F 0.100000 -j 0.150000 -p 4'. The panel includes a 'Visualize' button and a 'main' link. Below the command, there is a table with 4 columns: '1. Seqname', '2. Source', '3. Feature', and '4. Start'. The table contains 6 rows of data for chr19, showing transcripts and exons with their start positions.

1. Seqname	2. Source	3. Feature	4. Start
chr19	Cufflinks	transcript	33480
chr19	Cufflinks	exon	33480
chr19	Cufflinks	transcript	33490
chr19	Cufflinks	exon	33490
chr19	Cufflinks	transcript	33510
chr19	Cufflinks	exon	33510

Isn't it nice to

- To do all those things we talked about?
 - Use visualization to evaluate and refine analyses?
 - Expose some basic analyses in visualization to make it more informative?
 - Make that analyze-visualize-refine loop seamless and fast? That is, integrate the two?
 - Use visualization to learn tools and explore their parameter space?
 - Not be tied to a predefined reference genome?

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- 9:00 Welcome
- 9:20 Basic Analysis with Galaxy
- 10:20 Basic Analysis into Reusable Workflows
- 10:40 Break
- 11:00 RNA-Seq Example Part I
- 12:00 Galaxy Project Overview
- 12:20 Lunch
- 1:05 RNA-Seq Example Part II
 - Cufflinks, Visualization and Visual Analytics
- 1:55 **Sharing, Publishing and Reproducibility**
- 2:15 Break
- 2:35 Setting up your own Galaxy Cluster on AWS
- 4:30 Done

More Galaxy Terminology

Share:

Make something available to someone else

Publish:

Make something available to everyone

Galaxy Page:

Analysis documentation within Galaxy; easy to embed any Galaxy object

Let's all share...

Sharing & Publishing enables **Reproducibility**

Reproducibility: Everybody talks about it, but ...

Galaxy aims to push the goal of reproducibility from the bench to the bioinformatics realm

All analysis in Galaxy is recorded without any extra effort from the user.

Histories, workflows, visualizations and *pages* can be shared with others or published to the world.

Sharing & Publishing enables **Reproducibility**





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Windshield splatter analysis with the Galaxy metagenomic pipeline

Sergei Kosakovsky Pond^{1,2,6,9}, Samir Wadhawan^{3,6,7},
Francesca Chiaromonte⁴, Guruprasad Ananda^{1,3}, Wen-Yu Chung^{1,3,8},
James Taylor^{1,5,9}, Anton Nekrutenko^{1,3,9} and The Galaxy Team¹

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Footnotes

[Supplemental material is available online at <http://www.genome.org>. All data and tools described in this manuscript can be downloaded or used directly at <http://galaxyproject.org>. Exact analyses and workflows used in this paper are available at <http://usegalaxy.org/u/aun1/p/windshield-splatter>.]

Windshield splatter analysis with the Galaxy metagenomic pipeline: A live supplement

SERGEI KOSAKOVSKY POND^{1,2,*}, SAMIR WADHAWAN^{3,6*}, FRANCESCA CHIAROMONTE⁴, GURUPRASAD ANANDA^{1,3}, WEN-YU CHUNG^{1,3,7}, JAMES TAYLOR^{1,5}, ANTON NEKRUTENKO^{1,3} and THE GALAXY TEAM^{1*}

Correspondence should addressed to [SKP](#), [JT](#), or [AN](#).

How to use this document

This document is a live copy of supplementary materials for [the manuscript](#). It provides access to the **exact** analyses and workflows discussed in the paper, so you can play with them by re-running, changing parameters, or even applying them to your own data. Specifically, we provide the two histories and one workflow found below. You can view these items by clicking on their name to expand them. You can also import these items into your Galaxy workspace and start using them; click on the green plus to import an item. To import workflows you must [create a Galaxy account](#) (unless you already have one) – a hassle-free procedure where you are only asked for a username and password.

This is the Galaxy history detailing the comparison of our pipeline to MEGAN:

 **Galaxy History | Galaxy vs MEGAN**  
Comparison of Galaxy vs. MEGAN pipeline.

This is the Galaxy history showing a generic analysis of metagenomic data. (This corresponds to the "A complete metagenomic pipeline" section of the manuscript and **Figure 3A**):

 **Galaxy History | metagenomic analysis**  

This is the Galaxy workflow for generic analysis of metagenomic data. (This corresponds to the "A complete metagenomic pipeline" section of the manuscript and **Figure 3B**):

 **Galaxy Workflow | metagenomic analysis**  
Generic workflow for performing a metagenomic analysis on NGS data.

Accessing the Data

Windshield Splatter datasets analyzed in this manuscript can be accessed through this [Galaxy Library](#). From there, they can be analyzed through Galaxy using the shared workflows or downloaded.



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aun1

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Sharing for Galaxy Administrators Too

Data Libraries

Make data easy to find

Genome Builds

Care about a particular subset of life?

Galaxy Tool Shed

Wrapping tools and datatypes

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- 14:15 **Break**
- 14:35 Setting up your own Galaxy Cluster on AWS
- 16:30 Done

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AWS Credentials

<http://bit.ly/TGACAWS>

Galaxy CloudMan

<http://usegalaxy.org/cloud>

- Start with a **fully configured and populated** (tools and data) Galaxy instance.
- Allows you to scale up and down your compute assets as needed.
- Someone else manages the data center.
- **We are using this today.**



- **You will set up an instance now**

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

Instant CloudMan

The image shows two overlapping screenshots of the Galaxy web interface. The top screenshot displays the main Galaxy dashboard with a 'Cloud' menu item highlighted in the top navigation bar. A dropdown menu from 'Cloud' shows the option 'New Cloud Cluster'. The main content area features a 'Managing Data' section with the text 'Store, Manage, and Share data with Libraries' and 'An in-depth tutorial'. The left sidebar lists various data sources under 'Get Data', including 'Upload File from your computer', 'UCSC Main table browser', 'UCSC Archaea table browser', 'BX main browser', 'EBI SRA ENA SRA', 'BioMart Central server', 'GrameneMart Central server', 'Flymine server', 'modENCODE fly server', and 'modENCODE modMine server'. The bottom screenshot shows a 'Launch a Galaxy Cloud Instance' form with fields for 'Cluster Name', 'Password', 'Key ID', 'Secret Key', and 'Instance Share String (optional)'. The 'Instance Type' is set to 'Large'. A 'Submit' button is at the bottom, and a note states: 'Requesting the instance may take a moment, please be patient. Do not refresh your browser or navigate away from the page'.

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

Tools

search tools

Get Data

- [Upload File](#) from your computer
- [UCSC Main](#) table browser
- [UCSC Archaea](#) table browser
- [BX main](#) browser
- [EBI SRA](#) ENA SRA
- [BioMart](#) Central server
- [GrameneMart](#) Central server
- [Flymine](#) server
- [modENCODE fly](#) server
- [modENCODE modMine](#) server

Managing Data
Store, Manage, and Share
data with Libraries
An in-depth tutorial

0 bytes

Your history is empty. Click 'Get Data' on the left pane to start

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

Launch a Galaxy Cloud Instance

Cluster Name

Password

Key ID

Secret Key

Instance Share String (optional)

Instance Type
Large

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

Or, Step by Step

 **Galaxy Wiki**

Login | Search:

CloudMan/AWS/GettingStarted

Getting Started with Galaxy CloudMan

This page provides a step-by-step instructions on how to start your own instance of Galaxy on [Amazon Web Services \(AWS\) Elastic Compute Cloud \(EC2\)](#). More general information and instructions about Galaxy CloudMan (GC) can be found [here](#).

AWS
Get Started
Capacity Planning
AMIs
↑ CloudMan

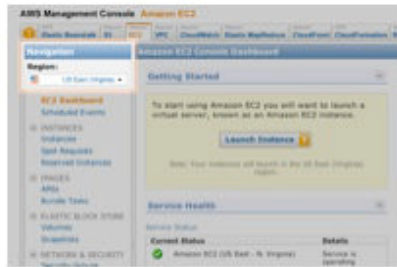
Contents

- 1. [Step 1: One Time Amazon Setup](#)
- 2. [Step 2: Starting a Master Instance](#)
- 3. [Step 3: Galaxy CloudMan Web Interface](#)
- 4. [Step 4: Use Galaxy as you normally would](#)
- 5. [Step 5: Shutting Down](#)

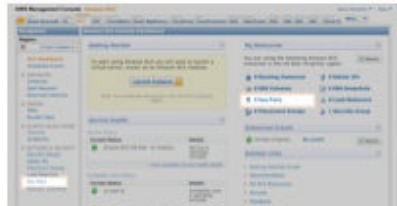
Step 1: One Time Amazon Setup

1. Because AWS services implement pay-as-you-go access model for compute resources, it is necessary for every user of the service to [register with Amazon](#). **You will need a credit card to register.** (You can apply for a [AWS Education Grant](#) after you register).
2. Once your account has been approved by Amazon (note that this may take up to one business day), [log into the EC2 AWS Management Console](#) and set your AWS Region to *US East (Virginia)*. This is the only region Galaxy CloudMan is fully supported in at this time (see [screenshot 1.2](#)).
3. Click **Network & Security** → **Key Pairs** or **My Resources** → **n Key Pairs** (see [screenshot 1.3](#) - if it does not look like this, then try using the Chrome browser) and then click **Create Key Pair**. Enter a memorable name for the key pair, e.g., *GalaxyCloud* and click **Create**.
4. *Save your private key!* The previous step creates the key pair and downloads a copy to your machine with the name *MemorableName.pem*. Save this file and protect it like you would your password. The key pair can be used to access started instances from

Step 1 Screenshots



1.2. Set region



<http://bit.ly/GXYAWSGetStarted>

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NIH NSF Huck Institute

Penn State University Emory University

Feedback Please!

<http://bit.ly/TGACfeedback>

Thanks



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<http://bit.ly/TGACfeedback>