

Installation and Usage of Chromatra

Version

- Chromatra: 1.0.0
- README: 1.0.1

Package content

- `chromatral.py` - the Chromatra_L module
- `chromatral.xml` - the Chromatra_L tool description for Galaxy
- `chromatrat.py` - the Chromatra_T module
- `chromatrat.xml` - the Chromatra_T tool description for Galaxy
- `H2AZ_WT_AllData_sample.gff3` - sample data for chr 1
- `sample_transcripts_for_Chromatra_L.tsv` - sample data for chr 1
- `sample_transcripts_for_Chromatra_T.tsv` - sample data for chr 1
- `README.pdf` - this PDF

Installation

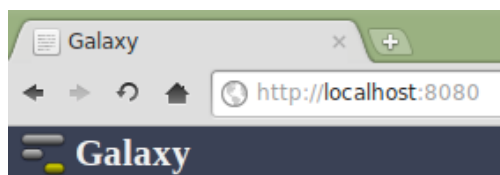
- Create a folder named `chromatra` inside `<galaxy_install_dir>/tools/` and copy the package content into it.
- Edit `<galaxy_install_dir>/tool_conf.xml` and add the following lines in the `<toolbox>` section:

```
<section name="CHROMATRA" id="chromatra">
  <tool file="chromatra/chromatral.xml" />
  <tool file="chromatra/chromatrat.xml" />
</section>
```
- Restart Galaxy

Usage

Since the workflow for both Chromatra modules is nearly identical, the following section demonstrates the process for Chromatra_T only.

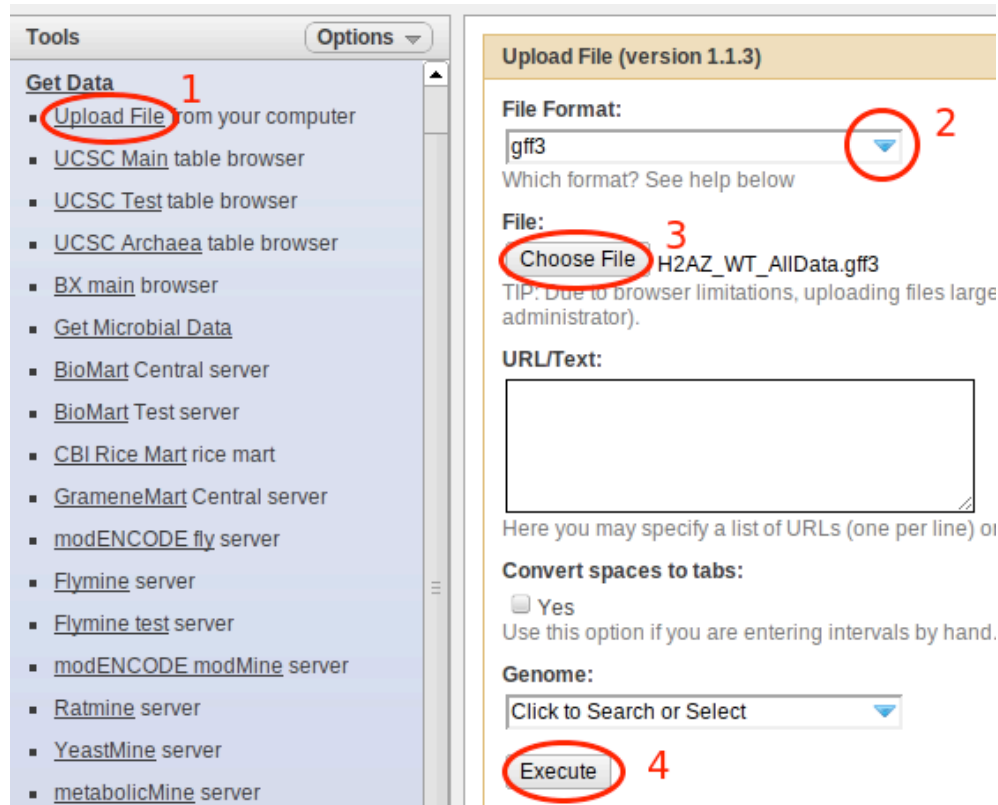
Once the Chromatra modules are installed, point your browser to the running Galaxy instance. The default setting would be: `http://localhost:8080` if Galaxy is running on a local installation.



From the *Tools* menu, select *Get Data* and then *Upload File*. Choose the *GGF3* format and select the *H2AZ_WT_AllData_sample.gff3* file from the Chromatra installation package. This is a sample line of data from that file illustrating its layout:

seqID	source	type	start	end	score	strand	phase	attributes
chr1	.	Z_over_Input	1	25	0.89557	.	.	.

This file contains the normalized enrichment scores for chromosome 1 derived from a ChIP-on-chip experiment looking at the histone variant H2A.Z in *S. cerevisiae*:

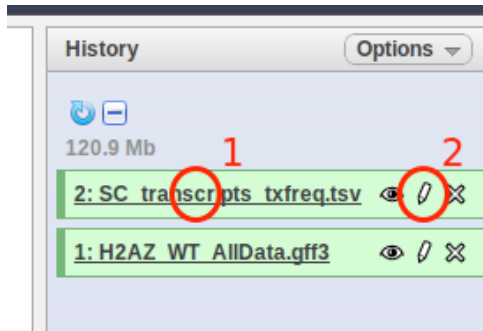


Repeat the process and upload the *sample_transcripts_for_Chromatra_T.tsv* file, which contains the transcript description for chromosome 1. This is the data layout of the file for Chromatra_T: (for Chromatra_L the last column does not exist, otherwise the layout is identical)

feature symbol	chr	strand	start	end	txrate
YAL062W	1	1	31144	33042	0.4

In the upload dialog, Leave the *File Format* option on *Auto-detect*, and wait for both files to appear in the *History* panel of Galaxy. Each entry should be highlighted in green.

Click on the transcript file to open a preview of its content and then the pen icon to adjust the attributes:



Change the file attributes as follows to adjust the column order:

Edit Attributes

Name:

Info:

Database/Build:

Number of comment lines:

Chrom column:

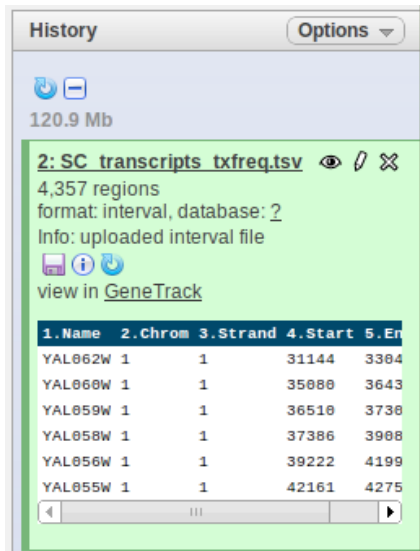
Start column:

End column:

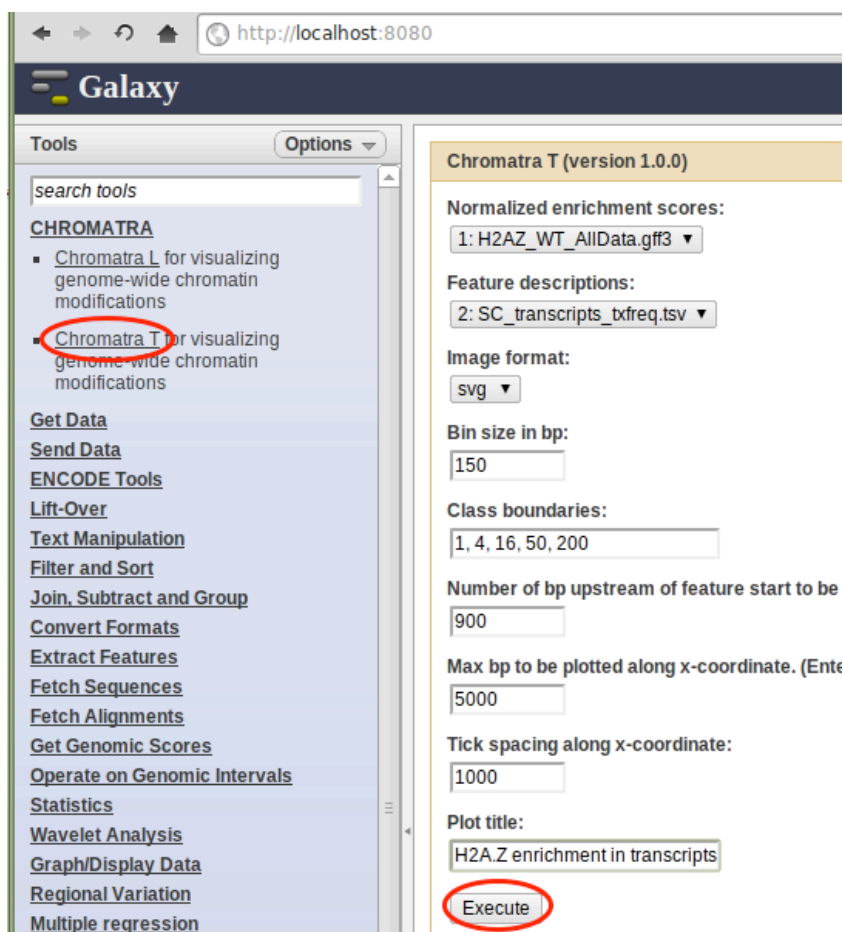
Strand column (click box & select):

Name/Identifier column (click box & select):

After saving the adjustments, the *History* panel should look like this for the transcript file: (Note the order of column names.)



From the *Tools* menu, select *Chromatra T* from the *Chromatra* section. Use the H2A.Z data as input for the enrichment scores, the transcript file as input for the feature descriptions and adjust the remaining parameters as follows:



Upon clicking *Execute*, a new entry in the *History* panel will appear that should be highlighted in green shortly after. Clicking on the eye icon will open the *Chromatra_T* plot in the main panel.

Downloading the image can be done by clicking on the floppy disk icon in the *History* panel entry for the plot:

The screenshot displays the Galaxy web interface. The main panel shows a heatmap titled "H2A.Z enrichment in transcripts of S. c." with a color scale from -8 to 8. The x-axis is "Distance from feature start (bp)" ranging from -900 to 5000. The y-axis is "Feature class (low to high)". The heatmap shows a vertical line at 0 bp, with enrichment values ranging from approximately -8 to 8. The History panel on the right shows a list of jobs, with the top job "2: Chromatran on data 2 and data 2" circled in red. A red "1" is next to the job name and a red "2" is next to the floppy disk icon. Below the heatmap is a "Tools" panel with various analysis options.