Chromosome tissue interaction analysis and visualisation software `HiCInteractionExplorer`

Short description

`HiCInteractionExplorer` is designed to visualize tissue interaction for a particular chromosome as a graph diagram using data from the file in JSON format.

Setup

Software module `HiCInteractionExplorer.html` together with data file `segmTissueBitsGraph.json` should be copied in the same directory and at the same level there should be directory `Utils` containing the following `JavaScript` files:

- `draw.js,`
- `st.js,`
- `bootstrap.min.js,`
- `bootstrap.min.css,`
- `d3.min.js,`
- `vis-network.min.js,`
- `vis-network.min.css,`
- `jquery-3.1.1.min.js,`
- `underscore-min.js.`

File `HiCInteractionExplorer.html` should be executed. The data file may be replaced by another data file in the same format.

Supported Browsers

`HiCInteractionExplorer.html` is designed and tested for Firefox version 62.0.3

Main window

Fig. 1. Tool ribbons

In the Fig.1 main tools of the `HiCInteractionExplorer` are depicted: two ribbons - one with radio buttons for chromosome selection and the second with checkboxes for choosing tissues. For starting computations and visualization, there is the main button "Upload chr" at the right.

To start the process, one chromosome should be chosen (radio button from the upper ribbon should be checked) and one or more tissues should be chosen (checkboxes from the lower ribbon checked). After that button "Upload chr" should be pushed and graph diagram will appear at the lower part of the screen. Example of the obtained diagram is given in Fig. 2.

It should be emphasized that together with visualization there appears also additional tools (checkbox "freeze layout" and button "Upload settings") and information panel at the top of the screen.

In the information panel chosen visualization parameters (number of the chromosome, list of the chosen tissues) together with statistics of the graph diagram (number of nodes and edges, distribution of connected component sizes) are given.
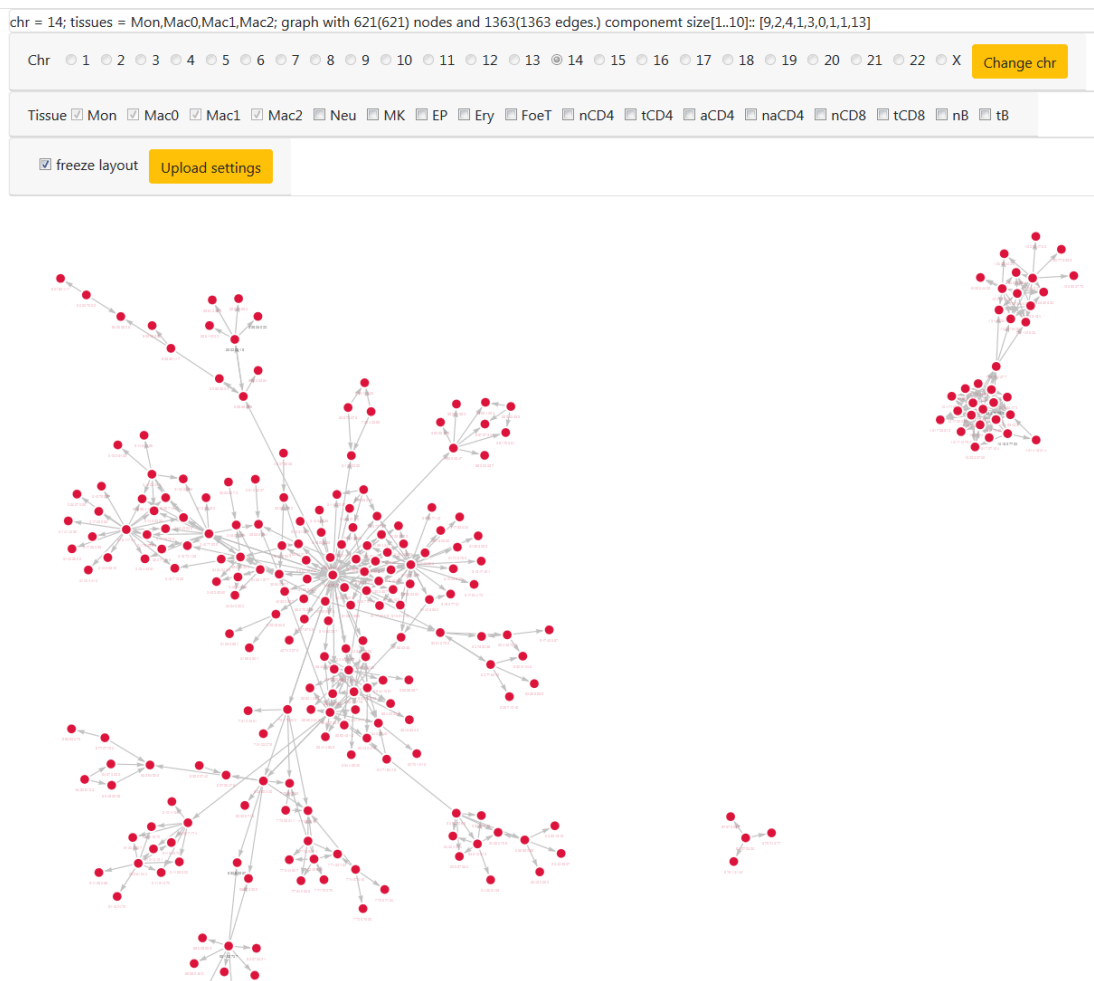

Fig. 2. Example of the base diagram (chromosome:14, tissues: Mon, Mac0, Mac1, Mac2).

Further data analysis can be made by choosing additional tissues. After tissues are chosen, analysis and visualisation can be performed by pressing "Upload settings".

Chr ○1 ○2 ○3 ○4 ○5 ○6 ○7 ○8 ○9 ○10 ○11 ○12 ○13 ◉14 ○15 ○16 ○17 ○18 ○19 ○20 ○21 ○22 ○X [Change chr]

Tissue ☑Mon ☑Mac0 ☑Mac1 ☑Mac2 ☐Neu ☐MK ☑EP ☑Ery ☐FoeT ☐nCD4 ☐tCD4 ☐aCD4 ☐naCD4 ☐nCD8 ☐tCD8 ☐nB ☐tB

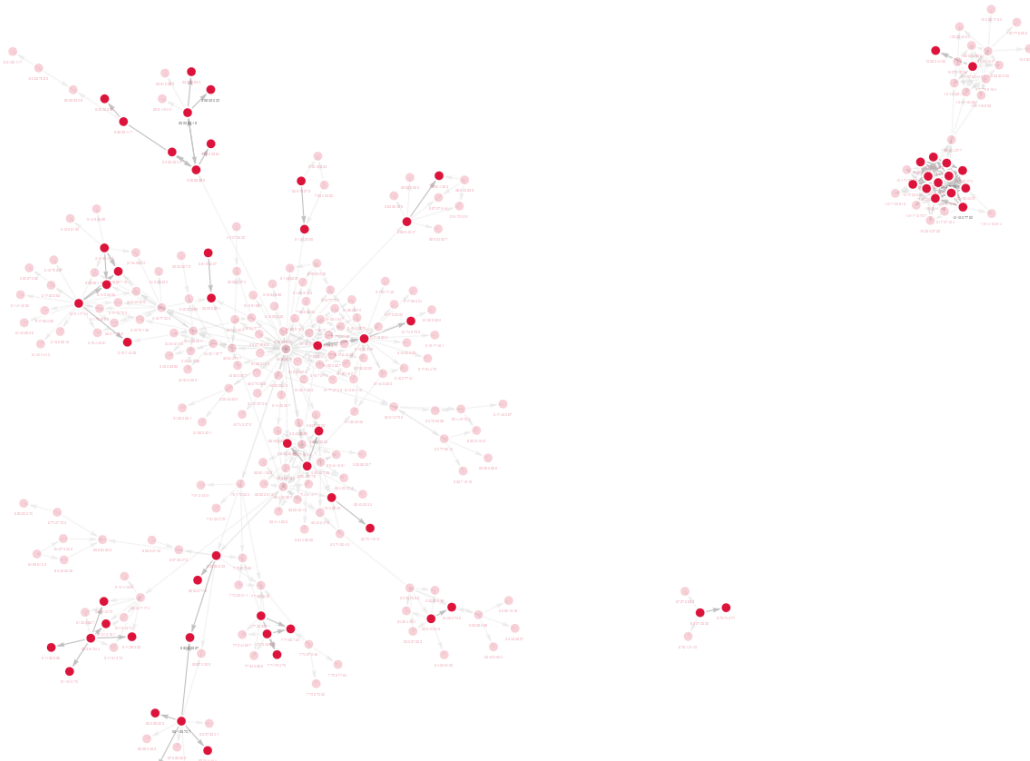☑freeze layout [Upload settings]

Fig. 3. Example of the updated diagram after adding tissues EP and Ery.

Part of interactions not corresponding to the updated set of tissues is shown as dim while actual interactions still are bright.

Checkbox "freeze layout" can be used to prevent movement of diagram nodes and stop them at particular positions.