

# Galaxy for NGS Data Analysis

Matt Shirley

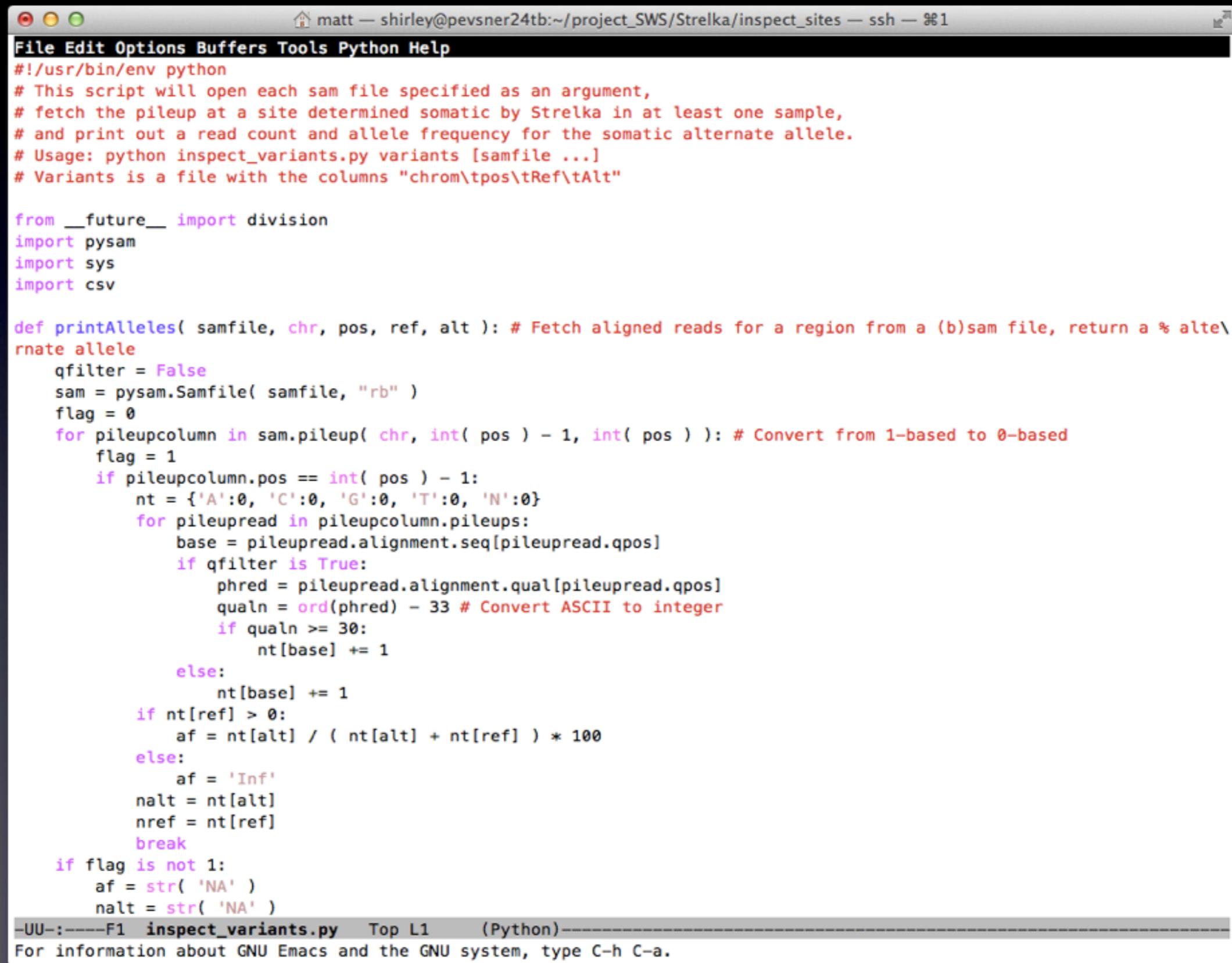
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Slides available at <http://mattshirley.com/talks>

# Contents

- What is Galaxy?
- Interface elements
- Retrieving data
- Creating and running workflows
- A FASTQ quality statistics workflow
- Galaxy on Amazon Web Services (AWS)
  - Automatic configuration through clouaunch
  - Monitoring your AWS charges
  - (optional) Manual configuration through AWS console

# Who wants to do this? :(



A screenshot of a terminal window titled "matt — shirley@pevsner24tb:~/project\_SWS/Strelka/inspect\_sites — ssh — #1". The window contains Python code for inspecting variants in SAM files. The code uses the `pysam` library to read SAM files and calculate allele frequencies. It includes a function `printAlleles` that takes a SAM file, chromosome, position, reference base, and alternate base as arguments. The code handles various edge cases and calculates the percentage of reads for each base.

```
File Edit Options Buffers Tools Python Help
#!/usr/bin/env python
# This script will open each sam file specified as an argument,
# fetch the pileup at a site determined somatic by Strelka in at least one sample,
# and print out a read count and allele frequency for the somatic alternate allele.
# Usage: python inspect_variants.py variants [samfile ...]
# Variants is a file with the columns "chrom\tpos\tRef\tAlt"

from __future__ import division
import pysam
import sys
import csv

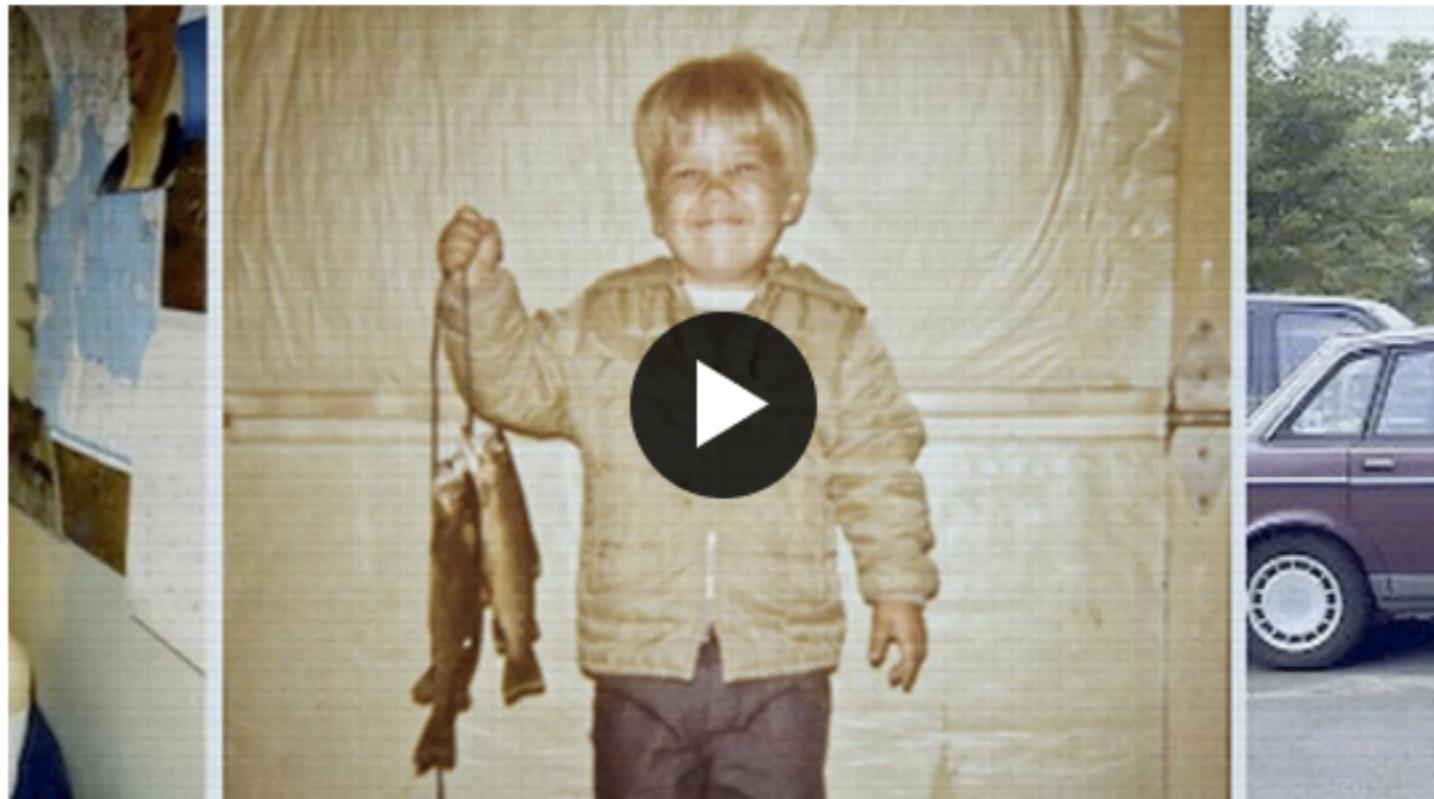
def printAlleles( samfile, chr, pos, ref, alt ): # Fetch aligned reads for a region from a (b)sam file, return a % alternate allele
    qfilter = False
    sam = pysam.Samfile( samfile, "rb" )
    flag = 0
    for pileupcolumn in sam.pileup( chr, int( pos ) - 1, int( pos ) ): # Convert from 1-based to 0-based
        flag = 1
        if pileupcolumn.pos == int( pos ) - 1:
            nt = {'A':0, 'C':0, 'G':0, 'T':0, 'N':0}
            for pileupread in pileupcolumn.pileups:
                base = pileupread.alignment.seq[pileupread.qpos]
                if qfilter is True:
                    phred = pileupread.alignment.qual[pileupread.qpos]
                    qualn = ord(phred) - 33 # Convert ASCII to integer
                    if qualn >= 30:
                        nt[base] += 1
                else:
                    nt[base] += 1
            if nt[ref] > 0:
                af = nt[alt] / ( nt[alt] + nt[ref] ) * 100
            else:
                af = 'Inf'
            nalt = nt[alt]
            nref = nt[ref]
            break
        if flag is not 1:
            af = str( 'NA' )
            nalt = str( 'NA' )
-UU-----F1  inspect_variants.py  Top L1      (Python)-----
For information about GNU Emacs and the GNU system, type C-h C-a.
```

# Wouldn't you rather do this?

**facebook**

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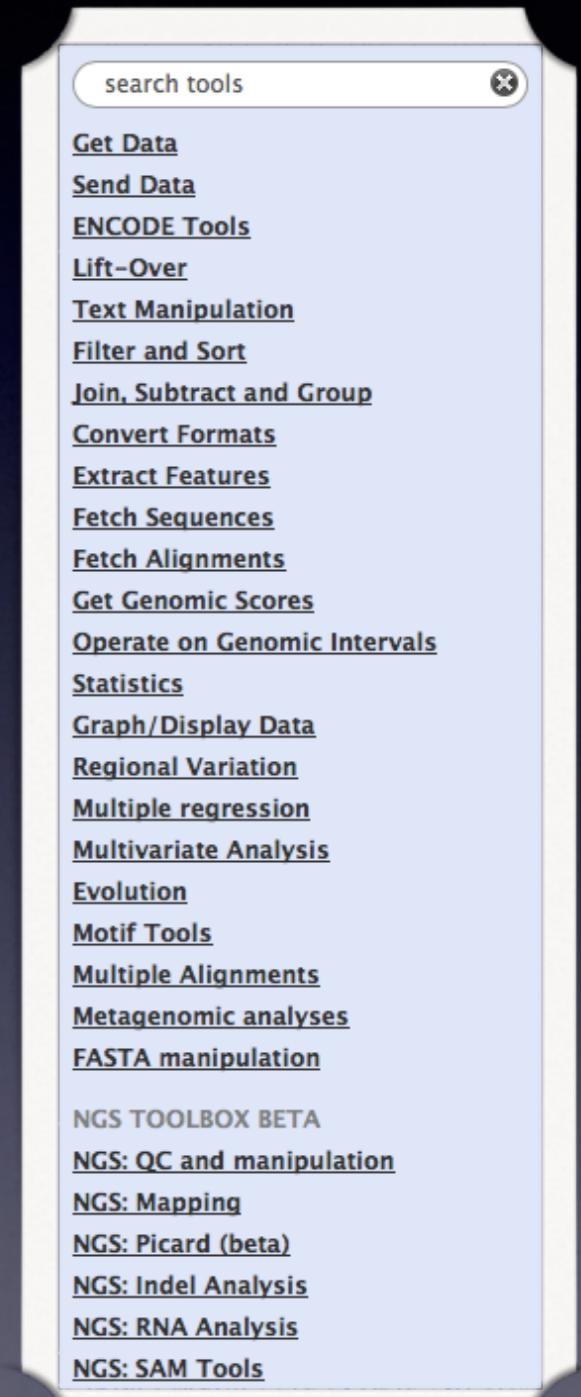


A photograph of a young boy with blonde hair, wearing a yellow jacket, standing in front of a yellow curtain. He is holding up two small fish by their tails. A large black play button is overlaid in the center of the image. To the left and right of the main image are smaller, partially visible thumbnail images.

# What is Galaxy?

Galaxy is framework for running bioinformatics tools for:

- data conversion and manipulation
- statistical analysis
- next generation sequencing analysis
- data display
- ...



- Have a tool that currently doesn't work within the Galaxy framework?
- Galaxy is **extensible**, allowing any program to run within the context of your web browser
- <Tool "wrapper"> + bowtie2 = bowtie2 in Galaxy
- Many tools available for installation via the toolshed
- The tools are **no different** than their command-line counterparts.

# What is Galaxy?

## Citation

If you use this tool, please cite [Blankenberg D, Gordon A, Von Kuster G, Coraor N, Taylor J, Nekrutenko A; Galaxy Team. Manipulation of FASTQ data with Galaxy. Bioinformatics. 2010 Jul 15;26\(14\):1783–5.](#)

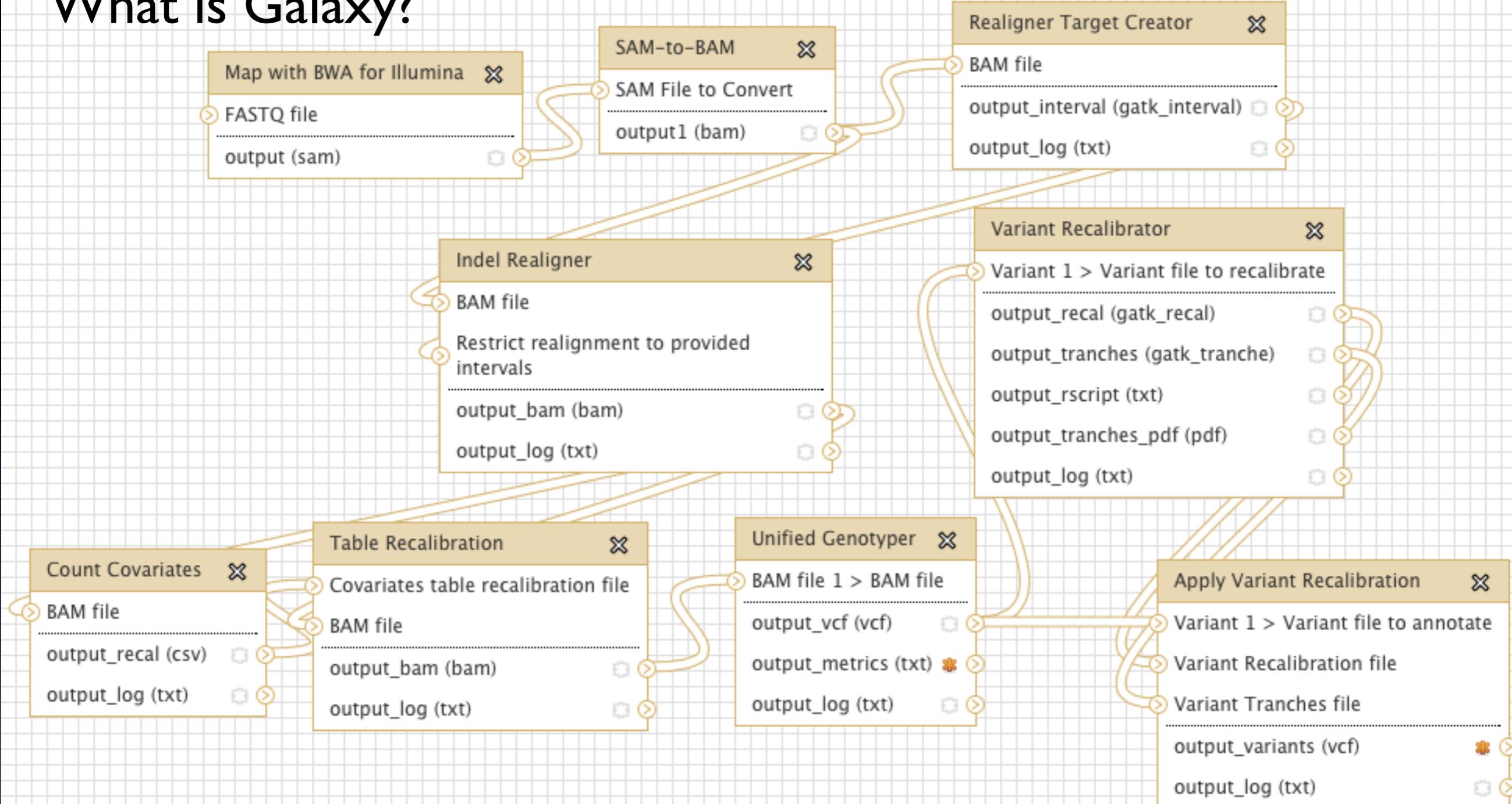
- Based on **peer-reviewed** and **open-source** implementations of each tool
- Galaxy provides integration with useful tools, targeted toward “bench” scientists as well as data scientists
- Unified and consistent interface for easy exploration

# What is Galaxy?

- Data library: management and sharing for collaborative analysis
- Data sources: download data from multiple online databases

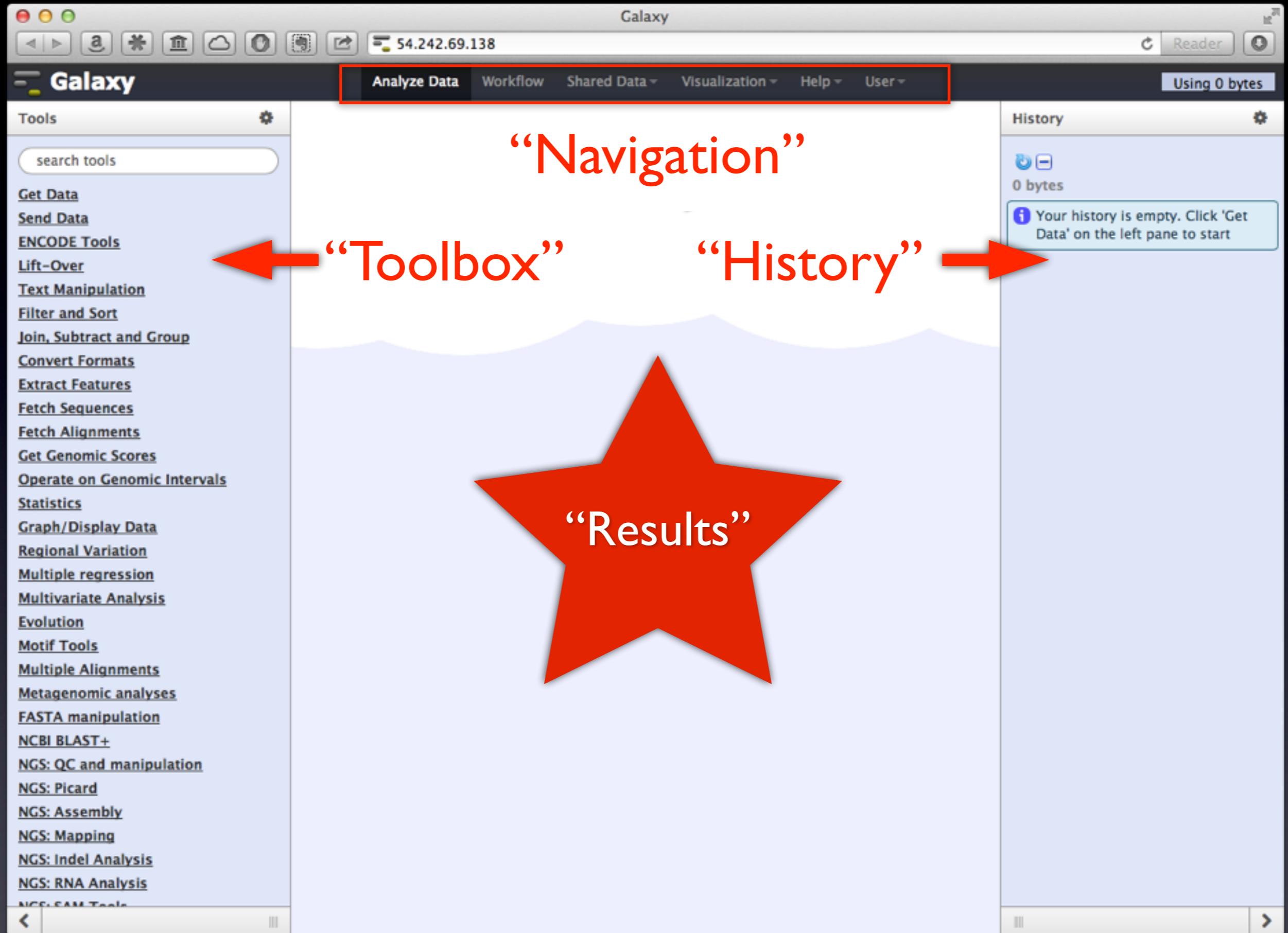
Data Libraries	
<input type="text" value="search dataset name, info, message, dbke"/> <input type="button" value=""/>	
<a href="#">Advanced Search</a>	
Data library name ↓	Data library description
<a href="#">1000 Genomes</a>	Data from the 1000 Genomes Project FTP site
<a href="#">AC-exome</a>	
<a href="#">Bushman</a>	Data for Nature Letter "Complete Khoisan and
<a href="#">ChIP-Seq Mouse Example</a>	Data used in examples that demonstrate analy
<a href="#">Chobi</a>	
<a href="#">CloudMap</a>	Contains userguide, reference files, and config
<a href="#">Codon Usage Frequencies</a>	
<a href="#">Coleman</a>	IonPGM
<a href="#">Denisovan sequences</a>	Files from 'A high-coverage genome sequence
<a href="#">Erythroid Epigenetic Landscape</a>	Dynamics of the epigenetic landscape during e
<a href="#">Evolutionary Trajectories in a Phage</a>	Experimental evolution (Illumina)
<a href="#">GATK</a>	
<a href="#">GCAT</a>	Consortium
<a href="#">Genome Diversity</a>	Nucleotide polymorphisms for several threatener
<a href="#">guru_1000GP</a>	
<a href="#">He-2010</a>	
<a href="#">Heteroplasmy</a>	Data for Genome Biology 2011 manuscript
<a href="#">iGenomes</a>	Selected files from Illumina iGenomes collectio

# What is Galaxy?



Workflows that enable  
reproducible research





# The “toolbox”



Contains links for :

- retrieving (“get”) data
- manipulating data (lift-over, filter, sort, set operations, format conversions)
- data analysis (statistics, sequence alignment, variant calling and annotation)

# “Get” data

In addition to uploading files from your computer, you may:

- Choose a file in the “shared data” library
- Import from UCSC, EBI SRA, BioMart, CBI Rice Map, modENCODE, Ratmine, Flymine, YeastMine, WormBase, EuPath, Microbial Genome Project, EncodeDB, EpiGRAPH, HbVar, GenomeSpace

Galaxy

54.242.69.138

Analyze Data Workflow Shared Data Visualization Help User Using 0 bytes

Tools

search tools

**Get Data**

- Upload File from your computer**
- UCSC Main table browser
- UCSC Test table browser
- UCSC Archaea table browser
- BX main browser
- Get Microbial Data
- BioMart Central server
- BioMart Test server
- CBI Rice Mart rice mart
- GrameneMart Central server
- modENCODE fly server
- Flymine server
- Flymine test server
- modENCODE modMine server
- Ratmine server
- YeastMine server
- metabolicMine server
- modENCODE worm server
- WormBase server
- Wormbase test server
- EuPathDB server
- EncodeDB at NHGRI
- EpiGRAPH server
- EpiGRAPH test server

Upload File (version 1.1.3)

**File Format:**

Auto-detect

Which format? See help below

**File:**

Choose File no file selected

TIP: Due to browser limitations, uploading files larger than 2GB is guaranteed to fail. To upload large files, use the URL method (below) or FTP (if enabled by the site administrator).

**URL/Text:**

https://s3.amazonaws.com/Sijung\_Yun\_NGS/1000\_tags.fastq.gz

Here you may specify a list of URLs (one per line) or paste the contents of a file.

**Files uploaded via FTP:**

File	Size	Date
------	------	------

Please [create](#) or [log in](#) to a Galaxy account to view files uploaded via FTP.

This Galaxy server allows you to upload files via FTP. To upload some files, log in to the FTP server at localhost using your Galaxy credentials (email address and password).

**Convert spaces to tabs:**

Yes

Use this option if you are entering intervals by hand.

**Genome:**

Click to Search or Select

**Execute**

**Auto-detect**

The system will attempt to detect Axt, Fasta, Fastqsolexa, Gff, Gff3, Html, Lav, Maf, Tabular, Wiggle, Bed and Interval (Bed with headers) formats. If your file is not detected properly as one of the known formats, it most likely means that it has some format problems (e.g., different numbers of columns, etc.).

History

0 bytes

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



Galaxy

Analyze Data Workflow Shared Data Visualization Help User Using 2.1 Mb

Tools

- Multivariate Analysis
- Evolution
- Motif Tools
- Multiple Alignments
- Metagenomic analyses
- FASTA manipulation
- NCBI BLAST+
- NGS: QC and manipulation
  - FASTQC: FASTQ/SAM/BAM
    - Fastqc: Fastqc QC using FastQC from Babraham
    - ILLUMINA FASTQ
    - FASTQ Groomer convert between various FASTQ quality formats
    - FASTQ splitter on joined paired end reads
    - FASTQ joiner on paired end reads
    - FASTQ Summary Statistics by column
  - ROCHE-454 DATA
    - Build base quality distribution
    - Select high quality segments
    - Combine FASTA and QUAL into FASTQ
  - AB-SOLID DATA
    - Convert SOLID output to fastq
    - Compute quality statistics for SOLID data
    - Draw quality score boxplot for SOLID data

History

1: https://s3.amazonaws.com/Sijung\_Yun\_NGS/1000\_tags.fastq 2.1 Mb

Edit Attributes

Name: https://s3.amazonaws.com/Sijung\_Yun\_NGS/1000\_tags.fastq

Info: uploaded fastq file

Database/Build: Click to Search or Select

Save

Auto-detect

This will inspect the dataset and attempt to correct the above column values if they are not accurate.

Convert to new format

Convert FASTQ files to seek locations

This will create a new dataset with the contents of this dataset converted to a new format.

Convert

Change data type

New Type: fastqsanger

This will change the datatype of the existing dataset but *not* modify its contents. Use this if Galaxy has incorrectly guessed the type of your dataset.

Save

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Galaxy

Analyze Data Workflow Shared Data Visualization Help User Using 2.1 Mb

**Tools**

- Multivariate Analysis
- Evolution
- Motif Tools
- Multiple Alignments
- Metagenomic analyses
- FASTA manipulation
- NCBI BLAST+
- NGS: QC and manipulation
  - FASTQC: FASTQ/SAM/BAM
  - Fastqc: Fastqc QC using FastQC from Babraham
  - ILLUMINA FASTQ
  - FASTQ Groomer convert between various FASTQ quality formats
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  - FASTQ joiner on paired end reads
  - FASTQ Summary Statistics by column
  - ROCHE-454 DATA
  - Build base quality distribution
  - Select high quality segments
  - Combine FASTA and QUAL into FASTQ
  - AB-SOLID DATA
  - Convert SOLID output to fastq
  - Compute quality statistics for SOLID data
  - Draw quality score boxplot for SOLID data
- GENERIC FASTQ MANIPULATION

**FASTQ Summary Statistics (version 1.0.0)**

**FASTQ File:**  
1: [https://s3.amazonaws.com/Sijung\\_Yun\\_NGS/1000\\_tags.fastq](https://s3.amazonaws.com/Sijung_Yun_NGS/1000_tags.fastq)

**Execute**

This tool creates summary statistics on a FASTQ file.

**TIP:** This statistics report can be used as input for the Boxplot and Nucleotides Distribution tools.

**The output file will contain the following fields:**

column = column number (1 to 36 for a 36-cycles read Solexa file)  
count = number of bases found in this column.  
min = Lowest quality score value found in this column.  
max = Highest quality score value found in this column.  
sum = Sum of quality score values for this column.  
mean = Mean quality score value for this column.  
Q1 = 1st quartile quality score.  
med = Median quality score.  
Q3 = 3rd quartile quality score.  
IQR = Inter-Quartile range (Q3-Q1).  
lW = 'Left-Whisker' value (for boxplotting).  
rW = 'Right-Whisker' value (for boxplotting).  
outliers = Scores falling beyond the left and right whiskers (comma separated list).  
A\_Count = Count of 'A' nucleotides found in this column.  
C\_Count = Count of 'C' nucleotides found in this column.  
G\_Count = Count of 'G' nucleotides found in this column.  
T\_Count = Count of 'T' nucleotides found in this column.  
N\_Count = Count of 'N' nucleotides found in this column.  
Other\_Nucs = Comma separated list of other nucleotides found in this column.  
Other\_Count = Comma separated count of other nucleotides found in this column.

For example:

#column	count	min	max	sum	mean	Q1	med	Q3	IQR	lW	rW	outliers	A_Count	C_Count
1	14336356	2	33	450600675	31.4306281875	32.0	33.0	33.0	33.0	1.0	31	33		
2	14336356	2	34	441135033	30.7703737965	30.0	33.0	33.0	33.0	3.0	26	34		
3	14336356	2	34	433659182	30.2489127642	29.0	32.0	33.0	33.0	4.0	23	34		
4	14336356	2	34	433635331	30.2472490917	29.0	32.0	33.0	33.0	4.0	23	34		
5	14336356	2	34	432498583	30.167957813	29.0	32.0	33.0	33.0	4.0	23	34		

**History**

Unnamed history 2.1 Mb

1: [https://s3.amazonaws.com/Sijung\\_Yun\\_NGS/1000\\_tags.fastq](https://s3.amazonaws.com/Sijung_Yun_NGS/1000_tags.fastq)

Galaxy

Analyze Data Workflow Shared Data Visualization Help User

Using 2.1 Mb

The following job has been successfully added to the queue:

2: FASTQ Summary Statistics on data 1

You can check the status of queued jobs and view the resulting data by refreshing the History pane. When the job has been run the status will change from 'running' to 'finished' if completed successfully or 'error' if problems were encountered.

History

Unnamed history 2.1 Mb

2: FASTQ Summary Statistics on data 1

1: https://s3.amazonaws.com/Sijung\_Yun\_NGS/1000\_tags.fastq

This screenshot shows the Galaxy web interface. The left sidebar contains a 'Tools' section with various analysis categories like Multivariate Analysis, Evolution, Motif Tools, etc. The main area displays a success message about a job being added to the queue. The right sidebar shows the 'History' pane with a list of submitted jobs, one of which is highlighted with a red border. The URL for the job's output file is also shown.

Galaxy

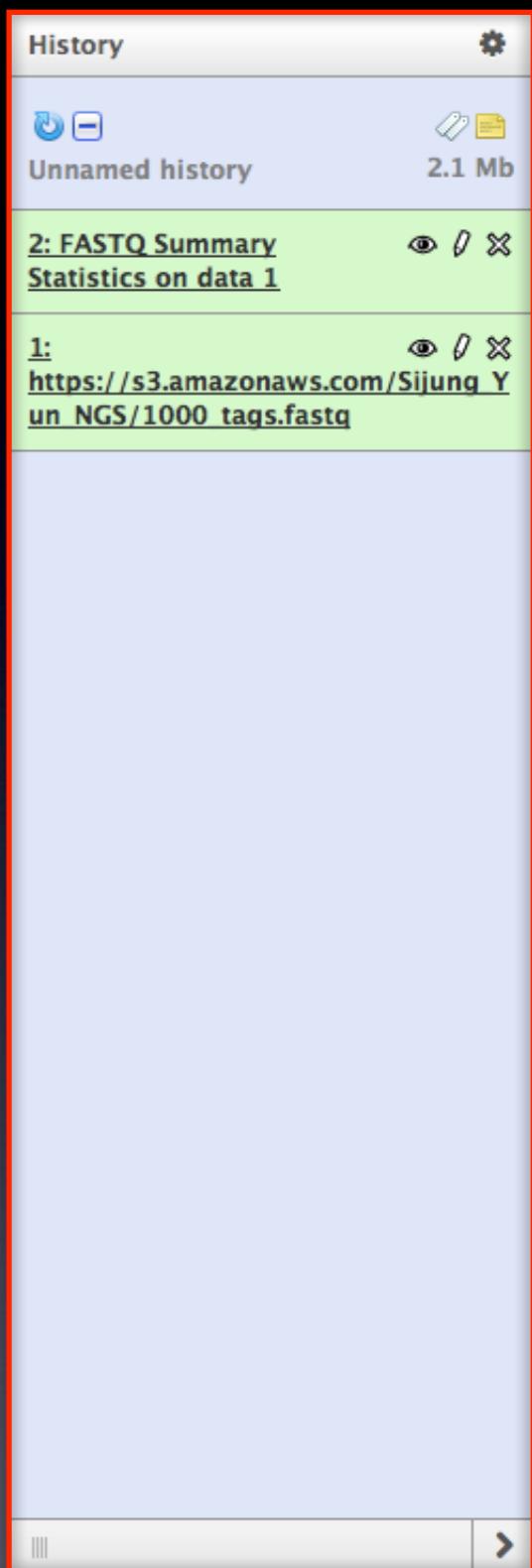
54.242.69.138

Analyze Data Workflow Shared Data Visualization Help User Using 2.1 Mb

Tools	#column	count	min	max	sum	mean	Q1	med	Q3	IQR	lW	rW	History
<u>Multivariate Analysis</u>	1	10000	2	40	358994	35.8994	35.0	38.0	39.0	4.0	29	40	
<u>Evolution</u>	2	10000	2	40	356075	35.6075	35.0	38.0	39.0	4.0	29	40	
<u>Motif Tools</u>	3	10000	2	40	355450	35.545	35.0	38.0	39.0	4.0	29	40	
<u>Multiple Alignments</u>	4	10000	2	40	354268	35.4268	35.0	38.0	39.0	4.0	29	40	
<u>Metagenomic analyses</u>	5	10000	2	40	355691	35.5691	35.0	38.0	39.0	4.0	29	40	
<u>FASTA manipulation</u>	6	10000	2	40	357066	35.7066	35.0	38.0	39.0	4.0	29	40	
<u>NCBI BLAST+</u>	7	10000	2	40	357335	35.7335	35.0	38.0	39.0	4.0	29	40	
<u>NGS: QC and manipulation</u>	8	10000	2	40	356799	35.6799	35.0	38.0	39.0	4.0	29	40	
FASTQC: FASTQ/SAM/BAM	9	10000	2	40	355891	35.5891	35.0	38.0	39.0	4.0	29	40	
▪ <u>Fastqc: Fastqc QC using FastQC from Babraham</u>	10	10000	2	40	356335	35.6335	35.0	38.0	39.0	4.0	29	40	
ILLUMINA FASTQ	11	10000	2	40	357109	35.7109	35.0	38.0	39.0	4.0	29	40	
▪ <u>FASTQ Groomer</u> convert between various FASTQ quality formats	12	10000	2	40	357572	35.7572	35.0	38.0	39.0	4.0	29	40	
▪ <u>FASTQ splitter</u> on joined paired end reads	13	10000	2	40	358956	35.8956	35.0	38.0	39.0	4.0	29	40	
▪ <u>FASTQ joiner</u> on paired end reads	14	10000	2	40	360000	36.0	35.0	38.0	39.0	4.0	29	40	
▪ <u>FASTQ Summary Statistics</u> by column	15	10000	2	40	356901	35.6901	35.0	38.0	39.0	4.0	29	40	
ROCHE-454 DATA	16	10000	2	40	350223	35.0223	34.0	38.0	39.0	5.0	27	40	
▪ <u>Build base quality distribution</u>	17	10000	2	40	351943	35.1943	34.0	38.0	39.0	5.0	27	40	
▪ <u>Select high quality segments</u>	18	10000	2	40	351757	35.1757	34.0	38.0	39.0	5.0	27	40	
▪ <u>Combine FASTA and QUAL</u> into FASTQ	19	10000	2	40	351216	35.1216	34.0	38.0	39.0	5.0	27	40	
AB-SOLID DATA	20	10000	2	40	351567	35.1567	34.0	38.0	39.0	5.0	27	40	
▪ <u>Convert SOLID output to fastq</u>	21	10000	2	40	349414	34.9414	34.0	38.0	39.0	5.0	27	40	
▪ <u>Compute quality statistics</u> for SOLID data	22	10000	2	40	350206	35.0206	34.0	38.0	39.0	5.0	27	40	
▪ <u>Draw quality score boxplot</u> for SOLID data	23	10000	2	40	350242	35.0242	34.0	38.0	39.0	5.0	27	40	
GENERIC FASTQ MANIPULATION	24	10000	2	40	351490	35.149	34.0	38.0	39.0	5.0	27	40	
	25	10000	2	40	349360	34.936	34.0	37.0	39.0	5.0	27	40	
	26	10000	2	40	353087	35.3087	35.0	38.0	39.0	4.0	29	40	
	27	10000	2	40	351412	35.1412	35.0	38.0	39.0	4.0	29	40	
	28	10000	2	40	352640	35.264	35.0	38.0	39.0	4.0	29	40	
	29	10000	2	40	352542	35.2542	35.0	38.0	39.0	4.0	29	40	
	30	10000	2	40	349193	34.9193	34.0	38.0	39.0	5.0	27	40	
	31	10000	2	40	354332	35.4332	35.0	38.0	39.0	4.0	29	40	
	32	10000	2	40	347471	34.7471	34.0	38.0	39.0	5.0	27	40	
	33	10000	2	40	354691	35.4691	35.0	38.0	39.0	4.0	29	40	
	34	10000	2	40	352285	35.2285	35.0	38.0	39.0	4.0	29	40	
	35	10000	2	40	348150	34.815	34.0	38.0	39.0	5.0	27	40	
	36	10000	2	40	350222	35.0222	35.0	38.0	39.0	4.0	29	40	

# The “history”

- Displays a list of your analysis steps
- Allows interaction with analysis results
- Each item in the history is a “**data-set**”
- Multiple concurrent histories allowed
- Maintains the order of analysis steps, allowing extraction of workflows on-demand



# Extracting workflows from histories

The screenshot shows the Galaxy web interface. On the left, a vertical sidebar titled "History" lists several histories. The second history, titled "2: FASTQ Statistics", is highlighted in green. A red arrow points from the "Extract Workflow" option in the context menu of this history to the resulting workflow diagram on the right.

**History**

- HISTORY LISTS
  - Saved Histories
  - Histories Shared with Me
- 2: FASTQ Statistics**
- 1: https://s...un NGS/1**
- CURRENT HISTORY
- Create New
- Clone
- Copy Datasets
- Share or Publish
- Extract Workflow**
- Dataset Security
- Show Deleted Datasets
- Show Hidden Datasets
- Purge Deleted Datasets
- Show Structure
- Export to File
- Delete
- Delete Permanently
- OTHER ACTIONS
- Import from File

**Extracted Workflow Diagram:**

```
graph LR; A[Input dataset] -- output --> B[FASTQ Summary Statistics]; B --> C[FASTQ File]; C -- output_file(tabular) --> D
```

**Histories and workflows result in reproducible research**

# NGS analysis in Galaxy

- QC and manipulation: filter, trim, mask, and convert fastq files
- Picard: a Java implementation of many samtools functions
- Mapping: align to reference genome with BWA, Bowtie, Bowtie2, BFAST, PerM, Mosaik, Lastz
- RNA: Tophat, Cufflinks (gapped alignment and transcript assembly)
- GATK: advanced analysis tools from BROAD
- Peak Calling: ChIP-Seq analysis tools

[NGS: QC and manipulation](#)  
[NGS: Picard \(beta\)](#)  
[NGS: Mapping](#)  
[NGS: Indel Analysis](#)  
[NGS: RNA Analysis](#)  
[NGS: SAM Tools](#)  
[NGS: GATK Tools \(beta\)](#)  
[NGS: Peak Calling](#)

# Visualizations

*Trackster* linear genome browser supports most interval, continuous, and discreet data formats

*Circster* “circos” style connectivity browser with interactive zooming

Visual parametric optimization allows the user to pick the most optimum local parameters, then optionally apply these globally

# Strengths and Weaknesses

## Strengths:

- Each tool has similar user interface elements, leading to a much lower learning curve
- Histories and workflows allow reproducibility
- Cluster and cloud compute-compatible
- Extensible tool set via Python scripting

## Weaknesses:

- Administrative overhead
- Limited set of parameters for some tools

# Local vs. Public

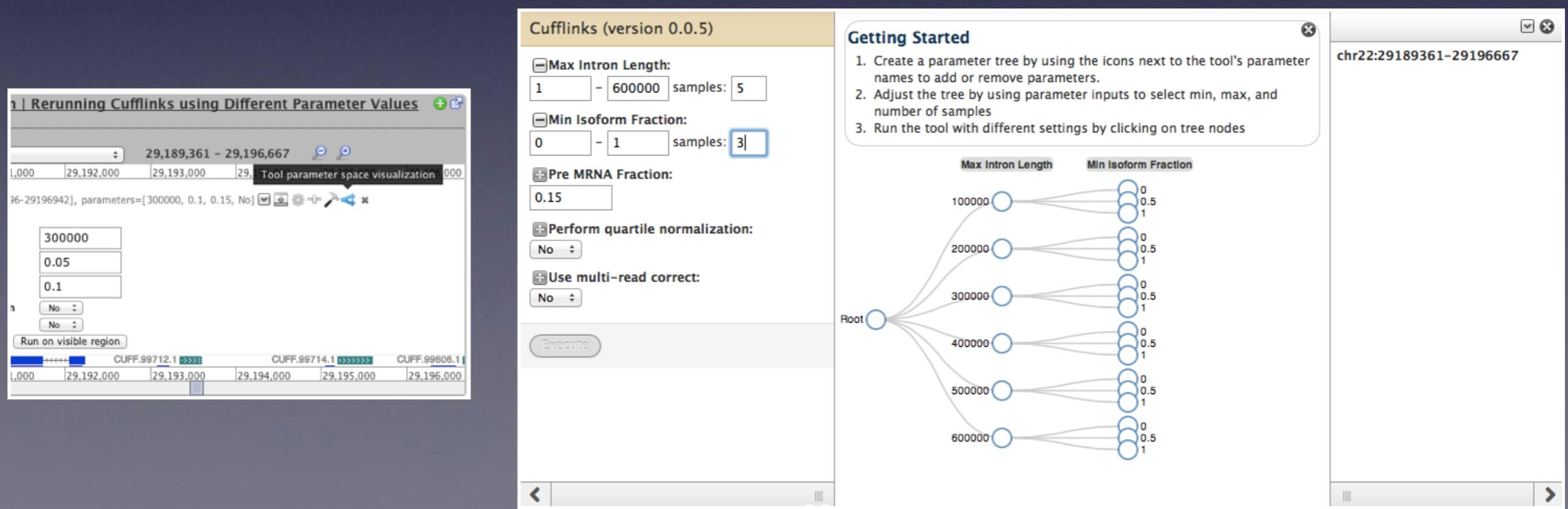
- Public Galaxy server is accessible at  
<http://usegalaxy.org>
- Learn about installing local instances at  
<http://getgalaxy.org>
- NGS analysis involves *large* data, and long compute times.
- For NGS analysis, a local (or cloud) installation of Galaxy is recommended.

# Questions?

Slides available at <http://mattshirley.com/presentations>

# Examples

- Basic protocols for Galaxy: Using Galaxy to Perform Large-Scale Interactive Data Analyses
- Parameter-space visualization: TopHat/CuffLinks RNA-seq optimization



# Galaxy on AWS (“the cloud”)



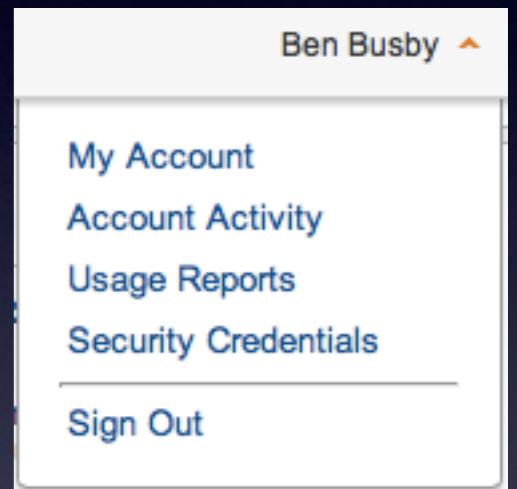
<http://xkcd.com/1117/>

# Using the “cloud launch” tool at Galaxy Main

## I. Log in to AWS EC2 management console

<http://console.aws.amazon.com/ec2>

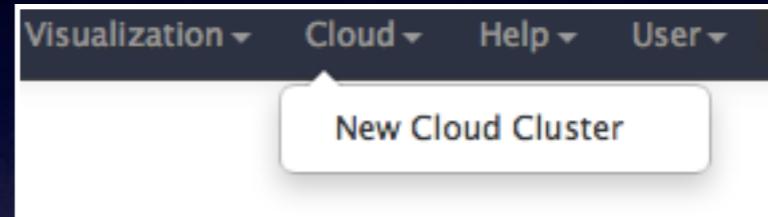
- Access your *Security Credentials* page
- Save your Access Key ID and Secret Access Key



Your Access Keys				
Created	Access Key ID	Secret Access Key	Status	
October 3, 2012	AKIAJRBU4D36GXYROQWQ	<a href="#">Show</a>	Active <a href="#">(Make Inactive)</a>	

# Automatic Galaxy cloud initialization

- I. Click “New Cloud Cluster” from “Cloud” toolbar of the main public instance.



Alternative mirror (please use sparingly)

2. Enter your AWS access key ID and secret key

**Launch a Galaxy Cloud Instance**

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

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

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

# Final steps before initialization

3. Enter a name for your cluster

4. Enter a password you can remember

5. Either choose an existing keypair or let the tool generate one for you

6. Select at least a “Large” instance type

7. Submit

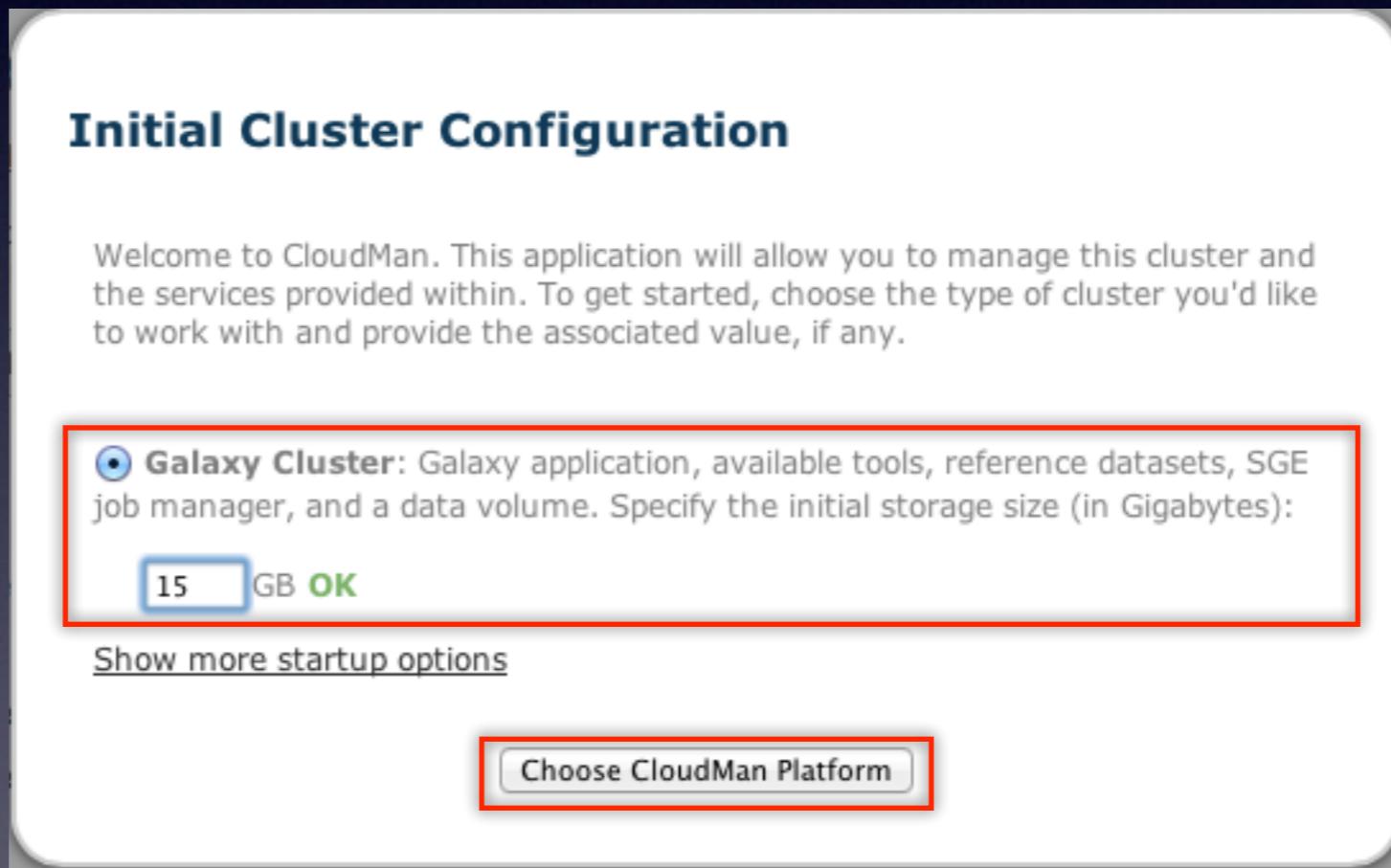
The screenshot shows a configuration interface for setting up a new AWS Lambda function. The fields include:

- Key ID:** Your Access Key ID (text input)
- Secret Key:** Your Secret Key (text input)
- Cluster Name:** NGS Cluster (dropdown menu)
- Cluster Password:** (redacted)
- Cluster Password - Confirmation:** (redacted)
- Key Pair:** clouzman\_keypair (dropdown menu)
- Instance Type:** Large (dropdown menu)

Below the form, a message reads: Requesting the instance may take a moment, please wait. A **Submit** button is at the bottom right.

# Galaxy on AWS (“the cloud”)

8. After logging in using the previously specified “cluster name” and “password”, specify the initial storage for the Galaxy cluster (you may need more than 15GB)



# Galaxy on AWS (“the cloud”)

9. After a few minutes, the Access Galaxy button will become accessible, signaling success

- Note that performance will be improved if autoscaling is turned on

**CloudMan Console**

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

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

**Status**

**Cluster name:** plato

**Disk status:** 51M / 15G (1%)

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

**Service status:** Applications Data

[Cluster status log](#)

# You're ready to analyze some data!

Next:

1. Learn how to shut down your cluster when you have finished.
2. Learn how to monitor your AWS usage.

# Terminate your cluster from within Cloudman

**CloudMan Console**

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

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

**Status**

**Cluster name:** plato

**Disk status:** 51M / 15G (1%)

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

**Service status:** Applications  Data

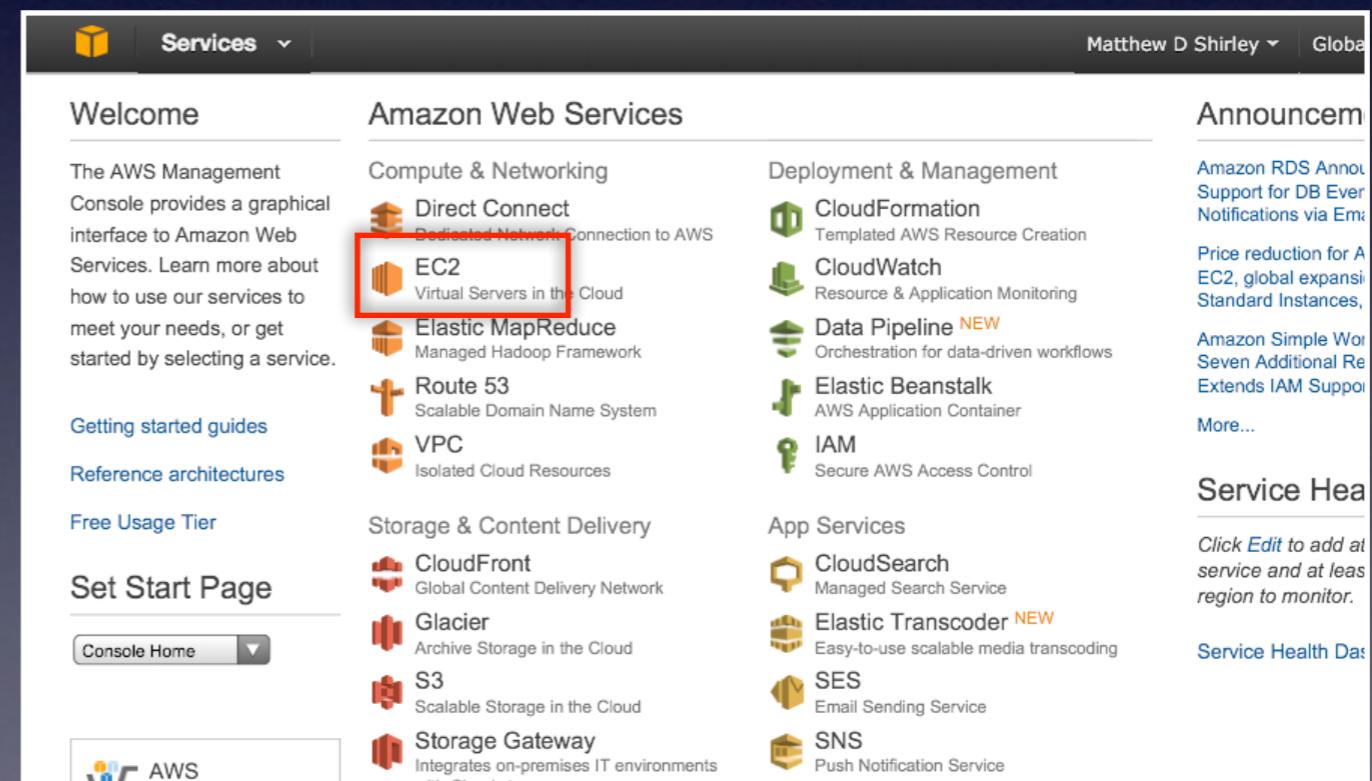
Autoscaling is **off**. Turn [on?](#)

[Cluster status log](#)

# Terminate your cluster from within AWS

1. Log in to your AWS console

2. Select EC2



# Shutting down your cluster

3. Select "instances" on the left and terminate any running EC2 instances

The screenshot shows the AWS EC2 Instances page. On the left, the navigation menu is open, with the 'Instances' section selected and highlighted with a red box. In the main 'My Instances' section, there are two EC2 instances listed:

Name	Type	Status	Status Checks	Alarm Status	Mon
empty	m1.large	terminated		none	basic
empty	m1.large	running	2/2 checks passed	none	basic

In the 'Instance Actions' dropdown menu, the 'Terminate' option is highlighted with a red box.

**Navigation**

**Region:** US East (N. Virginia)

**EC2 Dashboard**

**Events**

**INSTANCES**

**Instances** (highlighted with a red box)

Spot Requests

Reserved Instances

**IMAGES**

AMIs

Bundle Tasks

**ELASTIC BLOCK STORE**

Volumes

Snapshots

**NETWORK & SECURITY**

Security Groups

Elastic IPs

Placement Groups

Load Balancers

Key Pairs

Network Interfaces

**My Instances**

**Viewing:** All Instances

**Instance Management**

- Connect
- Get System Log
- Get Windows Admin Password
- Create Image (EBS AMI)
- Add/Edit Tags
- Change Security Group
- Change Source/Dest. Check
- Bundle Instance (instance store AMI)
- Launch More Like This
- Disassociate IP Address
- Change Termination Protection
- View/Change User Data
- Change Instance Type
- Change Shutdown Behavior
- Attach Network Interface
- Detach Network Interface
- Manage Private IP Addresses

**1 EC2 Instance selected**

**EC2 Instance**

ec2-54-242-6

**Description**

**AMI:** galaxy-cloudmar

**Zone:**

**Type:**

**Scheduled Events:** No scheduled events

**VPC ID:** -

**Instance Actions**

Terminate (highlighted with a red box)

Reboot

Stop

Start

**CloudWatch Monitoring**

Enable Detailed Monitoring

Disable Detailed Monitoring

Add/Edit Alarms

**Alarm Status:** none

**Security Groups:** galaxy, view rules

**State:** running

**Owner:** 994862681730

**Subnet ID:** -

# Shutting down your cluster

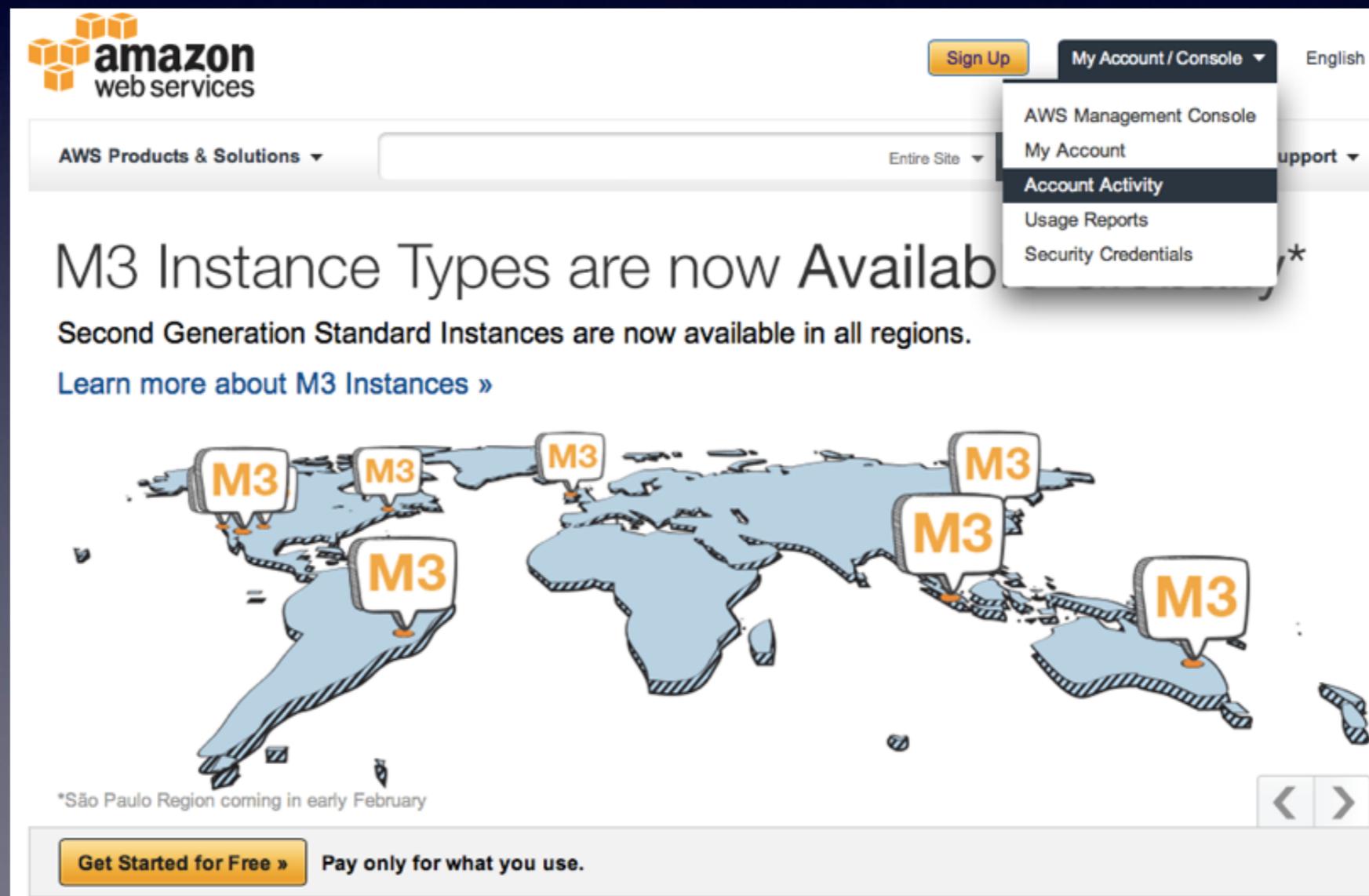
4. Also remember to delete any EBS volumes that persist

The screenshot shows the AWS Management Console interface for managing EBS volumes. On the left, there is a navigation sidebar with various service links. The 'VOLUMES' link under the 'ELASTIC BLOCK STORE' section is highlighted with a red box. The main content area is titled 'EBS Volumes' and displays a table of four volumes. The columns in the table are: Name, Volume ID, Capacity, Volume Type, Snapshot, Created, Zone, State, and Alarm. The volumes listed are all named 'empty' and have a status of 'in-use'. At the bottom of the main content area, a message says '0 Volumes selected' and 'Select a volume above'.

Name	Volume ID	Capacity	Volume Type	Snapshot	Created	Zone	State	Alarm
empty	vol-f2abf088	15 GiB	standard	snap-a95003c5	2012-10-07T00:02:01	us-east-1d	in-use	none
empty	vol-c5da81bf	700 GiB	standard	snap-5b030634	2012-10-07T00:10:58	us-east-1d	in-use	none
empty	vol-5dd88327	10 GiB	standard	snap-cf3746b3	2012-10-07T00:11:16	us-east-1d	in-use	none
empty	vol-16d8836c	15 GiB	standard	--	2012-10-07T00:11:29	us-east-1d	in-use	none

# Monitoring your usage!

I. Go to [aws.amazon.com](http://aws.amazon.com) and select “Account Activity”



# Monitoring your usage!

2. On your account activity page, select “Set your first billing alert”

**Account Activity**

Welcome Matthew D Shirley | Sign Out  
Account Number 8638-7837-2088

Your account is enabled for monitoring estimated charges. Set your first billing alert to receive an e-mail when charges reach a threshold you define. [Learn More](#)

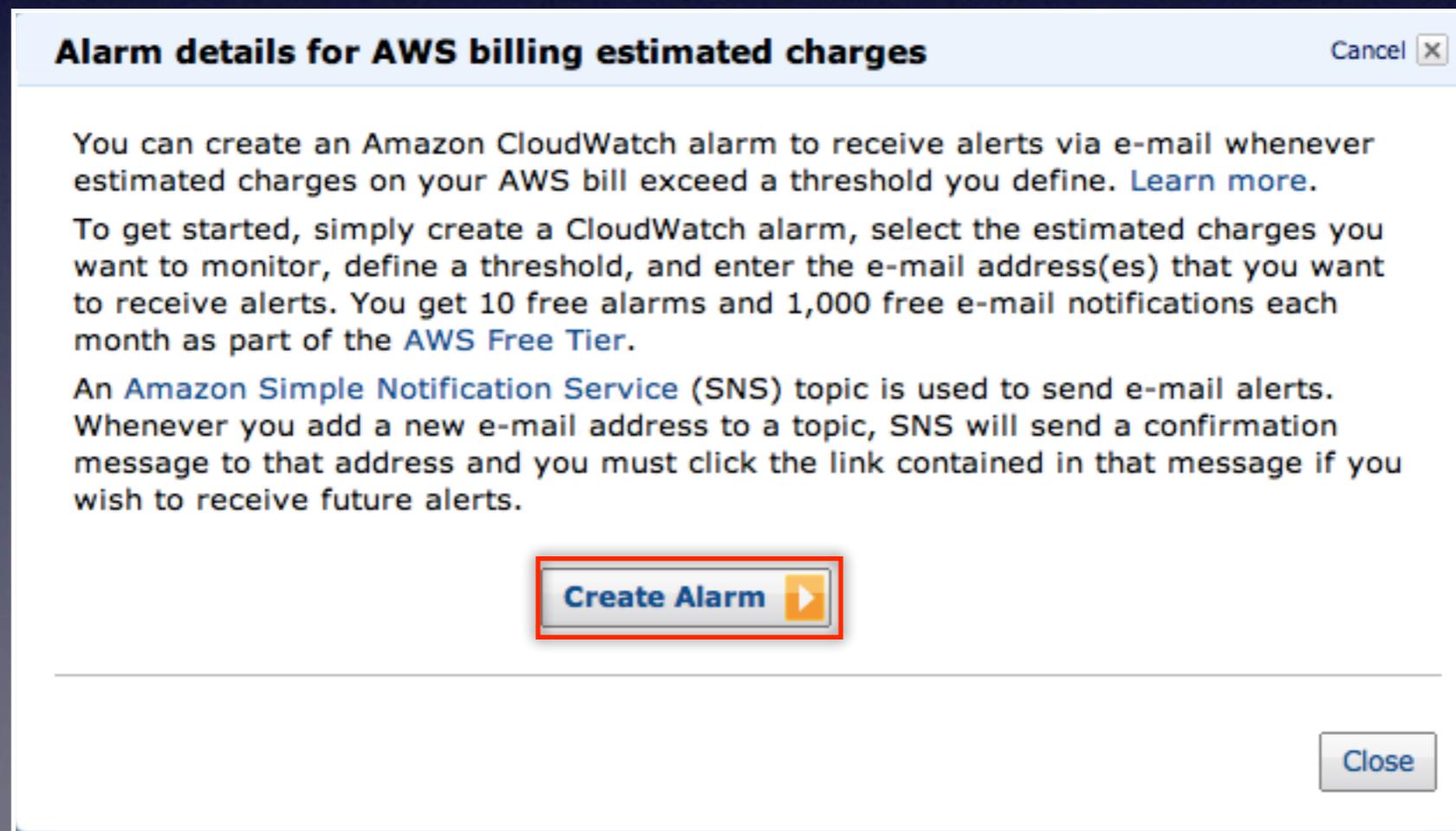
**This Month's Activity as of February 6, 2013**

The statement period for this report is February 1 - February 28, 2013. The charges on this page currently show activity through approximately 02/06/2013 09:43 GMT.

Select a different statement:

# Monitoring your usage!

## 3. Select “Create Alarm”



# Monitoring your usage!

4. Select an email address to send notifications to, and enter a threshold of total AWS service charges above which you wish to be notified.

**Create Billing Alarm**

Create an Amazon CloudWatch alarm to receive alerts via e-mail whenever estimated charges on your AWS bill exceed a threshold you define. The actual charges you will be billed in this statement period may differ from the charges shown on the notification. [Learn more](#).

To create an alarm, first choose whom to notify and then define when the notification should be sent

**Send a notification to:** NotifyMe (mdshw5@gmail.com) [create topic](#)

**With these recipients:** mdshw5@gmail.com

**Whenever charges for:** AWS Service Charges (total)

**Exceed:** USD \$ 100

Last statement period: USD 1.67 - AWS Service Charges (total)

**Name this alarm:** awsbilling-AWS-Service-Charges-total

**EstimatedCharges (None)**

1/26 1/29 2/1 2/4

0:00 0:00 0:00 0:00

[Cancel](#) [Create Alarm](#)