

Tools



search tools

[Get Data](#)[Send Data](#)[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[Filter GTF data by attribute values list](#)[Join, Subtract and Group](#)[Convert Formats](#)[Extract Features](#)[Fetch Sequences](#)[Fetch Alignments](#)

Filter (version 1.1.0)



Filter:

4: UCSC Main on Human: knownGene (genome)



Dataset missing? See TIP below.

With following condition:

c1=='chr22'

Double equal signs, ==, must be used as shown above. To filter for an arbitrary string, use the Select tool.

Number of header lines to skip:

0

Execute

Double equal signs, ==, must be used as "equal to" (e.g., c1 == 'chr22')

TIP: Attempting to apply a filtering condition may throw exceptions if the data type (e.g., string, integer) in every line of the columns being filtered is not appropriate for the condition (e.g., attempting certain numerical calculations on strings). If an exception is thrown when applying the condition to a line, that line is skipped as invalid for the filter condition. The number of invalid skipped lines is documented in the resulting history item as a "Condition/data issue". **TIP:** If your data is not TAB delimited, use *Text Manipulation->Convert*

Syntax

The filter tool allows you to restrict the dataset using simple conditional statements.

Columns are referenced with **c** and a **number**. For example, **c1** refers to the first column of a tab-delimited file

Make sure that multi-character operators contain no white space (e.g., <= is valid while < = is not valid)

History



search datasets



Unnamed history

6 shown, 7 [deleted](#)

11.5 MB

[13: Summary Statistics on data 4](#)

1 line, 1 comments

format: **tabular**, database: **hg19**

1	2	3	4
#sum	mean	stdev	0%
5.85083e+12	7.05259e+07	5.62337e+07	0

[5: Select first on data 4](#)[4: UCSC Main on Human: knownGene \(genome\)](#)

82,960 regions

format: **bed**, database: **hg19**display in IGB [View](#)display at Ensembl [Current](#)display at RViewer [main](#)display at UCSC [main](#)

1.Chrom	2.Start	3.End	4.Name	5	6.
chr1	11873	14409	uc001aaa.3	0	+