BRAINNET VIEWER MANUAL

A visualization tool for brain network

For v1.7, Released on October 31st, 2019

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1 Overview

The human brain is a complex system whose topological organization can be represented using connectomics. Recent studies have shown that human connectomes can be constructed using various neuroimaging technologies and further characterized using sophisticated analytic strategies, such as graph theory. These methods reveal the intriguing topological architectures of human brain networks in healthy populations and explore the changes throughout normal development and aging and under various pathological conditions. However, given the huge complexity of this methodology, toolboxes for graph-based network visualization are still lacking.

Here, we developed a graph-theoretical network visualization toolbox, called BrainNet Viewer, which can help researchers to visualize structural and functional connectivity patterns from different levels in a quick, easy and flexible way. BrainNet Viewer functions as follows:

    1) display combinations of the brain surface, nodes, edges and volumes in multi-views;

    2) adjust the color and size of both nodes and edges in different ways;

    3) provide interactive operations, such as zoom and rotate;

    4) support various kinds of image format exporting;

    5) support command line calling;

    6) provide codes to generate node files from NIfTI atlas

    7) export figures as commonly used image file formats or demonstration videos.

BrainNet Viewer helps researchers to visualize brain networks in an easy, flexible and quick manner, and this software is freely available on the NITRC website (www.nitrc.org/projects/bnv/).

BrainNet Viewer is developed using MATLAB (The MathWorks Inc., Natick, MA, US) as a programming language, with a user-friendly GUI, under a 64-bit Windows (Microsoft Corp., Redmond, WA, US) environment. The toolbox includes functions of Statistical Parametric Mapping 8 (SPM, http://www.fil.ion.ucl.ac.uk/spm/) for loading NIfTI, Analyze format and GIfTI surface files (*.nii; *.img; *.gii). This toolbox has been successfully tested under a variety of operating systems with MATLAB installed, including Windows (XP, 7, 8, 10 and Server versions), Linux (Ubuntu and CentOS) and Mac OS in both 32- and 64-bit versions.

Citation: Please cite as '... was/were visualized with the BrainNet Viewer (Xia et al., 2013, http://www.nitrc.org/projects/bnv/)' while using the package to make publicized pictures.

Reference: Xia M, Wang J, He Y (2013) BrainNet Viewer: A Network Visualization Tool for Human Brain Connectomics. PLoS ONE 8: e68910.

BrainNet Viewer is developed by Dr. Mingrui Xia, National Key Laboratory of Cognitive Neuroscience and Learning, Beijing Key Laboratory of Brain Imaging and Connectomics, IDG/McGovern Institute for Brain Research, Beijing Normal University, Beijing, China.

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2 Installation

2.1 Run BrainNet Viewer on a PC with Matlab

1) Run Matlab. (A version of R2010b or above is recommended)

2) Add BrainNet Viewer path to Matlab search path:
   Click 'File' in Matlab menu -> Click 'Set Path' -> Click 'Add with Subfolders...' button in the popup dialog -> Select the 'BrainNet Viewer' folder on the machine -> Click 'OK' button -> Click 'Save' Button.

3) Run BrainNet.m:
   *Type 'BrainNet' in the command window of Matlab.*

2.2 Run BrainNet Viewer on a PC without Matlab

The standalone version and the download link of Matlab Components Runtime are now available on the NITRC website (http://www.nitrc.org/projects/bnv/).

Install Matlab Components Runtime (MCRInstall.exe for Windows OS, or MCRInstaller.bin for Linux and Mac OS, ~800MB) using default settings.

Restart your computer (strongly recommended).

Run BrainNet.exe for Windows OS, run_BrainNet.sh for Linux or BrainNet.app for Mac OS, it should take about one minute to start. You can find the interface below (Fig. 1) after successfully running the BrainNet Viewer.
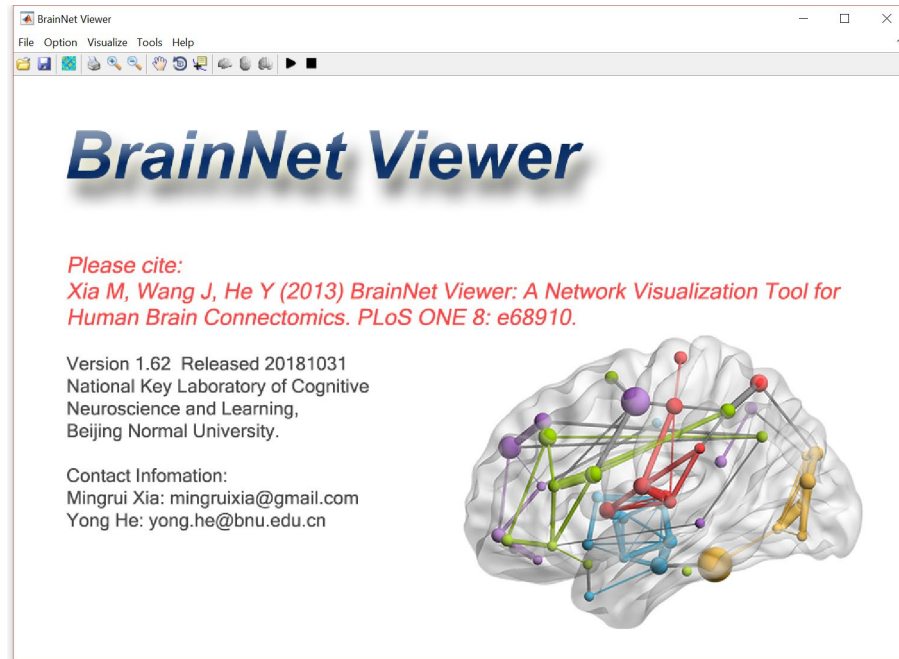
**Fig. 1 The main window of BrainNet Viewer**

3 Pictures

BrainNet Viewer doesn't require to load surface, node, edge and volume file together. Instead, the following combinations are acceptable and different combinations will generate different network pictures (Fig. 2):
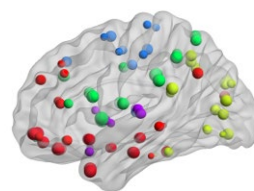
1) Brain surface: load brain surface file only. See section 4.1 for file preparation and section 5.3 for visualization options.
2) Nodes: load node file only. See section 4.2 for file preparation and section 5.4 for visualization options.
3) Brain surface and nodes: load both brain surface and node files. See sections 4.1 and 4.2 for file preparation and section 5.3 and 5.4 for visualization options.
4) Nodes and edges: load both node and edge files. See sections 4.2 and 4.3 for file preparation and section 5.4 and 5.5 for visualization options.
5) Brain surface, nodes, and edges: load brain surface, node, and edge files together. See sections 4.1 to 4.3 for file preparation and section 5.3 to 5.5 for visualization options.
6) Volume mapping to the surface: load brain surface and volume files. See section 4.1 and 4.4 for file preparation and section 5.3 and 5.6 for visualization options.
7) Volume mapping to surface with node: load brain surface, node and volume files. See section 4.1, 4.2 and 4.4 for file preparation and section 5.3, 5.4 and 5.6 for visualization options.
8) Volume mapping to surface with node and edge: load brain surface, node, edge and volume files. See sections 4.1 to 4.4 for file preparation and section 5.3 to 5.6 for visualization options.
9) ROI cluster drawing in volume: load brain surface and volume files. See section 4.1 and 4.4 for file preparation and section 5.3 and 5.6 for visualization options.
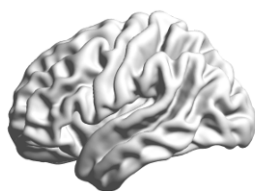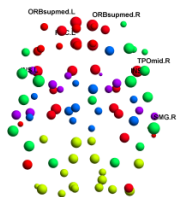
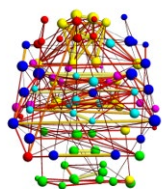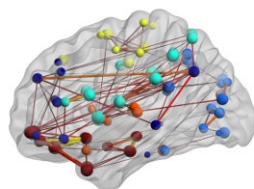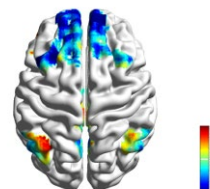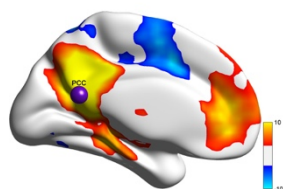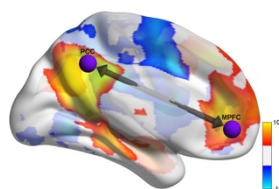1) Brain Surface 2) Nodes 3) Surface & Nodes
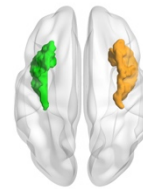
4) Nodes & Edges 5) Surface, Nodes & Edges 6) Surface mapping

7) Surface mapping & node 8) Surface mapping with node & edge 9) ROI in Volume

Fig. 2 Brain network pictures from different file combinations

4 Load Files

To draw a brain network, some kinds of files such as brain surface, node file or edge file should be loaded in the first step. Click the 'Load File' button on the toolbar or 'File\Load File' in the menu to open the Load File dialog shown below (Fig. 3). Select files to draw the required graph.

In BrainNet Viewer, we provided several brain surface templates and example files (which were made from various brain parcellation methods) including (1) Colin brain, smoothed Colin brain, Colin brain with cerebellum, ICBM152 brain (MNI/Talaraich), smoothed ICBM152 brain (MNI/Talaraich), hemispheres of ICBM152, hemispheres of smoothed ICBM152 brain surface and a cerebellum surface in the folder '.\Data\SurfTemplate'; and (2) node and edge files for Automated Anatomical Labeling (AAL, 90 regions) (Tzourio-Mazoyer et al., 2002), Brodmann areas (82 regions) (Brodmann, 1909), Desikan-Killiany Atlas (68 regions) (Desikan et al., 2006), Harvard-Oxford Atlas (HOA, 112 regions) (Smith et al., 2004), ROIs defined by Dosenbach et al.(160 ROIs) (Dosenbach et al., 2010), ROIs defined by Fair et al. (34 ROIs) (Fair et al., 2009), LONI Probabilistic Brain Atlas (40 regions) (Shattuck et al., 2008), ROIs defined by Power et al. (264 ROIs) (Power et al., 2011) and others (e.g., customized ROIs by users) in the folder '.\Data\ExampleFiles'.
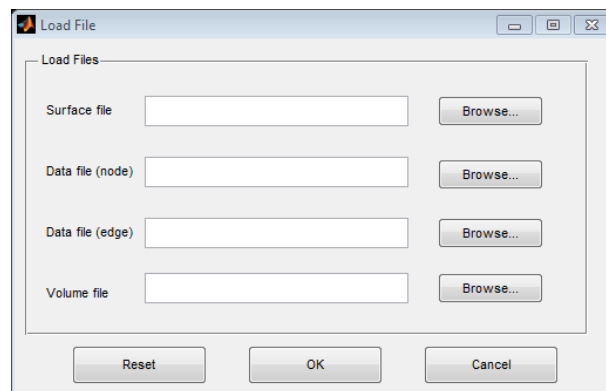
Fig. 3 Load File dialog

4.1 Load a surface file

Click the 'Browse...' button next to the 'Surface file' in the 'Load File' dialog, and then select the required brain surface file in the popup dialog. BrainNet Viewer provides several brain surfaces based on two different brain templates, ICBM152 (.\Data\SurfTemplate\BrainMesh_ICBM152.nv) and Colin27 (.\Data\SurfTemplate\BrainMesh_ch2.nv), and separate hemisphere surfaces (.\Data\SurfTemplate\ICBM152Left.nv, ICBM152Right.nv). In the below example, the ICBM152 template is selected (Fig. 4). Note that the surface with a name ended with 'tal' is in the Talaraich space, otherwise,

it is in the MNI space.
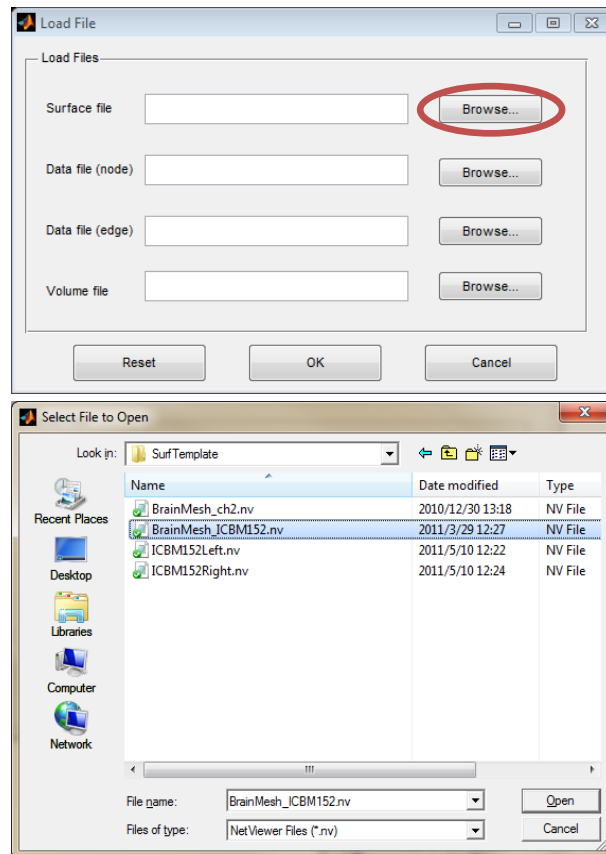
Fig. 4 Select brain surface (ICBM152 is selected)

The information below is about the definition of the surface file. Usually, you don't need to generate a new surface file. Please read the file if interested or if you want to make a surface by yourself. The brain surface file is defined as an ASCII text file with suffix 'nv' and contains four fields:

1) Vertex number;
2) Vertex coordinate;
3) Triangle faces number;
4) Index of vertex making up the triangles.

The ICBM152 brain surface was provided by Prof. Alan Evans (Montreal Neurological Institute, McGill University) and the Colin27 brain surface was made by BrainVISA (http://brainvisa.info/). We transferred and merged the original bilateral hemisphere files into one '.nv' file. A surface merge tool is provided in the tools menu (see more details in section 6.4 'Menus\Tool').

BrainNet Viewer supports a number of different surface formats, including the '*.pial' files generated by

FreeSurfer, (only hemisphere mesh), the '*.mesh' files generated by BrainVISA '*.g' files generated by BrainWorks software, '*.obj' files, '*.gii' files of GIfTI surface and '*.mz3' of Surf Ice.

4.2 Load a node file
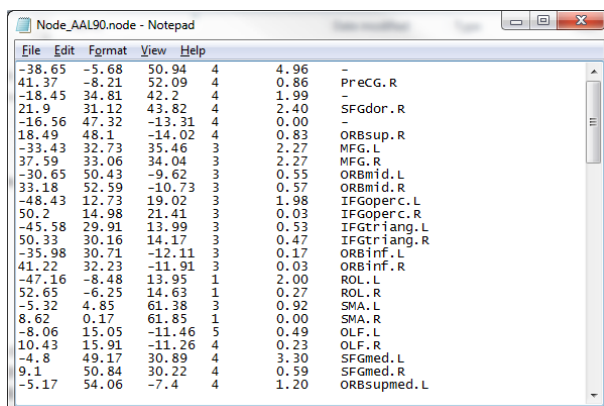
The file represents the information from nodes obtained from the AAL90, Brodmann82, Desikan-Killiany68, HOA112, Dos160, Fair34, LPBA40, Power264 and others (e.g., customized ROIs by users). All files are stored in folder '.\Data\ExampleFiles\', corresponding to its template name, respectively. Click the 'Browse…' button next to 'Data file (node)' in the Load File dialog and select the required node file. The AAL90 node file is selected as an example in Fig. 5.
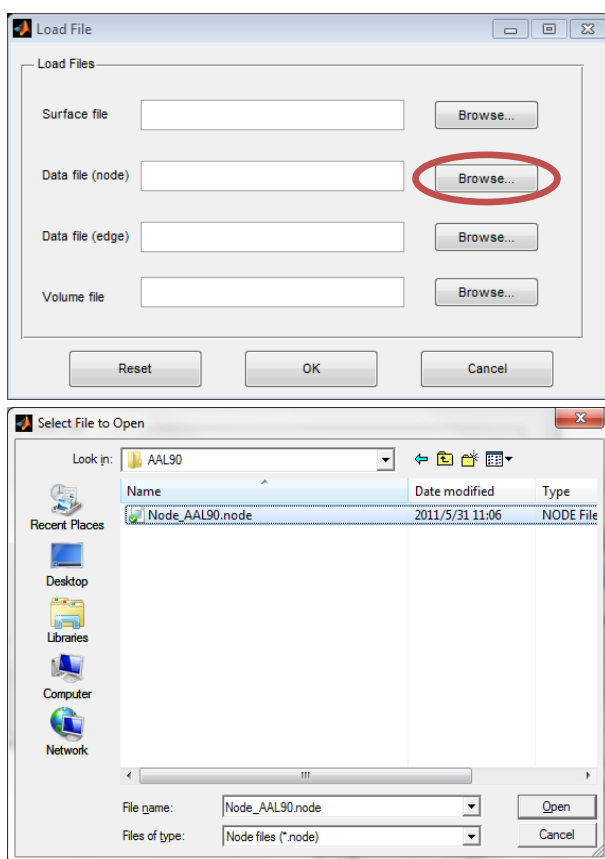
Fig. 5 Select node file (AAL90 is selected)

The node file is defined as an ASCII text file with the suffix 'node'. In the node file, there are 6 columns: columns 1-3 represent node coordinates, column 4 represents node colors, column 5 represents node sizes, and the last column represents node labels. Please note, a symbol '-' (no '') in column 6 means no labels and **blank characters in label would cause an error**. The user may put the modular information of

the nodes into column 4, like '1, 2, 3…' or other information to be shown by color. Column 5 could be set as nodal degree, centrality, T-value, etc. to emphasize nodal differences by size. The generation of node file is flexible depending on different requirements.

Fig. 6 Node file (AAL90)

4.3 Load an edge file

The brain edge file is defined as an ASCII text file with suffix 'edge', representing a connectivity (e.g., correlations) matrix among the ROIs, which could be either weighted or binarized, and therefore, the dimensions of the matrix must correspond to the number of nodes. AAL90, Brodmann82, HOA112, Dos160, Fair34, LPBA40, and other (e.g., customized ROIs by users) files are provided, and each file is in the folder '.\Data\ExampleFiles\' corresponding to its template name.
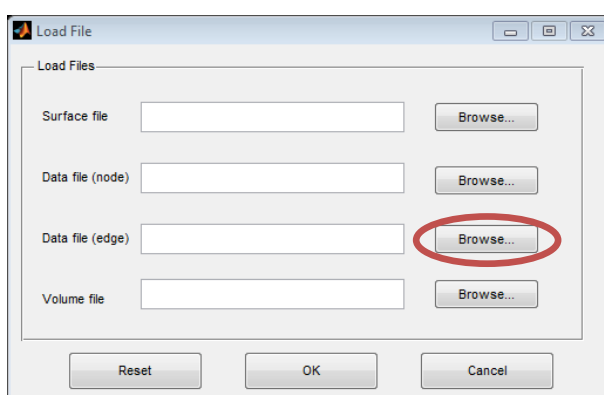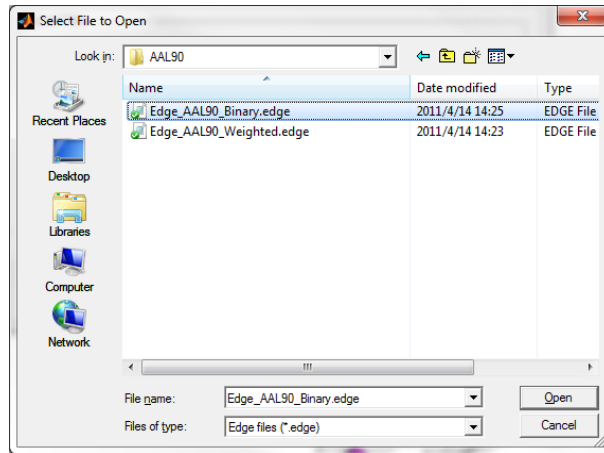
Fig. 7 Select an edge file (AAL90 binary file is selected)
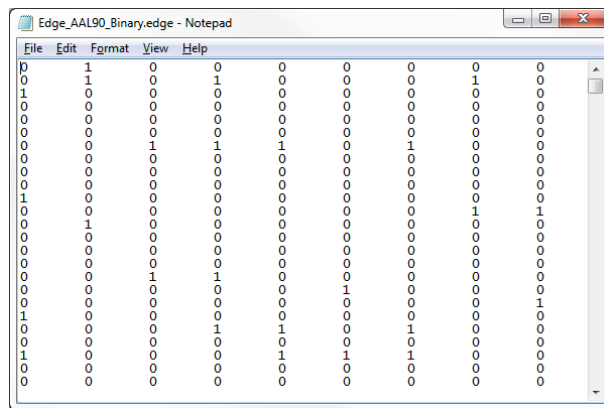
Fig. 8 Edge file (AAL90, Binarized)

Both node and edge files can be generated/edited with text editors or Excel.

Notably, the size of the matrix should correspond to the number of nodes and comments can be added with # at the beginning of the line in surface, node and edge files.

4.4 Load a volume file

This function lets users map the volume data to the brain surface. The volume file should be a 3D NIFTI format, which could be T-map, Z-map, atlas or any other volume data, either paired files or a single nii file are accepted. Besides, a text file containing an n $\times$ 1 vector is also accepted, in which n equals to the vertex number of the brain surface (81924 vertexes in ICBM whole-brain surface). The principle of volume mapping is to transfer the vertex coordinates on the brain surface to the volume space and assign vertices with corresponding values by using different algorithms. The principle of ROI drawing is to reconstruct voxels with the same index in the image file to 3D volume.
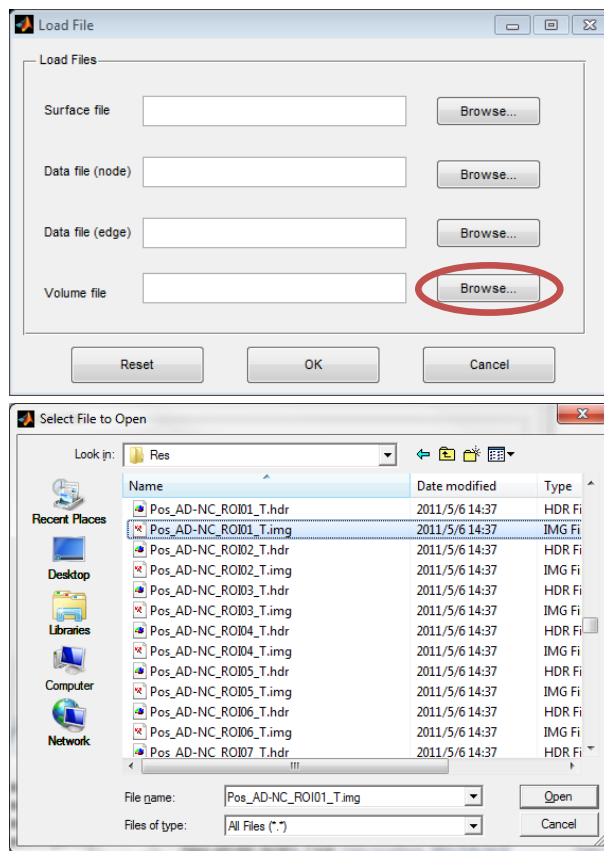
Fig. 9 Volume file (a paired NIFTI file of T-test Map is selected)

5 Visualize option

The option panel has three parts (Fig. 10). The list box on the left includes 'Layout', 'Global, 'Surface', 'Node', 'Edge', 'Volume' and 'Image,' which represent different aspects of the figure. The main panel on the right shows the detailed options of each part; click the text in the list box to change the panel. There are six buttons on the bottom of the panel: use the 'Load' and 'Save' to acquire or save options as a .mat file; 'Reset' to return all parameters to their original state; 'OK' to draw graph and close option panel; 'Apply' to draw graph but keep option panel and 'Cancel' to exit the panel without changes.

Fig. 10 Option panel

5.1 Layout panel

The layout panel (Figure 10) is primarily responsible for setting the output view of the brain model, in which five types of views are provided:

Single view: Show only one brain model in the figure.

Sagittal Shows the brain in a sagittal view (left side).

Axial Shows the brain in an axial view (dorsal side).

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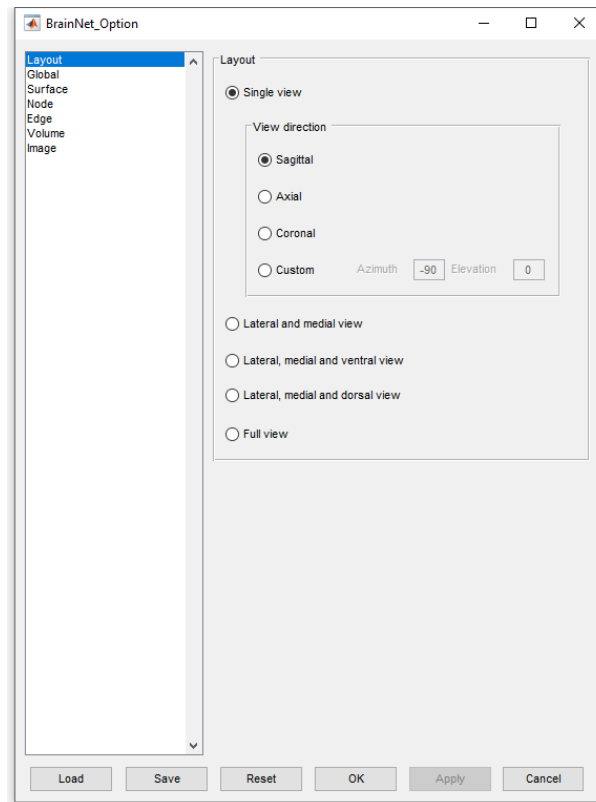
Coronal Shows the brain in a coronal view (frontal side).

Custom Shows the brain in a custom viewpoint, defined by azimuth and elevation (see more detail of function 'view' in Matlab help).

Lateral and medial view: Show the lateral and medial side of each hemisphere in the figure. The top row contains the lateral views of the left and right hemispheres while the bottom row contains the medial views of the left and right hemispheres.

Lateral, medial and ventral view: Show lateral, medial and ventral side of each hemisphere in the figure. The top row contains the lateral views of the left and right hemispheres, the middle row contains the medial views of the left and right hemispheres and the bottom row contains the ventral view of the left and right hemispheres.

Lateral, medial and dorsal view: Show the lateral and medial sides of each hemisphere and the dorsal side of the brain in the figure. The top row contains lateral view of left and right hemispheres, the bottom row contains medial view of left and right hemispheres and the whole-brain is displayed from the dorsal side in the center.

Full view: Show six or eight (depending on whether the brain surface can be divided into left and right hemispheres) brain models. In the six-brain mode, the top row from left to right are left side, top side, and frontal side, while the bottom row from left to right are the right side, bottom side and backside. In the eight-brain mode, the first row from left to right are lateral view of left hemisphere, topside, lateral view of right hemisphere, the second row from left to right are medial view of left hemisphere, bottom side, medial view of right hemisphere, and the third row are frontal side and backside. See Fig. 11.

Single view: Sagittal

Single view: Axial

Single view: Coronal

Single view: Custom,
Az -130, El 30

Lateral and medial view

Lateral, medial and ventral view

Lateral, medial and dorsal view

Full View, six brain

Full View, eight brain
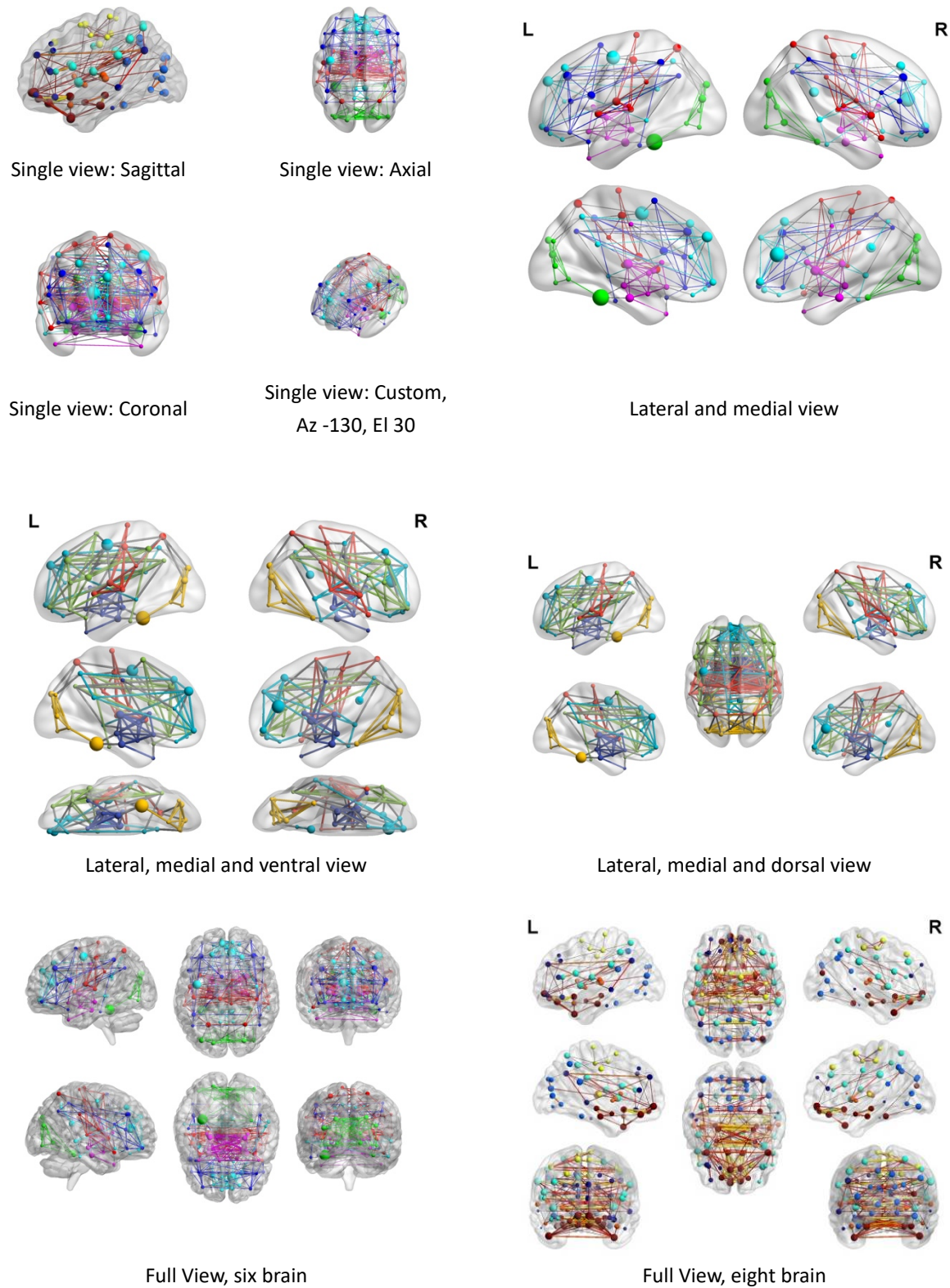
Fig. 11 Different layouts

5.2 Global panel

The global panel provides several different choices for the adjustment of the global figure, particularly the display properties of these objects. (Fig 12)

Background Color: Change the color of the background. Click on the color square button right beside the text 'Background Color', and select the desired color in the popup dialog.

Object Material: Provide four manners to define the material of the model in the figure, 'Shiny', 'Dull'(default), 'Metal' and 'Custom' which the ambient, diffuse, and specular can be freely defined.

Shading properties: Set color shading properties, 'Flat', 'Faceted' and 'Interp'.
Flat, each triangle of the mesh has a constant color, appropriate for atlas or ROI display.
Faceted, show edges of the mesh.
Interp, varies the color of the triangle by interpolating the colormap, appropriate for functional connectivity, ALFF, ReHo or any volume with continuous data (default).

Lighting algorithm: Set lighting algorithm, 'Flat', 'Gouraud', 'Phong' and 'None'.
Flat, produces uniform lighting across each of the faces of the object.
Gouraud, calculates the vertex normal and interpolates linearly across the triangles.
Phong, interpolates the vertex normal across each face and calculates the reflectance at each pixel. (Better but costly than Gouraud, default)
None, turn off light.

Light direction: Set where the light comes from, 'Headlight', 'Right' (default) and 'Left'.

Renderer: Set the render method, 'OpenGL' (default) and 'zbuffer'. The displayed texts are sometimes upside down with some type of AMD ATI graphic cards when using OpenGL mode. Turn this option to zbuffer would solve this problem. However, the texts in the saved image are in the right direction.

Graph detail: Set the level of object detail by adjusting the numbers of vertex of nodes and edges when drawing a graph theoretical network figure, 'High' (default), 'Moderate' and 'Low'

Mark left and right: Display marker 'L' and 'R' in the figure.
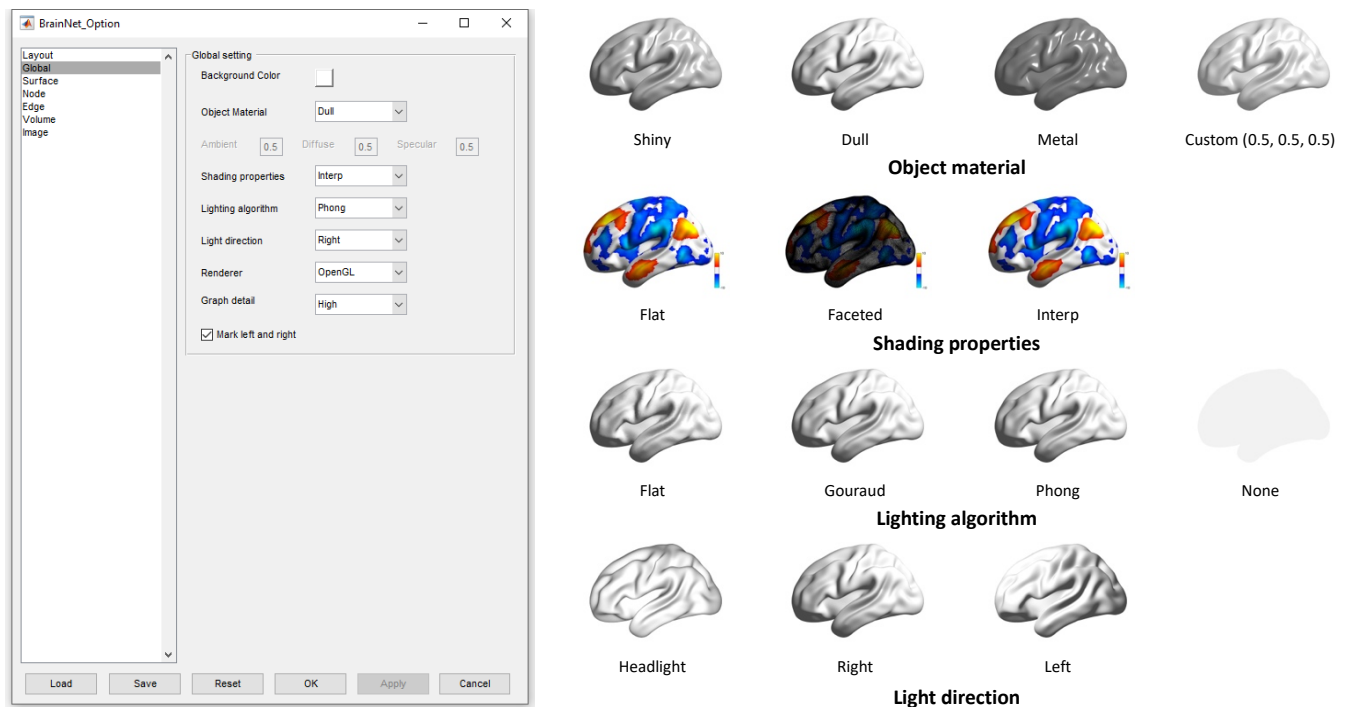
Fig. 12 Global panel

5.3 Surface panel

The surface panel is available for adjusting the properties of the brain surface.

Color: set the color of the brain surface.

Same, set the brain surface with a single color.

Load from file, load a txt file to define the color of each vertex on the surface. The txt file including an n*3 matrix, where n corresponding to the number of vertices of the surface, and the 3-column corresponding to the RGB color index (range: 0~1).

Opacity: drag the slider bar or enter a number range from 0~1 in the edit box to change the transparency of the brain surface.

Boundary: draw boundary of parcellation or cluster on the brain surface. Click the color square button to choose the required color.

None, do not draw a boundary.

Auto extract, automatically draw the boundary for brain atlas or cluster mapping.

Threshold, draw boundary for regions having a value above the threshold.

Load, load a pre-saved boundary file (should be used with the corresponding surface file, the boundary

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file can be saved using the command in the menu).

Double Brain: click to display two brain models in one figure, usually used to display the relationship between nodes in two-time points. To display such a figure, please arrange node and edge files as follow.

Node file: duplicate the node information and adjust it with your data at the end of the file. The first half would be placed in the brain model on the left and the last half would be placed in the brain model on the right. For instance, an original AAL90 node file includes 90 rows; they will be shown on the left. Then copy them and paste as the row 91 to 180, this part would be shown on the right.

Edge file: the edge file includes intra- and inter-brain association matrix. For instance, the original AAL90 edge file includes a 90×90 matrix. In the double brain model, please arrange an edge file with 180× 180 matrix, in which the matrix (1:90, 1:90) and (91:180, 91:180) are intra-brain connections of each brain, and (1:90, 91:180) and (91:180, 1:90) are inter-brain connections between the two brains.
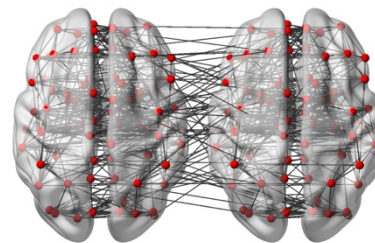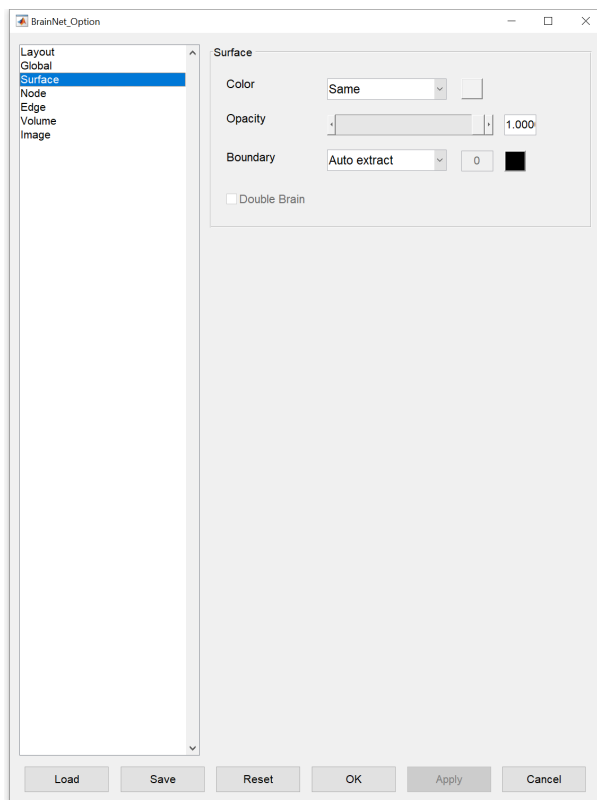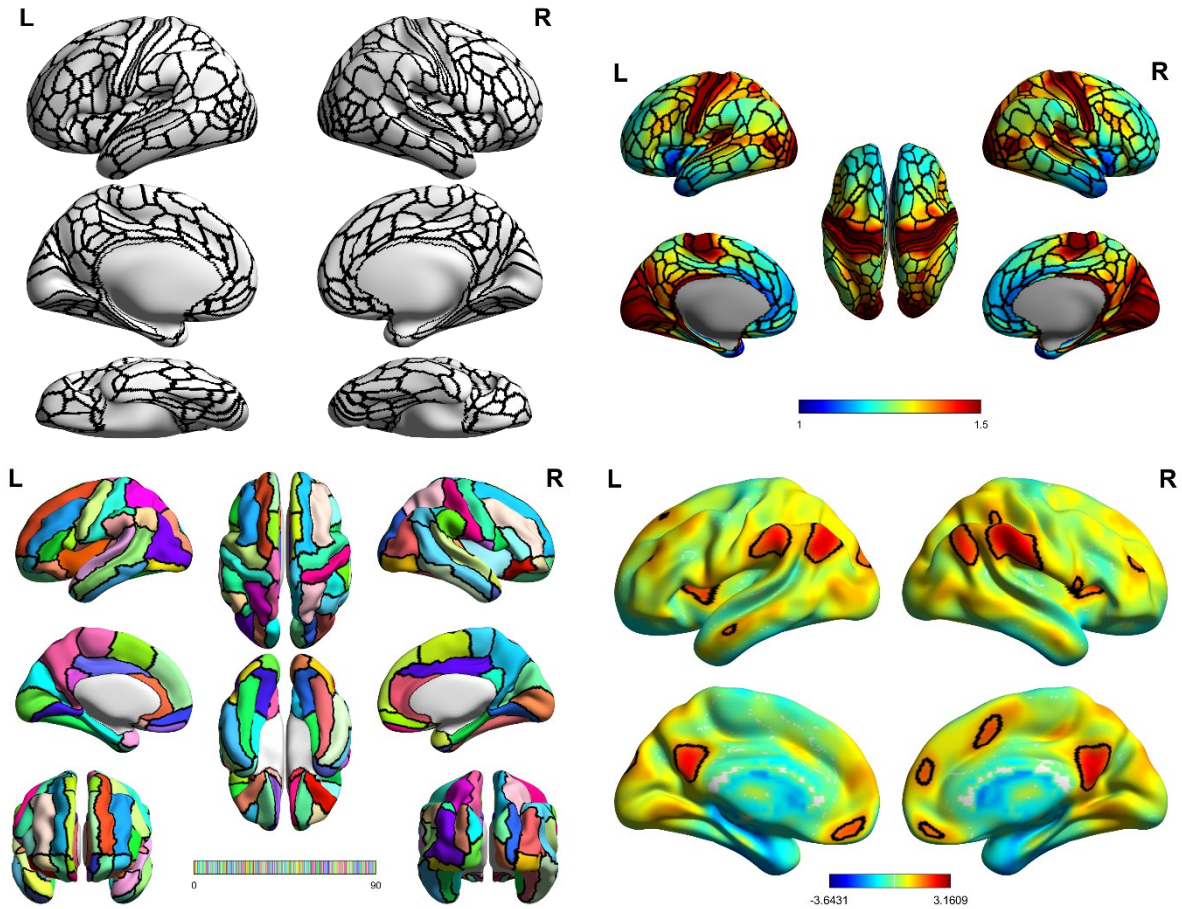
Fig. 13 The surface panel, double brain model, and examples for boundary

5.4 Node panel

The node panel is developed with four zones to select node drawing, set labels, and adjust the node size and color, respectively. All settings are dependent on the nodal information in the nodal file.
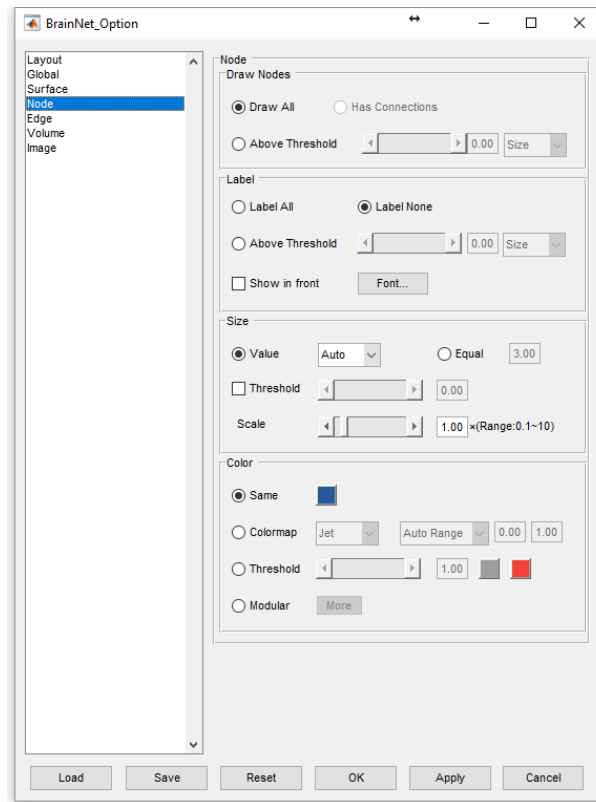
Fig. 14 Node panel

Draw nodes:

This function is used to decide which nodes are to be drawn.

Draw All: draw all nodes in the file.

Has Connections: only draw those nodes that have connections in the edge file.

Above Threshold: set a threshold of color or size corresponding to column 4 or column 5 to draw those nodes with a higher value than the threshold.

Nodal label:

This panel is used to control the nodal label. Three options are available: 'Label All', 'Label None' or by a threshold that only label those nodes with a higher value than the threshold on size or color. Click the 'Font...' button to change the font of the labels in the popup dialog.

Show in front: display nodal labels above the brain surface.

Nodal size:

There are two ways to set the size of the nodes:

Value: use the value in column 5 in the node file. In this manner, you can choose 'Auto' to arrange the sizes of nodes to a proper range (radius: 2-7) by their value automatically, or choose 'Raw' to use the original value in column 5 in the node file. When a threshold is selected, the nodes below the threshold will be a small size (radius: 1), while those above the threshold will display by their Auto/Raw size. Drag the slider bar or enter the threshold in the edit box. The range must be the same as that in column 5 in the node file.

Equal: set all nodes to an equal size ignoring the size value in the file, and the size can be defined in the edit box.

*Scale: t*he volume ratio option is used to adjust the size of all nodes together, and the scale factor ranges from 0.1 to 10.

Nodal color:

This panel provides four ways to control nodal color:

Same: to use the same color for all nodes ignoring the color index in the file, click the color square button and select the required color from the popup dialog.

Colormap: use a color map to display the value of the nodes from low end to high end corresponding to column 4 in the node file. 13 kinds of color maps and custom colormap can be selected (see the right picture for detail). The custom colormap is an n*3 matrix, in which the columns represent the red, green and blue channels, respectively, and the range of the values should be 0 to 1 (e.g., [0 0 0] represents black while [1 1 1] represents white). Colormap range can be set as auto or fixed. In auto mode, the minimum and maximum value in column 4 of node file will be used while in fixed mode, users are allowed to input any values they want.

Threshold: to binarize the color by a given threshold, drag the slider bar or enter the threshold in the edit box, but the range must be the same as the range stated in column 4 of the node file. The nodes with the higher value will have one fixed color, while the nodes with the lower value will have another fixed color. Click the color square button to select the color – the left one represents the higher value color while the right one represents the lower value color.

Modular: modular color can be used to display different nodal colors for different modules. Set the values of column 4 as '1, 2, 3…' corresponding to modular 1, modular 2… in the node file. The maximum number of modules is 21 at present. Click to open the modular color dialog, and the left picture will display six modules with their color on the right. Click the popup menus on the left to select other modules in the list and the color square will change to the corresponding one. Click the color square button to change color as described above.
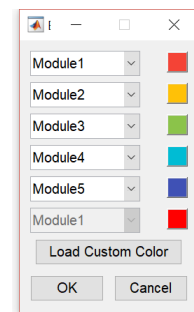
Load Custom Color: Load a .txt file which includes a color bar for modules. The color bar should be arranged as an n*3 matrix, where n refers to the number of modules, and the values represent the red, green and blue channels.

5.5 Edge panel

The edge panel is similar to the node panel, with three parts that separately control edge extraction, edge size, and edge color.
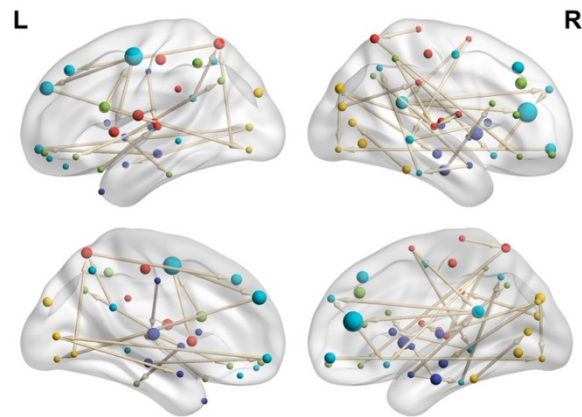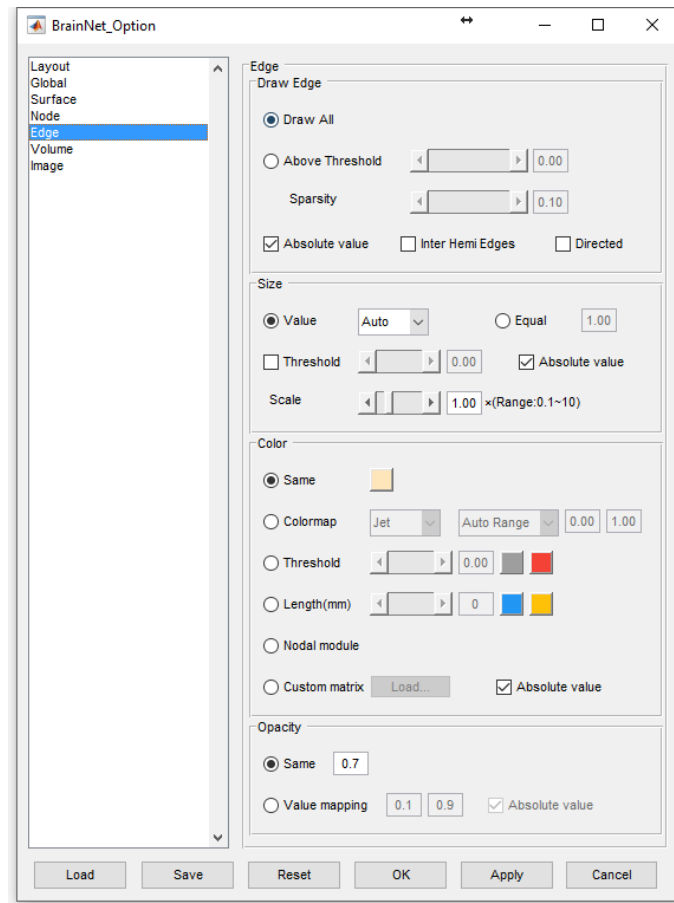
Fig. 15 Edge panel and directed random network

Draw Edge:

This panel is used to extract edge information from the correlation matrix contained in the edge file, and to decide whether all or parts of them are to be drawn.

Draw All: extract and draw all edges (all values not equal to zero) in the correlation matrix.

Threshold: extract the edge above a threshold. This threshold can be set as a value in the matrix or the sparsity of the matrix.

Absolute value: use absolute value to extract edges from the matrix.

Inter Hemi Edges: extract edges that travel across two hemispheres.

Directed: draw edges with direction.

Note that BrainNet Viewer will treat the value zero (0) in the matrix as a null edge, and only the right upper triangle of the matrix will be considered in undirected mode. Always remember to change the threshold when a weighted matrix is loaded, or it will draw the full connection among the nodes, which would require a lot of time.

Edge size:
There are two ways to set the size of edges (here, size means the radius of the edge);

Value: employ the correlation matrix value in the edge file. In this manner, you can choose 'Auto' to assign the edge sizes a proper range (radius: 0.3-1.5) by their value automatically or choose 'Raw' to use the original value of the correlation matrix in the edge file. When a threshold is selected, the edges with values lower than the threshold will have a fixed, smaller size while the edges above the threshold will be shown as Auto/Raw size. Drag the slider bar or enter the threshold into the edit box, but the range must be the same as the correlation matrix in the edge file.

Equal: set all edges to equal size, and the size can be defined in the edit box.

Scale: the scale option is used to adjust the size of all edges together. The scale factor ranges from 0.1 to 10.

Absolute value: use absolute value in matrix to calculate edge radius.

Edge color:
This panel provides six ways to control edge color:
Same: adopt the same color for all edges, click the color square button and select the required color from the popup dialog.

Colormap: use a colormap to render the value of the edge from low to high corresponding to the values

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of the correlation matrix in the edge file. 13 kinds of colormaps and custom colormap, same as the nodal colormaps can be selected. The custom colormap is an n*3 matrix, in which the columns represent the red, green and blue channels, respectively, and the range of the values should be 0 to 1 (e.g., [0 0 0] represents black while [1 1 1] represents white). Colormap range can be set as auto or fixed. In auto mode, the minimum and maximum value edge file will be used while in fixed mode, users are allowed to input any values they want.

Threshold: binarize the color by a given threshold, drag the slider bar or enter the threshold into the edit box. The range must be the same as the correlation matrix in the edge file. Click the color square button to select colors – the left one represents the lower value while the right one represents the higher value.

Length: binarize the color by a given threshold of Euclidean distance between two nodes (mm). The edges with a longer length have one fixed color, while the shorter ones have another fixed color. Drag the slider bar or enter the threshold in the edit box; the threshold can range from zero to 100. Click the color square button to select colors, the left one represents the higher value while the right one represents the lower value.

Nodal module: assign edge color according to the color of nodes it links. If two nodes of the edge have the same color, the edge will be set as the same color. If the two nodes are with different colors, the edge will be colored gray.

Custom matrix: load a matrix with the same size to the network, in which the edges can be assigned with color indices. For instance, edges in the network (n×n) were required to be rendered with three different colors. Do follows: i) generate a matrix (n ×n); ii) assign each edge with an index value (1, 2 or 3) and save the matrix as a text file; iii) load this file in this panel and set the color for each index in the popup window.
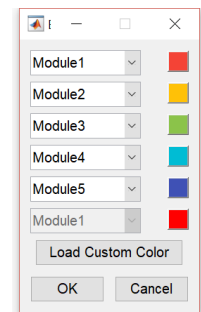
Absolute value: use absolute value in matrix to calculate edge color.

Edge opacity:
There are two ways to set the opacity of edges;

Same: set all edges with same opacity, default = 0.7;

Mapping: scale the edges' opacity according to their values. The minimum and maximum opacity can be set in the panel.

Absolute value: use absolute value in the matrix to calculate edge opacity.

5.6 Volume panel

The volume panel is set to control the volume-to-surface mapping and draw ROI clusters with the brain surface. The volume file could be a T-map, Z-map, an atlas image, etc.
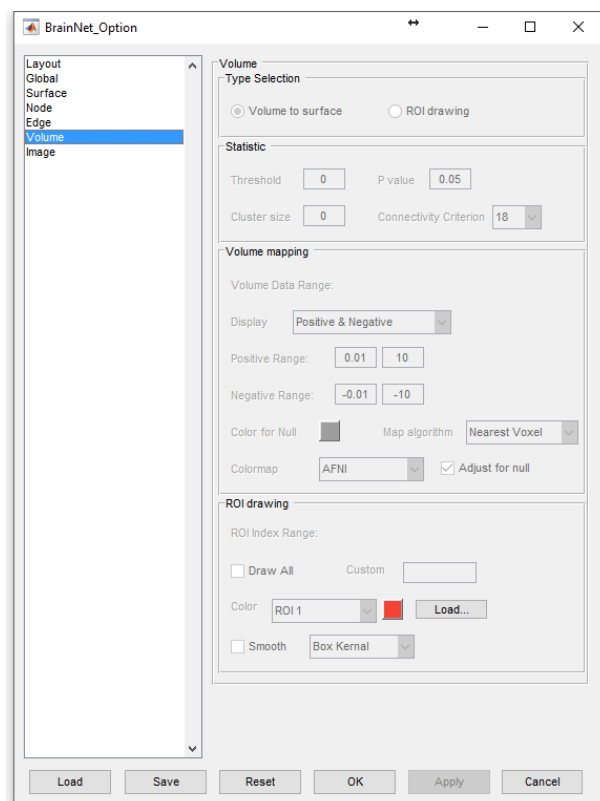
Fig. 16 Volume panel

Type Selection: select to map the volume to brain surface or to draw ROI volume in the brain surface.
Statistic zone:
Threshold: set a threshold that only using the voxels with a value higher than the threshold or lower than the negative threshold.

P value: work with the statistical volumes generated by SPM, REST or DPABI.

Cluster size: set a threshold to select and display clusters have larger voxel number.

Connectivity Criterion: set connectivity criterion for voxel connections. 6 for surface connected, 18 for edge connected and 26 for corner connected.

Volume mapping zone:

Volume Data Range: show the minimum and maximum values of the volume file.

Display: contain three mapping manner, 'Positive & Negative', 'Positive only' and 'Negative only'. 'Positive & Negative' sets the range of color bar from the minimum negative value to the maximum positive value, and 'Positive only' and 'Negative only' just set the range of the color bar in positive value or negative value separately.

Positive Range and *Negative Range*: set the range of the color bar. The edit boxes on the left define the value near zero on the color bar, while the right ones define the value away from zero. Take the above picture as an example. When 'Positive & Negative' is chosen, the color bar would be arranged from -3 to 3, and -0.01 to 0.01 would be set as the null value range; if 'Positive only' is selected, the color bar would be arranged from 0.01 to 3, any value below 0.01 would be set as a null value; and if 'Negative only' is selected, the color bar would be arranged from -0.01 to -3, and any value above -0.01 would be set as a null value (see Fig. 17).
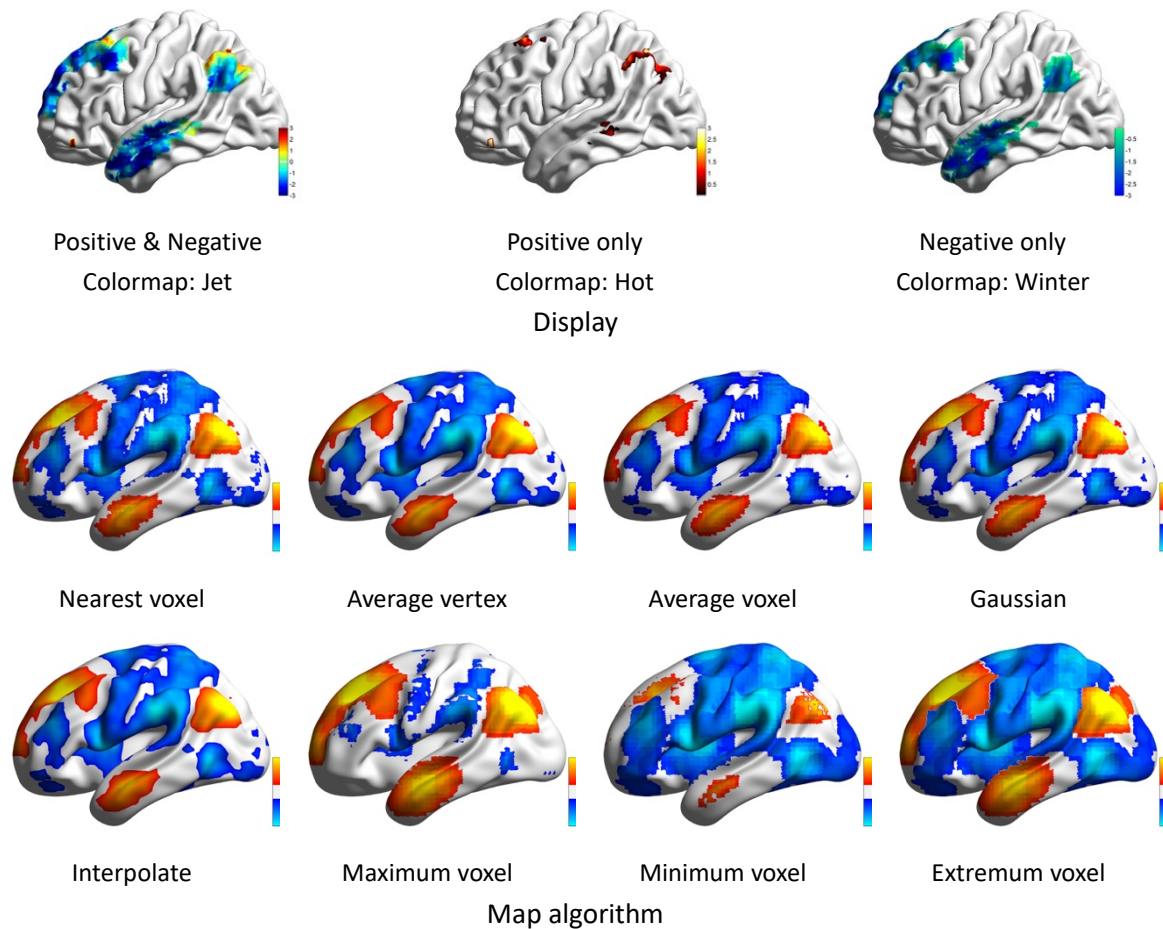
Color for Null: define the color for the null value part on the surface. Click the color square button and select the required color.

Adjust for Null: when this option is selected, the colormap will be adjusted for null value vertex. Specifically, in Positive & Negative mode, the vertex with value between high end of negative interval and low end of positive interval will be set as color for null; in only positive mode, the vertex with value below the low end of positive interval will be set as color for null; and in only negative mode, the vertex with value larger than the low end of positive interval will be set as color for null.

Colormap: provide 24 kinds of colormaps including custom colormap. The custom colormap is an n*3 matrix, in which the columns represent the red, green and blue channels, respectively, and the range of the values should be 0 to 1 (e.g., [0 0 0] represents black while [1 1 1] represents white).

Map algorithm: eight mapping algorithms are provided to determine the vertex values in BrainNet Viewer: 'Nearest Voxel', assign the vertex with the value of the voxel in volume that is nearest to it, suitable to display an atlas or mask; 'Average Vertex', assign the vertex with the value of the voxel in volume that is nearest to it, and then average the vertex across its neighbors (high time consumption); 'Average Voxel', assign the vertex with average value of the voxel and its neighbors in volume that is nearest to it; 'Gaussian', the volume first employs convolutions with a Gaussian kernel and then assigns the vertex with the value of the voxel in volume that is nearest to it; 'Interpolated', the coordinate of the

vertex is determined in the volume space, and a trilinear interpolate method is then used across its neighbors to calculate the value; 'Maximum Voxel', assign the vertex with the maximum value of the voxel and its neighbors in volume that is nearest to it; 'Minimum Voxel', assign the vertex with the minimum value of the voxel and its neighbors in volume that is nearest to it; 'Extremum Voxel', assign the vertex with the extremum value of the voxel and its neighbors in volume that is nearest to it.

Positive & Negative
Colormap: Jet

Positive only
Colormap: Hot

Negative only
Colormap: Winter

Display

Nearest voxel   Average vertex   Average voxel   Gaussian

Interpolate   Maximum voxel   Minimum voxel   Extremum voxel

Map algorithm

Fig. 17 Volume mapping

ROI drawing zone: (Please ensure your volume data is arranged with natural number index)
ROI Index Range: show the minimum and maximum index of the volume file, number 0 is out of use.

Draw All: construct and draw each ROI volume in sequence according to their index.

Custom: input the index number of ROIs, these ROIs will be selected to reconstruct and draw.

Color: set the color of each ROI volume. The 'Load...' button next to the color button allows users to load

a custom-defined color table for each ROI. This color table should be saved as a '.txt' file including n*3 matrix, where n corresponds to the number of ROIs and the columns represent the red, green and blue channels, respectively. The range of the values should be 0 to 1 (e.g., [0 0 0] represents black while [1 1 1] represents white).

Smooth: smooth the surface of ROI volume. Two smooth kernels, 'Box' and 'Gaussian' are provided. Please see the help for function 'smooth3' in Matlab for further information.

Fig. 18 ROI volume drawing

5.7 Image panel

In the image panel, the configurations are related to the size and resolution of the output images. The width and height of the image can be adjusted in pixel dimensions for screen display or in real units (centimeter or inch) for document use. The resolution of the output image can also be modified in dots per inch (DPI). (Fig. 19).
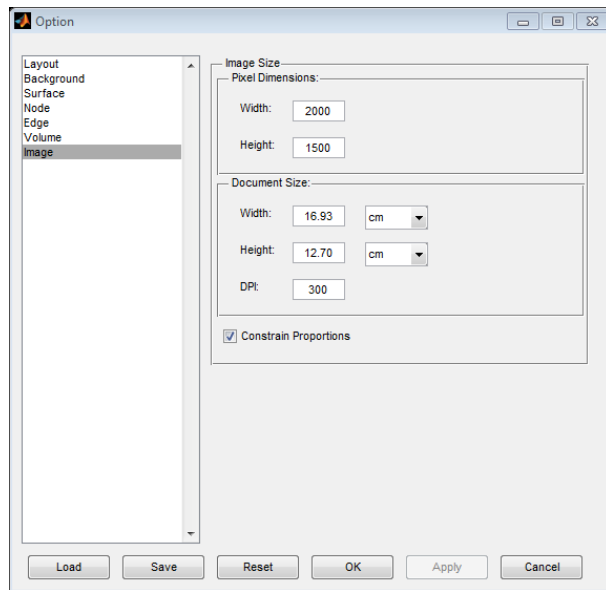
Fig. 19 Image panel

6 Menu

6.1 Files

Load files:
Click to open the load files panel (for more details, see Section 'Load Files').

Save Image:
After visualization, click here to save the present figure as an image. At present, TIFF, BMP, EPS, JPEG, and PNG image formats are supported. The parameters of the image such as pixel dimension, document size, and dpi can be adjusted in the 'Option panel\Image'. After the image is saved, a message box appears (see right picture).
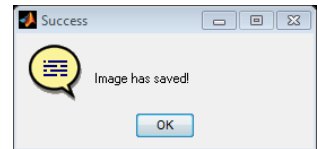
Save Movie:
This function helps users to save a demonstration movie for network visualization. It produces a 12 seconds long, 30 FPS, 735×534, avi file in which the brain network rotates clockwise in a circle, one degree per frame. This operation will take about 10 minutes. Please drink a cup of coffee to wait before playing the movie. Note that this function should only be used in the 'Single View' layout. Pictures below show different frames at different times. For example, see http://www.nitrc.org/docman/view.php/504/1023/Demo%20Video%20of%20Brain%20Network%20(14M)

3s   6s   9s
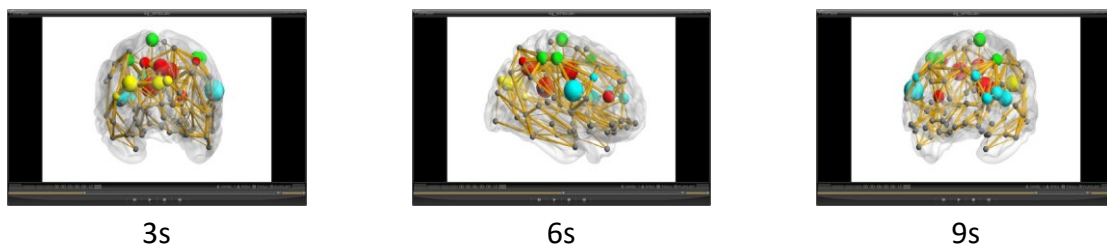
Fig. 20 Frames of the network movie

Exit: Click to exit BrainNet Viewer.

6.2 Option

Option: Click to open the option panel (see more details in the section 'Visualize Option').

Load Option: Load a previously saved visualize option file.

Save Option: Save current visualize option as a *.mat file.

Colormap Editor: Call colormap editor to edit colormap manually.

Apply Colormap: Apply edited colormap by colormap editor to all graphs in the figure.

Save Colormap: save colormap as a text file. The saved colormap can be used by copy its text into custom colormap in the option panel.

6.3 Visualize

Redraw:
Clear figure and redraw network using the data and option last loaded.

Clear Figure:
Remove the brain network and display the default information of BrainNet Viewer.

6.4 Tools

Merge Mesh:
This tool is used to merge the left and right hemisphere surface files extracted from FreeSurfer (*.pial) or BrainVISA (*.mesh) from two separate files into one BrainNet Viewer surface template file (*.nv), or to convert a one hemisphere surface file to a BrainNet Viewer surface template file (*.nv). When both 'Left Mesh' and 'Right Mesh' files are selected, the new mesh will combine two hemisphere files into one file. If only one of the input files is selected, the new mesh file will convert only that hemisphere file (Fig .21).
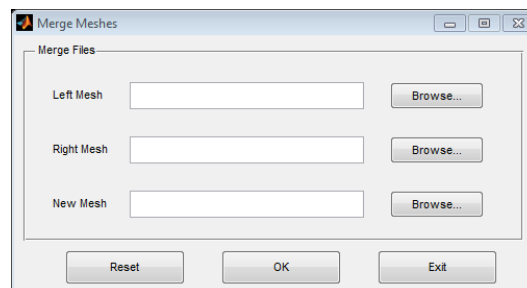
Fig. 21 Merge Meshes tool

Save Boundary:

Save the current boundary as a txt file, which can be loaded for further use.

6.5 Help

Manual:

Open this manual for help.

About:

Show version, author and contact information of BrainNet Viewer in a dialog.

7 Toolbar

The toolbar (Fig. 22) provides frequently-used and interaction commands to operate the brain network graph, most of them are not included in the menu.
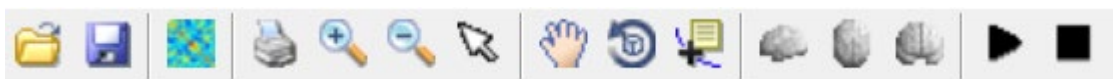

Fig. 22 Toolbar

7.1 Load Files & Save as Image

These two commands are included in the menu, see details in section 'Load Files', and section 'Menu\File\Save Images'.

7.2 Print & Zoom

The Print command lets users print the current graph conveniently. A print panel like the one below will pop up after the Print button is clicked.
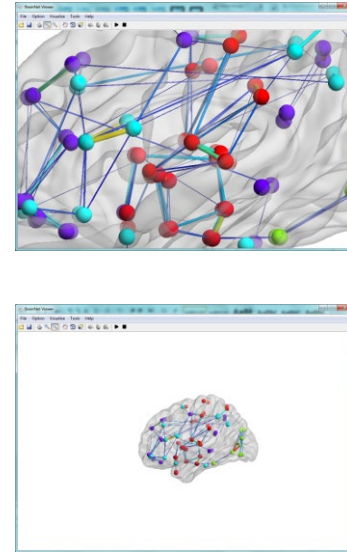
The zoom in and zoom out functions help to observe the local or global status of the brain network.

7.3 Plot Edit

The Plot Edit button can activate the figure edit mode of MATLAB, which allows the users to flexibly set the detailed configuration of the figure.
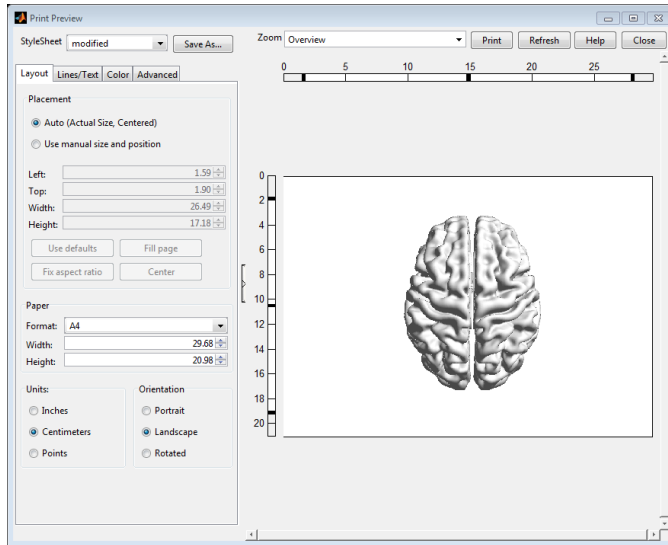
Print panel   Zoom in & Zoom out

Fig. 23 Print panel and Zoom function

## 7.4 Move, Rotate & Get position

Click the 'Move' button and drag the brain anywhere in the window.

When the 'Rotate' button is pressed, hold the left button of the mouse and move the mouse to rotate the brain. When the rotate button is deselected, the light cam in the window will re-render the brain model depending on the current orientation.

Click the 'Get position' button, and then click on the surface of the brain to display the coordinates and value of the vertex on the surface, and it also provides the corresponding brain region labels in terms of AAL and Brodmann atlases. Right-click anywhere in the figure window, and select 'Delete All Datatips' to remove all coordinate labels.

7.5 Standard view

Shortcuts for three standard views, sagittal, axial and coronal, are available to quickly observe networks from different standard views. These buttons should only be used for 'Single view' visualized brain networks. Click twice to see the opposite side of the brain.

| Sagittal View | Axial View | Coronal View |
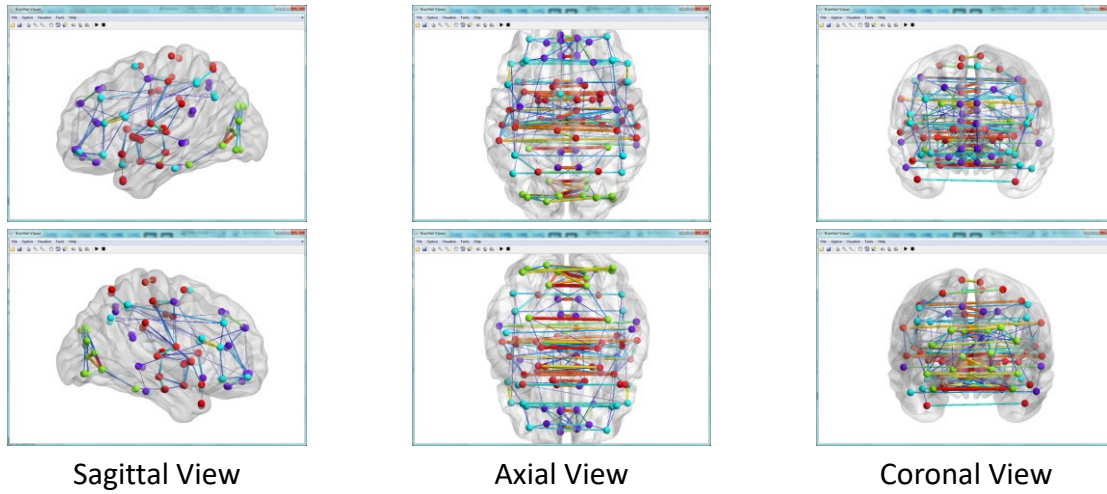
Fig. 24 Standard views

7.6 Demo

Press the black triangle button to make the brain rotate clockwise until the black square button is pressed. This function only works for 'Single View' visualizations.

8 Command-line

Considering the growing requirements for batched brain connectome figure mapping, such as dynamic brain functional connectomes, the functionality to generate brain network figures in the command line is provided. The function is called according to the following command line:

BrainNet_MapCfg(filename1, filename2…);

where the variables of filenames can be any one of the brain surface, node, edge and volume files. Once the files are loaded, BrainNet Viewer draws the graphs with default configurations. For instance, a command line of

BrainNet_MapCfg('BrainMesh_ICBM152.nv','Node_AAL90.node');

will draw the brain surface of 'BrainMesh_ICBM152.nv' and nodes in 'Node_AAL90.node' files using default settings.

A pre-saved configuration file can also be included in this command line. For example, the command line

BrainNet_MapCfg('BrainMesh_ICBM152_smoothed.nv','OneSample_T.nii','Cfg.mat');

would map the volume 'OneSample_T.nii' onto brain surface 'BrainMesh_ICBM152_smoothed.nv' using the settings pre-saved in the 'Cfg.mat' file.

The command line also supports exporting the brain network figure as an image file. The names of the required image files are added to the command line

BrainNet_MapCfg('Node_AAL90.node','Edge_AAL90_Binary.edge', 'Net.jpg');

Using this command, BrainNet Viewer draws a network in which the node information is obtained from 'Node_AAL90.node' and the edge information is obtained from 'Edge_AAL90_Binary.edge' using default settings, and this figure will be saved as a JPEG image as 'Net.jpg'. The order of these inputted filenames is exchangeable, and the combinations of files are similar to the GUI version.

Acknowledgments

We thank the following colleagues for their kind helps during BrainNet Viewer developing and manual revising:

Gaolang Gong, Ni Shu, Zhilei Xu, Jiaying Zhang, and Yapei Xie, Beijing Normal University, China;

Alan C Evans and Xindi Wang, McGill University, Canada;

Jinhui Wang, South China Normal University, China;

Chaogan Yan, Chinese Academy of Sciences, China;

Zhengjia Dai, Sun Yat-sen University, China;

Teng Xie, Peking University No.6 Hospital, China;

Qixiang Lin, Emory University, USA;

Miao Cao, Fudan University, China;

Jin Liu, Stanford University, USA

We also thank the developers of the following softwares and toolboxes whose source codes or file formats were referenced during our package developing:

Matlab: www.mathworks.com/products/matlab/

SurfStat: www.math.mcgill.ca/keith/surfstat/

FreeSurfer: http://surfer.nmr.mgh.harvard.edu/

BrainVISA: http://brainvisa.info/

SPM: www.fil.ion.ucl.ac.uk/spm/

REST: www.restfmri.net/

Surf Ice: www.nitrc.org/projects/surfice/

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