

ENIGMA Viewer User Guide

[\(http://enigma-viewer.org/\)](http://enigma-viewer.org/)

1. Acknowledgement

This program is a collaborated work from the following organizations:

IVCL, University of Maryland, Baltimore County

University of Maryland, School of Medicine

ENIGMA Consortium

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3. Program Overview

The ENIGMA viewer is a web-based program that can be executed on most modern browsers. It is recommended to use the latest version of Chrome for best compatibility.

The program interface is shown as in Figure 1. It contains three major views. From left to right, these views are plot view, spatial view and chart view.

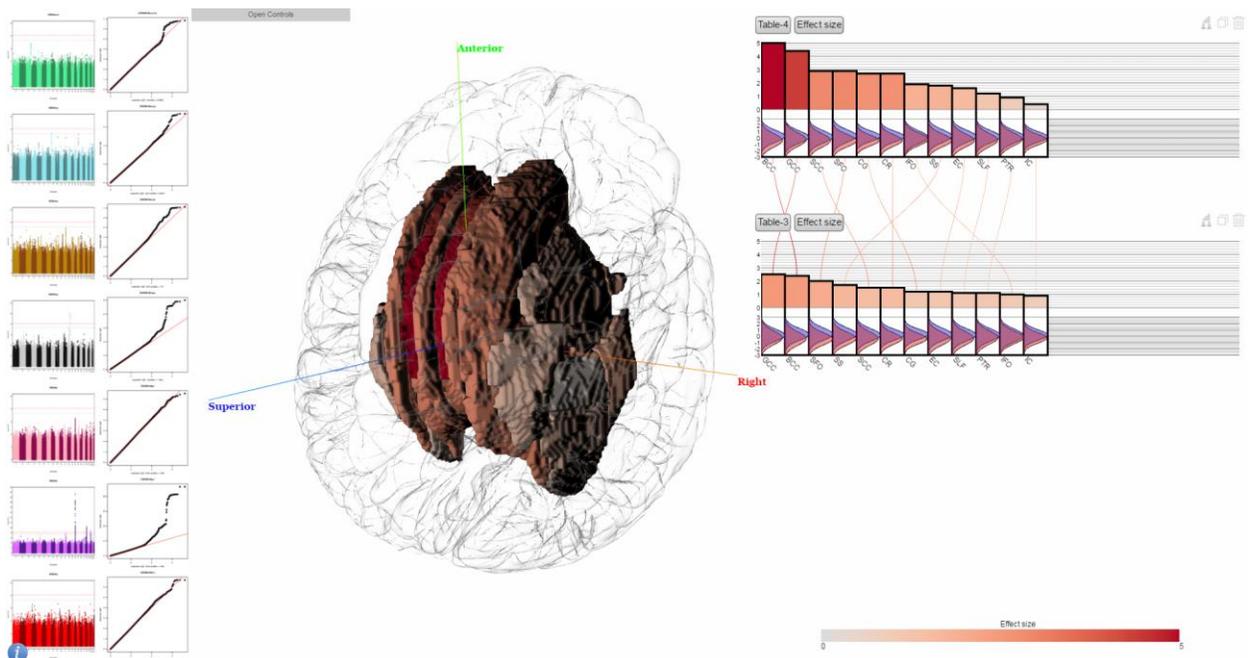


Figure 1 Program Overview.

The plot view on the left places images of Manhattan and QQ plots of several subcortical brain regions. Clicking on these images will make the corresponding brain regions be shown in the spatial view.

The spatial view in the middle display brain regions of interest (ROIs), including both cortical and subcortical regions. The cortical regions are displayed as transparent meshes while the subcortical regions are solid meshes. The 3D model can be rotated and scaled. Clicking on a mesh will remove it from the spatial view. Hovering over a mesh will display the related information on the tooltip.

The chart view on the right displays the statistics, namely effect size and p values of the corresponding ROIs. If population data is available, the FA value distribution will be drawn as Gaussian curves. The bars can be moved and scaled horizontally together by dragging and scrolling. Clicking on each of the bars will toggle the display of the ROI meshes in the spatial

view. Hovering over a bar will display the related information on the tooltip. The legend of the color encoding is shown on the bottom of this view.

4. Spatial View

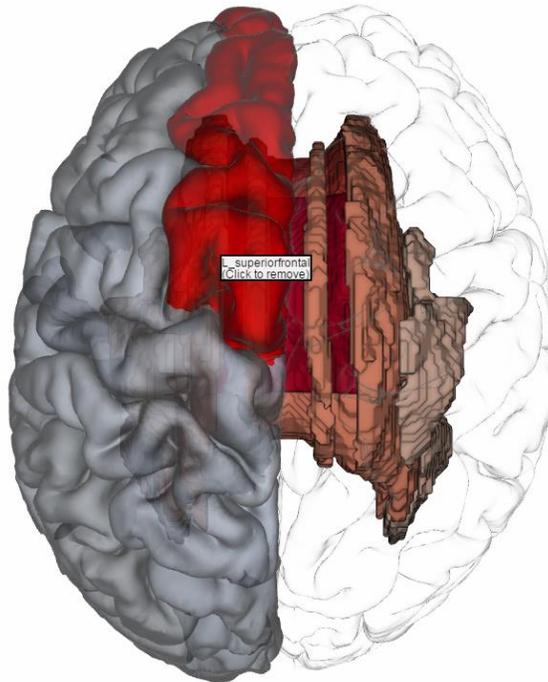


Figure 2 Spatial view.

1. Add/Remove an ROI to the view

Spatial view displays both cortical and subcortical ROIs showing as meshes displayed in a 3D glass brain model. The meshes are added to the spatial view by clicking a bar representing the corresponding ROI in the chart view. The ROIs are colored based on the bar color. To remove a mesh, simply click on the mesh in the spatial view.

2. Interactions

Rotate. To view the 3D model from different angles, simply drag the mouse using left buttons. A trackball like model is used to decide the rotation.

Zoom. By scrolling using the mouse wheel, the model will be put closer to the viewer.

Hover. Hover the mouse cursor over an ROI mesh in the spatial view will display the information about the ROI at the cursor location.

5. Chart View

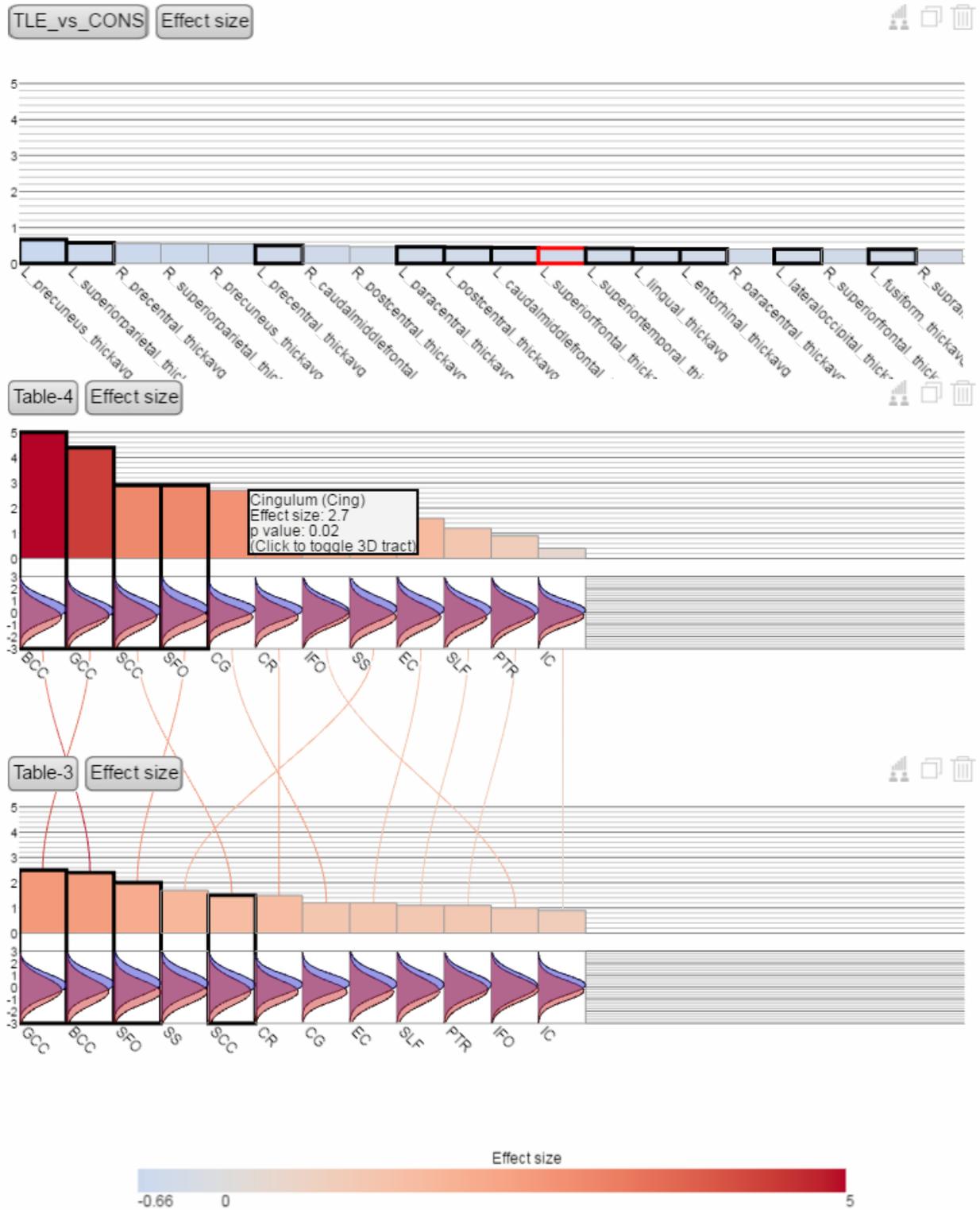


Figure 3 Chart view.

Chart view displays the statistics from each study as bar chart. The legend of the color encoding is displayed at the bottom.

1. Bar chart representation.

The chart representation uses both height and color to represent the statistics. Colors are always globally normalized, i.e. the same color always represents the same statistical values across bar chart. Bar height, by default is also globally normalized but can be changed to locally normalized so that the highest bar always occupies the entire vertical space within a chart.

2. Add/Remove an ROI to the spatial view

Clicking on a bar chart representing one ROI will add the mesh representation into the spatial view. Those with meshes displayed in the spatial view will have a thick black bounding boxes highlight the bars. The ROI that are currently hovered by mouse cursor in the spatial view has red bounding box instead as shown in Figure 4.

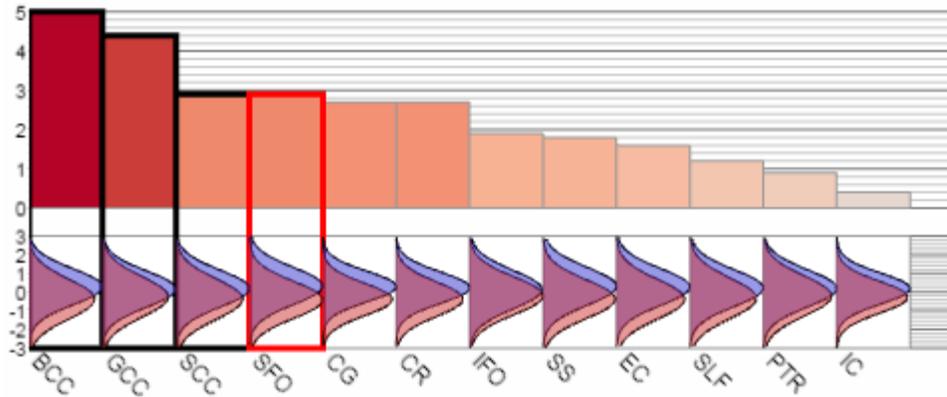


Figure 4 Highlighted bars.

3. Interactions

Translate. In case there are too many bars to be displayed and there is not enough horizontal space to show them all at once, these bars can be dragged to move along the horizontal lines. To do this, dragging the chart in the blank space (do not click on the bars) and move the mouse along the x axis.

Zoom. By scrolling using the mouse wheel, the width of the bars will be scaled accordingly.

Hover. Hover the mouse cursor over a bar will display the related ROI information on the tooltip.

Drag. Pressing on the most top left button, which displays the name of the dataset like this **Table-3** and drag will move the chart as a whole. The chart can be dropped to other location to arrange the location of different bar charts. It can also be dropped to the spatial view which result in all the ROIs in the chart being added to the spatial view. Multiple charts can be added to the spatial view, as shown in Figure 5

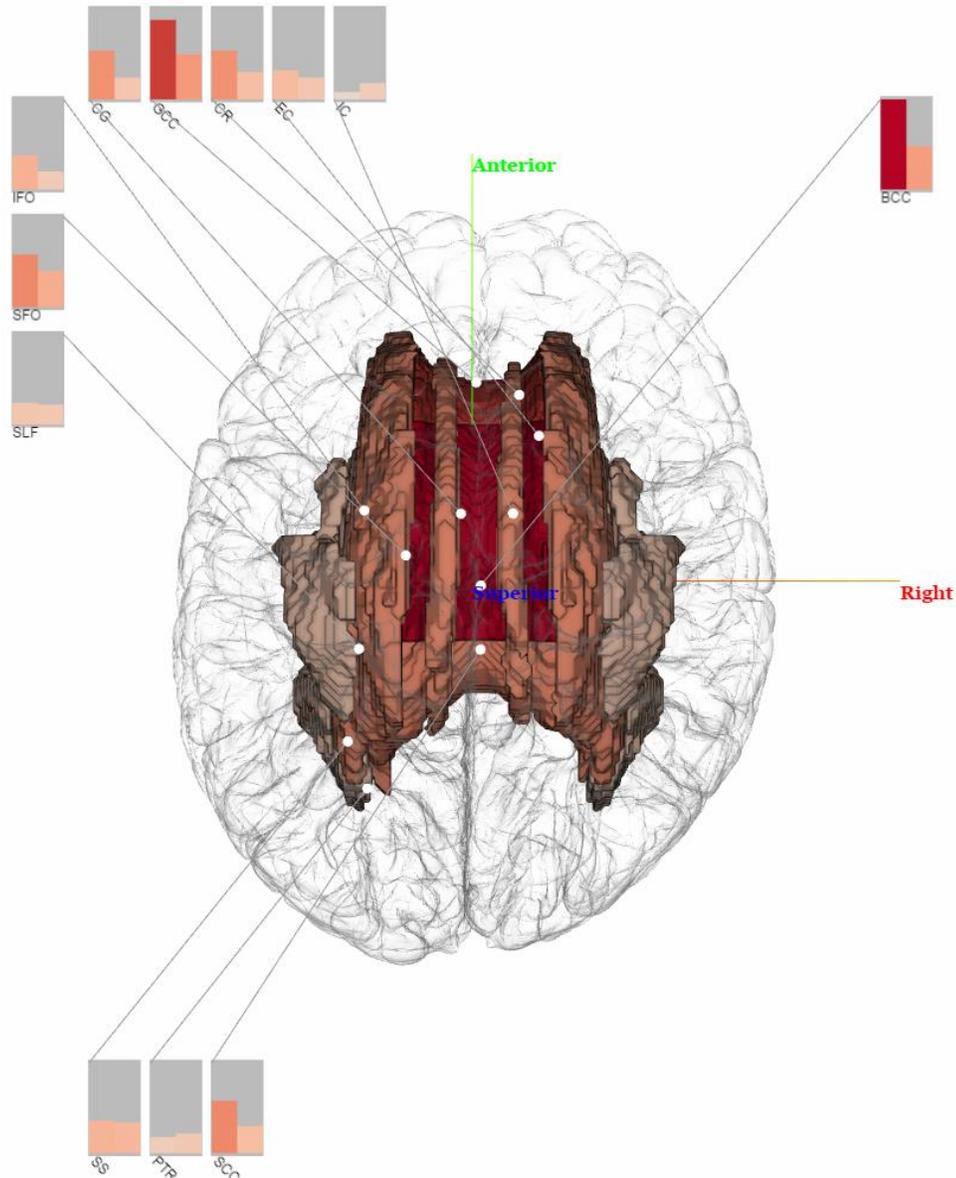


Figure 5 Charts in spatial view.

Switch statistics. Press the button on the right to the most top left button, which displays the name of statistics, will switch to next available statistics. Current there are two statistics that are used for the visualization: effect size and p value. Clicking on the button will switch between the statistics and change the bar chart display accordingly, as shown in Figure 6.

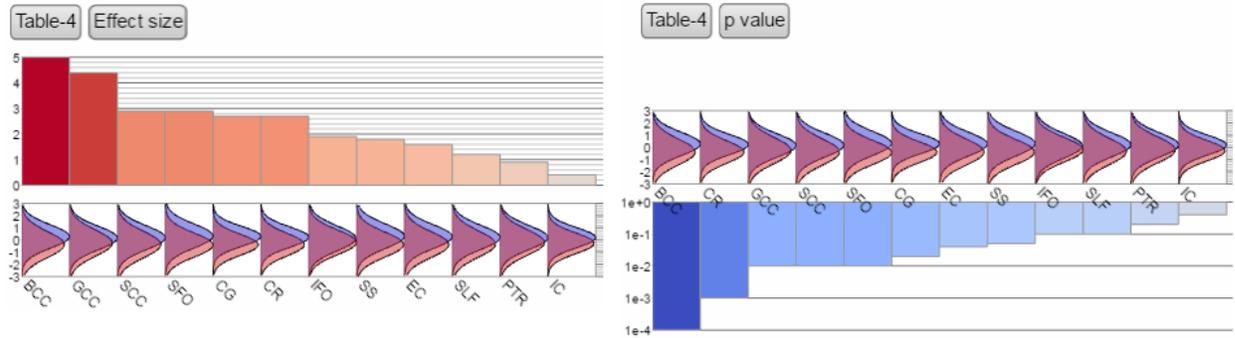


Figure 6 Switch statistics.

4. Other functions

As shown in Figure 3, there are several smaller buttons on the top right corner of each chart. These buttons are for toggling ROIs, copy chart and delete chart.

Toggling ROI button  is used to temporarily dismiss several ROI bars by making them smaller, as shown in Figure 7. By clicking this button, all selected ROI bars in the chart will become much narrower and their labels will be hidden. Those that are already dismissed will become normal if they are selected where clicking the toggling ROI button.

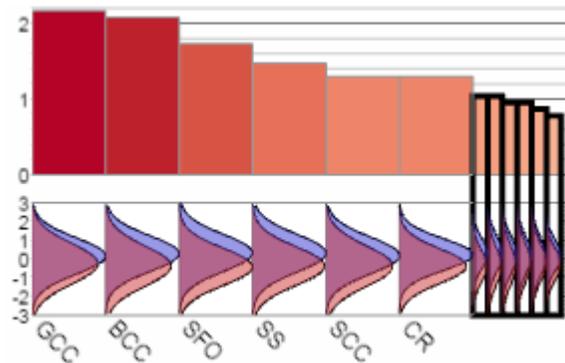


Figure 7 ROI bar dismissal.

Copy and delete buttons   are used to make a copy of the current chart and delete the current chart. Copying the chart is useful if you want different statistics to be displayed for the same dataset.

6. Plot View

Plot view displays the Manhattan plots (left) and QQ plots (right) of several subcortical regions.

Click on one of the plot will display the corresponding subcortical region in the spatial view. The region will have the same color as used in the Manhattan plot.

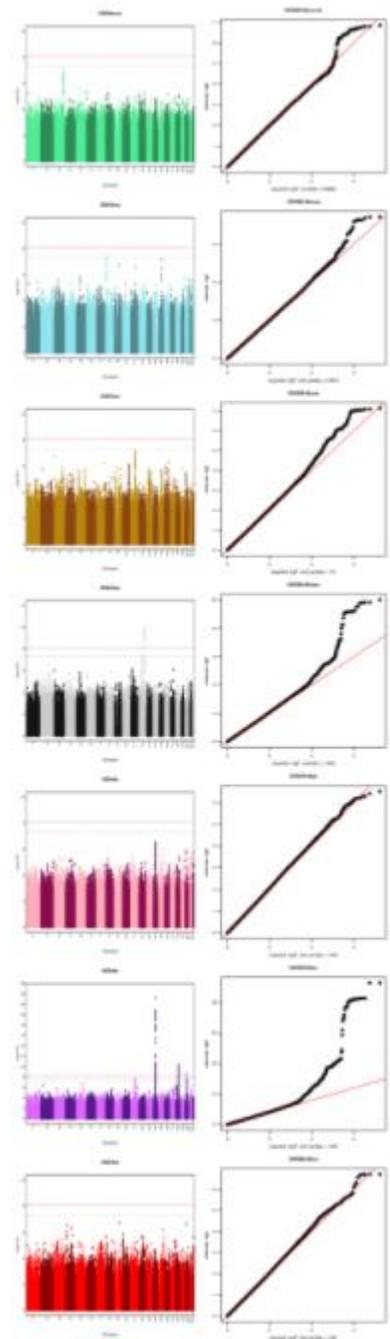


Figure 8 Plot view.

7. Control Panel



Figure 9 Control Panel.

By default, the control panel is a small gray box located on the top left corner of the spatial view as in Figure 9 left. When clicking, it will expand to show its options as Figure 9 middle. A fully expanded control panel is shown in Figure 9 right.

There are four major categories, controls for spatial view, chart view, spatial view camera and loading data.

1. Spatial view controls

Left hemisphere/Right hemisphere: toggle the display of left/right hemisphere display of the glass brain model.

Show axis: toggle the display of the axes showing anterior, superior and right direction.

Show boundary: toggle the display of boundary lines when a cortical mesh is added to the spatial view.

Transparency: adjust the transparency of the glass brain and the cortical meshes.

AutoVerticesSort: sort the vertices of the mesh so the transparency blending is rendered correctly. This sorting is expensive in terms of computation time. Note when checked, it will

immediately execute the sorting. If keep checked, the sorting will be executed whenever a mouse rotation is completed, i.e. when releasing the mouse button after rotating the model. It is recommended to left it unchecked and execute a one-time check and uncheck whenever the proper viewing angle is found.

2. Chart view controls

ROI tracts: toggle the generation and display of subcortical fiber tracts that pass through the subcortical ROI when a subcortical ROI is added to the spatial view. For example, when the ROI BCC is selected while the ROI tracts is checked, a transparency mesh is added to the spatial view with the BCC mesh as shown in Figure 10. See the density threshold below for description on the transparent tract mesh generation.



Figure 10 ROI tracts.

Density threshold: the tract mesh from one subcortical ROI is generated from a density field. The density field describes on each voxel the percentage of subject that has fiber passing through the selected ROI. The density threshold slider bar adjusts the threshold based on which an iso-

contour is generated as the tract mesh. Note the value from this bar only affects the mesh being generated afterwards. Previously generated tract meshes will not be adjusted to newer density threshold because mesh generation on the density field is an expensive operation for the web application. To adjust this parameter on a previously generated tract mesh, click the old mesh to remove it and click the ROI bar again to let the program re-generate a new tract mesh based on the new threshold.

Global: toggle whether or not the bar heights are normalized globally or locally.

Stacker view: merge all chart views into a single stacker view where all effect size values belong to the same ROI are stacked together, as shown in Figure 11.

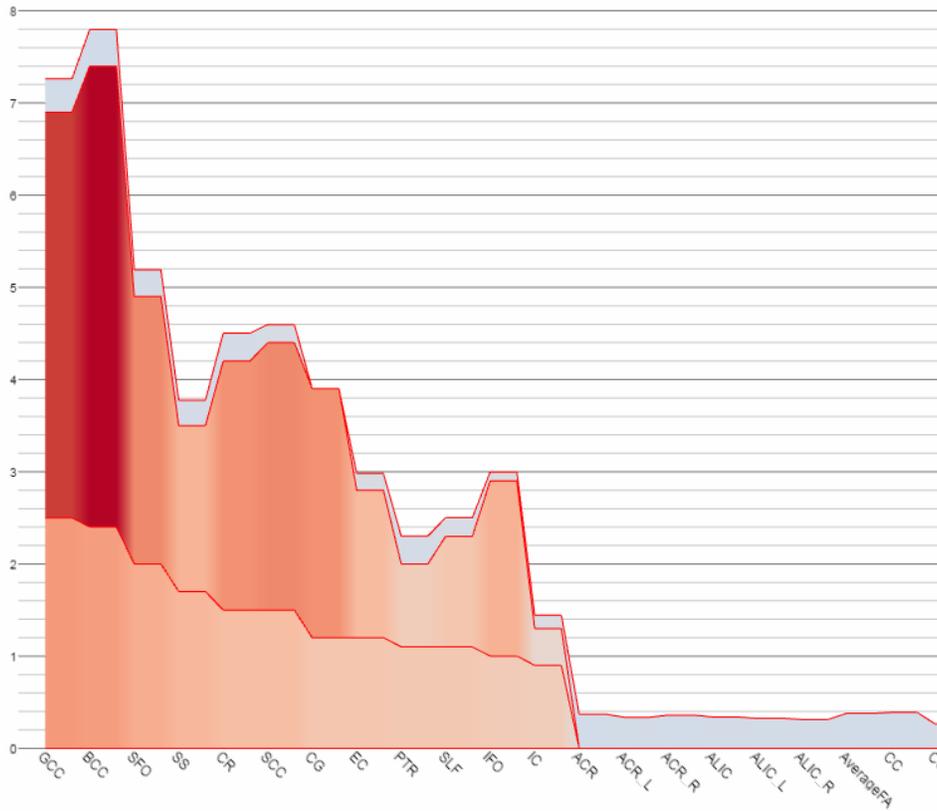


Figure 11 Stack view.

Show links: toggle whether or not the links that connect the same ROIs across adjacent chart views are displayed, as shown in Figure 12. The link from an ROI bar is colored according to the color of its connected bars.

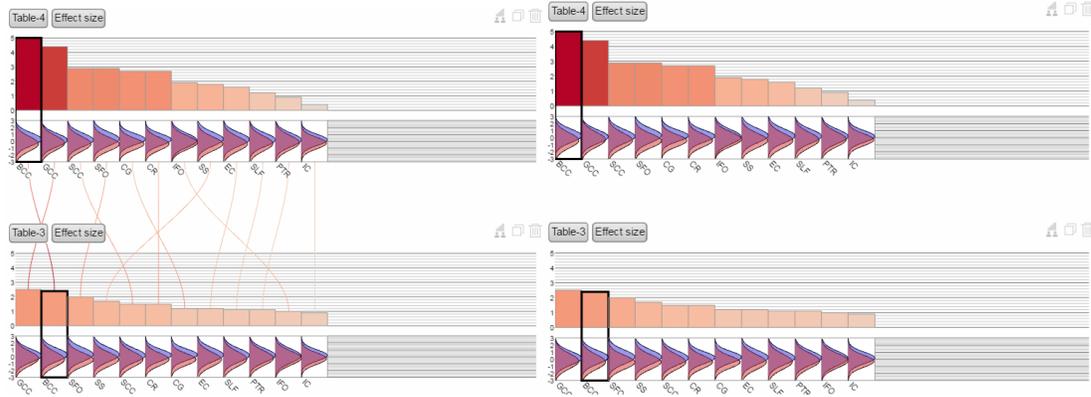


Figure 12 Show links.

3. Camera control

Reset camera: this will reset the camera to the default viewing angle.

4. Data

Load data: upload a CSV file to add a new chart to the visualization.

The data format is as follows:

Table 1 Data format-subcortical

roi	ACR	ACR_L	ACR_R	ALIC	ALIC_L
meta_d	-0.37086	-0.33769	-0.36108	-0.33922	-0.3255
meta_pval	6.72E-09	1.33E-07	9.14E-09	4.66E-08	3.82E-07

The table shown above are the content being read from the program. The content that triggers data input are the first column which must be named “roi”, “meta_d” and “meta_pval”, which refer to the ROI name row, effect size row and p value row respectively. The ROI row contains ROI names. For subcortical regions, the names must be included in the JHU/ENIGMA white matter template look up table.

Table 2 Data format-cortical

roi	L_precuneus_thickavg	L_superiorparietal_thickavg	R_precentral_thickavg
meta_d	-0.66762	-0.57735	-0.56487
meta_pval	8.66E-07	1.45E-04	1.17E-16

The above table shows the same table for cortical regions. The only difference is the format of names. Since the white matter template does not contain cortical regions. The names are currently in the above format.

Note the CSV file can contain other rows but only rows that begins with the aforementioned three names (“roi”, “meta_d” and “meta_pval”) will be read.