#Introduction to Galaxy Analyses tools

From peaks to genes tools

Goal to turn list of genomic regions into a list of possible target genes

	What for	What in	What out	Example operation, link
UCSC Main table browser	**Retrieve and export data from the Genome Browser** annotation track database	What in: **select** dataset, **define** region of interest (genome | position + identifiers), **retrieve and display data** **Send output to Galaxy:** displays results of query in Galaxy, a framework for interactive genome analysis. **Send output to GREAT:** displays the functional enrichments of the query results in GREAT, a tool for analysis of the biological function of cis-regulatory regions. **get output:** Submits a data query based on the specified parameters and returns the output. **Summary/statistics:** Displays statistics about the data specified by the parameters.	output formats BED - browser extensible data all fields from selected table selected fields from primary and related tables sequence GTF - gene transfer format (limited) BED - browser extensible data custom track hyperlinks to Genome Browser file type returned **plain text** - data is in ASCII format ***.gzip** compressed archieve format for Linux|Unix	https://genome.ucsc.edu/cgi-bin/hgTables?GALAXY_URL=https%3A//usegalaxy.eu/tool_runner&tool_id=ucsc_table_direct1&sendToGalaxy=1&hgta_compressType=none&hgta_outputType=bed Retrieve list of genes of an animals, viruses, insects for i.e. mice etc.
Select last lines from a dataset (tail)	**Keep the last X lines in a file**. It is a tool from text processing tools	**Keep last lines**| Keep from this line on Input file chr1 10 20 geneA chr1 50 80 geneB chr5 10 40 geneL	Result, the same file with last chosen lines chr1 50 80 geneB chr5 10 40 geneL	https://usegalaxy.eu/root?tool_id=toolshed.g2.bx.psu.edu/repos/bgruening/text_processing/tp_tail_tool/1.1.0 to compare the two files, to make sure that the chromosome names follow the same format
Replace Text in a specific column	**Performs find & replace operation** on a specified column in a given file. For more complex patterns, use the ***awk*** tool.	**Parameters** **In column:** i.e. 5 **Find pattern:** i.e. any symbol or letter expression „hello“ **Replace with:** text, or & (ampersand) and \\1 \\2 \\3 **Insert Replacement** (add new replacement for a new column)	The same text file in a *.gzip with replacement or replacements	*https://usegalaxy.eu/root?tool_id=toolshed.g2.bx.psu.edu/repos/bgruening/text_processing/tp_replace_in_column/1.1.3* For i.e. to convert the chromosome names, to change 20 and 21 to X and Y

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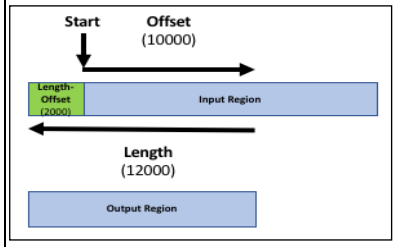
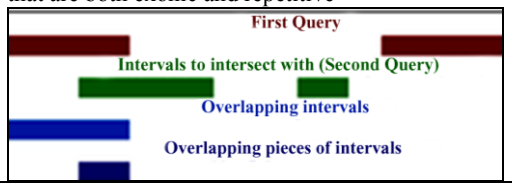
Get flanks returns flanking region/s for every gene	**This tool finds the upstream and/or downstream flanking region(s)** of all the selected regions in the input file.	Every line should contain at least 3 columns: Chromosome number, Start and Stop co-ordinates. **Parameters** **Region:** Whole feature| Around start | Around end **Location of the flanking region/s:** **Offset:** Use positive values to offset co-ordinates in the direction of transcription and negative values to offset in the opposite direction. **Length of the flanking region(s)** Use non-negative value	**Result** BED format file with flanking regions for every gene	https://usegalaxy.eu/root?tool_id=toolshed.g2.bx.psu.edu/repos/devteam/get_flanks/get_flanks1/1.0.0  Adding promoter regions, i.e. to get regions 2kb bases upstream of the start of the gene to 10kb bases downstream of the start (12kb in length)
Convert Genomic Intervals To BED	**Converts** Genomic Intervals To BED	Genomic intervals file	BED file	https://usegalaxy.eu/root?tool_id=CONVERTER_interval_to_bed_0
Intersect	**Intersect the intervals** of two datasets	Use "edit attributes" to set chromosome, start, end, and strand columns to set file to interval format if it doesn't appear in the pulldown menu The order of the datasets is important **Parameters** **Return:** Overlapping intervals | Overlapping pieces of intervals **Of** first dataset: **[the UCSC file format BED]** **that intersect** second dataset**:** **for at least: [1 or more]**	The intersection of two queries that are found.	https://usegalaxy.eu/root?tool_id=toolshed.g2.bx.psu.edu/repos/devteam/intersect/gops_intersect_1/1.0.0 i.e. task could be to extract the genes which overlap/intersect with peaks regions in a dataset **OR** e.g. to find all exons containing repeats **OR** all regions that are both exonic and repetitive 
Group data by a column and perform aggregate operation on	This tool allows you to group the input dataset by a particular column and perform aggregate functions: Mean, Median, Mode, Sum, Max, Min,	**Select Data:** [Data input 'input1' (tabular)] **Group by column**: [column number] **Ignore case while grouping:** [on|off] **Ignore lines beginning with these characters** [character's list]	File Group on data with executed grouping operations in TAB format	https://usegalaxy.eu/root?tool_id=Grouping1

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other columns.	Count, Concatenate, and Randomly pick on any column(s).	**Operation:** insert operation **[type e.g. mean & on column & round &replace non numeric data** | leave empty for no replacements.] You can add several operations following one by one. If your data is not TAB delimited, use *Text Manipulation->Convert*		
Compute an expression on every row	This tool computes an ex pression for every row of a dataset and appends the result as a ne w column (field).	Tool needs TAB data **Parameters** **Add expression**: *[e.g. c2+c5]* **as a new column to**: [the interval format file] **Round result?:** No | Yes **Avoid scientific notation:** No | Yes **Input has a header line with column names?** No | Yes Columns are referenced with **c** and a **number**. For example, **c1** refers to the **first column** of a tab-delimited file c3-c2 will add a length column to the dataset if c2 and c3 are start and end position	TAB file with computation, for e.g. in a new added column	https://usegalaxy.eu/root?tool_id=toolshed.g2.bx.psu.edu/repos/devteam/column_maker/Add_a_column1/1.6 To generate a new BED file from the peak file that contains the positions of the peak summits.
Cut columns from a table	This tool selects (cuts out) specified columns from the dataset.	WARNING: This tool breaks column assignments. **To re-establish column assignments run the tools and click on the pencil icon in the latest history item.** **Parameters** **Cut columns** for e.g. c1, c2 **Delimited by** Tab | Whitespace | Dot | Comma etc. **From** [dataset in csv.]	The output of this tool is always in tabular format (e.g., if your original delimiters are commas, they will be replaced with tabs). a , is , b c , is , d → a b c d	https://usegalaxy.eu/root?tool_id=Cut1 **Input dataset c1,c2,c3,c4,c5,c6** a 1 # %0 + b 2 $ %0 + **cut** on **c1,c4,c6** a 1 # %0 + → a %+ b 2 $ %0 + → b %+ **cut** on columns "**c6,c5,c4,c1**" returns + 0 %a + 0 %b **cut** on **c8,c7,c4** . . % . . %

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<table>
<tr>
<td>Join two Datasets side by side on a specified field</td>
<td>This tool joins lines of two datasets on a common field.</td>
<td>⚠This tool will force the ouput datatype to tabular. To change metadata assignments click on the "edit attributes" link of the history item generated by this tool.
ℹTIP: If your data is not TAB delimited, use Text Manipulation->Convert
Parameters
Join [file as tabular]
using column [column by its number e.g. 3 refers to third column]
with [file as tabular]
and column [column number e.g. 5]</td>
<td></td>
<td>https://usegalaxy.eu/root?tool_id=join1
To add in the end of BED file list of Gene names to RefSeq Gene identifiers in the table -> i.e. join two files
Joining 4th column of Dataset1
<table><tr><td>chr1</td><td>10</td><td>20</td><td>geneA</td></tr><tr><td>chr1</td><td>50</td><td>80</td><td>geneB</td></tr><tr><td>chr5</td><td>10</td><td>40</td><td>geneL</td></tr></table>
With the 1st column of Dataset2
<table><tr><td>geneA</td><td>tumor suppressor</td></tr><tr><td>geneB</td><td>Foxp2</td></tr><tr><td>geneC</td><td>Gnas1</td></tr><tr><td>geneE</td><td>INK4a</td></tr></table>
Result (Keep the header lines –No)
<table><tr><td>chr1</td><td>10</td><td>20</td><td>geneA</td><td>geneA</td><td>Tumor suppressor</td></tr><tr><td>chr1</td><td>50</td><td>80</td><td>geneB</td><td>geneB</td><td>Foxp2</td></tr></table>
Keep the header lines –Yes
<table><tr><td>chr1</td><td>10</td><td>20</td><td>geneA</td><td>geneA</td><td>Tumor suppressor</td></tr><tr><td>chr1</td><td>50</td><td>80</td><td>geneB</td><td>geneB</td><td>Foxp2</td></tr><tr><td>chr5</td><td>10</td><td>40</td><td>geneL</td><td></td><td></td></tr></table></td>
</tr>
<tr>
<td>Sort data in ascending or descending order</td>
<td>The tools sorts the input file</td>
<td>Sort Query
Parameters
Number of header lines
Column selection
On column
in Ascending | Descending order
Flavor Fast numeric sort (-n), General numeric sort (scientific notation -g),Natural/Version sort (-V) Alphabetical sort ,Human-readable numbers (-h) Random order (-R)</td>
<td>Output file contains</td>
<td>https://usegalaxy.eu/root?tool_id=toolshed.g2.bx.psu.edu/repos/bgruening/text_processing/tp_sort_header_tool/1.1.1
For listing unique genes that was unsorted.
Example of alphabetical order
<table><tr><td>chr13</td></tr><tr><td>chr2</td></tr><tr><td>chr20</td></tr><tr><td>chr4</td></tr></table></td>
</tr>
</table>

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Formats from Peaks and Genes

GNU zip (gzip) –compressed archive format for Linux and Unix systems

Txt. – plain text file

Interval format is a Galaxy format for representing genomic intervals. It is tab-separated, but has the added requirement that three of the columns must be:

- chromosome ID
- start position (0-based)
- end position (end-exclusive)

An optional strand column can also be specified, and an initial header row can be used to label the columns, which do not have to be in any special order. Unlike BED format (see below) arbitrary additional columns can also be present.

The **BED - Browser Extensible Data** format provides a flexible way to encode gene regions. BED lines have three required fields:

- chromosome ID
- start position (0-based)
- end position (end-exclusive)

There can be up to and nine additional optional fields, but the number of fields per line must be consistent throughout any single set of data.

UCSC Formats https://genome.ucsc.edu/FAQ/FAQformat.html

GFF (General Feature Format) lines are based on the Sanger **GFF2 specification**. GFF lines have nine required fields that must be tab-separated. If the fields are separated by spaces instead of tabs, the track will not display correctly.

TAB One or more columns of text data separated by tabs.