

Introduction to Galaxy

Washington University

St. Louis, Missouri

May 1, 2013

Dave Clements, Emory University

<http://galaxyproject.org/>



Agenda

- 9:00 **Welcome**
- 9:20 Basic Analysis with Galaxy
- 10:40 Break
- 11:00 Basic Analysis into Reusable Workflows
- 11:20 RNA-Seq Example Part I
- 12:20 Lunch (on your own)
- 1:35 Galaxy Project Overview
- 1:55 RNA-Seq Example Part II
- 2:45 Break
- 3:05 Sharing, Publishing and Reproducibility
- 3:25 Setting up your own Galaxy Cluster on AWS
- 5:00 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://cloud1.galaxyproject.org/>

<http://cloud2.galaxyproject.org/>

<http://cloud3.galaxyproject.org/>

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

Exons & Repeats: A General Plan

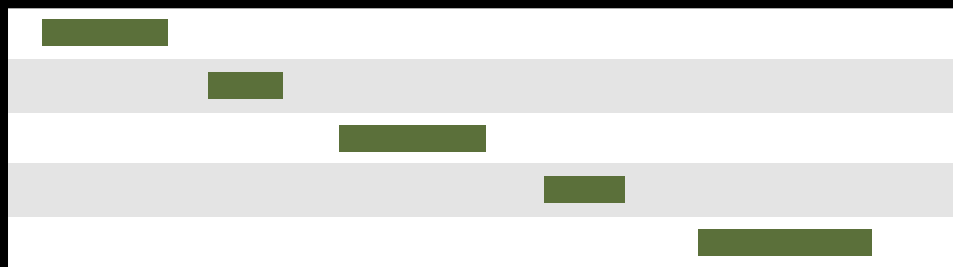
- Get some data
 - Coding exons on chromosome 22
 - Repeats on chromosome 22
- Mess with it
 - Identify which exons have repeats
 - Count repeats per exon
 - Save, download, ... exons with most repeats

<http://cloud1.galaxyproject.org/>

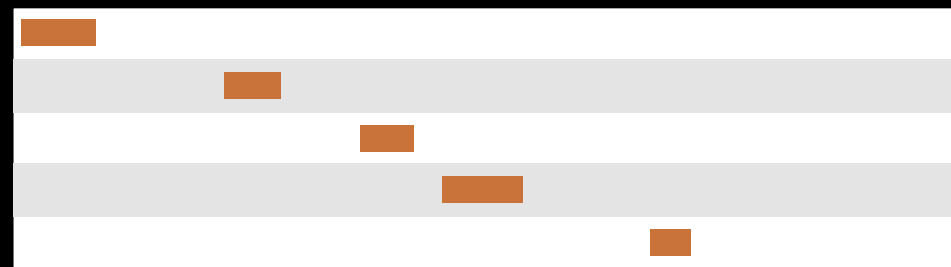
<http://cloud2.galaxyproject.org/>

<http://cloud3.galaxyproject.org/>

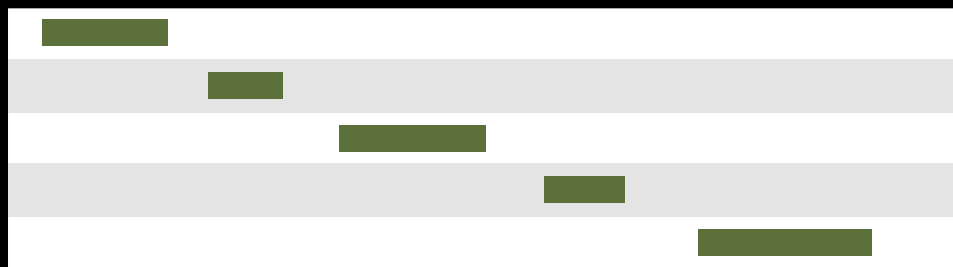
(~ <http://usegalaxy.org/galaxy101>)



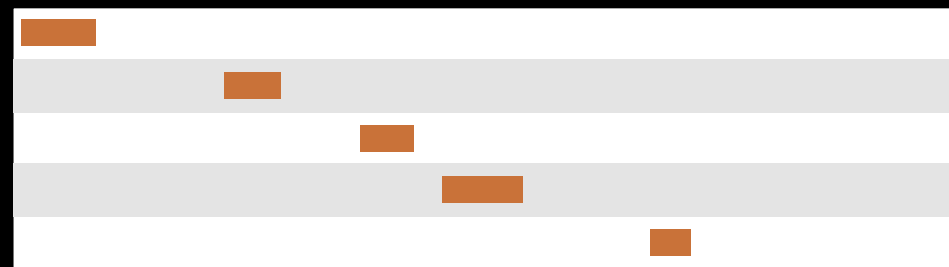
Exons, from UCSC



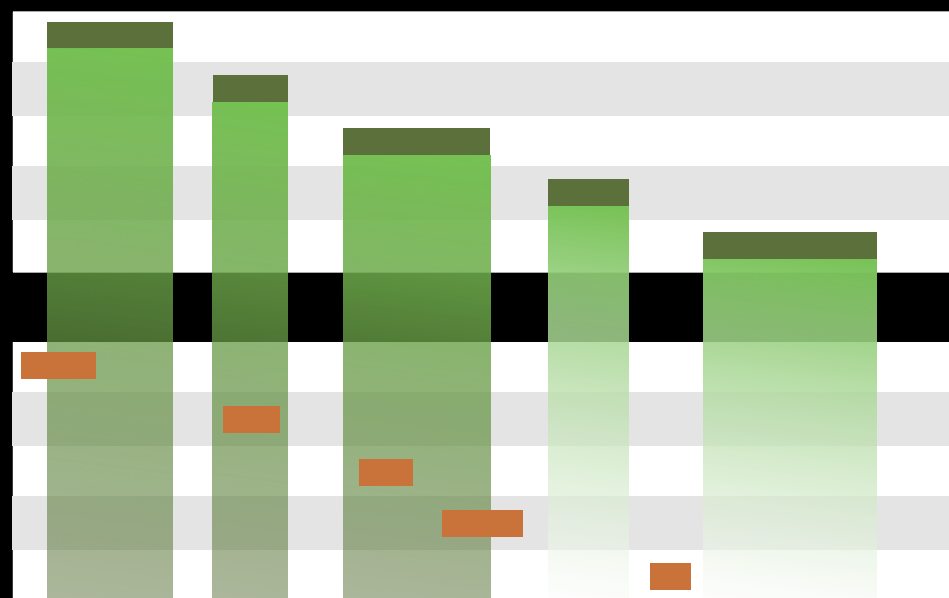
Repeats, from UCSC



Exons, from UCSC



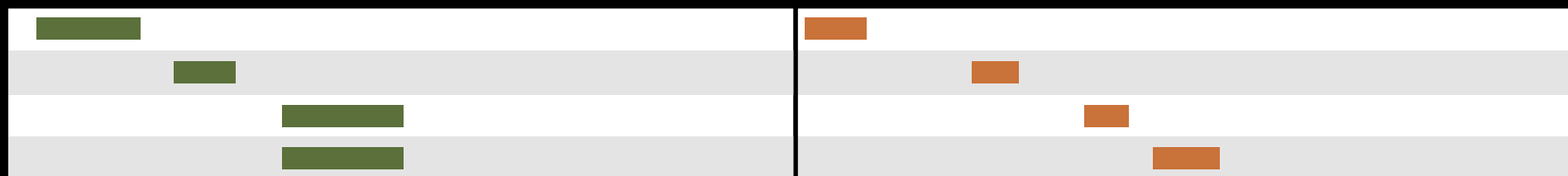
Repeats, from UCSC

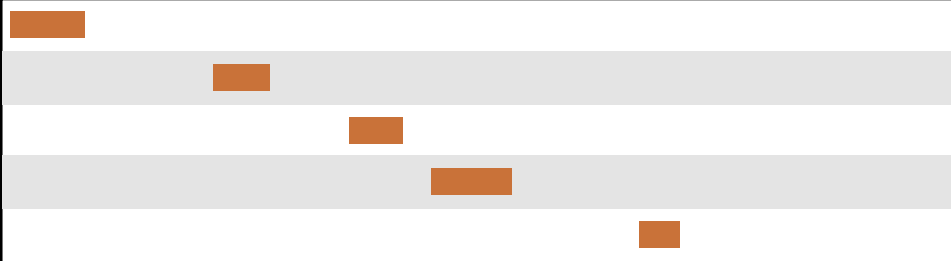
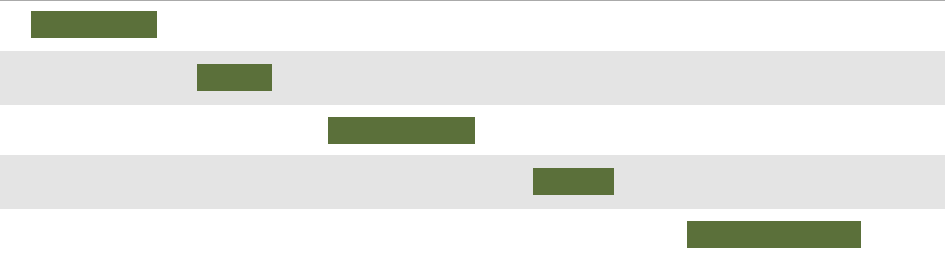


Exons, from UCSC

Repeats, from UCSC

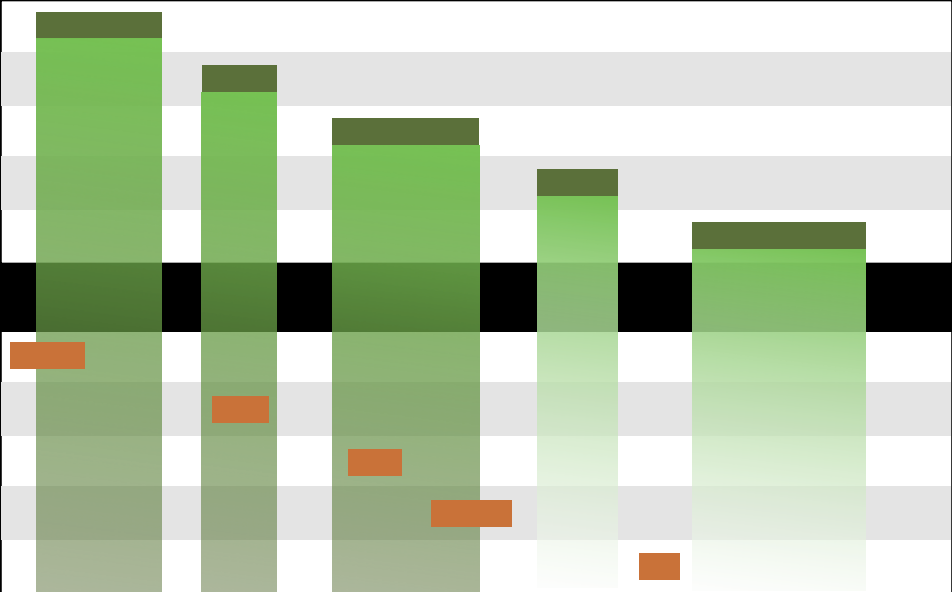
Overlap pairings





Exons, from UCSC

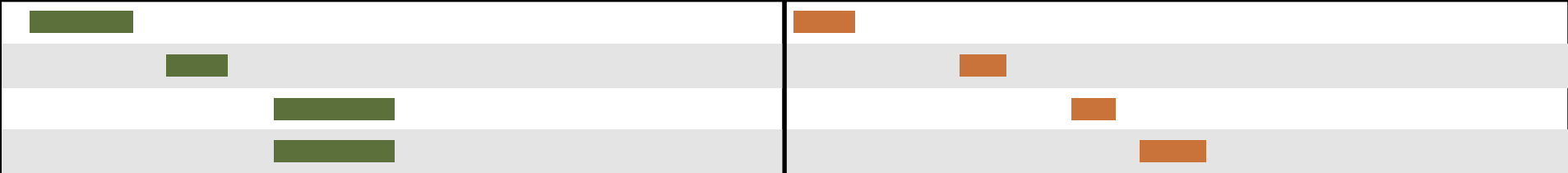
Repeats, from UCSC



Exons, from UCSC

Repeats, from UCSC

Overlap pairings

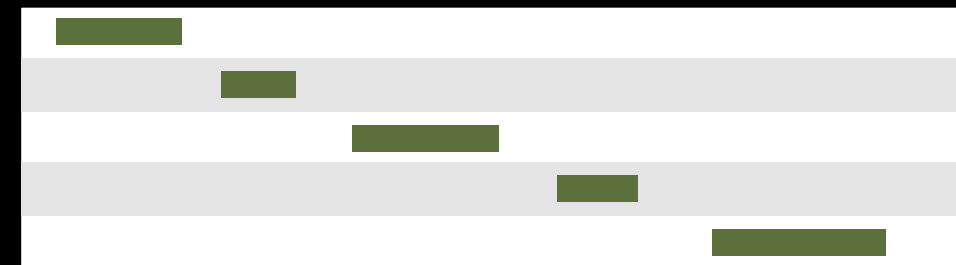


	1
	1
	2

Exon overlap counts



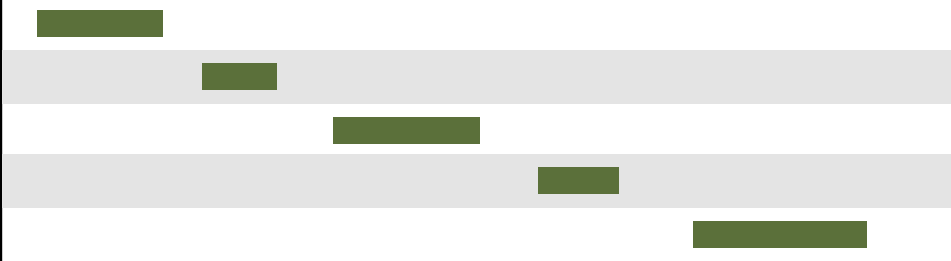
Exon overlap counts





Exons, from UCSC

	1
	1
	2

Exon overlap counts






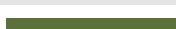
Exons, from UCSC

	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

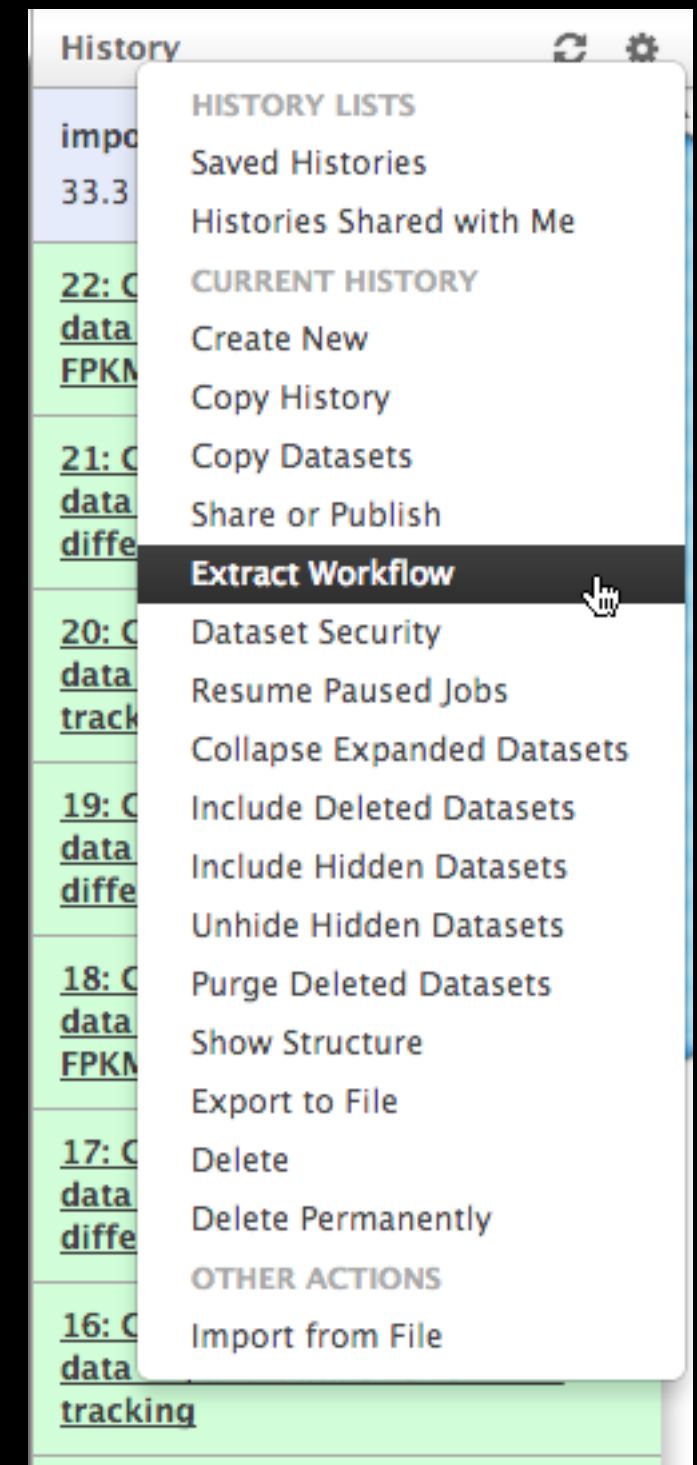
Guided: rerun with same inputs

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

Shared Data → Published Pages

→ RNA-Seq Analysis Exercise

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
- Run Cuffdiff on Tophat output to find significant differences

RNA-seq Exercise: A Plan, Except ...

- At WashU, these steps have likely already been done:
 - Trim as we see fit.
 - Map the reads to the human reference using Tophat
- So, we won't run them today, but we will explain them.

GTAC: <http://bit.ly/WashURNA>

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
- Shared Data → Published Histories → RNA-Seq with QC through Tophat

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

Look at quality Options 1 & 2:

1. NGS QC and Manipulation → Compute Quality Statistics and then Draw quality score boxplot

No control over how it is calculated or presented.

2. NGS QC and Manipulation → FastQ Summary Statistics,
Graph / Display Data → Boxplot of quality statistics

Lots of control over what the box plot looks like, info available in both graphical and text formats

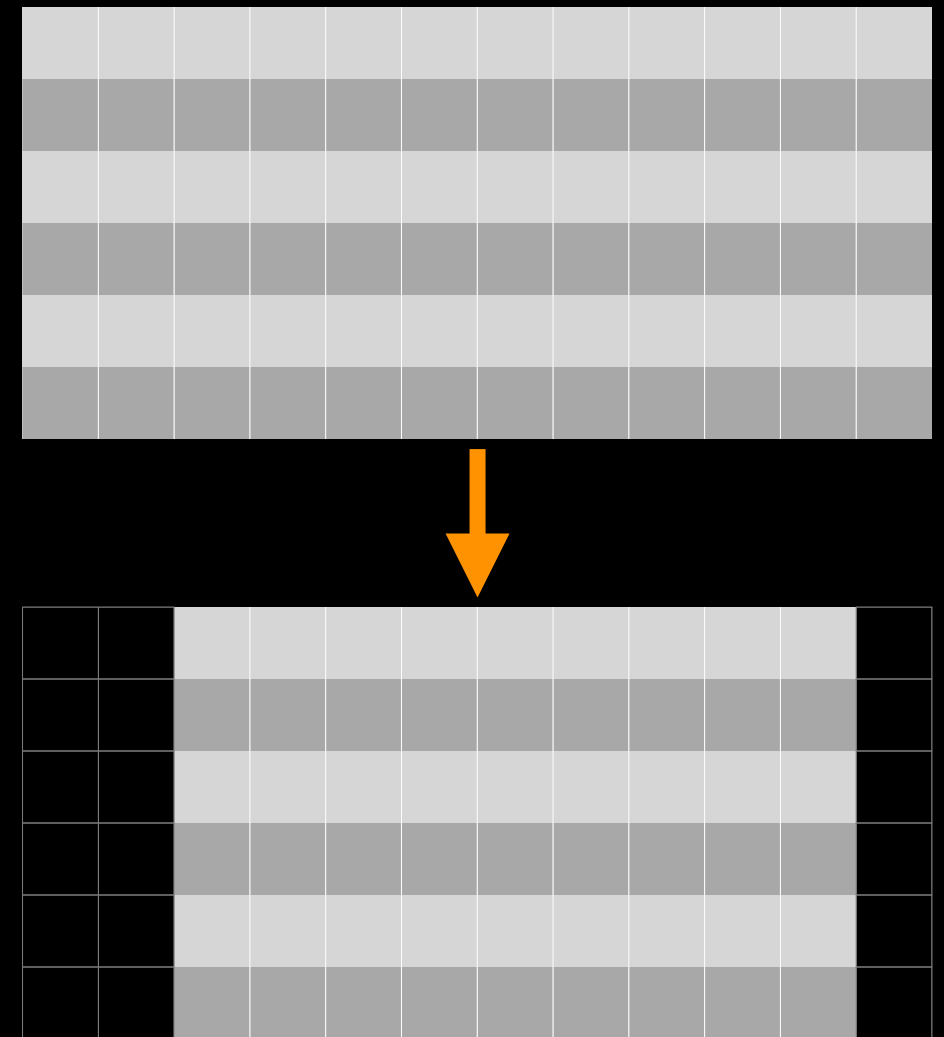
RNA-seq Exercise: A Plan

- 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.
- This is what we have done

*“For the love of all that is **holy**, please trim your reads!”*

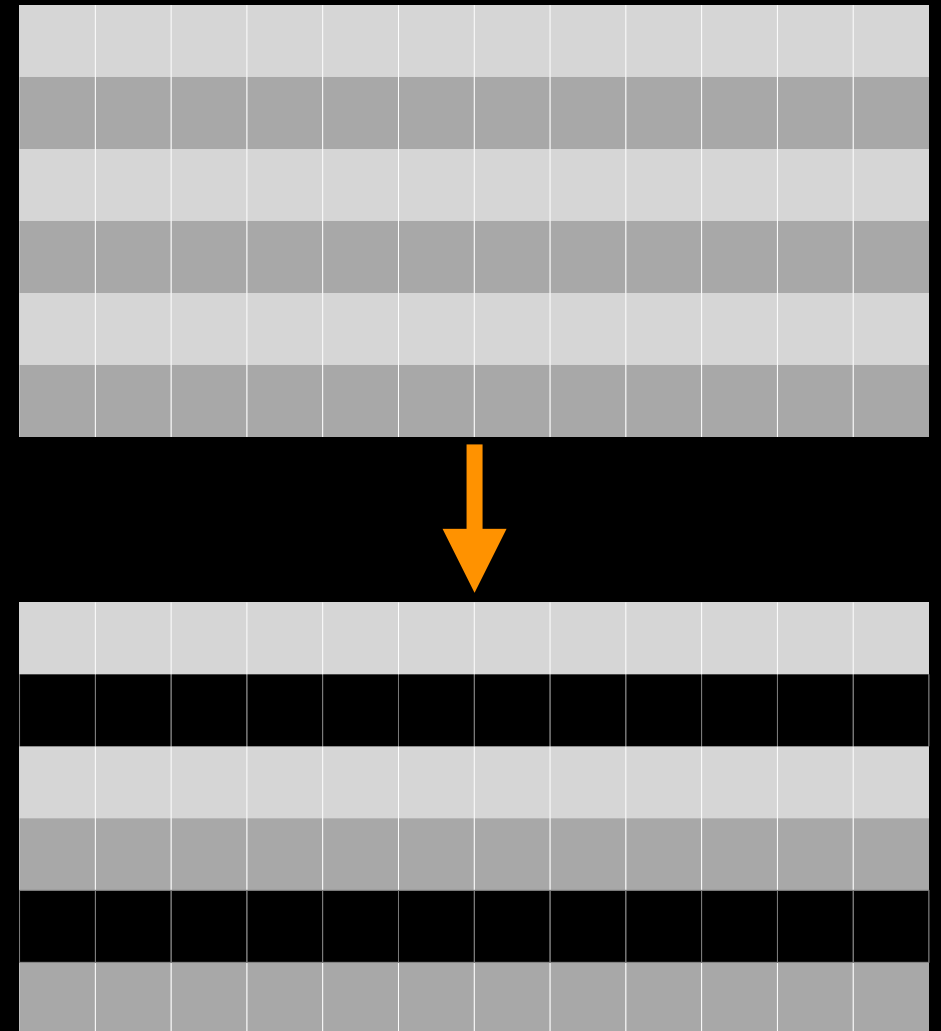
Chris Mason, ABRF NGS Study Report, March 4, 2013

- 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



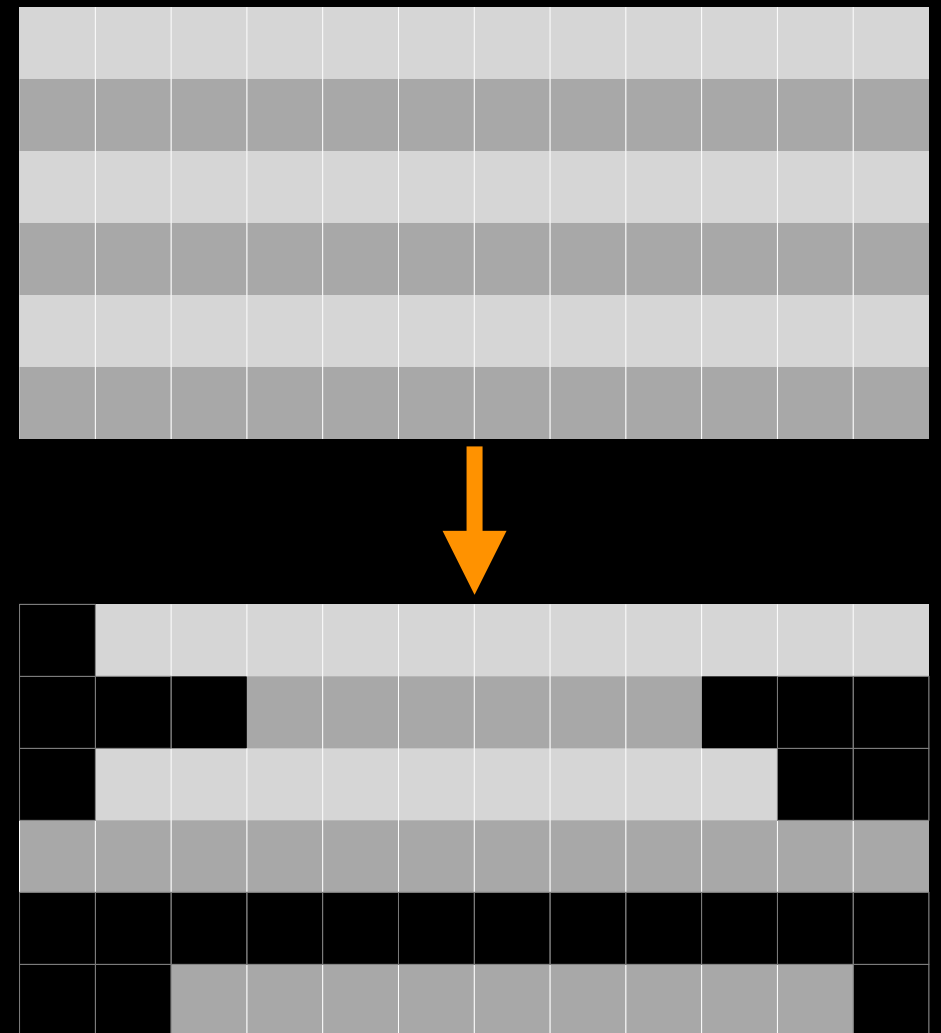
RNA-seq Exercise: A Plan

- 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.

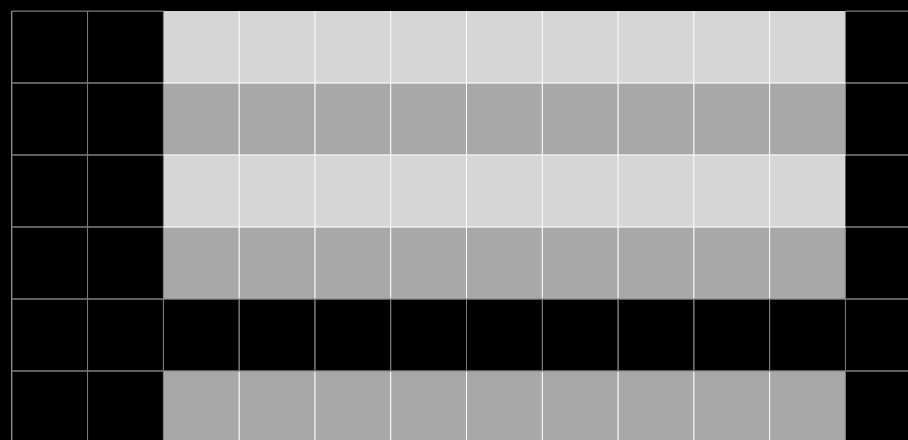
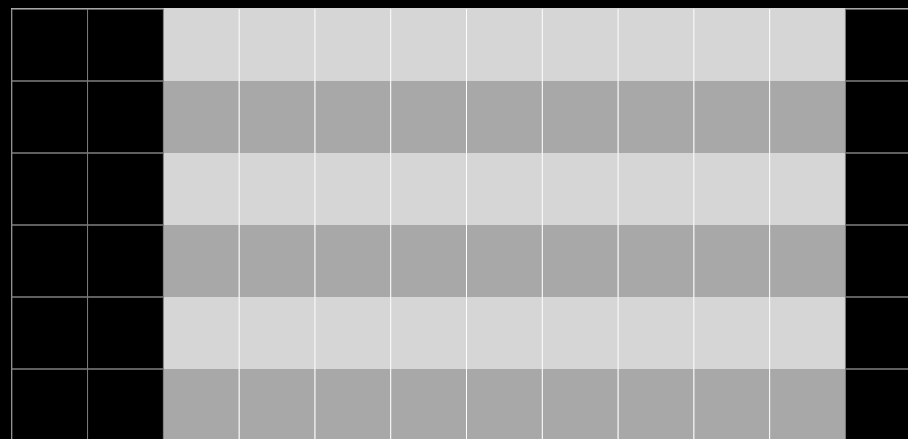
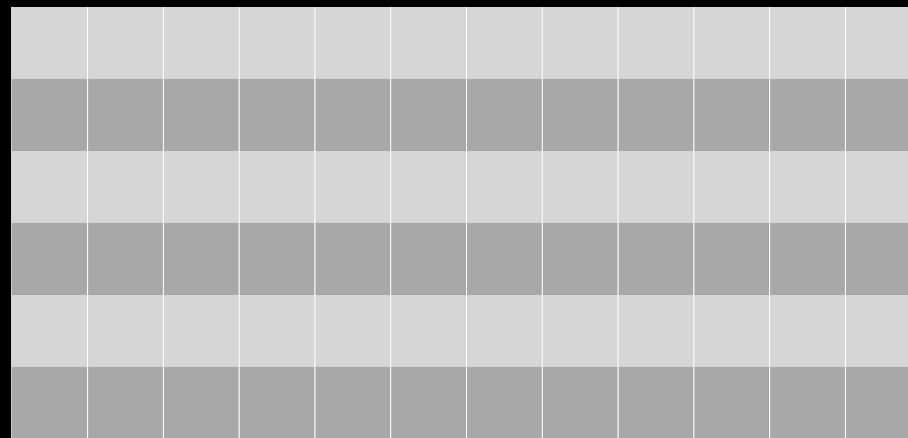


RNA-seq Exercise: A Plan

- 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**



Options are
not mutually
exclusive



Trim? *As we see fit?*

- Introduced 3 options
 - One preserves original read length, two don't
 - One preserves number of reads, two don't
 - Two keep/make every read the same length, one does not
 - One preserves pairings, two don't

Trim? *As we see fit?*

- Choice depends on downstream tools
- Find out assumptions & requirements for downstream tools and make appropriate choice(s) now.
- How to do that?
 - <http://biostars.org/>
 - <http://seqanswers.com/>
 - <http://galaxyproject.org/search>



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.*
 - And thanks to GTAC, we won't run it today.

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.*

<http://bit.ly/11Qvnwh>: Lance Parsons' RNA-Seq Tutorial

<http://bit.ly/Y7yKzv>: UC Davis (Nik Joshi?) RNA-Seq Tutorial

<http://bit.ly/Yfl0E0>: UAB RNA-Seq Tutorial @ GCC2012

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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>

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>

The screenshot shows the Galaxy Tool Shed interface for the 'clustalomega' repository. The left sidebar contains links: 'Browse by category', 'Browse all repositories', and 'Login to create a repository'. The main content area displays the repository revision '2:bb1847435ec1' with a 'repository tip' label. Below this, it provides the clone URL 'hg clone http://toolshed.g2.bx.psu.edu/repos/clustalomega/clustalomega', the name 'clustalomega', a synopsis 'multiple sequence alignment program for proteins', and a detailed description 'Clustal Omega is a general purpose multiple sequence alignment program for proteins. It produces high quality alignments'. It also shows the revision '2:bb1847435ec1', owner 'clustalomega', and 'Times downloaded: 39'. At the bottom, there is a table titled 'Tools - click the name to preview the tool and use the pop-up menu to inspect all metadata' with one entry: 'Clustal Omega' with description 'multiple sequence alignment program for proteins', version '1.0.2', and requirements 'none'.

The screenshot shows the Galaxy Tool Shed interface displaying a list of repositories. The left sidebar is the same as the previous screenshot. The main content area has a search bar and a table of repositories. The table has columns: 'Name', 'Synopsis', 'Revision', 'Category', and 'Owner'. The repositories listed are:

Name	Synopsis	Revision	Category	Owner
abyss_toolsuite	This suite contains Abyss and Abyss-PE config files and wrappers for Galaxy	0:92636934a189	Assembly	edward-kirton
agile_wrapper	Quickly match reads to a reference genome or sequence file	0:d6a426afaa46	Next Gen Mappers, Sequence Analysis	simonl
asdf	asdf	-1:000000000000	Statistics, Text Manipulation	vivek
assemblystats	Summarise an assembly (e.g. N50 metrics)	0:6544228ea290	Next Gen Mappers, Sequence Analysis	konradpaszkiewicz
bam_to_bigwig	Generate BigWig coverage files from BAM files. Allows gapped reads to be split (useful for RNA-Seq). Calculates	5:5b40b93ebae3	Convert Formats, SAM, Visualization	lparsons

Encourage **Public** Galaxy Instances

<http://bit.ly/gxyServers>

Interested in:

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

Plus many more

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

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

Google™ Custom Search


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](#)

 Galaxy Web Search

chip-seq

All Tools Email Source code Shared Documentation Abstracts Requests

About 444 results (0.06 seconds)

 Galaxy | Accessible Data | 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

Community can create, vote and comment on issues

The screenshot displays a Trello board titled "Galaxy: Development Inbox" with a "Public" status. The board is organized into four main columns:

- Inbox:** Contains five cards with titles like "To add cards, use the http://galaxyproject.org/tr ello", "Filter and Sort: 'Select' tool not dealing with special characters right", "Uploaded fastq file datatype not usable in BWA", "Reference genome request: GATK-ordered hg19", and "Feature request: manually hide datasets".
- Developer ideas:** Contains five cards including "Anonymous use of workflows/visualizations", "Feature Request: the ability to restart a failed workflow from the point of failure;", "Google Drive / Dropbox / Box / ... integration", "Bug report: always import deleted datasets", and "Standalone web application(s) for visualizations".
- Bug Reports:** Contains five cards such as "Issues with workflow step hiding not persisting", "Workflow View Broken in Toolshed?", "Unable to run jobs when user job limits are set", "Fix tool tip FASTQ Summary Statistics", and "Bug when using data_column".
- Issues from Bitbucket:** Contains five cards including "5: Option to disable automatic history creation", "6: Option to require that histories have names", "8: More flexible output handlers", "10: Allow overriding parameters when running a workflow", and "20: Suggestion: new tag in tool's XML file - 12/9/08 email from Assaf Gordon".

On the right side of the board, 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" section showing recent actions, such as "Dannon Baker added API: Library Contents to Developer ideas and" and "g2roboto on Feature request: manually hide datasets".

<http://bit.ly/gxyissues>

http://wiki.galaxyproject.org

Galaxy Wiki

FrontPage

Locked History Actions

Galaxy

Galaxy

Community

Conference

OSLO

30 June - 2 July

2013

University of Oslo

Poster abstracts due 3 May

Use Galaxy

Use Main (about) Use Others! • 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

Wiki

Help • All Pages

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.

usegalaxy.org

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

getgalaxy.org

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!

Events

News

Galaxy Wiki

Login | Search:

Titles



Events

Locked

History






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	Contact
April 29 - May 2	Introduction to Galaxy Workshops 2013 Galaxy Workshop Tour	Washington University in St. Louis	Dave Clements
		Saint Louis University	
		University of Missouri Columbia	
May 14-16	Tutorial: <i>Exploring and Enabling Biomedical Data Analysis with Galaxy</i>	Great Lakes Bioinformatics Conference (GLBIO) 2013, Pittsburgh, Pennsylvania, United States	Anton Nekrutenko
May 15	GalaxyAdmins May 2013 Meetup	GalaxyAdmins web meetup	Srinivas Maddhi, Dave Clements
May 16-17	Galaxy Workflows for Bioinformatics Analysis, and Workshop 1A - Galaxy Workflows for Bioinformatics Analysis	Workshop in Next-Generation Sequence Analysis and Metabolomics (WINGS), UNC-Charlotte, North Carolina, United States	James Taylor
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	Sandra Dérozier, Valentin Loux, Véronique Martin <veronique.martin AT jouy DOT inra DOT fr>
May 22 May 30	Analyse de données issues de séquenceurs nouvelle génération sous Galaxy Les deux ateliers sont maintenant complets		Jean-François Gibrat, Valentin Loux, Véronique Martin <veronique.martin AT jouy DOT inra DOT fr>
May 24 June 19	Introduction to Galaxy		Nikhil Joshi <najoshi AT ucdavis DOT edu>
	A Genomics Virtual Lab for Cancer Research	UC Davis Bioinformatics Core Davis, California, United States	Dominique Gorse
	Next-Gen Sequencing		

Galaxy Wiki

Login | Search:

Titles

Text

News

Locked

History

Actions

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

Environmental Metabolomics + Galaxy

A new UK-China collaboration in environmental metabolomics between the University of Birmingham, BGI and *GigaScience* has received funding from the UK's Natural Environment Research Council (NERC).

The first metabolomics project will send a developer from the University of Birmingham's School of Biosciences, to Hong Kong to work with *GigaScience* personnel on extending Galaxy for use in metabolomics data analyses.

"Metabolomics involves the detection and quantification of small molecules (metabolites) in living organisms and can provide an indication of their cellular condition and health. The toxicological responses of organisms to pollutants can be studied using environmental metabolomics, enabling researchers to discover diagnostic markers for monitoring and risk assessment of our environment. Research at Birmingham focuses extensively on the metabolic responses of the freshwater model organism, *Daphnia*, to both pollutants and engineered nanomaterials."

See the [official announcement](#) for more details.

Peter Li
[GigaScience](#)

Posted to the [Galaxy News](#) on 2013-04-22

Galaxy @ ASMS 2013

Galaxy will have a significant presence at the 61st ASMS Conference on Mass Spectrometry and Allied Topics being held in Minneapolis, Minnesota, June 9-13. Galaxy related content includes the [Galaxy Framework as a Solution for MS-based Informatics](#) workshop and at least 9 posters either directly about or using Galaxy.

If you do research in proteomics than please consider attending.

Dave Clements

Posted to the [Galaxy News](#) on 2013-04-19

April 8, 2013 Galaxy Security Release

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galaxyproject.org/GCC2013



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Poster abstracts due **May 3**



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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



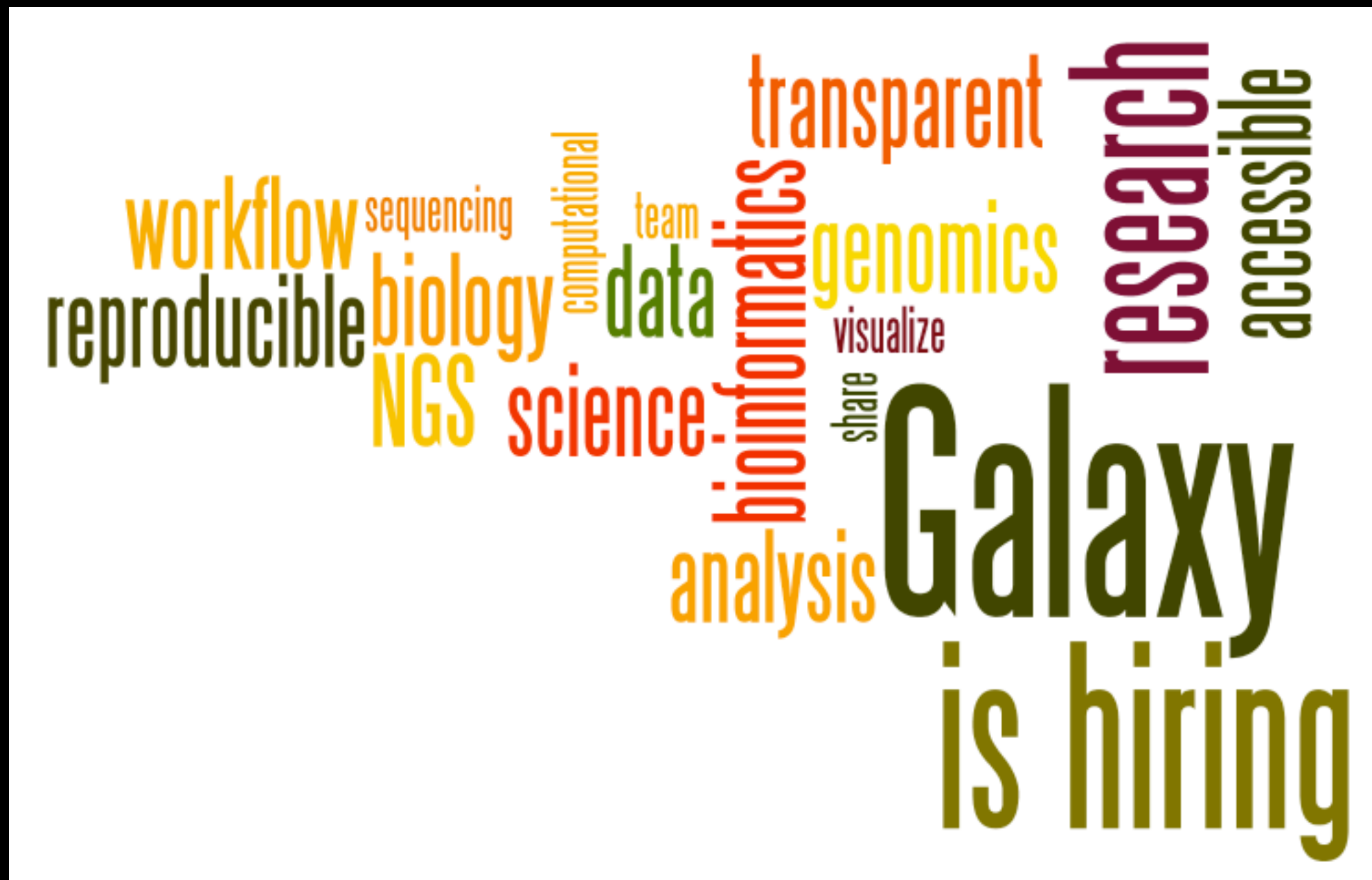
Anton Nekrutenko



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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- 9:00 Welcome
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- 11:20 RNA-Seq Example Part I
- 12:20 Lunch (on your own)
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- 1:55 **RNA-Seq Example Part II**
- 2:45 Break
- 3:05 Sharing, Publishing and Reproducibility
- 3:25 Setting up your own Galaxy Cluster on AWS
- 5:00 Done

RNA-seq Exercise: A Plan

- ...
- Run Cufflinks on Tophat output to assemble reads into transcripts
- Run Cuffdiff on Tophat output compare expression
 - *Imagine pages and pages of discussion on the intricacies and pitfalls of RNA-seq differential expression analysis here.*

RNA-seq Exercise: A Different (*better?*) Plan

- We've now walked through the analysis
- Suggests our level of iteration / experimentation is the whole workflow.
- Use Visualization as we go, to guide analysis as we go.

Visualizing Genomics

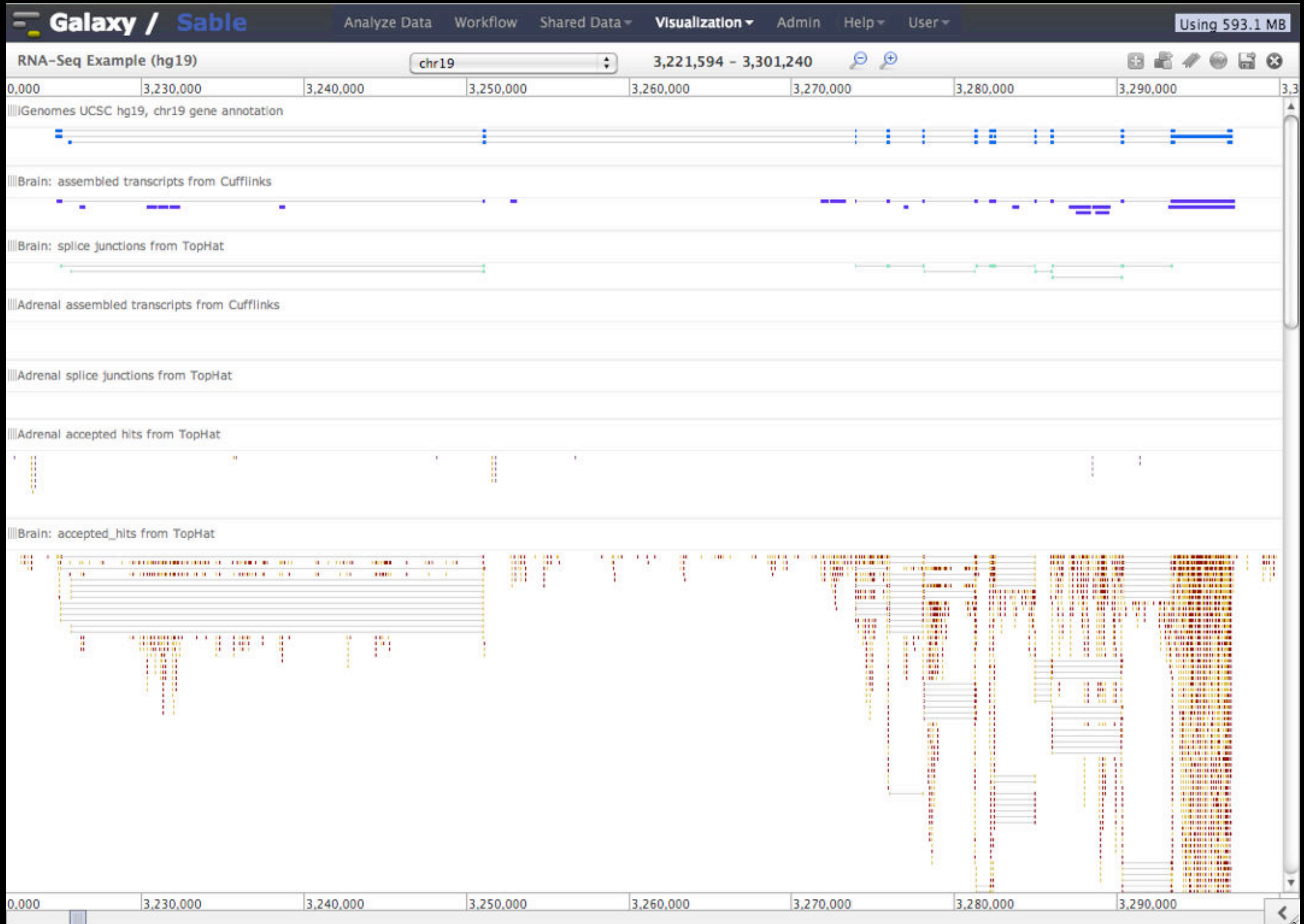
Supported external browsers

- UCSC
- Ensembl
- GBrowse
- IGB
- IGV

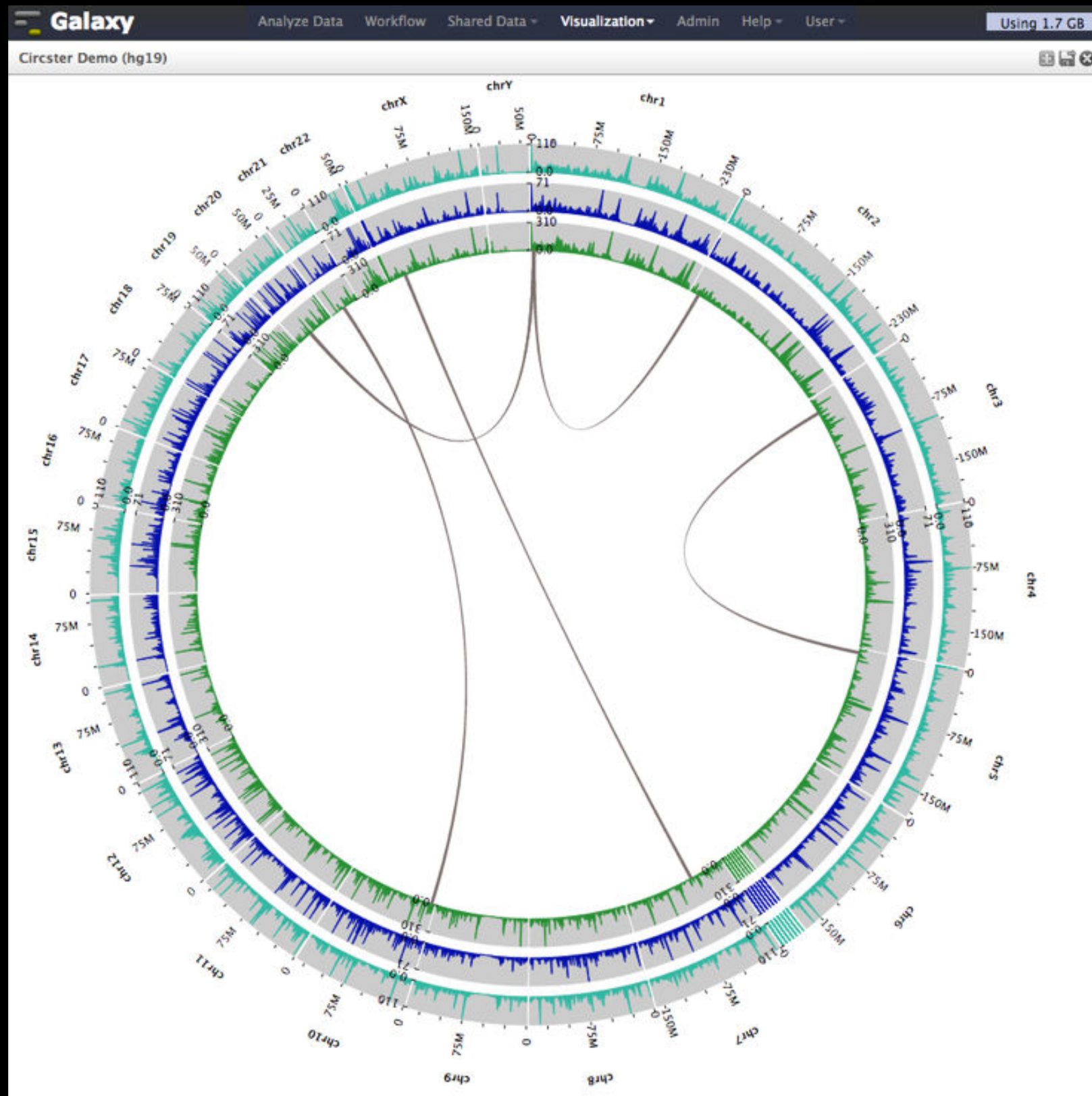
Traditional browser strengths:

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

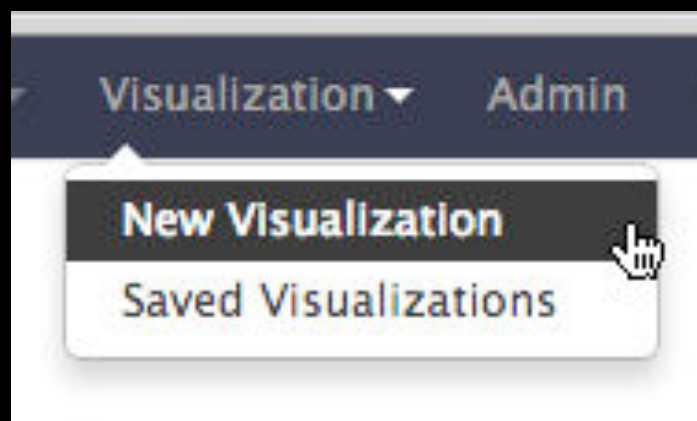
Trackster: Galaxy's embedded track browser



Circster



Create a visualization in Galaxy



or

A screenshot of a Galaxy track visualization. The track is titled '28: Brain: assembled transcripts from Cufflinks' and contains 211 lines of data. The format is gtf, and the database is hg19. The track shows a list of transcripts and exons for chromosome 19. A 'Visualize' button is highlighted with a mouse cursor.

28: Brain: assembled transcripts from Cufflinks
211 lines
format: gtf, database: hg19
Info: cufflinks v2.0.2
cufflinks -q --no-update-check -l 300000 -F 0.100000 -j 0.150000 -p 4

display at [HESC](#) main
display at Ensembl [Current](#)

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

Vizualization inside Galaxy

- Leverages visualization to **evaluate and refine analyses**
- **Exposes basic analyses in visualization** to make it more informative
- Makea that **analyze-visualize-refine loop seamless and fast**
- Enables **learning tools and exploring their parameter space**
- Supports custom genome browsers, **without a predefined reference genome**

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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

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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This Article

Published in Advance October 9, 2009, doi: 10.1101/gr.094508.109
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Current Issue

October 2010, 20 (10)



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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](#)

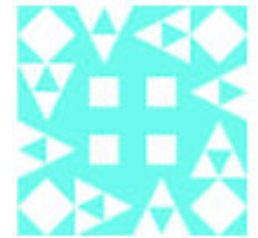

This is the Galaxy workflow for generic analysis of metagenomic data. (This corresponds to the "A complete metagenomic pipeline" section of the manuscript and **Figure 3B**):


[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.



Author

aun1

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<http://usegalaxy.org/u/aun1/p/windshield-splatter>

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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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>

Could do this step by step, but ...

<http://bit.ly/GXYAWSGetStarted>

Galaxy Wiki

CloudMan/AWS/GettingStarted

Login | Search:

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](#).

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](#)

AWS

Get Started

Capacity Planning

AMIs

↑ CloudMan

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



Instant CloudMan

<http://usegalaxy.org/cloudlaunch>

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 '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'. The bottom screenshot shows the 'Launch a Galaxy Cloud Instance' form, which includes input fields for Cluster Name, Password, Key ID, and Secret Key, an optional Instance Share String, and a dropdown for Instance Type (set to 'Large'). A 'Submit' button is at the bottom, and a message 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

Instant CloudMan

AWS Credentials

<http://bit.ly/WashUWed>

Instant Feedback

<http://bit.ly/20130501Gxy>

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Penn State University Emory University

<http://bit.ly/20130501Gxy>

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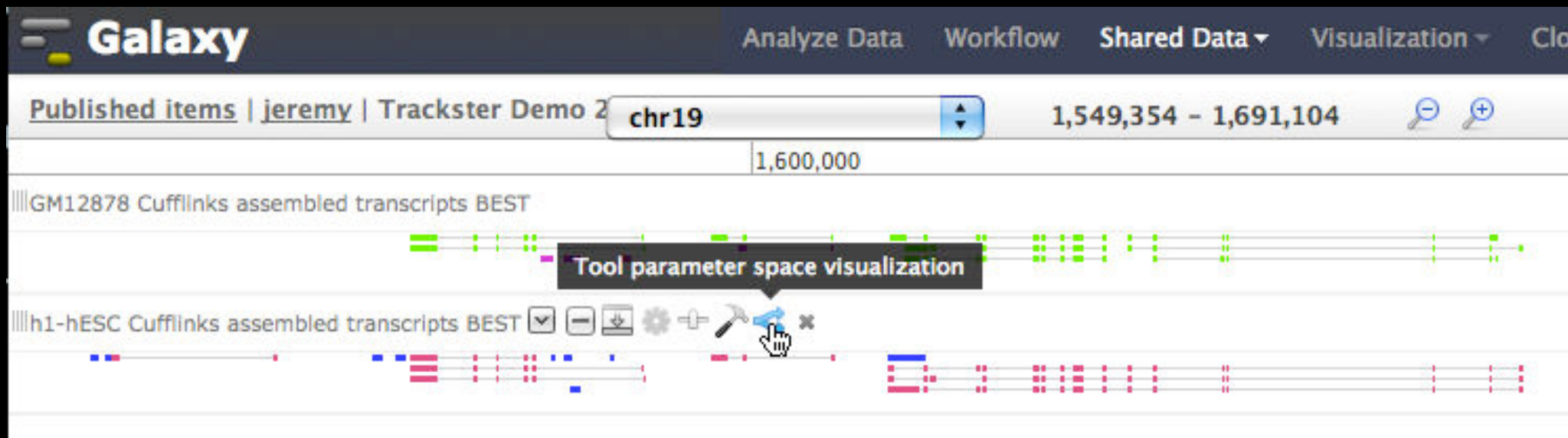
<http://bit.ly/20130501Gxy>



Thanks

<http://bit.ly/20130501Gxy>

Exploring Parameter Space with Trackster



Galaxy interface showing the Cufflinks (version 0.0.5) tool configuration and a parameter space visualization tree.

Cufflinks (version 0.0.5)

- ☐ Max Intron Length: 200000 - 400000 samples: 3
- ☐ Min Isoform Fraction: 0.1 - 0.2 samples: 3
- ☒ Pre mRNA Fraction: 0.15
- ☐ Perform quartile normalization: No, Yes
- ☒ Use multi-read correct: No

Getting Started

1. Create a parameter tree by using the icons next to the tool's parameter names to add or remove parameters.
2. Adjust the tree by using parameter inputs to select min, max, and number of samples
3. Run the tool with different settings by clicking on tree nodes

Parameter Space Visualization Tree:

- Root
 - Max Intron Length
 - 200000
 - Perform quartile normalization
 - No
 - Min Isoform Fraction
 - 0.1
 - 0.15
 - 0.2
 - Yes
 - Min Isoform Fraction
 - 0.1
 - 0.15
 - 0.2
 - 300000 (selected)
 - 400000
 - Perform quartile normalization
 - No
 - Min Isoform Fraction
 - 0.1
 - 0.15
 - 0.2
 - Yes
 - Min Isoform Fraction
 - 0.1
 - 0.15
 - 0.2