

<http://bit.ly/gxyeshg2015>

Variant Analysis with Galaxy

ESHG 2015

Glasgow, United Kingdom
6 June 2015

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Outline

Introduction: The Galactic Landscape

Variant Analysis: A worked example

Variant Analysis: Other options

Galaxy: Resources and Community

Done

Slides at <http://bit.ly/gxyeshg2015>

Goals

Provide a basic introduction to using Galaxy for bioinformatic analysis.

Demonstrate how Galaxy can help you explore and learn options, perform analysis, and then share, repeat, and reproduce your analyses.

Not Goals

This workshop will *not* cover

- details of how tools are implemented, or
- new algorithm designs, or
- which variant caller or assembler or mapper or peak caller or ... is best for you.

What is Galaxy?

Data integration and analysis platform that emphasizes accessibility, reproducibility, and transparency

A free (for everyone) web server

Open source software

These options result in several ways to use Galaxy

<http://galaxyproject.org>

Galaxy is available online, for free

<http://usegalaxy.org>

As a free (for everyone) web server integrating a wealth of tools, compute resources, petabytes of reference data and permanent storage



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

Galaxy is available as Open Source Software

Galaxy is installed in locations around the world.

Some of them are free for anyone to use too.

<http://getgalaxy.org>

bit.ly/gxyServers

Galaxy is available on the Cloud



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

<http://globus.org/>

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

We are using the cloud today.

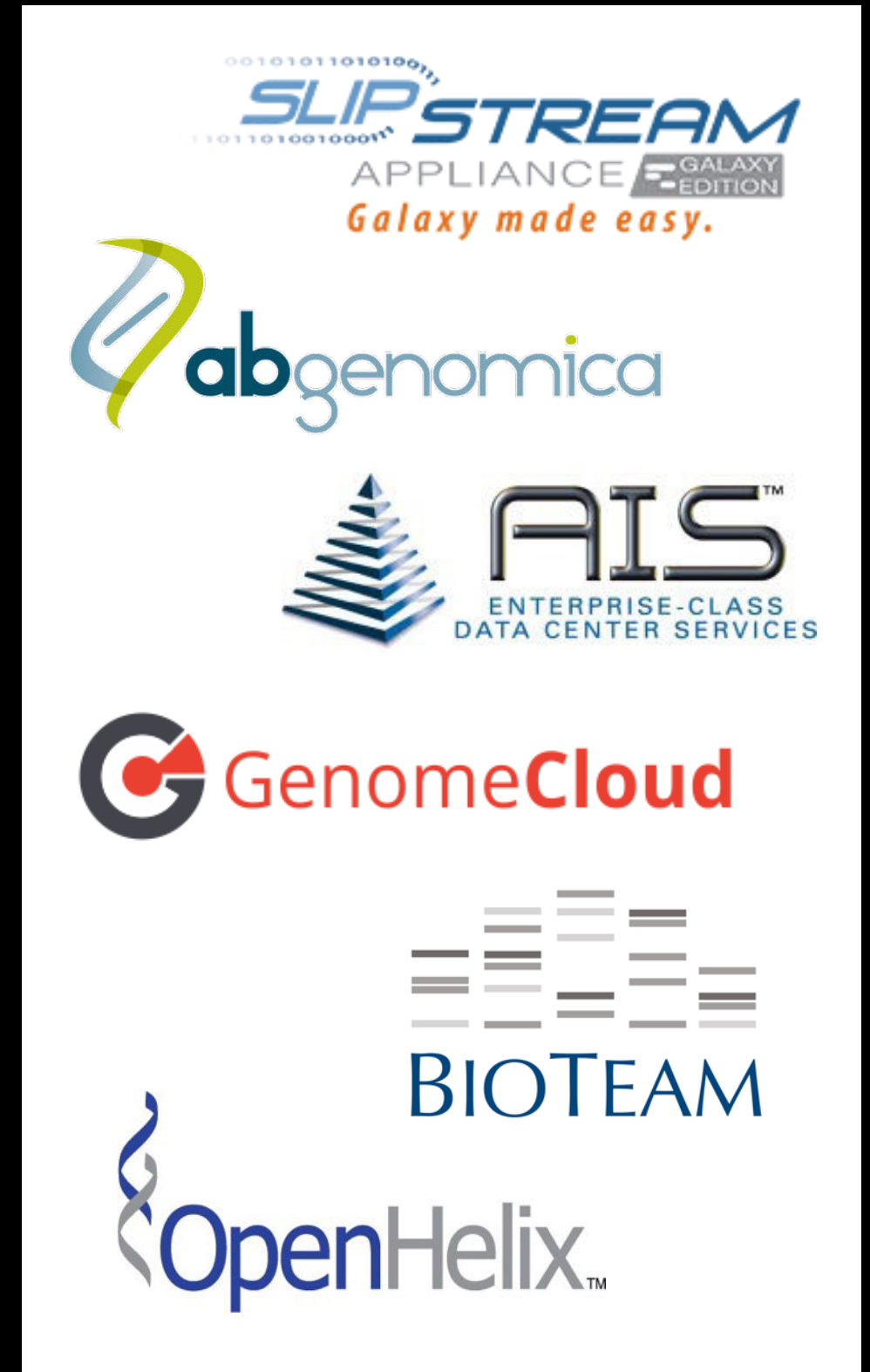
Galaxy is available **with Commercial Support**

A ready-to-use appliance
(BioTeam)

Cloud-based solutions
(ABgenomica, AIS,
GenomeCloud)

Consulting & Customization
(BioTeam, Deena
Bioinformatics)

Training
(OpenHelix)



Galaxy Project: Further reading & Resources

<http://galaxyproject.org>

<http://usegalaxy.org>

<http://getgalaxy.org>

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

<http://bit.ly/gxychoices>

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Galaxy 101 NGS: Introduction to Polymorphism Detection via Variant Analysis

Heteroplasmy: Mother–Child mtDNA Variant Polymorphism

heteroplasmy ismb2010-demo

This tutorial

Galaxy

Analyze Data Workflow Shared Data Visualization Cloud Help User

Published Pages | aun1 | heteroplasmy

- Import Sequence
- Interpret FASTQ
- Execute a series
- Execute one com
- Filter key results

Dynamics of mitochondrial heteroplasmy in three families investigated via a repeatable re-sequencing study

Hiroki Goto¹, Benjamin Dickins², Enis Afgan^{3,5}, Ian M. Paul⁴, James Taylor^{3,5}, Kateryna D. Makova¹, and Anton Nekrutenko^{2,5}

Published in Genome Biology on June 23, 2011

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What is Heteroplasmy

The heteroplasmy is a phenomenon where a cell contains more than one type of mitochondrial DNA (mtDNA) heteroplasmy. This is a common occurrence in the field of mitochondrial research.

Being heteroplasmy

Go ahead, start with the tutorial

Experiment

Import child and mother mtDNA data (*where Q20 indicates quality score) and convert the results to a VCF file using FreeBayes. Note: Variant Annotator is not required.

Explore the results

Questions:

- Can you identify the heteroplasmy?
- Can you identify the heteroplasmy?
- How could this heteroplasmy have arisen?
- Are any SNPs shared between the two samples?
- Do any polymorphisms exist in the mtDNA (per individual)?

* Source at Illumina

Input NGS Data

F1

M9

blood

6,106,214

1. How to use Galaxy

This document is intended to be used with them by re-sequencing a sample in a hassle-free procedure.

access our dataset

re-use workflows

view and import the data

In addition, we can

Watch the analysis

Watch how the code works

If you experience

2. Accessing the data

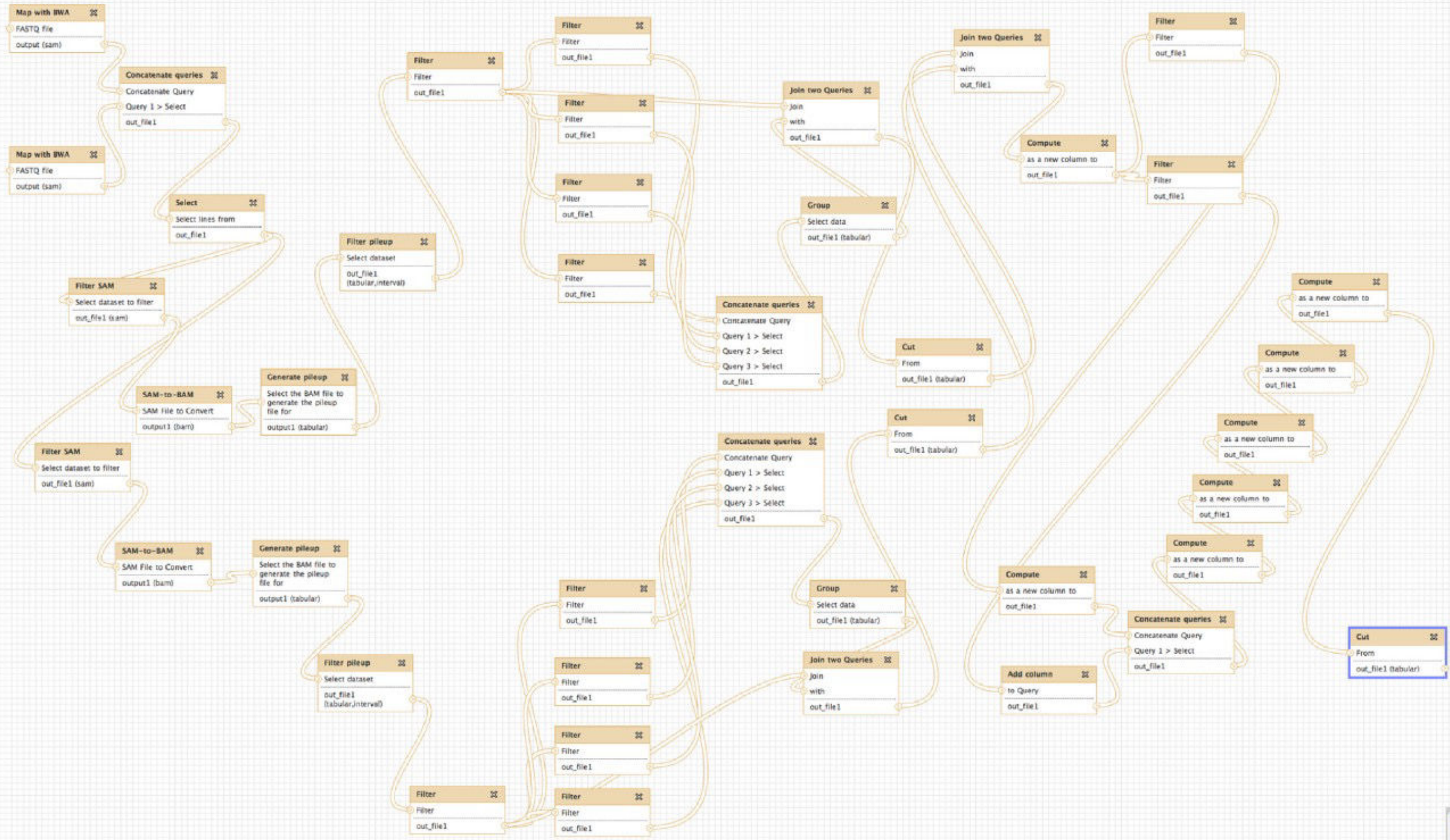
All datasets discussed in this tutorial are available in the Galaxy Library.

A Galaxy Library

An S3 bucket on the Galaxy server

From there these datasets can be downloaded.

family is "F4", "F7", "F8", "F9", "F10", "F11", "F12", "F13", "F14", "F15", "F16", "F17", "F18", "F19", "F20", "F21", "F22", "F23", "F24", "F25", "F26", "F27", "F28", "F29", "F30", "F31", "F32", "F33", "F34", "F35", "F36", "F37", "F38", "F39", "F40", "F41", "F42", "F43", "F44", "F45", "F46", "F47", "F48", "F49", "F50", "F51", "F52", "F53", "F54", "F55", "F56", "F57", "F58", "F59", "F60", "F61", "F62", "F63", "F64", "F65", "F66", "F67", "F68", "F69", "F70", "F71", "F72", "F73", "F74", "F75", "F76", "F77", "F78", "F79", "F80", "F81", "F82", "F83", "F84", "F85", "F86", "F87", "F88", "F89", "F90", "F91", "F92", "F93", "F94", "F95", "F96", "F97", "F98", "F99", "F100", "F101", "F102", "F103", "F104", "F105", "F106", "F107", "F108", "F109", "F110", "F111", "F112", "F113", "F114", "F115", "F116", "F117", "F118", "F119", "F120", "F121", "F122", "F123", "F124", "F125", "F126", "F127", "F128", "F129", "F130", "F131", "F132", "F133", "F134", "F135", "F136", "F137", "F138", "F139", "F140", "F141", 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Variant analysis

Goal is to find variation in these individuals' mitochondria
I'm going to run this on **usegalaxy.org**

The screenshot displays the Galaxy web interface. The top navigation bar includes links for Analyze Data, Workflow, Shared Data, Visualization, Cloud, Help, and User. The left sidebar lists various tools and categories such as Get Data, Text Manipulation, NGS: QC and manipulation, and NGS: Mapping. The main content area features a banner for 'Try Galaxy on the Cloud' and a 'Tweets' section with recent updates from the Galaxy Project and Nate Coraor. The right sidebar shows the 'History' section, which is currently empty. The footer includes logos for Penn State, Johns Hopkins University, TACC, and iPlant Collaborative.

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

Tools

search tools

[Get Data](#)
[Lift-Over](#)
[Text Manipulation](#)
[Convert Formats](#)
[Filter and Sort](#)
[Join, Subtract and Group](#)
[NGS: QC and manipulation](#)
[NGS: Mapping](#)
[NGS: RNA-seq](#)
[NGS: SAMtools](#)
[NGS: BAM Tools](#)
[NGS: Picard](#)
[NGS: VCF Manipulation](#)
[Extract Features](#)
[Fetch Sequences](#)
[Fetch Alignments](#)
[Get Genomic Scores](#)
[Operate on Genomic Intervals](#)
[Statistics](#)
[Graph/Display Data](#)
[Phenotype Association](#)
[snpEff](#)
[BEDTools](#)
[Genome Diversity](#)
[EMBOSS](#)
[Regional Variation](#)
[FASTA manipulation](#)
[Evolution](#)
[Multiple Alignments](#)

Galaxy is an open source, web-based platform for data intensive biomedical research. If you are new to Galaxy [start here](#) or consult our [help resources](#).

Try Galaxy on the Cloud

Now you can have a personal Galaxy within the infinite Universe

Tweets

Galaxy Project @galaxyproject 5h
We are formalizing code procedures of #usegalaxy & adding committers to the project. Welcome!
[github.com/galaxyproject/...](#)
[pic.twitter.com/4KcJk0DBrI](#)

Nate Coraor @natefoo 4 Jun
Merged! Thanks @Eric_Rasche for the improvements to #usegalaxy deps docker-build (+ much input from @bjoerngruening)
[github.com/galaxyproject/...](#)
 Retweeted by Galaxy Project

Tweet to @galaxyproject

History

search datasets

Unnamed history

0 bytes

This history is empty. You can [load your own data](#) or [get data from an external source](#)

PENNSTATE
1855

JOHNS HOPKINS UNIVERSITY

TACC

iPlant Collaborative

The Galaxy Team is a part of the Center for Comparative
This instance of Galaxy is utilizing infrastructure

Variant analysis: First steps

Login / register

Start a new history

**Shared Data → Data Libraries → Training → Heteroplasmy →
M512**

Select all

Import to current history

These are 4 paired end reads from mother and child,
from blood or cheek.

Variant analysis: Quality Control

NGS QC is a workshop until itself

Should address it here.

We will actually get to it later.

See <http://bit.ly/ngs101qc> for more on QC.

Variant analysis: Mapping

Map mother and child paired end datasets using

NGS Mapping → Map with BWA-MEM

Reference genome → HG19

Select M512-bl_1 and M512-bl_2

Read Groups: basically metadata that allow tools to identify
different samples / platforms / lanes / ...

Set Read group ID, Read Group Sample Name , Library Name,
Platform unit

Variant analysis: Mapping

Now do it again, this time using
M512C2-bl_1 and **M512C2-bl_2**

Which can be kinda tedious.

Cheat #1: Rerun button

Variant analysis: Mapping

Now do it a third time, this time using

M512C2-ch_1 and M512C2-ch_2

Which now seems even more tedious.

Cheat #2: Multiple datasets button

Variant analysis: Mapping

Now do it a third time, this time using

M512C2-ch_1 and **M512C2-ch_2**

Which now seems even more tedious.

Cheat #2: Multiple datasets button

Why we didn't do that to begin with? (*and cheat #3, maybe*)

Variant analysis: Mapping

Cheat #4: Jamie's 30 Minute Meals!

Shared Data → Published Histories →
ESHG 1: Through BWA Mapping w/ RG →
Import History

One thing we aren't showing that we also ran is:

NGS: Picard → MergeSamFiles

Variant analysis: BAM Cleanup & Manipulation

Use only the good stuff!

NGS BAM Tools → Filter

Mapping Quality → ≥ 20

Insert Filter → **isProperPair: Yes**

Insert Filter → **reference: chrM**

Variant analysis: BAM Cleanup & Manipulation

But not too much good stuff: **remove duplicates**

NGS Picard → MarkDuplicates

Remove Duplicates → Yes

Variant analysis: BAM Cleanup & Manipulation

Miscellaneous tidying

NGS Picard → CleanSam

Variant analysis: BAM Cleanup & Manipulation

Downsample it (hey, it's a workshop)

NGS Picard → Downsample SAM/BAM

~ 10%

Variant analysis

NGS Variant Analysis -> Naive Variant Caller

- 100 Minimum number of reads need to consider a REF/ALT
- 30 Minimum base quality
- 20 Minimum mapping quality
- 1 Ploidy
- chrM Restrict to regions
- Yes Report counts by strand

Produces a VCF file listing variants

Variant analysis: Only positions with variation

Lots of information in a VCF file
Can filter based on most of it.

NGS VCF Manipulation → VCFfilter

Get only positions with alternate allele frequency of 5%+

Specify filtering expression → -f "AF > 0.05"

Variant analysis: Annotation

NGS Variant Analysis -> Variant Annotator

- 1.0 Minor Allele Frequency threshold (in percent)
- 100 Coverage threshold (in reads per strand)
- No Do not filter sites or alleles
- Yes Output stranded base counts
- Yes Write header line

Outline

Introduction: The Galactic Landscape

Variant Analysis: A worked example

Variant Analysis: Other options

Galaxy: Resources and Community

Done

Galaxy	Galaxy	Galaxy	Galaxy
Tools	Tools	Tools	Tools
<p>NGS: Variant Analysis</p> <p><u>BamLeftAlign</u> indels in BAM datasets</p> <p><u>FreeBayes</u> – Bayesian genetic variant detector</p> <p><u>Slice VCF</u> to get data from selected regions</p> <p><u>MAF boxplot</u> Minor Allele Frequency Boxplot</p> <p><u>Phylorelatives</u> Relatedness of minor allele sequences in NJ tree</p> <p><u>CloudMap: in silico complementation</u> Perform in silico complementation analysis on multiple tabular snpEff output files</p> <p><u>CloudMap: Variant Discovery Mapping with WGS data</u> Map a mutation using in silico bulk segregant linkage analysis using variants that are already present in the mutant strain of interest (rather than those introduced by a cross to a polymorphic strain).</p> <p><u>CloudMap: Hawaiian Variant Mapping with WGS data</u> Map a mutation by plotting recombination frequencies resulting from crossing to a highly polymorphic strain</p> <p><u>CloudMap: EMS Variant Density</u></p>	<p><u>CloudMap: EMS Variant Density Mapping</u> Map a mutation by linkage to regions of high mutation density using WGS data</p> <p><u>Variant Annotator</u> process variant counts</p> <p><u>FASTA from allele counts</u> Generate major and minor allele sequences from alleles table</p> <p><u>Naive Variant Caller</u> – tabulate variable sites from BAM datasets</p> <p><u>Annotate</u> a VCF dataset with custom filters</p> <p><u>Varscan</u> for variant detection</p> <p><u>ANNOVAR</u> Annotate VCF with functional information using ANNOVAR</p> <p>NGS: VCF Manipulation</p> <p><u>VCFfixup</u>: Count the allele frequencies across alleles present in each record in the VCF file</p> <p><u>VCFprimers</u>: Extract flanking sequences for each VCF record</p> <p><u>VCFcombine</u>: Combine multiple VCF datasets</p> <p><u>VCFbreakCreateMulti</u>: Break multiple alleles into multiple records, or combine overallpoing alleles into a single record</p>	<p><u>VcfAllelicPrimitives</u>: Split allelic primitives (gaps or mismatches) into multiple VCF lines</p> <p><u>VCFfilter</u>: filter VCF data in a variety of attributes</p> <p><u>VCFrandomSample</u>: Randomly sample sites from VCF dataset</p> <p><u>VCFgenotype-to-haplotype</u>: Convert genotype-based phased alleles into haplotype alleles</p> <p><u>VCFcommonSamples</u>: Output records belonging to samples common between two datasets</p> <p><u>VCFselectsamples</u>: Select samples from a VCF dataset</p> <p><u>VCFleftAlign</u>: Left-align indels and complex variants in VCF dataset</p> <p><u>VCFtoTab-delimited</u>: Convert VCF data into TAB-delimited format</p> <p><u>VCFaddinfo</u>: Adds info fields from the second dataset which are not present in the first dataset</p> <p><u>VCFannotate</u>: Intersect VCF records with BED annotations</p> <p><u>VCF-VCFintersect</u>: Intersect two VCF datasets</p> <p><u>VCFannotateGenotypes</u>:</p>	<p><u>VCFannotateGenotypes</u>: Annotate genotypes in a VCF dataset using genotypes from another VCF dataset</p> <p><u>VCFcheck</u>: Verify that the reference allele matches the reference genome</p> <p><u>VCFsort</u>: Sort VCF dataset by coordinate</p> <p><u>VCFgenotypes</u>: Convert numerical representation of genotypes to allelic</p> <p><u>VCFhetHomAlleles</u>: Count the number of heterozygotes and alleles, compute het/hom ratio</p> <p><u>VCF-BEDintersect</u>: Intersect VCF and BED datasets</p> <p><u>VCFdistance</u>: Calculate distance to the nearest variant</p> <p>snpEff</p> <p><u>CloudMap: Check snpEff Candidates</u> Marks up a snpEff output file with matches to a gene candidate list.</p> <p><u>SnpSift Filter</u> Filter variants using arbitrary expressions</p> <p><u>SnpEff</u> Variant effect and annotation</p> <p>BEDTools</p> <p>EMBOSS</p>

2857 valid tools on Dec 16, 2014

- Search**
- [Search for valid tools](#)
 - [Search for workflows](#)
- Valid Galaxy Utilities**
- [Tools](#)
 - [Custom datatypes](#)
 - [Repository dependency definitions](#)

Repositories by Category

search repository name, description

Name	Description	Repositories
Assembly	Tools for working with assemblies	36
ChIP-seq	Tools for analyzing and manipulating ChIP-seq data.	10

Transcriptomics	Tools for use in the study of Transcriptomics.	16
Variant Analysis	Tools for single nucleotide polymorphism data such as WGA	164
Visualization	Tools for visualizing data	45

Data Source	Tools for retrieving data from external data sources	17
Fasta Manipulation	Tools for manipulating fasta data	42

Getting help on Variant Calling

- <http://biostars.org/>
- <http://seqanswers.com/>
- <http://galaxyproject.org/search>



Outline

Introduction: The Galactic Landscape

Variant Analysis: A worked example

Variant Analysis: Other options

Galaxy: Resources and Community

Done

Galaxy Community Resources

Galaxy Community Resources: Galaxy **Biostar**

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

Absolutely have to **encourage community support**.

Project traditionally used mailing list

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



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

Galaxy Community Resources: Mailing Lists

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

Galaxy-Dev

Questions about developing for and deploying Galaxy

High volume (3246 posts in 2014, 1000+ members)


Galaxy-Announce


Project announcements, low volume, moderated

Low volume (34 posts in 2014, 4400+ members)

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

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

 **Galaxy Web Search**



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

 **Galaxy Web Search**

About 444 results (0.06 seconds)

[Galaxy | Accessible Page | ChIP-seq exercise](#)



Galaxy is an open, web-based platform for *accessible*, *reproducible*, and *transparent* computational biomedical research.

- **Accessible:** Users without programming experience can easily specify parameters and run tools and workflows.
- **Reproducible:** Galaxy captures information so that any user can repeat and understand a complete computational analysis.
- **Transparent:** Users share and publish analyses via the web and create Pages, interactive, web-based documents that describe a complete analysis.

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

Use Galaxy

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



Community & Project

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

- [Community](#)

Deploy Galaxy

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

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



Contribute


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



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Events

News

Galaxy Event Horizon

Events with Galaxy-related content are listed here.

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

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

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

Upcoming Events



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

News Items

Opening at McMaster University

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



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

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

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

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

December 2014 Galaxy Newsletter

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

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

Dave Clements and the *crisp* Galaxy Team

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

Bioinformaticians, Freiburg

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



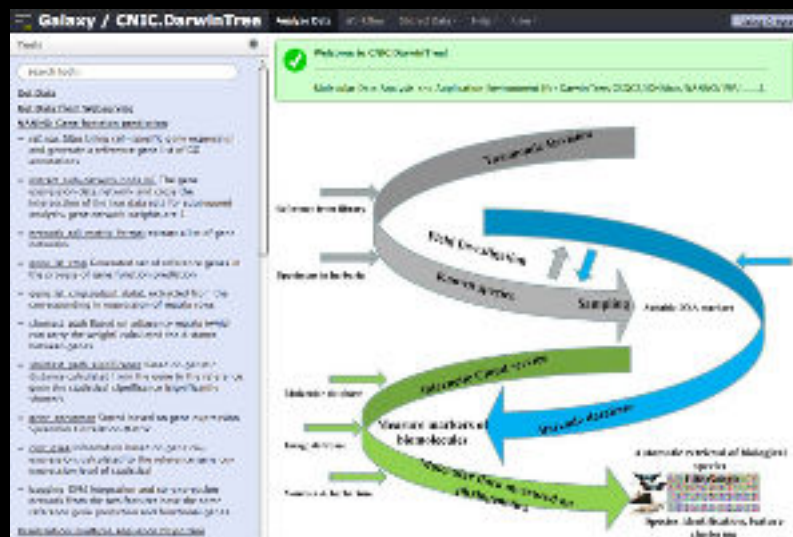
• primary analysis of deep-sequencing data and quality controls



Cistrome

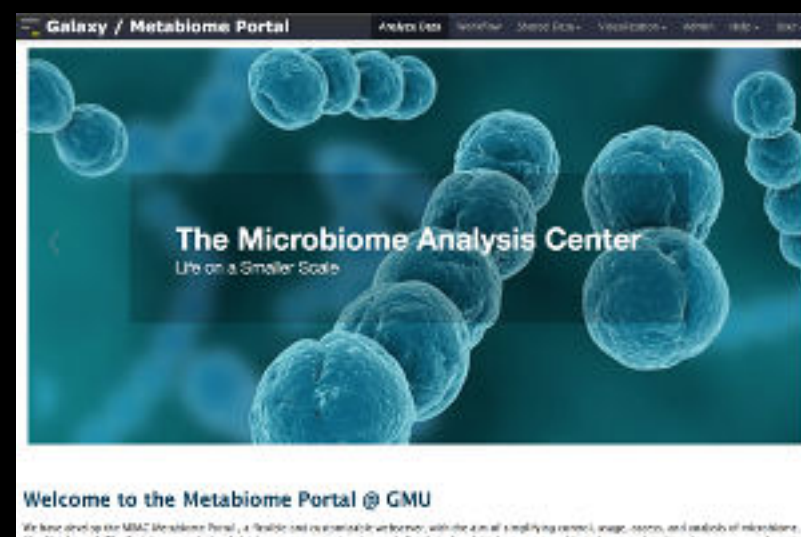
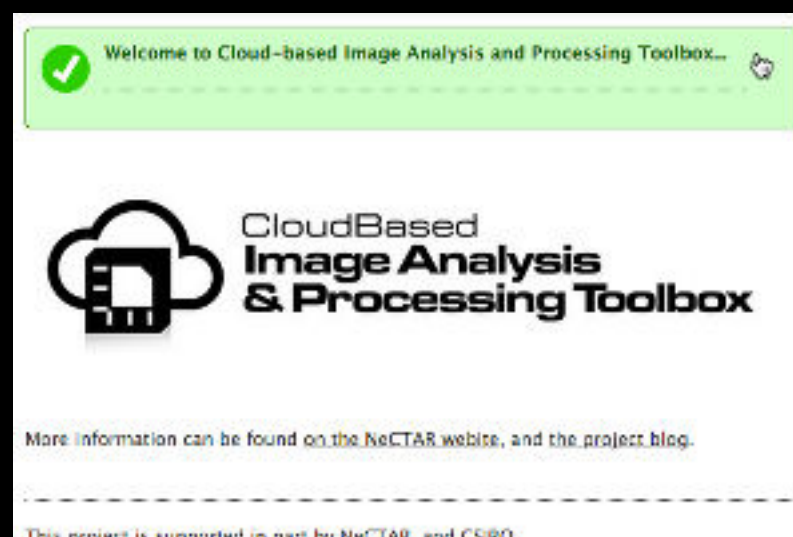
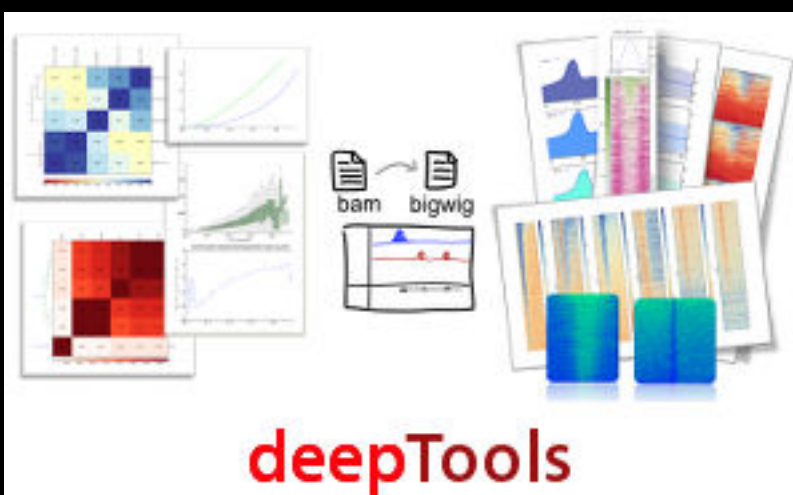


A Galaxy Server dedicated to ChIP-* analysis



ballaxy

Powered by the
Biochemical
Algorithms
Library
Project



bit.ly/gxyServers

Community can create, vote and comment on issues

The screenshot displays a Trello board titled "Galaxy: Development" with a "Public" setting. The board is organized into columns: "Inbox", "Tool Requests", "Bug Reports", "Ideas", "Pull Requests", and "Members". Each column contains cards representing different issues or tasks. Cards include titles, descriptions, vote counts, comment counts, and user avatars. A sidebar on the right shows a "Menu" with "Members" and "Activity" sections. The "Activity" section shows a recent comment by Lance Parsons on a pull request.

HOME TOUR GOLD BUSINESS CLASS BLOG

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

Galaxy: Development Public

Inbox

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

Tool Requests

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

Bug Reports

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

Ideas

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

Pull Requests

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

Menu

Members

Activity

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

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

today at 3:52 pm

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

<http://bit.ly/gxytrello>



GALAXY

COMMUNITY CONFERENCE

BALTIMORE, MD | JUNE 30 - JULY 2, 2014

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





GCC 2015

Galaxy Community Conference

~~4-6~~ 6-8th July 2015

The Sainsbury Laboratory
Norwich, UK

gcc2015.tsl.ac.uk



GCUK IS LIVE!

We also support
community
organized efforts
and events.



Galaxy Resources & Community: Videos

The screenshot shows the Vimeo channel for the Galaxy Project. The header includes the Vimeo logo and navigation links: Me, Videos, Create, Watch, Tools, Upload. A search bar is located in the top right. The channel name 'Galaxy Project' is displayed with a 'PLUS' badge and a note 'Joined 1 month ago'. Below this, a statistics bar shows: 54 Videos, 0 Likes, 0 Following, 1 Group, 6 Channels, and 0 Albums. The 'Recently Uploaded' section features four video thumbnails. The first two are titled 'Using Galaxy protocol 3' and 'Using Galaxy protocol 2', both by 'CPB Using Galaxy' and uploaded 5 days ago. The third is 'Using Galaxy protocol 1' by 'CPB Using Galaxy 1', also uploaded 5 days ago. The fourth is 'FASTQ Prep Illumina' by 'FASTQ Prep - Illumina', uploaded 1 week ago. A sidebar on the left contains a 'Settings' button and a paragraph of text about the Galaxy project.

Galaxy Project PLUS
Joined 1 month ago

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

Recently Uploaded + See all 54 videos

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

Settings

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

“How to”
screencasts on
using and
deploying
Galaxy

Talks from
previous
meetings.

<http://vimeo.com/galaxyproject>

Galaxy Resources & Community: CiteULike Group



CiteULike Group: Galaxy Search Register Log in

Group: Galaxy - library 2336 articles

Search Copy Export Sort Hide Details

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

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

■ Abstract

✓ Genomic and experimental evidence for multiple metabolic functions in the RidA/YjgF/YER057c/U

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

■ Abstract

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

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

✓ Repression by H-NS of genes required for the biosynthesis of the Vibrio cholerae biofilm matrix is mediated by the

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

■ Abstract

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



Group Tags

All tags in the group Galaxy

Filter:

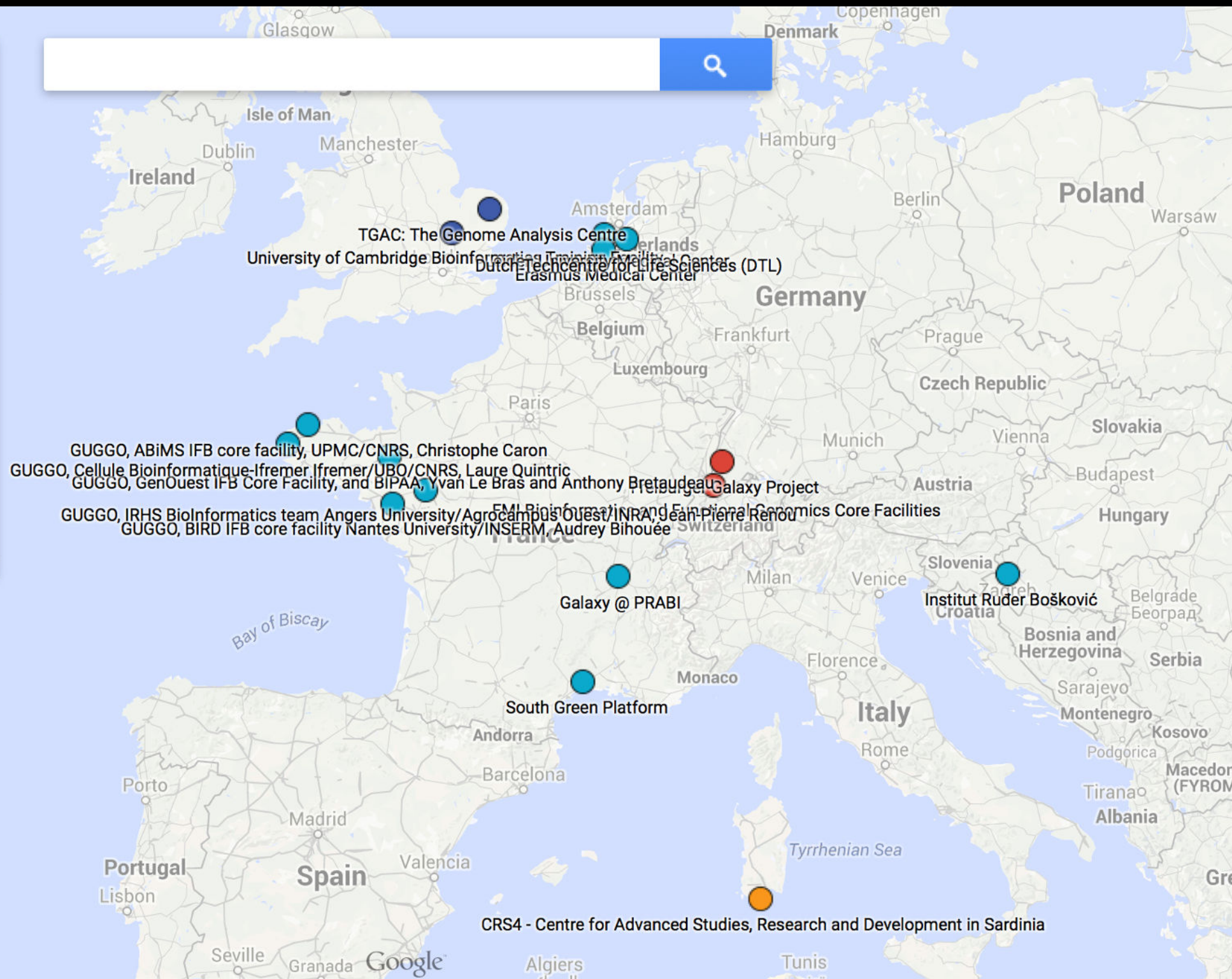
[\[Display as Cloud\]](#)

methods	1149
workbench	702
usemain	233
tools	169
usepublic	129
isgalaxy	124
uselocal	90
cloud	89
shared	81
other	68
refpublic	57
unknown	53
reproducibility	51
howto	45
project	43
visualization	15
usecloud	4

Now
over
2300
papers

<http://bit.ly/gxycul>

Scaling Training



Galaxy Training Network launched In October.

bit.ly/gxygtn

Outline

Introduction: The Galactic Landscape

Variant Analysis: A worked example

Variant Analysis: Other options

Galaxy: Resources and Community

Done (almost)

The Galaxy Team



Enis Afgan



Dannon Baker



Dan Blankenberg



Dave Bouvier



Marten Cech



John Chilton



Dave Clements



Nate Coraor



Carl Eberhard



Jeremy Goecks



Sam Guerler



Jen Jackson



Ross Lazarus



Anton Nekrutenko



Nick Stoler



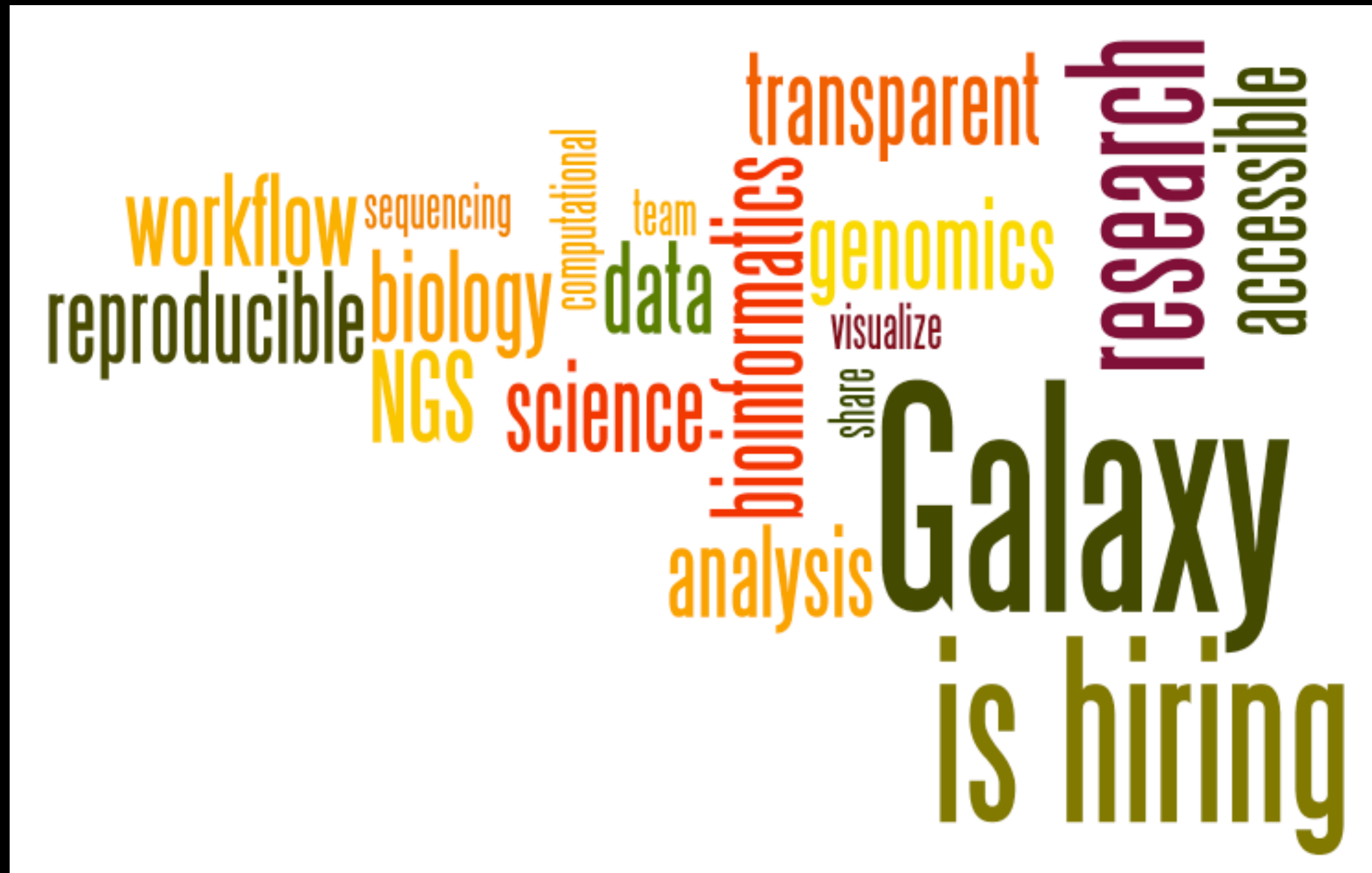
James Taylor



Nitesh Turaga

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

Galaxy is hiring post-docs and software engineers



Please help.

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

Also Thanks To



National Institutes of Health

Brunhilde Wirth
Stephen
Carole

Outline

Introduction: The Galactic Landscape

Variant Analysis: A worked example

Variant Analysis: Other options

Galaxy: Resources and Community

Done

Slides at <http://bit.ly/XXXXX>

Thanks



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