

EINVis Software User Manual

This document describes the “Input Dataset Format”, “User Interfaces” and “User Interactions” for the EINVis software.

1. Input Dataset Format

EINVis needs two input files: Nodes file and Edges file.

Nodes file: Each line contains the information for one SNP. Each line contains four tokens: chromosome id, gene name, SNPs name and single-locus test statistic. The four tokens are separated by space symbol “ ”. The SNPs are ordered by their positions on the chromosomes. One example Nodes file is shown as follows:

Table 1. Nodes file format

Line #	chrom_id gene_name SNP_name single-locus_test_statistic
1	1 CA6 rs7513804 0.382463
2	2 IL1A rs1894399 0.712872
3	7 MTPN rs1488004 0.477534
4	11 CD3E rs3782040 0.490576
5	21 CSTB rs743466 0.12148
6	22 TIMP3 rs130293 0.889259

Edges file: Each line contains a SNP-pair and its two-locus test statistic. Each line contains three tokens: Index of the First SNP, Index of Second SNP, and Two-Locus Test Statistic. The “Index of SNP” means the index in the list of SNPs in the “Nodes file”. The index begins from “0”. The three tokens are separated by space symbol “ ”. The SNP-pairs are sorted in descending order by their two-locus test statistics. One example of this file is shown as follows:

Table 2. Edges file format

Line #	SNP1-Index SNP2-Index two-locus_test_statistic
1	5 1 1
2	2 0 0.895698
3	2 3 0.741046
4	4 1 0.638908
5	0 5 0.000631648
6	3 4 0

From this example, we can see that the first line “5 1 1” means that SNPs “22 TIMP3 rs130293” (the 6th line of the Table 1) and “2 IL1A rs1894399” (the 2nd line of the Table 1) have an interaction with the test value 1.

The single-locus test value should be between 0 and 1. We recommend that single-locus test value is normalized among the single-locus test values of all the SNPs. Two-locus test values also should be

between 0 and 1. The user can select the top ranked SNP-pairs, e.g., the top-400 SNP-pairs. Then the two-locus test values should be normalized among the selected SNP-pairs.

2. User Interfaces

EINVis contains two bubbles: tree ring view bubble, as show in Figure 1; and matrix view bubble, as shown in Figure 2.

In the tree ring view bubble, the left part shows the tree ring view, and the right column shows the control panel. The functions of these controls are described in Table 3. The node color is mapped from single-locus test statistics; and the edge color is mapped from two-locus test statistics. We provide user mouse interactions to let the user to select, expand or collapse the nodes. These user mouse interactions are listed in Table 4.

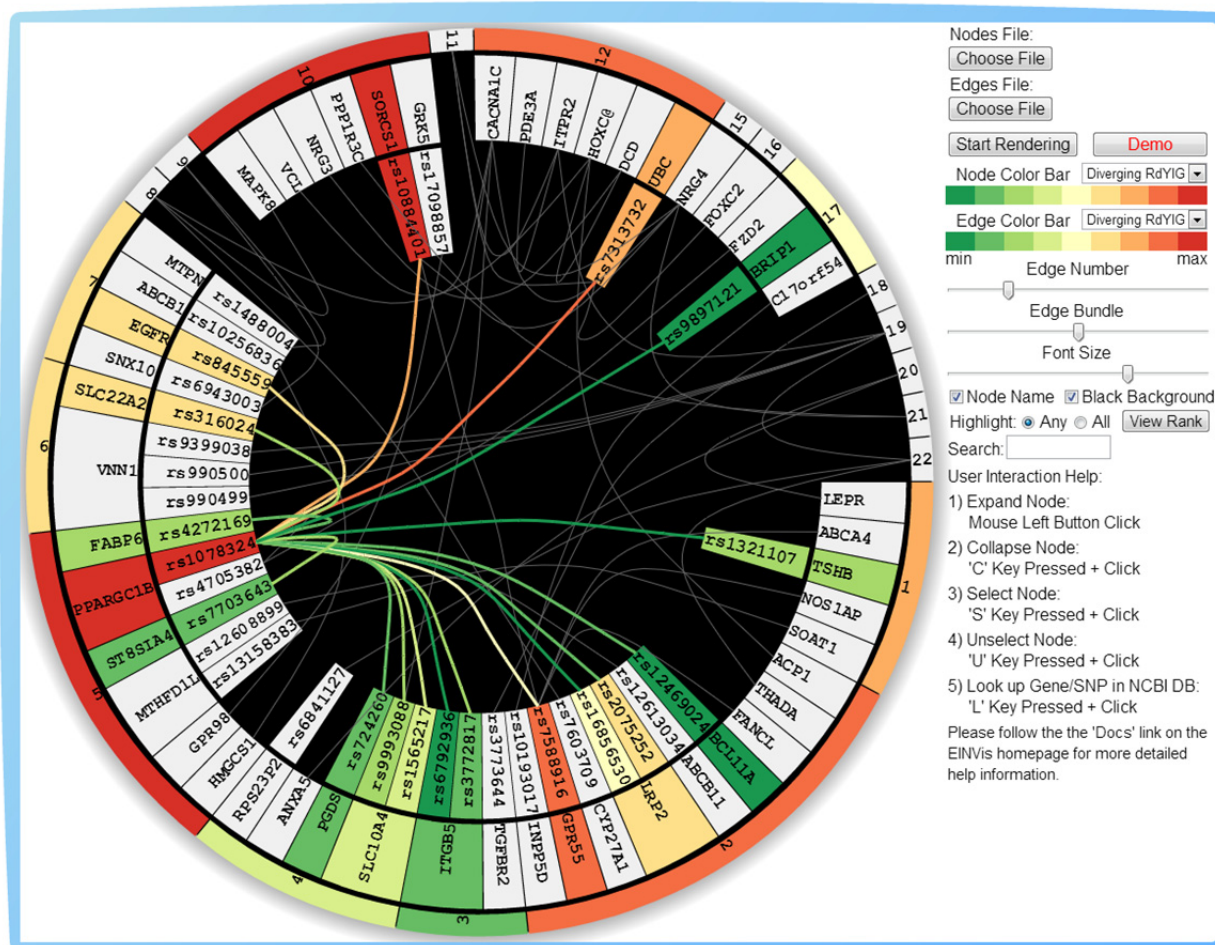


Figure 1. Tree Ring View Bubble

The Matrix View is an auxiliary view for the Tree Ring View. The color scheme is the same as that used in the tree ring view. The left margin and top margin shows the SNP name list in the format of “gene.SNP_name”. And the background color represents the single-locus test value. In the matrix, each square represents whether or not the two SNPs have interactions. If the small square is gray, then there is no interaction. If it has a color, then the color represents the two-locus test value. Since the view space is limited, we can only show part of the interaction matrix at one time. We provide the pan function, so that the user can pan the matrix to view other parts of the matrix view. This mouse interaction is in Table 4.

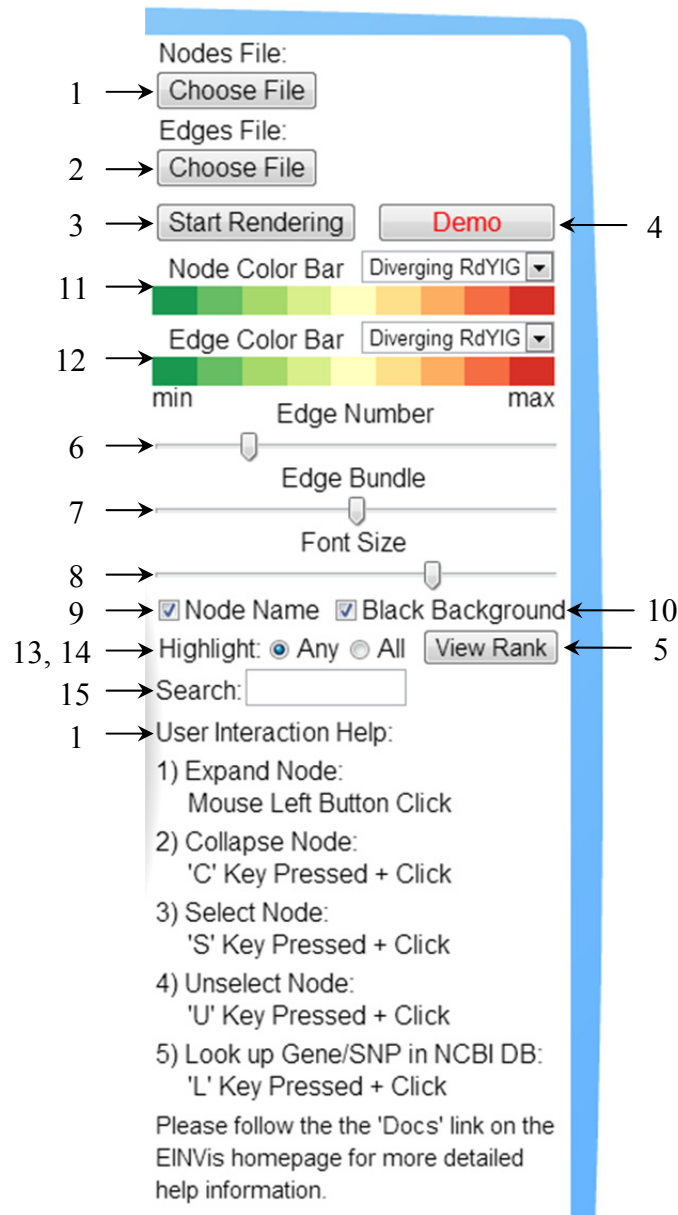


Figure 3. Control Pannel with Labels.

The control functions in the tree ring view are listed in the following table. You can find these controls in the controls panel (right column) in tree ring view bubble, as shown in Figure 1. You can also find these control in Figure 3, with the labels for each control. The number index shown in Figure 3 corresponds to the number in the “Index” column in Table 3.

Table 3. Control Function in the Tree Ring View bubble

Control Type	Index	Control Name	Functions
Button	1	Choose File (Nodes File)	Choose the Nodes File
	2	Choose File (Edges File)	Choose the Edges File
	3	Start Rendering	Start to render the views after user choose the Nodes File and Edges File.
	4	Demo	Start to render the demo. EINVis will load the demo Nodes File and Edges File automatically from server.
	5	View Rank	Open a new webpage to show the table of rank of SNPs based on their degree.
Slider	6	Edge Number	Control how many edges are shown in tree ring view and matrix view. Minimum: 10%, Maximum: 100% (All the edges), Delta: 10%.
	7	Edge Bundle	Control the edge bundle strength. Minimum: 0.0 (Straight Line), Maximum: 1.00, Delta: 0.1.
	8	Font Size	Control the font size of the node name text shown in the tree ring view. Minimum: “10 px”, Maximum: “20 px”, Delta: “1 px”. When user decrease the font size, the width of three levels in the tree ring view will also decrease.
Checkbox	9	Node Name	Control that whether or not show the node name text in the tree ring view. If unchecked, the node name will disappear; if checked, the node name will appear.
	10	Black Background	Control whether use black background in tree ring view. If checked, render black background, which will be much clear; if unchecked, render white background.
Drop-Down Menu	11	Node Color Bar	Select one Node Color bar from the drop-down menu, the contents is listed in Table 5.
	12	Edge Color Bar	Select one Edge Color bar from the drop-down menu, the contents is listed in Table 5.
Radio	13	Highlight Any	If user switches to this radio button and user has selected multiple nodes, then the nodes related to any of the selected nodes and induced edges will be highlighted with color.
	14	Highlight All	If user switches to this radio button and user has selected multiple nodes, then the nodes related to all of the selected nodes and induced edges will be highlighted with color.
Input Text Box	15	Search	Input the Gene name or SNPs ID in this text box, then, EINVis will highlight all the matched Genes or SNPs.

The mouse user interactions are listed in the following table.

Table 4. User Mouse Interactions

Domains	Functions	Interactions
Bubbles	Move one bubble	Drag on the frame of the bubble (the blue frame region)
	Change Layer	Click on one bubble, it will become the most forward layer
Tree Ring View	Expand one node	Left Button Down in one ring sector region
	Collapse one node	“C” key pressed + Left Button Down in one ring sector region
	Select one node	“S” key pressed + Left Button Down in one ring sector region
	Unselect one node	“U” key pressed + Left Button Down in one ring sector region
	Link to NCBI Database	“L” key pressed + Left Button Down in one ring sector region, then it will link to NCBI database.
Matrix View	Pan the matrix view	Left Button Down + Mouse Move (Drag mouse) in the Inner Matrix View Region

The color bar drop-down menu contains the items listed in the following Table.

Table 5. Items in Node and Edge Color Bar Drop-Down Menu

Item Names	Color Bars
Sequential YIGn	
Sequential YIGnBu	
Sequential YIOBr	
Sequential YIORd	
Sequential PuRd	
Sequential Greys	
Diverging PiYG	
Diverging PRGn	
Diverging PuOr	
Diverging RdBu	
Diverging RdYIBu	
Diverging RdYIGn	
Continuous RdGn	

Note: the “Sequential” and “Diverging” color bars are selected from ColorBrewer website.

The node and edge color bar drop-down menu share the common items in the above Table. However, they are independent. If you change node color bar, it will not affect the edge color.

Please visit the homepage of EINVis: <http://filer.case.edu/yxw407/einvis> , we provide video tutorials about EINVis software there: <http://filer.case.edu/yxw407/einvis/tutorial.html> . And, if you want to run EINVis online, please visit this link: <http://filer.case.edu/yxw407/einvis/run> . Enjoy the visualization tool!

In conclusion, this document describes the “Input Data Format”, “User Interfaces” and “User Interactions” for the EINVis software.