

Getting started in Reveal

Günter Jäger

1 Getting started

1.1 Starting Reveal

In order to start Reveal one has to start Mayday first. Reveal can then be found in the Mayday-Menu.

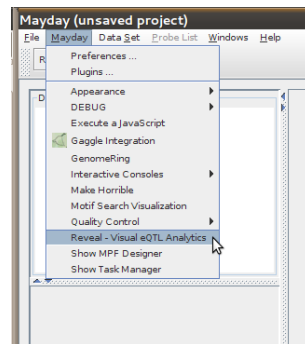


Abbildung 1: Starting Reveal

1.2 GUI Elements

Reveal consists mainly of two parts. On the left the different data types are listed in the data overview frame. On the right the different available visualizations are grouped using tabs.

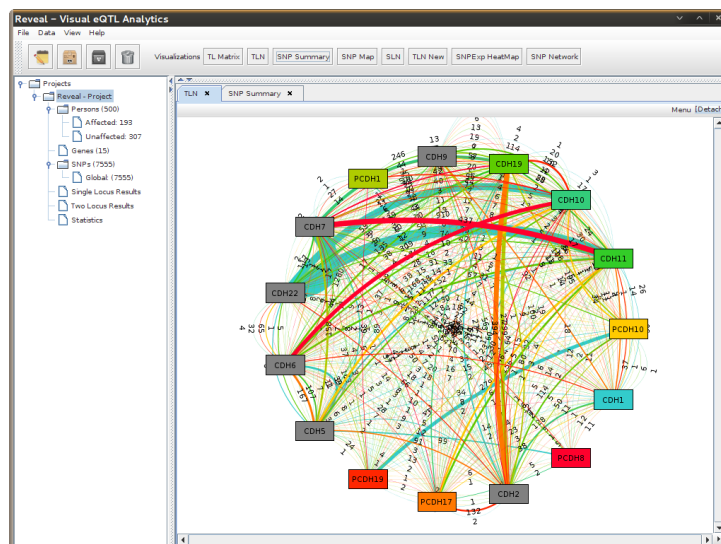


Abbildung 2: Reveal's Graphical User Interface

1.3 Creating a new project

New projects can be created by selecting “New Project” from the File-Menu. A file loading dialog pops up, where the user can define the paths to the different files needed for the analysis.

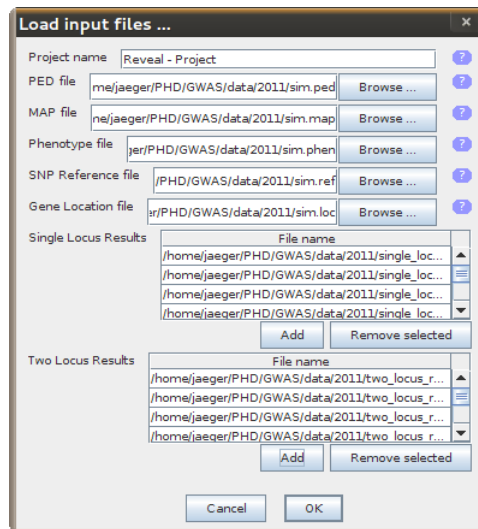


Abbildung 3: Creating a new project using the BioVis 2011 Contest data set.

After that some file specific information can be given in order to correctly parse the input files. For the BioVis 2011 data set the default values are fine and the parsing process can be started.

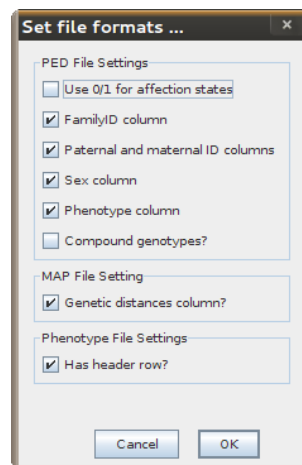


Abbildung 4: Setting file specific parameters to ensure correct parsing.

1.4 Visualizing the data

In order to visualize your data in Reveal, simply select one of the available visualizations from the icon-bar or from the corresponding View-Menu in the menubar. Visualizations are created automatically using the necessary available data from the project selected in the data overview frame. New visualizations appear as a new tab in the visualization frame. However, visualizations can also be detached from the Reveal-GUI via the corresponding “Detach-Button” on the upper right of each visualization.

If different visualizations from the same project are created, these visualizations are linked to each other automatically. This means, that selections (e.g. of SNPs) in one visualization automatically result in a selection of the same elements in all the other visualizations that were created for the specific project.

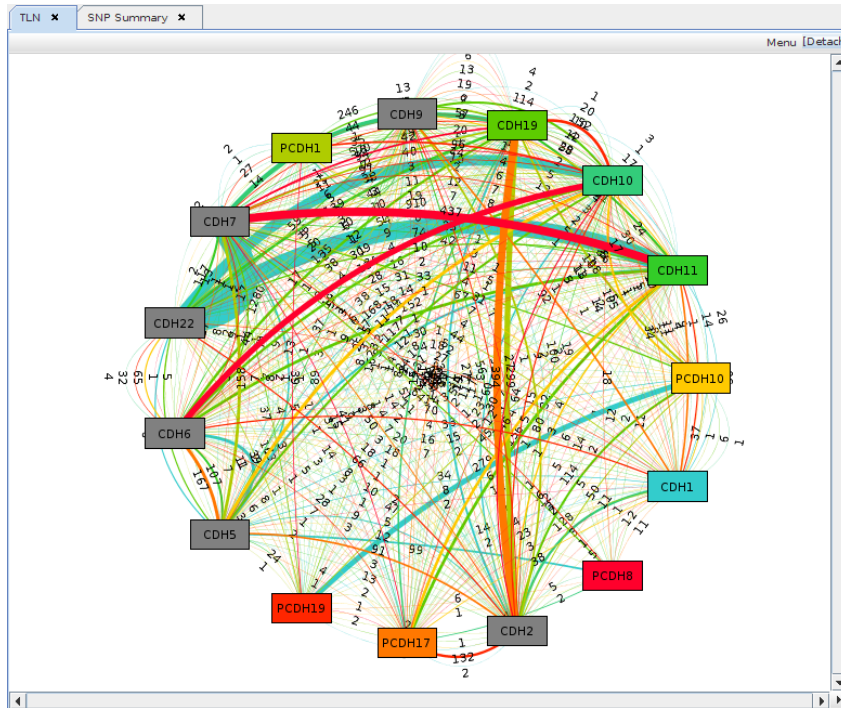


Abbildung 5: Example visualization in Reveal. Visualizations can be detached using the corresponding “Detach-Button” on the upper right.

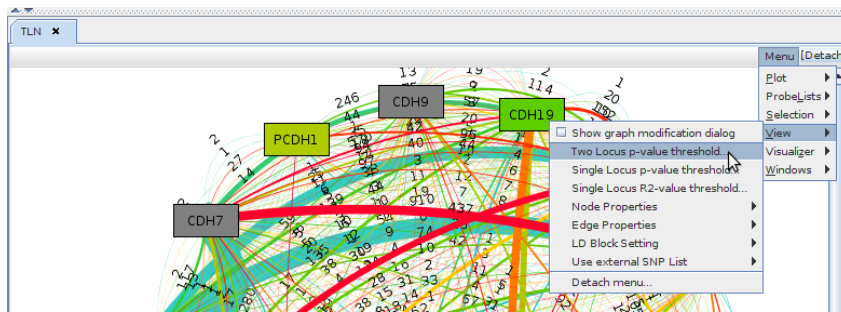


Abbildung 6: Example showing the View-Menu of the Association Gene Network Visualization (TLN).

2 Visualizations

Every visualization in Reveal allows for several types of interaction. Usually zooming is implemented for all visualizations. Furthermore, every visualization has a specific Menu that offers further possibilities to explore the displayed data. The Menu is located on the upper right next to the “Detach-Button”. This Menu contains an additional submenu “View” that shows all possibilities for manipulating a specific visualization.

2.1 Association Graph

The easiest way to display the association graph is by clicking on the TLN-Button in the iconbar. This creates a new tab showing the unfiltered association graph. The association graph allows for different types of interaction, such as zooming (Mouse-Wheel), moving the network around (drag&drop in “Transformation Mode”), selecting nodes or edges (mouse click in “Picking Mode”) and some more. The user can switch between the two mouse modes by clicking on the little arrow on the bottom right of the association graph.

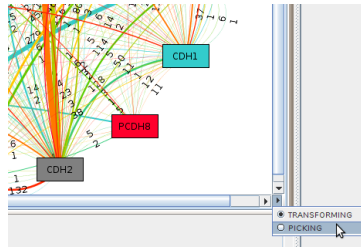


Abbildung 7: Changing the mouse mode in the association graph.

Further interaction possibilities, such as edge filtering, edge layout, node layout and many more can be applied via the “View-Submenu” from the association graph’s “Menu”.

2.2 Genotype View

The genotype view can be created by clicking on the “SNP Summary-Button” from Reveal’s iconbar. As the association graph the genotype view also has a individual menu that allows one to interact with the visualizations in order to e.g. filter for specific SNPs based statistical values, selections in an other visualization etc. The genotype view by itself also offers some direct interaction possibilities, such as selecting SNPs of interest (mouse click on the specific SNP column).

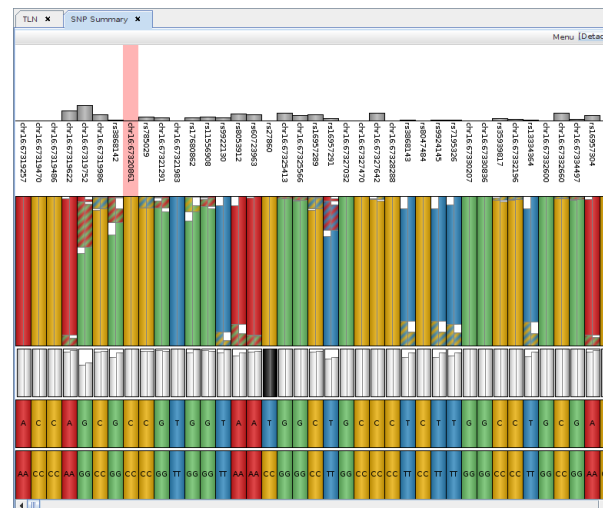


Abbildung 8: Example of the Genotype View with one selected SNP. The selected SNP is highlighted with a red background.

2.3 Mayday Visualizations

For detailed information on how to use Mayday and its visualizations please read the documentations on the Mayday Website (<http://www.microarray-analysis.org>).

3 Further Comments

Reveal is an ongoing project and many new features are currently under heavy development. As soon as those features are bug-free and ready to be used they will also be described in this tutorial.