An Introduction to Galaxy

Daniel Blankenberg
The Galaxy Team
http://UseGalaxy.org

Overview

What is Galaxy?

What you can do in Galaxy

- analysis interface, tools and datasources
- data libraries
- workflows
- visualization
- sharing
- Pages

Galaxy 101 Exercise

The Vision

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

What is Galaxy?

GUI for genomics

- for complete analyses: analyze, visualize, share, publish

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

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Galaxy 101 Exercise

Galaxy Analysis Workspace

Galaxy

http://main.g2.bx.psu.edu/

Google

Galaxy

Analyze Data | Workflow | Shared Data | Visualization | Help | User

Tools — Options

Get Data
Send Data
ENCODE Tools
Lift-Over
Text Manipulation
Convert Formats
FASTA manipulation
Filter and Sort
Join, Subtract and Group
Extract Features
Fetch Sequences
Fetch Alignments
Get Genomic Scores
Operate on Genomic Intervals
Statistics
Graph/Display Data
Regional Variation
Multiple regression
Multivariate Analysis
Evolution
Metagenomic analyses
EMBOSS

NGS TOOLBOX BETA

NGS: QC and manipulation
NGS: Mapping
NGS: SAM Tools
NGS: Indel Analysis
NGS: Peak Calling

RGENETICS

SNP/WGA: Data; Filters
SNP/WGA: QC; LD; Plots
SNP/WGA: Statistical Models

Workflows

Map with Bowtie for Illumina

Will you select a reference genome from your history or use a built-in index?:
Use a built-in index
Built-ins were indexed using default options

Select a reference genome:
mm9
if your genome of interest is not listed - contact Galaxy team

Is this library mate-paired?:
Paired-end

Forward FASTQ file:
1: E18 PE.1 Reads
Must have Sanger-scaled quality values with ASCII offset 33

Reverse FASTQ file:
1: E18 PE.1 Reads
Must have Sanger-scaled quality values with ASCII offset 33

Maximum insert size for valid paired-end alignments (-X):
1000

The upstream/downstream mate orientation for valid paired-end alignment against the forward reference strand (--fr/--rf/--ff):
FR (for Illumina)

Bowtie settings to use:
Commonly used
For most mapping needs use Commonly used settings. If you want full control use Full parameter list

Suppress the header in the output SAM file:
Bowtie produces SAM with several lines of header information by default

Execute

What it does

Bowtie is a short read aligner designed to be ultrafast and memory-efficient. It is developed by Ben Langmead and Cole Trapnell. Please cite: Langmead B, Trapnell C, Pop M, Salzberg SL. Ultrafast and memory-efficient alignment of short DNA sequences to the human genome. Genome Biology 10:R25.

History — Options

imported: SNP Pileup Analysis for Sample E18

15: Variants from sample E18, consensus different, in RefSeq Genes
14: UCSC mm9 RefSeq Genes
13: Variants from sample E18 where consensus base different than ref. base
10: Variants from sample E18
9: Generate pileup on data 8
8: SAM-to-BAM on data 7
7: Map with Bowtie for Illumina on data 6 and data 5
6: E18 PE.2 Reads Groomed, Trimmed
5: E18 PE.1 Reads Groomed, Trimmed
4: E18 PE.2 Reads Groomed
3: E18 PE.1 Reads Groomed
2: E18 PE.2 Reads
1: E18 PE.1 Reads

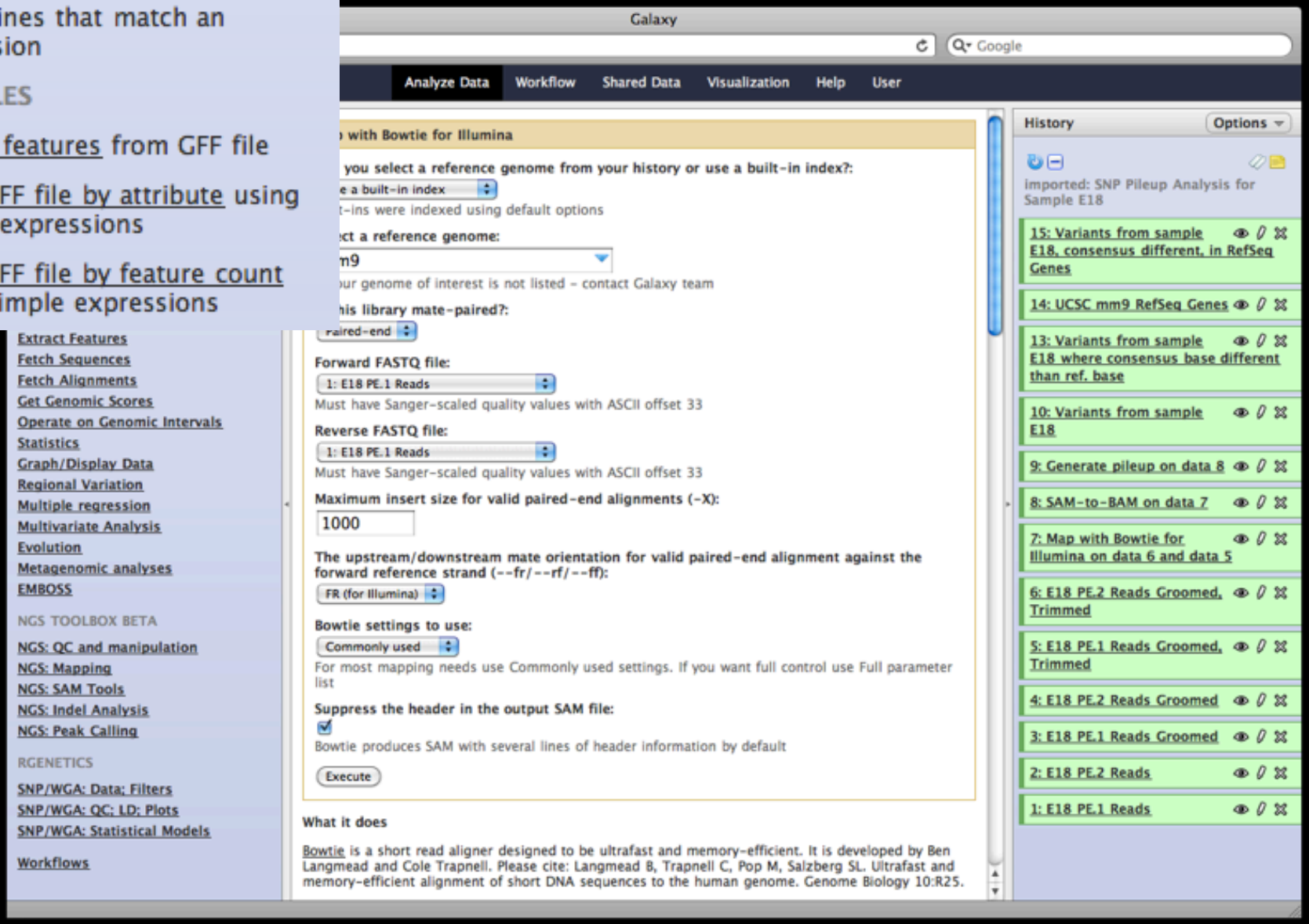
xy Analysis Workspace

Filter and Sort

- Filter data on any column using simple expressions
- Sort data in ascending or descending order
- Select lines that match an expression

GFF FILES

- Extract features from GFF file
- Filter GFF file by attribute using simple expressions
- Filter GFF file by feature count using simple expressions



xy Analysis Workspace

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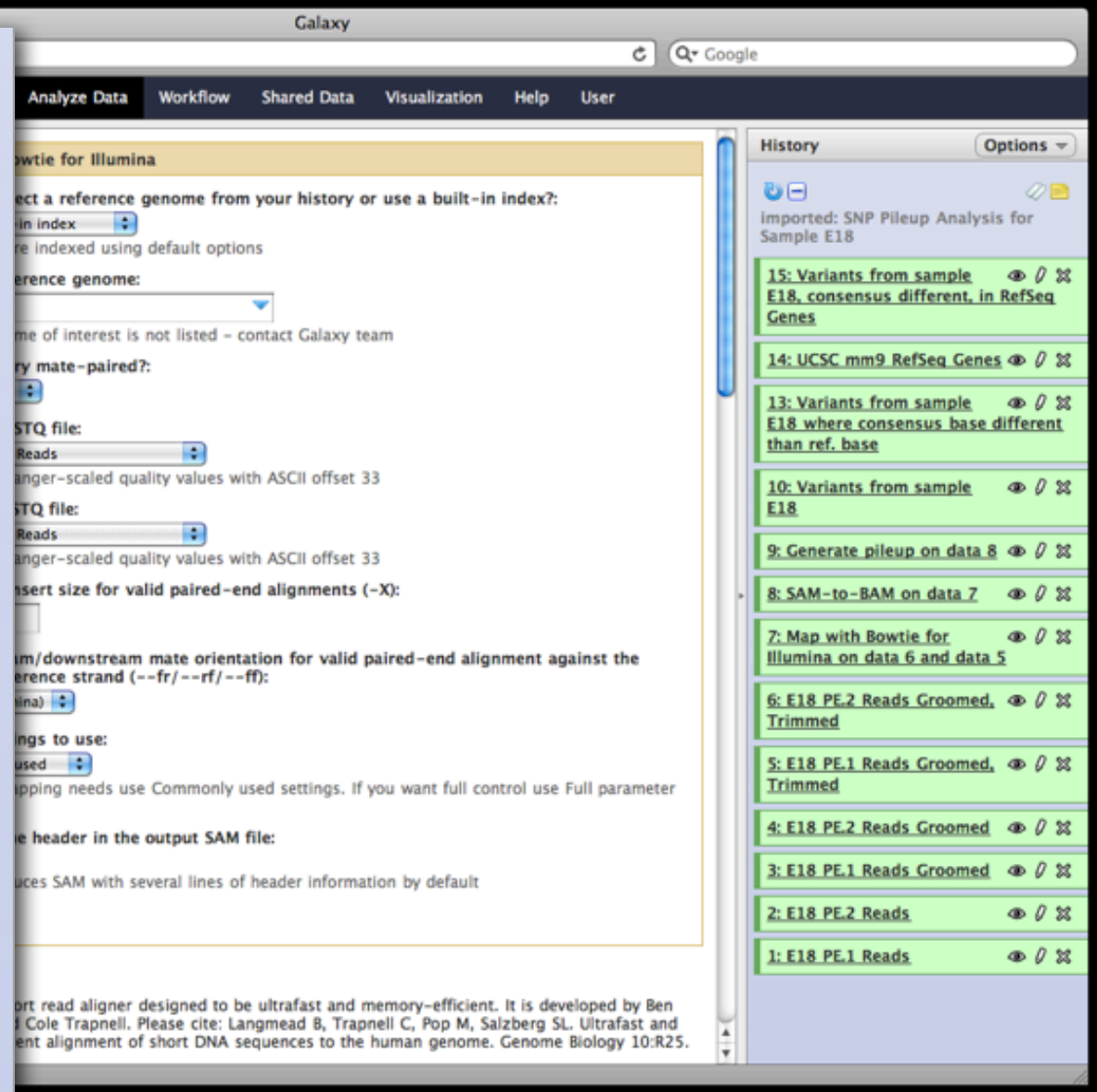
- E
- Fi si
- Fi u

Operate on Genomic Intervals

- Intersect the intervals of two queries
- Subtract the intervals of two queries
- Merge the overlapping intervals of a query
- Concatenate two queries into one query
- Base Coverage of all intervals
- Coverage of a set of intervals on second set of intervals
- Complement intervals of a query
- Cluster the intervals of a query
- Join the intervals of two queries side-by-side
- Get flanks returns flanking region/s for every gene
- Fetch closest feature for every interval
- Profile Annotations for a set of genomic intervals



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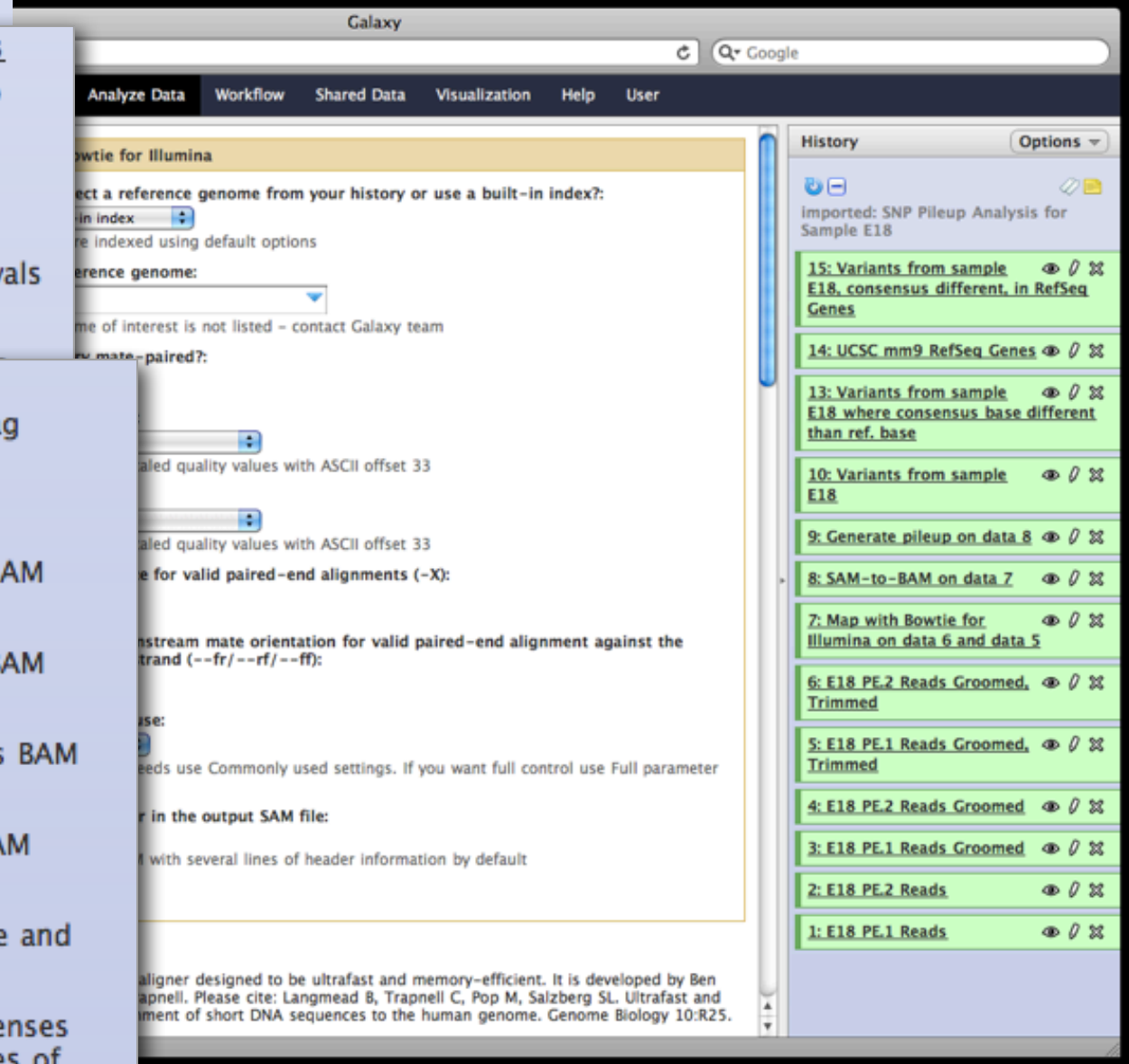
NGS: SAM Tools

- Filter SAM on bitwise flag values
- Convert SAM to interval
- SAM-to-BAM converts SAM format to BAM format
- BAM-to-SAM converts BAM format to SAM format
- Merge BAM Files merges BAM files together
- Generate pileup from BAM dataset
- Filter pileup on coverage and SNPs
- Pileup-to-Interval condenses pileup format into ranges of bases



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NGS: SAM Too

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Filter pileup

Select dataset:

10: Variants from sample E18

which contains:

Pileup with six columns (simple)

See "Types of pileup datasets" below for examples

Do not consider read bases with quality lower than:

20

No variants with quality below this value will be reported

Do not report positions with coverage lower than:

3

Pileup lines with coverage lower than this value will be skipped

Only report variants?:

Yes

See "Examples 1 and 2" below for explanation

Convert coordinates to intervals?:

No

See "Output format" below for explanation

Print total number of differences?:

No

See "Example 3" below for explanation

Print quality and base string?:

Yes

See "Example 4" below for explanation

Execute

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Options

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Variants from sample consensus different, in RefSeq es

UCSC mm9 RefSeq Genes

Variants from sample where consensus base different n ref. base

Variants from sample

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Analysis

Filter and Sort

- Filter data on any co simple expressions
- Sort data in ascendir descending order
- Select lines that mat

Operate on Geno

- Intersect the in queries
- Subtract the int queries
- Merge the over of a query

NGS: SAM To

- Filter SAM values
- Convert SA
- SAM-to-BA format to
- BAM-to-SA format to
- Merge BAM files togeth
- Generate p dataset
- Filter pileup on coverage and SNPs
- Pileup-to-Interval condenses pileup format into ranges of bases

This dataset is large and only the first megabyte is shown below.
Show all | Save

chr10	6882036	6882037	A	A	107	0	60	32	.$..,.....C.....
chr10	14243075		14243076		G	G	96	0	60 35 t.
chr10	14243079		14243080		C	C	106	0	60 35 ..
chr10	14465082		14465083		T	K	173	176	60 35 GG
chr10	14465083		14465084		G	K	144	144	60 35 ..
chr10	14465084		14465085		T	T	117	0	60 38 ..
chr10	14465085		14465086		G	G	70	0	60 38 ..
chr10	14465257		14465258		C	C	79	0	60 42 ..
chr10	14465258		14465259		A	A	137	0	60 46 ..
chr10	14465263		14465264		A	A	136	0	60 61 ..
chr10	14465366		14465367		A	A	101	0	60 38 g$
chr10	14465371		14465372		G	G	137	0	60 50 .$
chr10	14465410		14465411		G	G	184	0	60 69 .$
chr10	14465447		14465448		T	T	186	0	60 65 .$
chr10	14465456		14465457		G	G	193	0	60 70 ..
chr10	14465465		14465466		T	T	177	0	60 63 .$
chr10	14465485		14465486		C	T	129	129	60 34 t$
chr10	14465569		14465570		T	T	219	0	60 84 .
chr10	14465581		14465582		G	G	240	0	60 84 ,$
chr10	14465586		14465587		C	C	248	0	60 82 .$
chr10	14465621		14465622		C	C	134	0	60 49 ..
chr10	14465658		14465659		C	C	134	0	60 49 ,,
chr10	14465660		14465661		T	T	153	0	60 55 ,
chr10	14465691		14465692		G	G	128	0	60 42 .$
chr10	14465778		14465779		C	C	89	0	60 34 ,$
chr10	14465791		14465792		G	G	104	0	60 33 ,$
chr10	14465881		14465882		G	G	110	0	60 41 ..
chr10	17445088		17445089		A	A	103	0	60 34 ..
chr10	17445271		17445272		A	A	55	0	60 34 ..
chr10	17731269		17731270		T	T	113	0	60 42 ,$
chr10	19928287		19928288		G	A	135	135	60 36 AA
chr10	19928468		19928469		C	T	132	132	60 35 T$
chr10	19928488		19928489		A	A	119	0	60 44 ..
chr10	19928494		19928495		C	T	138	138	60 37 TT
chr10	19928527		19928528		A	A	134	0	60 45 ,
chr10	19928538		19928539		G	G	144	0	60 52 ,$
chr10	19928543		19928544		A	G	147	147	60 40 Gg
chr10	19928741		19928742		T	T	80	0	60 30 ,
chr10	20799826		20799827		G	G	117	0	60 37 ,$
chr10	28750217		28750218		C	T	138	138	60 37 TT
chr10	28750397		28750398		A	C	154	211	60 64 C$
chr10	28750401		28750402		A	A	128	0	60 47 ,$
chr10	28750423		28750424		C	T	113	113	60 35 T$
chr10	28750438		28750439		A	A	95	0	60 36 .$
chr10	28750446		28750447		A	G	165	165	60 46 G$
chr10	28750487		28750488		A	A	80	0	60 31 ,
chr10	28750512		28750513		G	G	220	0	60 72 .$
chr10	28750548		28750549		G	C	255	255	60 97 C$
chr10	28750574		28750575		T	T	237	0	60 83 .$
chr10	28750577		28750578		T	T	234	0	60 82 ,$
chr10	28750578		28750579		T	T	242	0	60 76 ,$
chr10	28750593		28750594		G	G	220	0	60 75 .$
chr10	28750640		28750641		T	C	165	165	60 46 Cc
chr10	28750746		28750747		G	A	202	202	60 58 AA
chr10	28750766		28750767		A	G	205	205	60 59 G$
chr10	28750769		28750770		T	C	175	175	60 49 cc

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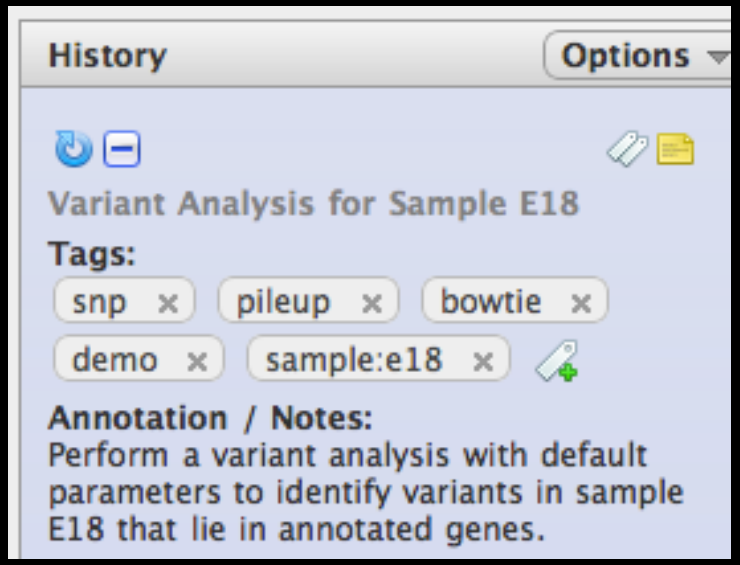
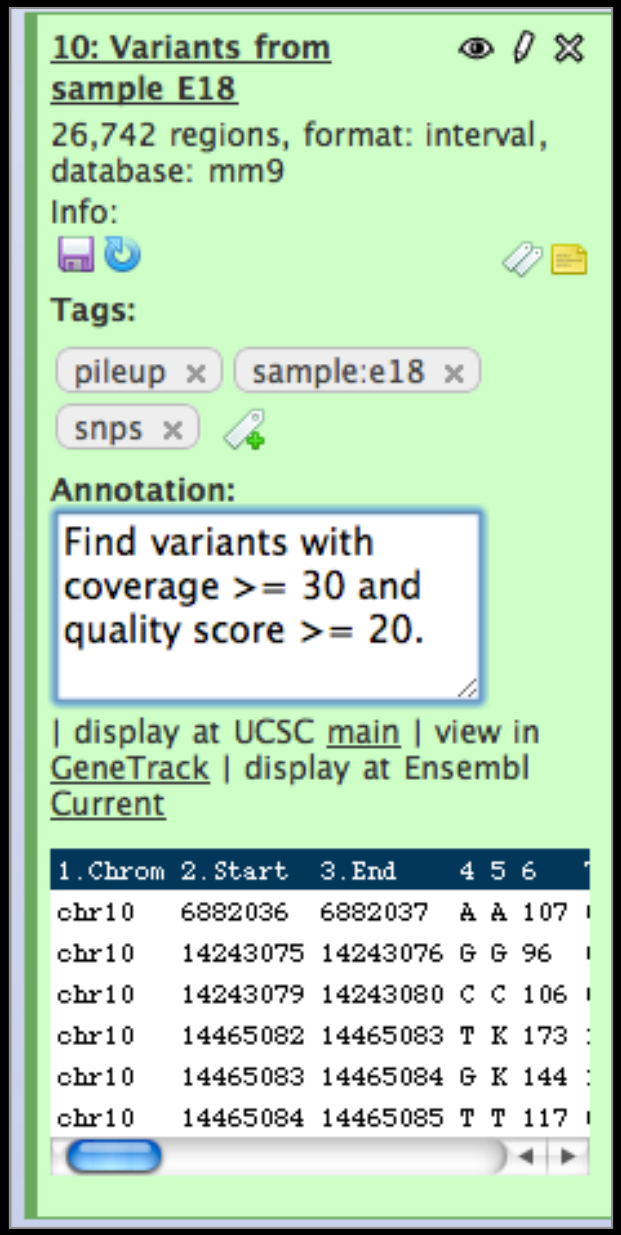
User Metadata





Datasources

Upload file from your computer

- FTP support for large datasets

UCSC table browser

BioMart

interMine / modMine

EuPathDB server

EncodeDB at NHGRI

EpiGRAPH server

Tool Suites

Text Manipulation
Format Converters
Filtering and Sorting
Join, Subtract, Group
Sequence Tools
Multi-species Alignment Tools
Genomic Interval Operations
Summary Statistics
Graphing / Plotting

Regional Variation
EMBOSS
Evolution / Phylogeny
RNA-seq
ChIP-seq
GATK
Picard
RGenetics
...and more

NGS: QC and manipulation

ILLUMINA DATA

- 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

GENERIC FASTQ MANIPULATION

- Filter FASTQ reads by quality score and length
- FASTQ Trimmer by column
- FASTQ Quality Trimmer by sliding window

Evolution

Metagenomic analyses

Human Genome Variation

EMBOSS

NGS TOOLBOX BETA

NGS: QC and manipulation

NGS: Mapping

ILLUMINA

- Map with Bowtie for Illumina
- Map with BWA for Illumina

ROCHE-454

- Lastz map short reads against reference sequence
- Megablast compare short reads against htgs, nt, and wgs databases
- Parse blast XML output

AB-SOLID

- Map with Bowtie for SOLiD

NGS: SAM Tools

NGS: Indel Analysis

NGS: Peak Calling

NGS: RNA Analysis

RGENETICS

SNP/WGA: Data; Filters

SNP/WGA: QC; LD; Plots

SNP/WGA: Statistical Models

Workflows

NGS TOOLBOX BETA

NGS: QC and manipulation

NGS: Mapping

NGS: SAM Tools

- Filter SAM on bitwise flag values
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- SAM-to-BAM converts SAM format to BAM format
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- Merge BAM Files merges BAM files together
- Generate pileup from BAM dataset
- Filter pileup on coverage and SNPs
- Pileup-to-Interval condenses pileup format into ranges of bases
- flagstat provides simple stats on BAM files

NGS: Indel Analysis

NGS: Peak Calling

NGS: RNA Analysis

RGENETICS

SNP/WGA: Data; Filters

SNP/WGA: QC; LD; Plots

SNP/WGA: Statistical Models

Workflows

NGS: SAM Tools

NGS: Indel Analysis

- Filter Indels for SAM
- Extract indels from SAM
- Indel Analysis

NGS: Peak Calling

- MACS Model-based Analysis of ChIP-Seq
- GeneTrack indexer on a BED file
- Peak predictor on GeneTrack index

NGS: RNA Analysis

RNA-SEQ

- Tophat Find splice junctions using RNA-seq data
- Cufflinks transcript assembly and FPKM (RPKM) estimates for RNA-Seq data
- Cuffcompare compare assembled transcripts to a reference annotation and track Cufflinks transcripts across multiple experiments
- Cuffdiff find significant changes in transcript expression, splicing, and promoter use

FILTERING

- Filter Combined Transcripts using tracking file

Dozens of tools for different HTS applications packaged with Galaxy

VCF Tools

- Intersect Generate the intersection of two VCF files
- Annotate a VCF file (dbSNP, hapmap)
- Filter a VCF file
- Extract reads from a specified region

NGS: Picard (beta)

QC/METRICS FOR SAM/BAM

- BAM Index Statistics
- Sam/bam Alignment Summary Metrics
- Sam/bam GC Bias Metrics
- Estimate Library Complexity
- Insertion size metrics for PAIRED data
- Sam/bam Hybrid Selection Metrics For (eg exome) targeted data

BAM/SAM CLEANING

- Add or Replace Groups
- Reorder SAM
- Replace Sam Header
- Paired Read Mate Fixer for paired data
- Mark Duplicate reads

FASTQC: FASTQ/SAM/BAM

- Fastqc: Fastqc QC using FastQC from Babraham

NGS: GATK Tools Alpha

REALIGNMENT

- Realigner Target Creator for use in local realignment
- Indel Realigner – perform local realignment

BASE RECALIBRATION

- Count Covariates on BAM files
- Table Recalibration on BAM files
- Analyze Covariates – perform local realignment

GENOTYPING

- Unified Genotyper SNP and indel caller

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Galaxy 101 Exercise

Data Library "Bushman"

Library Actions

These are the data underlying the analyses reported in the paper "Complete Khoisan and Bantu genomes from southern Africa" by S. C. Schuster et al., published in the journal Nature, February 18, 2010. Each data set can be downloaded and/or imported into a Galaxy history. Data will be updated as the project progresses.

Name	Information	Uploaded By	Date	File Size
All SNPs in personal genomes	Summary table of SNPs in all individuals	greg@bx.psu.edu	2010-01-28	676.8 Mb
Alu insertions in KB1		greg@bx.psu.edu	2010-02-10	14.9 Kb
Alu insertions in NB1		greg@bx.psu.edu	2010-02-10	6.5 Kb
KB1_microsatellites.txt		greg@bx.psu.edu	2010-02-15	3.5 Mb
NB1_microsatellites.txt		greg@bx.psu.edu	2010-02-15	828.5 Kb
amino acid differences with functional predictions		greg@bx.psu.edu	2010-02-05	1.1 Mb
gene copy number in HP2 and other personal genomes		greg@bx.psu.edu	2010-02-15	2.1 Mb
indels in ABT		greg@bx.psu.edu	2010-02-03	105.3 Kb
indels in KB1		greg@bx.psu.edu	2010-02-03	14.2 Mb
indels in MD8		greg@bx.psu.edu	2010-02-03	109.8 Kb
indels in NB1		greg@bx.psu.edu	2010-02-03	[illegible] Kb
indels in TK1		greg@bx.psu.edu	2010-02-03	123.2 Kb
novel SNPs in ABT		greg@bx.psu.edu	2010-02-09	9.4 Mb
novel SNPs in KB1		greg@bx.psu.edu	2010-02-09	16.9 Mb
novel SNPs in MD8		greg@bx.psu.edu	2010-02-09	594.1 Kb
novel SNPs in NB1		greg@bx.psu.edu	2010-02-09	4.1 Mb
novel SNPs in TK1		greg@bx.psu.edu	2010-02-09	722.6 Kb
sequenced exon-containing intervals		greg@bx.psu.edu	2010-02-03	3.1 Mb

For selected items: Import into your current history Go

http://usegalaxy.org/bushman

Managing Libraries

Loading Data

- Upload a single file
- Import datasets from a Galaxy history
- Upload a directory of files
- Directly from Sequencer using Sample Tracking System

Accessing Data

- Data contents on disk are not copied
- Dataset security: public, Role-based access control (RBAC)

Annotating Library Data: Library Templates

- Build user fillable forms
- Associate at Library, Folder or Dataset level

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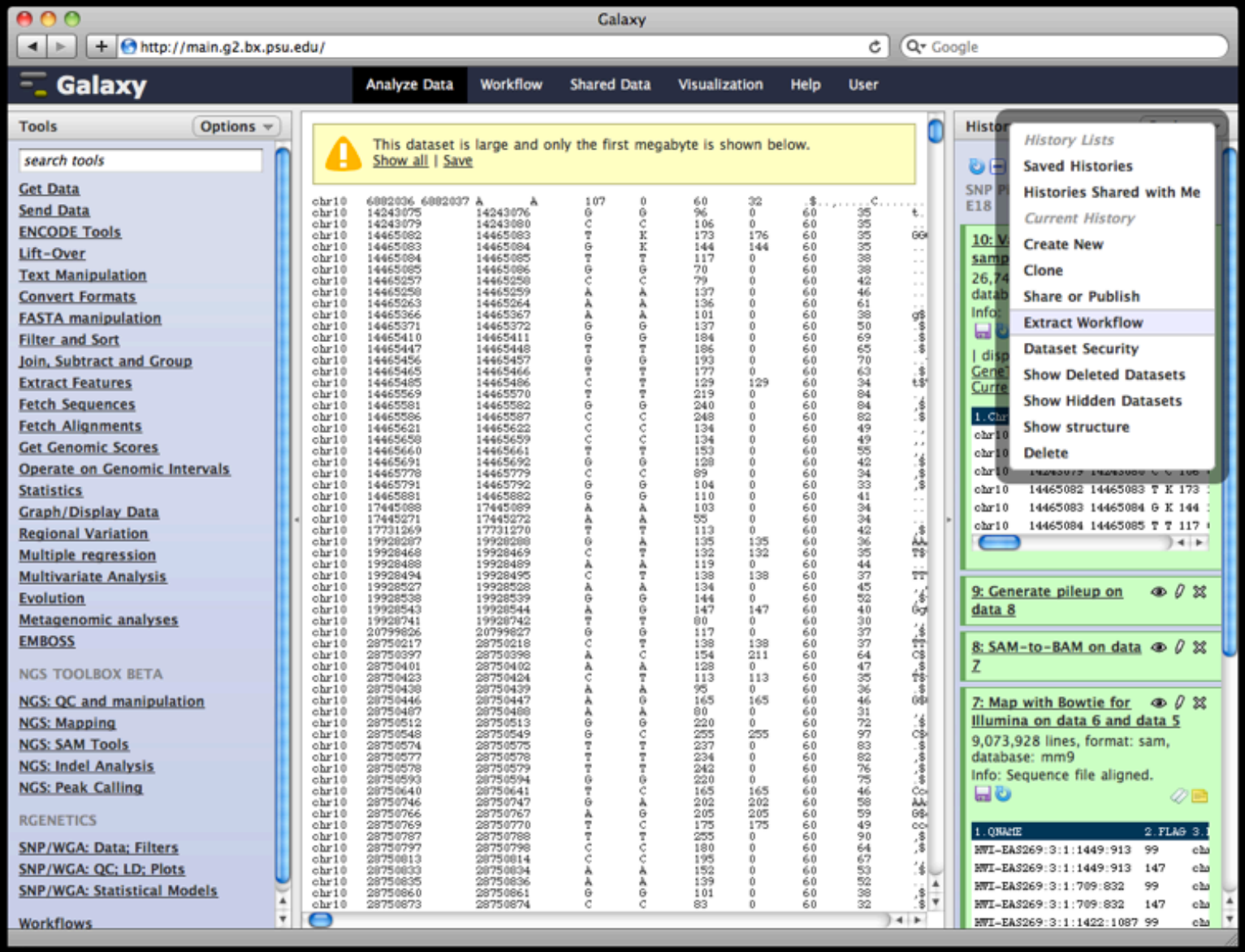
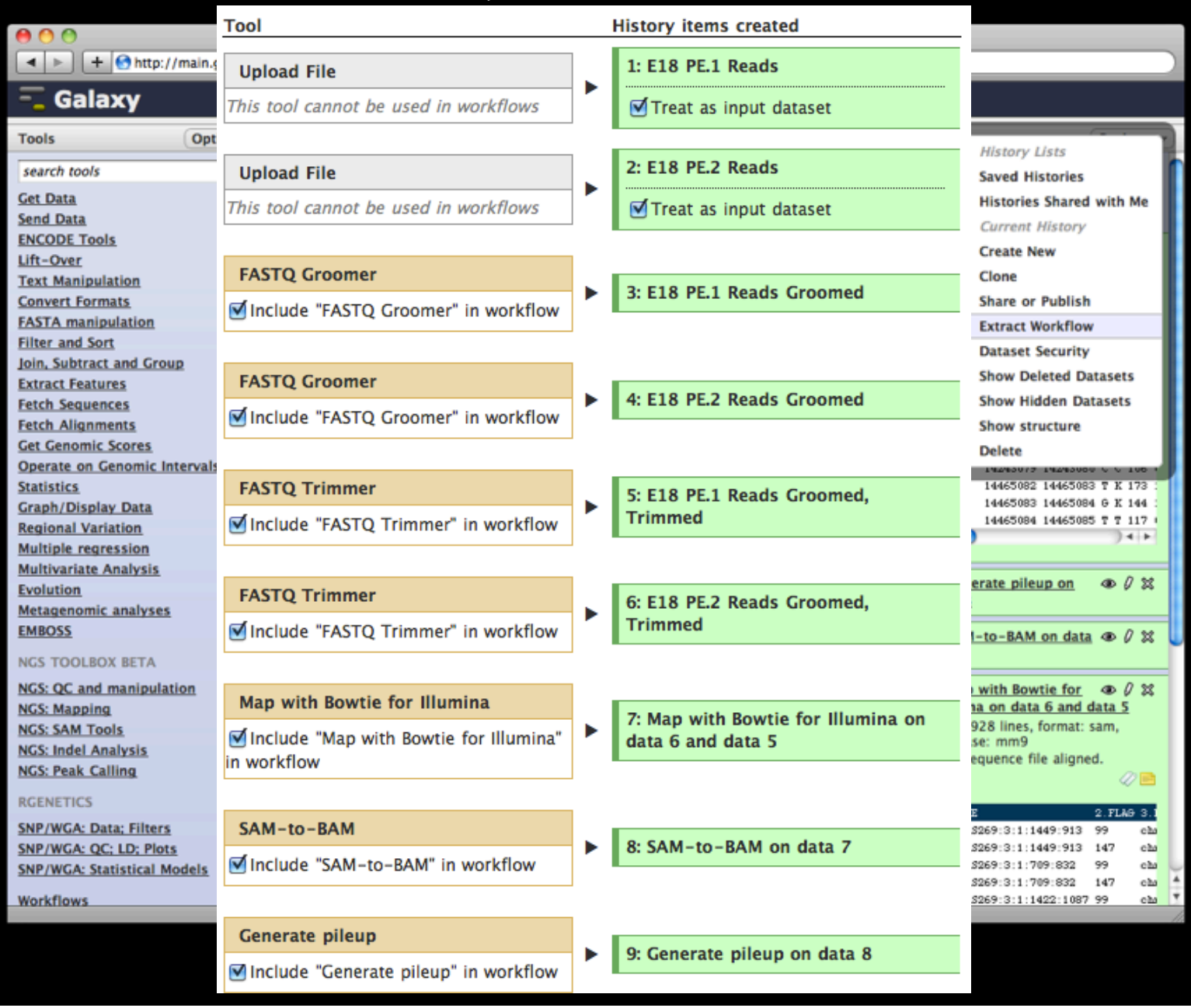
Galaxy Workflows



Galaxy Workflows



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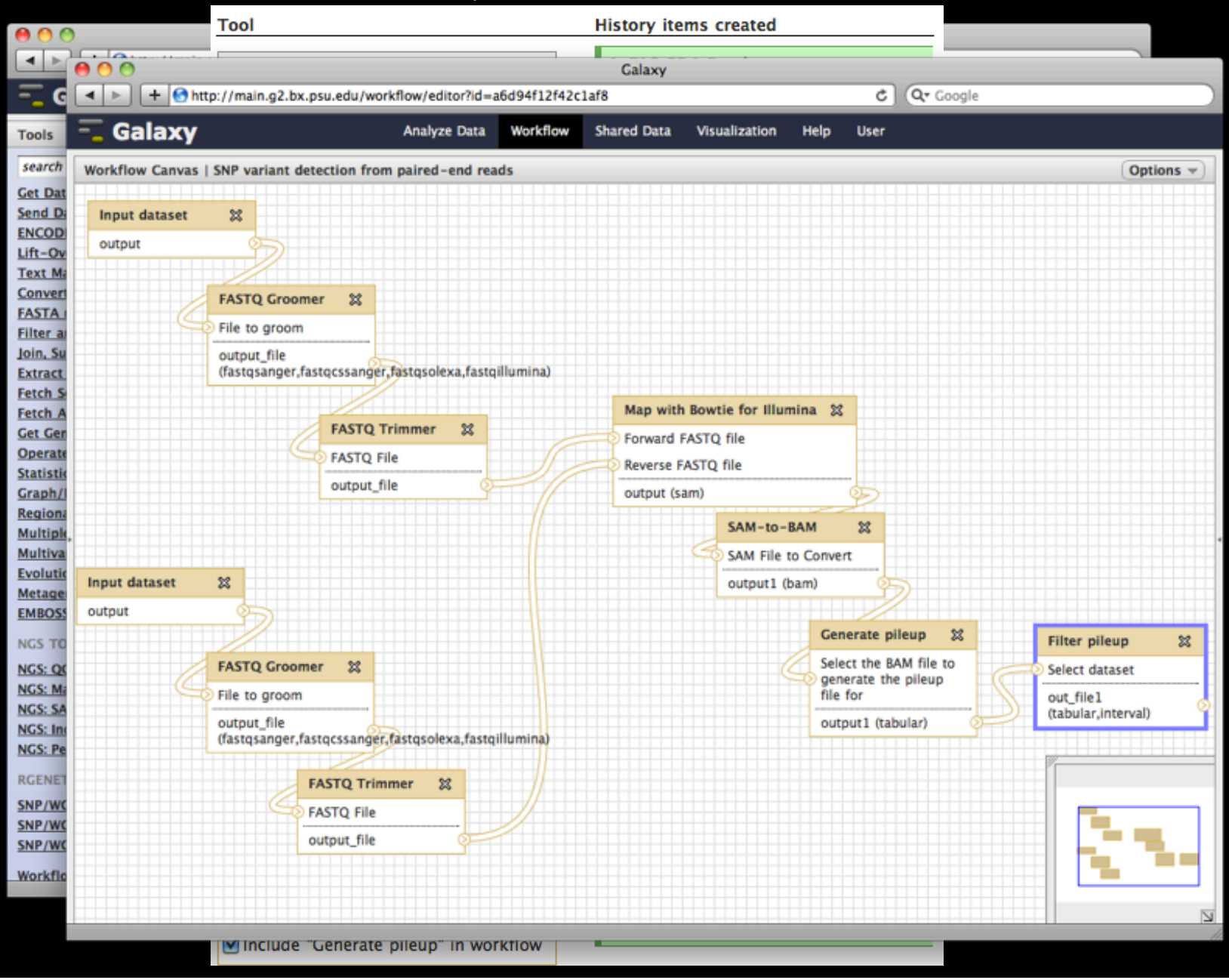

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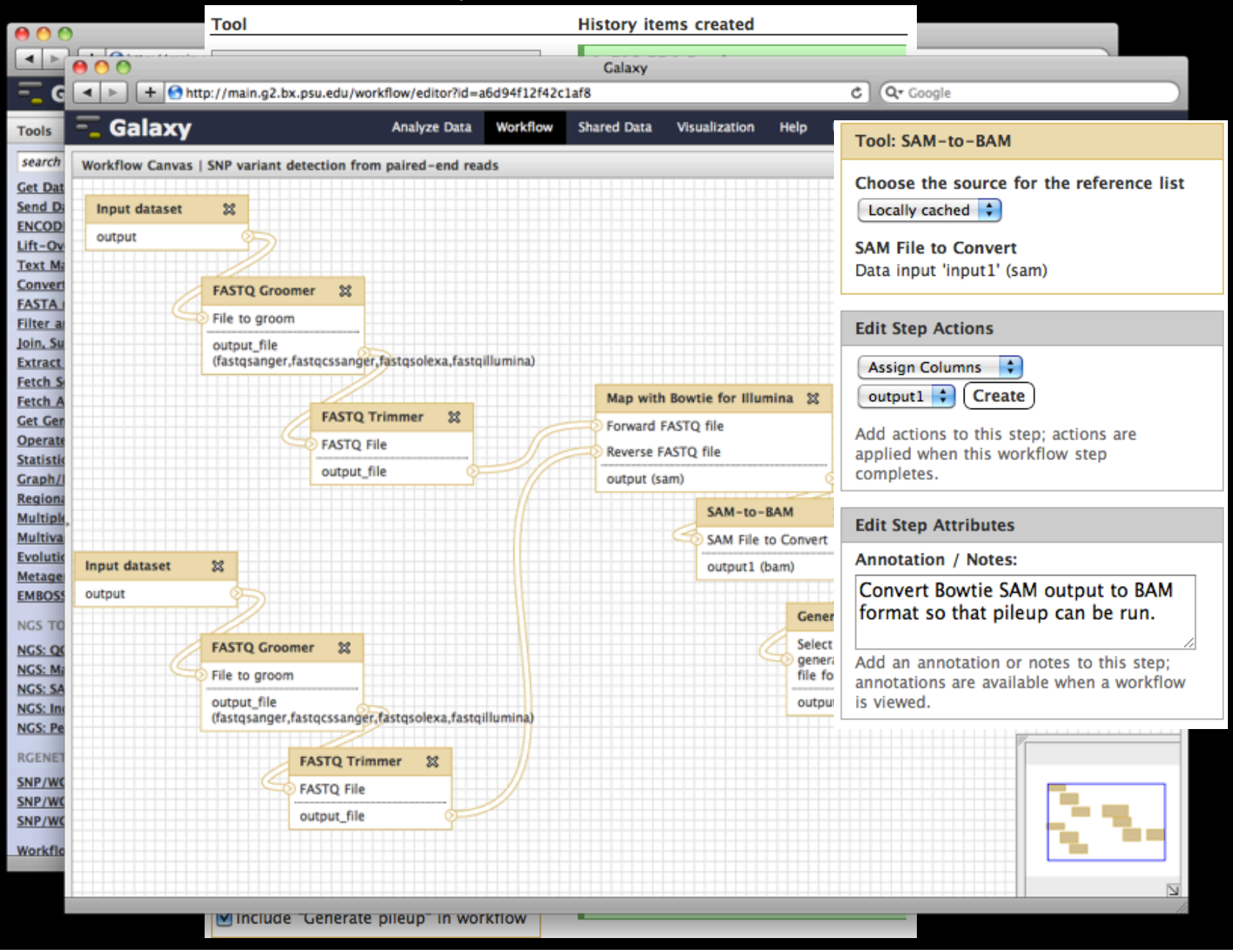
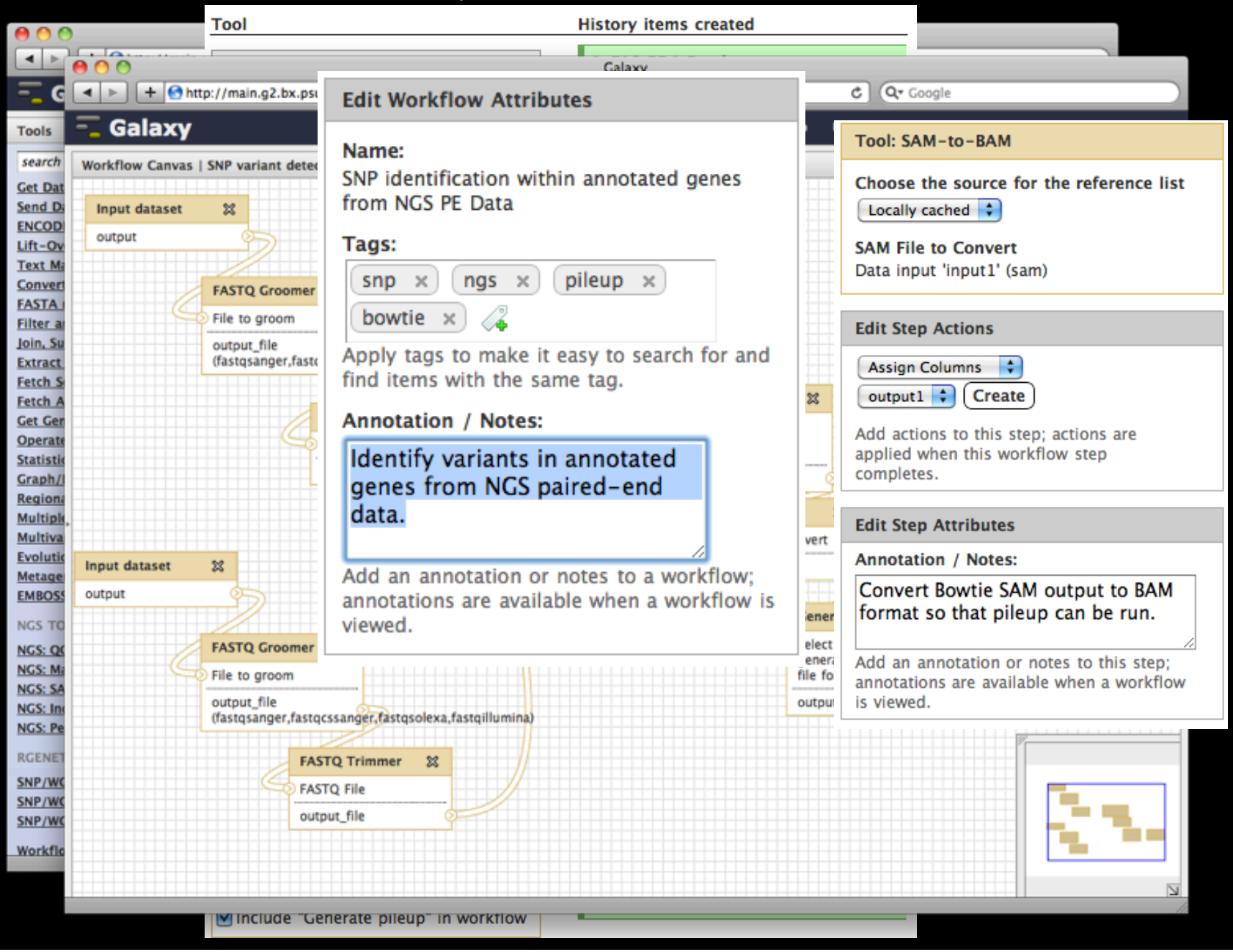
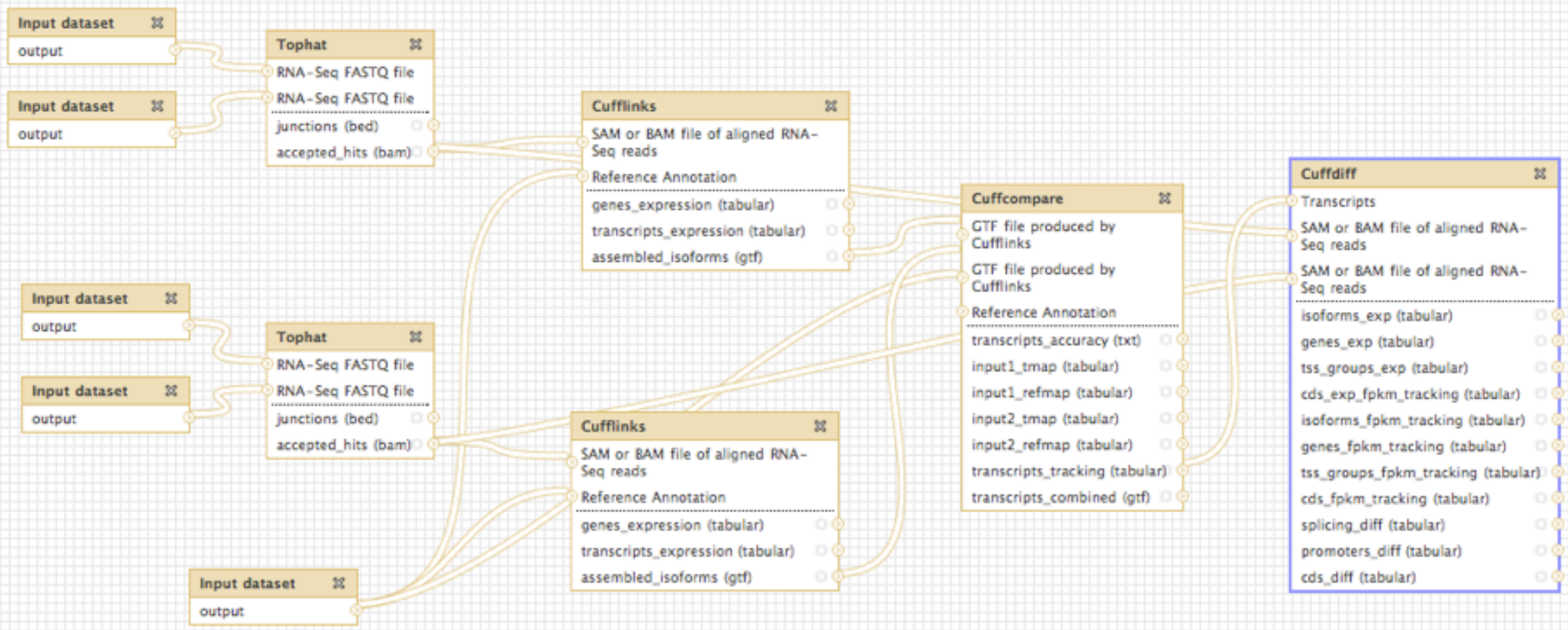
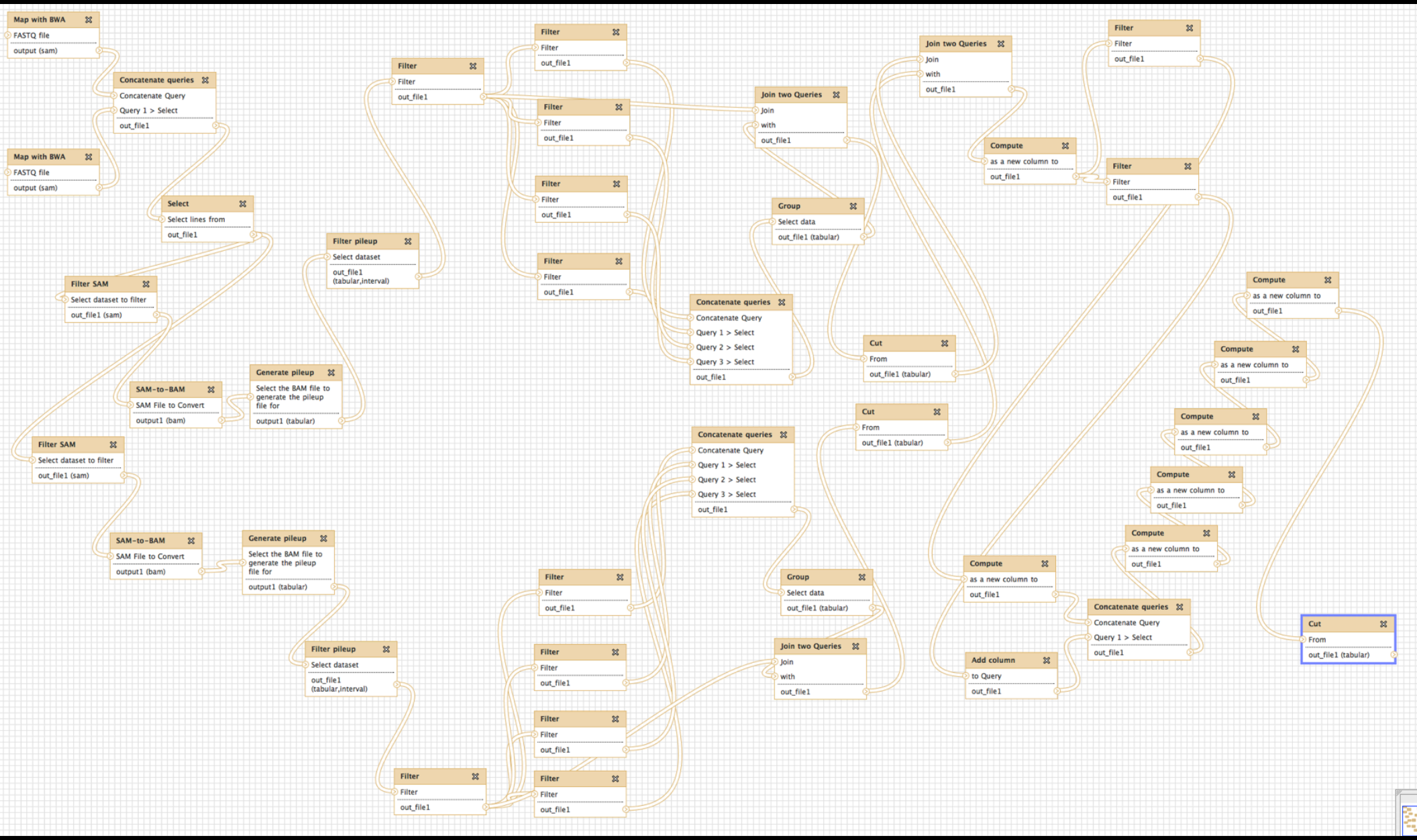


Galaxy Workflows





Example: Workflow for differential expression analysis of RNA-seq using Tophat/Cufflinks tools



Example: Diagnosing low-frequency heterosplasmic sites in two tissues from the same individual

Overview

What is Galaxy?

What you can do in Galaxy

- analysis interface, tools and datasources
- data libraries
- workflows
- visualization
- sharing
- Pages

Galaxy 101 Exercise

Visualize

Send data results to external genome browsers

Trackster: Galaxy's genome browser

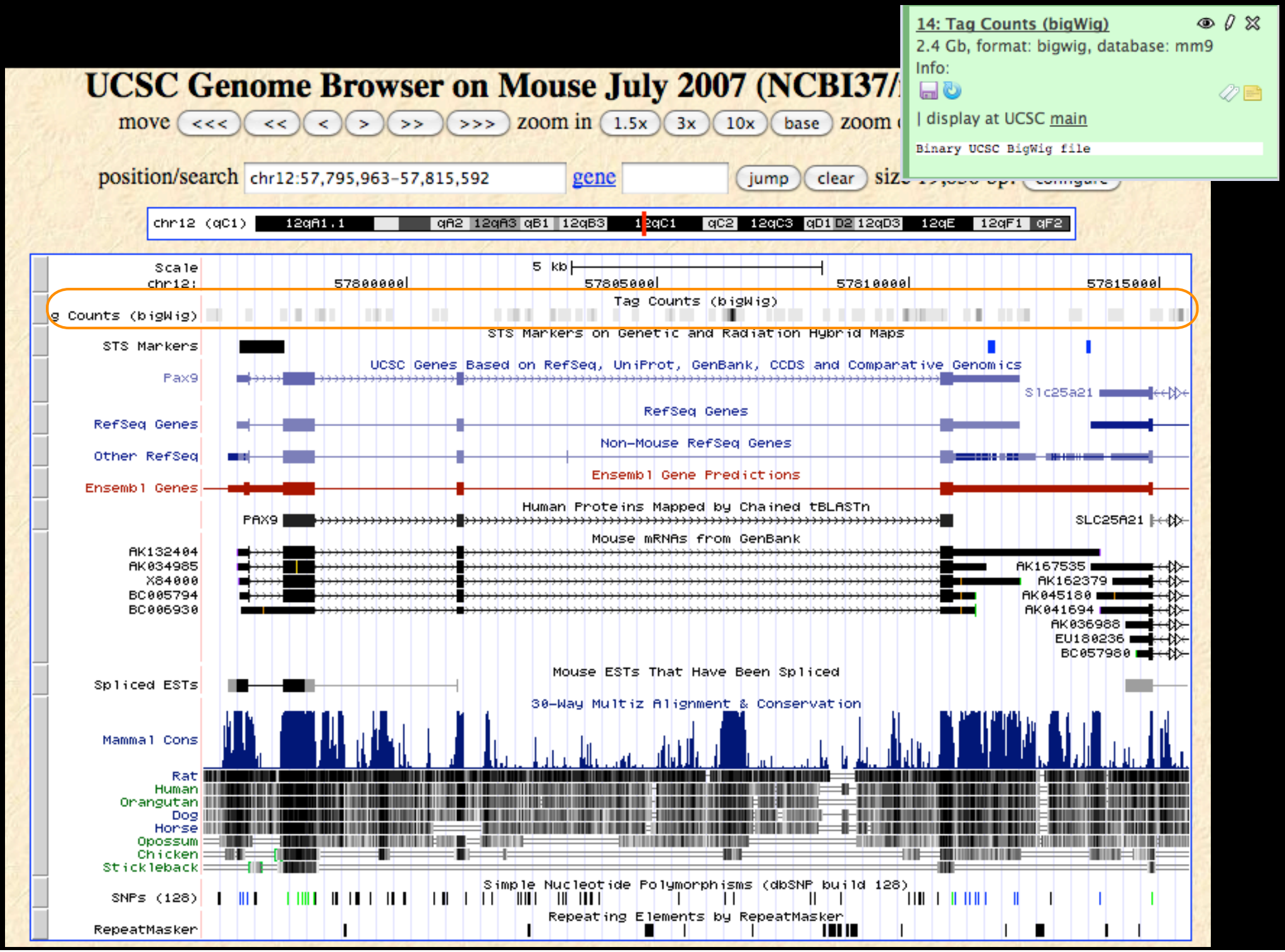
External Genome Browsers

UCSC

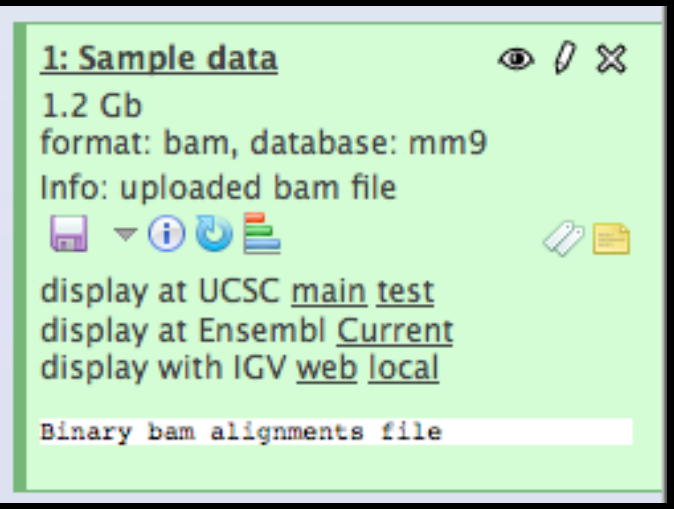
Ensembl

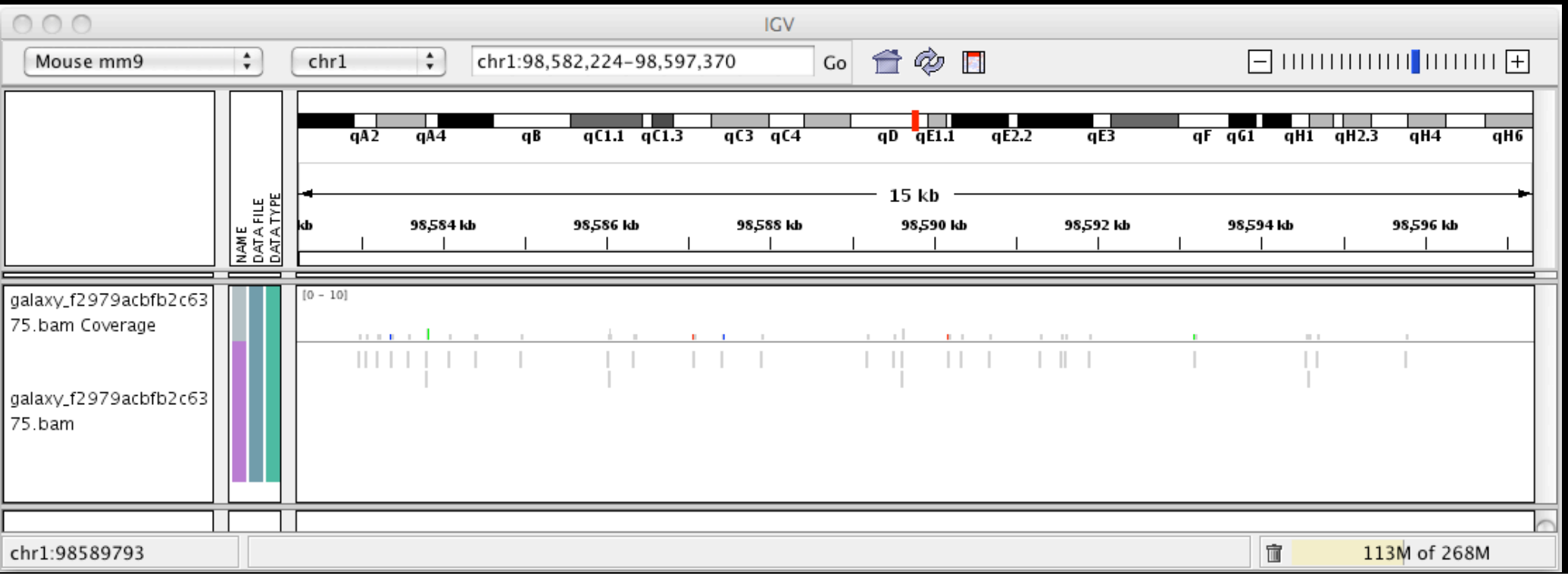
GBrowse

IGV


14: Tag Counts (bigWig)
2.4 Gb, format: bigwig, database: mm9
Info:
| display at UCSC main
Binary UCSC BigWig file
UCSC Genome Browser on Mouse July 2007 (NCBI37/
move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom
position/search chr12:57,795,963-57,815,592 gene jump clear
chr12 (qC1) 12qA1.1 qA2 12qA3 qB1 12qB3 12qC1 qC2 12qC3 qD1 D2 12qD3 12qE 12qF1 qF2
Scale
chr12:
5 kb
57800000
57805000
57810000
57815000
Tag Counts (bigWig)
STS Markers
STS Markers on Genetic and Radiation Hybrid Maps
UCSC Genes Based on RefSeq, UniProt, GenBank, CCDS and Comparative Genomics
Pax9
Slc25a21
RefSeq Genes
Other RefSeq
Non-Mouse RefSeq Genes
Ensembl Genes
Ensembl Gene Predictions
Human Proteins Mapped by Chained tBLASTn
PAX9
SLC25A21
Mouse mRNAs from GenBank
AK132404
AK034985
X84000
BC005794
BC006930
AK167535
AK162379
AK045180
AK041694
AK036988
EU180236
BC057980
Spliced ESTs
Mouse ESTs That Have Been Spliced
30-Way Multiz Alignment & Conservation
Mammal Cons
Rat
Human
Orangutan
Dog
Horse
Opossum
Chicken
Stickleback
SNPs (128)
Simple Nucleotide Polymorphisms (dbSNP build 128)
RepeatMasker
Repeating Elements by RepeatMasker

Integrative Genomics Viewer (IGV)





Galaxy

- tool integration framework
- heavy focus on usability
- sharing, publication framework

Genome Browser

- physical depiction of data
- visually identify correlations
- find interesting regions, features

Trackster

Trackster

View your data from within Galaxy

- No data transfers to external site
- Use it locally, even without internet access

Supports common filetypes

- BAM, BED, GFF/GTF, WIG

Unique features

- custom genomes
- highly interactive

Galaxy | Published Visualization | GCC2011-1: Viewing and Navigating

http://main.g2.bx.psu.edu/u/jeremy/v/gcc2011-1-viewing-and-navigating

Galaxy

Analyze Data | Workflow | Shared Data | Visualization | Help | User

Published Visualizations | jeremy | GCC2011-1: Viewing and chr19 1,290 - 4,168,475

0 | 1,000,000 | 2,000,000 | 3,000,000 | 4,000,000

UCSC Main on Human: knownGene (chr19) — Auto (Squish)

UCSC Main on Human: all_est (chr19) — Auto (coverage histogram)

11431

UCSC Main on Human: phyloP46wayPrimates (chr19) — Histogram

1

-1

h1-hESC Tophat Mapped Reads — Auto (coverage histogram)

8732

h1-hESC Cufflinks assembled transcripts — Auto (Squish)

0 | 1,000,000 | 2,000,000 | 3,000,000 | 4,000,000

Display a menu

Galaxy | Published Visualization | GCC2011-1: Viewing and Navigating

http://main.g2.bx.psu.edu/u/jeremy/v/gcc2011-1-viewing-and-navigating

Galaxy

Analyze Data | Workflow | Shared Data | Visualization | Help | User

Published Visualizations | jeremy | GCC2011-1: Viewing and chr19 625,719 - 682,581

630,000 640,000 650,000 660,000 670,000 680,000

UCSC Main on Human: knownGene (chr19) Auto (Squish)

UCSC Main on Human: all_est (chr19) Dense

UCSC Main on Human: phyloP46wayPrimates (chr19) Histogram

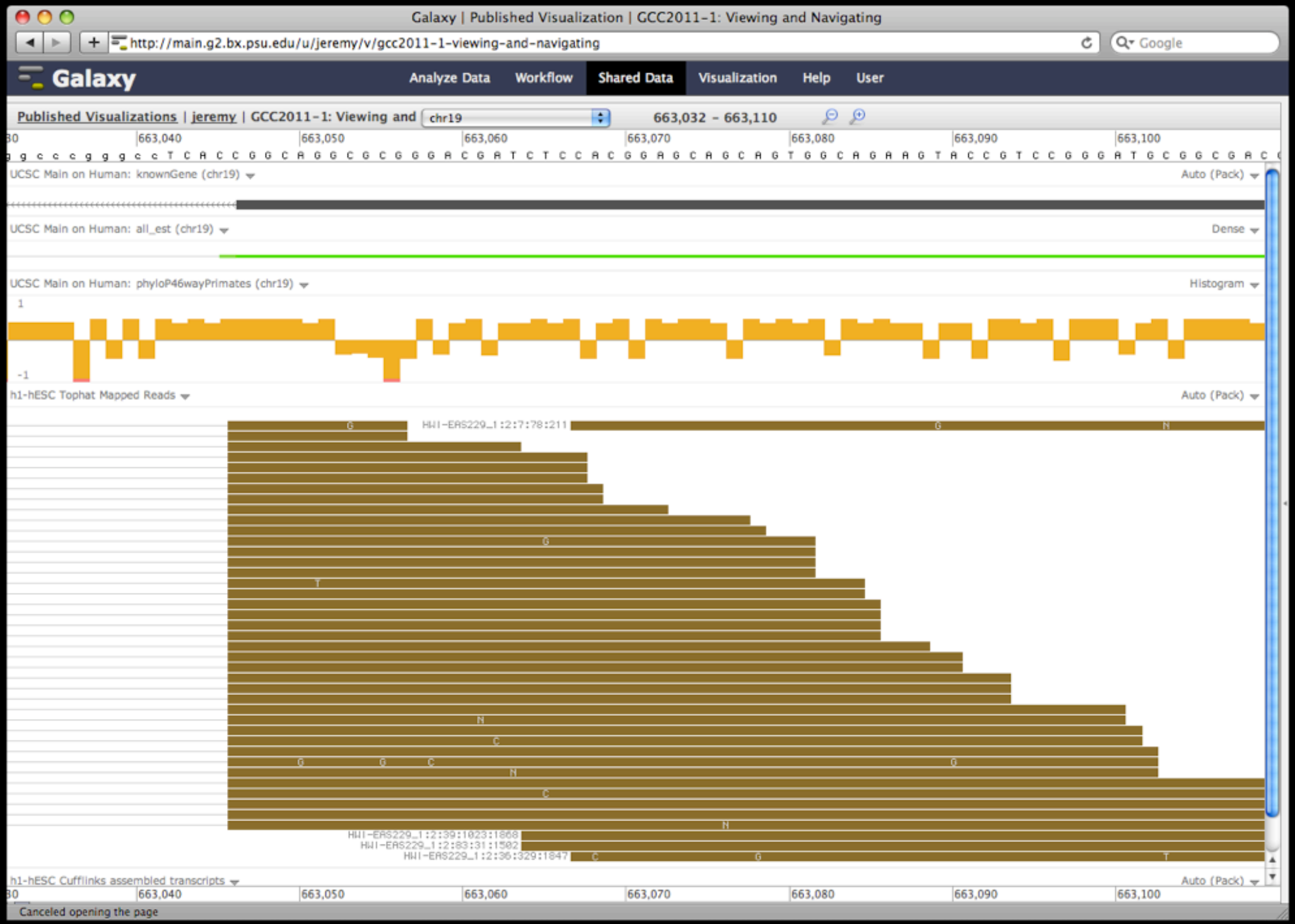
1

-1

h1-hESC Tophat Mapped Reads Auto (Squish)

630,000 640,000 650,000 660,000 670,000 680,000

Display a menu


Galaxy | Published Visualization | GCC2011-1: Viewing and Navigating
http://main.g2.bx.psu.edu/u/jeremy/v/gcc2011-1-viewing-and-navigating
Galaxy
Analyze Data
Workflow
Shared Data
Visualization
Help
User
Published Visualizations | jeremy | GCC2011-1: Viewing and
chr19
663,032 - 663,110
663,040
663,050
663,060
663,070
663,080
663,090
663,100
UCSC Main on Human: knownGene (chr19)
Auto (Pack)
UCSC Main on Human: all_est (chr19)
Dense
UCSC Main on Human: phyloP46wayPrimates (chr19)
Histogram
1
-1
h1-hESC Tophat Mapped Reads
Auto (Pack)
HWI-EAS229_1:2:7:78:211
HWI-EAS229_1:2:39:1023:1868
HWI-EAS229_1:2:83:31:1502
HWI-EAS229_1:2:36:329:1847
h1-hESC Cufflinks assembled transcripts
Auto (Pack)
Canceled opening the page

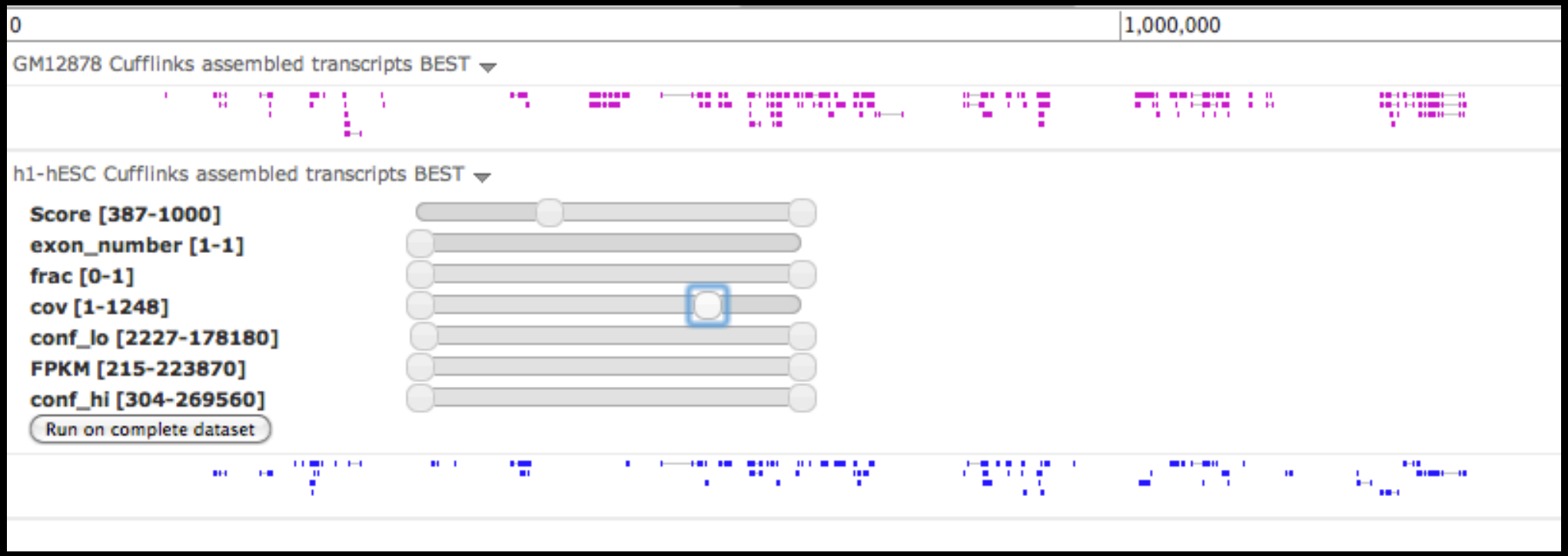
But really, why *another* genome browser

From static browsing to visual analysis

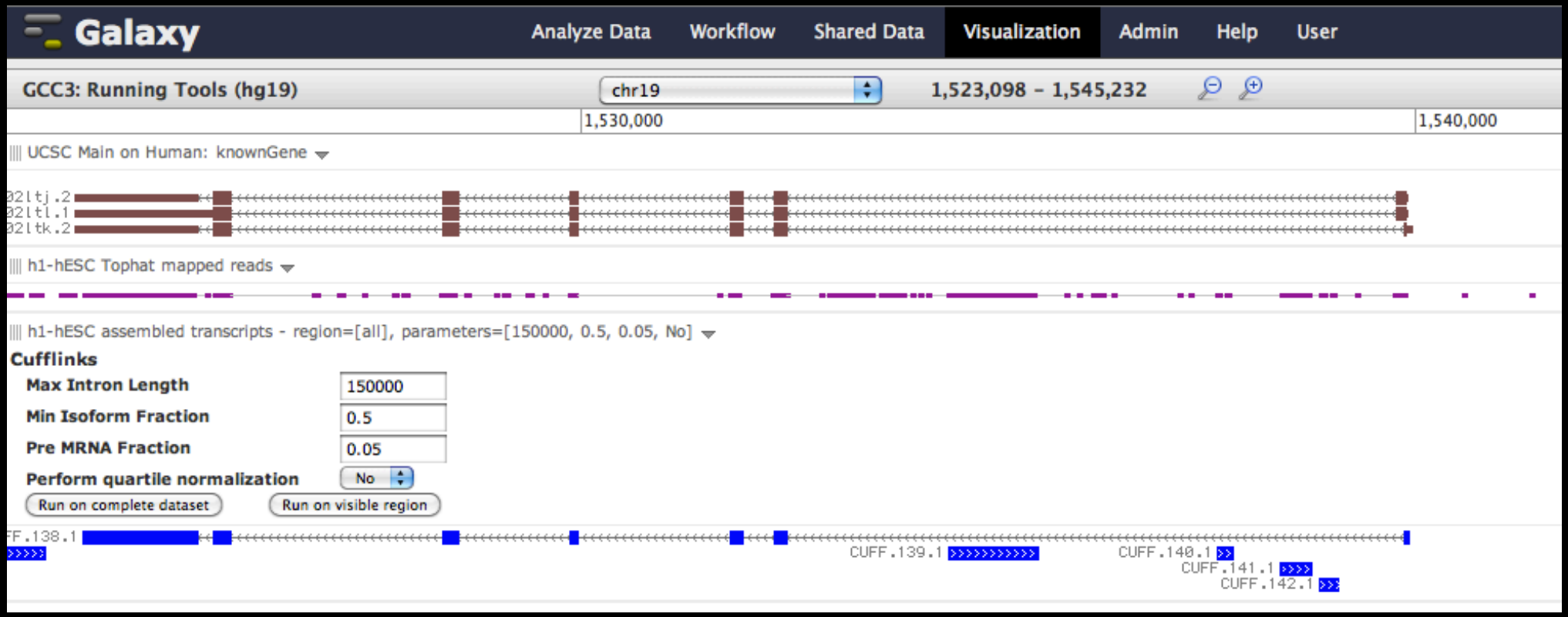
Visual feedback and experimentation needed for complex tools with many parameters

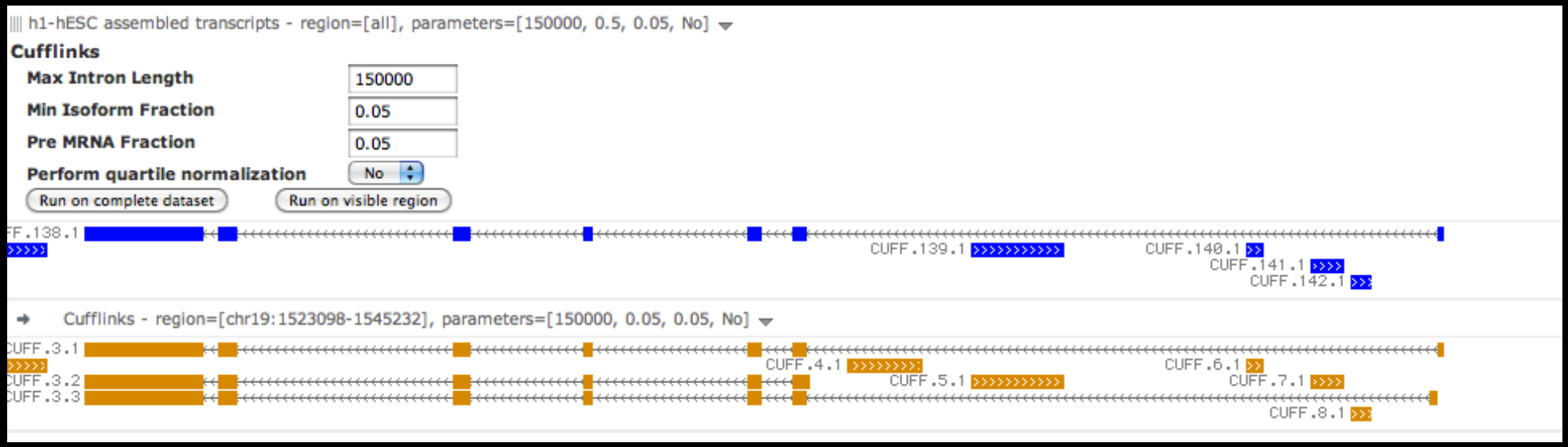
Leverage Galaxy strengths: a very sound model for abstracting interfaces to analysis tools and already integrates an enormous number

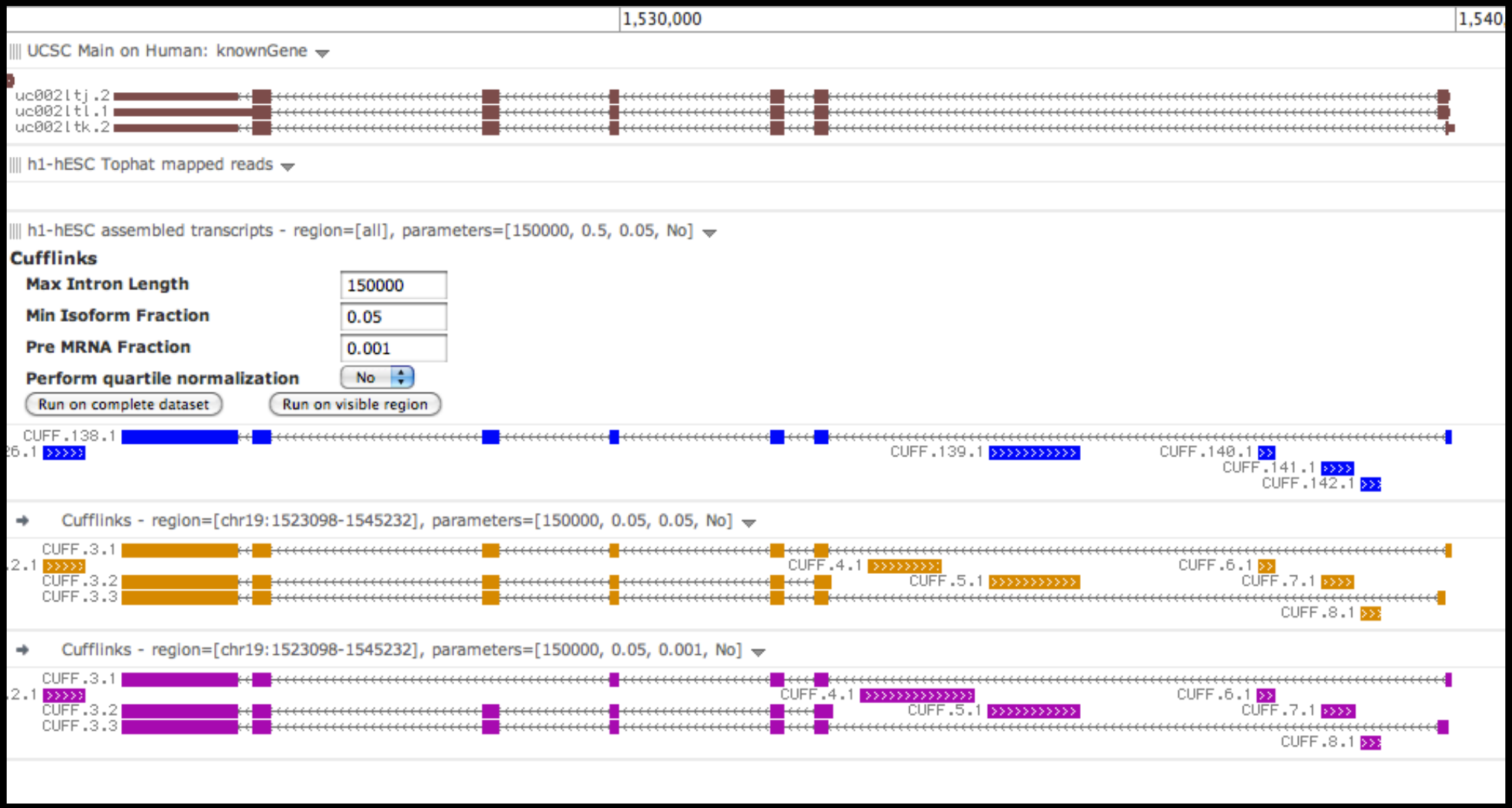
Dynamic Filtering



Integrating Tools and Visualization




h1-hESC assembled transcripts - region=[all], parameters=[150000, 0.5, 0.05, No]
Cufflinks
Max Intron Length
150000
Min Isoform Fraction
0.05
Pre MRNA Fraction
0.05
Perform quartile normalization
No
Run on complete dataset
Run on visible region
FF.138.1
CUFF.139.1
CUFF.140.1
CUFF.141.1
CUFF.142.1
Cufflinks - region=[chr19:1523098-1545232], parameters=[150000, 0.05, 0.05, No]
CUFF.3.1
CUFF.4.1
CUFF.6.1
CUFF.3.2
CUFF.5.1
CUFF.7.1
CUFF.3.3
CUFF.8.1


1,530,000
1,540
UCSC Main on Human: knownGene
uc002ltj.2
uc002ltl.1
uc002ltk.2
h1-hESC Tophat mapped reads
h1-hESC assembled transcripts - region=[all], parameters=[150000, 0.5, 0.05, No]
Cufflinks
Max Intron Length
150000
Min Isoform Fraction
0.05
Pre MRNA Fraction
0.001
Perform quartile normalization
No
Run on complete dataset
Run on visible region
CUFF.138.1
CUFF.139.1
CUFF.140.1
CUFF.141.1
CUFF.142.1
Cufflinks - region=[chr19:1523098-1545232], parameters=[150000, 0.05, 0.05, No]
CUFF.3.1
CUFF.4.1
CUFF.6.1
CUFF.3.2
CUFF.5.1
CUFF.7.1
CUFF.3.3
CUFF.8.1
Cufflinks - region=[chr19:1523098-1545232], parameters=[150000, 0.05, 0.001, No]
CUFF.3.1
CUFF.4.1
CUFF.6.1
CUFF.3.2
CUFF.5.1
CUFF.7.1
CUFF.3.3
CUFF.8.1

Overview

What is Galaxy?

What you can do in Galaxy

- analysis interface, tools and datasources
- data libraries
- workflows
- visualization
- sharing
- Pages

Galaxy 101 Exercise

Sharing and Publishing

Sharing and Publishing History 'Variant Analysis for Sample E18'

Making History Accessible via Link and Publishing It

This history is currently restricted so that only you and the users listed below can access it. You can:

Make History Accessible via Link

Generates a web link that you can share with other people so that they can view and import the history.

Make History Accessible and Publish

Makes the history accessible via link (see above) and publishes the history to Galaxy's Published Histories section, where it is publicly listed and searchable.

Sharing History with Specific Users

You have not shared this history with any users.

Share with a user

Back to Histories List

Sharing and Publishing

Sharing and Publishing History 'Variant Analysis for Sample E18'

Making History Accessible via Link and Publishing It

This history **accessible via link and published**.

Anyone can view and import this history by visiting the following URL:

http://main.g2.bx.psu.edu/u/jgoecks/h/variant-analysis-for-sample-e18

This history is publicly listed and searchable in Galaxy's Published Histories section.

You can:

Unpublish History

Removes history from Galaxy's Published Histories section so that it is not publicly listed or searchable.

Disable Access to History via Link and Unpublish

Disables history's link so that it is not accessible and removes history from Galaxy's Published Histories section so that it is not publicly listed or searchable.

Sharing History with Specific Users

You have not shared this history with any users.

Share with a user

Back to Histories List

Galaxy | Published History | Variant Analysis for Sample E18

http://main.g2.bx.psu.edu/u/jgoecks/h/variant-analysis-for-sample-e18

Galaxy

Analyze Data | Workflow | Shared Data | Visualization | Help | User

Published Histories | jgoecks | Variant Analysis for Sample E18

Galaxy History ' Variant Analysis for Sample E18'

Import history

Annotation: Perform a pileup analysis with default parameters to identify variants in sample E18.

Dataset	Annotation
1: E18 PE.1 Reads	Forward reads from sample E18.
2: E18 PE.2 Reads	Reverse reads from sample E18.
3: E18 PE.1 Reads Groomed	Groom reads to convert quality scores from Solexa 1.0 to Solexa 1.3
4: E18 PE.2 Reads Groomed	Groom reads to convert quality scores from Solexa 1.0 to Solexa 1.3
5: E18 PE.1 Reads Groomed, Trimmed	Trim reads from 3' end to remove low-quality nts.
6: E18 PE.2 Reads Groomed, Trimmed	Trim reads from 3' to remove low-quality nts.
7: Map with Bowtie for Illumina on data 6 and data 5	Map paired-end reads with default parameters.
8: SAM-to-BAM on data 7	Need to convert Bowtie SAM to BAM so that pileup analysis can be performed.
9: Generate pileup on data 8	Pileup analysis with default parameters
10: Filter pileup to get Variants from sample E18	Find variants with coverage >= 30.
13: Filter to get Variants from sample E18 where consensus base different than ref. base	Filter pileup to find variants where the consensus base is different than the reference base.
14: UCSC mm9 RefSeq Genes	UCSC mm9 RefSeq genes.
15: Intersect to get Variants from sample E18, consensus different, in RefSeq Genes	Variants with consensus different that occur in RefSeq genes.

About this History

Author

jgoecks

Related Histories

All published histories
Published histories by jgoecks

Rating

Community
(1 rating, 4.0 average)

Yours

Tags

Community:
snp | pileup | bowtie | demo | sample

Yours:
snp × | pileup × | bowtie × | demo × | sample:e18 ×

Galaxy | Published Workflow | SNP variant detection from paired-end reads

http://main.g2.bx.psu.edu/u/jgoecks/w/snp-variant-detection-from-paired-end-reads

Google

Galaxy

Analyze Data | Workflow | Shared Data | Visualization | Help | User

Published Workflows | jgoecks | SNP variant detection from paired-end reads

Step 6: FASTQ Trimmer

Trim reads to remove low-quality bases.

FASTQ File
Output dataset 'output_file' from step 4

Define Base Offsets as
Absolute Values

Offset from 5' end
0

Offset from 3' end
9

Keep reads with zero length
False

Step 7: Map with Bowtie for Illumina

Map reads using default parameter values.

Will you select a reference genome from your history or use a built-in index?
Use a built-in index

Select a reference genome
/galaxy/data/apiMel3/bowtie_index/apiMel3

Is this library mate-paired?
Paired-end

Forward FASTQ file
Output dataset 'output_file' from step 6

Reverse FASTQ file
Output dataset 'output_file' from step 5

Maximum insert size for valid paired-end alignments (-X)
1000

The upstream/downstream mate orientation for valid paired-end alignment against the forward reference strand (--fr/--rf/--ff)
FR (for Illumina)

Bowtie settings to use
Commonly used

Suppress the header in the output SAM file
True

Step 8: SAM-to-BAM

Convert Bowtie SAM output to BAM format so that pileup can be run.

Choose the source for the reference list
Locally cached

About this Workflow

Author

jgoecks

Related Workflows

All published workflows
Published workflows by jgoecks

Rating

Community
(0 ratings, 0.0 average)

Yours

Tags

Community:
snp bowtie

Yours:
snp bowtie

Galaxy | Published Histories

http://main.g2.bx.psu.edu/history/list_published

Galaxy

Analyze Data | Workflow | Shared Data | Visualization | Help | User

Published Histories

search | Advanced Search

Name	Annotation	Owner	Community Rating ↑	Community Tags	Last Updated
Galaxy vs MEGAN	Comparison of Galaxy vs. MEGAN pipeline.	aun1	★★★★★	metagenomics, megan, galaxy	Mar 19, 2010
metagenomic analysis		aun1	★★★★★	metagenomics, galaxy	Mar 19, 2010
SM_1186088	Datasets correspond to our paper published in Science by Peleg et al. entitled : Altered histone acetylation is associated with age-dependent memory impairment. Experiment layout: This history contains 4 datasets in the form of BED files of uniquely mapped reads produced after chip-seq for histone modifications H4K12ac and H3K9ac in mouse hippocampus of 3 months (young) and 16 months (old) mice after fear conditioning. For detailed information please refer to supplementary materials and methods of the respective work by peleg et al.	fischerlab	★★★★★		Apr 19, 2010
Variant Analysis for Sample E18	Perform a pileup analysis with default parameters to identify variants in sample E18.	jgoecks	★★★★☆	snp, pileup, bowtie, demo, sample	2 minutes ago
get longest exon		henri	☆☆☆☆☆	chr22, longest, marc, exon, human, workshop	Sep 02, 2010
FASTA to Tabular Test		JJ	☆☆☆☆☆		Aug 26, 2010
EKLF		yzc109	☆☆☆☆☆		Aug 24, 2010

Open "http://main.g2.bx.psu.edu/history/list_published?sort=rating&f-tags=All" in a new tab

Sharing Trackster Visualizations

"A picture is worth a 1000 words."

A fully-interactive visualization is worth many more words

Galaxy | Published Visualiza

main.g2.bx.psu.edu/u/jeremy/v/gcc2011-1-viewing-and-navigating

Galaxy

Analyze Data | Workflow | Shared Data | Visualization | Admin | Help | User

Published Visualizations | jeremy | GCC2011-1: Viewin chr19 1,290 - 4,168,475

0 | 1,000,000 | 2,000,000 | 3,000,000 | 4,000,00

UCSC Main on Human: knownGene (chr19) — Auto (Squish)

UCSC Main on Human: all_est (chr19) — Auto (coverage histogram)

11431

UCSC Main on Human: phyloP46wayPrimates (chr19) — Histogram

1

-1

h1-hESC Tophat Mapped Reads — Auto (coverage histogram)

8732

h1-hESC Cufflinks assembled transcripts — Auto (Squish)

0 | 1,000,000 | 2,000,000 | 3,000,000 | 4,000,00

About this Visualization

Author

jeremy

Related Visualizations

All published visualizations
Published visualizations by jeremy

Rating

Community
(1 rating, 5.0 average)

Yours

Tags

Community:
cool

Yours:

Overview

What is Galaxy?

What you can do in Galaxy

- analysis interface, tools and datasources
- data libraries
- workflows
- visualization
- sharing
- Pages

Galaxy 101 Exercise

Galaxy Pages

A web-based, interactive medium for presenting all aspects of an analysis: data, methods, and results

Galaxy Pages

Galaxy | Published Page | Variant Analysis for sample E18

http://main.g2.bx.psu.edu/u/jgoecks/p/variant-analysis-for-sample-e18

Galaxy | Analyze Data | Workflow | Shared Data | Visualization | Help | User

Published Pages | jgoecks | Variant Analysis for sample E18

Variant Analysis of Embryonic Mouse Brain Tissue

Jeremy Goecks, Anton Nekrutenko, James Taylor, and The Galaxy Team

Results

To demonstrate how Galaxy can support accessible, reproducible, and transparent NGS re-sequencing studies, we performed a simple variant analysis experiment. This experiment identifies variants from a set of 4,536,964 RNA-seq reads obtained from sequencing a sample of mm9 brain tissue from day 18 of embryonic development.

The initial analysis produced support for 27,742 possible variants. Of these possible variants, there are 5,625 where (a) the consensus base--as determined by the MAQ model--differs from the reference base and (b) read coverage at the base is 30x or greater. Of these potential variants, 2796 occur in known RefSeq Genes. These potential variants are:

Galaxy Dataset | Intersect to get Variants from sample E18, consensus different, in RefSeq Genes
Variants with consensus different that occur in RefSeq genes.

Method

In the first step of this analysis, the reads were groomed to convert their quality scores from Solexa 1.0 to Solexa 1.3/Fastqsanger. Next, the reads were trimmed from 36bp to 27bp to exclude base pairs with low quality scores; see [1] for this step's rationale and parameter choices. After grooming and trimming, the reads were mapped using the short-read mapper Bowtie [2]. A pileup analysis using SAMtools [3] was then performed and was filtered to identify variants supported by 30+ reads. The complete analysis is contained in this history:

Galaxy History | Variant Analysis for Sample E18
Perform a pileup analysis with default parameters to identify variants in sample E18.

Here is a workflow for performing this analysis:

Galaxy Workflow | Variant identification within annotated genes from NGS PE Data
Identify variants in annotated genes from NGS paired-end data.

References

[1] Han, X. et al. Transcriptome of embryonic and neonatal mouse cortex by high-throughput RNA sequencing. *Proceedings of the National Academy of Sciences* **106**, 12741-12746 (2009).

[2] Langmead, B., Trapnell, C., Pop, M. & Salzberg, S.L. Ultrafast and memory-efficient alignment of short DNA sequences to the human genome. Genome Biol 10, R25 (2009).

About this Page

Author

jgoecks

Related Pages

All published pages
Published pages by jgoecks

Rating

Community
(0 ratings, 0.0 average)

Yours

Tags

Community: none

Yours:

Galaxy Pages

Galaxy | Published Page | Variant Analysis for sample E18

http://main.g2.bx.psu.edu/u/jgoecks/p/variant-analysis-for-sample-e18

Galaxy | Analyze Data | Workflow | Shared Data | Visualization | Help | User

Published Pages | jgoecks | Variant Analysis for sample E18

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Galaxy History | Variant Analysis for Sample E18
Perform a pileup analysis with default parameters to identify variants in sample E18.

8: SAM-to-BAM on data 7	Need to convert Bowtie SAM to BAM so that pileup analysis can be performed.
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Here is a workflow for performing this analysis:

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Identify variants in annotated genes from NGS paired-end data.

References

About this Page

Author

jgoecks

Related Pages

All published pages
Published pages by jgoecks

Rating

Community
(0 ratings, 0.0 average)

Yours

Tags

Community: none

Yours:

Galaxy Pages

Galaxy | Dataset | Filter to get Variants from sample E18 where consensus base different than ref. base

http://main.g2.bx.psu.edu/u/jgoecks/d/fdcdbcfd1207fbd2

Galaxy

Analyze Data | Workflow | Shared Data | Visualization | Help | User

Dataset | Filter to get Variants from sample E18 where consensus base different than ref. base

Galaxy Dataset ' Filter to get Variants from sample E18 where consensus base different than ref. base'

Annotation: Filter pileup to find variants where the consensus base is different than the reference base.

This dataset is large and only the first megabyte is shown below. | Show all

chr10	14465082	14465083	T	K	173	176	60	35	GGGGG.GGGGGGGG.GG.....
chr10	14465083	14465084	G	K	144	144	60	35	.....T.....T..TTTTT
chr10	14465485	14465486	C	T	129	129	60	34	t$TTTTTTTTTTTTTTTTTTTT
chr10	19928287	19928288	G	A	135	135	60	36	AAAAAAAAAAAAAAAAAAAAAA
chr10	19928468	19928469	C	T	132	132	60	35	T$tttttTTttttttTttTTT
chr10	19928494	19928495	C	T	138	138	60	37	TTTTttttttttttTTttTttT
chr10	19928543	19928544	A	G	147	147	60	40	GgGgGgggGGGGGGGGgGGGGG
chr10	28750217	28750218	C	T	138	138	60	37	TTttttttTTTtTttTtTTTTTT
chr10	28750397	28750398	A	C	154	211	60	64	C$.$CCCCCCCCCCcC
chr10	28750423	28750424	C	T	113	113	60	35	T$ttTTTttttTTATTTTTtTT
chr10	28750446	28750447	A	G	165	165	60	46	G$GGGggGGggGGggGGGGGgg
chr10	28750548	28750549	G	C	255	255	60	97	CCCCC$CCCCCCCCCccC
chr10	28750640	28750641	T	C	165	165	60	46	CccccccccCCCCCCCCCCCCC
chr10	28750746	28750747	G	A	202	202	60	58	AAaaaaaaaaaaaAaaaaaaaa
chr10	28750766	28750767	A	G	205	205	60	59	GgGgG$gggggggggggG
chr10	28750769	28750770	T	C	175	175	60	49	ccccCccCCCCCcCccccccCc
chr10	28750924	28750925	C	T	182	217	60	64	TTttTtttTtTtTtTttTTg
chr10	28751092	28751093	a	A	147	0	60	123	,,,,,,,,,,,,gg,,gggg,
chr10	28751096	28751097	a	A	212	0	60	119	gg,,,,,,,,,,,,,,,,,,
chr10	28751114	28751115	g	A	225	235	60	85	aaaa,aaaaaaaaaaaaaaaa
chr10	28751117	28751118	T	A	191	198	60	79	aaaaaaaaaa,$
chr10	28918972	28918973	c	M	114	114	60	75	,$,$,$,$,,,,,,,,,,,,,,
chr10	28918975	28918976	a	A	177	0	60	63	,$,$,$...,c,,,,,,,,,,
chr10	28918995	28918996	C	M	154	154	60	48	a$aaaaaaaaaaaaaaaaaaaa
chr10	33613489	33613490	G	A	82	114	60	30	.AAAAAAAAAAAAAAAAA
chr10	36721501	36721502	G	K	129	129	60	43	TTTT..,,,,,,,,,,,,,,,,,
chr10	36721507	36721508	C	Y	51	51	60	54	.$.,,,,,,,,,,,,,,,,,,,,
chr10	36721695	36721696	T	A	120	120	60	31	aaaaaaaaaaa$
chr10	36805412	36805413	A	G	126	126	60	33	GGGGGGGGGGGGGGGGGGGGGG
chr10	36805605	36805606	A	G	120	120	60	31	gggggggggggggggggggggg
chr10	36853176	36853177	C	Y	138	138	60	35	.....T
chr10	36853265	36853266	A	R	17	17	60	37	.....
chr10	36854675	36854676	T	K	99	99	60	48	.....
chr10	36854678	36854679	A	M	94	94	60	48	.....
chr10	36855346	36855347	a	R	159	159	60	50	,,,,,,,,,,,,,,,,,,..GGG
chr10	36855350	36855351	a	R	156	156	60	56	,,,,,,,,,,,,,,,,,,,,GGG
chr10	36855356	36855357	a	A	134	0	60	49	,,,,g,,,,,,,,,,,,,,,,,
chr10	36855366	36855367	g	G	52	0	60	40	.....
chr10	36855370	36855371	g	G	25	0	60	32	.$.$.$.$.$.$.....
chr10	36855665	36855666	A	M	11	11	60	39	ccccc$,,,,,,,,,,,
chr10	39144591	39144592	G	C	126	126	60	33	CCCCCCCCCCCCCCCCCCCCCC
chr10	42722938	42722939	C	Y	63	63	60	34	ttttt$,,,,,,,,,,,,

About this Dataset

Author

jgoecks

Tags

Community: none

Yours:

Galaxy Pages

Galaxy | Published Page | Variant Analysis for sample E18

http://main.g2.bx.psu.edu/u/jgoecks/p/variant-analysis-for-sample-e18

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Published Pages | jgoecks | Variant Analysis for sample E18

The initial analysis produced support for 27,742 possible variants. Of these possible variants, there are 5,625 where (a) the consensus base--as determined by the MAQ model--differs from the reference base and (b) read coverage at the base is 30x or greater. Of these potential variants, 2796 occur in known RefSeq Genes. These potential variants are:

Galaxy Dataset | Intersect to get Variants from sample E18, consensus different, in RefSeq Genes
Variants with consensus different that occur in RefSeq genes.

Method

In the first step of this analysis, the reads were groomed to convert their quality scores from Solexa 1.0 to Solexa 1.3/Fastqsanger. Next, the reads were trimmed from 36bp to 27bp to exclude base pairs with low quality scores; see [1] for this step's rationale and parameter choices. After grooming and trimming, the reads were mapped using the short-read mapper Bowtie [2]. A pileup analysis using SAMtools [3] was then performed and was filtered to identify variants supported by 30+ reads. The complete analysis is contained in this history:

Import history

Galaxy History | Variant Analysis for Sample E18
Perform a pileup analysis with default parameters to identify variants in sample E18.

8: SAM-to-BAM on data 7	Need to convert Bowtie SAM to BAM so that pileup analysis can be performed.
9: Generate pileup on data 8	Pileup analysis with default parameters
10: Filter pileup to get Variants from sample E18	Find variants with coverage >= 30.
13: Filter to get Variants from sample E18 where consensus base different than ref. base	Filter pileup to find variants where the consensus base is different than the reference base.
14: UCSC mm9 RefSeq Genes	UCSC mm9 RefSeq genes.
15: Intersect to get Variants from sample E18, consensus different, in RefSeq Genes	Variants with consensus different that occur in RefSeq genes.

Here is a workflow for performing this analysis:

Galaxy Workflow | Variant identification within annotated genes from NGS PE Data
Identify variants in annotated genes from NGS paired-end data.

References

Open "http://main.g2.bx.psu.edu/history/imp?id=e0b8bd5d661b10c2" in a new tab

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jgoecks

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Tags

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Galaxy | Analyze Data | Workflow | Shared Data | Visualization | Help | User

Tools | Options

Get Data
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Lift-Over
Text Manipulation
Convert Formats
FASTA manipulation
Filter and Sort
Join, Subtract and Group
Extract Features
Fetch Sequences
Fetch Alignments
Get Genomic Scores
Operate on Genomic Intervals
Statistics
Graph/Display Data
Regional Variation
Multiple regression
Multivariate Analysis
Evolution
Metagenomic analyses
EMBOSS

NGS TOOLBOX BETA

NGS: QC and manipulation
NGS: Mapping
NGS: SAM Tools
NGS: Indel Analysis
NGS: Peak Calling

RGENETICS

SNP/WGA: Data; Filters
SNP/WGA: QC; LD; Plots
SNP/WGA: Statistical Models

Filter pileup

Select dataset:
9: Generate pileup on data 8

which contains:
Pileup with ten columns (with consensus)
See "Types of pileup datasets" below for examples

Do not consider read bases with quality lower than:
20
No variants with quality below this value will be reported

Do not report positions with coverage lower than:
30
Pileup lines with coverage lower than this value will be skipped

Only report variants?:
Yes
See "Examples 1 and 2" below for explanation

Convert coordinates to intervals?:
Yes
See "Output format" below for explanation

Print total number of differences?:
Yes
See "Example 3" below for explanation

Print quality and base string?:
Yes
See "Example 4" below for explanation

Execute

What it does

Allows one to find sequence variants and/or sites covered by a specified number of reads with bases above a set quality threshold. The tool works on six and ten column pileup formats produced with *samtools pileup* command. However, it also allows you to specify columns in the input file manually. The tool assumes the following:

- the quality scores follow phred33 convention, where input qualities are ASCII characters equal to the Phred quality plus 33.
- the pileup dataset was produced by the *samtools pileup* command (although you

History | Options

15: Variants from sample E18, consensus different, in RefSeq Genes

14: UCSC mm9 RefSeq Genes

13: Variants from sample E18 where consensus base different than ref. base

10: Variants from sample E18
26,742 regions, format: interval,

Run this job again

| display at UCSC main | view in GeneTrack | display at Ensembl Current

1.Chrom	2.Start	3.End	4	5	6
chr10	6882036	6882037	A	A	107
chr10	14243075	14243076	G	G	96
chr10	14243079	14243080	C	C	106
chr10	14465082	14465083	T	K	173
chr10	14465083	14465084	G	K	144
chr10	14465084	14465085	T	T	117

9: Generate pileup on data 8

8: SAM-to-BAM on data 7

7: Map with Bowtie for Illumina on data 6 and data 5

6: E18 PE.2 Reads

Open "http://main.g2.bx.psu.edu/tool_runner/rerun?id=1703758" in a new tab

Galaxy Pages

Galaxy | Published Page | Variant Analysis for sample E18

http://main.g2.bx.psu.edu/u/jgoecks/p/variant-analysis-for-sample-e18

Galaxy Analyze Data Workflow Shared Data Visualization Help User

Published Pages | jgoecks | Variant Analysis for sample E18

Variant Analysis of Embryonic Mouse Brain Tissue

Jeremy Goecks, Anton Nekrutenko, James Taylor, and The Galaxy Team

Results

To demonstrate how Galaxy can support accessible, reproducible, and transparent NGS re-sequencing studies, we performed a simple variant analysis experiment. This experiment identifies variants from a set of 4,536,964 RNA-seq reads obtained from sequencing a sample of mm9 brain tissue from day 18 of embryonic development.

The initial analysis produced support for 27,742 possible variants. Of these possible variants, there are 5,625 where (a) the consensus base--as determined by the MAQ model--differs from the reference base and (b) read coverage at the base is 30x or greater. Of these potential variants, 2796 occur in known RefSeq Genes. These potential variants are:

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Galaxy History | Variant Analysis for Sample E18
Perform a pileup analysis with default parameters to identify variants in sample E18.

Here is a workflow for performing this analysis:

Import workflow

Galaxy Workflow | Variant identification within annotated genes from NGS PE Data
Identify variants in annotated genes from NGS paired-end data.

References

[1] Han, X. et al. Transcriptome of embryonic and neonatal mouse cortex by high-throughput RNA sequencing. *Proceedings of the National Academy of Sciences* **106**, 12741-12746 (2009).

[2] Langmead, B., Trapnell, C., Pop, M. & Salzberg, S.L. Ultrafast and memory-efficient alignment of short DNA sequences to the human genome. Genome Biol 10, R25 (2009).

[3] Li, H. et al. The Sequence Alignment/Map format and SAMtools. *Bioinformatics* **25**, 2078 -2079 (2009).

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jgoecks

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Rating

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Community: none

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Galaxy | Analyze Data | Workflow | Shared Data | Visualization | Help | User

Page Editor | Title : Variant Analysis for sample E18 | Save | Close

Paragraph type | Insert Link to Galaxy Object | Embed Galaxy Object

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Here is a workflow for performing this analysis:

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Page Editor | Title : Variant Analysis for sample E18 — Save | Close

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Variant Analysis of Embr

Jeremy Goecks, Anton Nekrutenko, James Taylor,

Results

To demonstrate how Galaxy can support accessible, … variant analysis experiment. This experiment identifies variants from a set of 4,536,964 RNA-seq … bryonic development.

The initial analysis produced support for 27,742 pos … base--as determined by the MAQ model--differs from the reference base and (b) read coverage at the … Genes. These potential variants are:

Method

In the first step of this analysis, the reads were groo … t, the reads were trimmed from 36bp to 27bp to exclude base pairs with low quality scores; see [1] f … ads were mapped using the short-read mapper Bowtie [2]. A pileup analysis using SAMtools [3] was … complete analysis is contained in this history:

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[2] Langmead, B., Trapnell, C., Pop, M. & Salzberg, S.L. Ultrafast and memory-efficient alignment of short DNA sequences to the human genome. Genome Biol 10, R25 (2009).

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	Name	Tags	Last Updated ↑
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☐	Unnamed history	0 Tags	Sep 07, 2010
☐	Unnamed history	0 Tags	Dec 17, 2009
☐	imported: Hsitory with ~100 items	5 Tags	Dec 10, 2009
☐	imported: Galaxy vs MEGAN	0 Tags	Dec 04, 2009
☐	imported: Galaxy vs MEGAN	2 Tags	Oct 06, 2009
☐	imported: Galaxy vs MEGAN	0 Tags	Oct 06, 2009
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Page: 1 2 | Show all histories on one page

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Page Editor | Title : Variant Analysis for sample E18 | Save | Close

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Embedded Galaxy History "Variant Analysis for Sample E18"

[Do not edit this block; Galaxy will fill it in with the annotated history when it is displayed.]

Here is a workflow for performing this analysis:

References

[1] Han, X. et al. Transcriptome of embryonic and neonatal mouse cortex by high-throughput RNA sequencing. *Proceedings of the National Academy of Sciences* **106**, 12741-12746 (2009).

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Page Editor | Title : Variant Analysis for sample E18 | Save | Close

Paragraph type | Insert Link to Galaxy Object | Embed Galaxy Object

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Embedded Galaxy Dataset 'Variants from sample E18, consensus different, in RefSeq Genes'

[Do not edit this block; Galaxy will fill it in with the annotated dataset when it is displayed.]

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Embedded Galaxy History 'Variant Pileup Analysis for Sample E18'

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Here is a workflow for performing this analysis:

Embedded Galaxy Workflow 'SNP identification within annotated genes from NGS PE Data'

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References

[1] Han, X. et al. Transcriptome of embryonic and neonatal mouse cortex by high-throughput RNA sequencing. *Proceedings of the National Academy of Sciences* **106**, 12741-12746 (2009).

[2] Langmead, B., Trapnell, C., Pop, M. & Salzberg, S.L. Ultrafast and memory-efficient alignment of short DNA sequences to the human genome. Genome Biol 10, R25 (2009).

[3] Li, H. et al. The Sequence Alignment/Map format and SAMtools. *Bioinformatics* **25**, 2078 -2079 (2009).

The power of Galaxy publishing

Galaxy's publishing features facilitate access and reproducibility without any extra leg work

One click grants access to the *actual analysis* you performed to generate your original results

- Not just data access: the full pipeline
- Annotate each step
- Anyone can import your work and immediately reproduce or build on it

Overview

What is Galaxy?

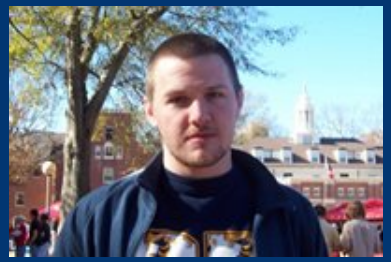
What you can do in Galaxy

- analysis interface, tools and datasources
- data libraries
- workflows
- visualization
- sharing
- Pages

Galaxy 101 Exercise

EMORY

Enis Afgan



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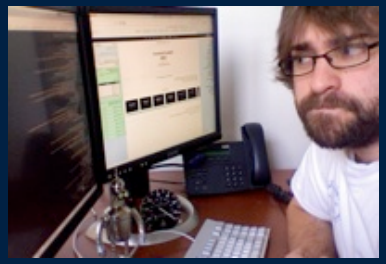


Nate Coraor

Jennifer Jackson

Greg von Kuster

Guru Ananda

Anton Nekrutenko

Supported by the **NHGRI** (HG005542, HG004909, HG005133), **NSF** (DBI-0850103), Penn State University, Emory University, and the Pennsylvania Department of Public Health

Galaxy 101
http://usegalaxy.org/galaxy101

A simple question...

- Which coding exons have highest number of single nucleotide polymorphisms?

Galaxy 101
http://usegalaxy.org/galaxy101

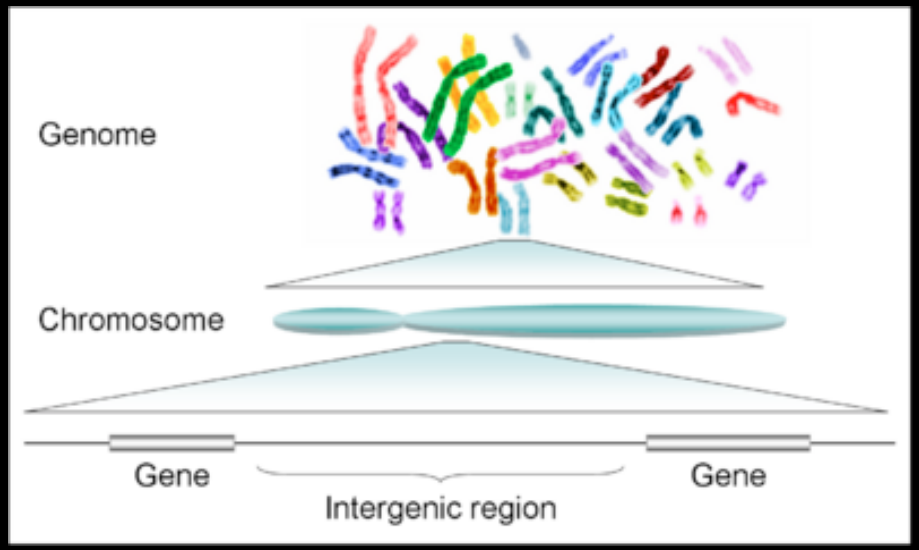
Overview

- Interactively Analyze Data
- Create reusable generic Workflow
- Share analysis Results, History, Workflow

Required Data

- Genomic Coordinates of coding exons and SNPs

Genomic Coordinates



http://library.kiwix.org:4201/A/Human_genome.html

>chr1
taaccctaaccctaaccctaaccctaaccctaaccctaaccctaaccctaacccta
accctaaccctaaccctaaccctaaccctaaccctaaccctaaccctaac

chrom	start	end	name	score	strand
chr1	0	10	first_ten_bases	0	+

see also:
https://bitbucket.org/galaxy/galaxy-central/wiki/GopsDesc
https://bitbucket.org/galaxy/galaxy-central/wiki/zero_based_coordinates.pdf

Galaxy 101: Basic Steps
http://usegalaxy.org/galaxy101

Get Genomic data from UCSC Table Browser

Determine each SNP that overlaps with a specific coding exon

Calculate count of overlapping SNPs for each exon

Sort and select exons by greatest SNP counts