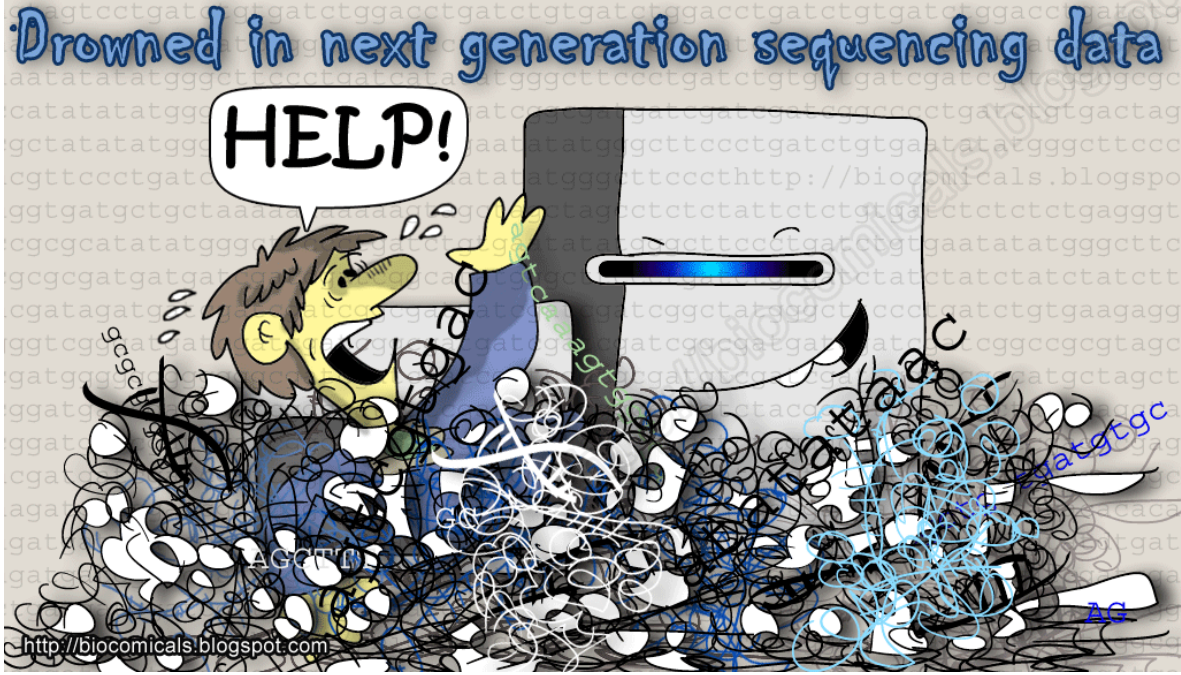
Popular bioinformatics tools in Galaxy: I

Yanbin Yin

Spring 2013

As creating and obtaining data has become easier, the key decision faced by many researchers is a practical one: where and how should an analysis be performed?



1. No need of programming experience.
2. Integrates many bioinformatics tools within one interface.
3. Keeps track of all the steps performed in an analysis. Even if you delete the datasets, the history keeps the tools used.

Galaxy (http://galaxyproject.org) is a software system that provides genomics data analysis support through a framework that gives experimentalists simple interfaces to powerful computational tools, while automatically managing the computational details.

Penn State U:
Anton Nekrutenko

Emory U:
James Taylor

Bioinformatics
Tools and analyses:

Accessibility
Reproducibility
Transparency

Galaxy is a metaserver that allows users to:

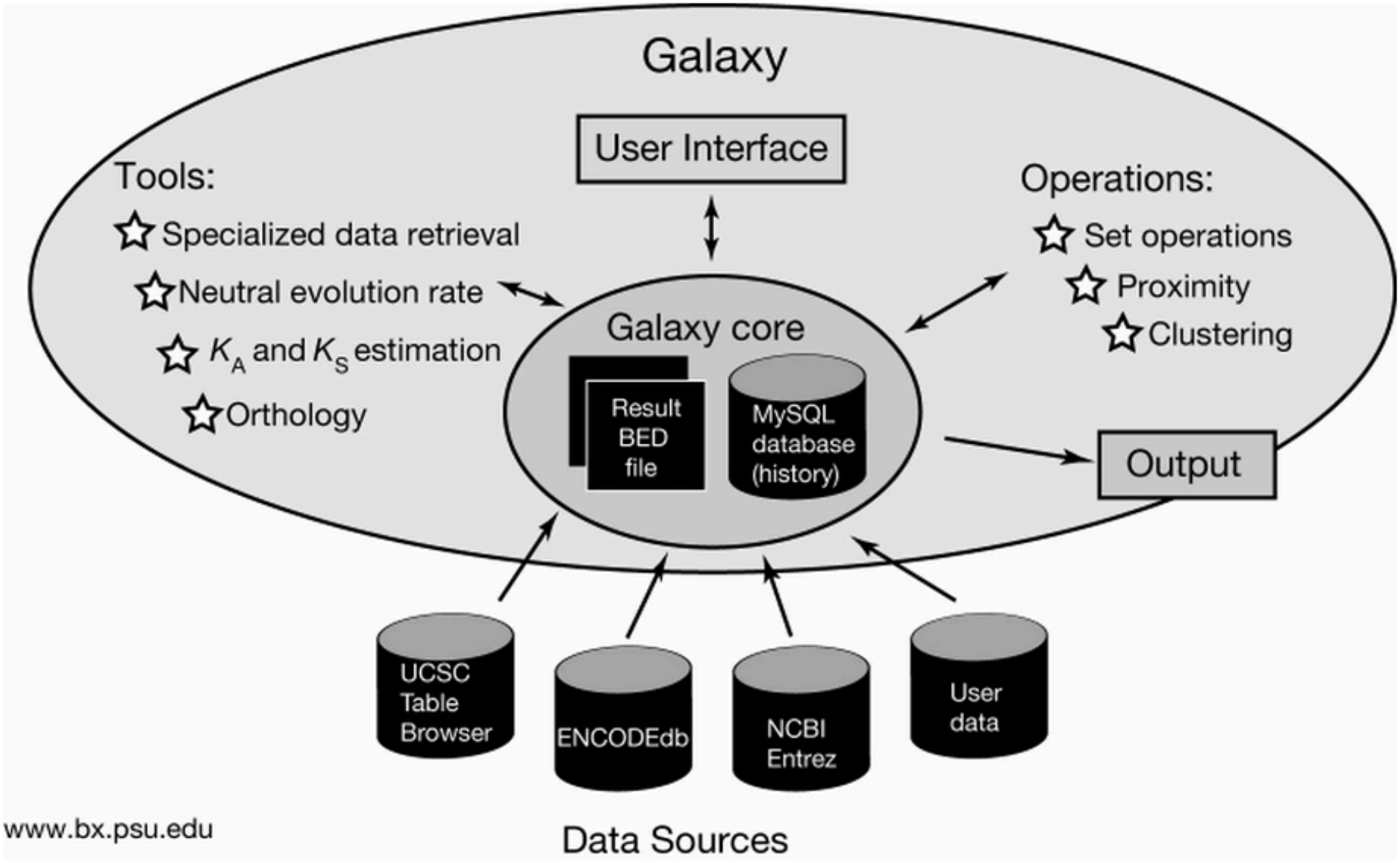
- retrieve information from multiple remote sources
- store, combine, and refine the information at a central site
- perform mathematical operations
- analyze the results using sophisticated tools

Galaxy is designed for the integration of:

- genomic sequences
- alignments of those sequences
- functional annotations

Galaxy combines the power of existing databases and visualization engines with seamless access to a wide variety of analytical tools.

http://www.bx.psu.edu/~giardine/Galaxy/posterCSH05v5.pdf


Galaxy
User Interface
Tools:
Specialized data retrieval
Neutral evolution rate
K_A and K_S estimation
Orthology
Operations:
Set operations
Proximity
Clustering
Galaxy core
Result BED file
MySQL database (history)
Output
UCSC Table Browser
ENCODEdb
NCBI Entrez
User data
www.bx.psu.edu
Data Sources

Hands on!

http://galaxyproject.org/

Galaxy

Data intensive biology *for everyone.*

Galaxy is an open, web-based platform for data intensive biomedical research. Whether on the free public server or your own instance, you can perform, reproduce, and share complete analyses.

Use Galaxy

Use the free public server

Get Galaxy

Install locally or in the cloud

Learn Galaxy

Screencasts, Galaxy 101, ...

Get Involved

Mailing lists, Tool Shed, wiki

Search all resources

The Galaxy Team is a part of BX at Penn State, and the Biology and Mathematics and Computer Science departments at Emory University. The Galaxy Project is supported in part by NHGRI, NSF, The Huck Institutes of the Life Sciences, The Institute for CyberScience at Penn State, and Emory University.

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

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

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

Tools

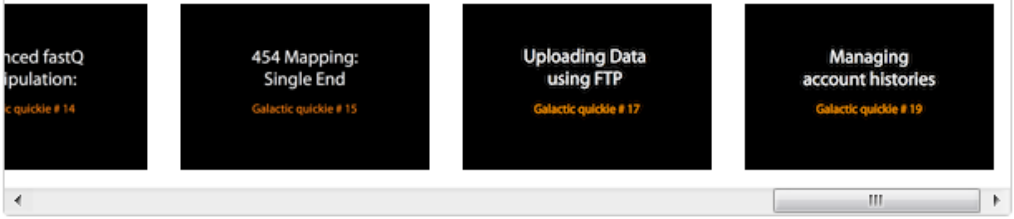
search tools

- 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
- Motif Tools
- Multiple Alignments
- Metagenomic analyses
- Genome Diversity
- Phenotype Association
- EMBOSS

NGS TOOLBOX BETA

- NGS: QC and manipulation
- NGS: Mapping
- NGS: SAM Tools
- NGS: GATK Tools (beta)

Live Quickies



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Galaxy build: **$Rev 8761:7b96c5b684d1$**

galaxyproject

History

Unnamed history

0 bytes

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

BUSY & SLOW !!!

http://galaxyproject.org/

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Get Galaxy: Galaxy Download and Installation

In addition to using the public Galaxy server (a.k.a. Main), you can also install your own instance of Galaxy (what this page is about), or create an instance of Galaxy on the cloud. Another option is to use one of the ever-increasing number of Public Galaxy Servers hosted by other organizations.

See Big Picture/Choices for help on deciding which of these options may be best for your situation.

Contents

Reasons to Install Your Own Galaxy

You only need to download Galaxy if you plan to:

1. Develop it further
2. Add new tools
3. Plug-in new datasources, or
4. Run a local production server for your site because you have
    1. Sensitive data (e.g., clinical)
    2. Large datasets or processing requirements that are too big to be processed on Main

Installation Procedure

131.156.41.196:8080/root

http://131.156.41.196:8080

Galaxy | Analyze Data | Workflow | Shared Data | Visualization | Help | User | Using 0 bytes

Tools

search tools

- Get Data
- Send Data
- ENCODE Tools
- Lift-Over
- Text Manipulation
- Filter and Sort
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- Multiple regression
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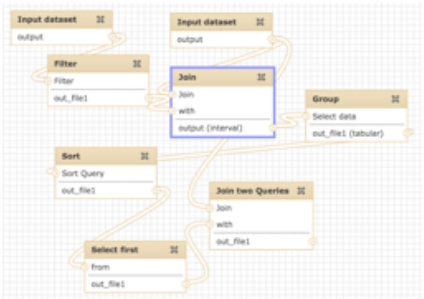
- Motif Tools
- Multiple Alignments
- Metagenomic analyses
- FASTA manipulation
- NGS: QC and manipulation
- NGS: Mapping
- NGS: Indel Analysis
- NGS: RNA Analysis
- NGS: SAM Tools
- NGS: GATK Tools (beta)
- NGS: Peak Calling
- NGS: Simulation

Hello world! It's running...

To customize this page edit `static/welcome.html`

WWFSMD?

grow noodly appendages...



usegalaxy.org

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http://cys.bios.niu.edu:8080

History

Unnamed history

0 bytes

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

http://galaxyproject.org/

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Galaxy Wiki

Login | Search:

Learn/Screencasts

Galaxy Screencasts and Demos

Contents

Screencasts are one of several ways to learn how to use Galaxy. These video tutorials cover many aspects of Galaxy, from simple tasks like uploading data, to complex analysis.

We are currently in the process of revamping Galaxy's screencast library. The current screencasts use a variety of technologies, including QuickTime (you may need to download the QuickTime player).

We hope to have both the screencast content and the screencast technology brought up to date by sometime in 2012.

Getting Started

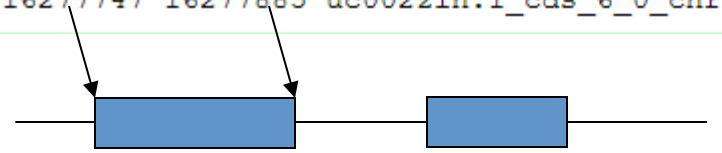
- Galaxy 101

What is the video about

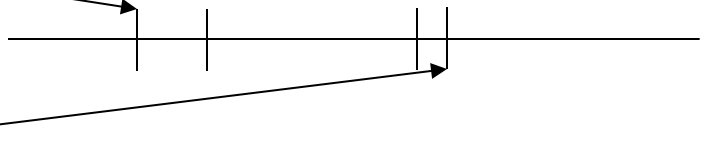
Find exons containing the largest number of SNPs in human chr22:

1. Download the exon data from UCSC
2. Download the SNP data from UCSC
3. Join the two files according to their chromosome locations
4. Count how many SNPs each exon has and generate a new file
5. Sort the file according to the number of SNPs in descending order
6. Check the top lines in the file

1.Chrom	2.Start	3.End	4.Name	5	6.Strand
chr22	16258185	16258303	uc002zlh.1_cds_1_0_chr22_16258186_r	0	-
chr22	16266928	16267095	uc002zlh.1_cds_2_0_chr22_16266929_r	0	-
chr22	16268136	16268181	uc002zlh.1_cds_3_0_chr22_16268137_r	0	-
chr22	16269872	16269943	uc002zlh.1_cds_4_0_chr22_16269873_r	0	-
chr22	16275206	16275277	uc002zlh.1_cds_5_0_chr22_16275207_r	0	-
chr22	16277747	16277885	uc002zlh.1_cds_6_0_chr22_16277748_r	0	-



1.Chrom	2.Start	3.End	4.Name	5	6.Strand
chr22	16050115	16050116	rs77005907	0	-
chr22	16050251	16050252	rs3016036	0	+
chr22	16050352	16050353	rs56342815	0	+
chr22	16050352	16050353	rs2334386	0	+
chr22	16050374	16050375	rs2844882	0	+
chr22	16050407	16050408	rs2844883	0	+



1.Chrom	2.Start	3.End	4.Name	5	6.Strand	7	8	9	10	11	12
chr22	16258185	16258303	uc002zlh.1_cds_1_0_chr22_16258186_r	0	-	chr22	16258278	16258279	rs2845178	0	+

Dataset 1

ctg15	10	49	Feature1
ctg15	70	119	Feature2
ctg15	170	209	Feature3
ctg15	180	229	Feature4

Dataset 2

ctg15	80	109	FeatureA
ctg15	150	199	FeatureB
ctg15	250	289	FeatureC
ctg15	270	309	FeatureD

Only records that are joined (INNER JOIN)

ctg15	70	119	Feature2	ctg15	80	109	FeatureA
ctg15	170	209	Feature3	ctg15	150	199	FeatureB
ctg15	180	229	Feature4	ctg15	150	199	FeatureB

All records of first dataset

ctg15	10	49	Feature1	.	.	.	.
ctg15	70	119	Feature2	ctg15	80	109	FeatureA
ctg15	170	209	Feature3	ctg15	150	199	FeatureB
ctg15	180	229	Feature4	ctg15	150	199	FeatureB

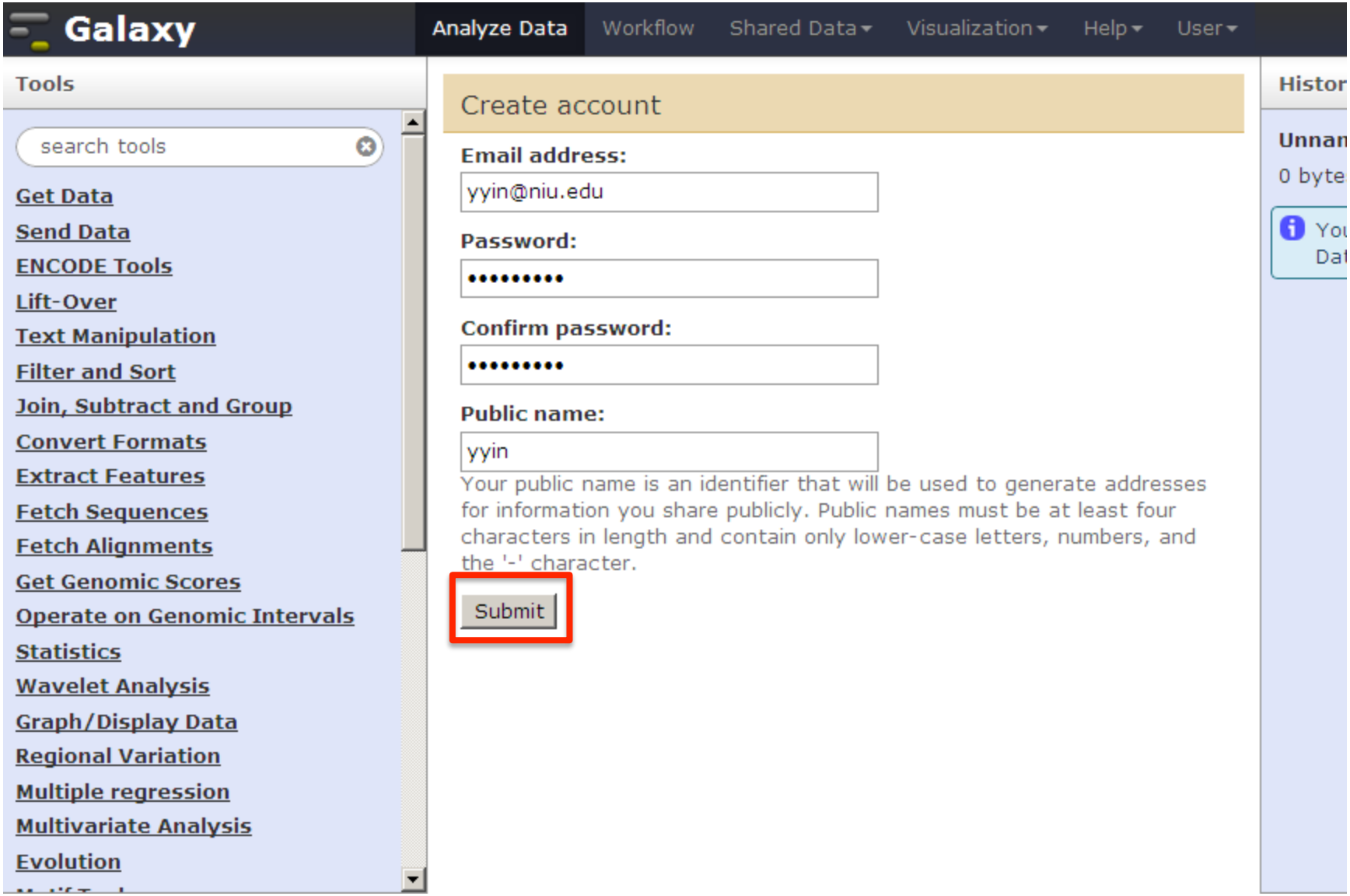
All records of second dataset

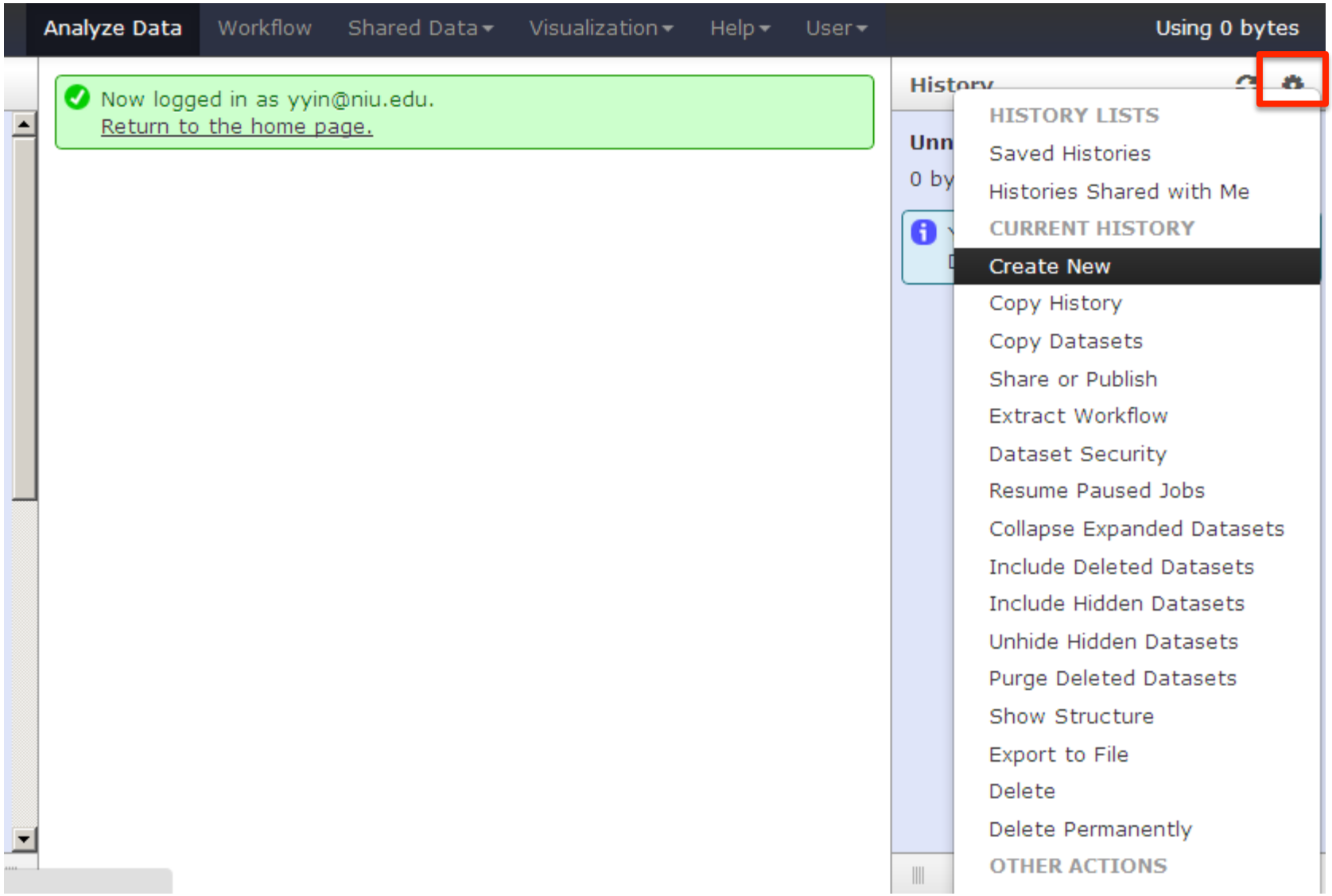
ctg15	70	119	Feature2	ctg15	80	109	FeatureA
ctg15	170	209	Feature3	ctg15	150	199	FeatureB
ctg15	180	229	Feature4	ctg15	150	199	FeatureB
.	.	.	.	ctg15	250	289	FeatureC
.	.	.	.	ctg15	270	309	FeatureD

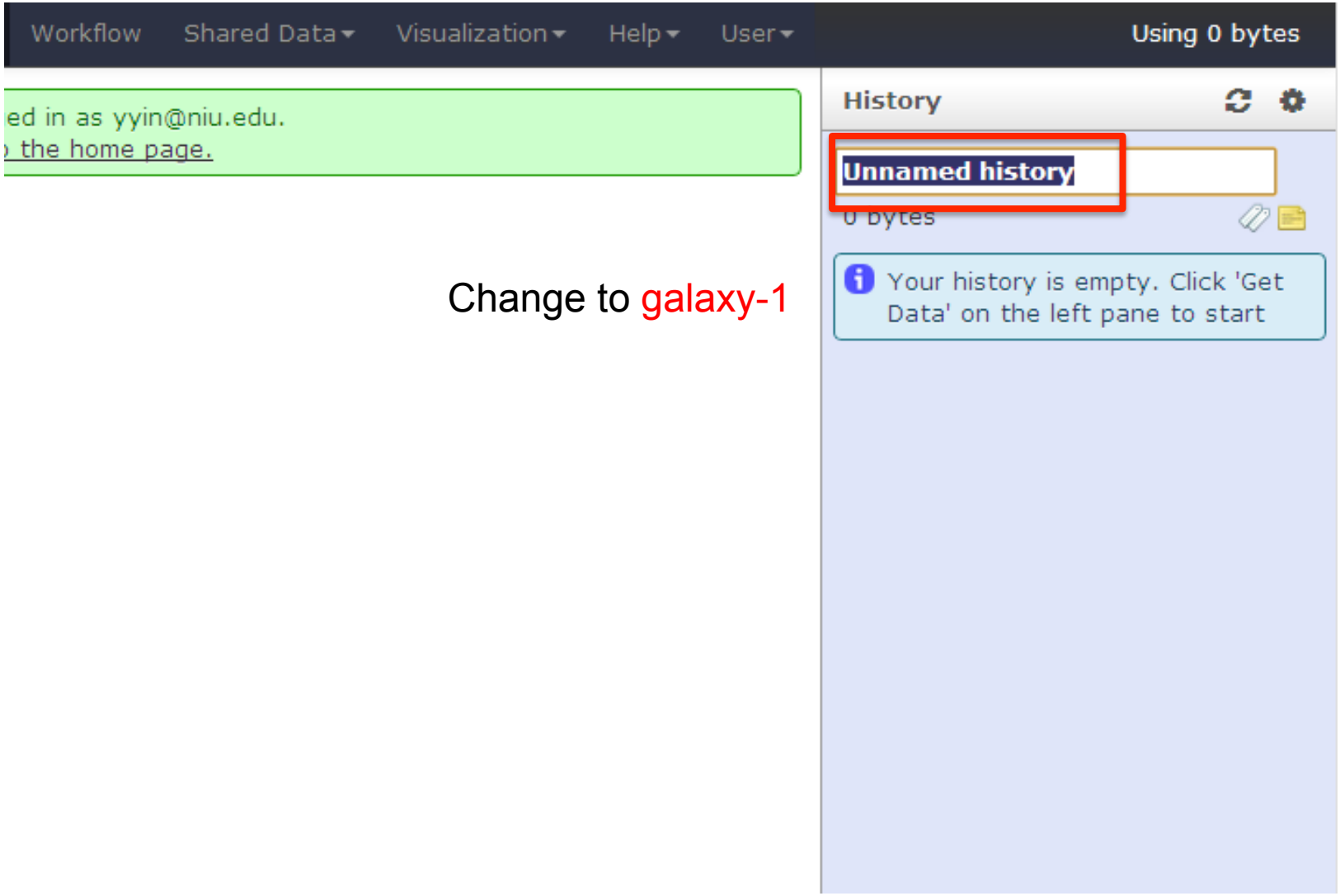
All records of both datasets

ctg15	10	49	Feature1	.	.	.	.
ctg15	70	119	Feature2	ctg15	80	109	FeatureA
ctg15	170	209	Feature3	ctg15	150	199	FeatureB
ctg15	180	229	Feature4	ctg15	150	199	FeatureB
.	.	.	.	ctg15	250	289	FeatureC
.	.	.	.	ctg15	270	309	FeatureD

Register an account

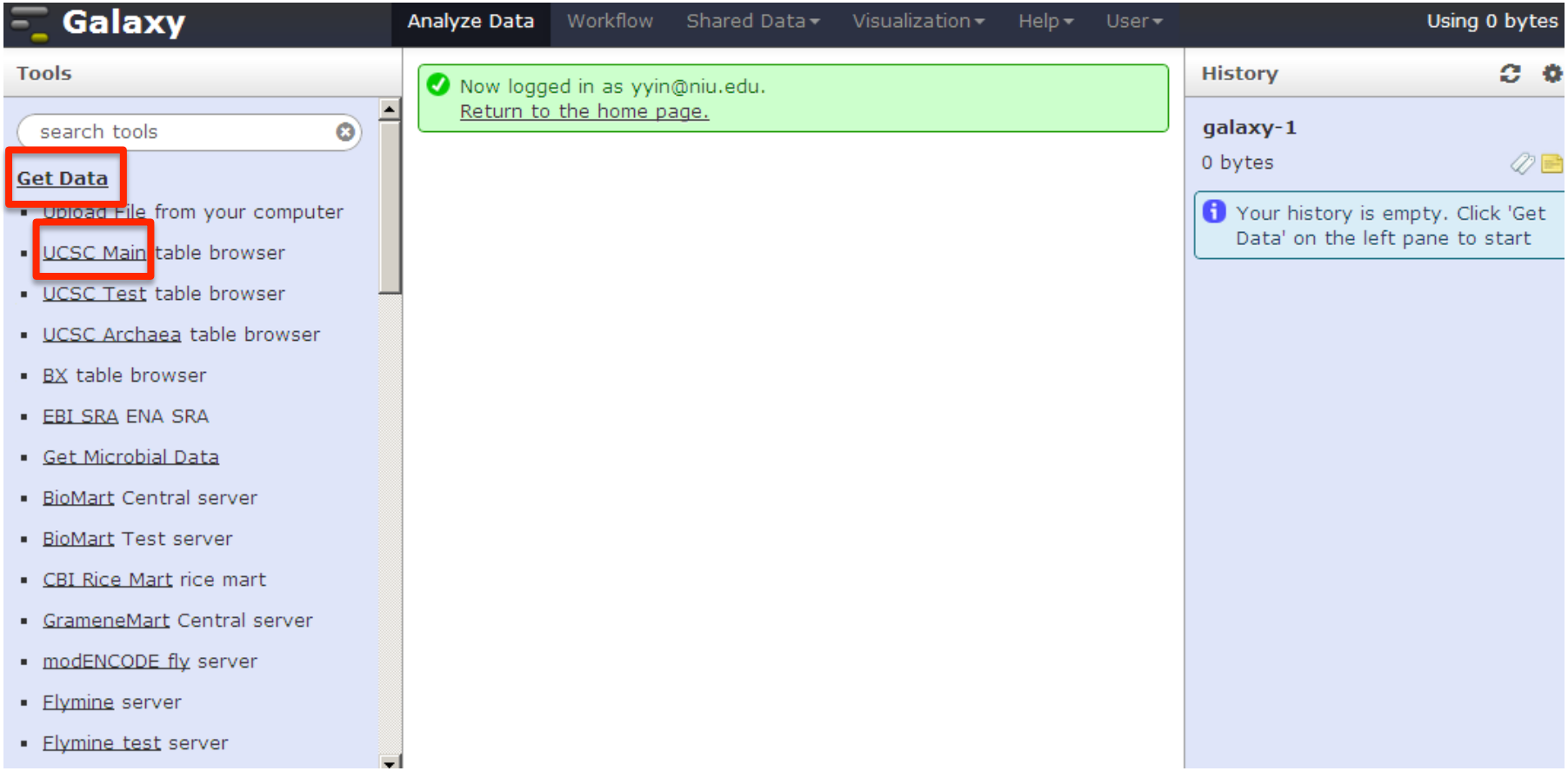

Galaxy
Analyze Data
Workflow
Shared Data
Visualization
Help
User
Tools
search tools
Get Data
Send Data
ENCODE Tools
Lift-Over
Text Manipulation
Filter and Sort
Join, Subtract and Group
Convert Formats
Extract Features
Fetch Sequences
Fetch Alignments
Get Genomic Scores
Operate on Genomic Intervals
Statistics
Wavelet Analysis
Graph/Display Data
Regional Variation
Multiple regression
Multivariate Analysis
Evolution
Create account
Email address:
yyin@niu.edu
Password:
Confirm password:
Public name:
yyin
Your public name is an identifier that will be used to generate addresses for information you share publicly. Public names must be at least four characters in length and contain only lower-case letters, numbers, and the '-' character.
Submit
Histor
Unnan
0 byte


Analyze Data
Workflow
Shared Data
Visualization
Help
User
Using 0 bytes
Now logged in as yyin@niu.edu.
Return to the home page.
History
HISTORY LISTS
Saved Histories
Histories Shared with Me
CURRENT HISTORY
Create New
Copy History
Copy Datasets
Share or Publish
Extract Workflow
Dataset Security
Resume Paused Jobs
Collapse Expanded Datasets
Include Deleted Datasets
Include Hidden Datasets
Unhide Hidden Datasets
Purge Deleted Datasets
Show Structure
Export to File
Delete
Delete Permanently
OTHER ACTIONS



Change to galaxy-1

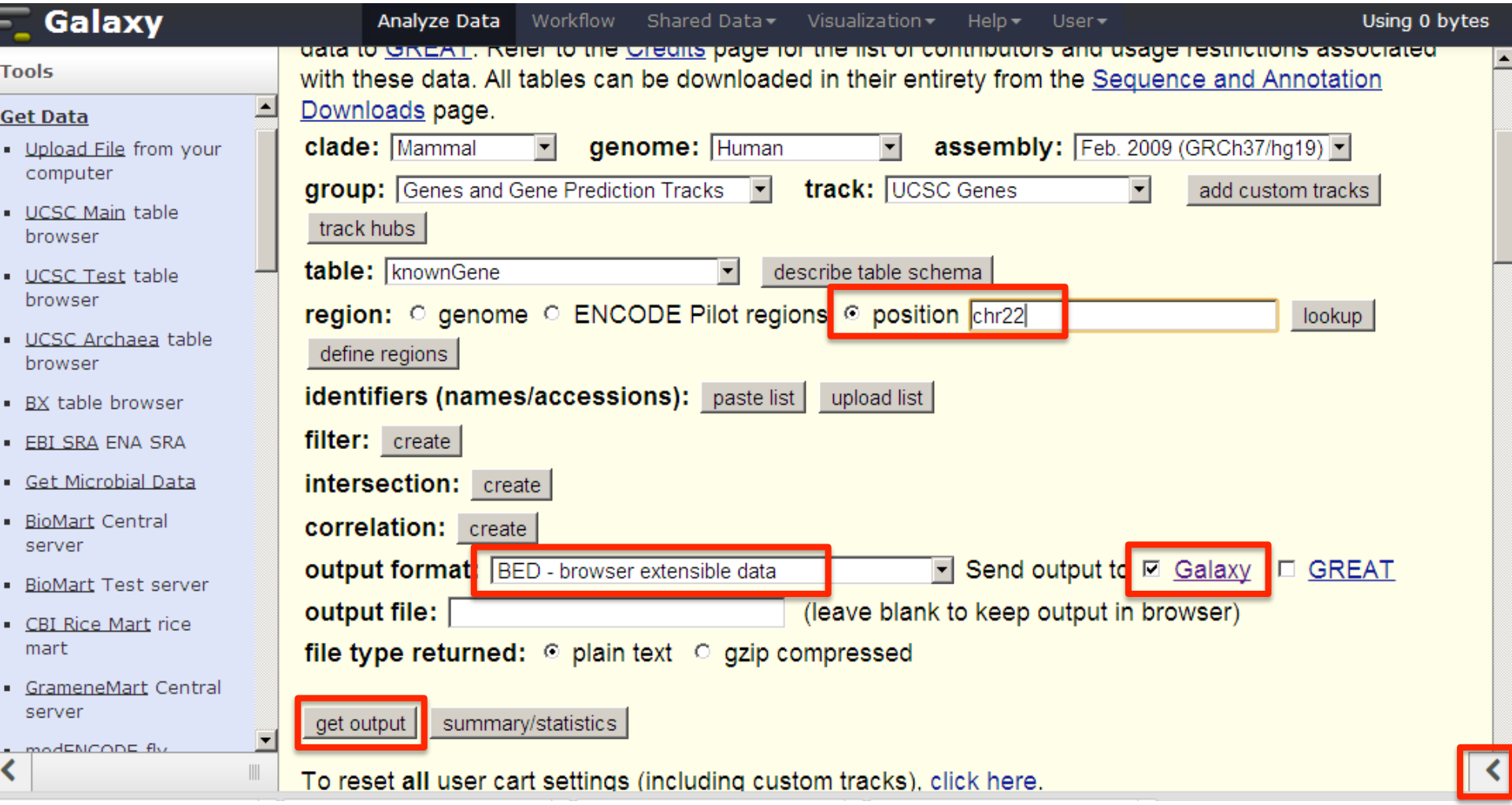
Step 1: get exon position data from UCSC



We are connected to UCSC genome browser

We are going to download the exon position data

Human -> knownGene -> chr22



Google ucsc bed format

BED format

Index ▷

BED format provides a flexible way to define the data lines that are displayed in an annotation track. BED lines have three required fields and nine additional optional fields. The number of fields per line must be consistent throughout any single set of data in an annotation track. The order of the optional fields is binding: lower-numbered fields must always be populated if higher-numbered fields are used.

If your data set is BED-like, but it is very large and you would like to keep it on your own server, you should use the bigBed data format.

The first three required BED fields are:

1. **chrom** - The name of the chromosome (e.g. chr3, chrY, chr2_random) or scaffold (e.g. scaffold10671).
2. **chromStart** - The starting position of the feature in the chromosome or scaffold. The first base in a chromosome is numbered 0.
3. **chromEnd** - The ending position of the feature in the chromosome or scaffold. The *chromEnd* base is not included in the display of the feature. For example, the first 100 bases of a chromosome are defined as *chromStart=0, chromEnd=100*, and span the bases numbered 0-99.

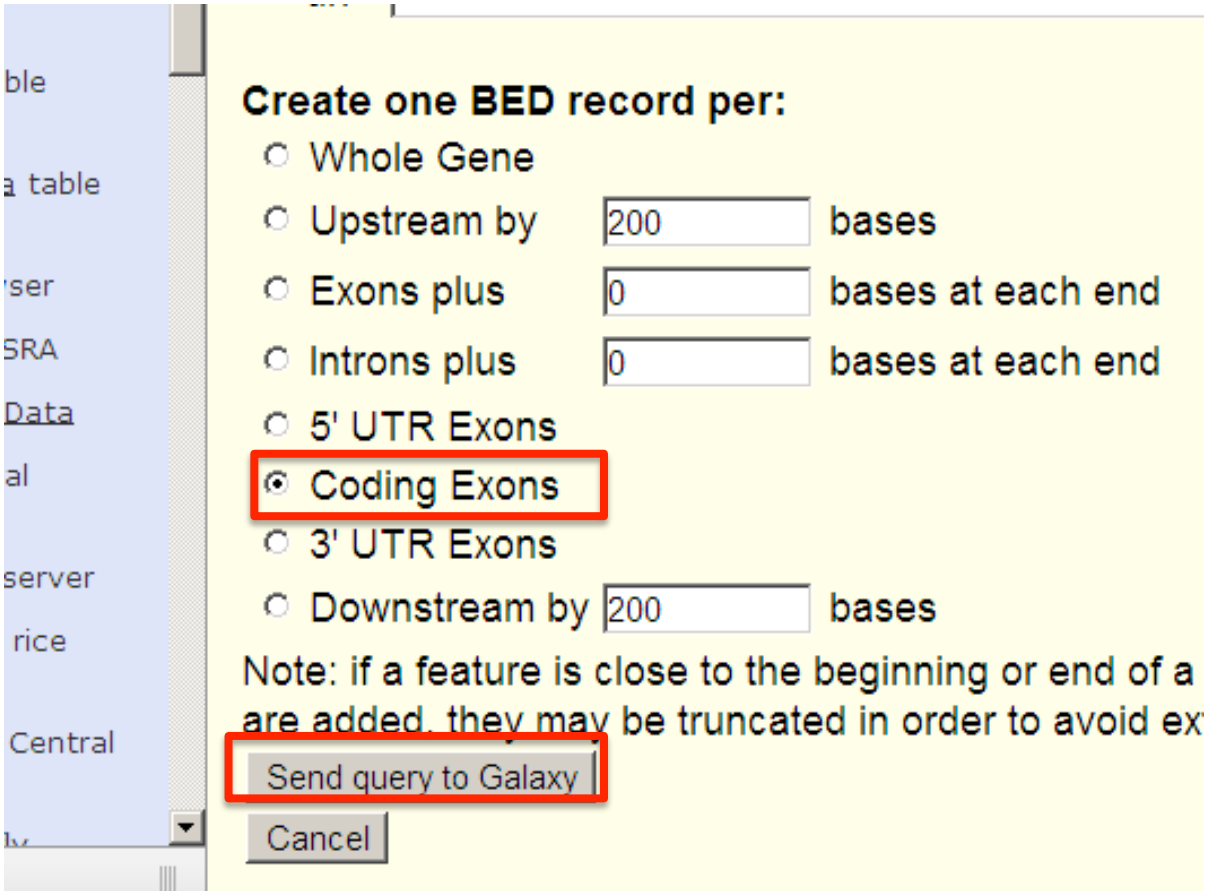
The 9 additional optional BED fields are:

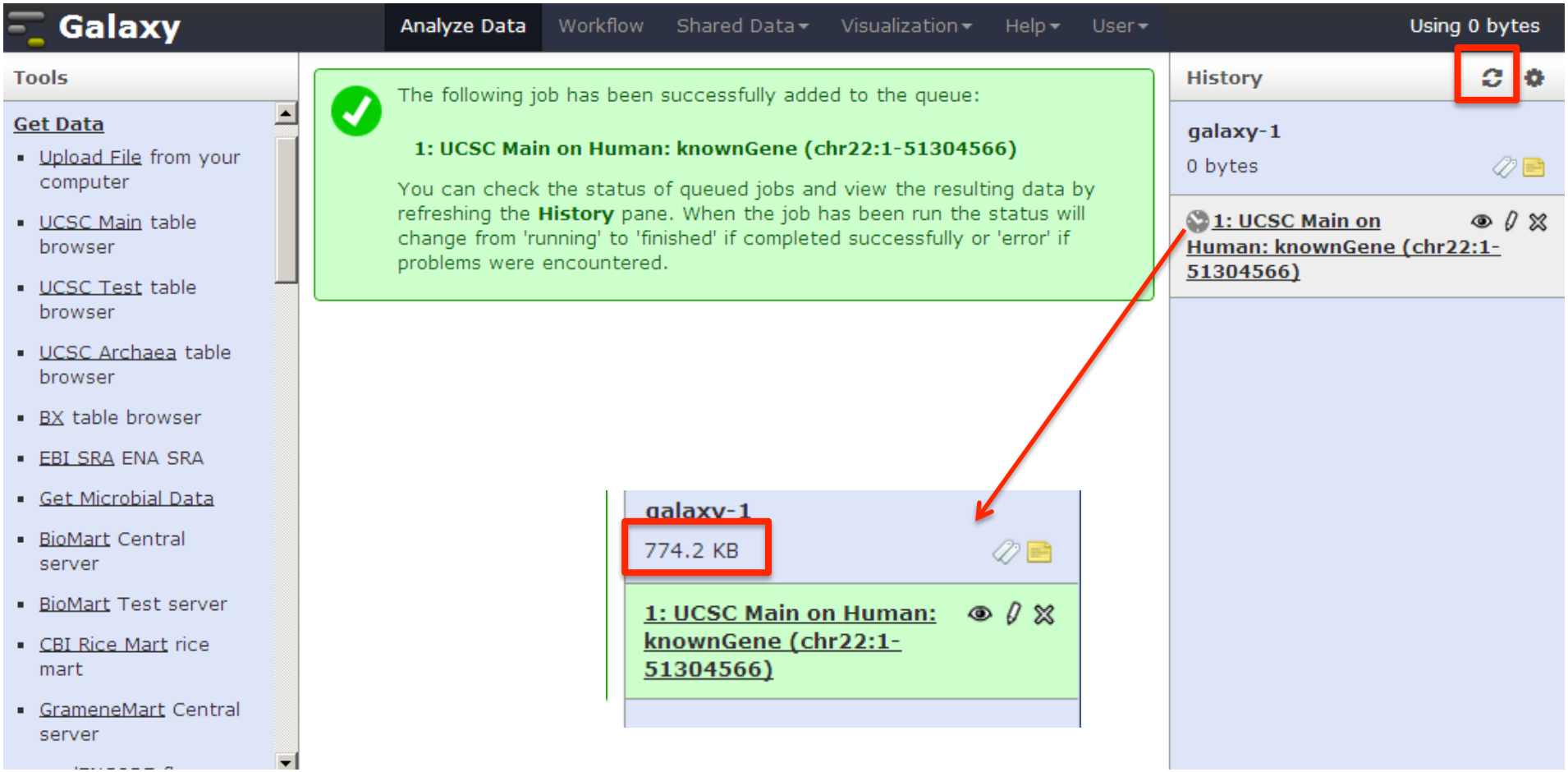
4. **name** - Defines the name of the BED line. This label is displayed to the left of the BED line in the Genome Browser window when the track is open to full display mode or directly to the left of the item in pack mode.
5. **score** - A score between 0 and 1000. If the track line *useScore* attribute is set to 1 for this annotation data set, the *score* value will determine the level of gray in which this feature is displayed (higher numbers = darker gray). This table shows the Genome Browser's translation of BED score values into shades of gray:

shade								
score in range	≤ 166	167-277	278-388	389-499	500-611	612-722	723-833	834-944	≥ 945

6. **strand** - Defines the strand - either '+' or '-'.
7. **thickStart** - The starting position at which the feature is drawn thickly (for example, the start codon in gene displays).
8. **thickEnd** - The ending position at which the feature is drawn thickly (for example, the stop codon in gene displays).
9. **itemRgb** - An RGB value of the form R,G,B (e.g. 255,0,0). If the track line *itemRgb* attribute is set to "On", this RBG value will determine the display color of the data contained in this BED line. NOTE: It is recommended that a simple color scheme (eight colors or less) be used with this attribute to avoid overwhelming the color resources of the Genome Browser and your Internet browser.
10. **blockCount** - The number of blocks (exons) in the BED line.

Choose coding exons

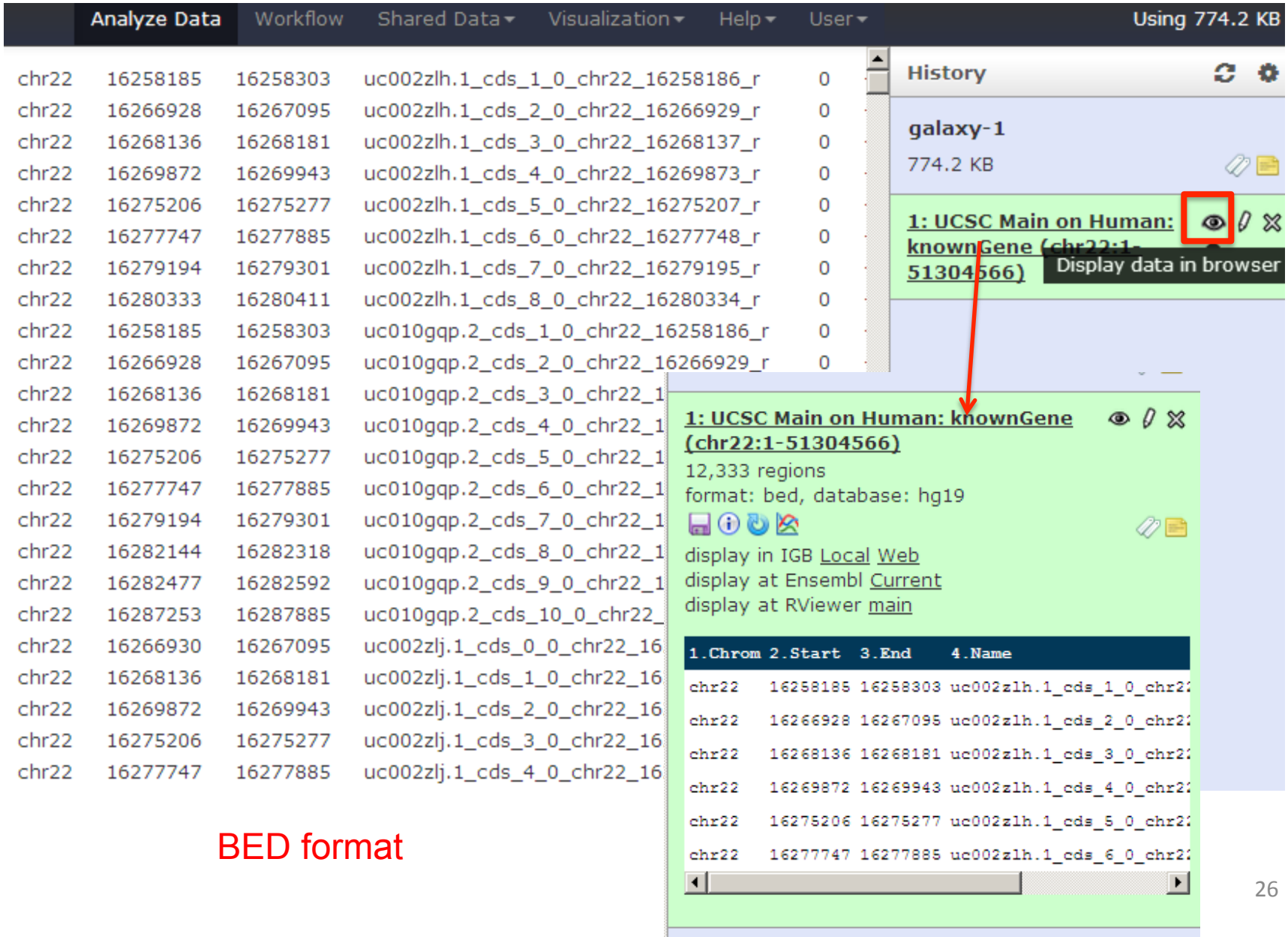



Galaxy
Analyze Data
Workflow
Shared Data
Visualization
Help
User
Using 0 bytes
Tools
Get Data
Upload File from your computer
UCSC Main table browser
UCSC Test table browser
UCSC Archaea table browser
BX table browser
EBI SRA ENA SRA
Get Microbial Data
BioMart Central server
BioMart Test server
CBI Rice Mart rice mart
GrameneMart Central server
The following job has been successfully added to the queue:
1: UCSC Main on Human: knownGene (chr22:1-51304566)
You can check the status of queued jobs and view the resulting data by refreshing the History pane. When the job has been run the status will change from 'running' to 'finished' if completed successfully or 'error' if problems were encountered.
History
galaxy-1
0 bytes
1: UCSC Main on Human: knownGene (chr22:1-51304566)
galaxy-1
774.2 KB
1: UCSC Main on Human: knownGene (chr22:1-51304566)

Tool tab

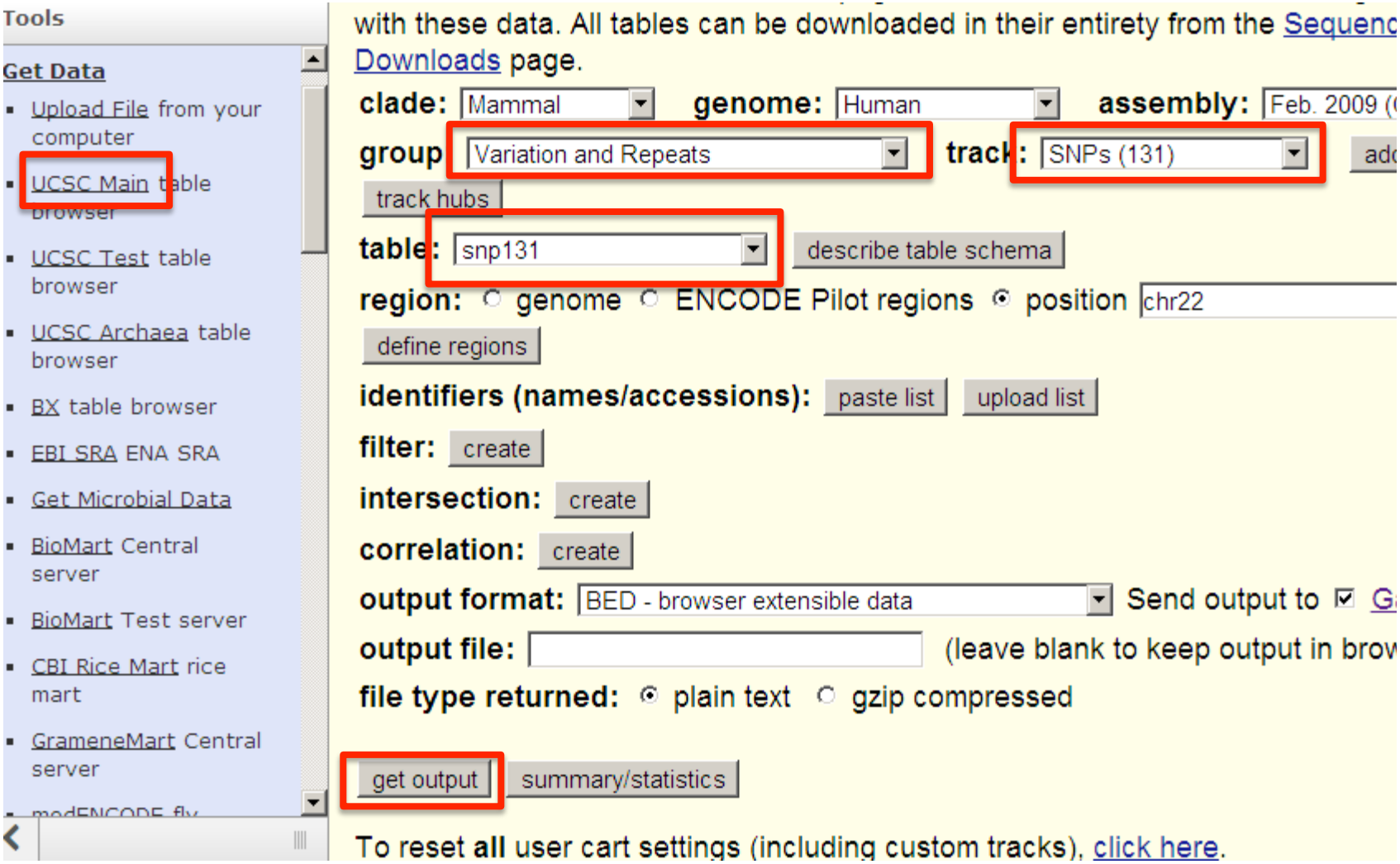
Browse tab

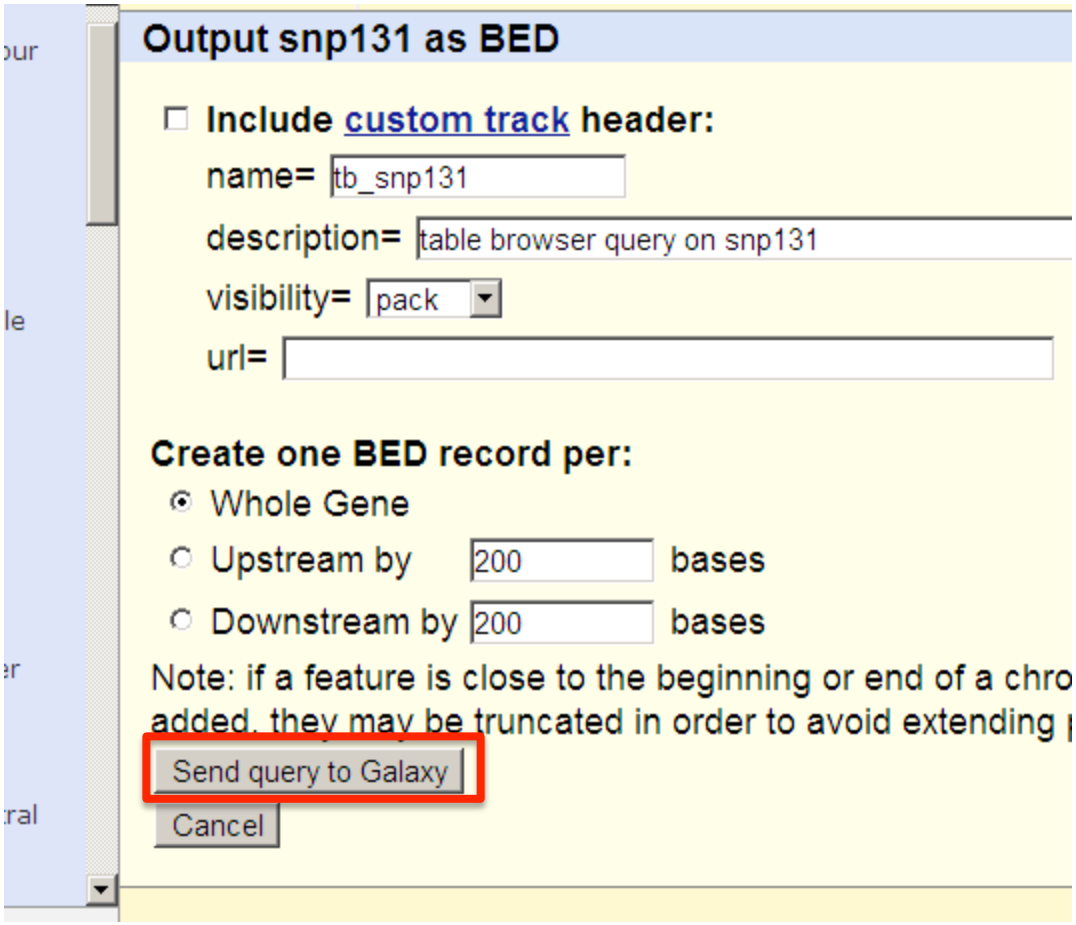
History tab

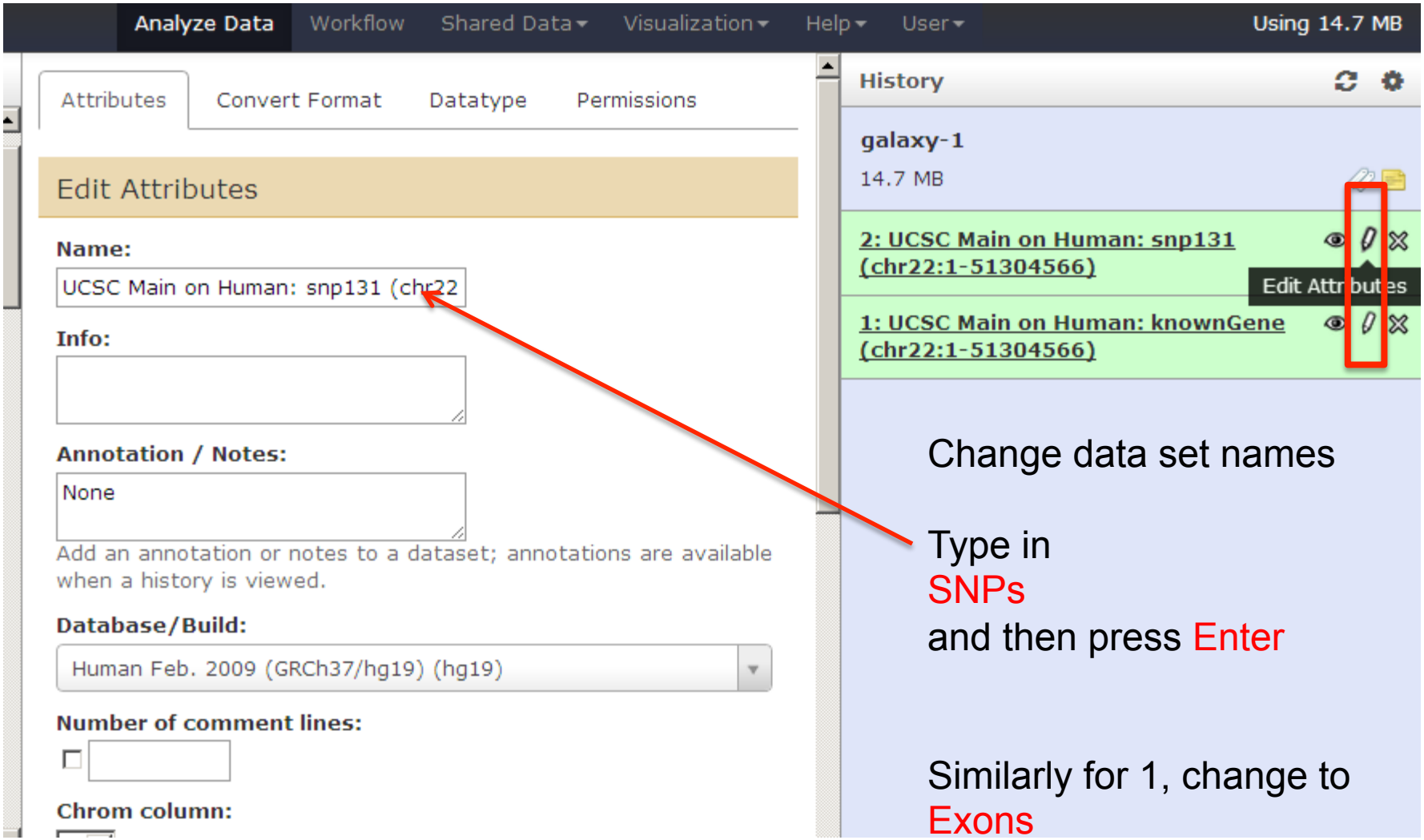


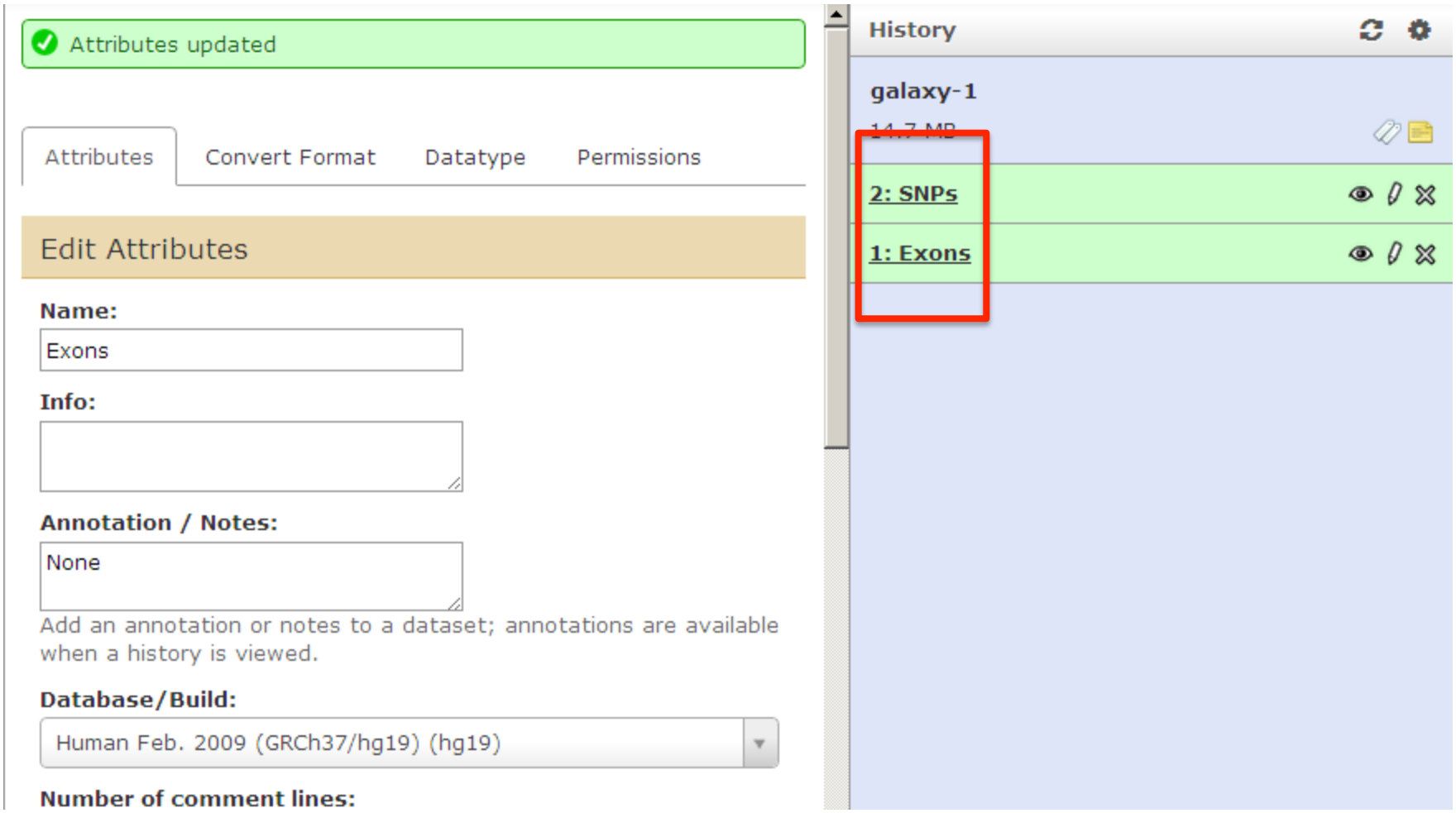
BED format

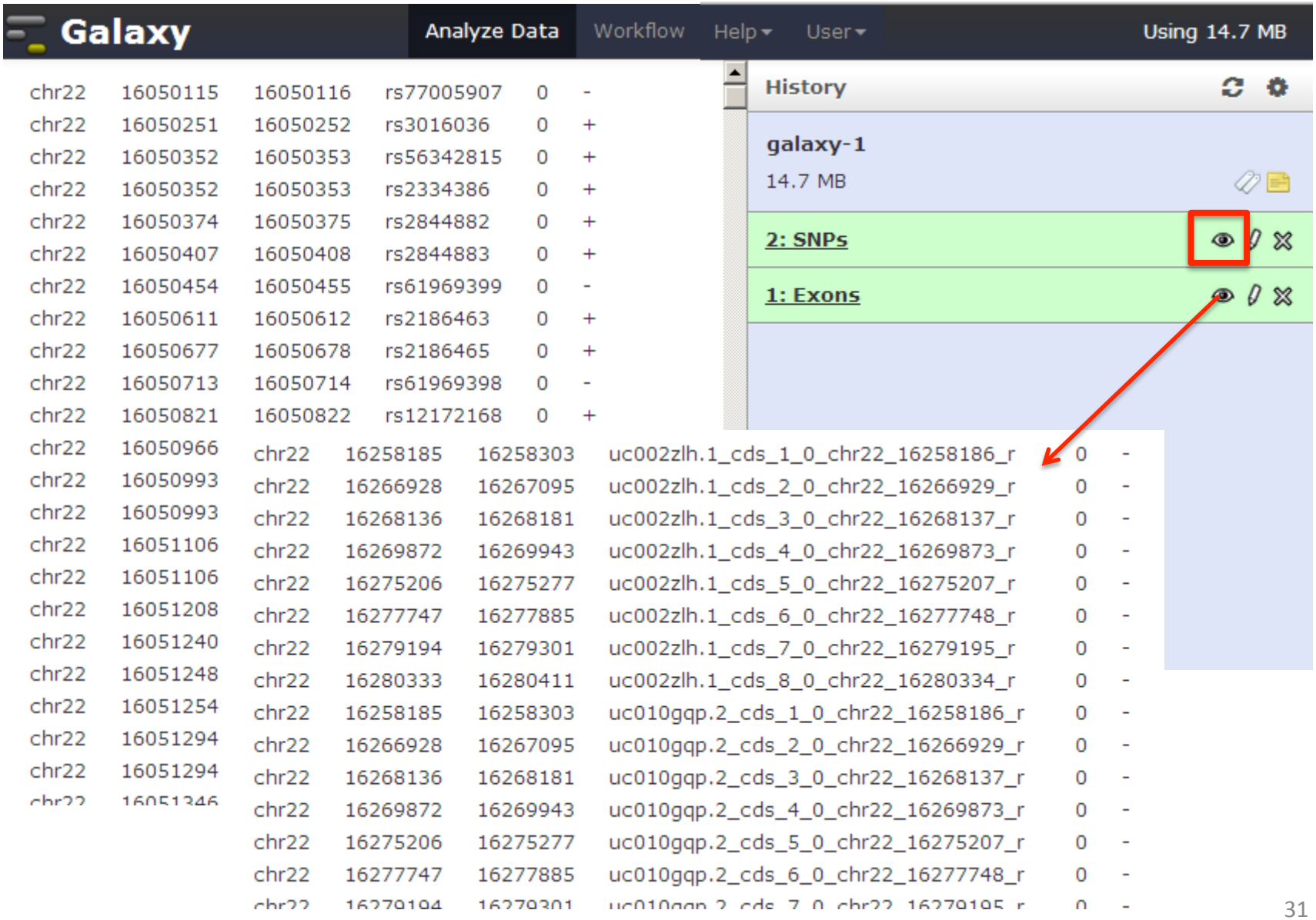
Now download SNP position data

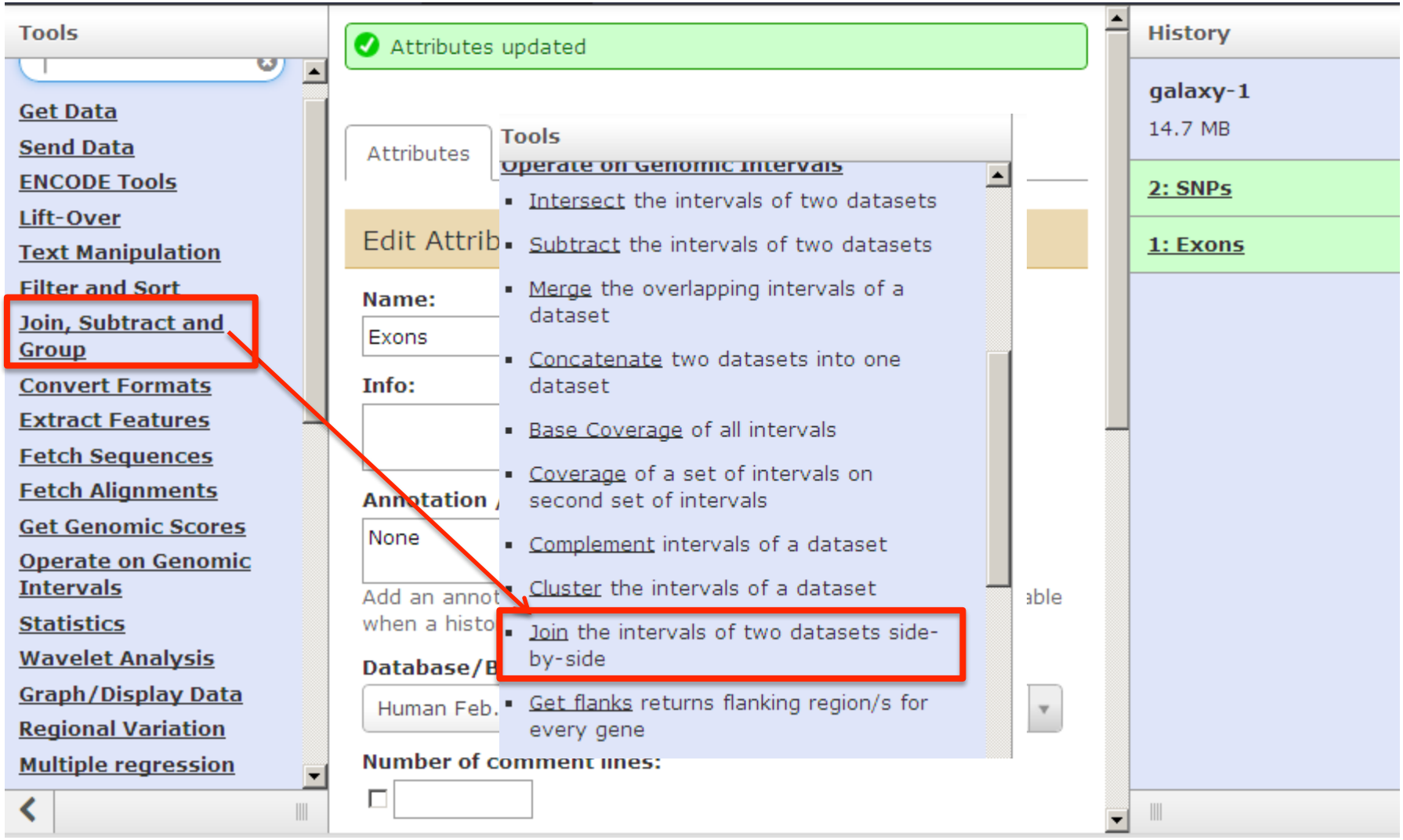


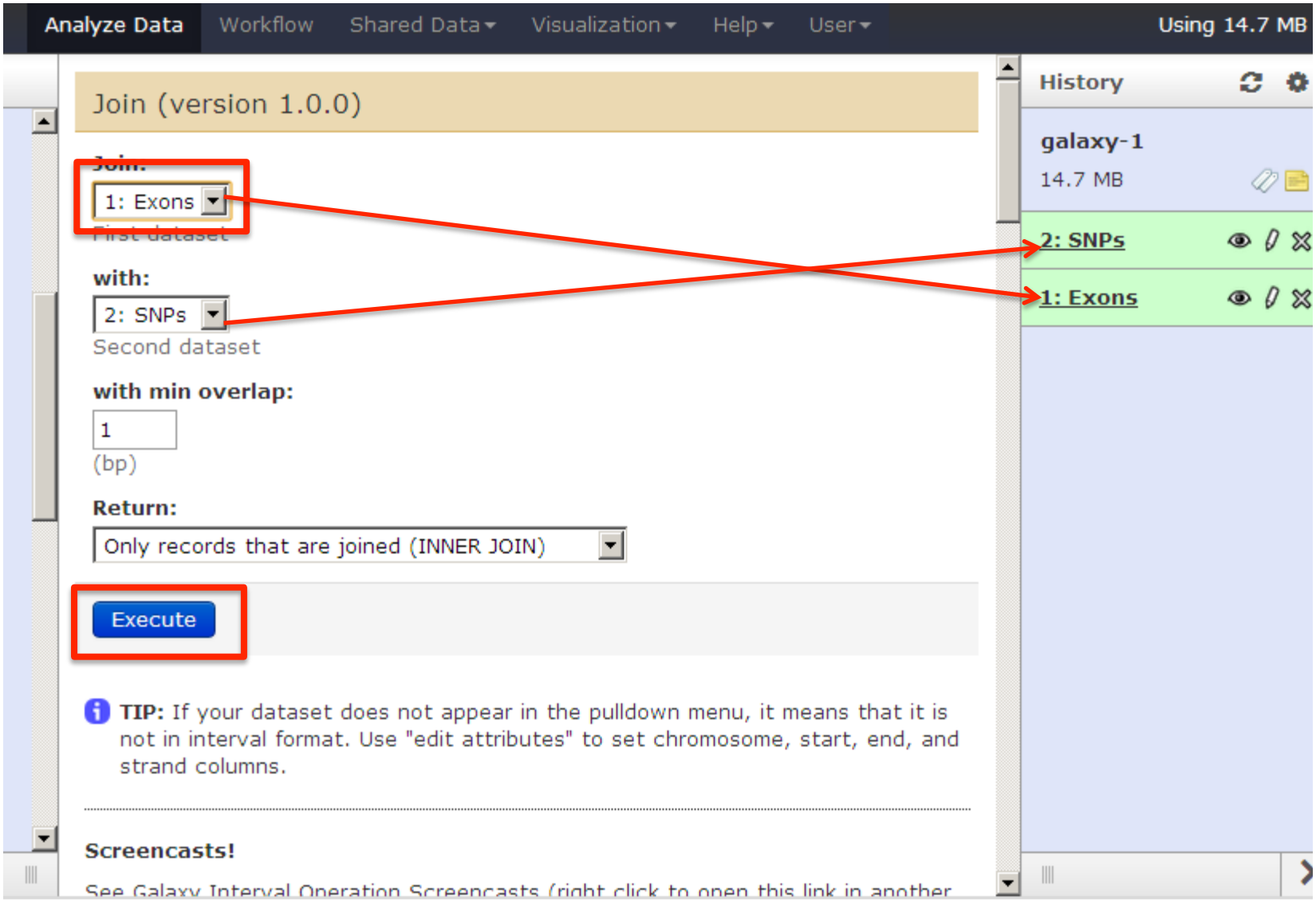

Output snp131 as BED
Include custom track header:
name= tb_snp131
description= table browser query on snp131
visibility= pack
url=
Create one BED record per:
Whole Gene
Upstream by 200 bases
Downstream by 200 bases
Note: if a feature is close to the beginning or end of a chro
added, they may be truncated in order to avoid extending
Send query to Galaxy
Cancel


Analyze Data
Workflow
Shared Data
Visualization
Help
User
Using 14.7 MB
Attributes
Convert Format
Datatype
Permissions
Edit Attributes
Name:
UCSC Main on Human: snp131 (chr22
Info:
Annotation / Notes:
None
Add an annotation or notes to a dataset; annotations are available when a history is viewed.
Database/Build:
Human Feb. 2009 (GRCh37/hg19) (hg19)
Number of comment lines:
Chrom column:
History
galaxy-1
14.7 MB
2: UCSC Main on Human: snp131 (chr22:1-51304566)
Edit Attributes
1: UCSC Main on Human: knownGene (chr22:1-51304566)
Change data set names
Type in
SNPs
and then press Enter
Similarly for 1, change to
Exons


Attributes updated
Attributes
Convert Format
Datatype
Permissions
Edit Attributes
Name:
Exons
Info:
Annotation / Notes:
None
Add an annotation or notes to a dataset; annotations are available when a history is viewed.
Database/Build:
Human Feb. 2009 (GRCh37/hg19) (hg19)
Number of comment lines:
History
galaxy-1
2: SNPs
1: Exons


Galaxy
Analyze Data
Workflow
Help
User
Using 14.7 MB
History
galaxy-1
14.7 MB
2: SNPs
1: Exons
chr22 16050115 16050116 rs77005907 0 -
chr22 16050251 16050252 rs3016036 0 +
chr22 16050352 16050353 rs56342815 0 +
chr22 16050352 16050353 rs2334386 0 +
chr22 16050374 16050375 rs2844882 0 +
chr22 16050407 16050408 rs2844883 0 +
chr22 16050454 16050455 rs61969399 0 -
chr22 16050611 16050612 rs2186463 0 +
chr22 16050677 16050678 rs2186465 0 +
chr22 16050713 16050714 rs61969398 0 -
chr22 16050821 16050822 rs12172168 0 +
chr22 16050966
chr22 16050993
chr22 16050993
chr22 16051106
chr22 16051106
chr22 16051208
chr22 16051240
chr22 16051248
chr22 16051254
chr22 16051294
chr22 16051294
chr22 16051346
chr22 16258185 16258303 uc002zlh.1_cds_1_0_chr22_16258186_r 0 -
chr22 16266928 16267095 uc002zlh.1_cds_2_0_chr22_16266929_r 0 -
chr22 16268136 16268181 uc002zlh.1_cds_3_0_chr22_16268137_r 0 -
chr22 16269872 16269943 uc002zlh.1_cds_4_0_chr22_16269873_r 0 -
chr22 16275206 16275277 uc002zlh.1_cds_5_0_chr22_16275207_r 0 -
chr22 16277747 16277885 uc002zlh.1_cds_6_0_chr22_16277748_r 0 -
chr22 16279194 16279301 uc002zlh.1_cds_7_0_chr22_16279195_r 0 -
chr22 16280333 16280411 uc002zlh.1_cds_8_0_chr22_16280334_r 0 -
chr22 16258185 16258303 uc010gqp.2_cds_1_0_chr22_16258186_r 0 -
chr22 16266928 16267095 uc010gqp.2_cds_2_0_chr22_16266929_r 0 -
chr22 16268136 16268181 uc010gqp.2_cds_3_0_chr22_16268137_r 0 -
chr22 16269872 16269943 uc010gqp.2_cds_4_0_chr22_16269873_r 0 -
chr22 16275206 16275277 uc010gqp.2_cds_5_0_chr22_16275207_r 0 -
chr22 16277747 16277885 uc010gqp.2_cds_6_0_chr22_16277748_r 0 -
chr22 16279194 16279301 uc010gqp.2_cds_7_0_chr22_16279195_r 0 -


Tools
Get Data
Send Data
ENCODE Tools
Lift-Over
Text Manipulation
Filter and Sort
Join, Subtract and Group
Convert Formats
Extract Features
Fetch Sequences
Fetch Alignments
Get Genomic Scores
Operate on Genomic Intervals
Statistics
Wavelet Analysis
Graph/Display Data
Regional Variation
Multiple regression
Attributes updated
Attributes
Tools
Operate on Genomic Intervals
Intersect the intervals of two datasets
Subtract the intervals of two datasets
Merge the overlapping intervals of a dataset
Concatenate two datasets into one dataset
Base Coverage of all intervals
Coverage of a set of intervals on second set of intervals
Complement intervals of a dataset
Cluster the intervals of a dataset
Join the intervals of two datasets side-by-side
Get flanks returns flanking region/s for every gene
Edit Attrib
Name:
Exons
Info:
Annotation
None
Database/B
Human Feb.
Number of comment lines:
History
galaxy-1
14.7 MB
2: SNPs
1: Exons


Analyze Data
Workflow
Shared Data
Visualization
Help
User
Using 14.7 MB
Join (version 1.0.0)
1: Exons
First dataset
with:
2: SNPs
Second dataset
with min overlap:
1
(bp)
Return:
Only records that are joined (INNER JOIN)
Execute
TIP: If your dataset does not appear in the pulldown menu, it means that 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
History
galaxy-1
14.7 MB
2: SNPs
1: Exons

The following job has been successfully added to the queue:

3: Join on data 2 and data 1

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

History

galaxy-1
14.7 MB

3: Join on data 2 and data 1

2: SNPs

1: Exons

Click on the link to expand the panel

galaxy-1
16.2 MB

3: Join on data 2 and data 1
15,469 regions
format: interval, database: hg19
display at Ensembl Current
display at RViewer main

1.Chrom	2.Start	3.End	4.Name
chr22	16258185	16258303	uc002zlh.1_c
chr22	16266928	16267095	uc002zlh.1_c
chr22	16266928	16267095	uc002zlh.1_c
chr22	16266928	16267095	uc002zlh.1_c
chr22	16266928	16267095	uc002zlh.1_c
chr22	16269872	16269943	uc002zlh.1_c

Becomes green after it is done

History

galaxy-1
16.2 MB

Change the name to Joined

3: Joined

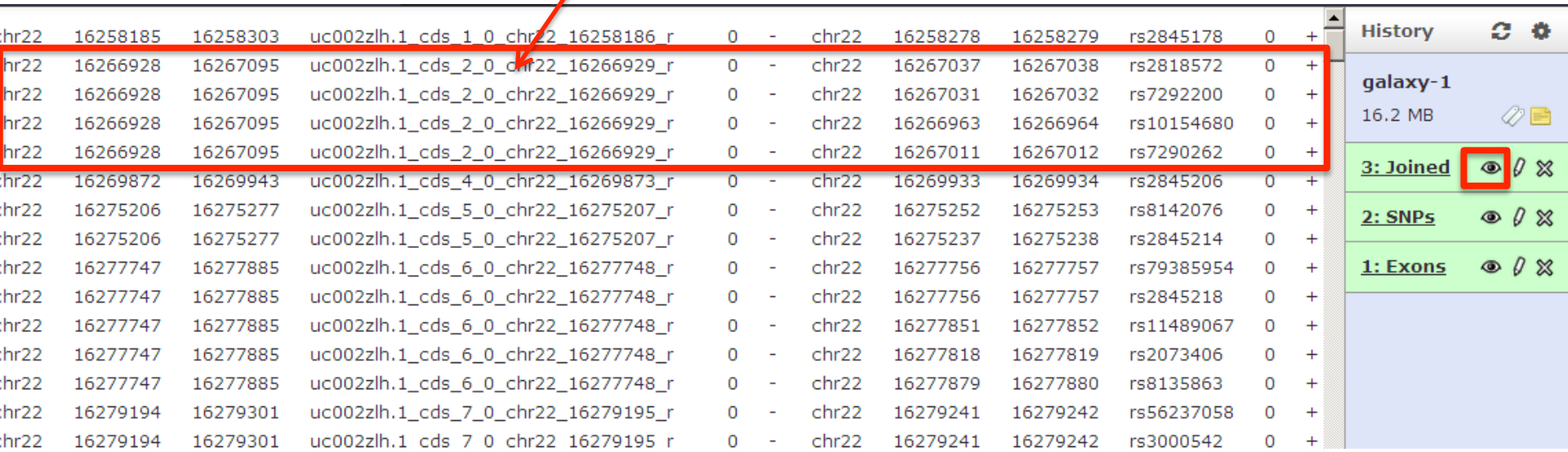
2: SNPs

1: Exons

4 SNPs are located in exon uc002zlh.1_cds_2_0_chr22_16266929_r

Now we need to count for each exon, in how many lines do they appear

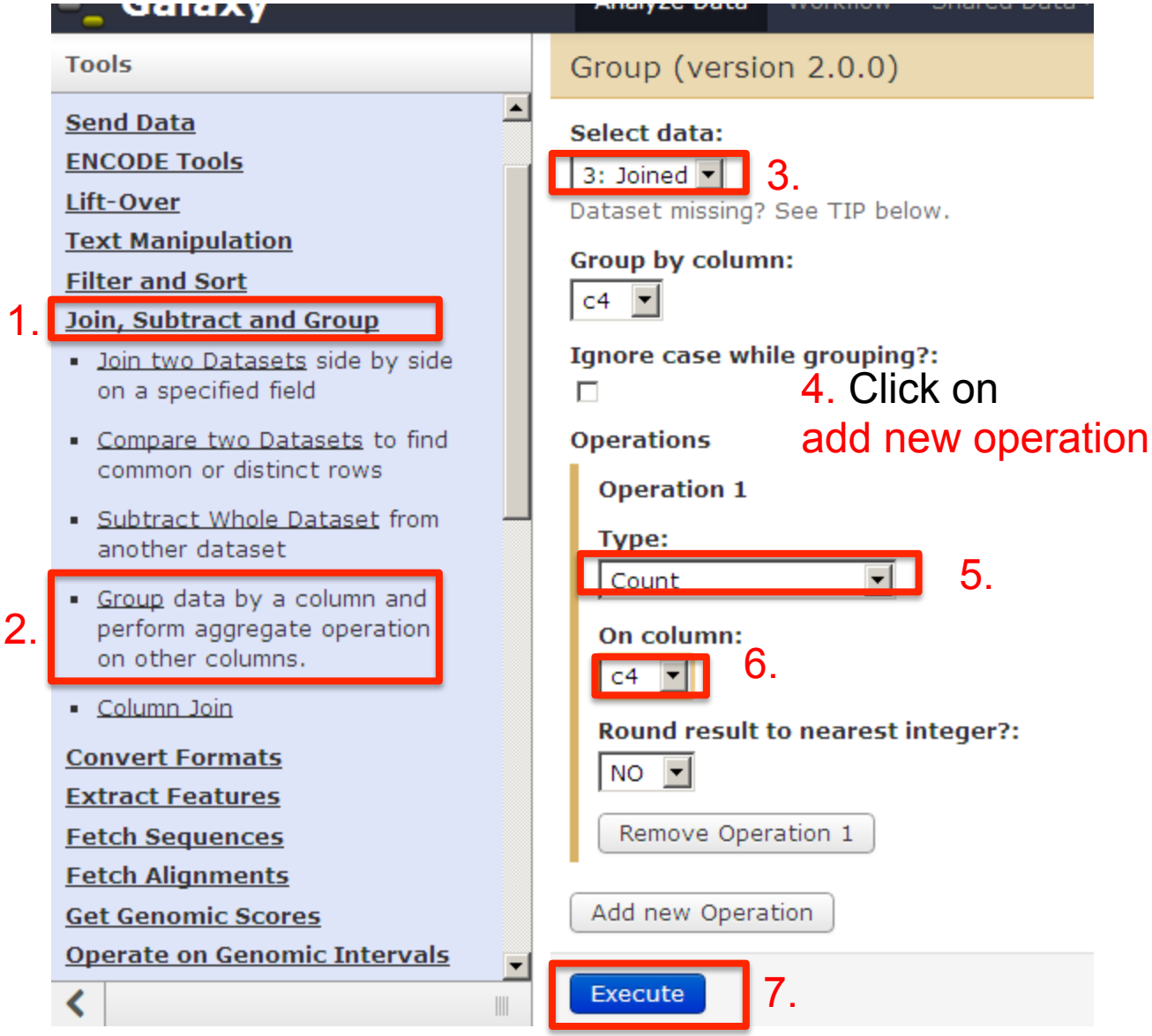
Or
more specifically, count how many times each word in column 4 appear if we group them



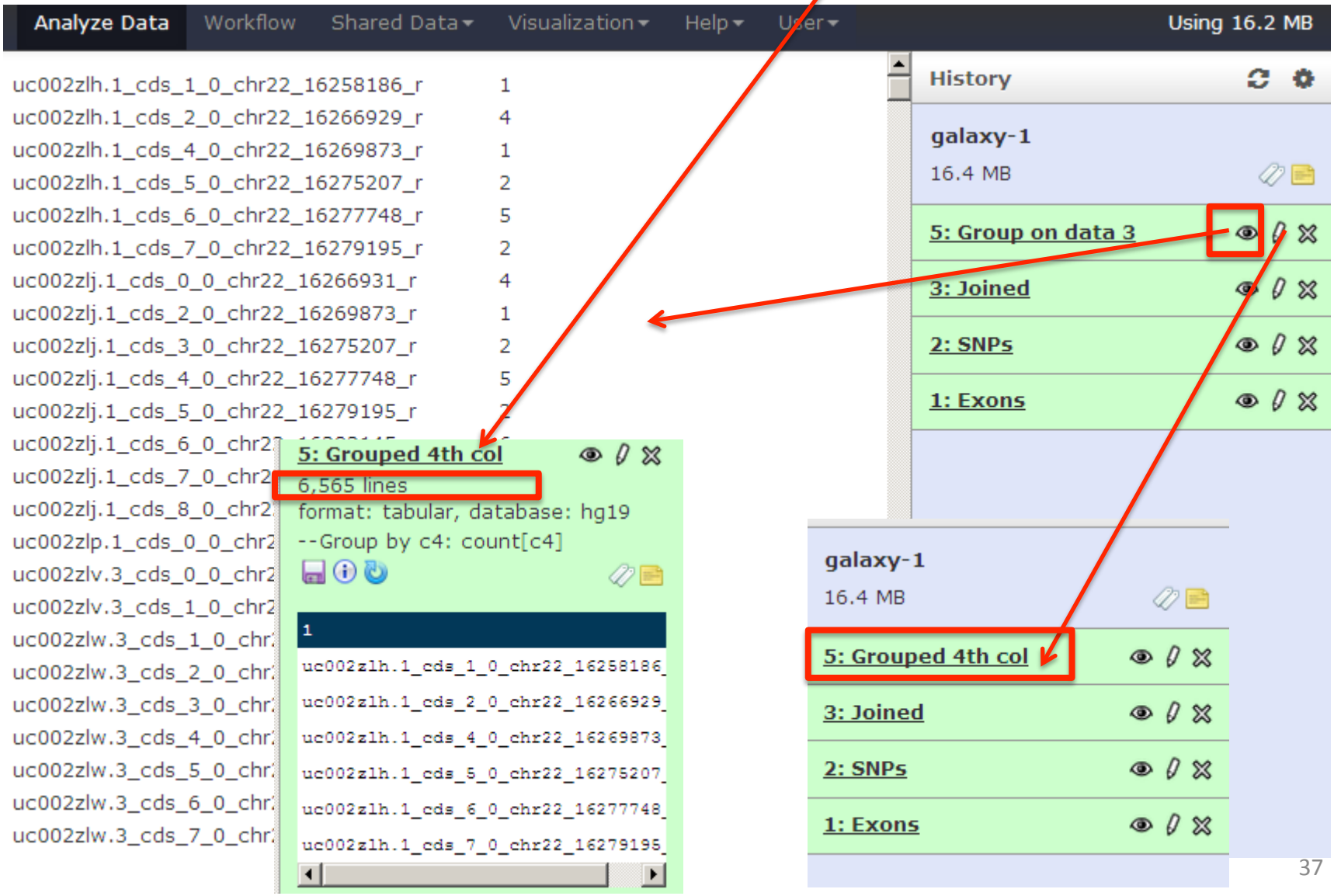
hr22	16258185	16258303	uc002zlh.1_cds_1_0_chr22_16258186_r	0	-	chr22	16258278	16258279	rs2845178	0	+
hr22	16266928	16267095	uc002zlh.1_cds_2_0_chr22_16266929_r	0	-	chr22	16267037	16267038	rs2818572	0	+
hr22	16266928	16267095	uc002zlh.1_cds_2_0_chr22_16266929_r	0	-	chr22	16267031	16267032	rs7292200	0	+
hr22	16266928	16267095	uc002zlh.1_cds_2_0_chr22_16266929_r	0	-	chr22	16266963	16266964	rs10154680	0	+
hr22	16266928	16267095	uc002zlh.1_cds_2_0_chr22_16266929_r	0	-	chr22	16267011	16267012	rs7290262	0	+
hr22	16269872	16269943	uc002zlh.1_cds_4_0_chr22_16269873_r	0	-	chr22	16269933	16269934	rs2845206	0	+
hr22	16275206	16275277	uc002zlh.1_cds_5_0_chr22_16275207_r	0	-	chr22	16275252	16275253	rs8142076	0	+
hr22	16275206	16275277	uc002zlh.1_cds_5_0_chr22_16275207_r	0	-	chr22	16275237	16275238	rs2845214	0	+
hr22	16277747	16277885	uc002zlh.1_cds_6_0_chr22_16277748_r	0	-	chr22	16277756	16277757	rs79385954	0	+
hr22	16277747	16277885	uc002zlh.1_cds_6_0_chr22_16277748_r	0	-	chr22	16277756	16277757	rs2845218	0	+
hr22	16277747	16277885	uc002zlh.1_cds_6_0_chr22_16277748_r	0	-	chr22	16277851	16277852	rs11489067	0	+
hr22	16277747	16277885	uc002zlh.1_cds_6_0_chr22_16277748_r	0	-	chr22	16277818	16277819	rs2073406	0	+
hr22	16277747	16277885	uc002zlh.1_cds_6_0_chr22_16277748_r	0	-	chr22	16277879	16277880	rs8135863	0	+
hr22	16279194	16279301	uc002zlh.1_cds_7_0_chr22_16279195_r	0	-	chr22	16279241	16279242	rs56237058	0	+
hr22	16279194	16279301	uc002zlh.1_cds_7_0_chr22_16279195_r	0	-	chr22	16279241	16279242	rs3000542	0	+

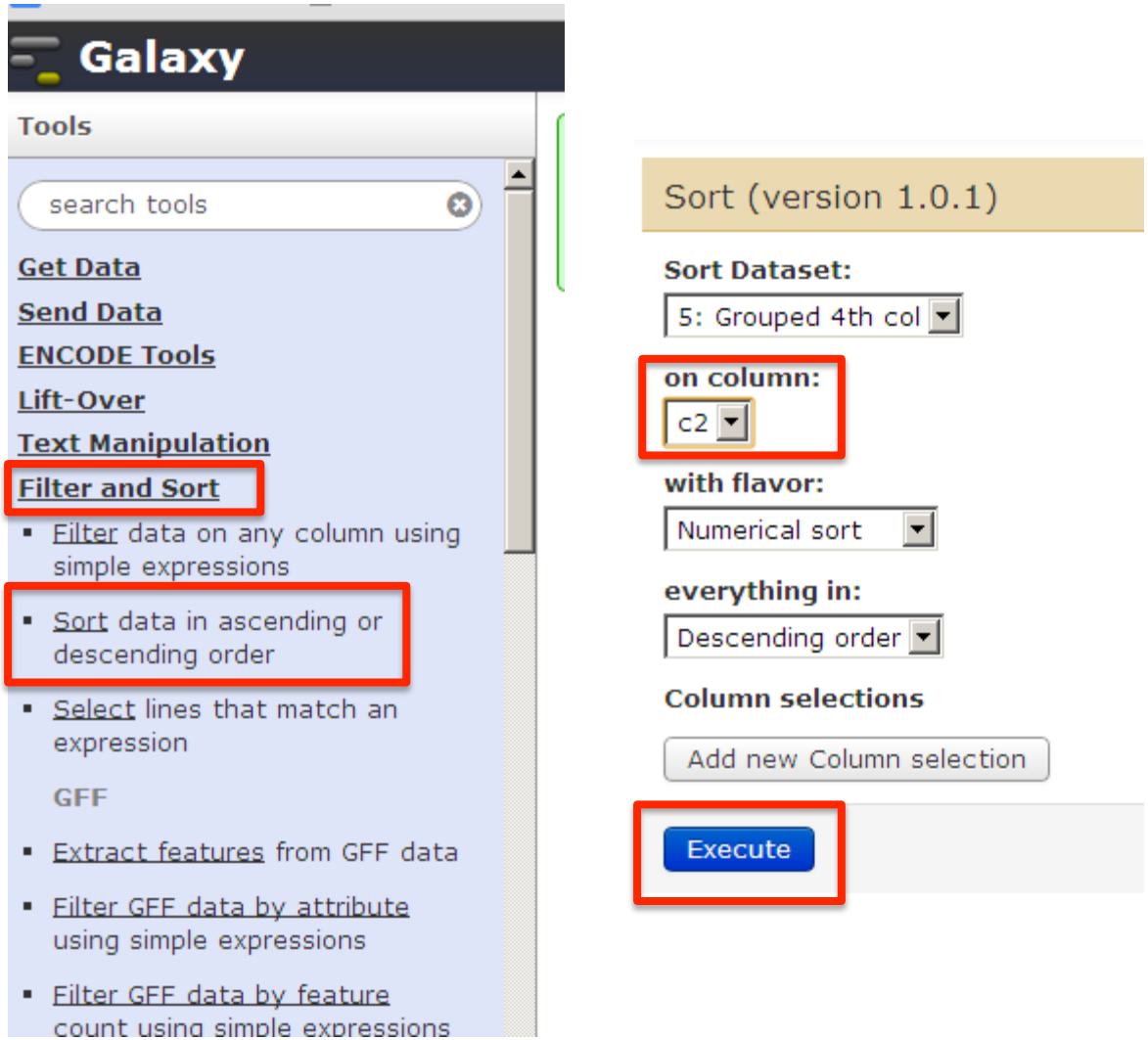
Exon data

SNP data

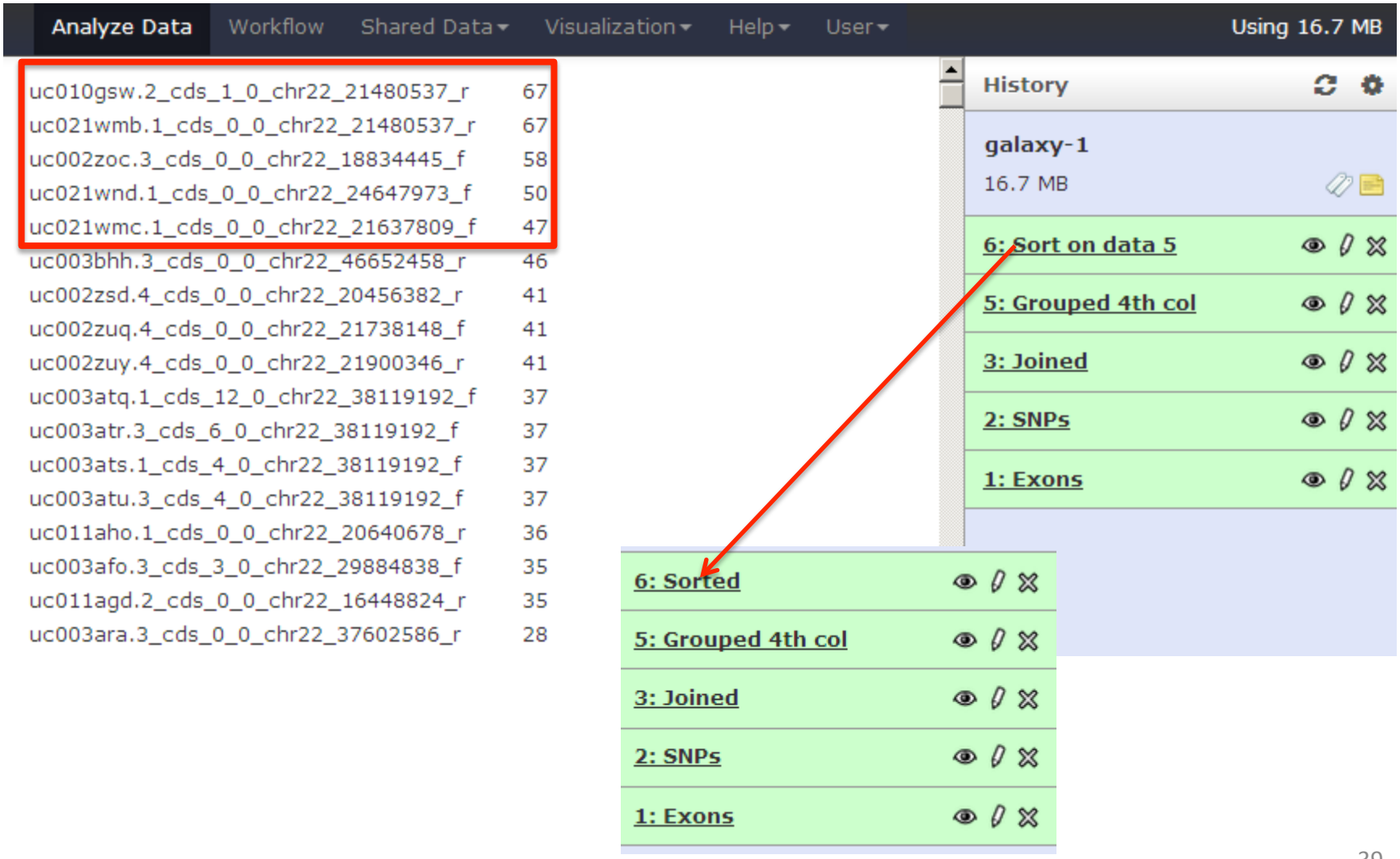

Tools
Send Data
ENCODE Tools
Lift-Over
Text Manipulation
Filter and Sort
1.
Join, Subtract and Group
Join two Datasets side by side on a specified field
Compare two Datasets to find common or distinct rows
Subtract Whole Dataset from another dataset
2.
Group data by a column and perform aggregate operation on other columns.
Column Join
Convert Formats
Extract Features
Fetch Sequences
Fetch Alignments
Get Genomic Scores
Operate on Genomic Intervals
Group (version 2.0.0)
Select data:
3: Joined
3.
Dataset missing? See TIP below.
Group by column:
c4
Ignore case while grouping?:
4. Click on
add new operation
Operations
Operation 1
Type:
Count
5.
On column:
c4
6.
Round result to nearest integer?:
NO
Remove Operation 1
Add new Operation
Execute
7.

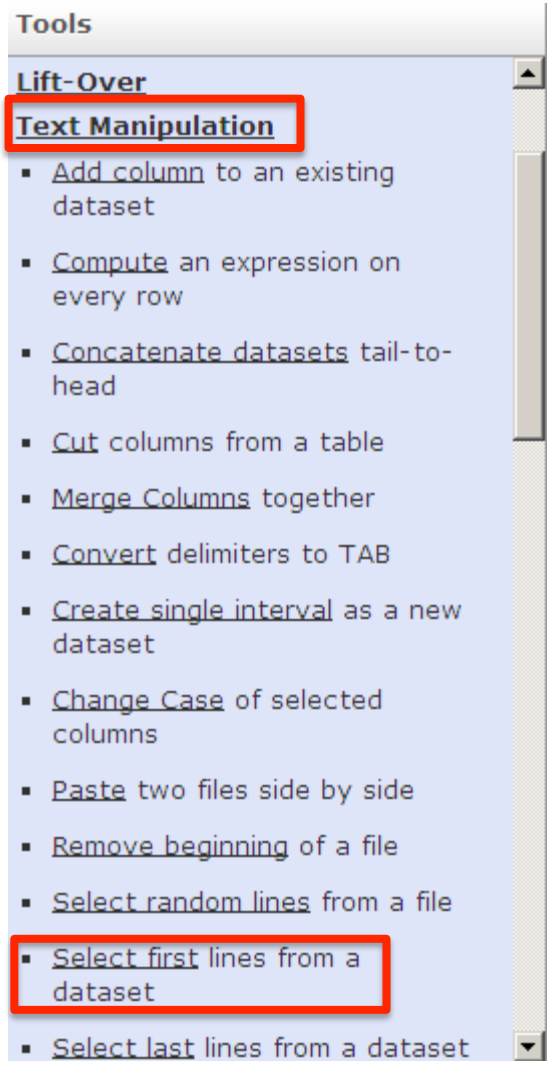
Now for each exon we know how many times they appeared in the previous "Joined" data file, i.e. the SNP numbers. However, we need to find out which one has the largest number in col 2. Note there are 6565 lines in the file

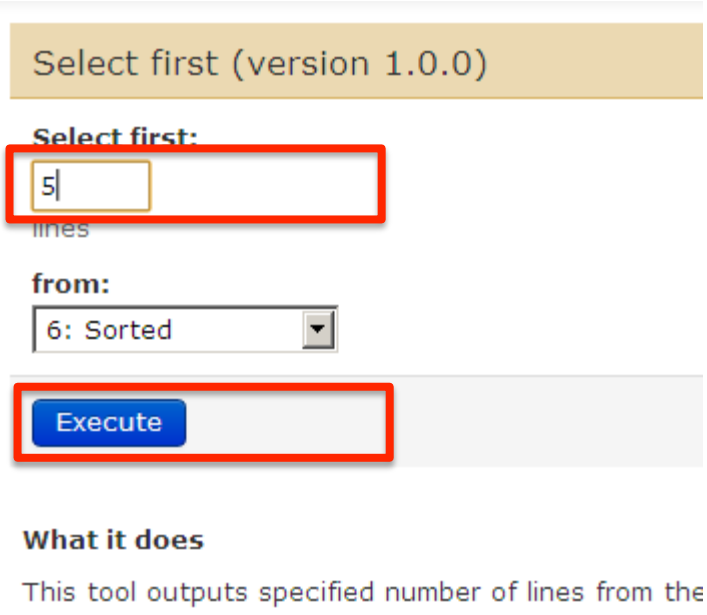



Galaxy
Tools
search tools
Get Data
Send Data
ENCODE Tools
Lift-Over
Text Manipulation
Filter and Sort
Filter data on any column using simple expressions
Sort data in ascending or descending order
Select lines that match an expression
GFF
Extract features from GFF data
Filter GFF data by attribute using simple expressions
Filter GFF data by feature count using simple expressions
Sort (version 1.0.1)
Sort Dataset:
5: Grouped 4th col
on column:
c2
with flavor:
Numerical sort
everything in:
Descending order
Column selections
Add new Column selection
Execute

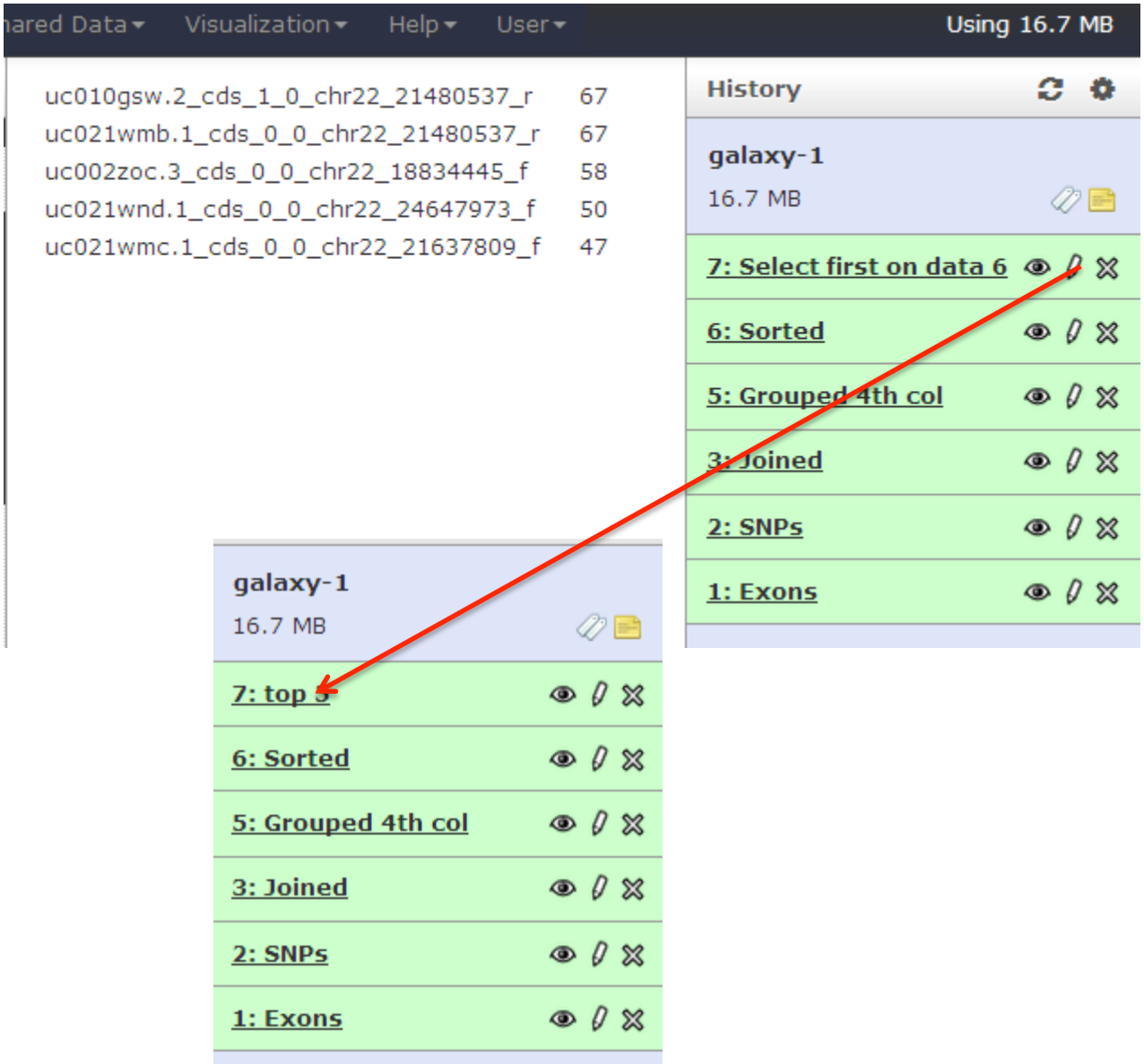
How do we pick out the top 5?

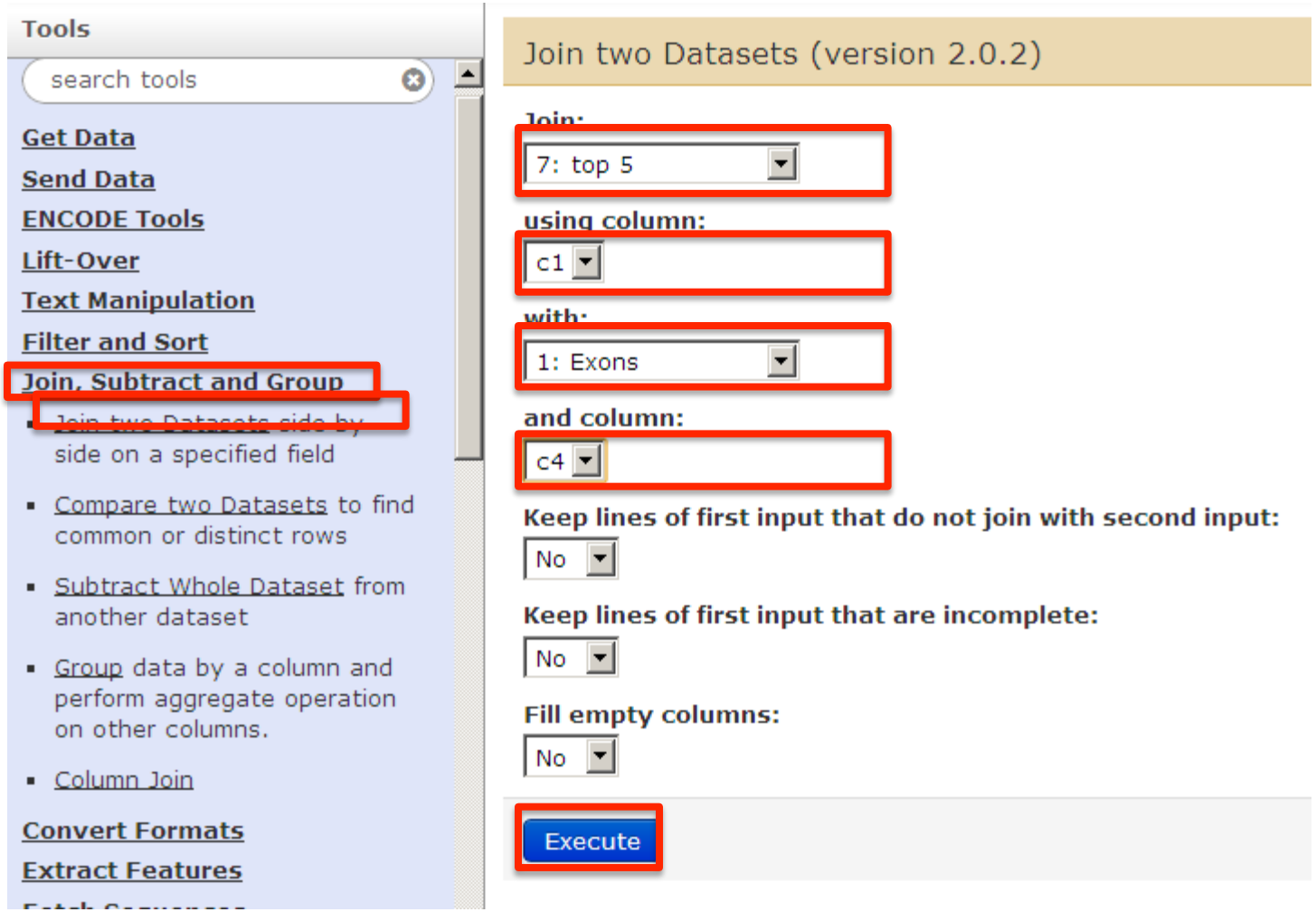



Tools
Lift-Over
Text Manipulation
Add column to an existing dataset
Compute an expression on every row
Concatenate datasets tail-to-head
Cut columns from a table
Merge Columns together
Convert delimiters to TAB
Create single interval as a new dataset
Change Case of selected columns
Paste two files side by side
Remove beginning of a file
Select random lines from a file
Select first lines from a dataset
Select last lines from a dataset

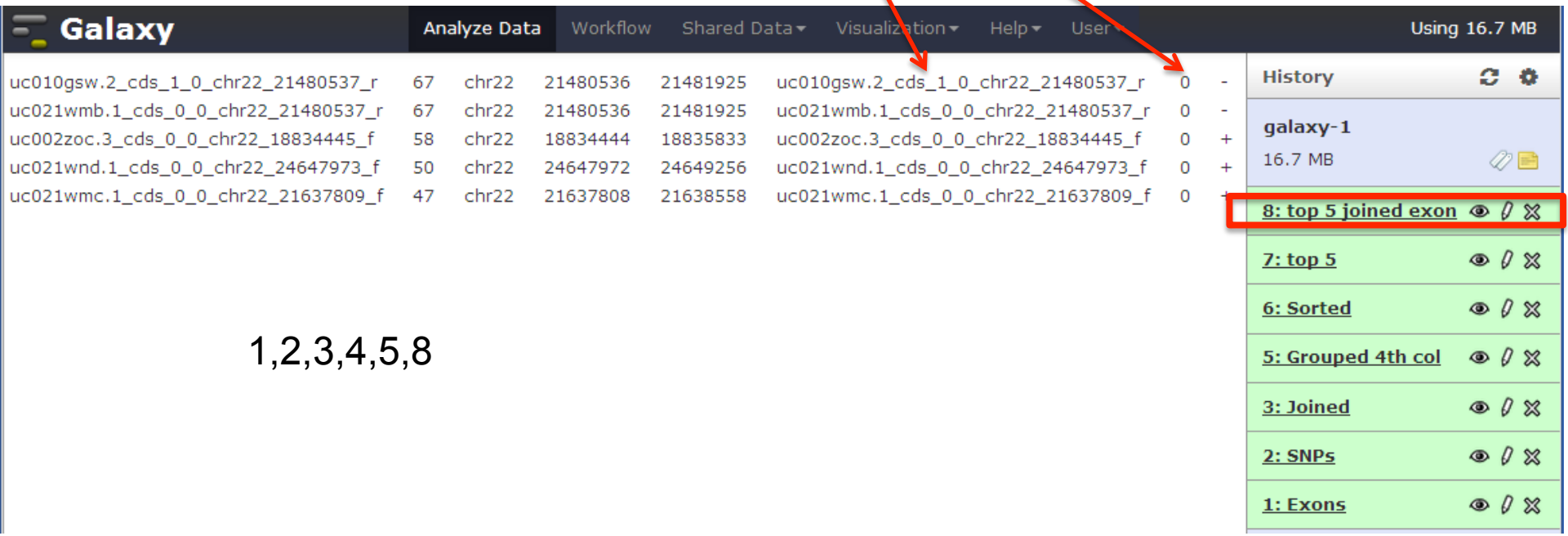

Select first (version 1.0.0)
Select first:
5
lines
from:
6: Sorted
Execute
What it does
This tool outputs specified number of lines from the

How do we find back the exon position info?

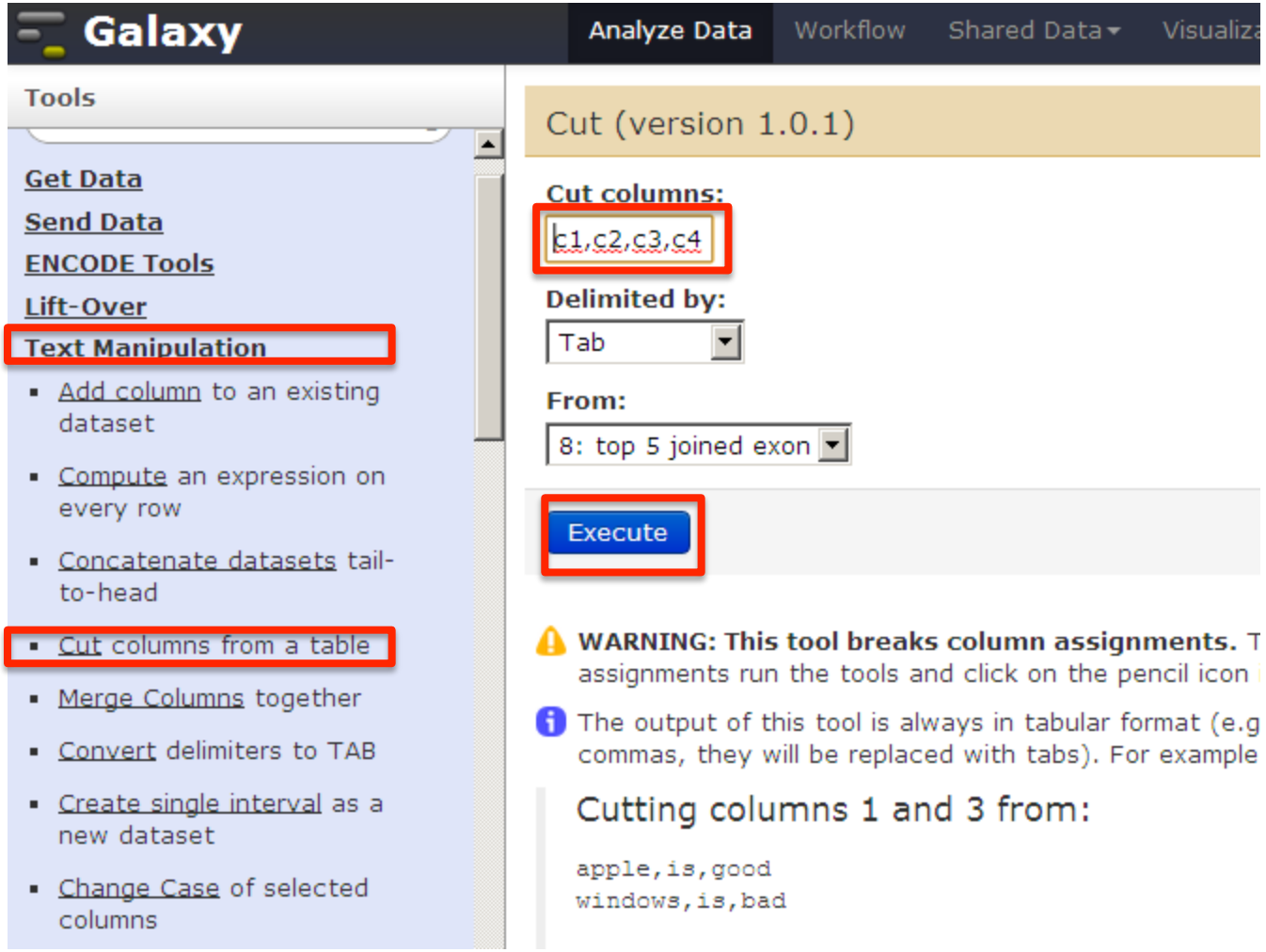



Tools
search tools
Get Data
Send Data
ENCODE Tools
Lift-Over
Text Manipulation
Filter and Sort
Join, Subtract and Group
Join two Datasets side by side on a specified field
Compare two Datasets to find common or distinct rows
Subtract Whole Dataset from another dataset
Group data by a column and perform aggregate operation on other columns.
Column Join
Convert Formats
Extract Features
Join two Datasets (version 2.0.2)
Join:
7: top 5
using column:
c1
with:
1: Exons
and column:
c4
Keep lines of first input that do not join with second input:
No
Keep lines of first input that are incomplete:
No
Fill empty columns:
No
Execute

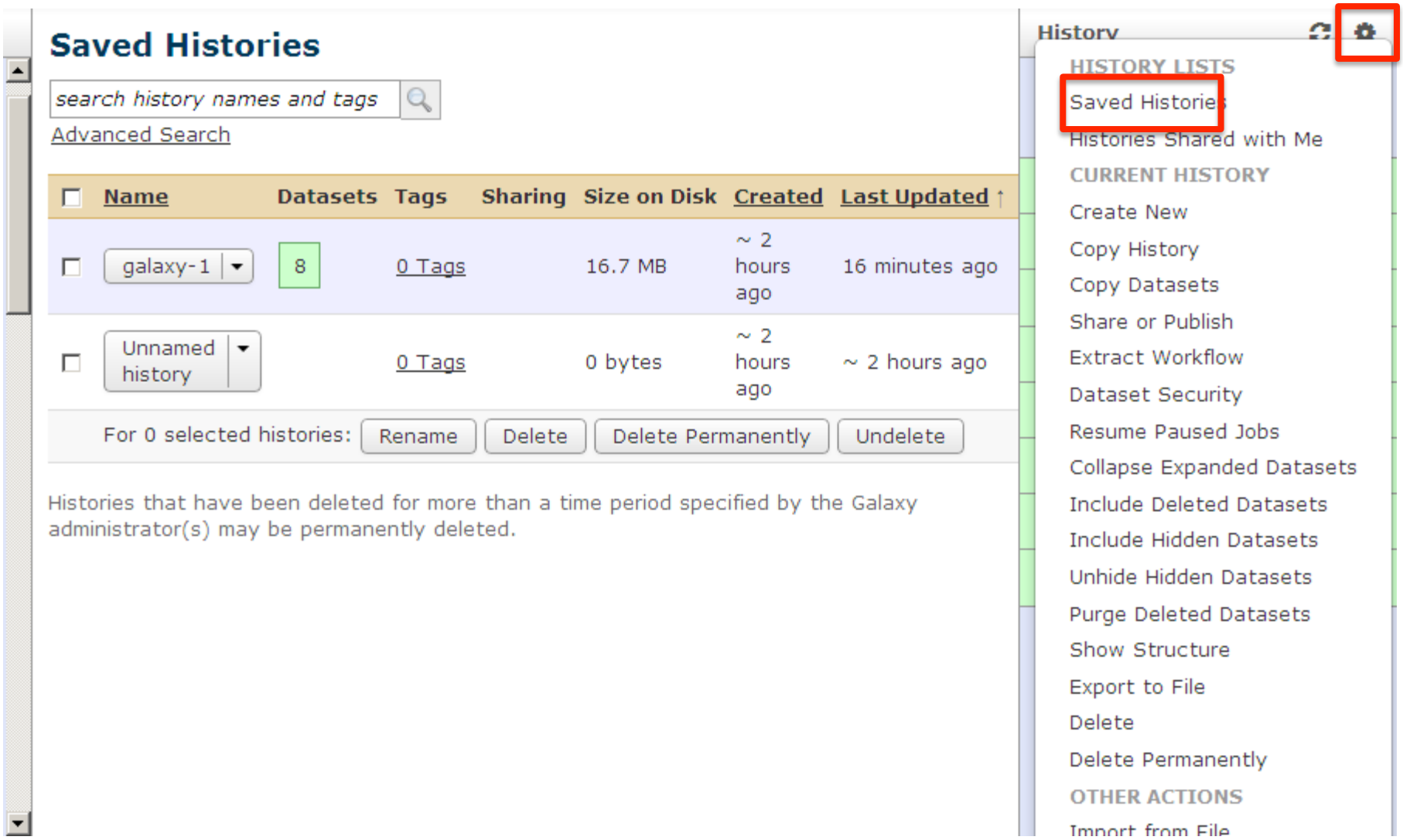
I do not need these columns

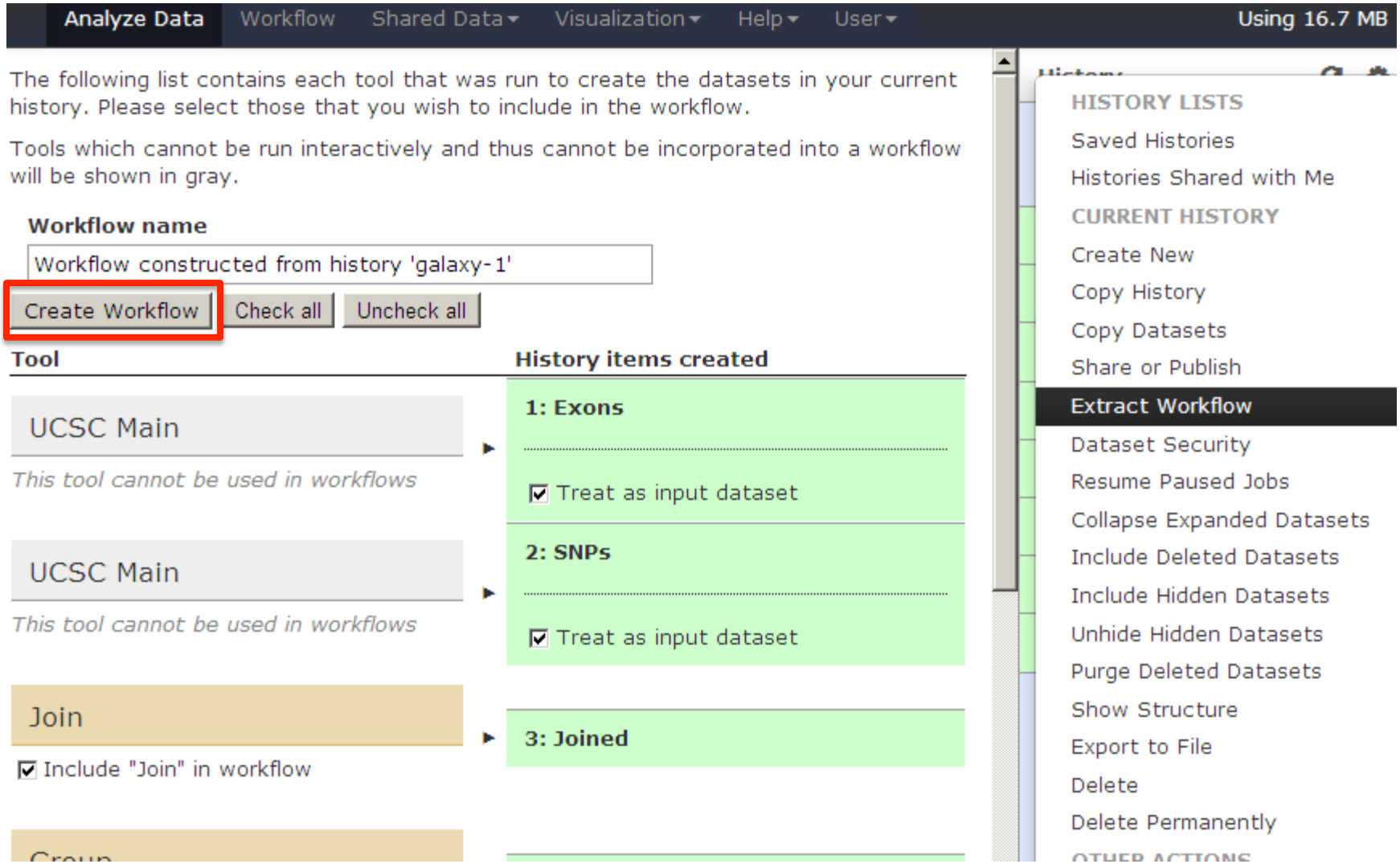


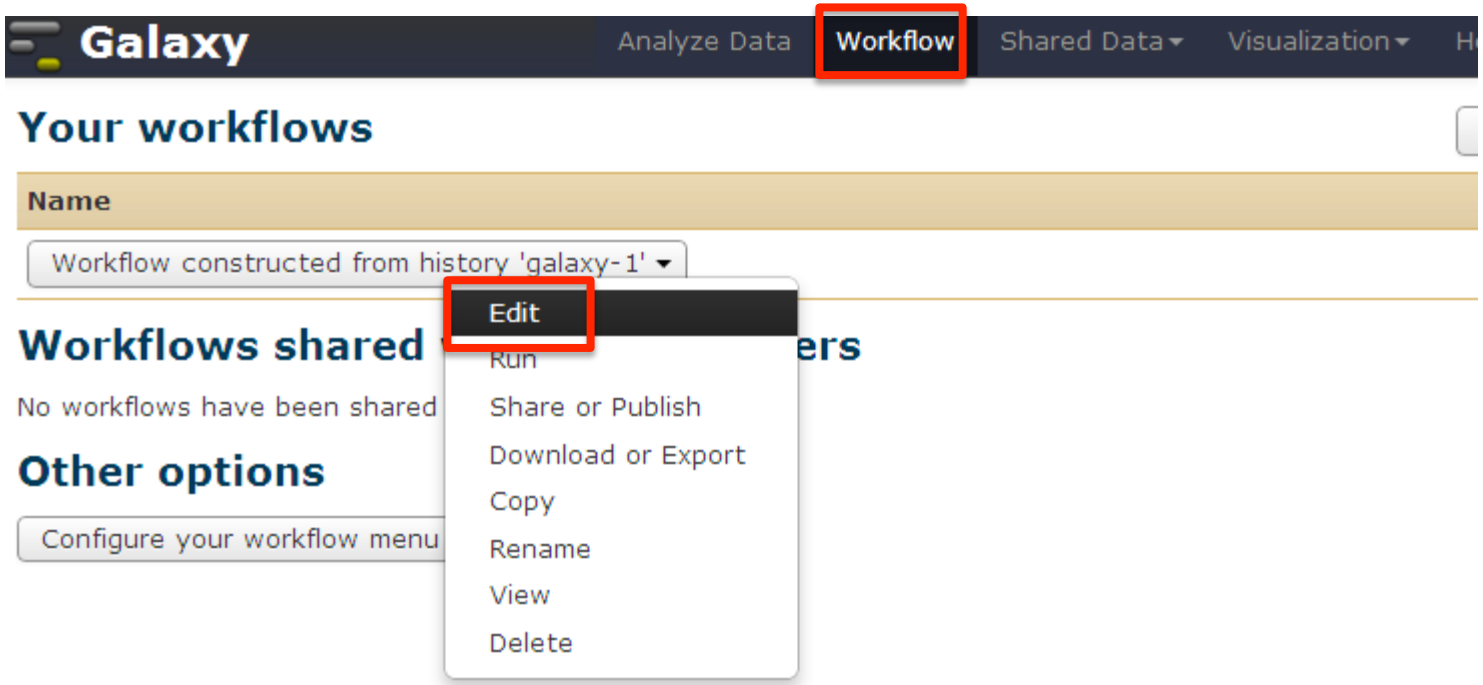
1,2,3,4,5,8

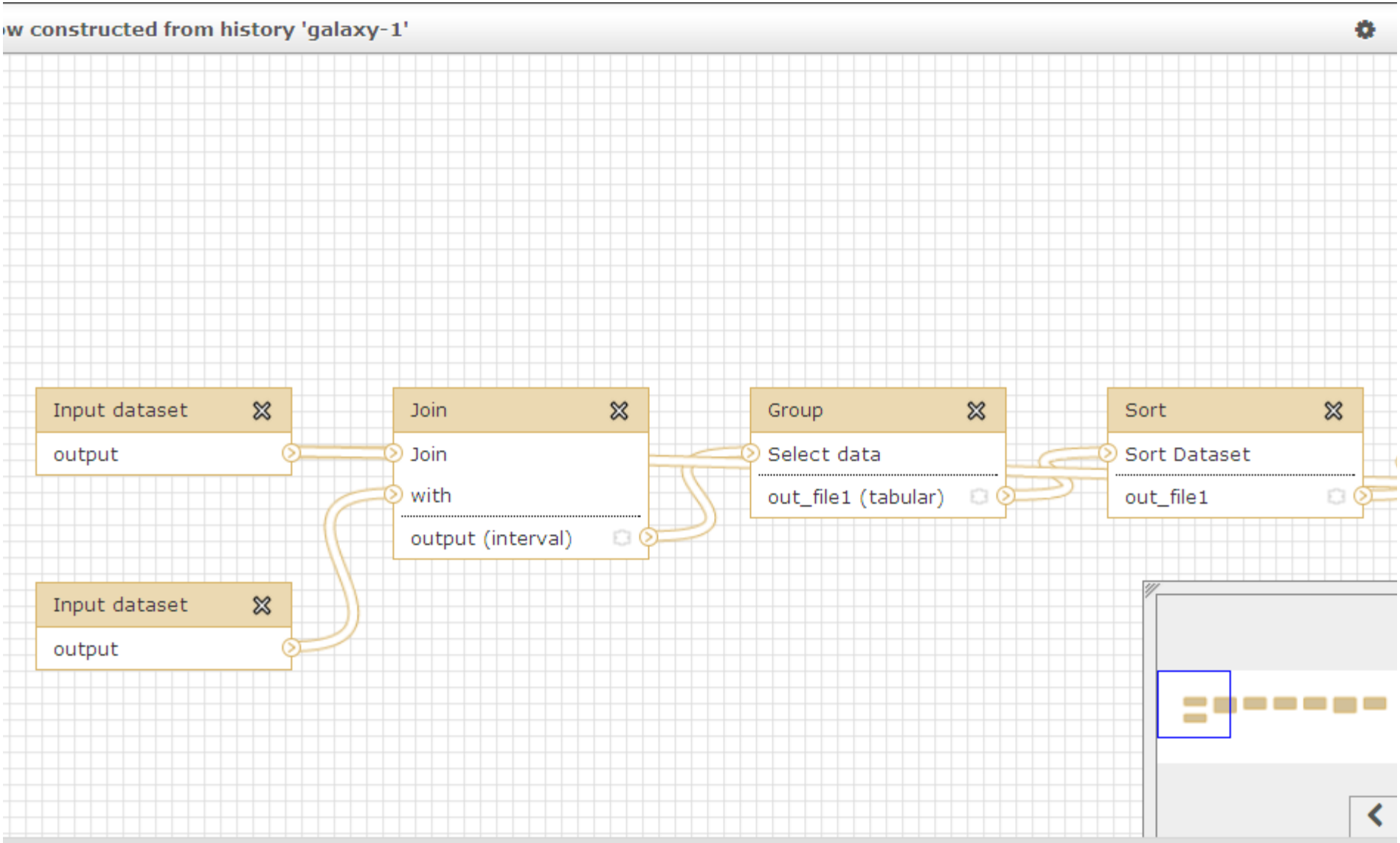

Galaxy
Analyze Data
Workflow
Shared Data
Visualiz
Tools
Get Data
Send Data
ENCODE Tools
Lift-Over
Text Manipulation
Add column to an existing dataset
Compute an expression on every row
Concatenate datasets tail-to-head
Cut columns from a table
Merge Columns together
Convert delimiters to TAB
Create single interval as a new dataset
Change Case of selected columns
Cut (version 1.0.1)
Cut columns:
c1,c2,c3,c4
Delimited by:
Tab
From:
8: top 5 joined exon
Execute
WARNING: This tool breaks column assignments. T
assignments run the tools and click on the pencil icon
The output of this tool is always in tabular format (e.g
commas, they will be replaced with tabs). For example
Cutting columns 1 and 3 from:
apple,is,good
windows,is,bad

uc010gsw.2_cds_1_0_chr22_21480537_r	67	chr22	21480536	21481925	-
uc021wmb.1_cds_0_0_chr22_21480537_r	67	chr22	21480536	21481925	-
uc002zoc.3_cds_0_0_chr22_18834445_f	58	chr22	18834444	18835833	+
uc021wnd.1_cds_0_0_chr22_24647973_f	50	chr22	24647972	24649256	+
uc021wmc.1_cds_0_0_chr22_21637809_f	47	chr22	21637808	21638558	+


Saved Histories
search history names and tags
Advanced Search
Name
Datasets
Tags
Sharing
Size on Disk
Created
Last Updated
galaxy-1
8
0 Tags
16.7 MB
~ 2 hours ago
16 minutes ago
Unnamed history
0 Tags
0 bytes
~ 2 hours ago
~ 2 hours ago
For 0 selected histories:
Rename
Delete
Delete Permanently
Undelete
Histories that have been deleted for more than a time period specified by the Galaxy administrator(s) may be permanently deleted.
History
HISTORY LISTS
Saved Histories
Histories Shared with Me
CURRENT HISTORY
Create New
Copy History
Copy Datasets
Share or Publish
Extract Workflow
Dataset Security
Resume Paused Jobs
Collapse Expanded Datasets
Include Deleted Datasets
Include Hidden Datasets
Unhide Hidden Datasets
Purge Deleted Datasets
Show Structure
Export to File
Delete
Delete Permanently
OTHER ACTIONS
Import from File


Analyze Data
Workflow
Shared Data
Visualization
Help
User
Using 16.7 MB
The following list contains each tool that was run to create the datasets in your current history. Please select those that you wish to include in the workflow.
Tools which cannot be run interactively and thus cannot be incorporated into a workflow will be shown in gray.
Workflow name
Workflow constructed from history 'galaxy-1'
Create Workflow
Check all
Uncheck all
Tool
History items created
UCSC Main
This tool cannot be used in workflows
1: Exons
Treat as input dataset
UCSC Main
This tool cannot be used in workflows
2: SNPs
Treat as input dataset
Join
Include "Join" in workflow
3: Joined
HISTORY LISTS
Saved Histories
Histories Shared with Me
CURRENT HISTORY
Create New
Copy History
Copy Datasets
Share or Publish
Extract Workflow
Dataset Security
Resume Paused Jobs
Collapse Expanded Datasets
Include Deleted Datasets
Include Hidden Datasets
Unhide Hidden Datasets
Purge Deleted Datasets
Show Structure
Export to File
Delete
Delete Permanently


Galaxy
Analyze Data
Workflow
Shared Data
Visualization
Your workflows
Name
Workflow constructed from history 'galaxy-1'
Edit
Run
Share or Publish
Download or Export
Copy
Rename
View
Delete
Workflows shared
ers
No workflows have been shared
Other options
Configure your workflow menu


w constructed from history 'galaxy-1'
Input dataset
output
Input dataset
output
Join
Join
with
output (interval)
Group
Select data
out_file1 (tabular)
Sort
Sort Dataset
out_file1

Re-use the workflow we just saved

Let’s try to use All SNP 137 and all the rest remains the same

Next lecture: Galaxy II