Introduction to Galaxy

Jeremy Goecks
The Galaxy Team
http://usegalaxy.org

Session Overview

What is Galaxy?

What you can do in Galaxy

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

Where you can use and build Galaxy

- public website
- local instance
- on the cloud
- tool shed/contributing tools

Galaxy 101 Exercise

Workshop Coverage

Session 1: Galaxy framework and support for analyses

- Galaxy is tool-agnostic

Session 2: Galaxy for HTS data analysis

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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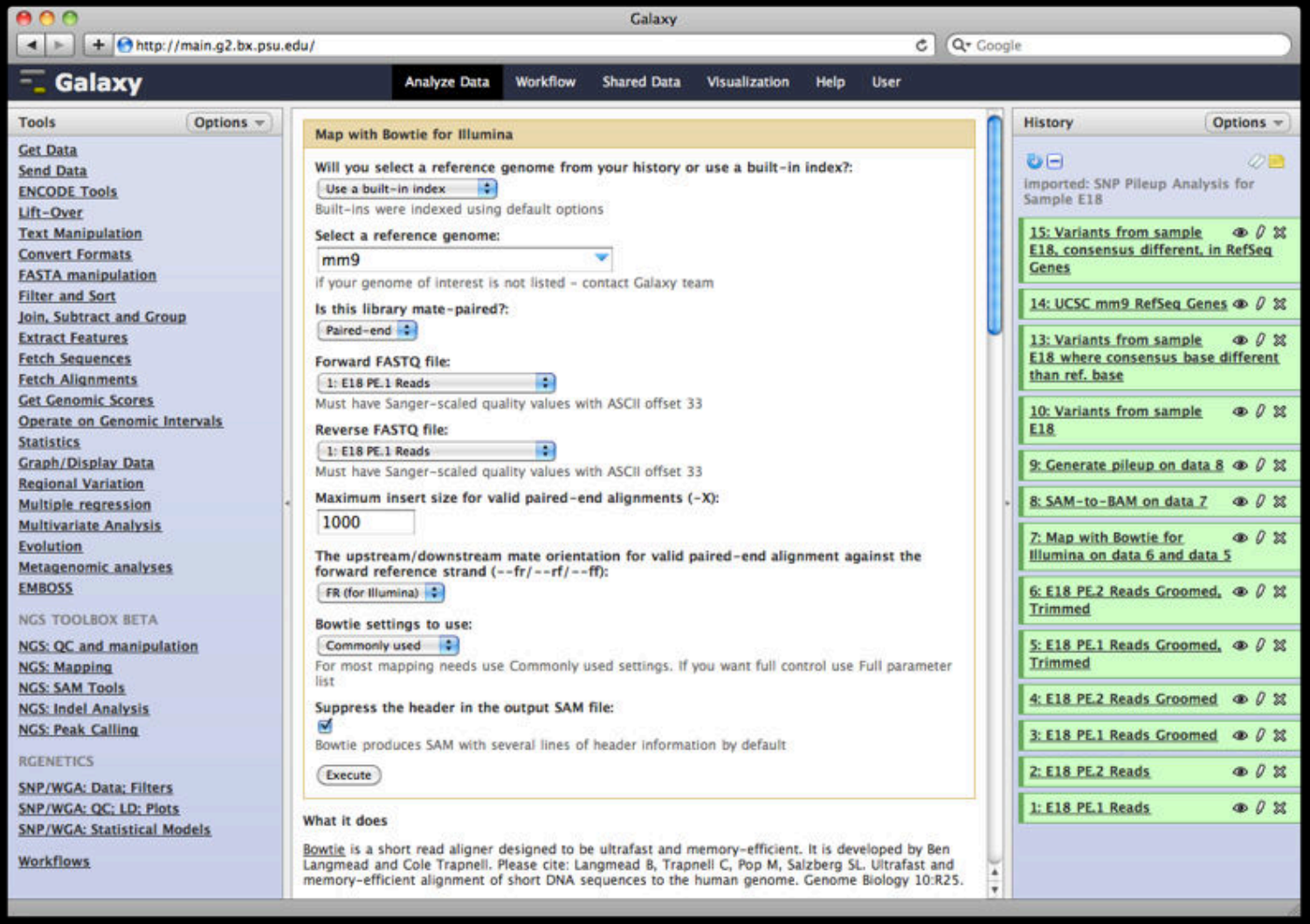
Galaxy 101 Exercise

Galaxy Analysis Workspace



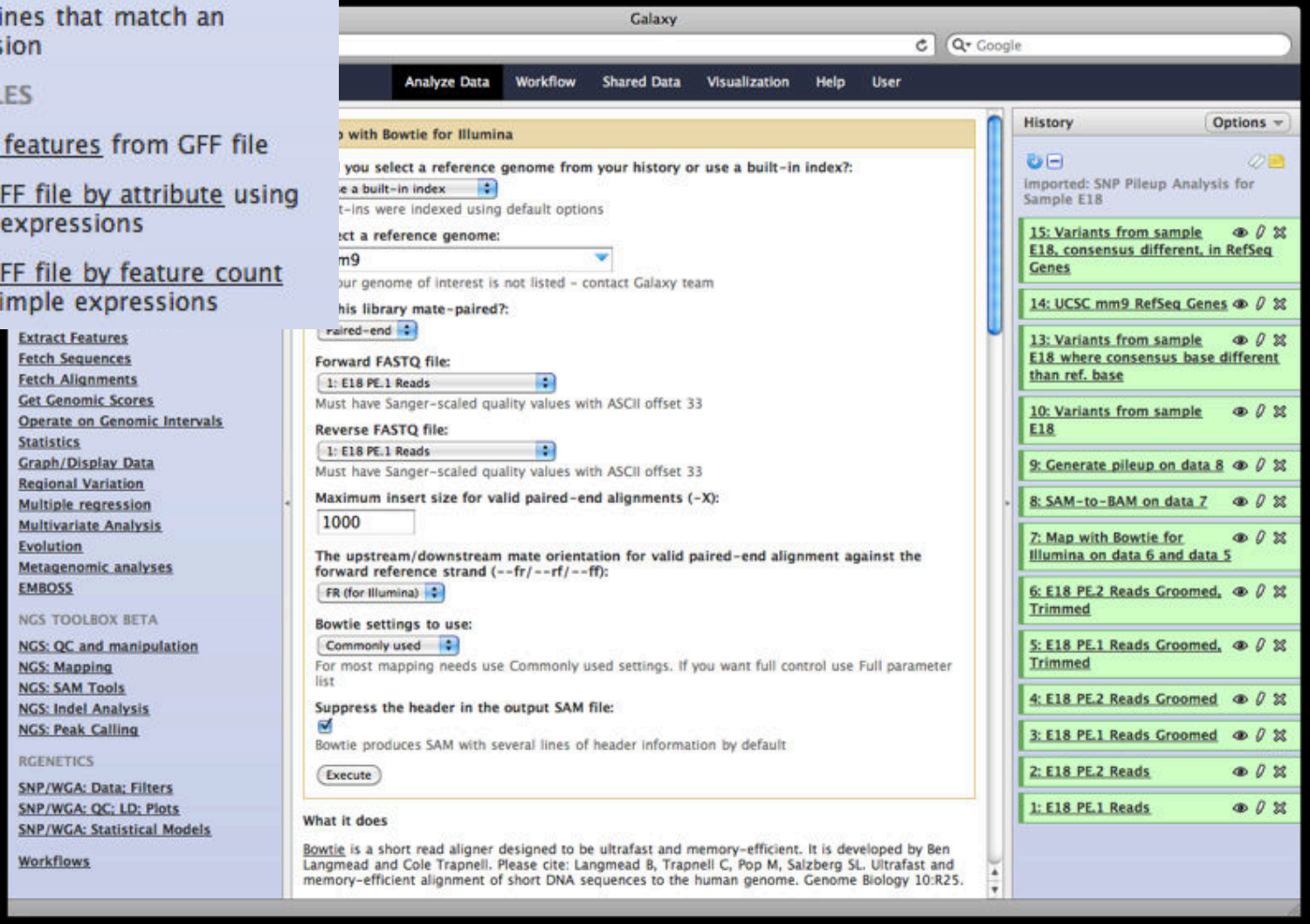
xy Analysis Workspace

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



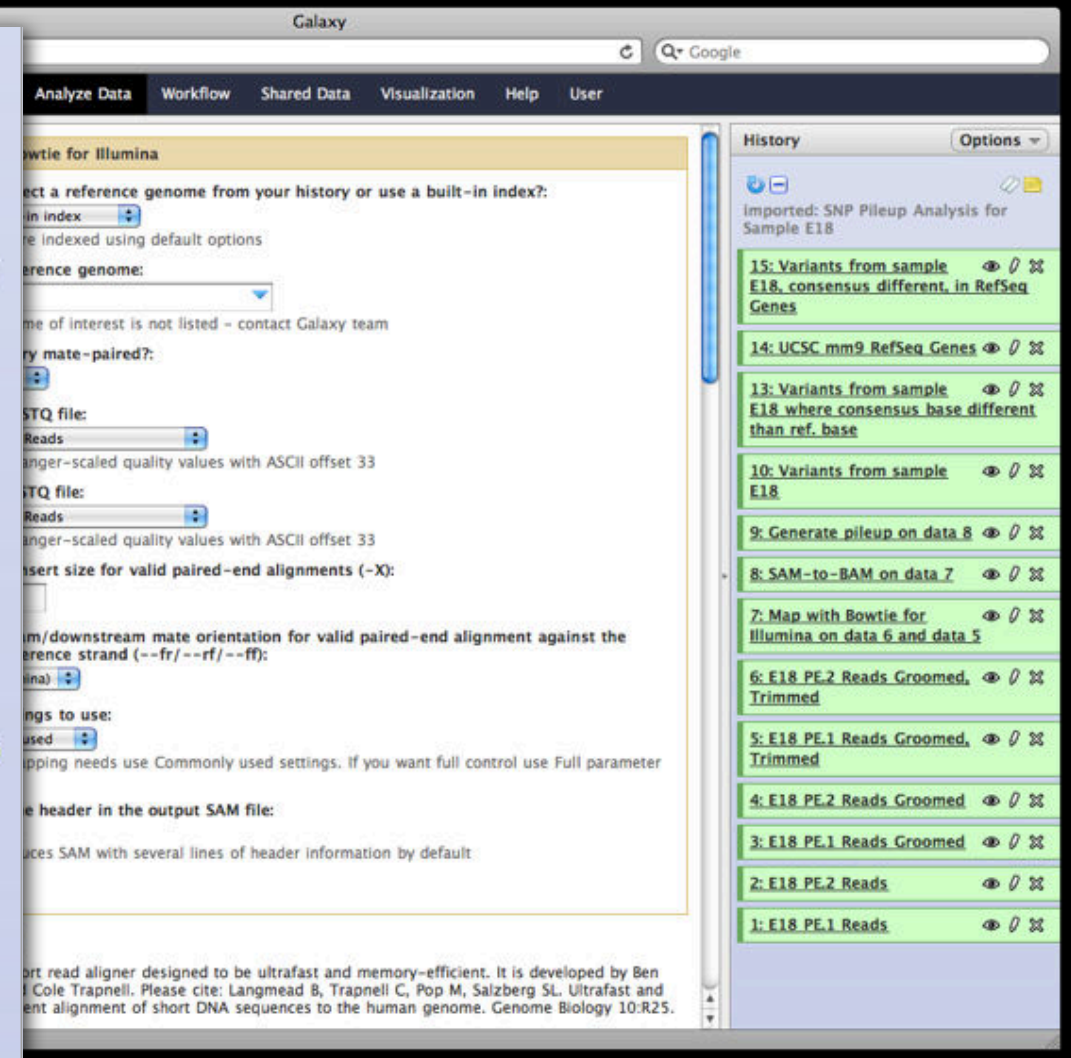
xy Analysis Workspace

Filter and Sort

- Filter data on any column using simple expressions
- Sort data in ascending or descending order
- Select lines that match an e
- 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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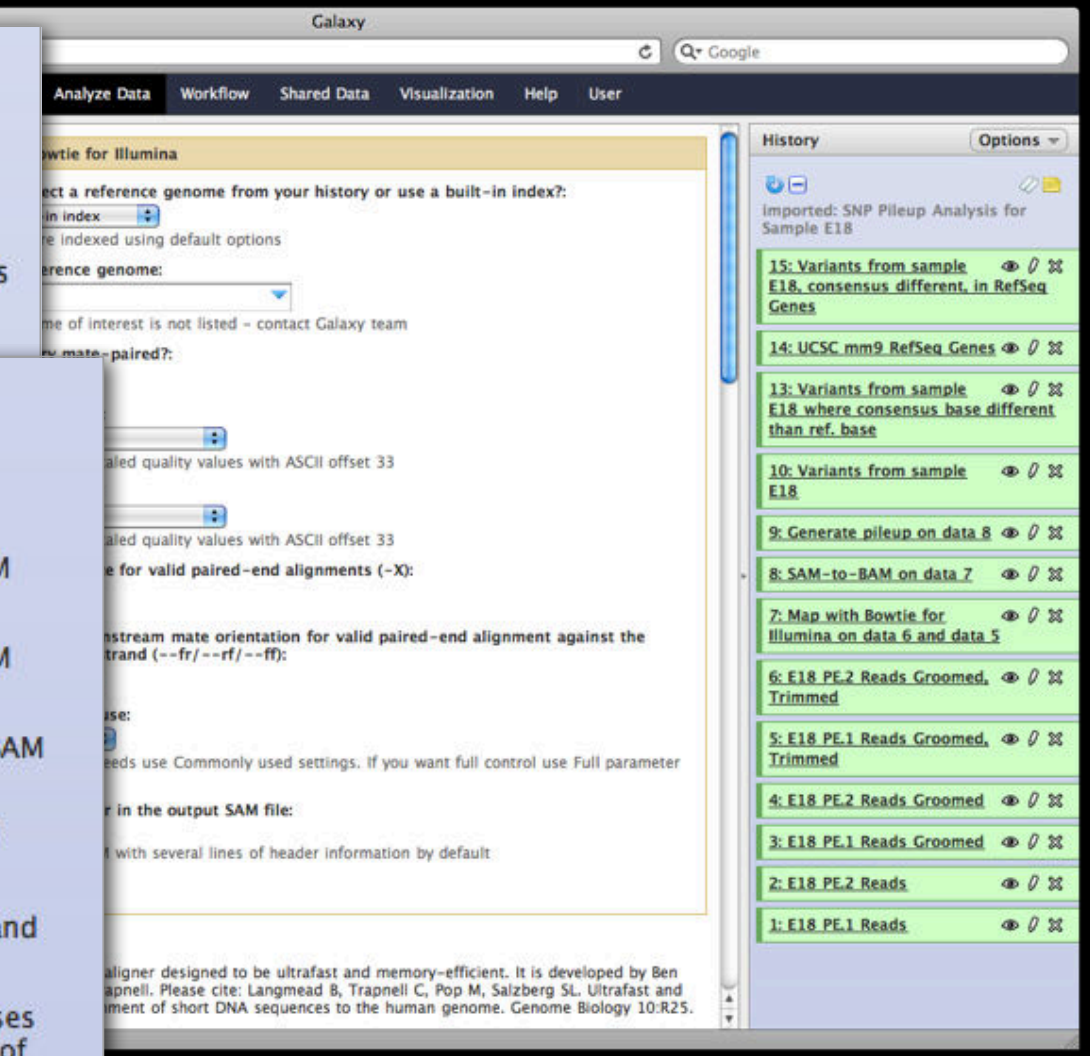
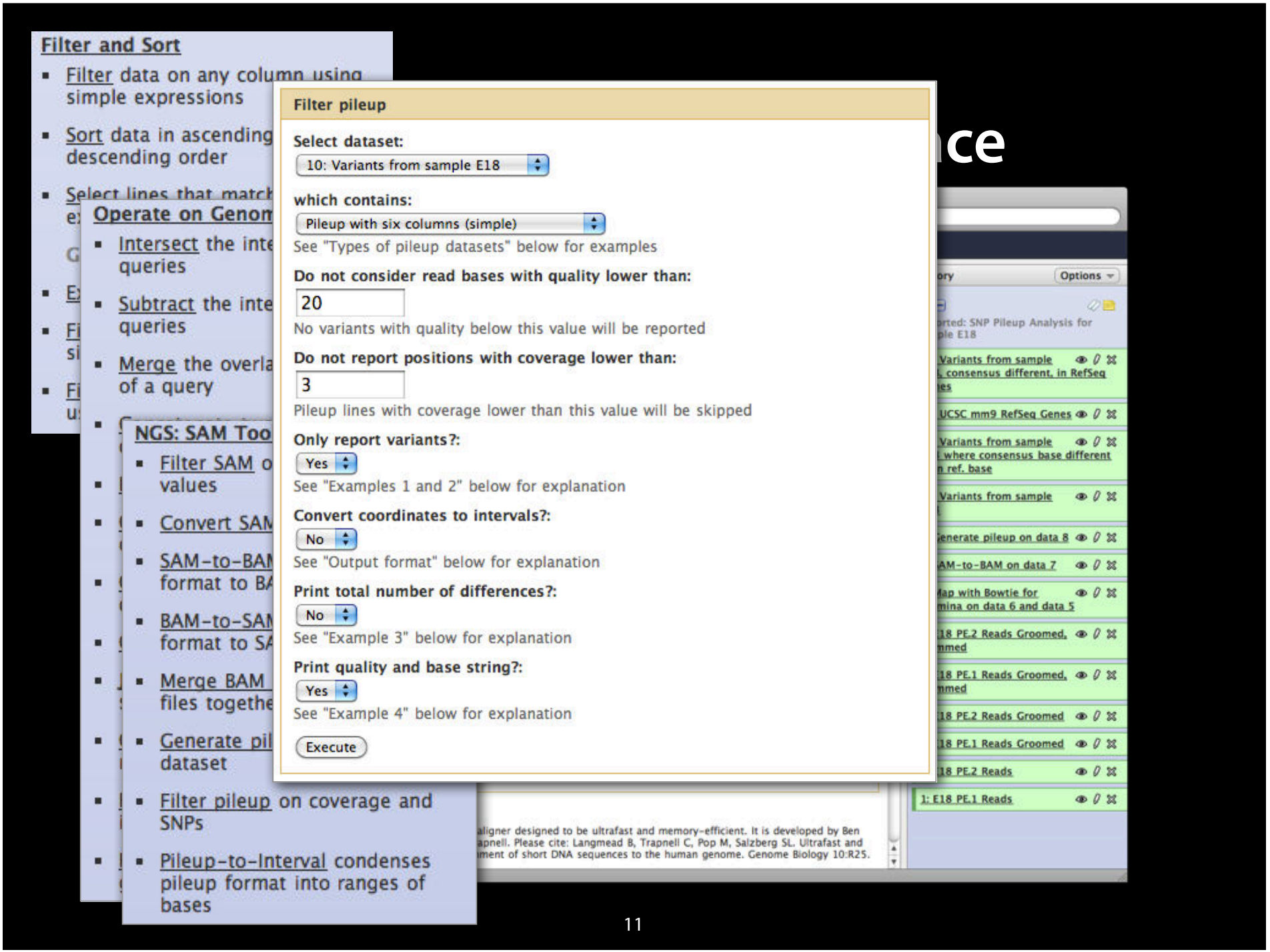
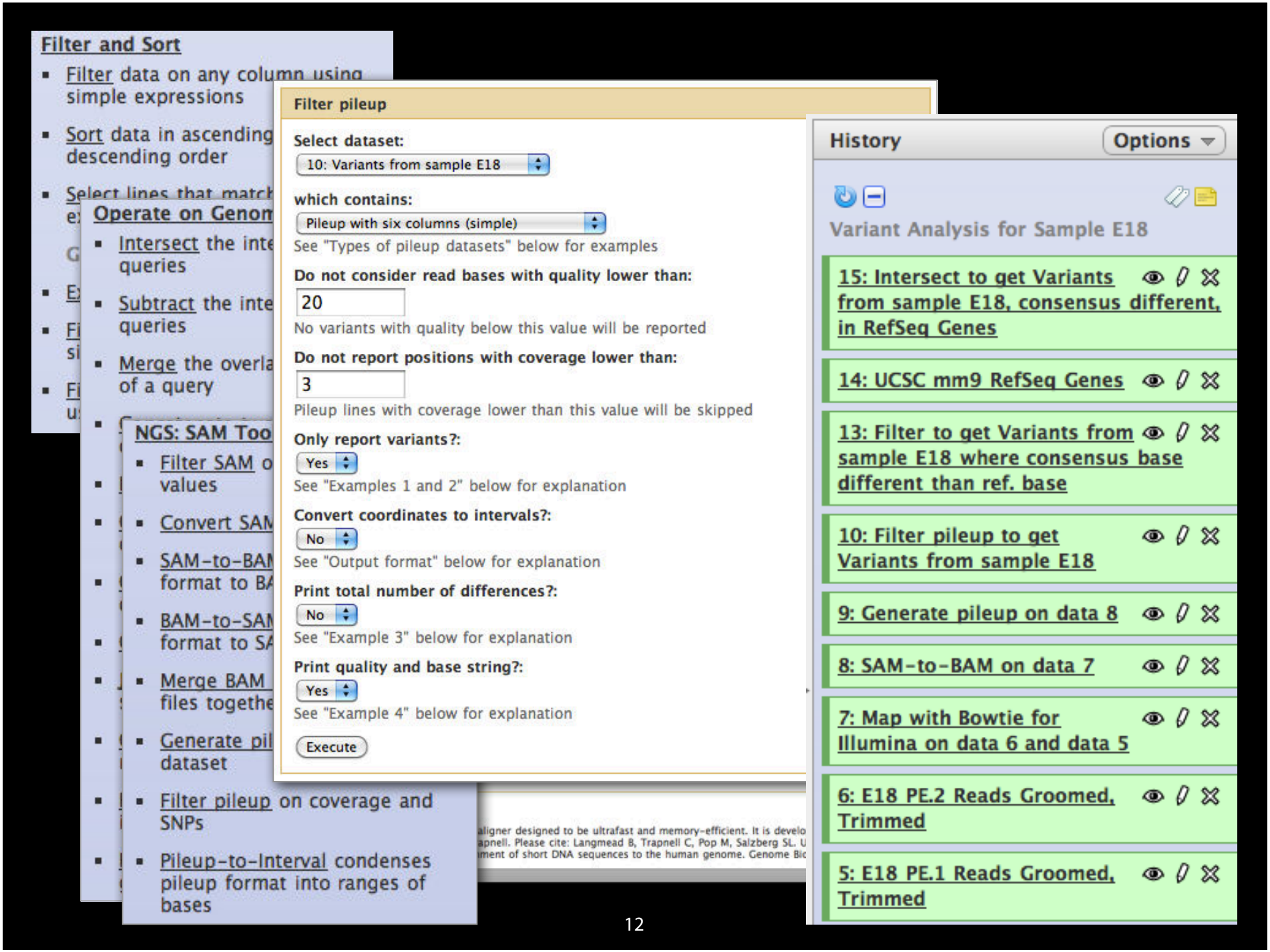
- Subtract the intervals of two queries
- Merge the overlapping intervals of a query

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




Filter and Sort
Filter data on any column using simple expressions
Sort data in ascending descending order
Operate on Genom
Intersect the inte queries
Subtract the inte queries
Merge the overla of a query
NGS: SAM Too
Filter SAM o values
Convert SAM
SAM-to-BAM format to BA
BAM-to-SAM format to SA
Merge BAM files togethe
Generate pil dataset
Filter pileup on coverage and SNPs
Pileup-to-Interval condenses pileup format into ranges of bases
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
Options
Variants from sample
consensus different, in RefSeq
UCSC mm9 RefSeq Genes
Variants from sample
where consensus base different
ref. base
Variants from sample
Generate pileup on data 8
AM-to-BAM on data 7
18 PE.2 Reads Groomed,
18 PE.1 Reads Groomed,
18 PE.2 Reads Groomed
18 PE.1 Reads Groomed
18 PE.2 Reads
1: E18 PE.1 Reads


Filter and Sort
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Intersect the inte queries
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Filter pileup
Select dataset:
10: Variants from sample E18
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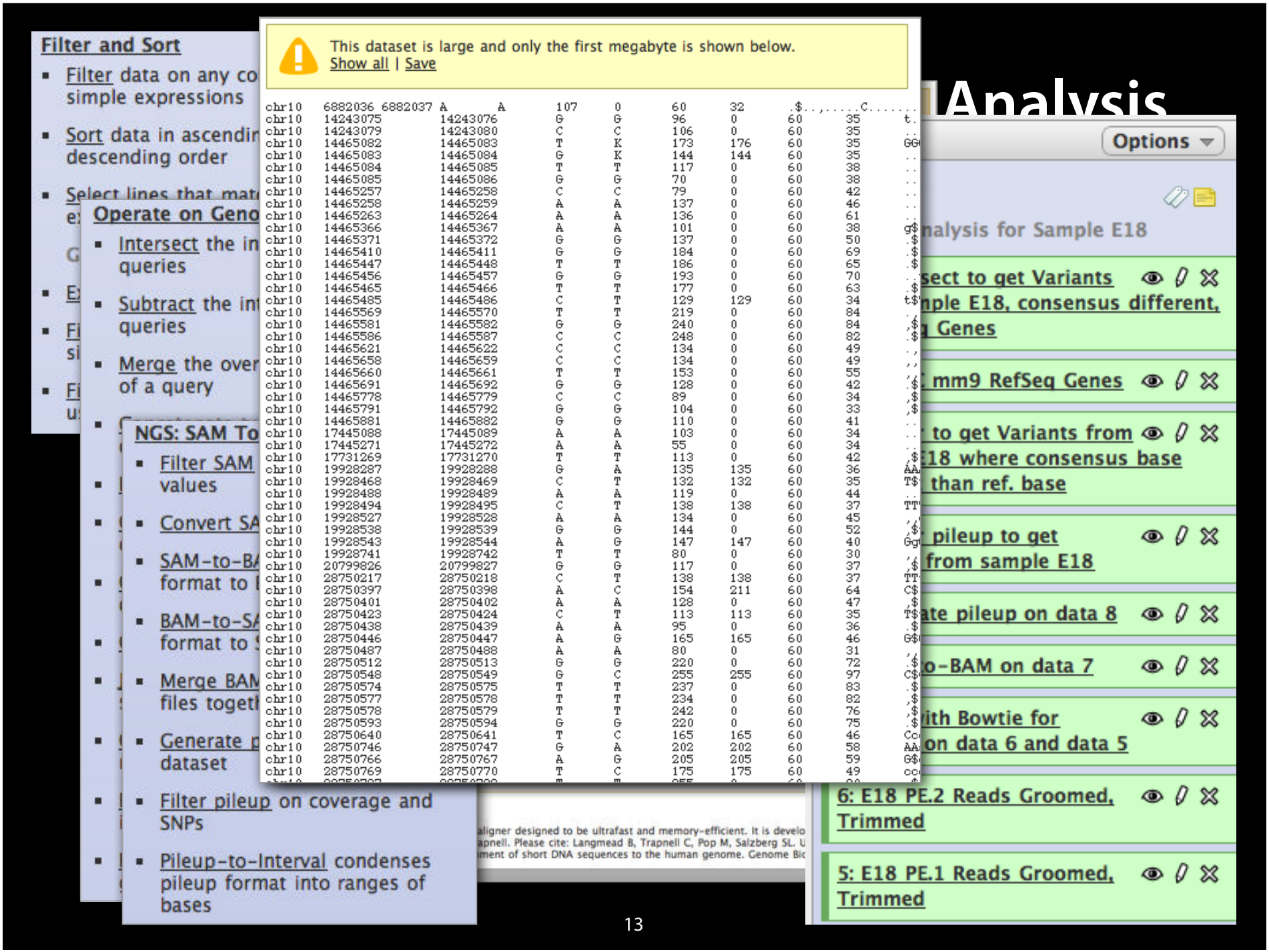
Pileup with six columns (simple)
See "Types of pileup datasets" below for examples
Do not consider read bases with quality lower than:
20
No variants with quality below this value will be reported
Do not report positions with coverage lower than:
3
Pileup lines with coverage lower than this value will 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
History
Options
Variant Analysis for Sample E18
15: Intersect to get Variants from sample E18, consensus different, in RefSeq Genes
14: UCSC mm9 RefSeq Genes
13: Filter to get Variants from sample E18 where consensus base different than ref. base
10: Filter pileup to get 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


Filter and Sort
Filter data on any co
simple expressions
Sort data in ascendir
descending order
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
Analysis
Options
nalysis for Sample E18
sect to get Variants
nple E18, consensus different,
Genes
mm9 RefSeq Genes
to get Variants from
E18 where consensus base
than ref. base
pileup to get
from sample E18
ate pileup on data 8
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ith Bowtie for
on data 6 and data 5
6: E18 PE.2 Reads Groomed, Trimmed
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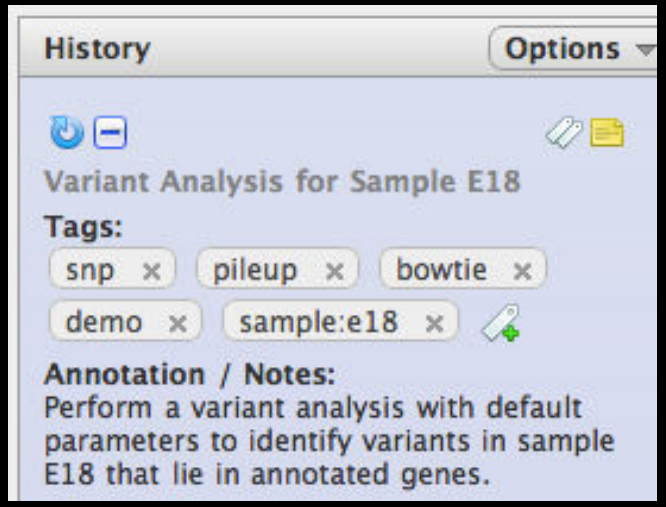
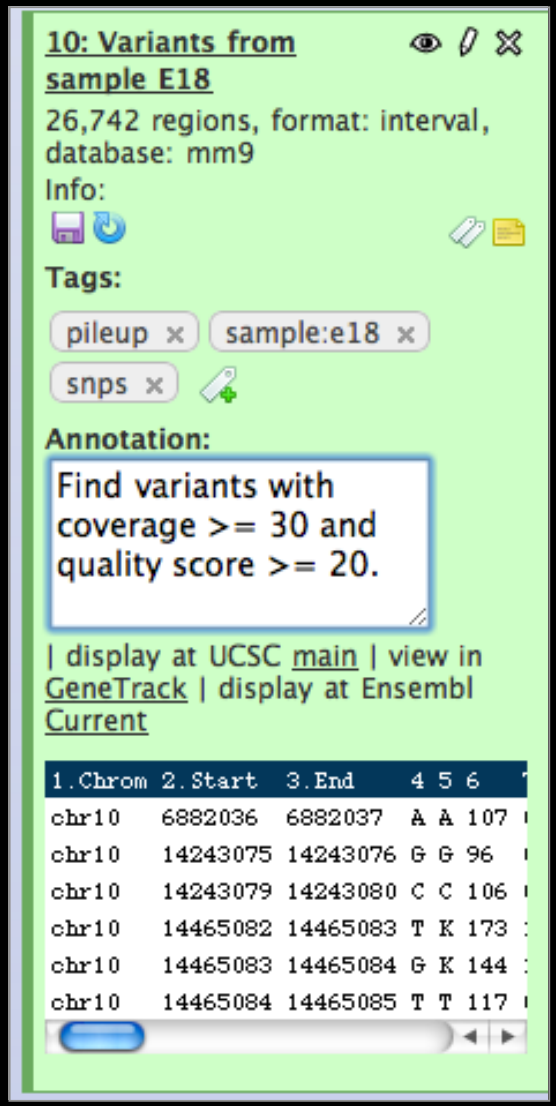
User Metadata





Datasources

Upload file from your computer

- FTP support for large datasets

UCSC table browser

BioMart

interMine / modMine

EuPathDB server

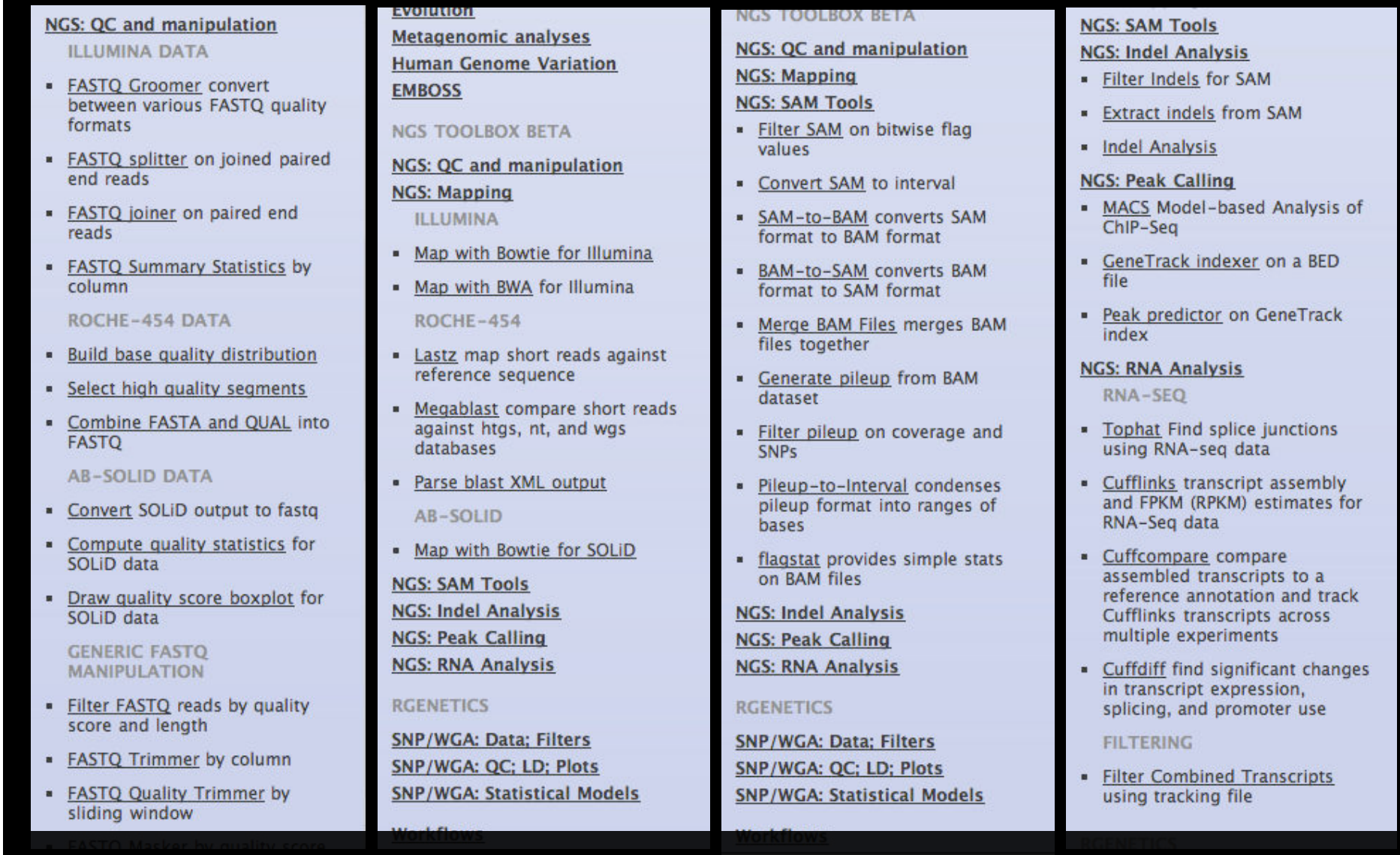
EncodeDB at NHGRI

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



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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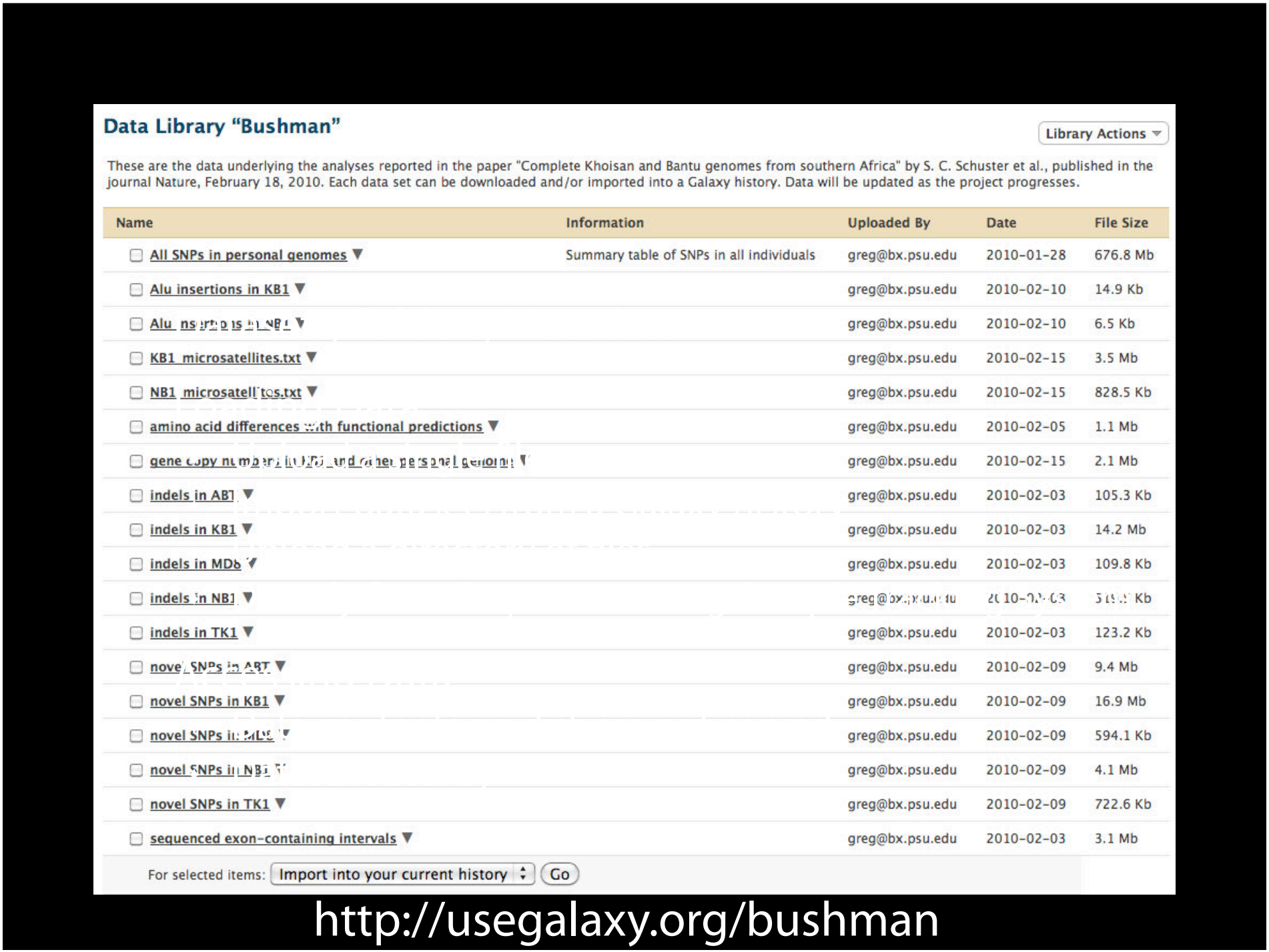
Galaxy 101 Exercise



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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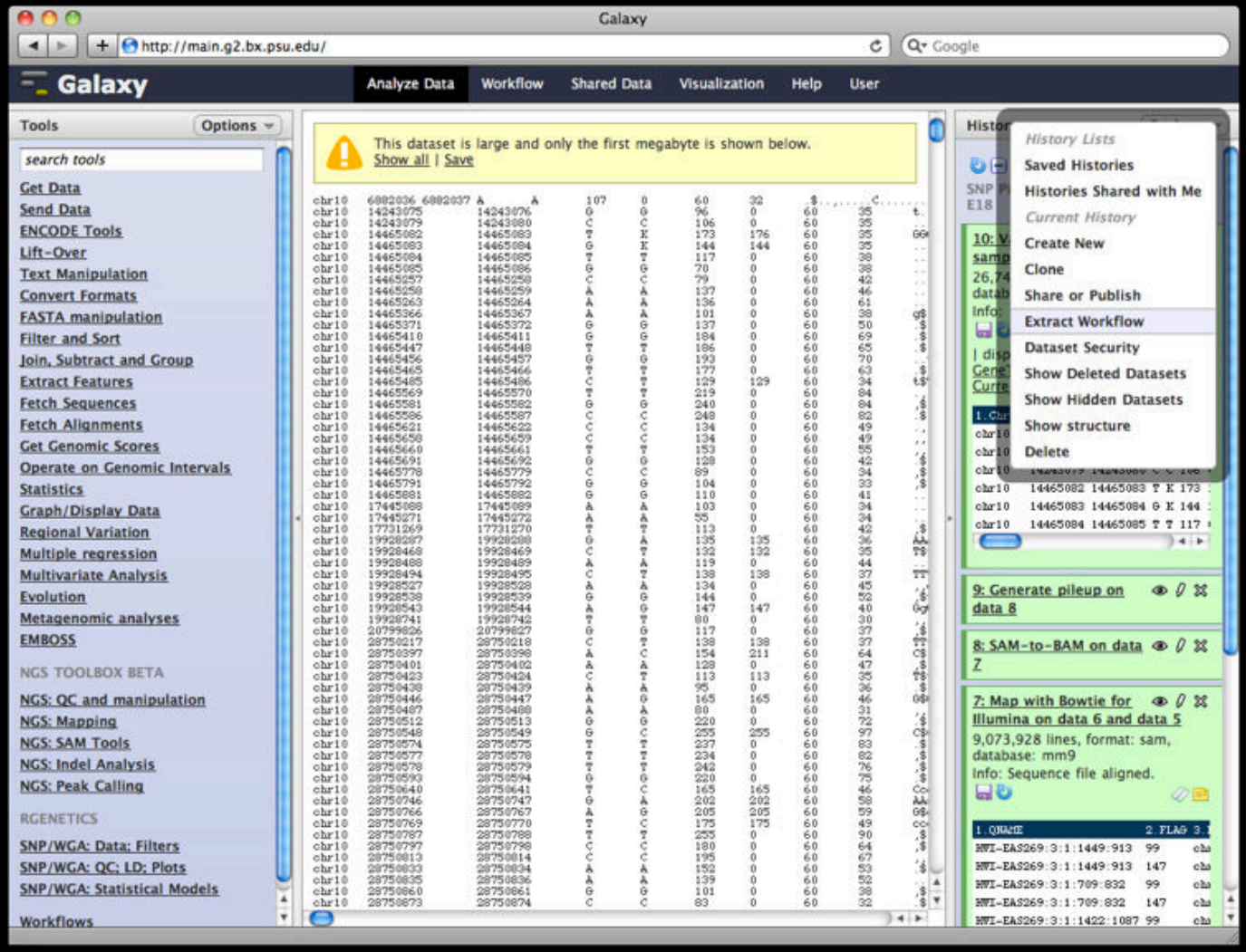
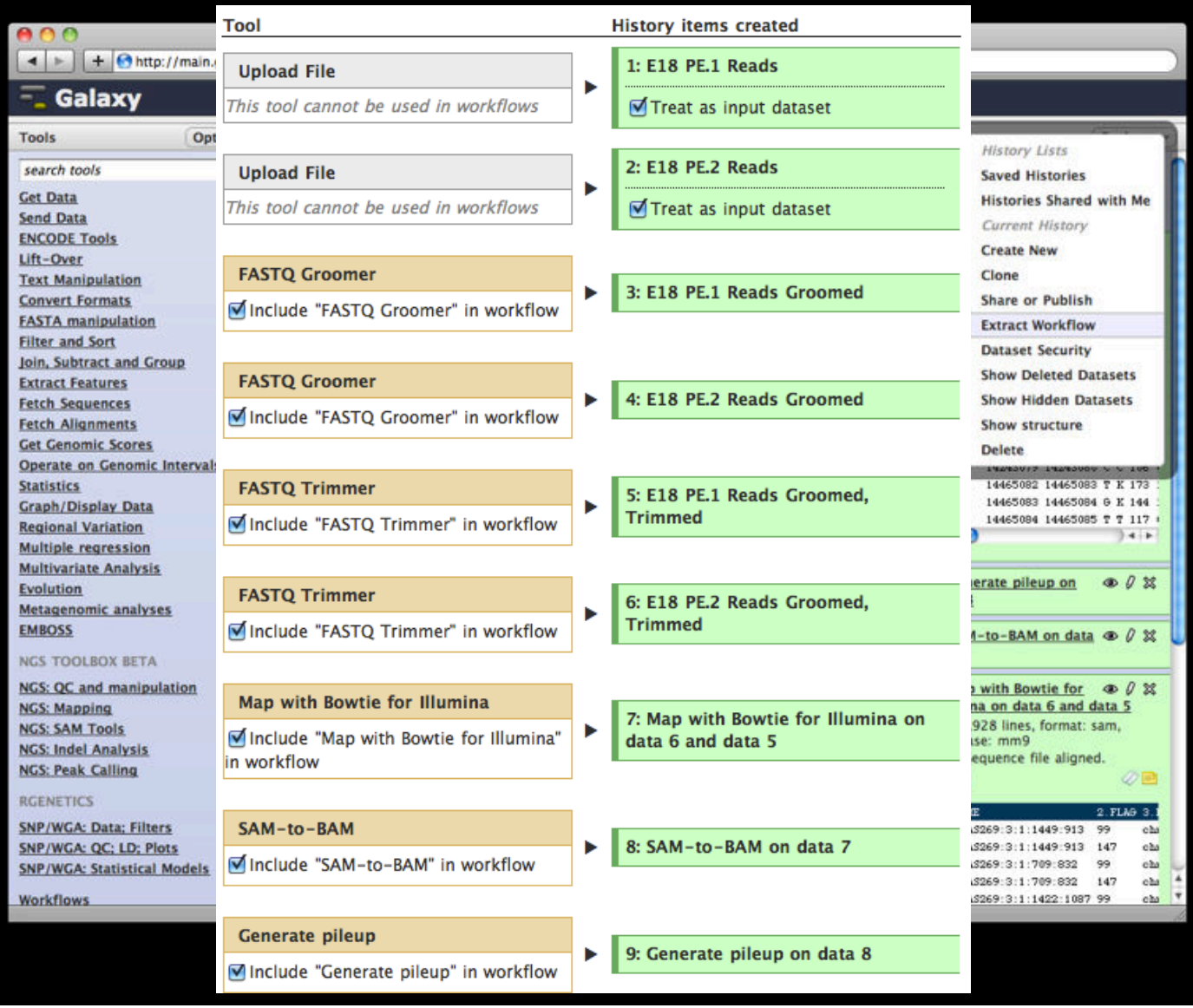
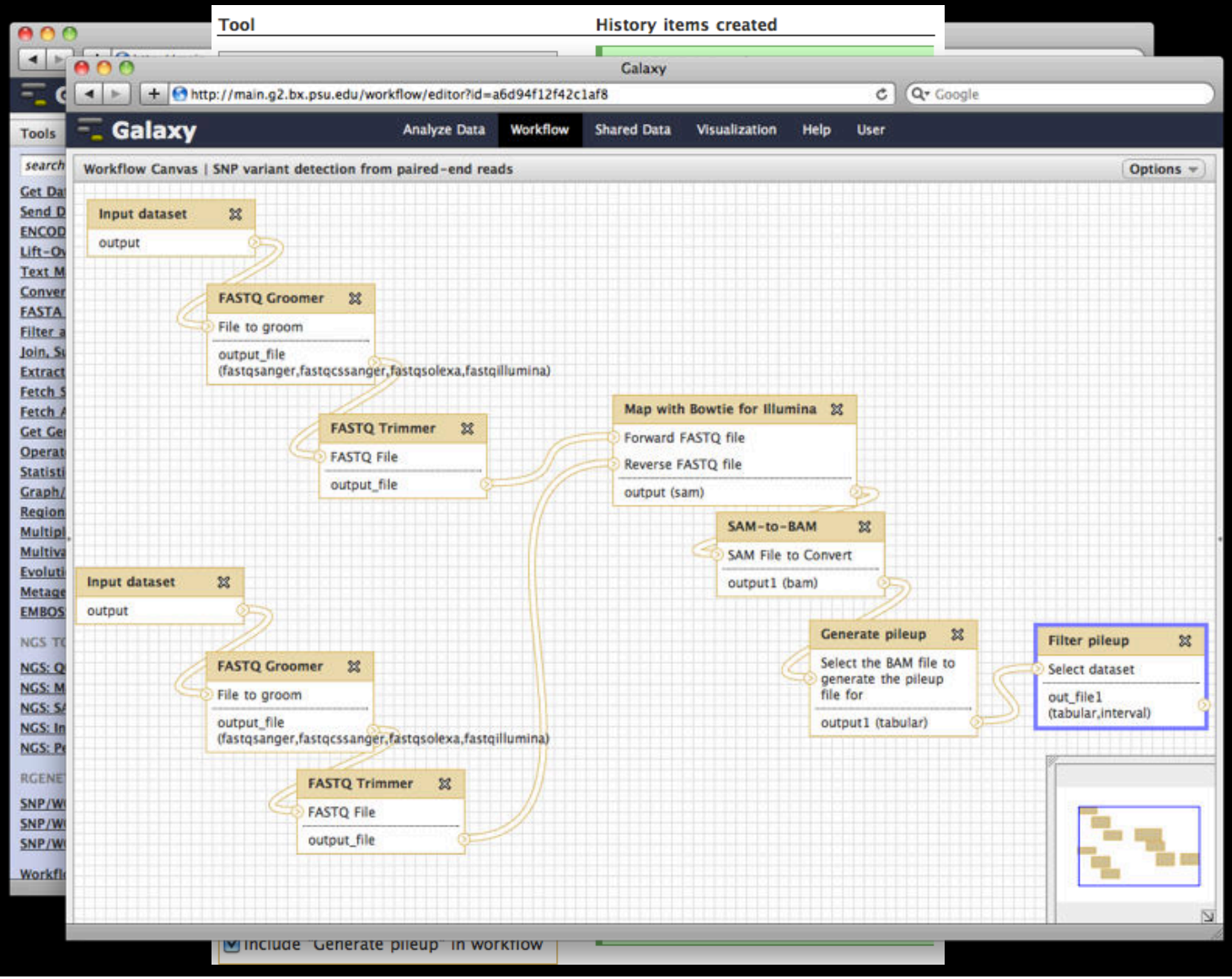
Galaxy Workflows



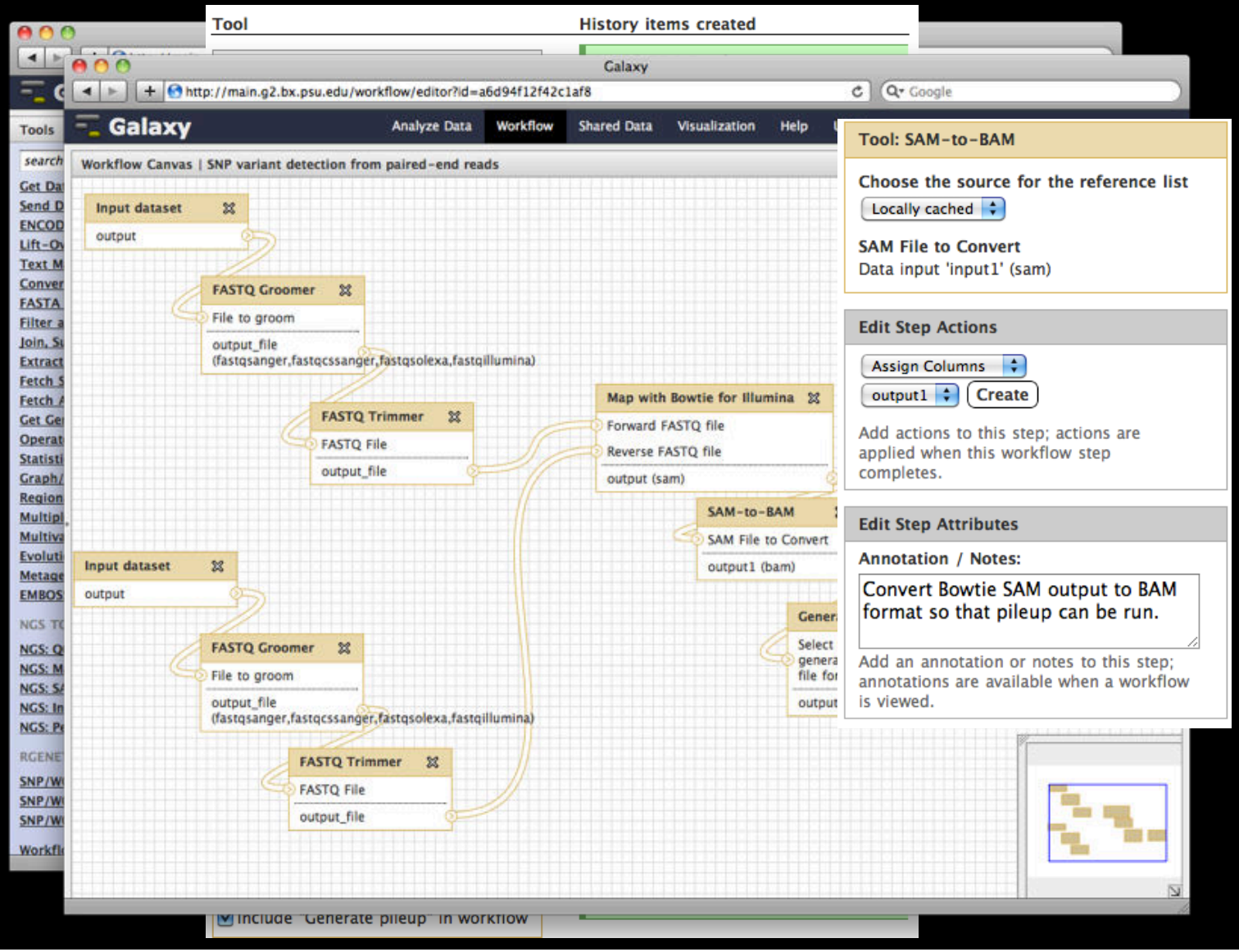
Galaxy Workflows



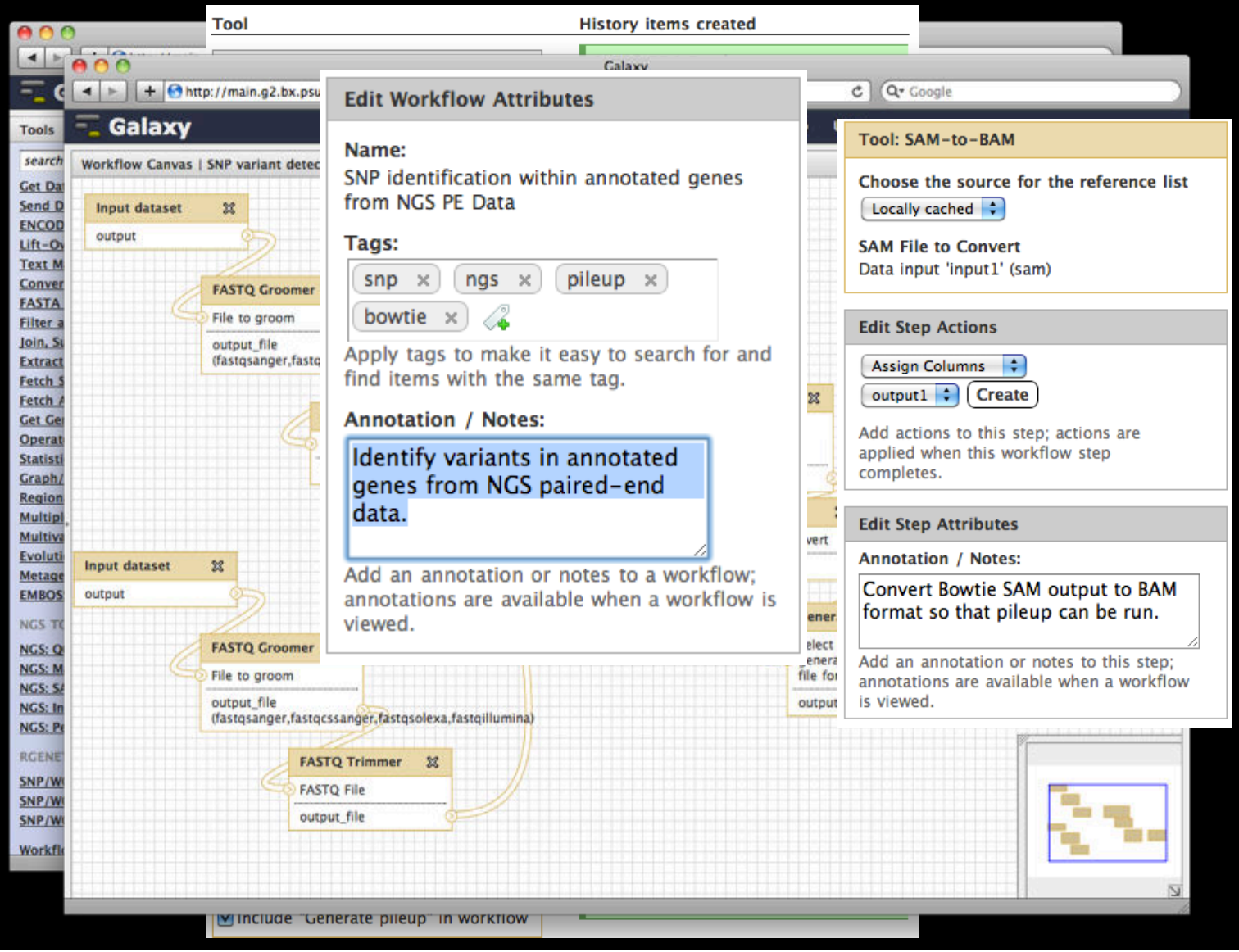
Galaxy Workflows

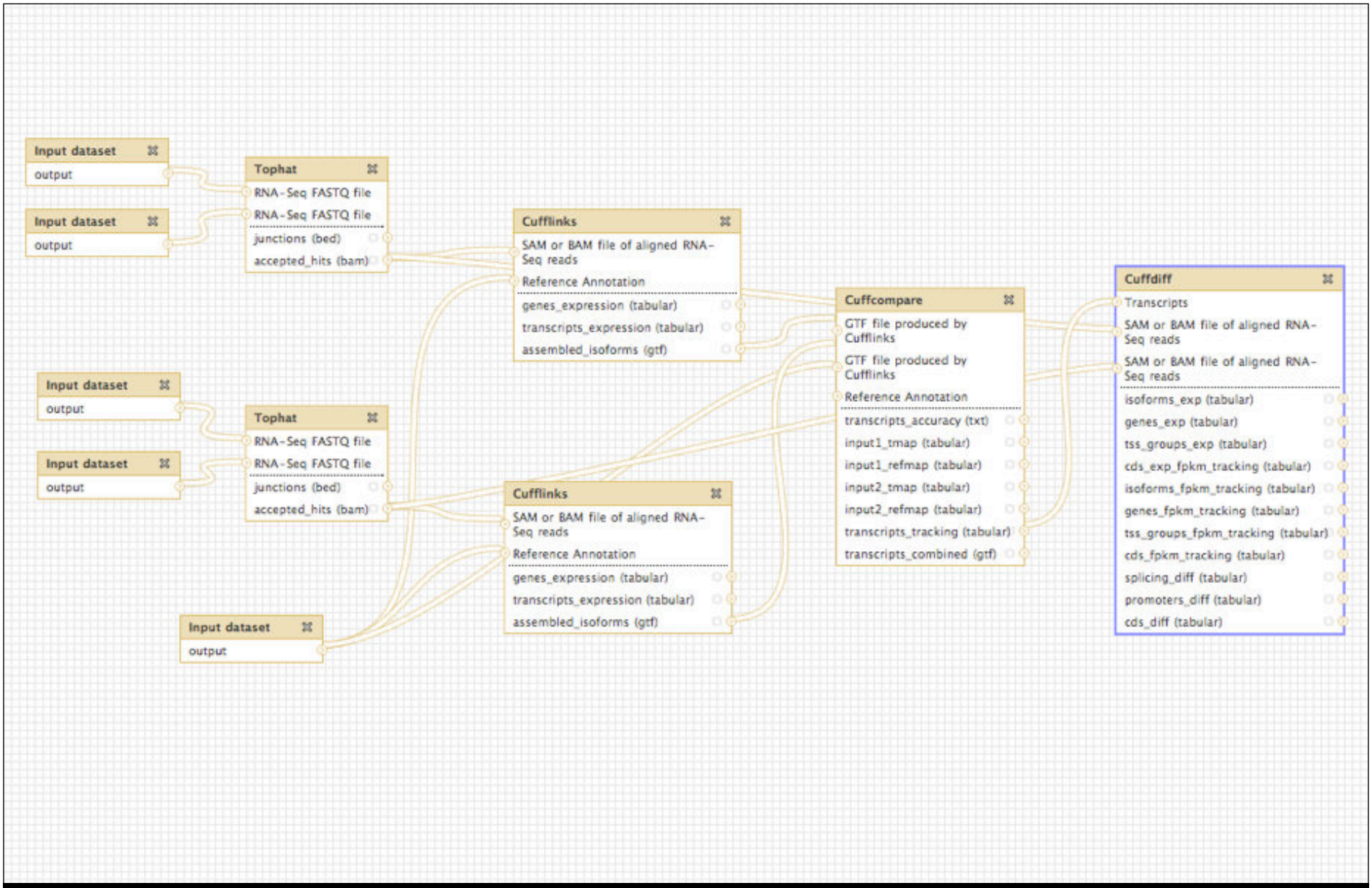


Galaxy Workflows

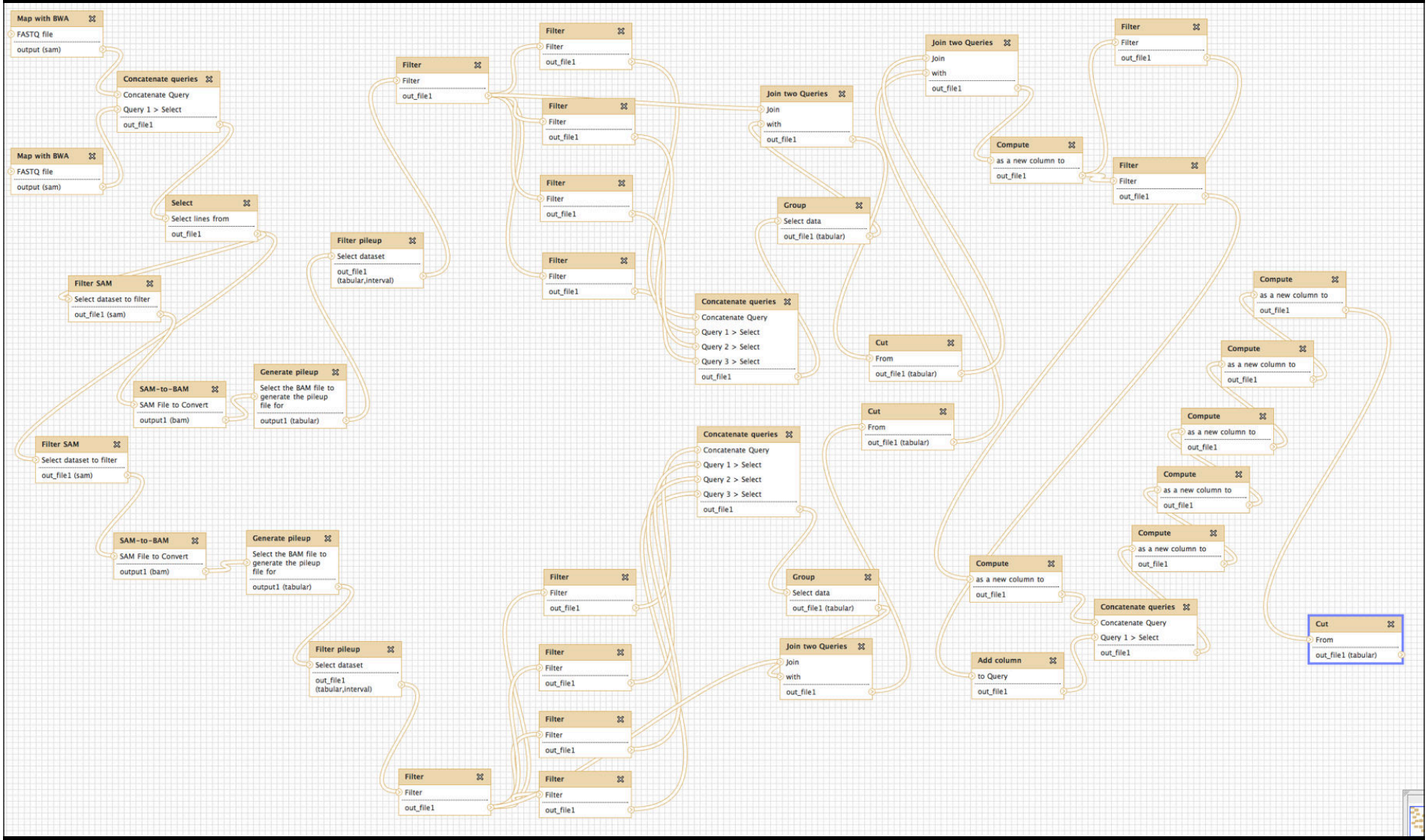


Galaxy Workflows





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

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Galaxy 101 Exercise

Visualize

Send data results to external genome browsers

Trackster: Galaxy's genome browser

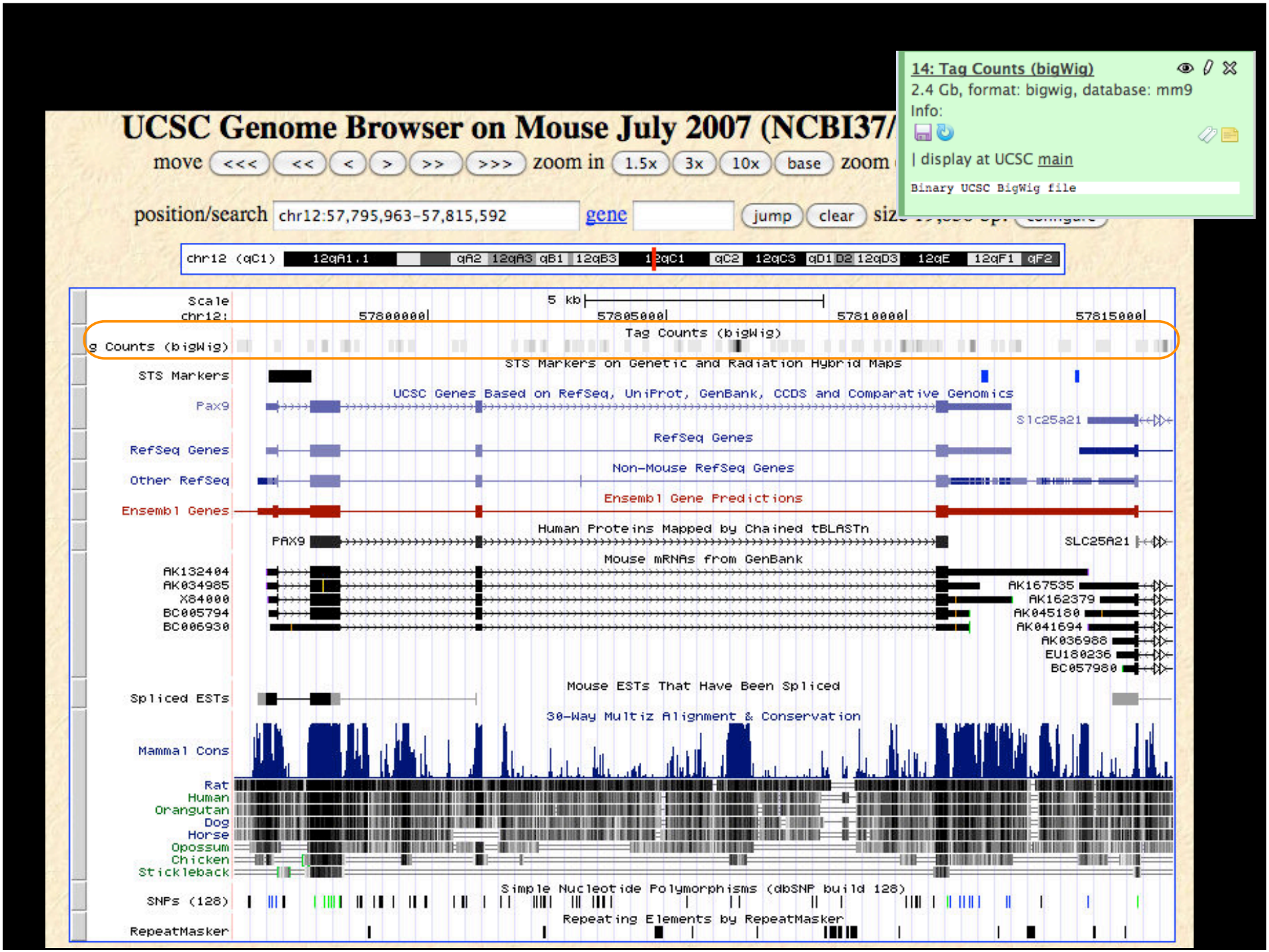
External Genome Browsers

UCSC

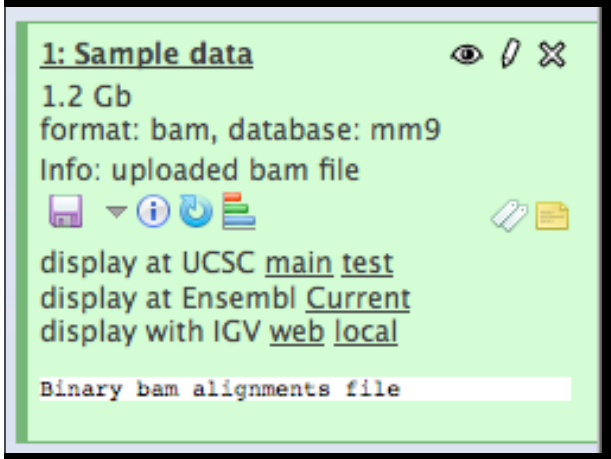
Ensembl

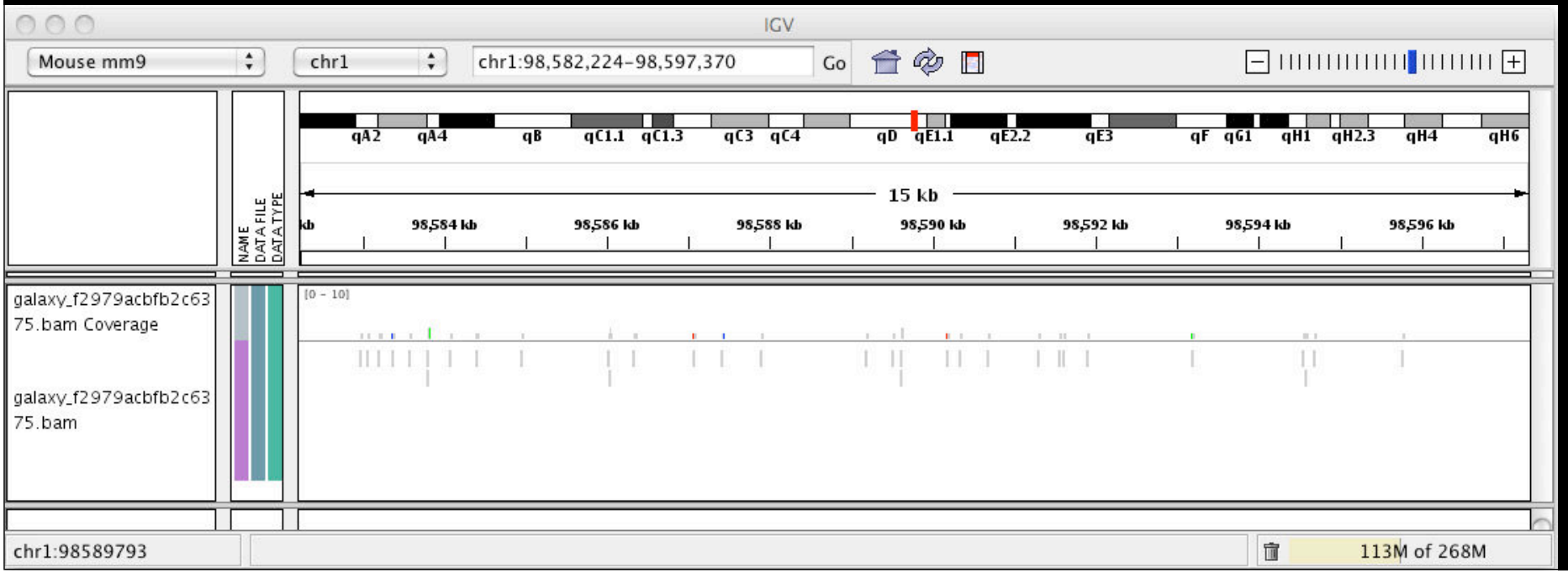
GBrowse

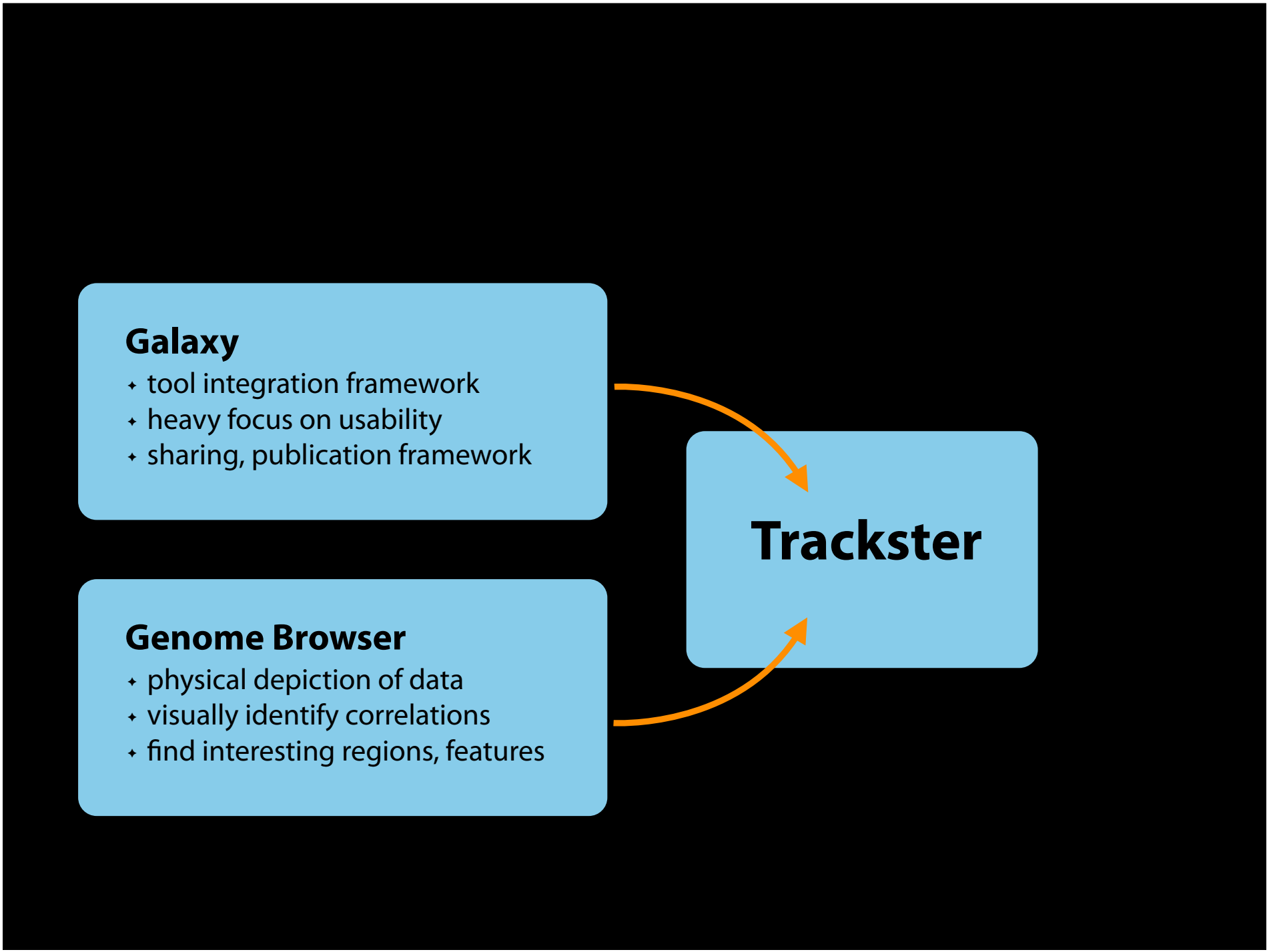
IGV


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)
g Counts (bigWig)
STS Markers on Genetic and Radiation Hybrid Maps
STS Markers
UCSC Genes Based on RefSeq, UniProt, GenBank, CCDS and Comparative Genomics
Pax9
Slc25a21
RefSeq Genes
RefSeq Genes
Non-Mouse RefSeq Genes
Other RefSeq
Ensembl Gene Predictions
Ensembl Genes
Human Proteins Mapped by Chained tBLASTn
PAX9
SLC25A21
Mouse mRNAs from GenBank
AK132404
AK034985
X84000
BC005794
BC006930
AK167535
AK162379
AK045180
AK041694
AK036988
EU180236
BC057980
Mouse ESTs That Have Been Spliced
Spliced ESTs
30-Way Multiz Alignment & Conservation
Mammal Cons
Rat
Human
Orangutan
Dog
Horse
Opossum
Chicken
Stickleback
Simple Nucleotide Polymorphisms (dbSNP build 128)
SNPs (128)
Repeating Elements by RepeatMasker
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

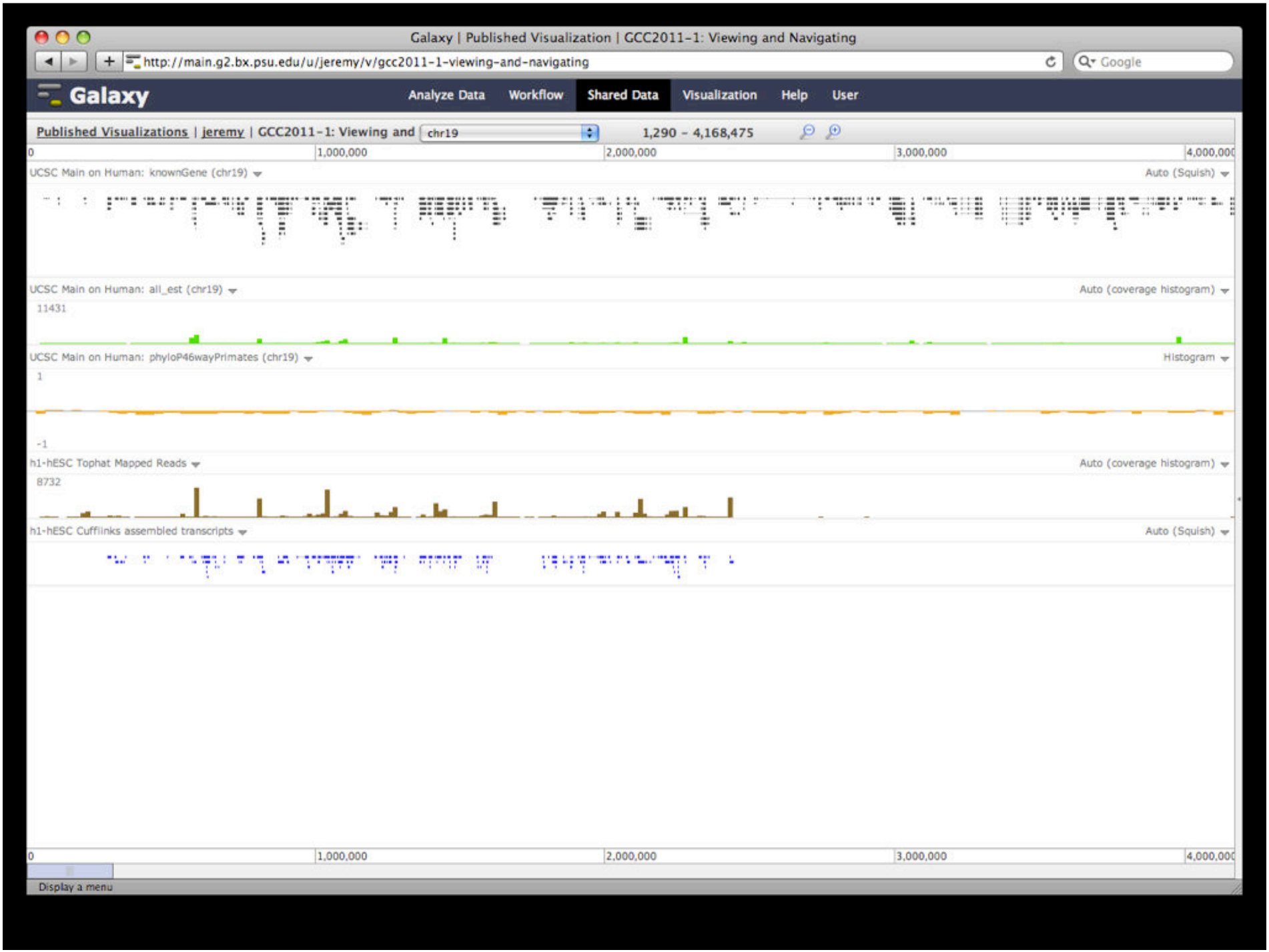
- No data transfers to external site
- Use it locally, even without internet access

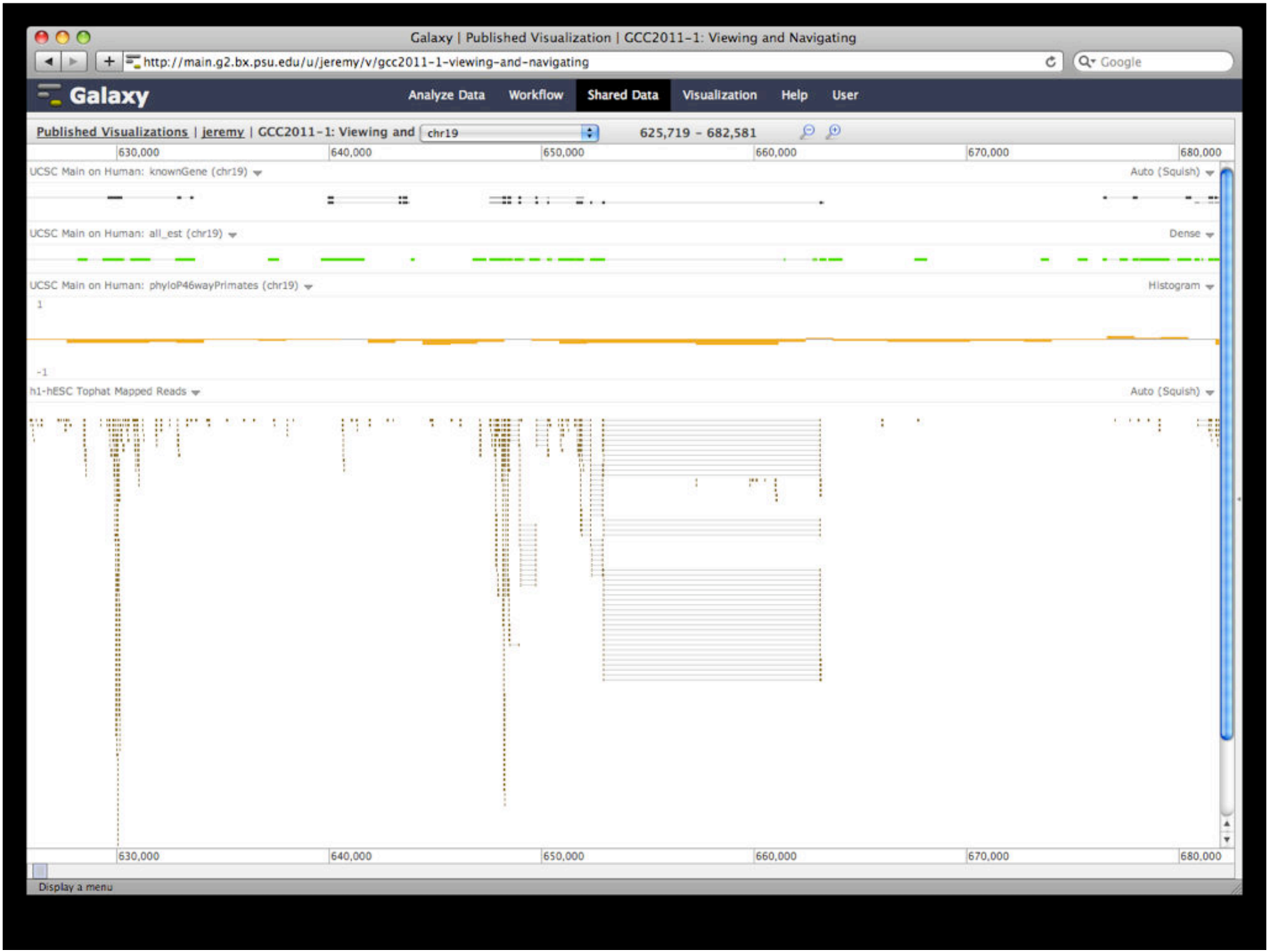
Supports common filetypes

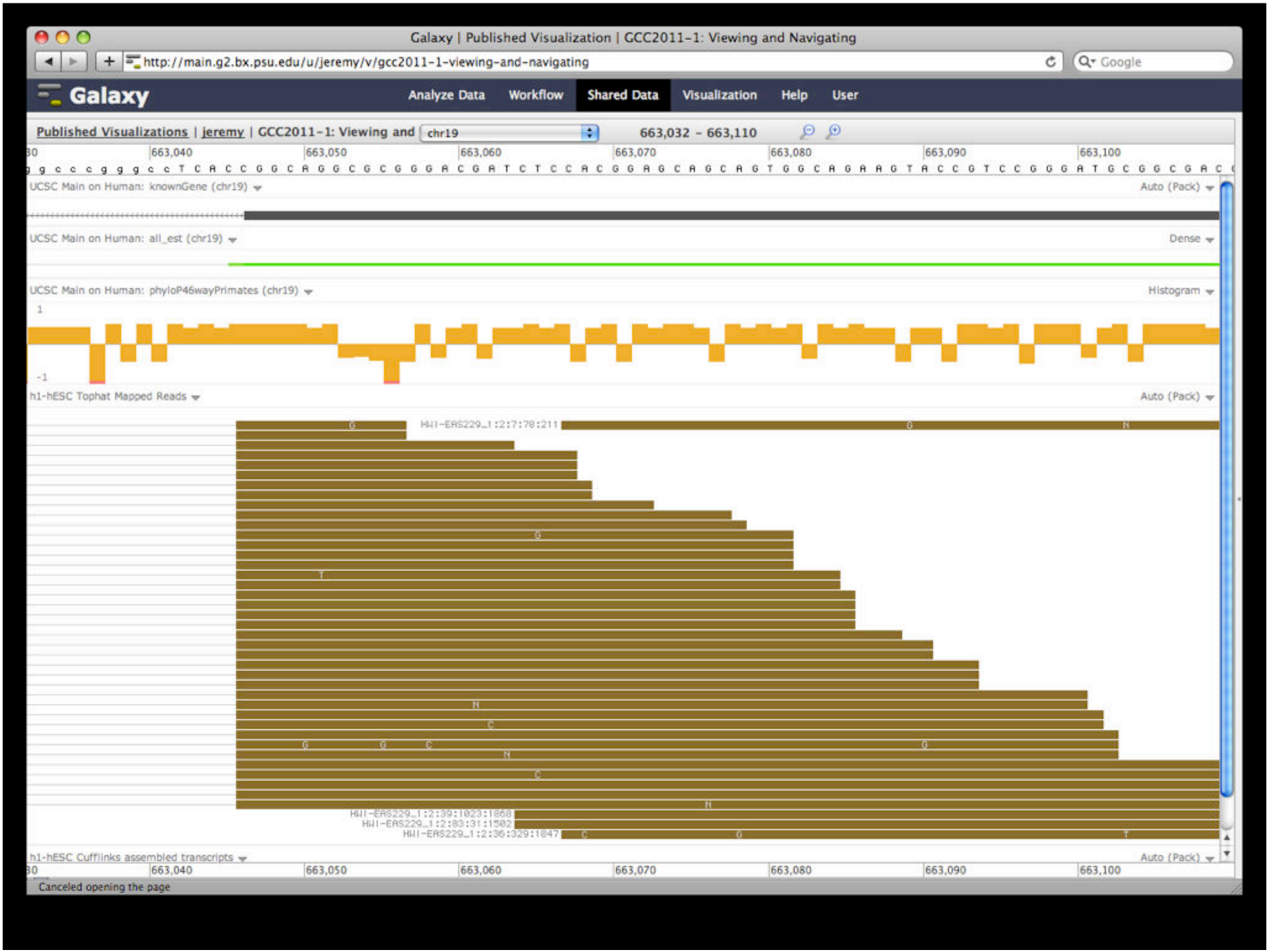
- BAM, BED, GFF/GTF, WIG

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
Google
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)
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
Google
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)
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
Google
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

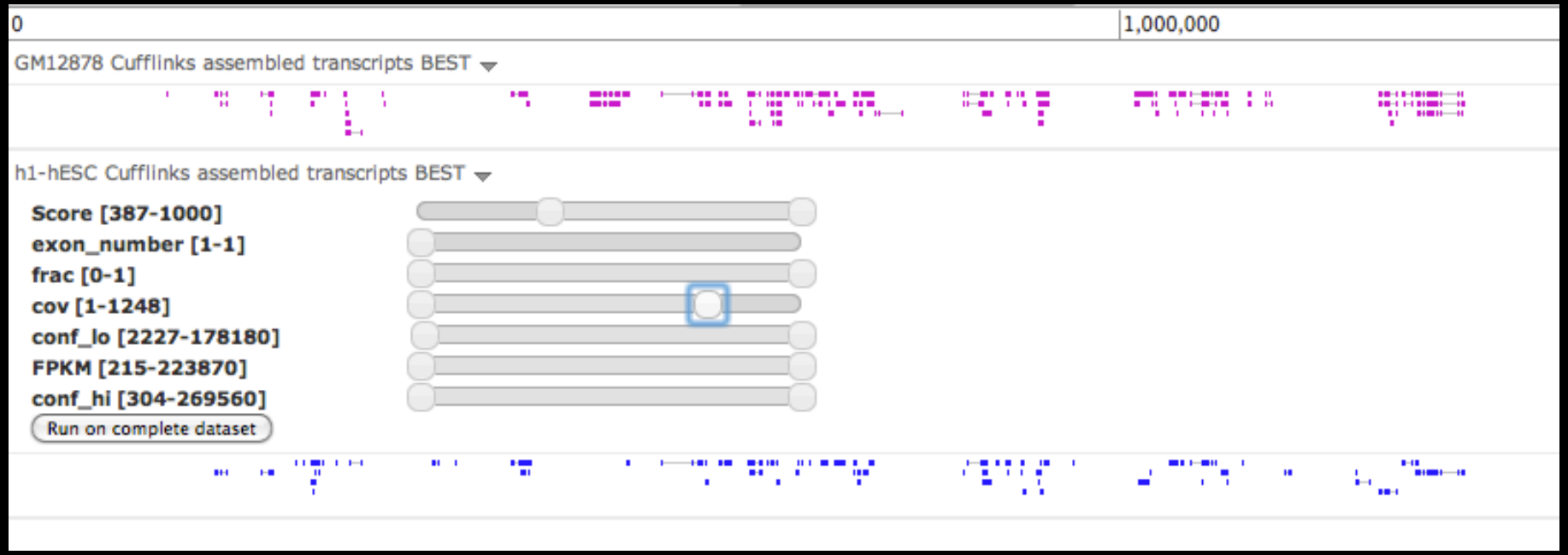
But really, why *another* genome browser

From static browsing to visual analysis

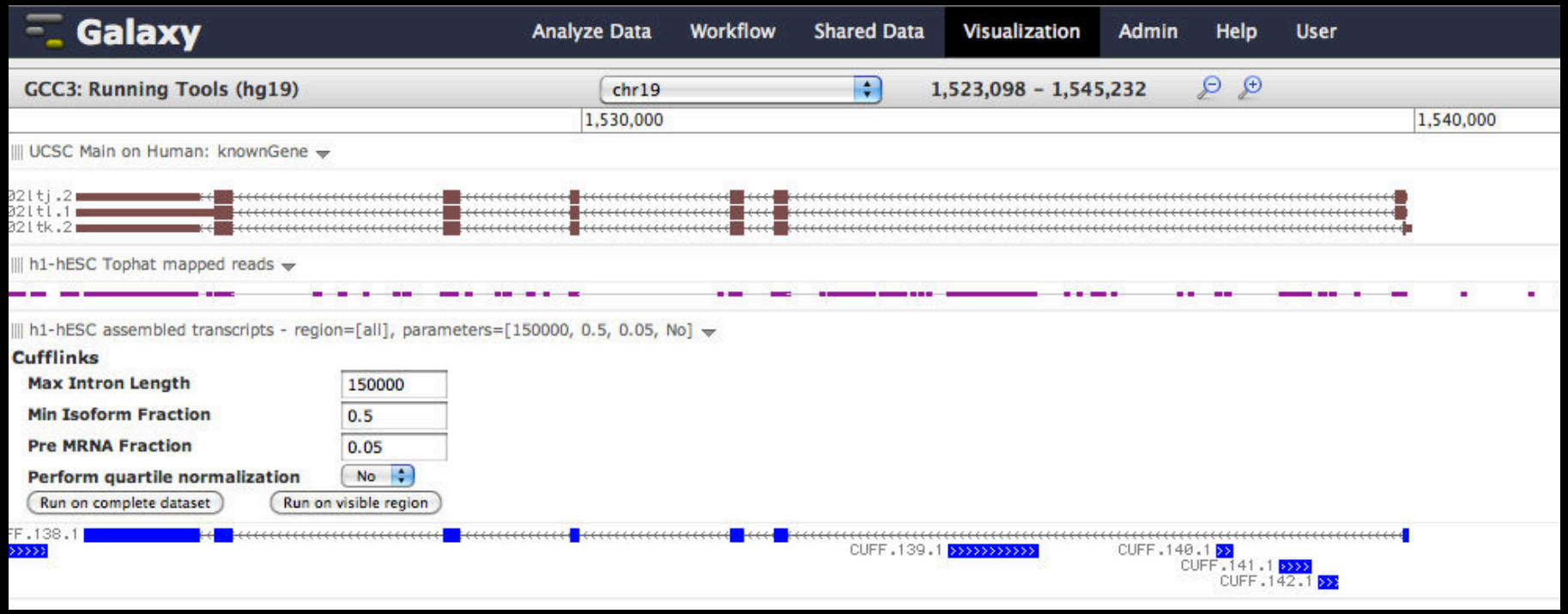
Visual feedback and experimentation needed for complex tools with many parameters

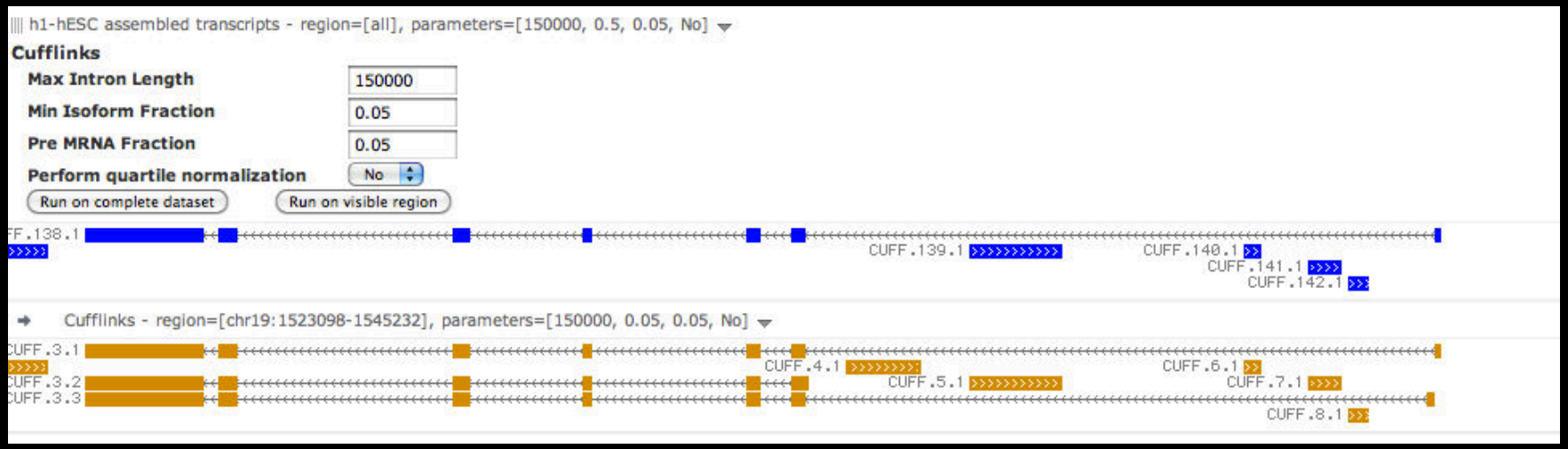
Leverage Galaxy strengths: a very sound model for abstracting interfaces to analysis tools and already integrates an enormous number

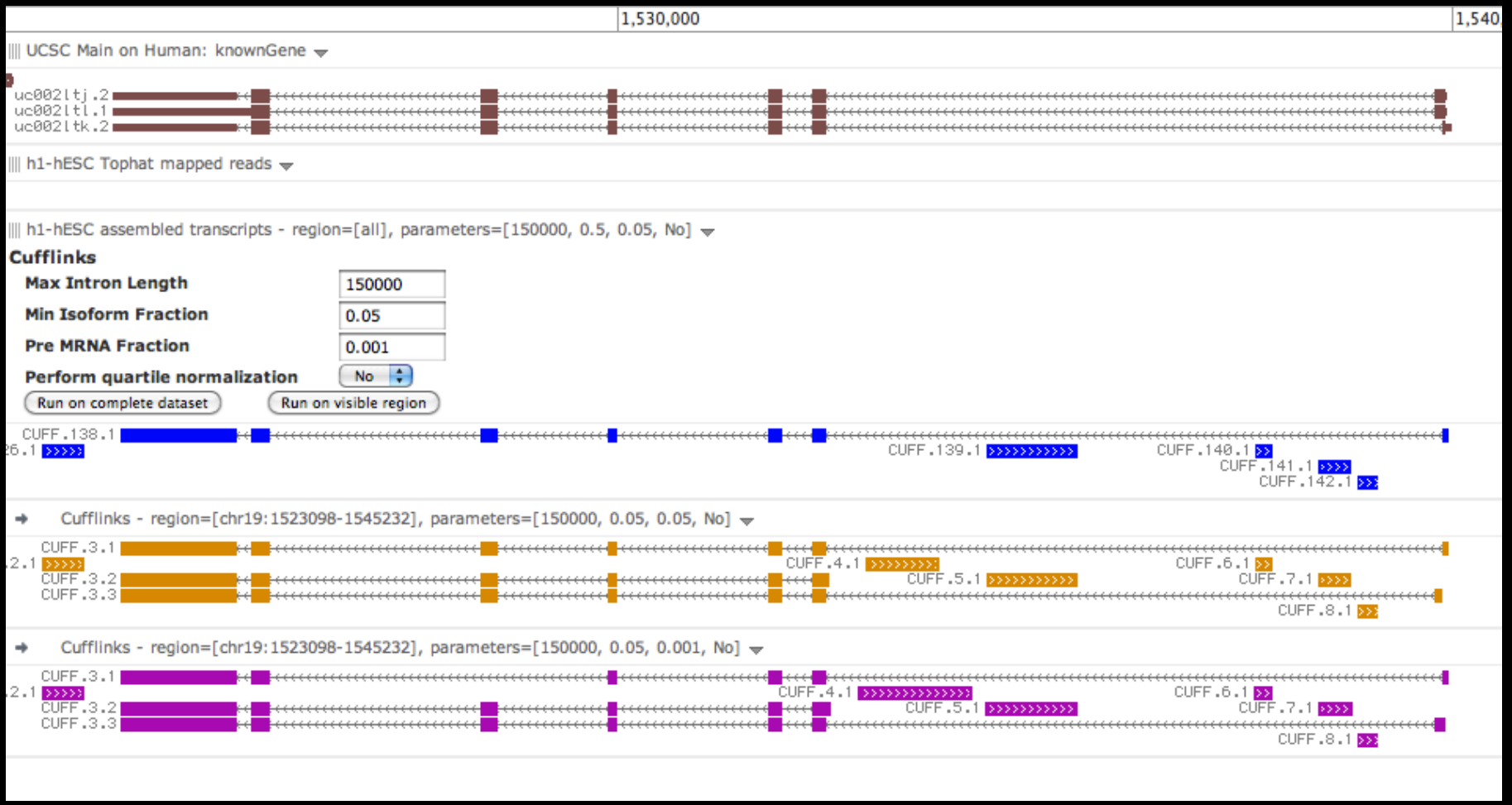
Dynamic Filtering



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.3.2
CUFF.3.3
CUFF.4.1
CUFF.5.1
CUFF.6.1
CUFF.7.1
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.3.2
CUFF.3.3
CUFF.4.1
CUFF.5.1
CUFF.6.1
CUFF.7.1
CUFF.8.1
Cufflinks - region=[chr19:1523098-1545232], parameters=[150000, 0.05, 0.001, No]
CUFF.3.1
CUFF.3.2
CUFF.3.3
CUFF.4.1
CUFF.5.1
CUFF.6.1
CUFF.7.1
CUFF.8.1

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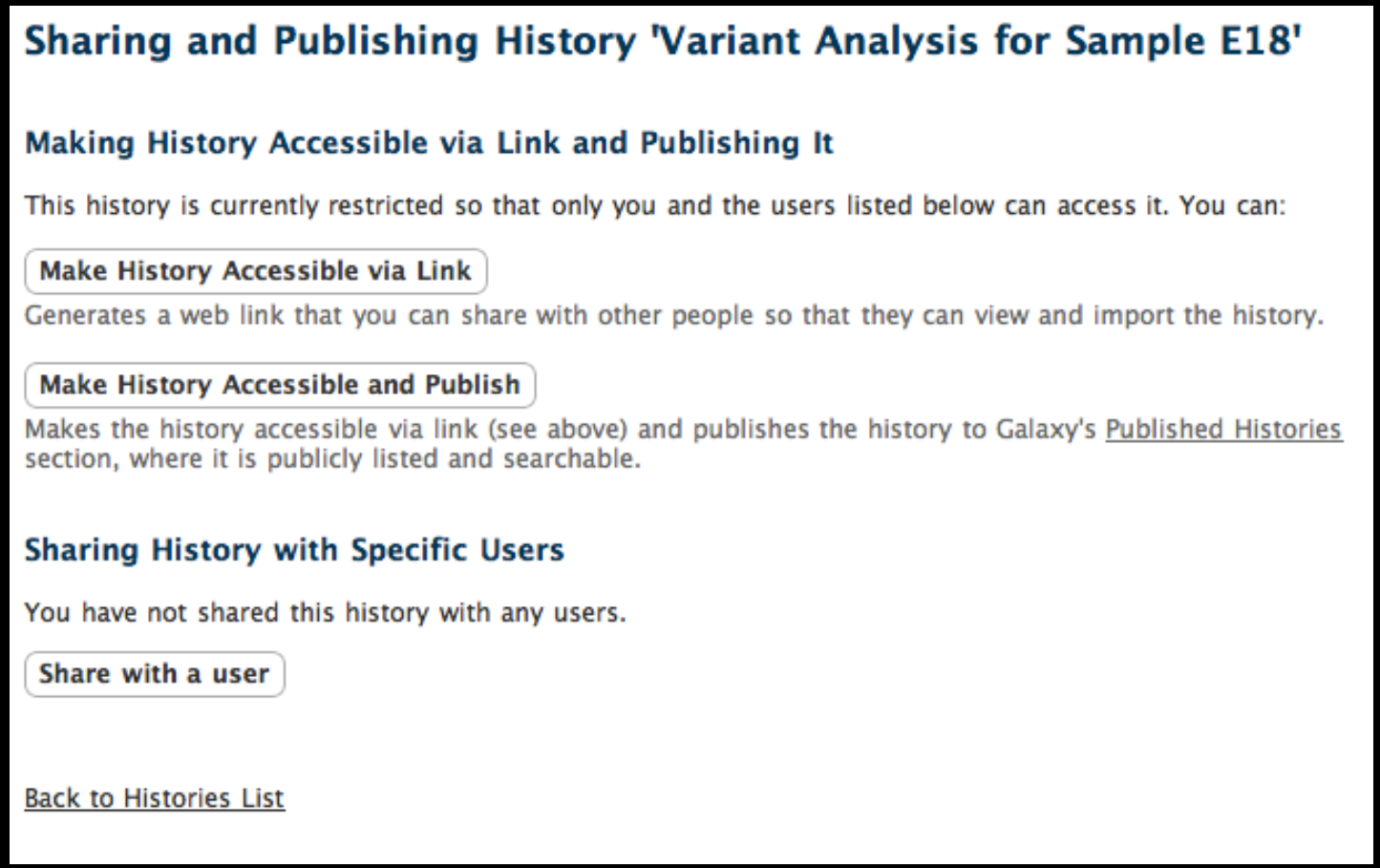
Galaxy 101 Exercise

Sharing and Publishing



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

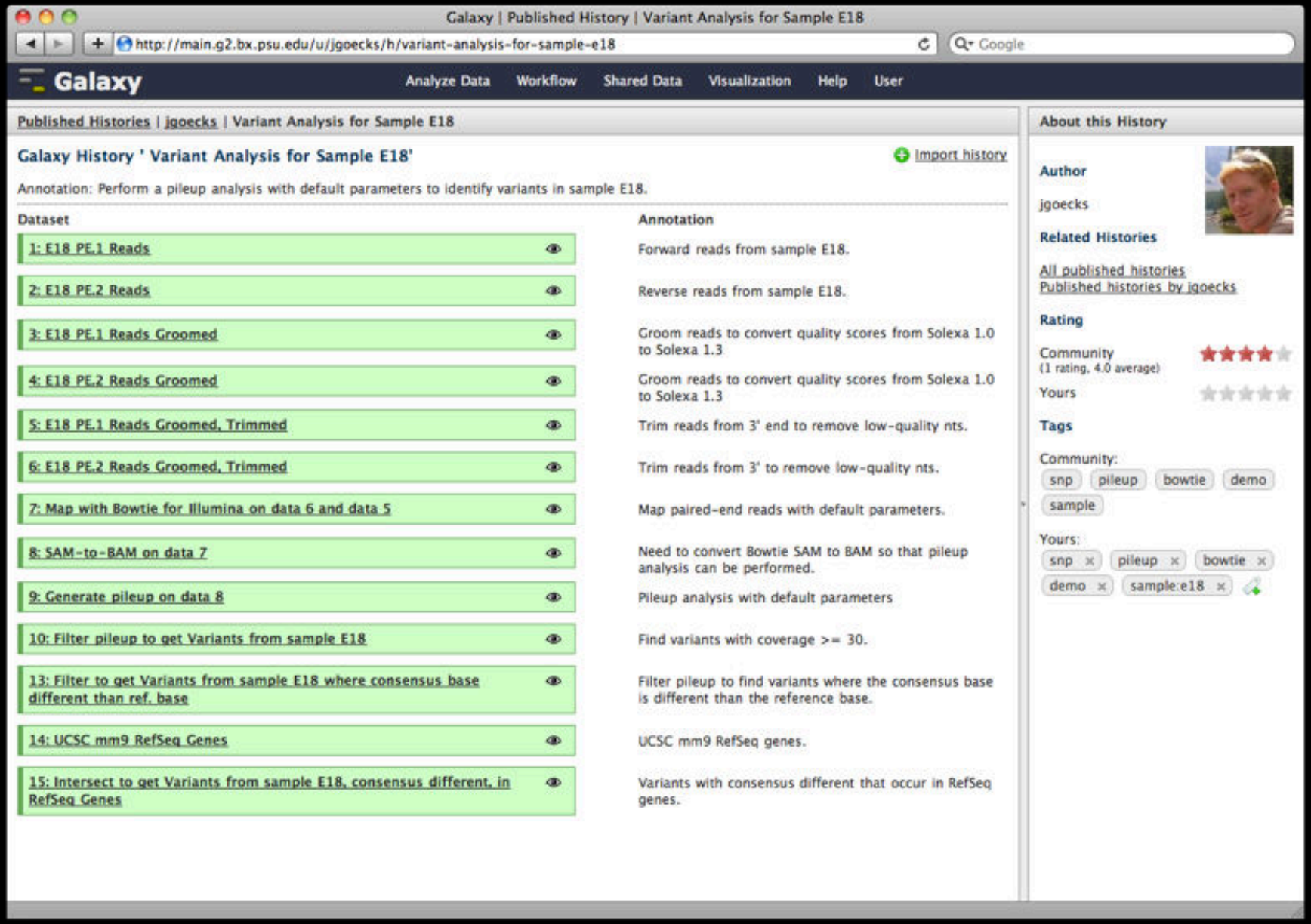
Disables history's link so that it is not accessible and removes history from Galaxy's Published Histories section so that it is not publicly listed or searchable.

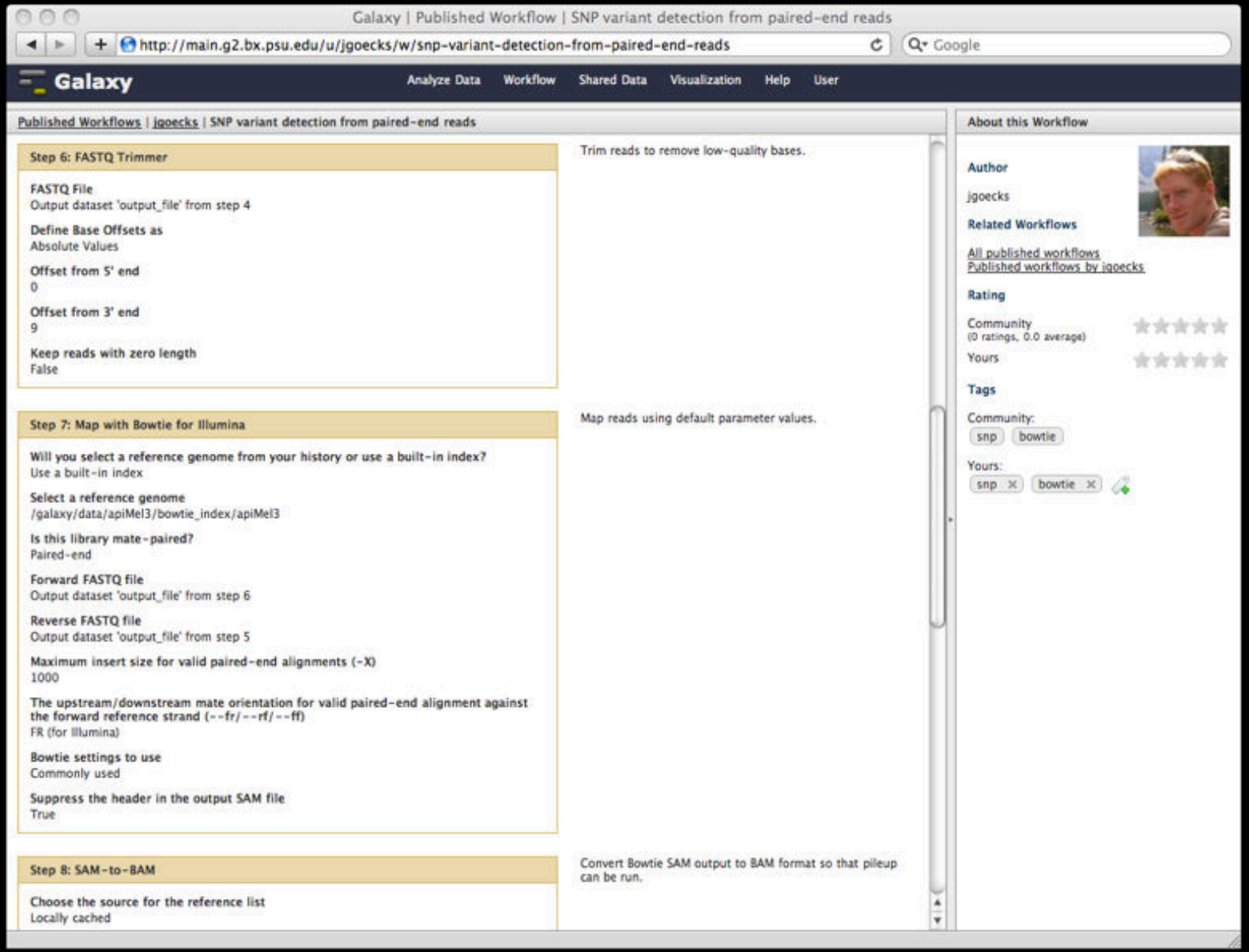
Sharing History with Specific Users

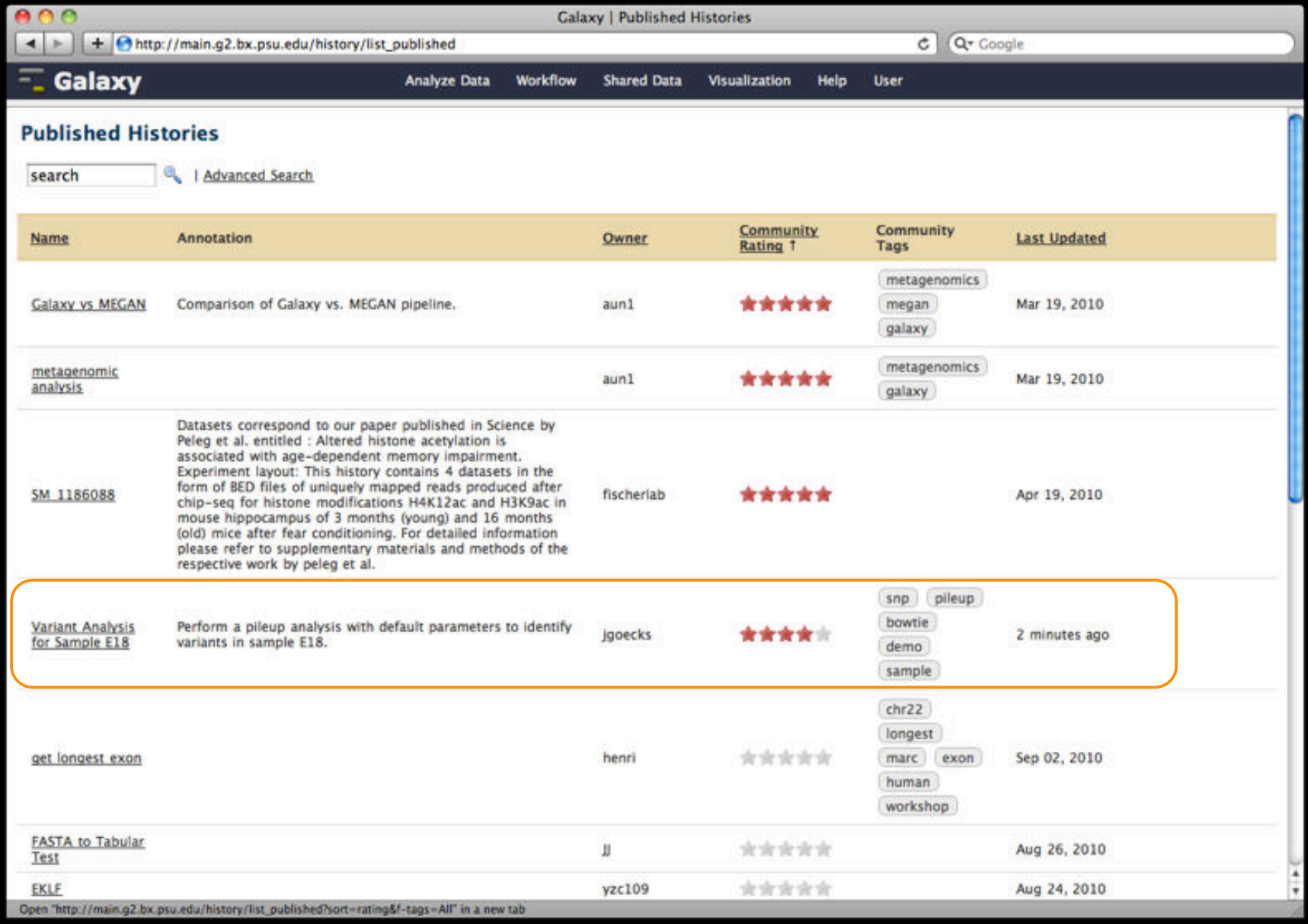
You have not shared this history with any users.

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
Google
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

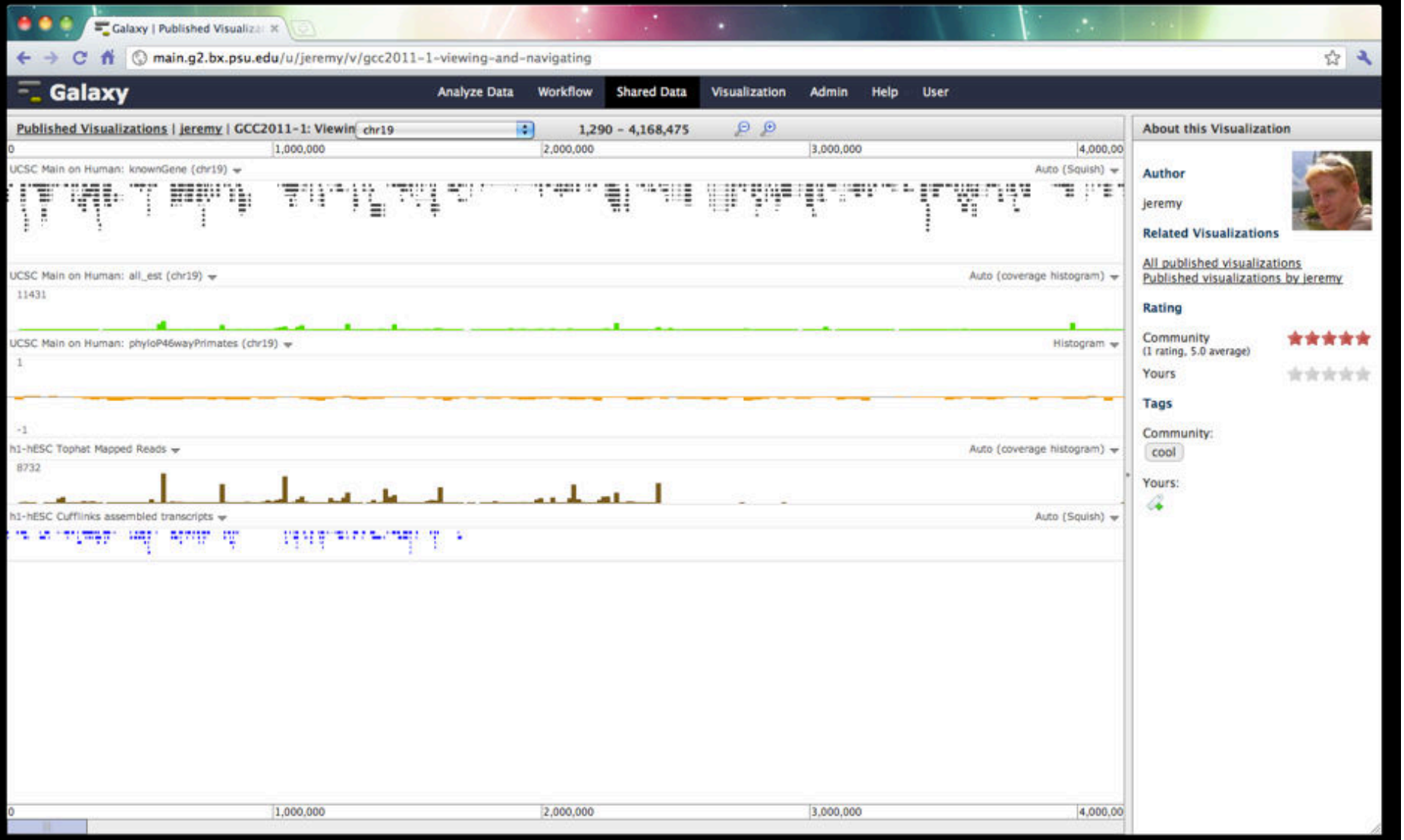

Galaxy | Published Workflow | SNP variant detection from paired-end reads
http://main.g2.bx.psu.edu/u/jgoecks/w/snp-variant-detection-from-paired-end-reads
Google
Galaxy
Analyze Data
Workflow
Shared Data
Visualization
Help
User
Published Workflows | jgoecks | SNP variant detection from paired-end reads
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
Google
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
FKLF
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 Visualiz
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)
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

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- workflows
- visualization
- sharing
- Pages

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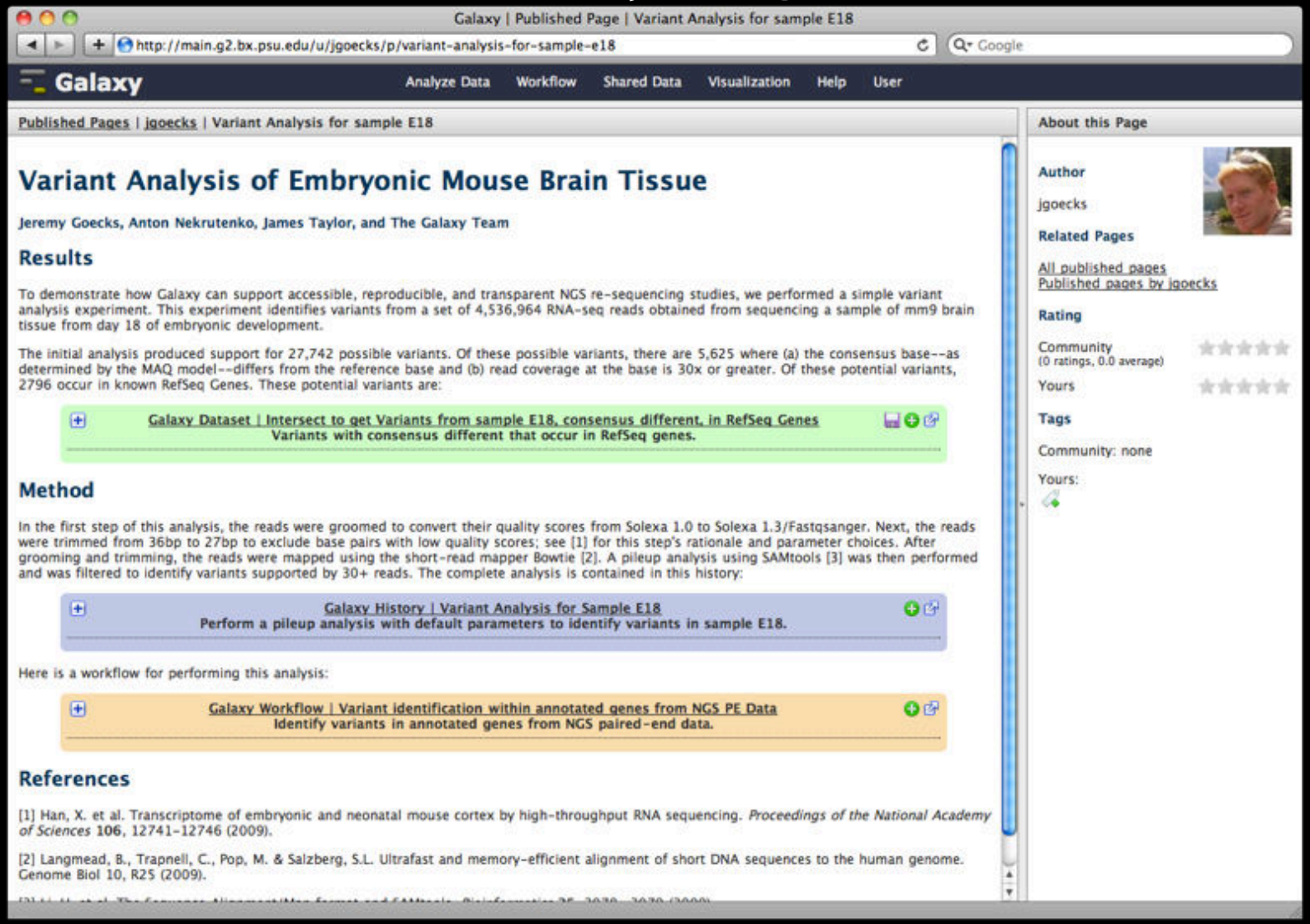
- on the cloud
- tool shed/contributing tools

Galaxy 101 Exercise

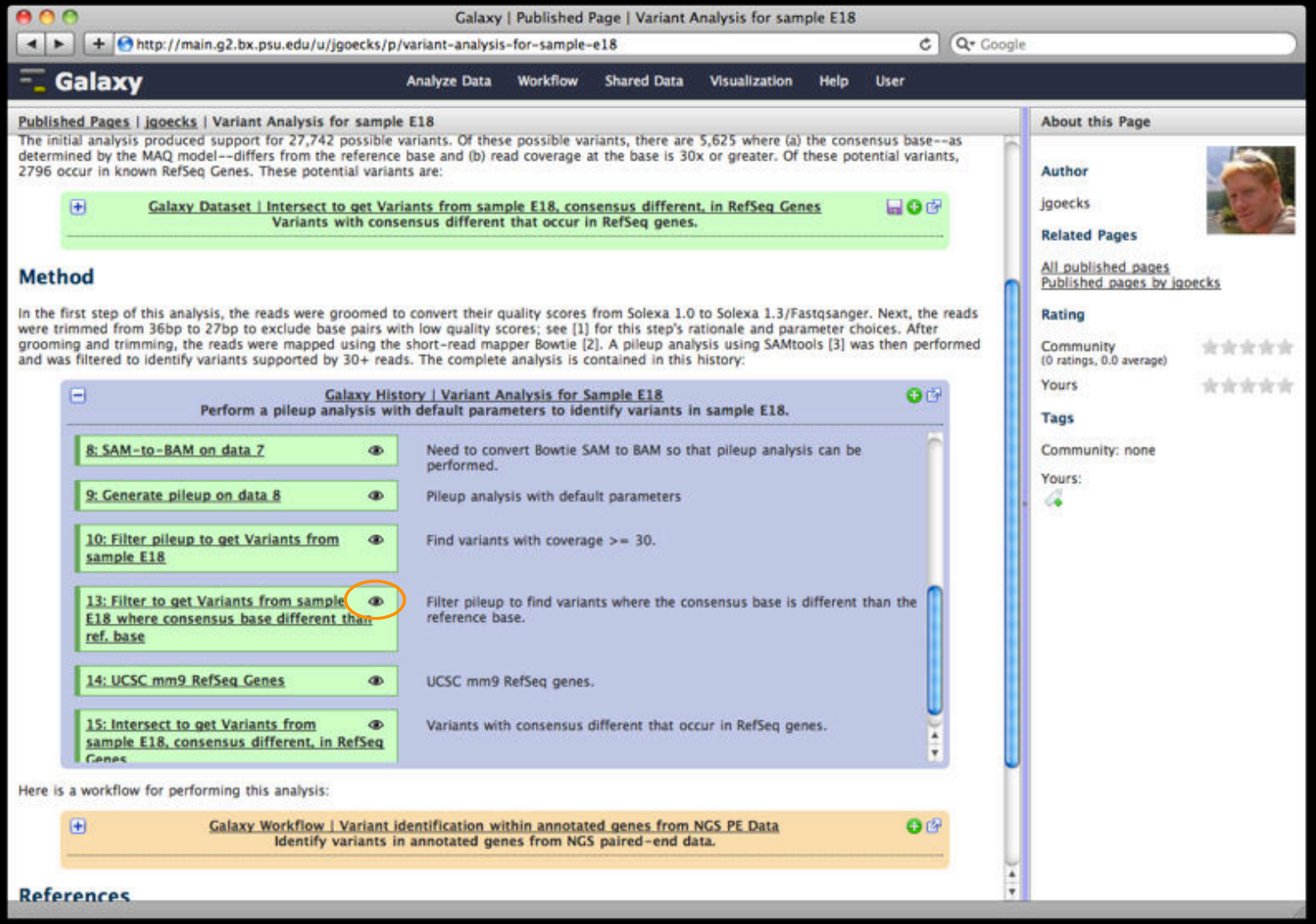
Galaxy Pages

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

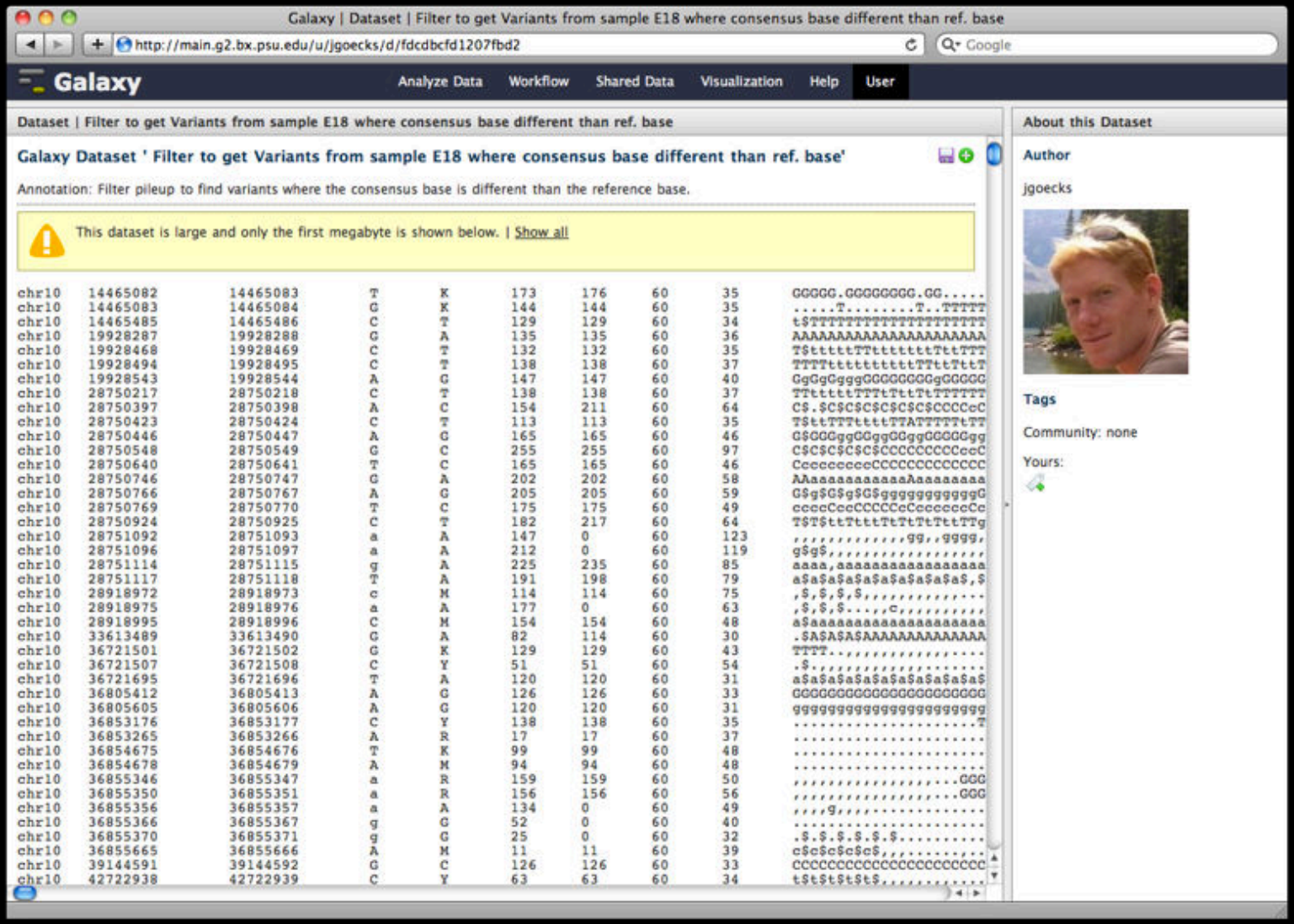
Galaxy Pages



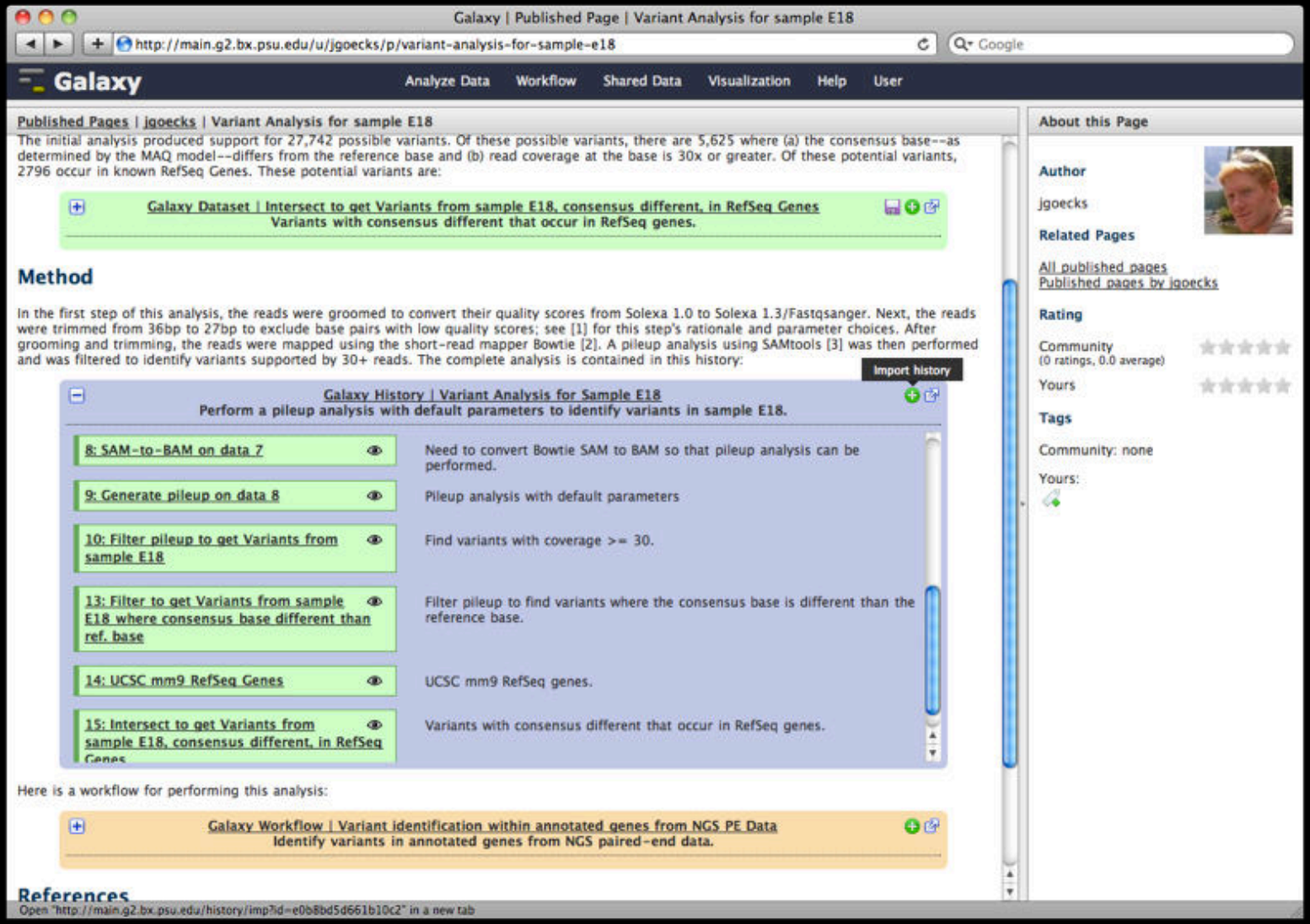
Galaxy Pages



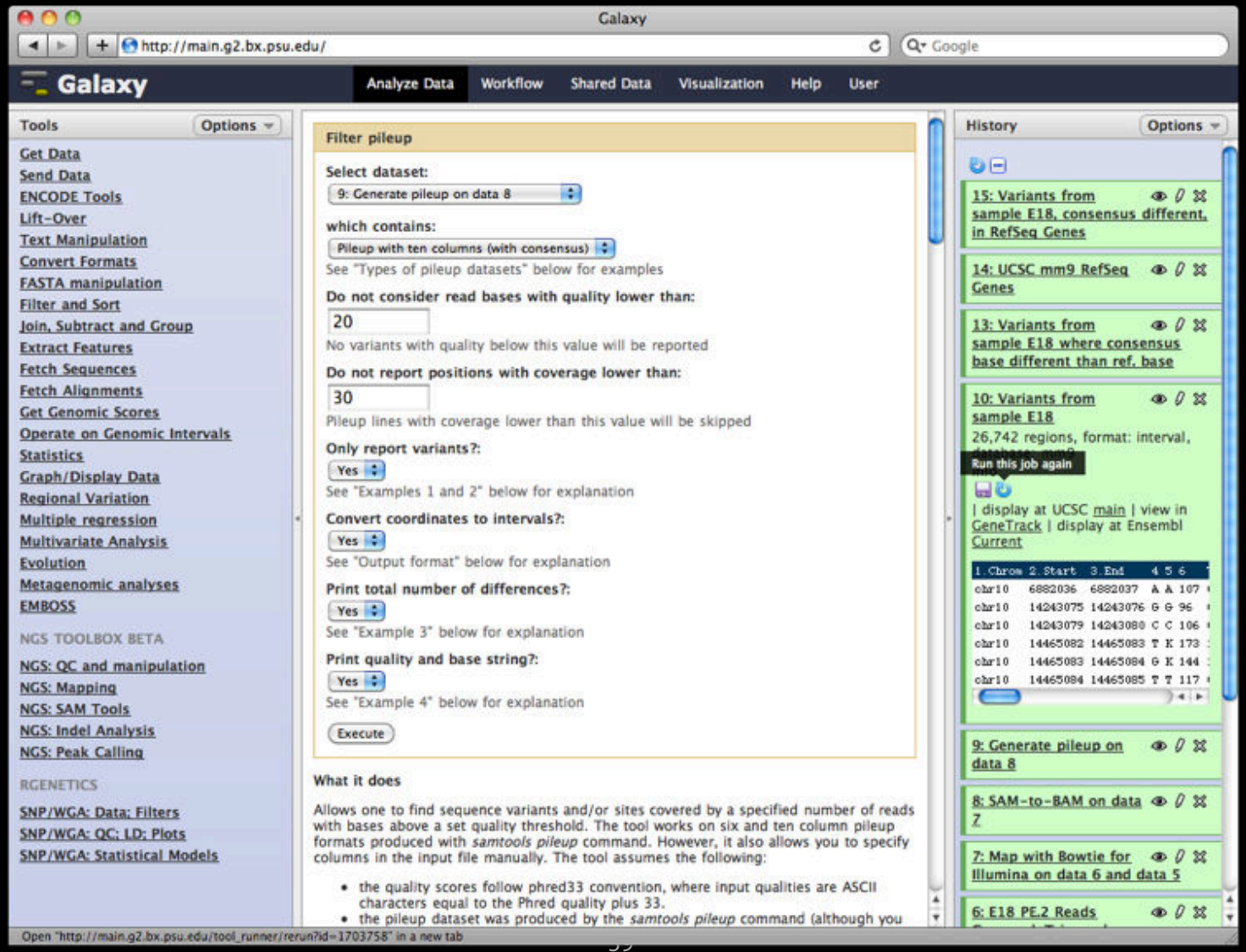
Galaxy Pages



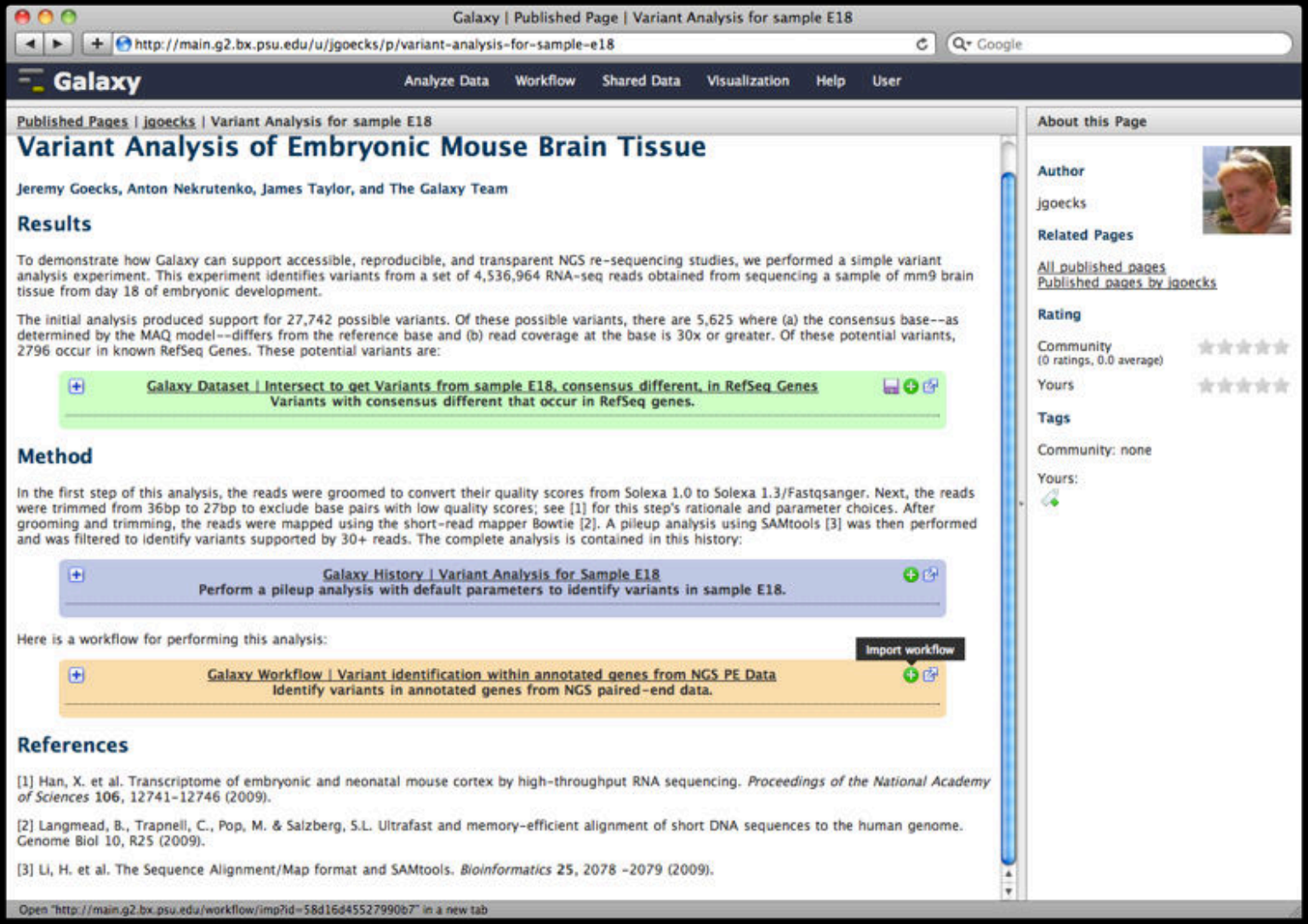
Galaxy Pages



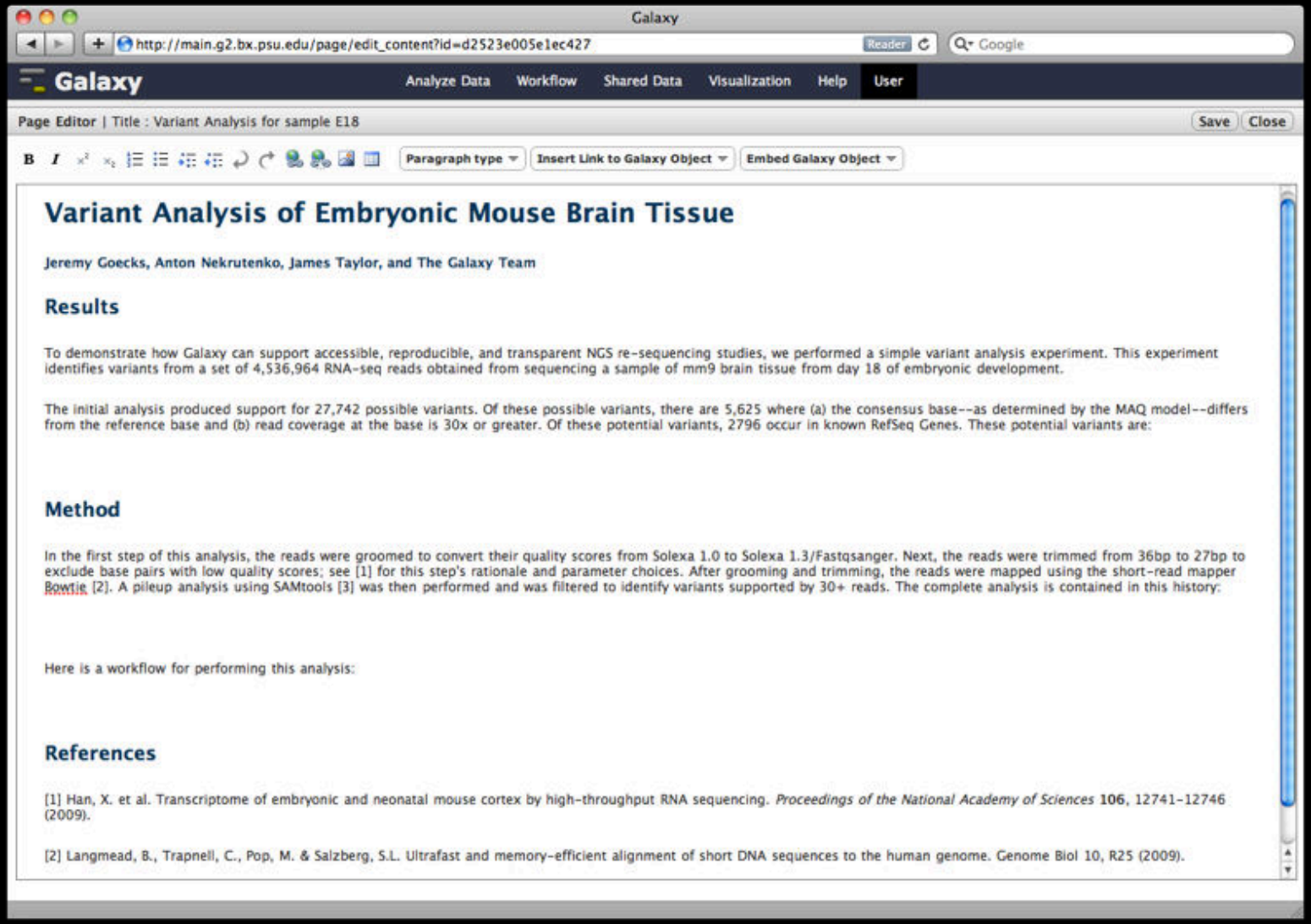
Galaxy Pages



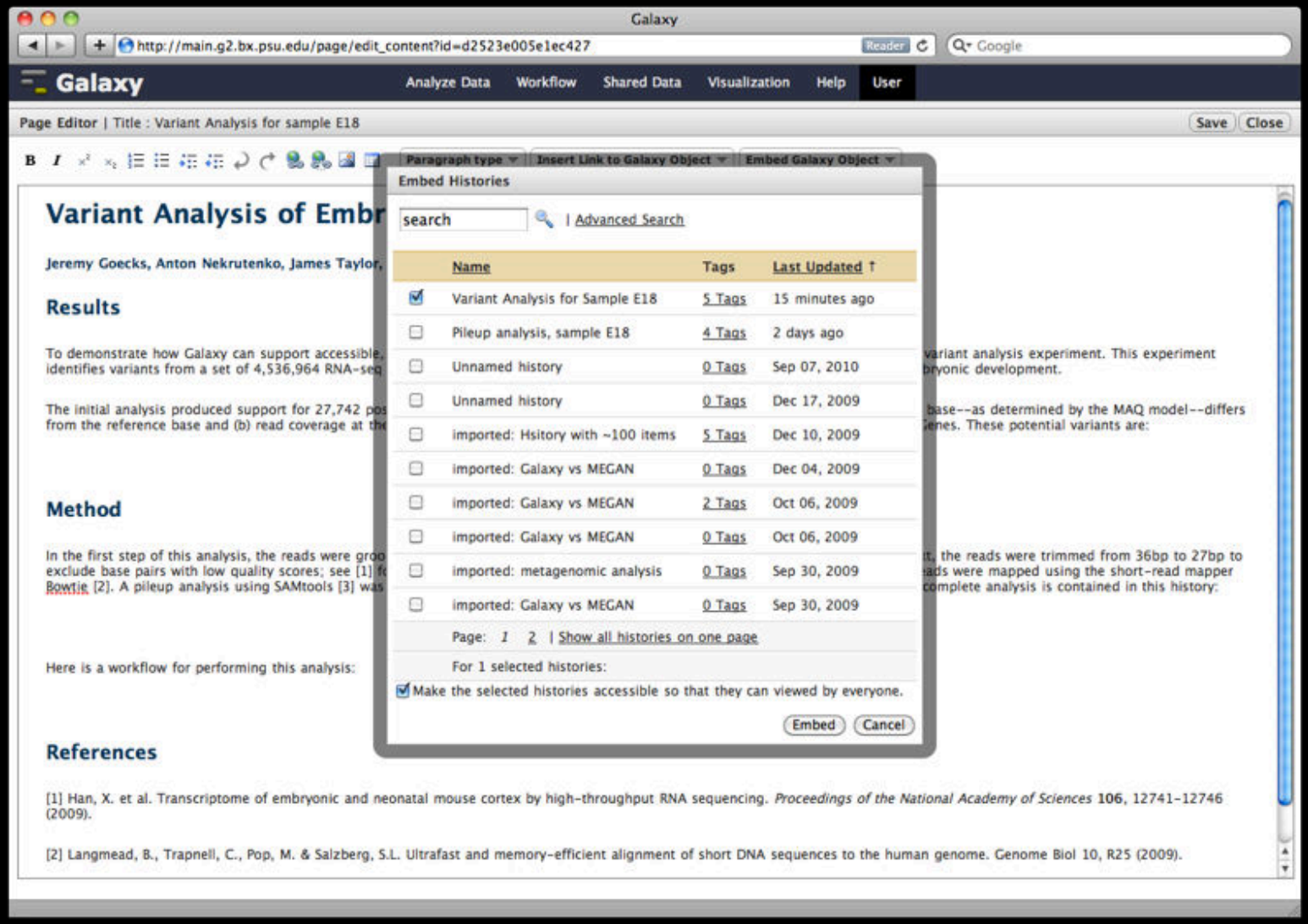
Galaxy Pages



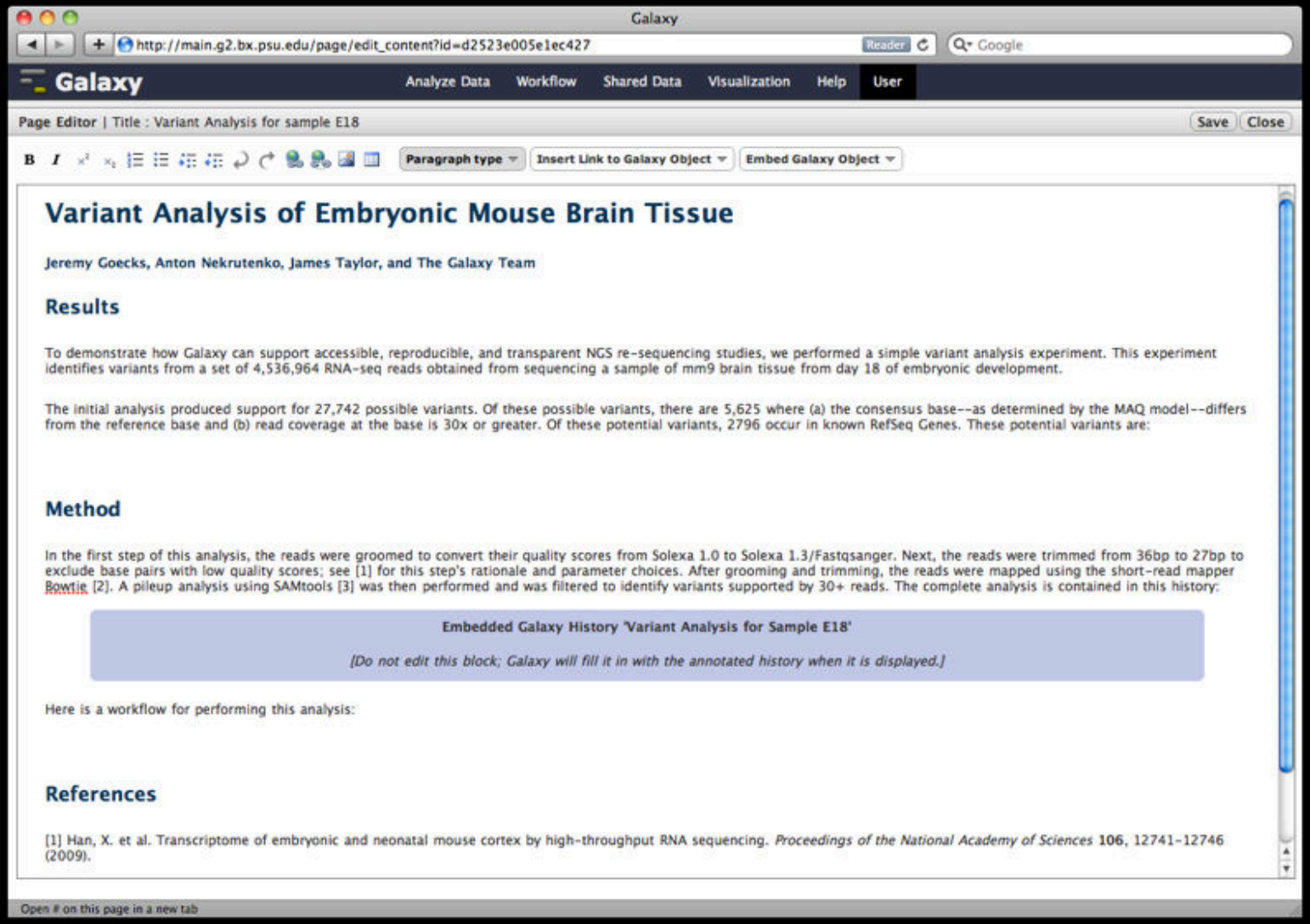
Creating a Page



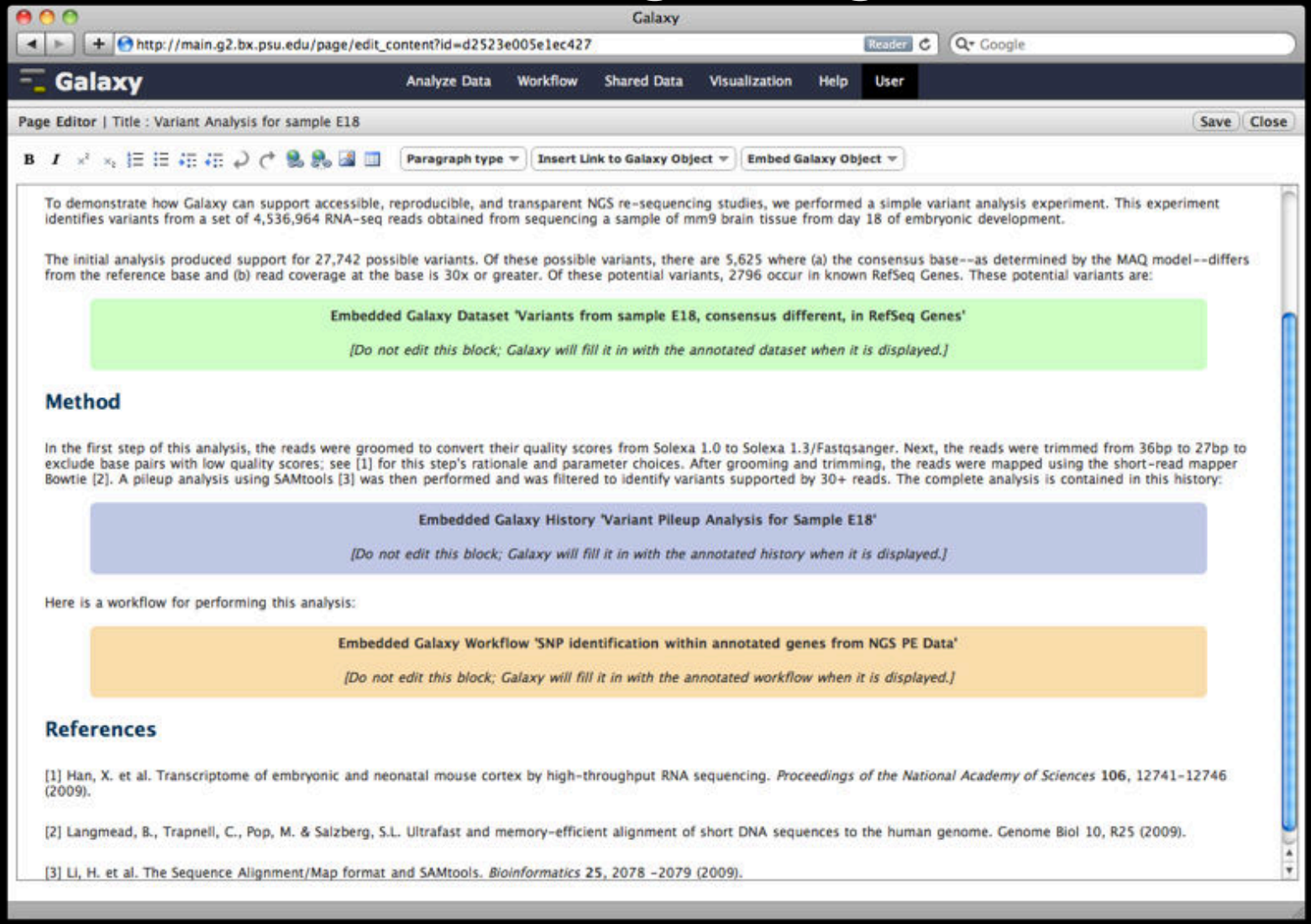
Creating a Page



Creating a Page



Creating a Page



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

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Galaxy 101 Exercise

How to get into Galaxy

Galaxy main site (http://usegalaxy.org)

Public web site, anybody can use

~500 new users per month, ~100 TB of user data, ~130,000 analysis jobs per month, every month is our busiest month ever...

Will continue to be maintained and enhanced, but with limits and quotas

Centralized solution cannot scale to meet data analysis demands

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Galaxy 101 Exercise

Local Galaxy instances (http://getgalaxy.org)

Galaxy is designed for local installation and customization

- Just download and run, completely self-contained
- Easily integrate new tools
- Easy to deploy and manage on nearly any (unix) system
- Run jobs on existing compute clusters

Especially useful for sensitive data

- can secure data and abide by regulations

Scale up on existing resources

Move intensive processing (tool execution) to other hosts

Frees up the application server to serve requests and manage jobs

Utilize existing resources

Supports any scheduler that supports DRMAA (most of them)

Running a Production Server

Use a real database server: PostgreSQL, MySQL

Run on compute cluster resources

External Authentication: LDAP, Kerberos, OpenID

Load balancing; proxy support

https://bitbucket.org/galaxy/galaxy-central/wiki/Config/ProductionServer

Lack IT knowledge or resources?

No problem, just use the Cloud

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Galaxy 101 Exercise

Cloud Computing

network accessible compute resources that can be rapidly acquired, configured, and released on demand

Infrastructure as a service

Compute resources provided and configured on demand (compute nodes, storage, network)

Public commercial: Amazon Web Services, Rackspace, ...
Build your own: Eucalyptus, Nimbus, OpenStack, ...

When to use the cloud?

Limited informatics expertise or infrastructure

Extended or particular resource needs

Cannot upload data to a shared resource

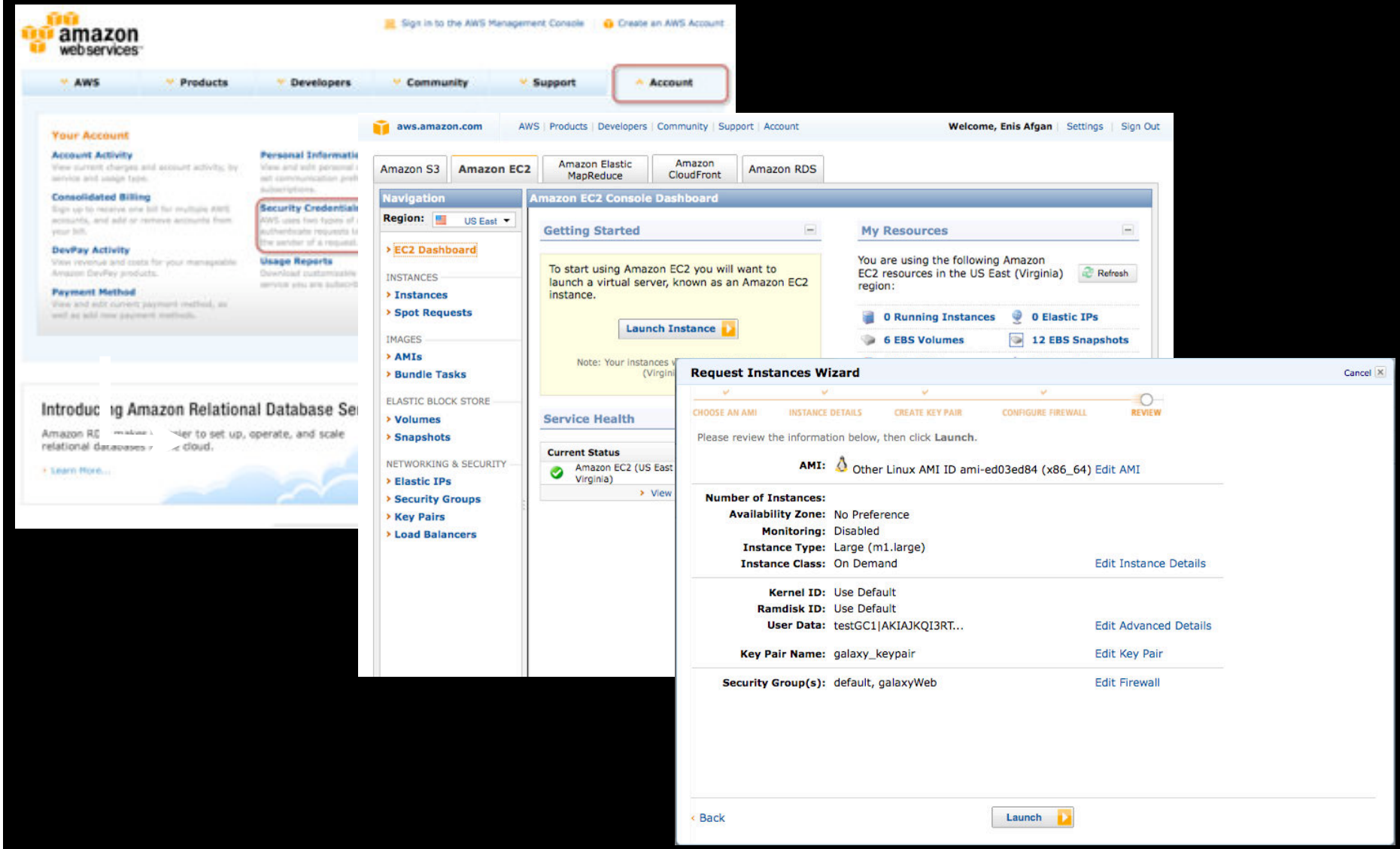
Need for customization

Have oscillating data volume

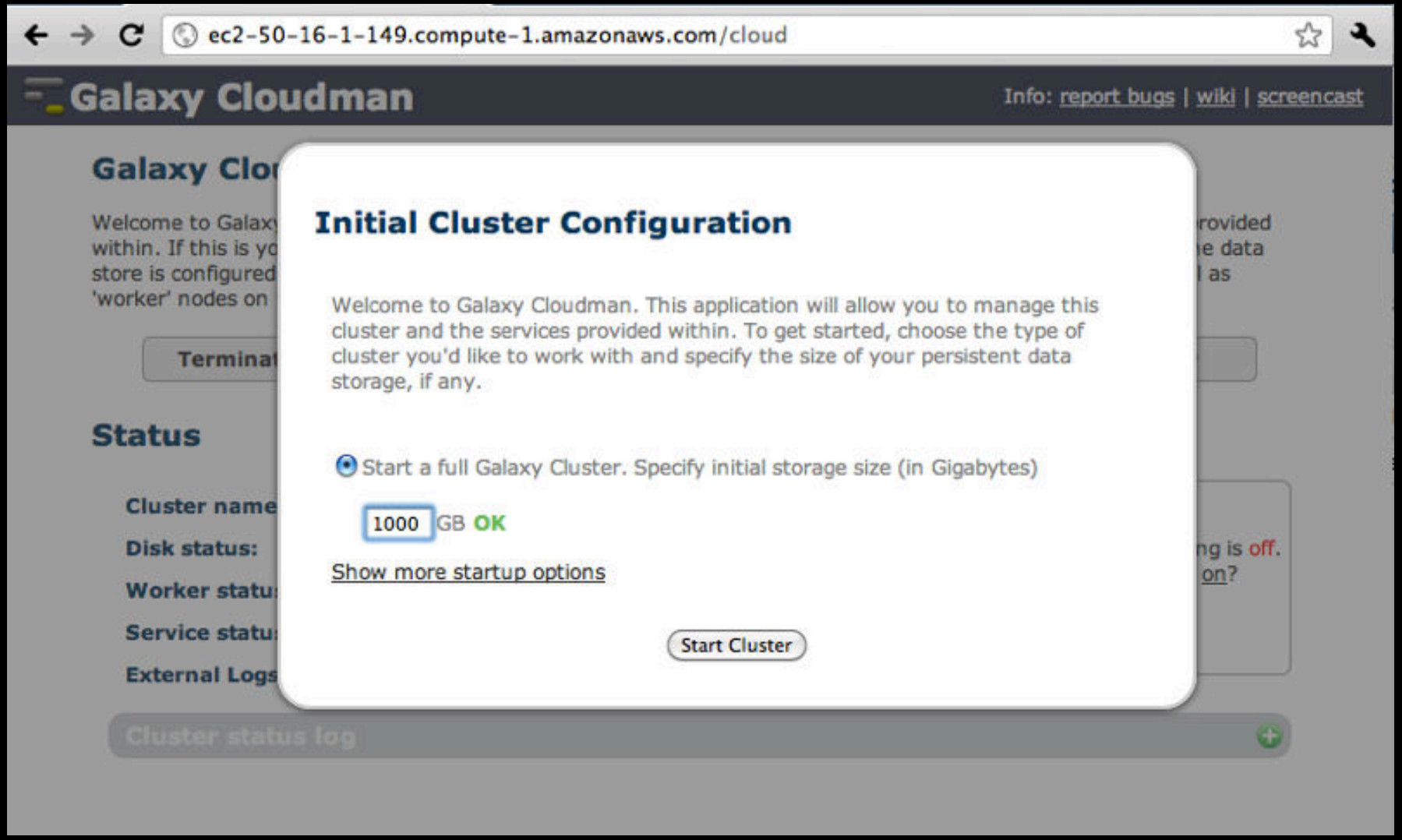
Deploying Galaxy on the AWS Cloud
http://usegalaxy.org/cloud

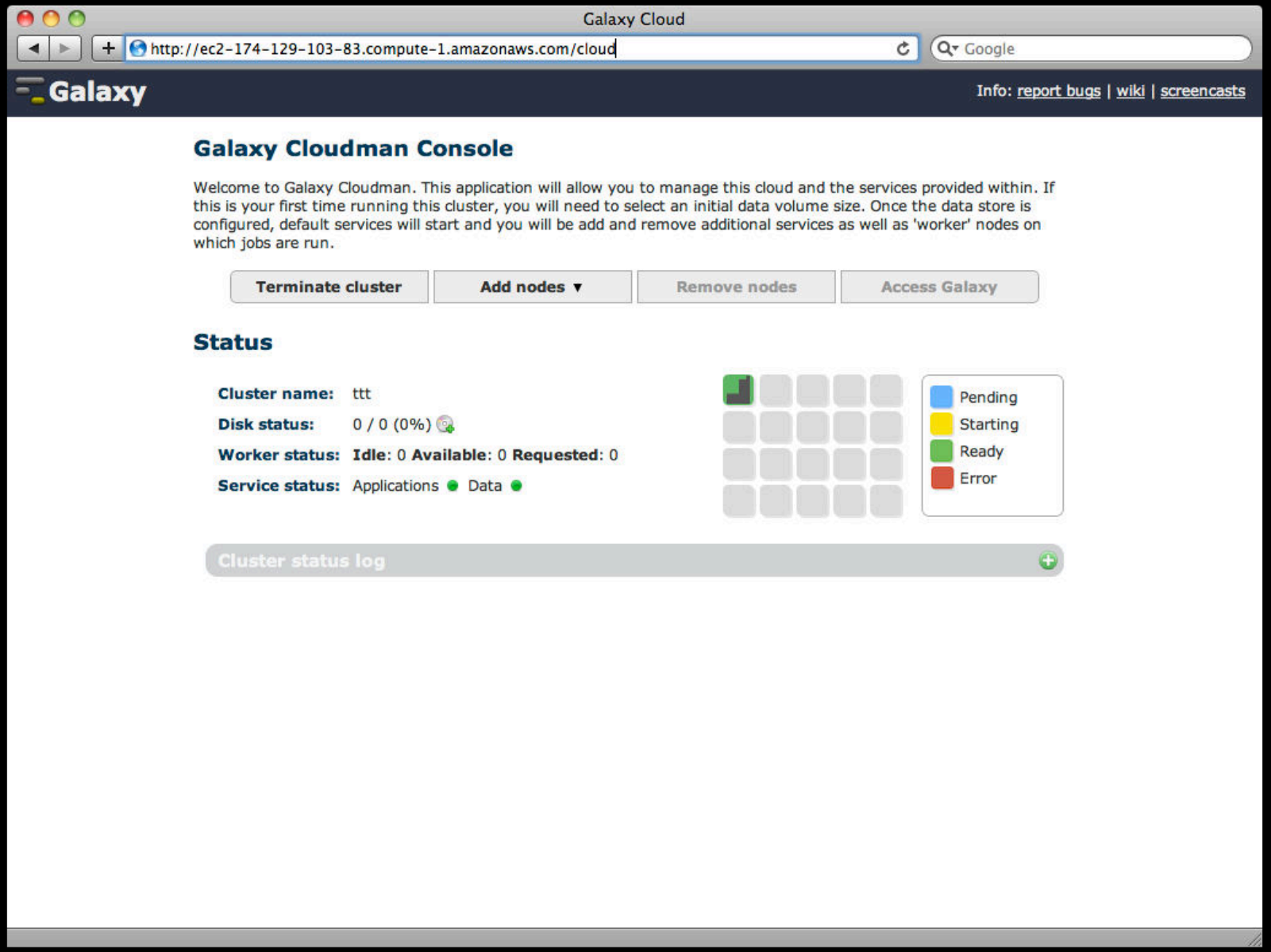
1. Open an AWS account (only once)
2. Use the AWS Management Console to start a master EC2 instance
3. Use the Galaxy CloudMan web interface on the master instance to manage the cluster

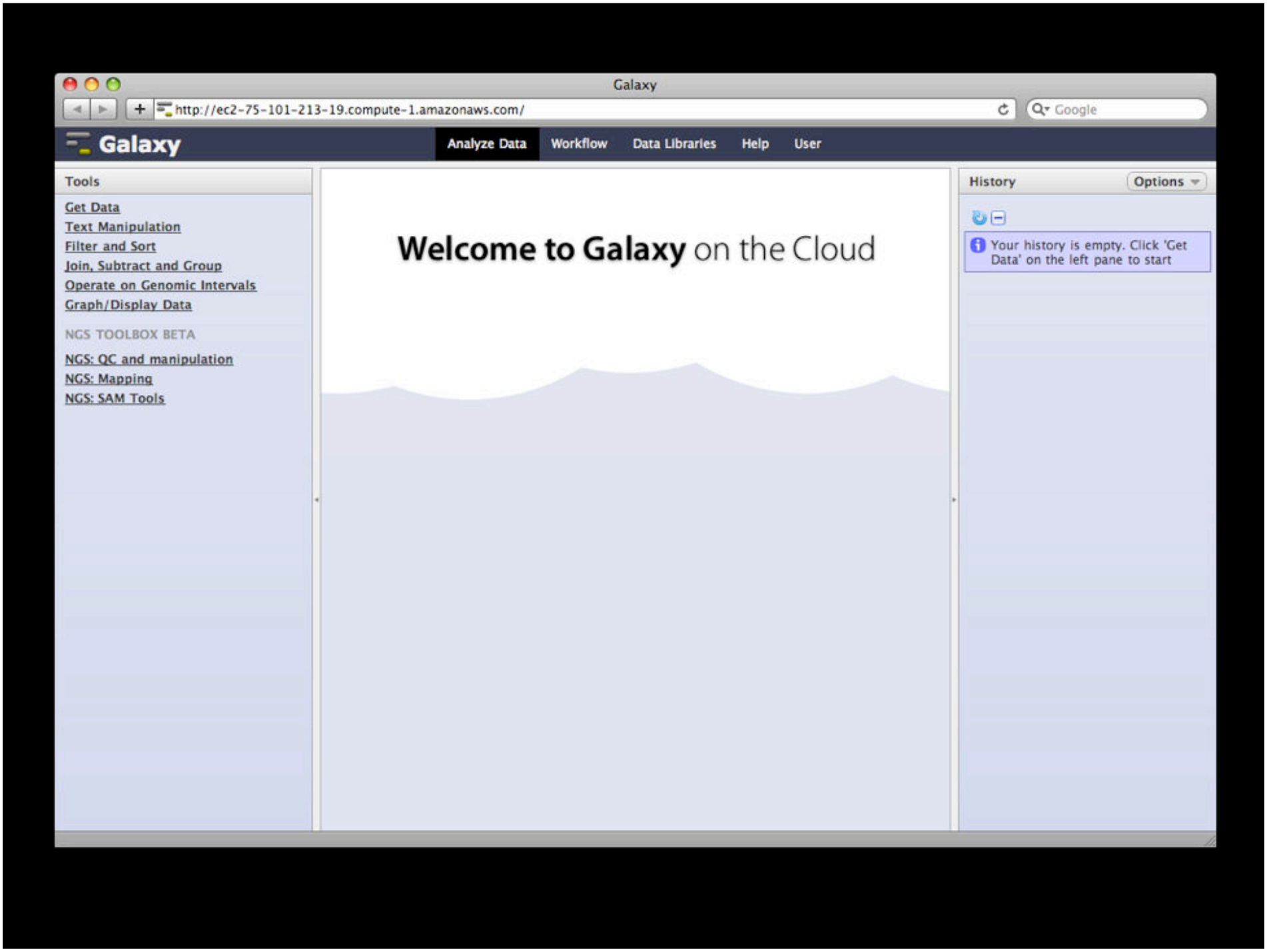
2. Start an EC2 Instance

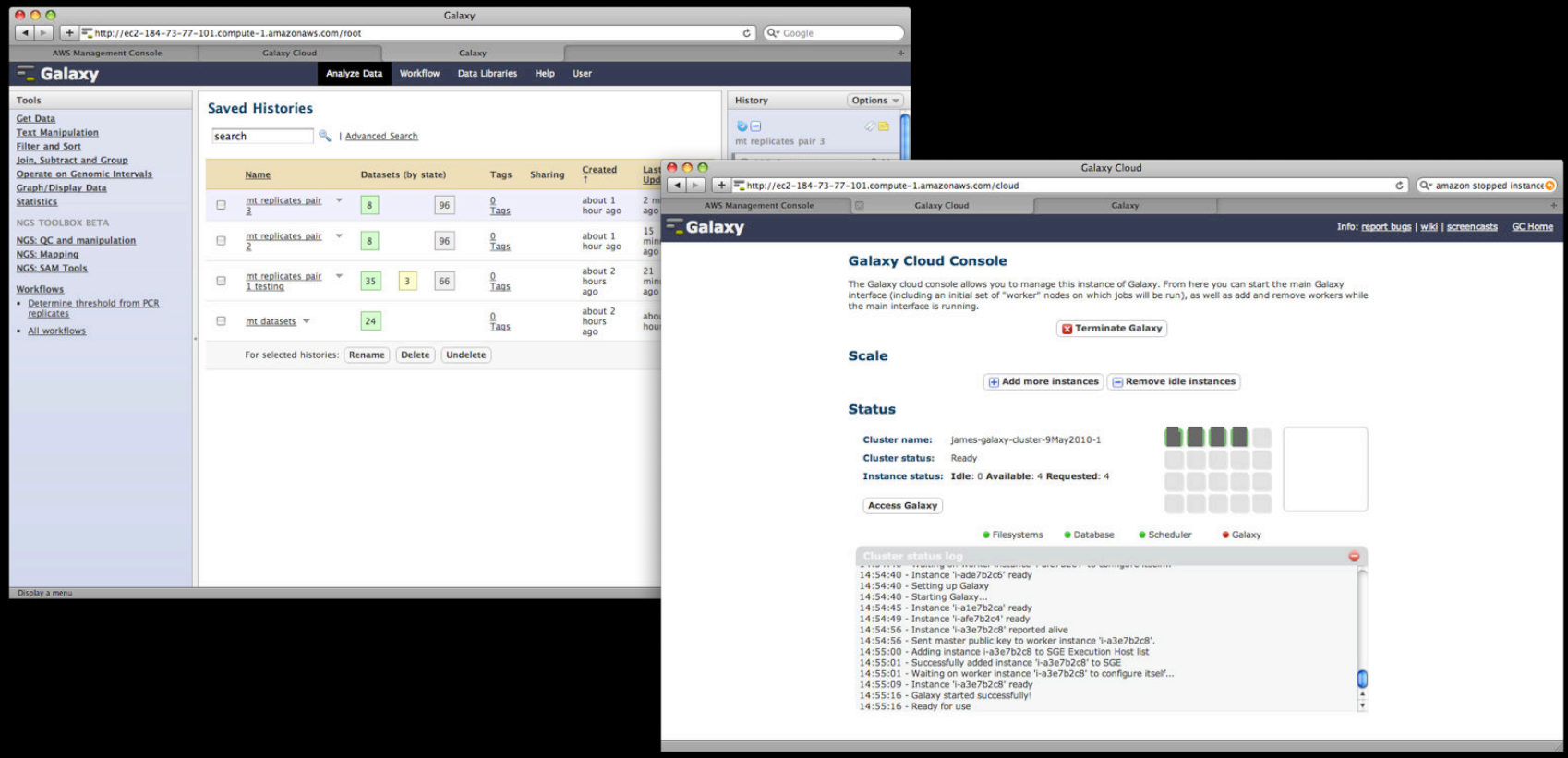


3. Configure Your Cluster

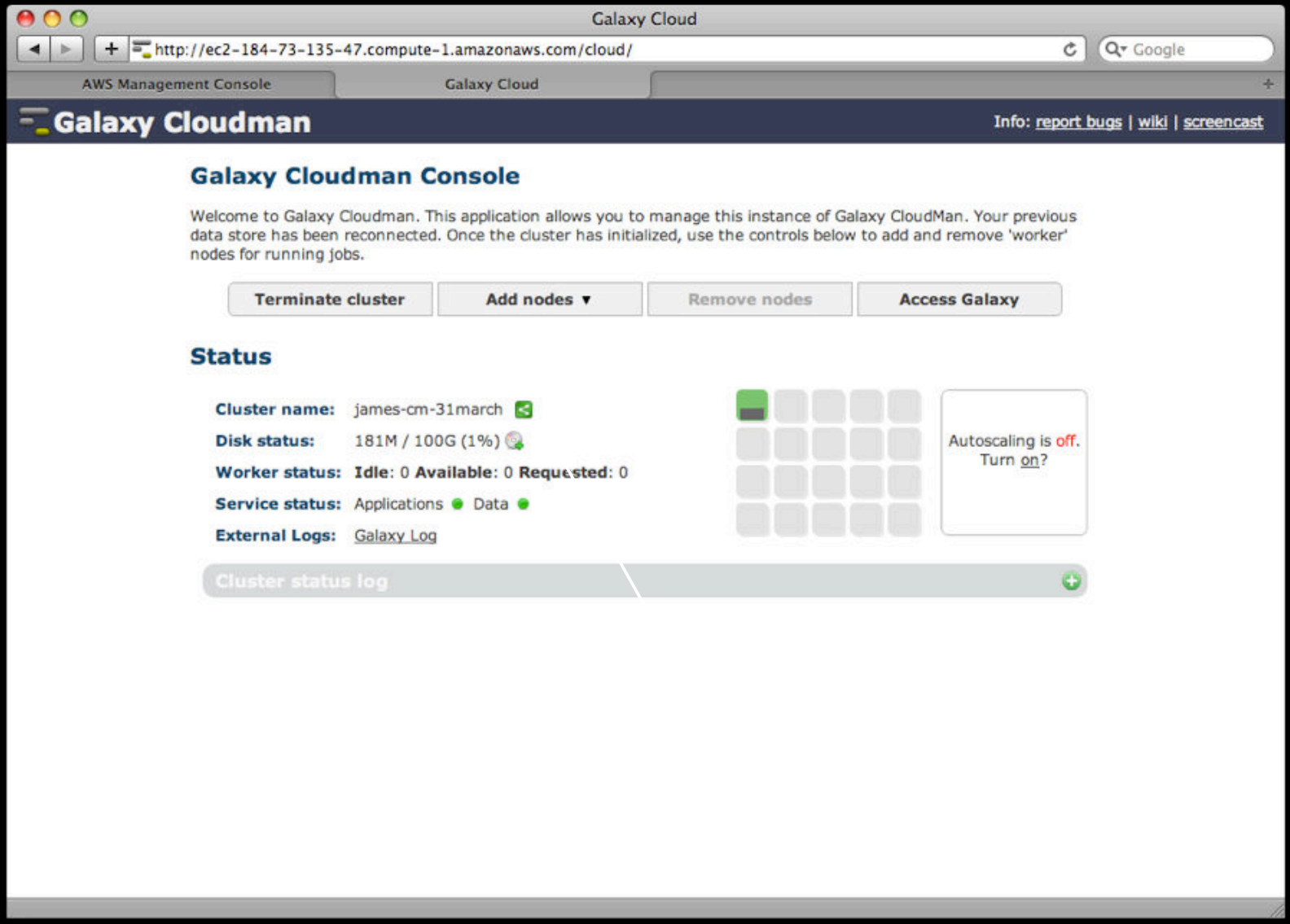


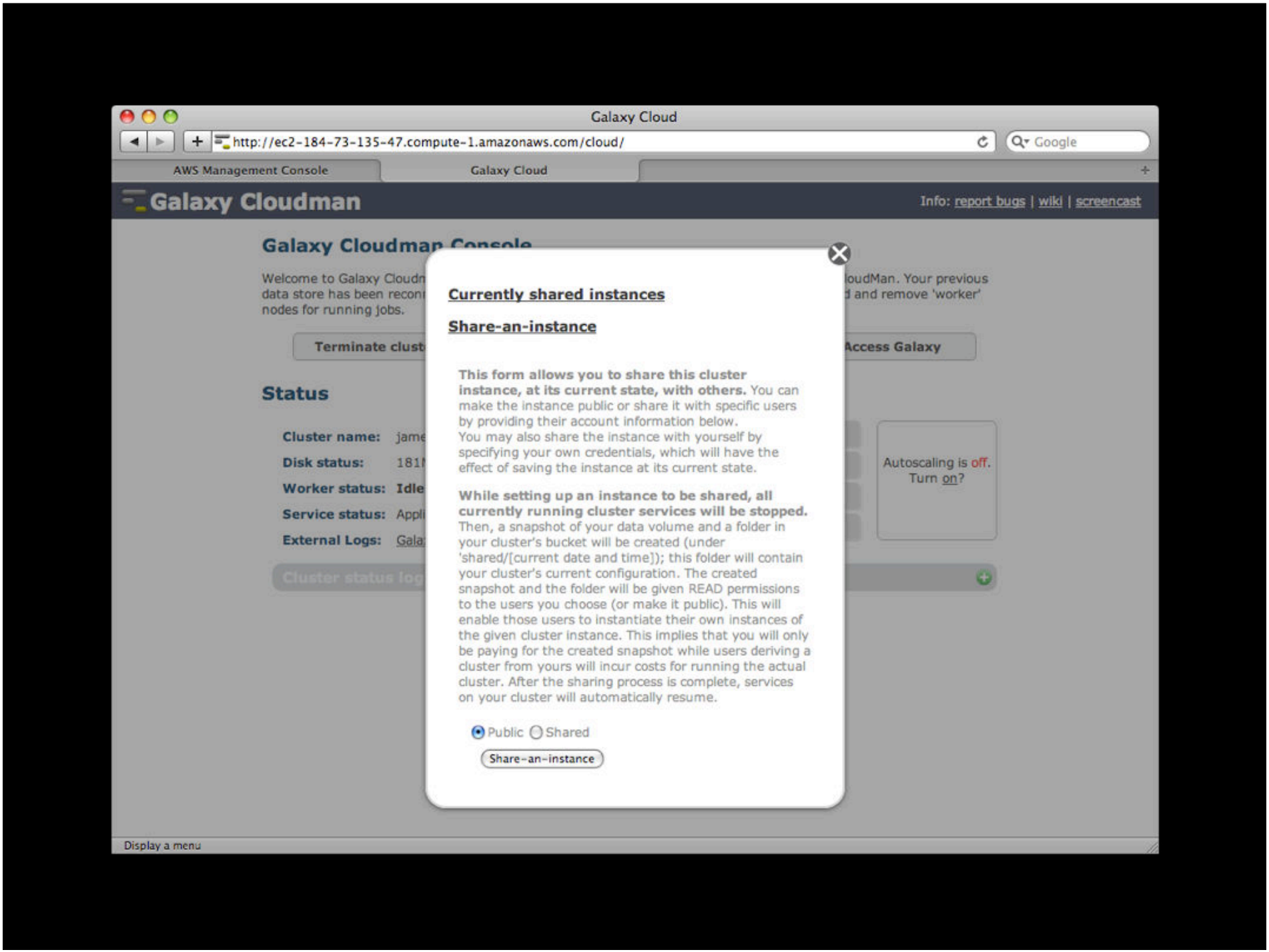

Galaxy Cloud
http://ec2-174-129-103-83.compute-1.amazonaws.com/cloud
Google
Galaxy
Info: report bugs | wiki | screencasts
Galaxy Cloudman Console
Welcome to Galaxy Cloudman. This application will allow you to manage this cloud and the services provided within. If this is your first time running this 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 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: ttt
Disk status: 0 / 0 (0%)
Worker status: Idle: 0 Available: 0 Requested: 0
Service status: Applications Data
Pending
Starting
Ready
Error
Cluster status log


Galaxy
http://ec2-75-101-213-19.compute-1.amazonaws.com/
Google
Galaxy
Analyze Data
Workflow
Data Libraries
Help
User
Tools
Get Data
Text Manipulation
Filter and Sort
Join, Subtract and Group
Operate on Genomic Intervals
Graph/Display Data
NGS TOOLBOX BETA
NGS: QC and manipulation
NGS: Mapping
NGS: SAM Tools
Welcome to Galaxy on the Cloud
History
Options
Your history is empty. Click 'Get Data' on the left pane to start



Can use like any other Galaxy instance, with additional compute nodes acquired and released (*automatically*) in response to usage


Galaxy Cloud
http://ec2-184-73-135-47.compute-1.amazonaws.com/cloud/
Google
AWS Management Console
Galaxy Cloud
Galaxy Cloudman
Info: report bugs | wiki | screencast
Galaxy Cloudman Console
Welcome to Galaxy Cloudman. This application allows you to manage this instance of Galaxy CloudMan. Your previous data store has been reconnected. Once the cluster has initialized, use the controls below to add and remove 'worker' nodes for running jobs.
Terminate cluster
Add nodes ▾
Remove nodes
Access Galaxy
Status
Cluster name: james-cm-31march
Disk status: 181M / 100G (1%)
Worker status: Idle: 0 Available: 0 Requested: 0
Service status: Applications Data
External Logs: Galaxy Log
Autoscaling is off.
Turn on?
Cluster status log


Galaxy Cloud
http://ec2-184-73-135-47.compute-1.amazonaws.com/cloud/
Google
AWS Management Console
Galaxy Cloud
Galaxy Cloudman
Info: report bugs | wiki | screencast
Galaxy Cloudman Console
Welcome to Galaxy Cloudn
data store has been recon
nodes for running jobs.
loudMan. Your previous
d and remove 'worker'
Terminate clust
Access Galaxy
Status
Cluster name: jame
Disk status: 181
Worker status: Idle
Service status: Appli
External Logs: Gala
Autoscaling is off.
Turn on?
Cluster status log
Currently shared instances
Share-an-instance
This form allows you to share this cluster instance, at its current state, with others. You can make the instance public or share it with specific users by providing their account information below.
You may also share the instance with yourself by specifying your own credentials, which will have the effect of saving the instance at its current state.
While setting up an instance to be shared, all currently running cluster services will be stopped. Then, a snapshot of your data volume and a folder in your cluster's bucket will be created (under 'shared/[current date and time]); this folder will contain your cluster's current configuration. The created snapshot and the folder will be given READ permissions to the users you choose (or make it public). This will enable those users to instantiate their own instances of the given cluster instance. This implies that you will only be paying for the created snapshot while users deriving a cluster from yours will incur costs for running the actual cluster. After the sharing process is complete, services on your cluster will automatically resume.
Public
Shared
Share-an-instance
Display a menu

Automation

Cloud instances include all tools available in main Galaxy and more

Tool installation and configuration, image creation, etc, all completely automated and extensible

Same automation approach can be used for configuring tool dependencies for a local Galaxy

VM image with tools (not data) also available, currently at
http://s3.amazonaws.com/usegalaxy/UseGalaxy.ova

Overview

What is Galaxy?

What you can do in Galaxy

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

Where you can use and build Galaxy

- public website
- local instance
- on the cloud
- tool shed/contributing tools

Galaxy 101 Exercise

The Problem

You have written a Python script to analyze genomic data and you want to share it with command-line averse colleagues

The Galaxy Solution

Solution: Integrate the script as a new Tool into your own Galaxy server

Steps:

- Obtain and install Galaxy source code (GetGalaxy.org)
- Write an XML file describing the inputs and outputs and how to execute the script
- Instruct Galaxy to load the tool

Adding your Own

Write or download a command-line executable

Determine number and kind of

- Input and Output Datasets
- Input Parameters

Construct a descriptive tool configuration XML file

- Write a wrapper script, only if required

Tool Configuration

Tool Action - Default tool action should be adequate (Upload tool uses custom tool action)

Tool Command

Inputs

- Action - Used by datasource tools
- Parameters

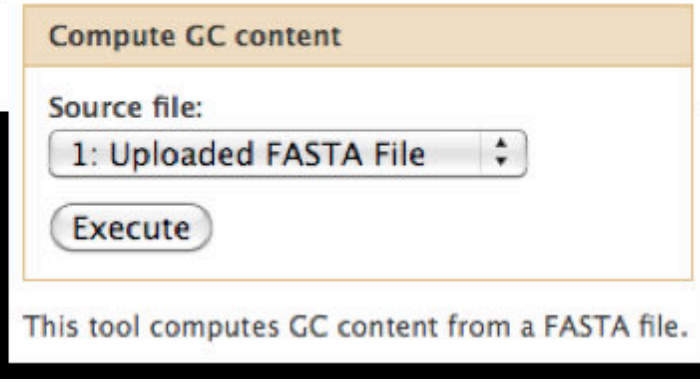
Outputs

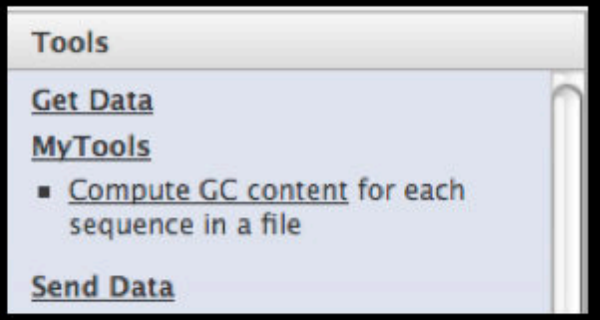
Help

Tests

A Basic Tool

```
<tool id="fa_gc_content_1" name="Compute GC content">
  <description>for each sequence in a file</description>
  <command interpreter="perl">toolExample.pl $input $output</command>
  <inputs>
    <param format="fasta" name="input" type="data" label="Source file"
  </inputs>
  <outputs>
    <data format="tabular" name="output" />
  </outputs>

  <tests>
    <test>
      <param name="input" value="fa_gc_content_input.fa"/>
      <output name="out_file1" file="fa_gc_content_output.txt"/>
    </test>
  </tests>

  <help>
This tool computes GC content from a FASTA file.
  </help>

</tool>
```






```
<section name="MyTools" id="mTools">
    <tool file="myTools/toolExample.xml" />
</section>
```

tool_conf.xml

Cluster

Cluster intervals of: 6: UCSC Main on Human: knownGene

max distance between intervals: 1 (bp)

min number of intervals per cluster: 2

Return type: Merge clusters into single intervals

Execute

TIP: If your query does not appear in the pulldown menu -> it is not in interval format. Use "edit attributes" to set chromosome, start, end, and strand columns

---

Screencasts!

See Galaxy Interval Operation Screencasts (right click to open this link in another window).

Syntax

- **Maximum distance** is greatest distance in base pairs allowed between intervals that will be considered "clustered". **Negative** values for distance are allowed, and are useful for clustering intervals that overlap.
- **Minimum intervals per cluster** allow a threshold to be set on the minimum number of intervals to be considered a cluster. Any area with less than this minimum will not be included in the ouput.
- **Merge clusters into single intervals** outputs intervals that span the entire cluster.
- **Find cluster intervals; preserve comments and order** filters out non-cluster intervals while maintaining the original ordering and comments in the file.
- **Find cluster intervals; output grouped by clusters** filters out non-cluster intervals, but outputs the cluster intervals so that they are grouped together. Comments and original ordering in the file are lost.

Example

cluster.xml

```
<tool id="gops_cluster_1" name="Cluster">
  <description>[[Cluster]] the intervals of a query</description>
  <command interpreter="python2.4">
    gops_cluster.py $input1 $output -1 $input1_chromCol,$input1_startC
                   -d $distance -m $minregions -o $returntype
  </command>
  <inputs>
    <param format="interval" name="input1" type="data">
      <label>Cluster intervals of</label>
    </param>
    <param name="distance" size="5" type="integer" value="1" help="(bp
      <label>max distance between intervals</label>
    </param>
    <param name="minregions" size="5" type="integer" value="2">
      <label>min number of intervals per cluster</label>
    </param>
    <param name="returntype" type="select" label="Return type">
      <option value="1">Merge clusters into single intervals</option>
      <option value="2">Find cluster intervals; preserve comments and
      <option value="3">Find cluster intervals; output grouped by clus
      <option value="4">Find the smallest interval in each cluster</op
      <option value="5">Find the largest interval in each cluster</opt
    </param>
   </inputs>
   <help>

.. class:: infomark

**TIP:** If your query does not appear in the pulldown menu -> it is n

-----

**Screencasts!**

See Galaxy Interval Operation Screencasts_ (right click to open this l

.. _Screencasts: http://www.bx.psu.edu/cgi-bin/trac.cgi/wiki/GopsDesc

-----

**Syntax**

- **Maximum distance** is greatest distance in base pairs allowed betw
- **Minimum intervals per cluster** allow a threshold to be set on the
- **Merge clusters into single intervals** outputs intervals that span
- **Find cluster intervals; preserve comments and order** filters out
- **Find cluster intervals; output grouped by clusters** filters out n
```

Line: 87 Column: 8 XML Soft Tabs: 2

Input Parameter types

Basic

- Text
- Integer
- Float
- Select
  - Static
  - Dynamic
- Boolean
- Genome build
- Data column
- Data
- Hidden
- Base URL
- File
- Drill down
- Grouping
  - Conditional
  - Repeat
- Config Files

Datasets and Datatypes

All datasets are associated with a Datatype

- File format
- Type of Data: genomic intervals, sequence, alignment
- Hierarchical structure useful for inputs
- Automatic conversion possible
- Metadata

datatypes_conf.xml and lib/galaxy/datatypes

https://bitbucket.org/galaxy/galaxy-central/wiki/AddingDatatypes

Adding your Own Display Application

Define An XML configuration which describes how and where to present the data to the External Web Application

- Static
- Dynamic - display options can be loaded from a file

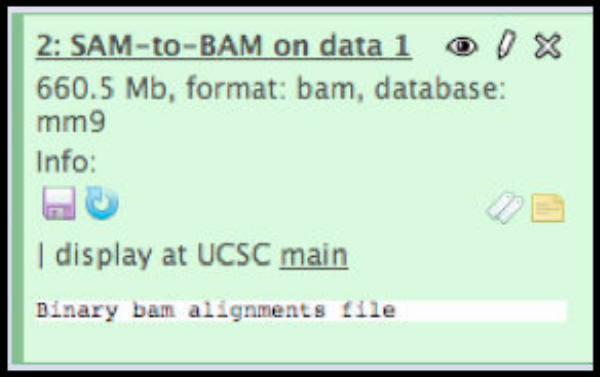
Inform Galaxy about the new display by adding to the appropriate datatype in datatypes_conf.xml

https://bitbucket.org/galaxy/galaxy-central/wiki/ExternalDisplayApplications/Tutorial

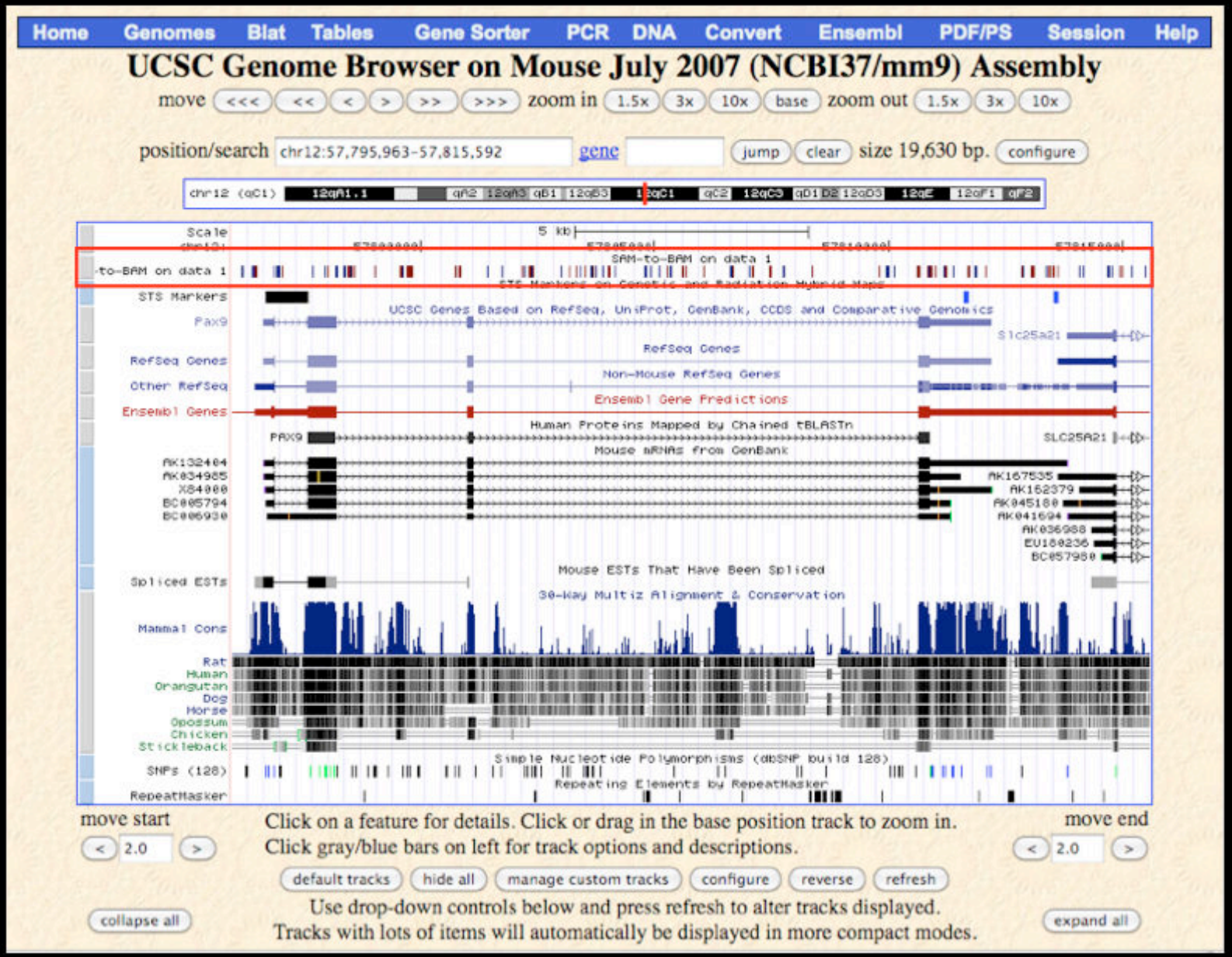
Static External Display Application

```
<display id="ucsc_bam" version="1.0.0" name="display at UCSC">
    <link id="main" name="main">
        <url>http://genome.ucsc.edu/cgi-bin/hgTracks?db=${qp($bam_file.dbkey)}&amp;hgt.customText=${qp($track.url)}</url>
        <param type="data" name="bam_file" url="galaxy.bam" strip_https="True" />
        <param type="data" name="bai_file" url="galaxy.bam.bai" metadata="bam_index" strip_https="True" />
        <param type="template" name="track" viewable="True" strip_https="True">
            track type=bam name="${bam_file.name}" bigDataUrl=${bam_file.url} db=${bam_file.dbkey}
        </param>
    </link>
</display>
```

```
<datatype extension="bam" type="galaxy.datatypes.binary:Bam"
    mimetype="application/octet-stream" display_in_upload="true">
    <display file="ucsc/bam.xml" />
</datatype>
```



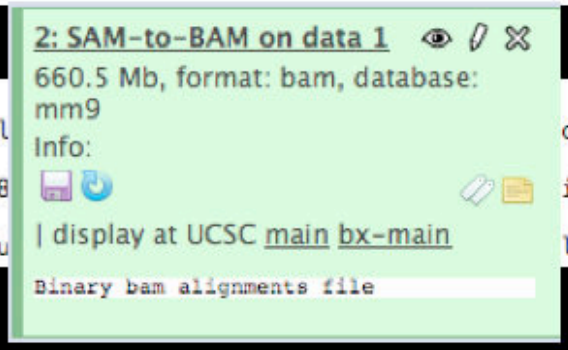
BAM at UCSC


Home Genomes Blat Tables Gene Sorter PCR DNA Convert Ensembl PDF/PS Session Help
UCSC Genome Browser on Mouse July 2007 (NCBI37/mm9) Assembly
move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x
position/search chr12:57,795,963-57,815,592 gene jump clear size 19,630 bp. configure
chr12 (qC1)
Scale
5 kb
SAM-to-BAM on data 1
STS Markers
UCSC Genes Based on RefSeq, UniProt, GenBank, CCDS and Comparative Genomics
Pax9
Slc25a21
RefSeq Genes
Non-Mouse RefSeq Genes
Other RefSeq
Ensembl Gene Predictions
Ensembl Genes
Human Proteins Mapped by Chained tBLASTn
PAX9
SLC25A21
Mouse mRNAs from GenBank
AK132404
AK034985
X84000
BC005794
BC006930
AK167535
AK152379
AK045180
AK041694
AK036988
EU150236
BC057980
Spliced ESTs
Mouse ESTs That Have Been Spliced
30-Way Multiz Alignment & Conservation
Mammal Cons
Rat
Human
Orangutan
Dog
Horse
Opossum
Chicken
Stickleback
Simple Nucleotide Polymorphisms (dbSNP build 128)
SNPs (128)
Repeating Elements by RepeatMasker
RepeatMasker
move start
< 2.0 >
Click on a feature for details. Click or drag in the base position track to zoom in.
Click gray/blue bars on left for track options and descriptions.
move end
< 2.0 >
default tracks hide all manage custom tracks configure reverse refresh
collapse all
Use drop-down controls below and press refresh to alter tracks displayed.
Tracks with lots of items will automatically be displayed in more compact modes.
expand all

Dynamic External Display Application

```
<display id="ucsc_bam" version="1.0.0" name="display at UCSC">
    <!-- Load links from file: one line to one link -->
    <dynamic_links from_file="tool-data/shared/ucsc/ucsc_build_sites.txt" skip_startswith="#" id="0" name="0">

        <!-- Define parameters by column from file, allow splitting on builds -->
        <dynamic_param name="site_id" value="0"/>
        <dynamic_param name="ucsc_link" value="1"/>
        <dynamic_param name="builds" value="2" split="True" separator="," />

        <!-- Filter out some of the links based upon matching site_id to a Galaxy application configuration parameter and b
        <filter>${site_id in $APP.config.ucsc_display_sites}</filter>
        <filter>${dataset.dbkey in $builds}</filter>

        <!-- We define url and params as normal, but values defined in dynamic_param are available by specified name -->
        <url>${ucsc_link}db=${qp($bam_file.dbkey)}&amp;hgt.customText=${qp($track.url)}</url>
        <param type="data" name="bam_file" url="galaxy_${DATASET_HASH}.bam" strip_https="True" />
        <param type="data" name="bai_file" url="galaxy_${DATASET_HASH}.bam.bai" metadata="bam_index" strip_https="True" />
        <param type="template" name="track" viewable="True" strip_https="True">
            track type=bam name="${bam_file.name}" bigDataUrl=${bam_file.url} db=${bam_file.dbkey}
        </param>

    </dynamic_links>
</display>
```

```
#Harvested from http://genome.ucsc.edu/cgi-bin/das/dsn
main    http://genome.ucsc.edu/cgi-bin/hgTracks?    anoCar1,ce6,ce4,ce2,rn3,l
#Harvested from http://archaea.ucsc.edu/cgi-bin/das/dsn
archaea http://archaea.ucsc.edu/cgi-bin/hgTracks?   therSibi1,symbTher_IAM148
#Harvested from http://main.genome-browser.bx.psu.edu/cgi-bin/das/dsn
bx-main http://main.genome-browser.bx.psu.edu/cgi-bin/hgTracks? oviAri1,eriEu
```

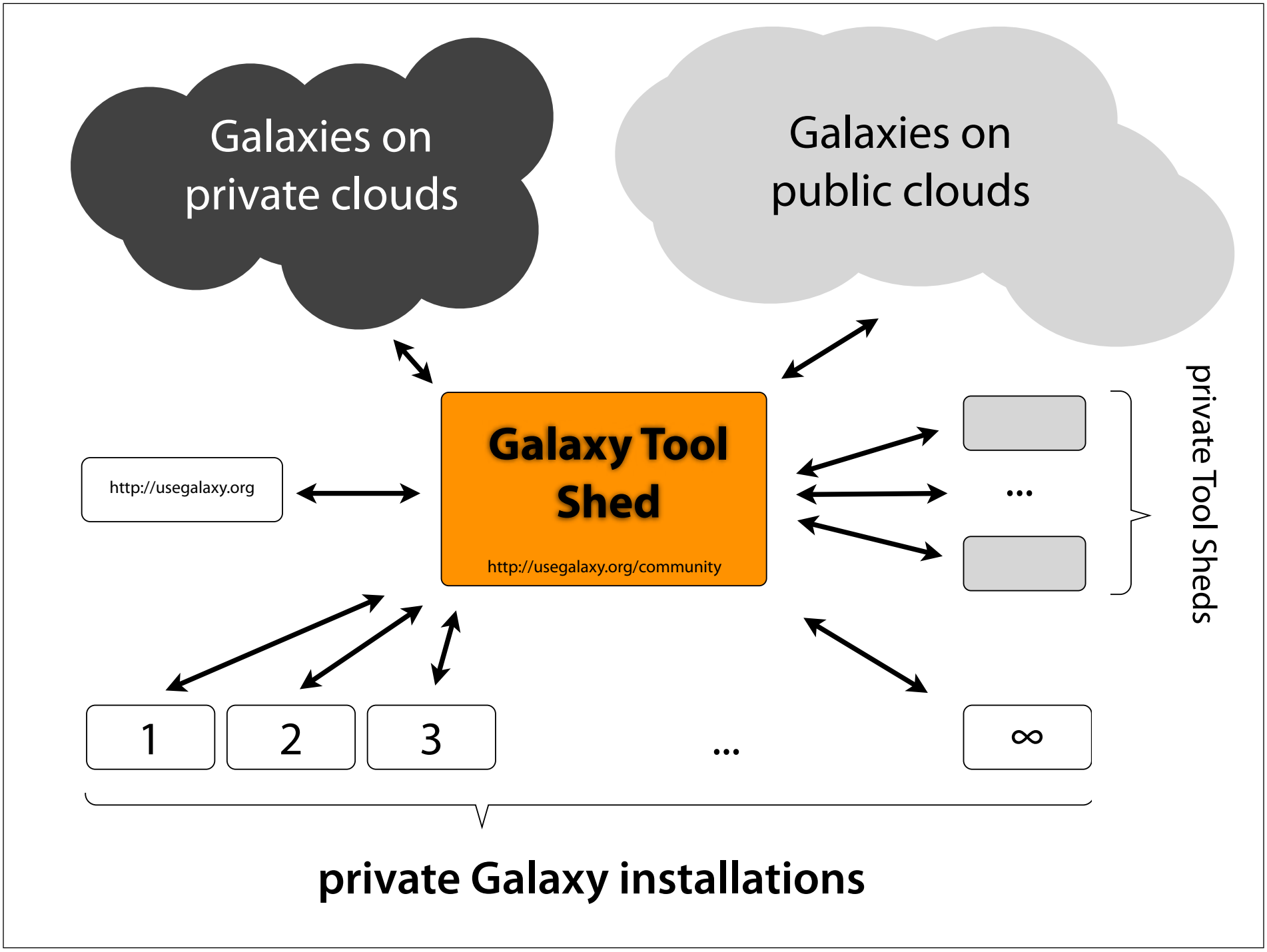


You added a tool, now what?

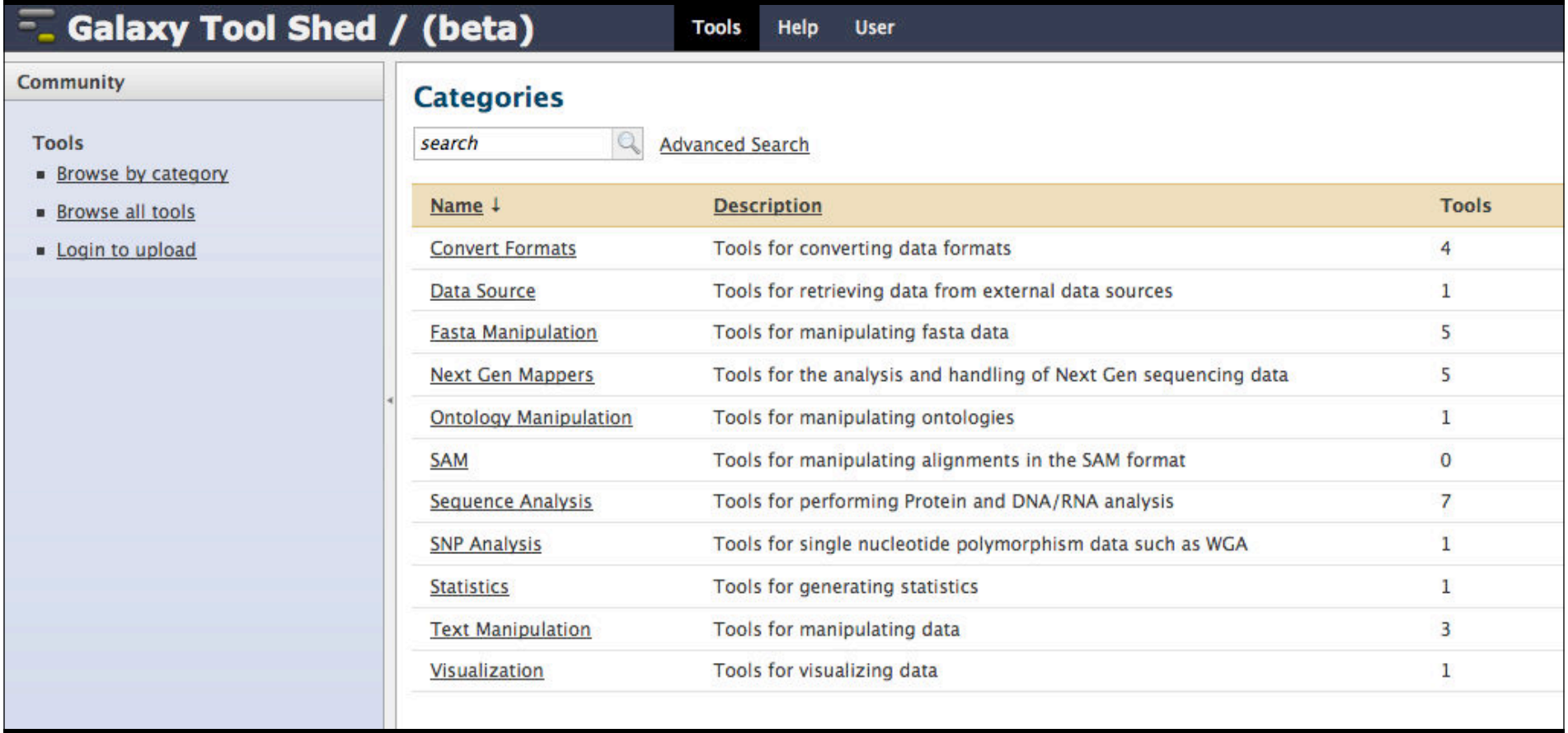
Share it with the community!

Galaxy Tool Shed

- Upload and Download contributed tools
- Rate and provide comments and feedback


Galaxies on private clouds
Galaxies on public clouds
Galaxy Tool Shed
http://usegalaxy.org/community
http://usegalaxy.org
private Tool Sheds
1
2
3
...
∞
private Galaxy installations

Get and Contribute Tools



http://usegalaxy.org/community

Using Galaxy

Use public Galaxy server: UseGalaxy.org

Download Galaxy source: GetGalaxy.org

Galaxy Wiki: GalaxyProject.org

Screencasts: GalaxyCast.org

Public Mailing Lists

- galaxy-bugs@bx.psu.edu
- galaxy-user@bx.psu.edu
- galaxy-dev@bx.psu.edu

EMORY

Enis Afgan

Dannon Baker

Dave Clements

Jeremy Goecks

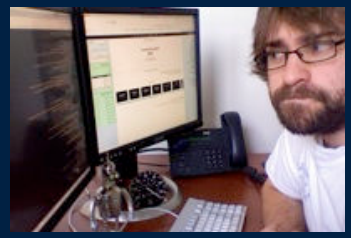
Kanwei Li

James Taylor

PENNSTATE

1855

Dan Blankenberg



Nate Coraor

Jennifer Jackson

Greg von Kuster

Kelly Vincent

Anton Nekrutenko

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

Overview

What is Galaxy?

What you can do in Galaxy

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

Where you can use and build Galaxy

- public website
- local instance
- on the cloud
- tool shed/contributing tools

Galaxy 101 Exercise

Galaxy 101
http://usegalaxy.org/galaxy101

http://usegalaxy.org/u/jeremy/p/usc-exercise-clusters

A simple question...

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

Galaxy 101
http://usegalaxy.org/galaxy101

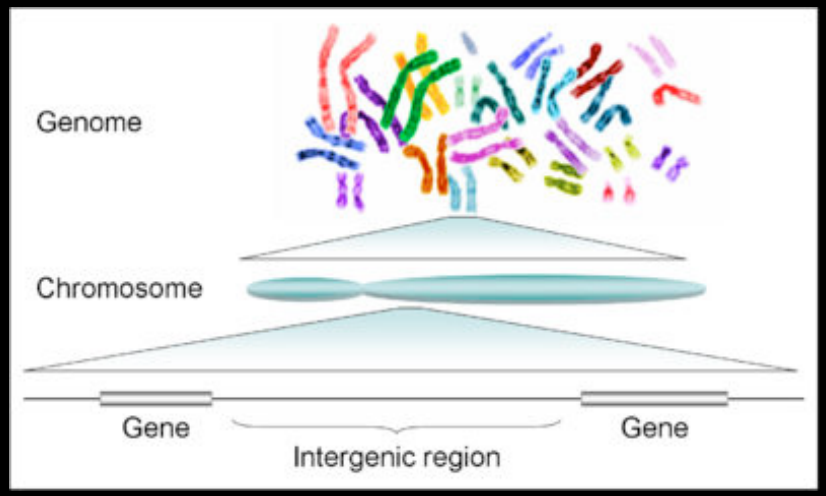
Overview

- 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
taaccctaaccctaaccctaaccctaaccctaaccctaaccctaacccta
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