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://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://usegalaxy.org/galaxy101 )
### Exon overlap counts

<table>
<thead>
<tr>
<th>Exon</th>
<th>Count</th>
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<tbody>
<tr>
<td>1</td>
<td>1</td>
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<tr>
<td>2</td>
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</table>

### Exons, from UCSC
### Exon overlap counts

<table>
<thead>
<tr>
<th>Exon 1</th>
<th>Exon 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1</td>
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<td>2</td>
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### Exons, from UCSC

<table>
<thead>
<tr>
<th>Exon 1</th>
<th>Exon 2</th>
<th>Join on exon name</th>
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<tbody>
<tr>
<td>1</td>
<td>1</td>
<td>0</td>
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<td>1</td>
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## Join on exon name
### Exon overlap counts

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### Join on exon name

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### Rearrange columns w/ cut

<table>
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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
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/gxytgac1

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

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

What is FASTQ?

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

```
@SEQ_ID
GATTTGGGGTTCAAAGCAGTATCGATCAAATAGTAATCCATTTGTCAACTCAGTTT
+
!''*(((****)))%%%++)(%%%%).1***--+++'))*55CCF>>>>>>CCCCCC65
```

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

```
SSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS
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.

[Link to exercise](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

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 more information but little control over how it is calculated or presented.

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

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.

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

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.*

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4:30  Done
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:**

- 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

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](http://galaxyproject.org/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 ...
- Related feature requests
- Papers using Galaxy for ...
- Documentation on ...
Community can create, vote and comment on issues

http://wiki.galaxyproject.org

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!
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@galaxypoint.org.

Upcoming Events

<table>
<thead>
<tr>
<th>Date</th>
<th>Topic/Event</th>
<th>Venue/Location</th>
</tr>
</thead>
<tbody>
<tr>
<td>February 4</td>
<td>Introduction to Galaxy Boot Camp</td>
<td>UC Davis Bioinformatics Core Davis, California, United States</td>
</tr>
<tr>
<td>March 2-5</td>
<td>Accessible, Transparent and Reproducible Analysis with Galaxy, part of GTL: Application of NGS Platforms for Whole Transcriptome and Genome Analysis</td>
<td>ABRF 2013, Palm Springs, California, United States</td>
</tr>
<tr>
<td>March 26-28</td>
<td>RNA Technologies and Analysis Workshop</td>
<td>DOE JGI User Meeting</td>
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<tr>
<td>April 5-6</td>
<td>2012 GMOD Meeting</td>
<td>Cambridge, United Kingdom</td>
</tr>
<tr>
<td>April 7-10</td>
<td>GO Galaxy Workshop</td>
<td>Boston, Massachusetts, United States</td>
</tr>
<tr>
<td>April 9-11</td>
<td>iii: Integrated Research Data Management for Next Gen Sequencing Analysis Using Galaxy and Globus Online Software-as-a-Service</td>
<td>BiOT World, Boston, Massachusetts, United States</td>
</tr>
<tr>
<td>May 14-16</td>
<td>Tutorial: Exploring and Enabling Biomedical Data Analysis with Galaxy</td>
<td>Great Lakes Bioinformatics Conference (GLBLIC) 2013, Pittsburgh, Pennsylvania, United States</td>
</tr>
<tr>
<td>May 21</td>
<td>Initiator à l'utilisation de Galaxy</td>
<td>Cycle &quot;Bioinformatique par la prati&quot; 2013, INRA Jouy-en-Josas, France</td>
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<tr>
<td>May 29</td>
<td>Analysa de dossiers juiss de sequences nouvelles generation sous galaxy</td>
<td>Les deux ateliers sont maintenant complexes</td>
</tr>
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<td>May 30</td>
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<tr>
<td>June 6-7</td>
<td>Informatics or High Throughput Sequencing Data Workshop</td>
<td>Toronto, Ontario, Canada</td>
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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
- Labs
- 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 panels
- Open Positions at five different institutions
- GCC2013 Training Day Topic voting, Registration, and Sponsorships
- January GalaxyAdmins Web Meetup slides and screen cast
- 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

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.
Talk abstracts due 12 April

@ galaxyproject.org/GCC2013

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
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
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       Cufflinks, Visualization and Visual Analytics
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RNA-seq Exercise: A Plan

- Trim as we see fit.
- 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/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  

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

[Image of Galaxy interface options]

[Image of Cufflinks transcript data]
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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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...
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.
Windshield splatter analysis with the Galaxy metagenomic pipeline

Sergei Kosakovsky Pond\textsuperscript{1,2,6,9}, Samir Wadhawan\textsuperscript{3,6,7}, Francesca Chiaromonte\textsuperscript{4}, Guruprasad Ananda\textsuperscript{1,3}, Wen-Yu Chung\textsuperscript{1,3,8}, James Taylor\textsuperscript{1,5,9}, Anton Nekrutenko\textsuperscript{1,3,9} and The Galaxy Team\textsuperscript{1}
Windshield splatter analysis with the Galaxy metagenomic pipeline

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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\textsuperscript{1,2,*}, SAMIR WADHAWAN\textsuperscript{3,6,*}, FRANCESCA CHIAROMONTE\textsuperscript{4}, GURUPRASAD ANANDA\textsuperscript{1,3}, WEN-YU CHUNG\textsuperscript{1,3,7}, JAMES TAYLOR\textsuperscript{1,5}, ANTON NEKRUTENKO\textsuperscript{1,3} and THE GALAXY TEAM\textsuperscript{1,*}

Correspondence should be addressed to SKP, IT, 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 these, they can be re-run through Galaxy using the above workflows and downloaded.

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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AWS Credentials

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.**

![Amazon Web Services](image)

- You will set up an instance now

http://aws.amazon.com/education
Instant CloudMan

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

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.
Submit
Or, Step by Step

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Helen Tunney

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You!

The Genome Analysis Centre

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NIH  NSF  Huck Institute
Penn State University  Emory University
Feedback Please!

http://bit.ly/TGACfeedback
Thanks

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Emory University
clements@galaxyproject.org

http://bit.ly/TGACfeedback