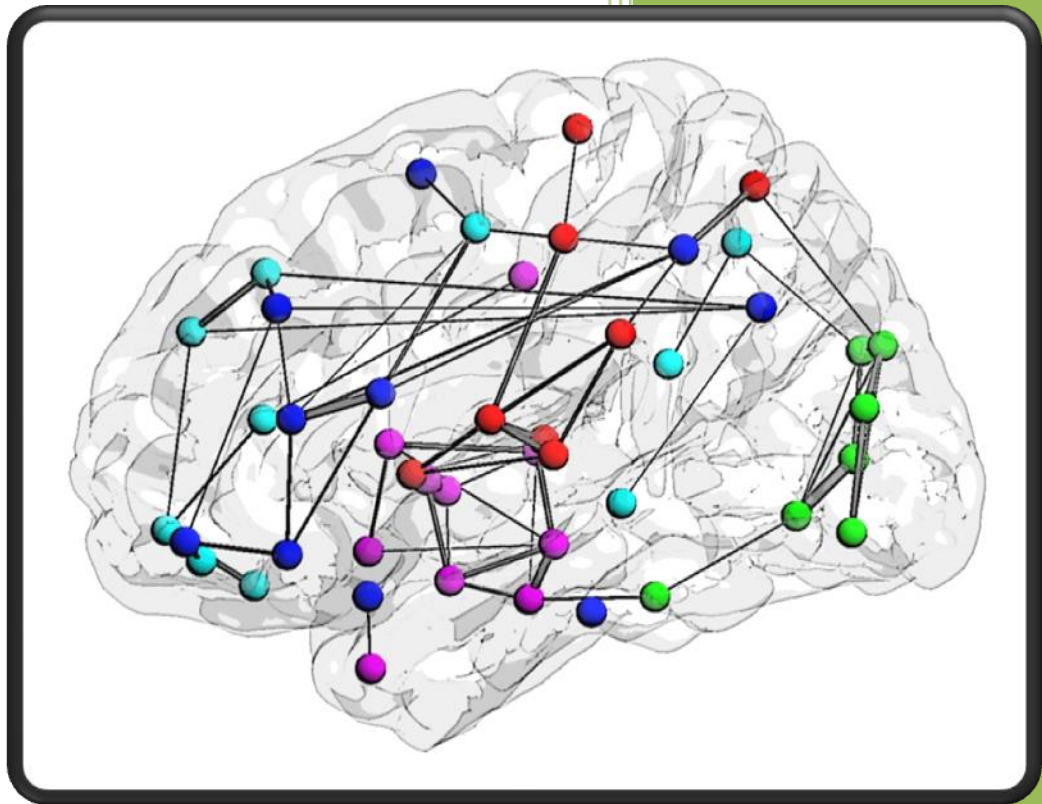# 2013

BrainNet Viewer Manual

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Version 1.42, Released 20130709

Contents

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1 Introduction

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 a brain network visualization tool, which can help researchers to visualize structural and functional connectivity patterns from different levels in a quick, easy and flexible way. It would be greatly appreciated if you have any suggestions about the package or manual.

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 and Analyze format files (*.nii; *.img). This toolbox has been successfully tested under a variety of operating systems with MATLAB installed, including Windows (XP, 7, 8 and Server versions), Linux (Ubuntu and CentOS) and Mac OS in both 32- and 64-bit versions.

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2 Installation

2.1 Run BrainNet Viewer on a PC with Matlab

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

Add BrainNet Viewer path to Matlab search path:
1) *Type 'Addpath('X:\...\BrainNet');', where 'X:\...\BrainNet' refers to the path of BrainNet Viewer on the machine.*

   or

2) *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. (**Recommended**)*

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

2.2 Run BrainNet Viewer on a PC without Matlab

Please contact us if you need standalone version. It cannot be found on the NITRC due to the large size.

Install Matlab Components Runtime (MCRInstall.exe for Windows OS, or MCRInstaller.bin for Linux and Mac OS, ~200MB) using default settings.

Restart your computer (strongly recommended).

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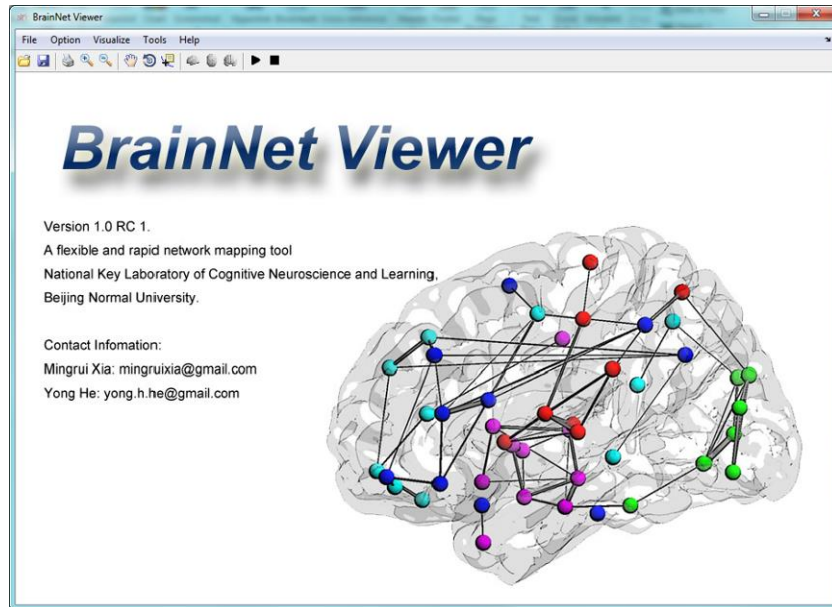
**Fig. 1 The interface of BrainNet Viewer**

3 Pictures

BrainNet Viewer will not load surface, node, edge and volume file together. The following combinations are acceptable and different combinations will generate different network pictures (see 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 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 and 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 section 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.
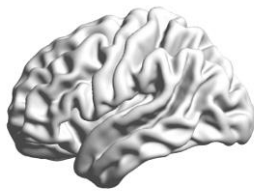
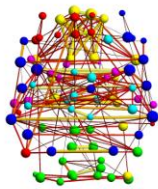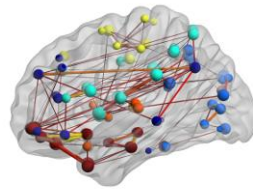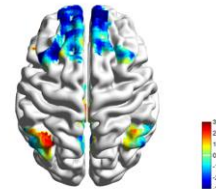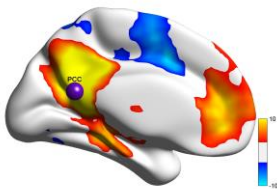1) Brain Surface
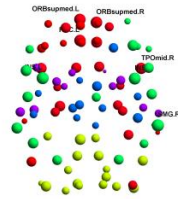
2) Nodes
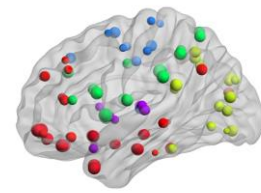
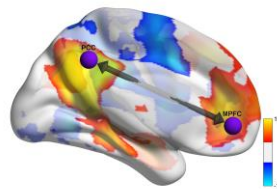3) Surface & Nodes

4) Nodes & Edges

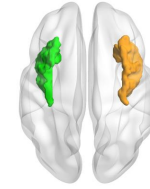5) Surface, Nodes & Edges

6) Surface mapping

7) Surface mapping & node

8) Surface mapping with node & edge

9) ROI in Volume

Fig. 2 Brain network pictures with the BrainNet Viewer

4 Load Files

To draw a brain network graph, some kinds of files such as brain surface, node file or edge file should be loaded in the first step. Click 'Load File' button on the toolbar or 'File\Load File' in the menu to open Load File dialog shown below (Fig. 3). Select files to draw 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, inflated Colin brain, Colin brain with cerebellum, ICBM152 brain (MNI/Talaraich), smoothed ICBM152 brain (MNI/Talaraich), hemispheres of ICBM152 and hemispheres of smoothed ICBM152 brain 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), 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) and others (e.g., customized ROIs by users) in the folder '.\Data\ExampleFiles'.
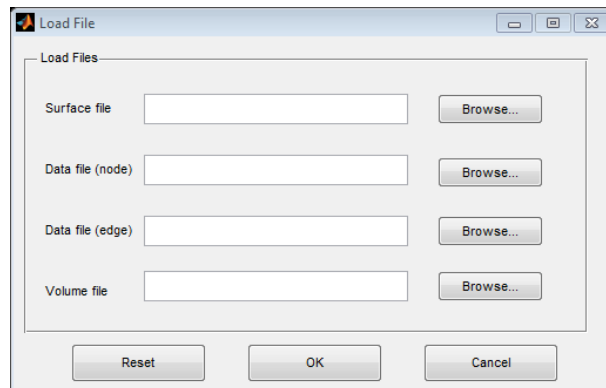

Fig. 3 Load File dialog

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).
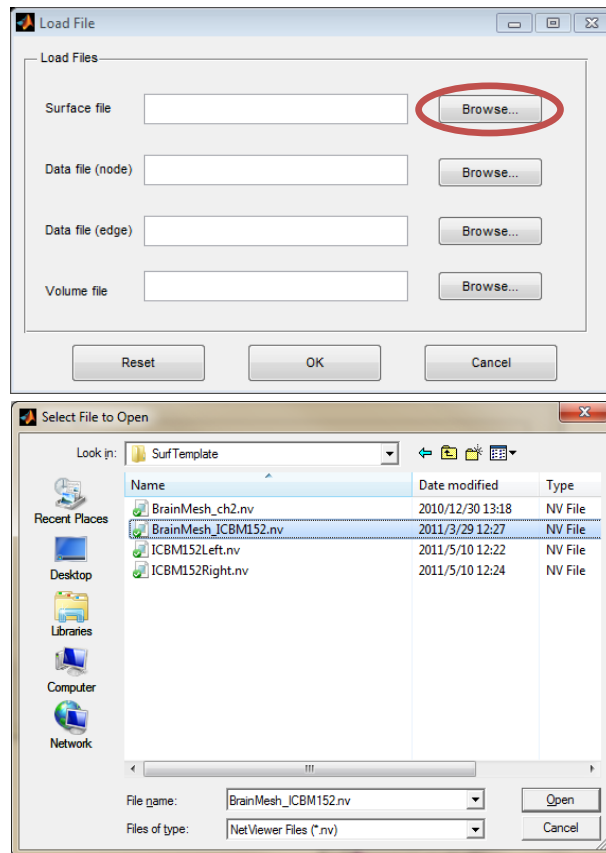
Fig. 4 Select brain surface (ICBM152 is selected)

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 derived from Freesurfer
(http://surfer.nmr.mgh.harvard.edu/) and the Colin27 brain surface was made by

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BrainVISA (http://brainvisa.info/). We transferred and merged the original bilateral hemisphere files into one '.nv' file. A surface merge tool is in the tools menu (see more details in section 6.4 'Menus\Tool').

Currently, the '*.pial' files generated by FreeSurfer, (only hemisphere mesh) and the '*.mesh' files generated by BrainVISA are supported, and these can be loaded and visualized directly. The FreeSurfer pial files are recommended as their vertex coordinates have been transformed into the MNI space, while the BrainVISA mesh files may need a manual transformation.

The ICBM152Left.nv and ICBM152Right.nv files are from Professor Alan Evans's group in the Montreal Neurological Institute, McGill University. Of note, the coordinates in the surfaces are located in the MNI space.

4.2 Load a node file

The file represents the information from ROIs obtained from the AAL90, Brodmann82, HOA112, Dos160, Fair34, LPBA40 and others (e.g., customized ROIs by users). Each file is in the folder '.\Data\ExampleFiles\' corresponding to its template name. 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 in Fig. 5.
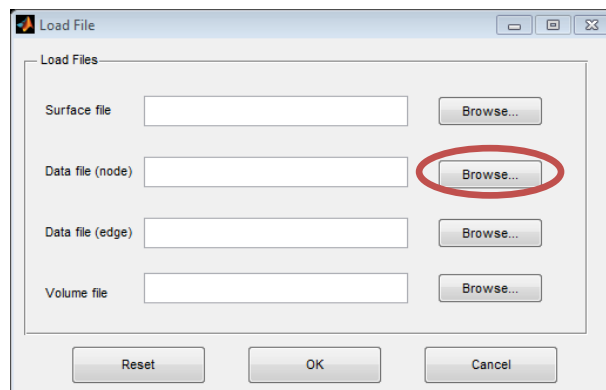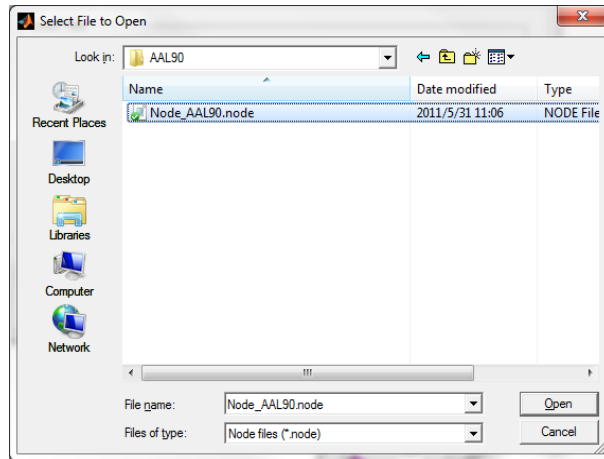
Fig. 5 Select node file (AAL90 is selected)

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. 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. You can generate your nodal file according to the 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 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. You can generate your edge file according to the requirements.

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.

4.4 Load a volume file

This function lets users map the volume data to the brain surface. The volume file should be NIFTI format, which could be T-map, Z-map, atlas or any other volume data, either paired files or nii file are accepted. Besides, a text file containing an n $\times$ 1 vector is 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 voxels in the image file using different algorithms, and assign vertices to corresponding values. The principle of ROI drawing is to reconstruct voxels with same index in the image file to 3D volume.
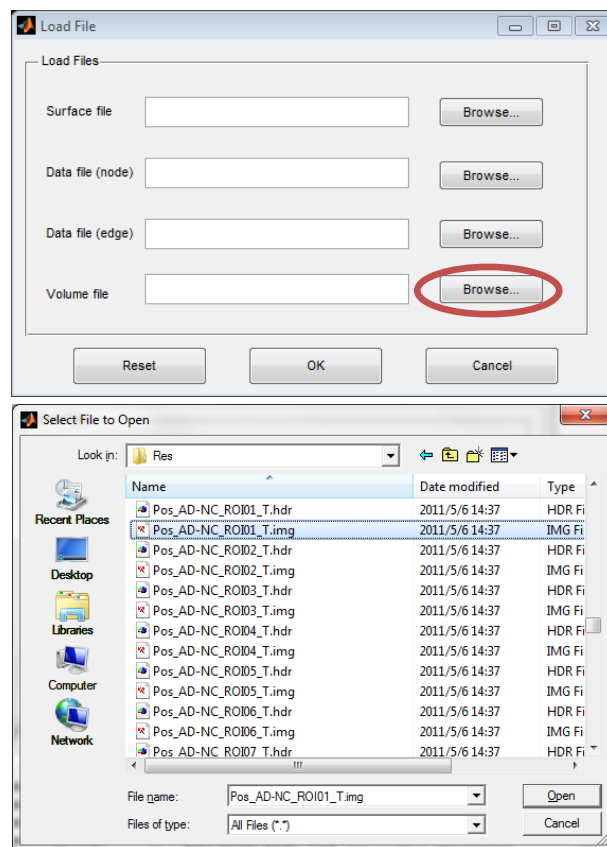

Fig. 9 Volume file (a paired NIFTI file of T-test Map is selected)

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.
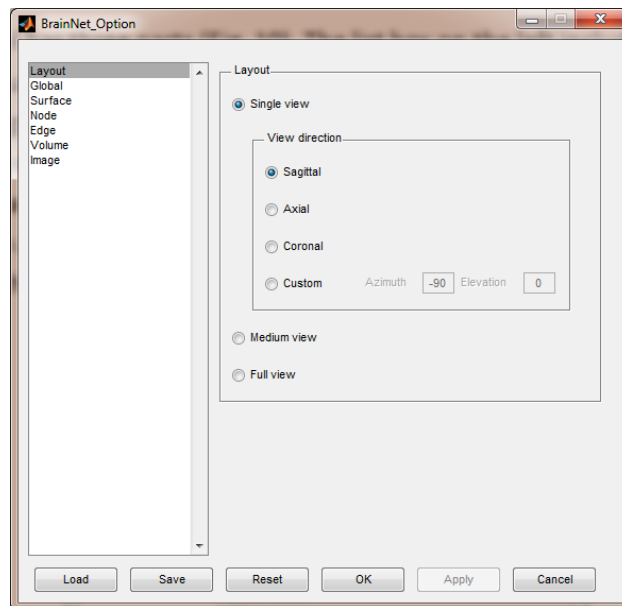
Fig. 10 Option panel

5.1 Layout panel

The layout panel (Figure 4A) is primarily responsible for setting the output view of the brain model, in which three types of views are provided:
Single view: Show only one brain model in the figure.
Sagittal Show the brain in sagittal view (left side).
Axial Show the brain in axial view (dorsal side).
Coronal Show the brain in coronal view (frontal side).
Custom Show the brain in a custom viewpoint, defined by azimuth and elevation (see

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more detail of function 'view' in Matlab help).

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

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 right side, bottom side and back side. In the eight brain mode, the first row from left to right are lateral view of left hemisphere, top side, 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 back side. See Fig. 11.
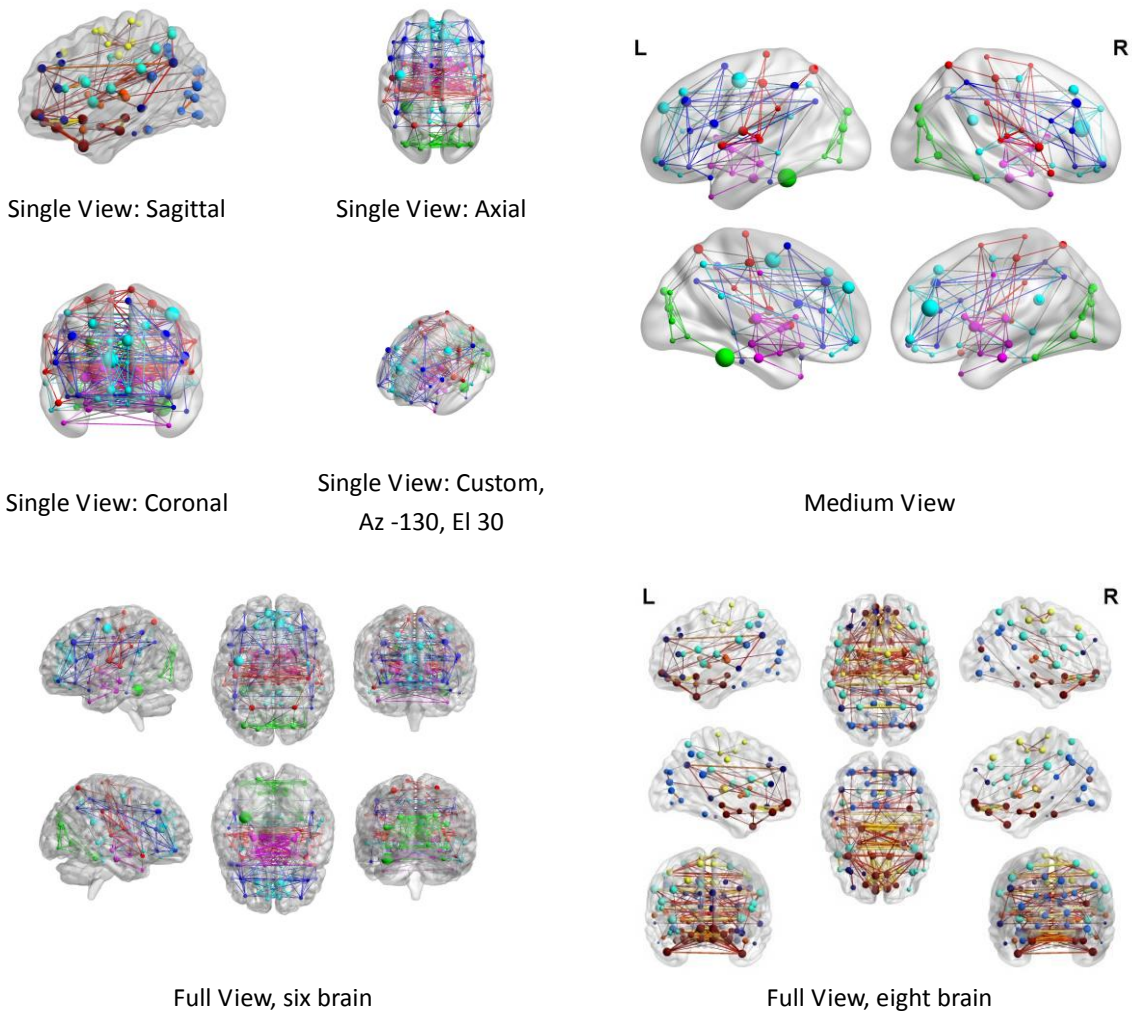

Single View: Sagittal

Single View: Axial

Single View: Coronal

Single View: Custom,
Az -130, El 30

Medium 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. Right-click on the color square right beside the text 'Background Color', and select the desired color in the popup dialog.

Object Material: Provide four manner to define material of the mode in 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 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 normals and interpolates linearly across the triangles.
Phong, interpolates the vertex normals 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'. Texts displayed 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 image is saved with texts in 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'
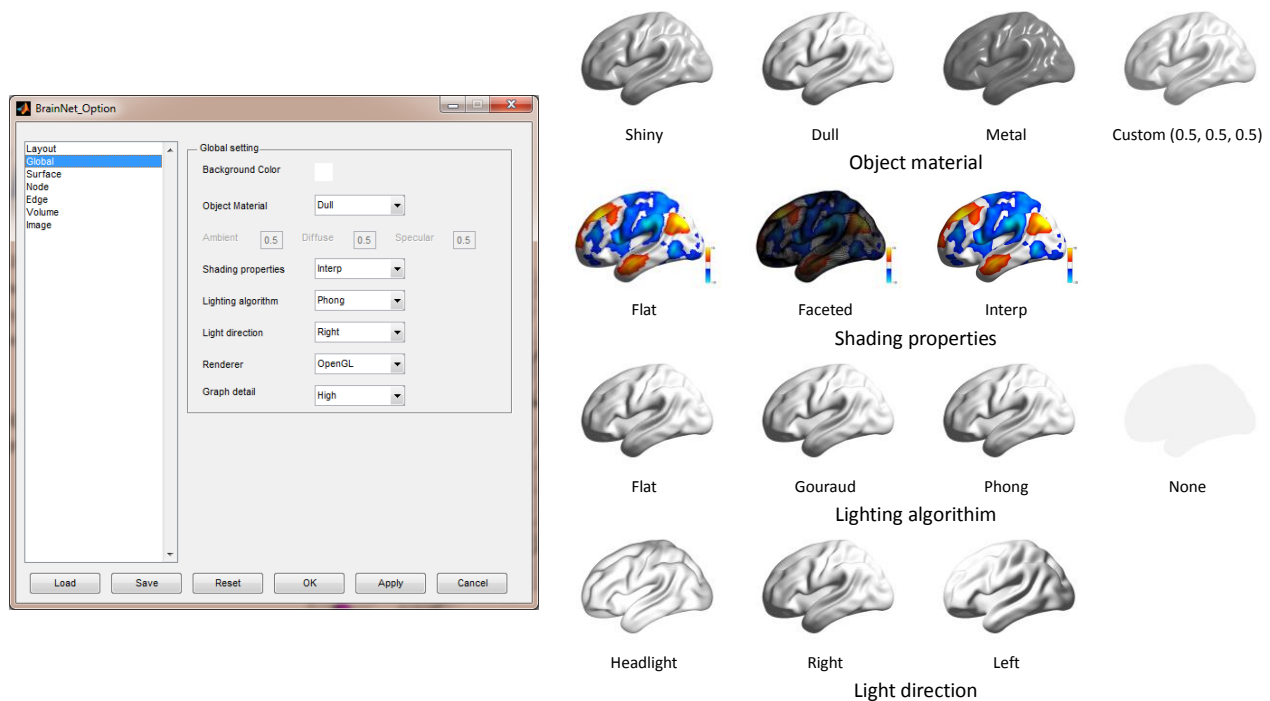
and 'Low'

Fig. 12 Global panel

5.3 Surface panel

The surface panel is available for adjusting the properties of the brain surface.
Color: right-click the color square and select required color in the popup dialog to change color of the brain surface.

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.

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 figure, please arrange node and edge files as follow.
Node file: duplicate the node information and adjust with your own 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.

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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 connections of each brain, and (1:90, 91:180) and (91:180, 1:90) are inter connections between the two brains.
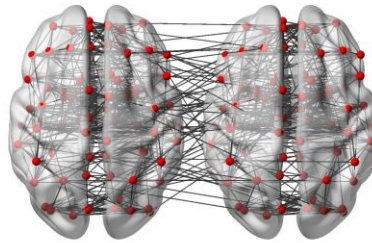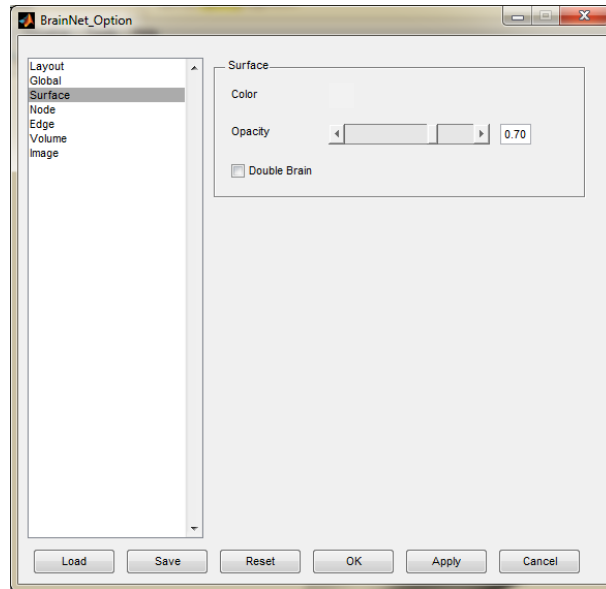

Fig. 13 Surface panel and double brain model

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.
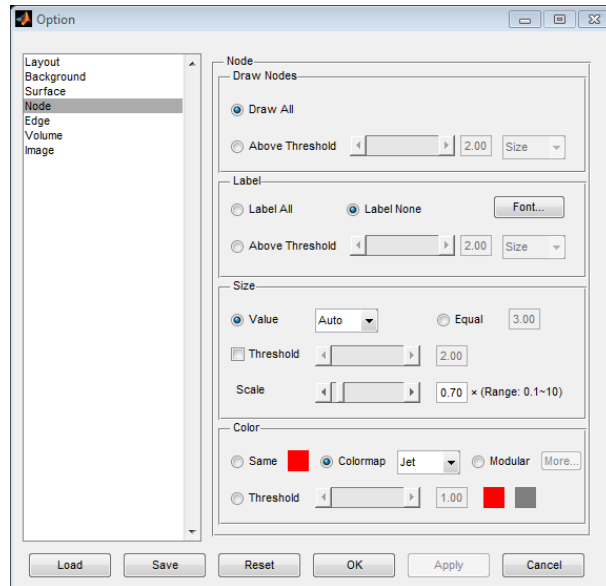
Fig. 14 Node panel

Draw nodes:

This function is used to decide which nodes are to be drawn. Select 'Draw All' to draw all nodes in the file, or set a threshold of color or size corresponding to column 4 or column 5 to draw those nodes with 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 higher value than the threshold on size or color. Click the 'Font…' button to change the font of the labels in the popup dialog.

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 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.

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*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, right-click the color square 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 can be selected (see the right picture for detail).
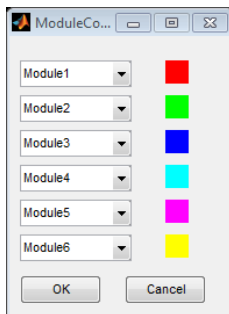
Modular: modular color can be used to display different nodal colors for different modules. Set the values of column 4 as '1, 2, 3…' corresponding to modular 1, modular 2… in the node file. The maximum number of modules is21 at present. Click to open the modular color dialog, and the left picture will 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. Right-click the color square to change color as described above.

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 higher value will have one fixed color, while the nodes with lower value will have another fixed color. Right-click the color square to select the color – the left one represents the higher value color while the right one represents the lower value color.

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.
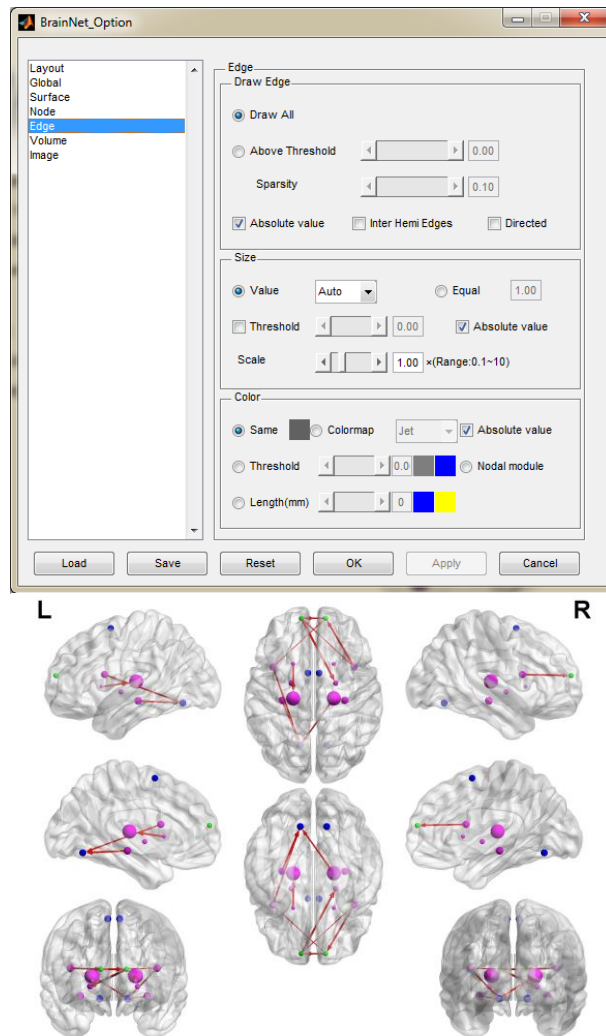
Fig. 15 Edge panel and directed network

(Image data is from M.Ghasemi, Tarbiat Modares University, Tehran, Iran)

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 in 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 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 an 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 five ways to control edge color:
Same: adopt the same color for all edges, right-click the color square 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 of the correlation matrix in the edge file. 13 kinds of colormaps, same as the nodal colormaps can be selected.

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. Right-click the color square 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 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. Right-click the color square 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 same color, the edge will be set as the same color. If the two nodes are with different color, the edge will be colored gray.

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

5.6 Volume panel

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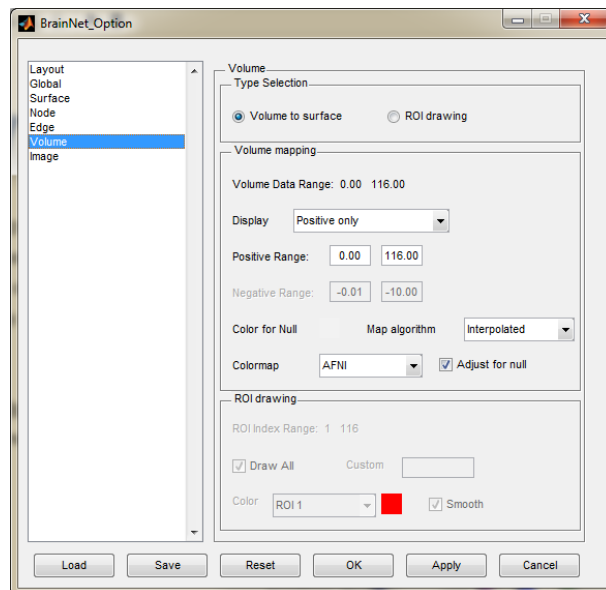

Fig. 16 Volume panel

Type Selection: select to map volume to brain surface or draw ROI volume in brain surface.

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 colorbar range from the minimum negative value to the maximum positive value, and 'Positive only' and 'Negative only' just set the range of the colorbar 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 null value part on the surface. Right-click the color square and select 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.

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.
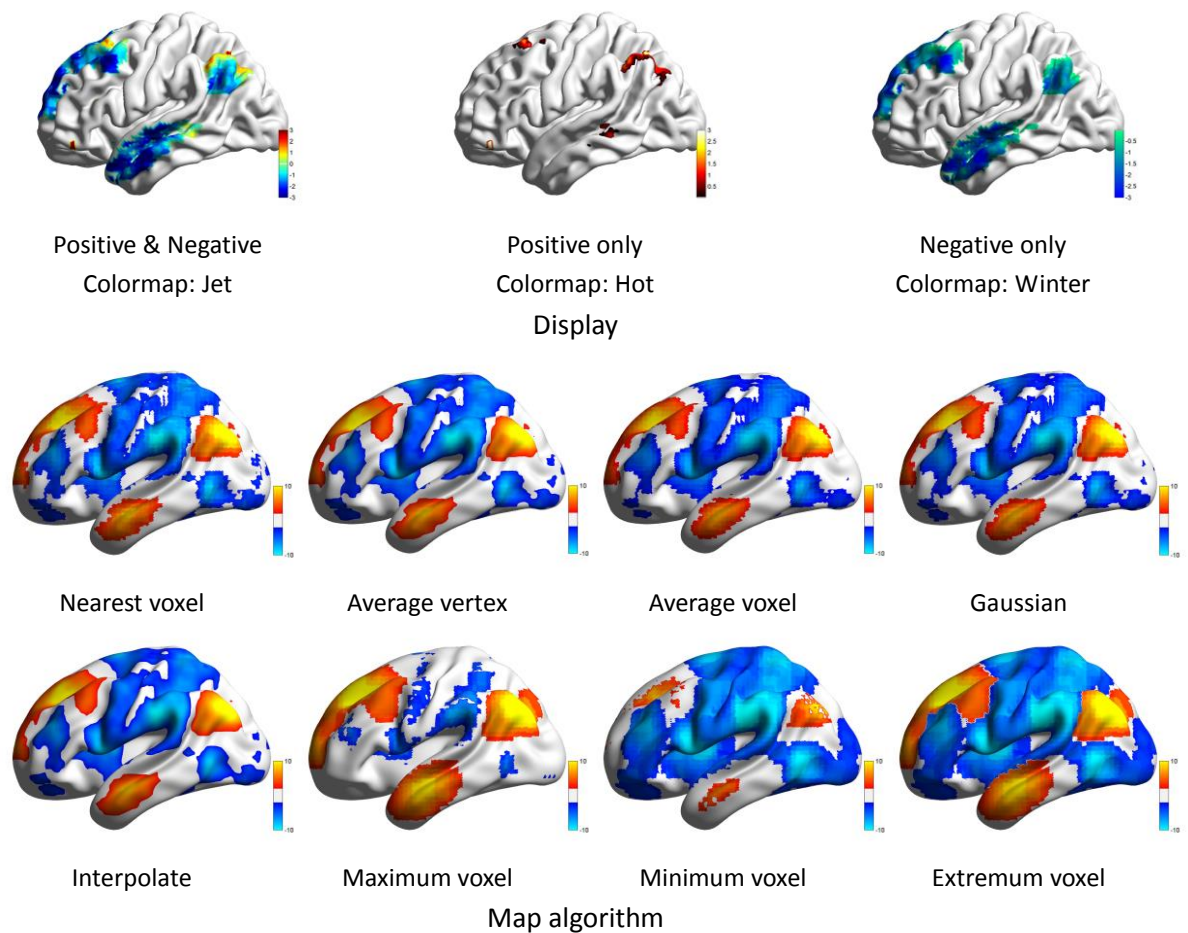

| Positive & Negative | Positive only | Negative only |
| Colormap: Jet | Colormap: Hot | Colormap: Winter |

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.
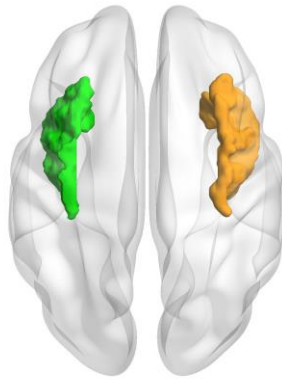
Smooth: smooth the surface of ROI volume.

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).
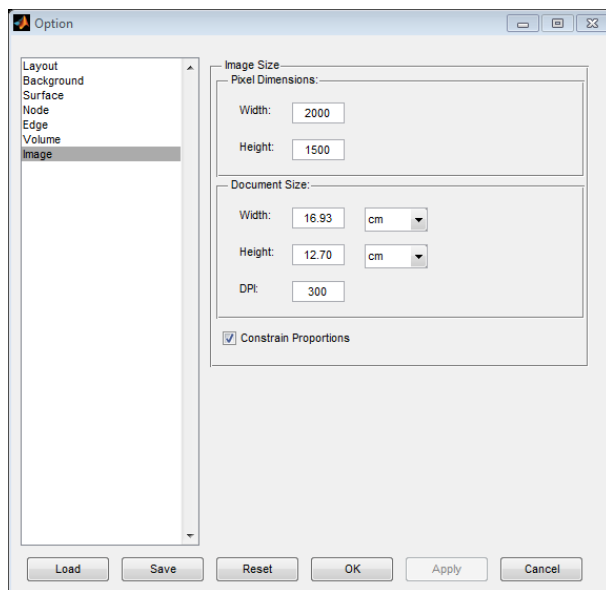
Fig. 19 Image panel

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6 Menu

6.1 Files

Load files:
Click to open 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).
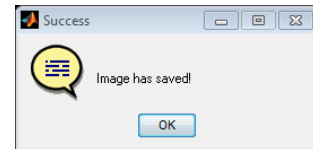
Save Movie:
This function helps users to save a demonstration movie for network visualization. It produces a 12 seconds long, 30 FPS, 735×534, avi file in which the brain network rotates clockwise in a circle, one degree per frame. This operation will take about 10 minutes. Please drink a cup of coffee 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 an example, see
http://www.nitrc.org/docman/view.php/504/1023/Demo%20Video%20of%20Brain%20Network%20(14M)
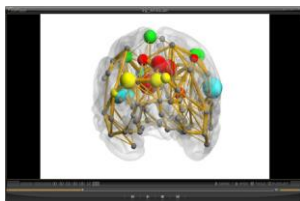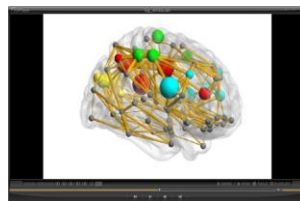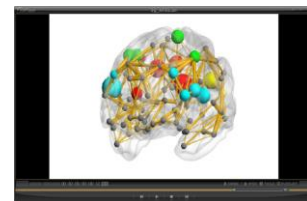
| 3s | 6s | 9s |

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 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 colomap editor to edit colormap manually.

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

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

6.3 Visualize

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

Clear Figure:
Remove 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).
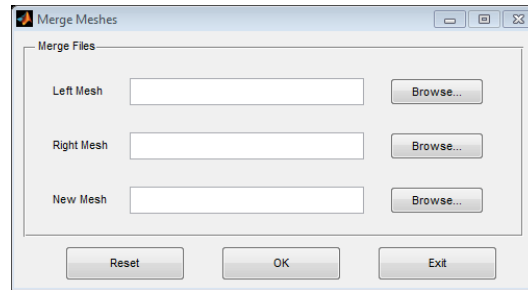
Fig. 21 Merge Meshes tool

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 menu, see details in section 'Load Files', and section 'Menu\File\Save Images'.
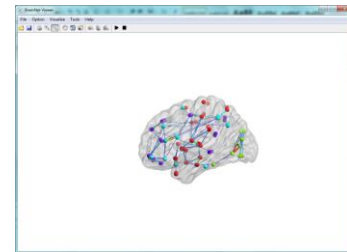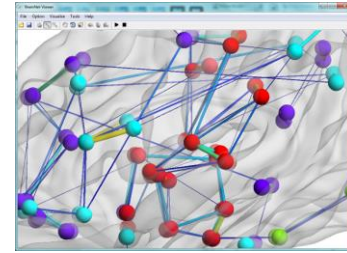
7.2 Print & Zoom

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.
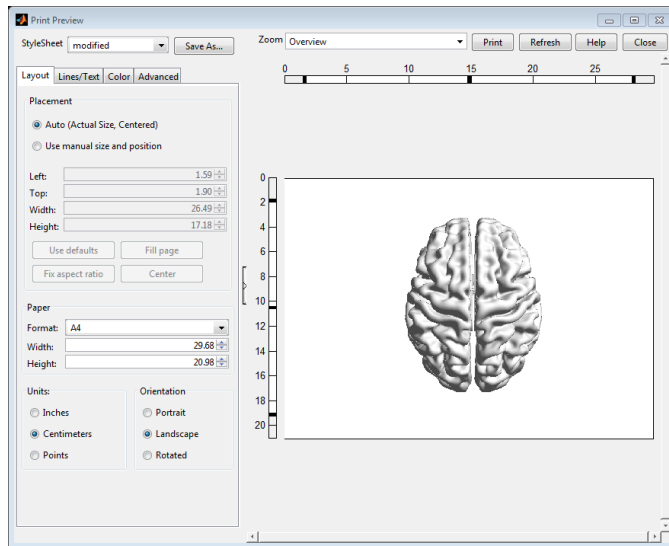
Print panel	Zoom in & Zoom out

Fig. 23 Print panel and Zoom function

7.3 Move, Rotate & Get position

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

When the 'Rotate' button is pressed, hold left button of the mouse and move mouse to rotate the brain. When 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.

7.4 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.
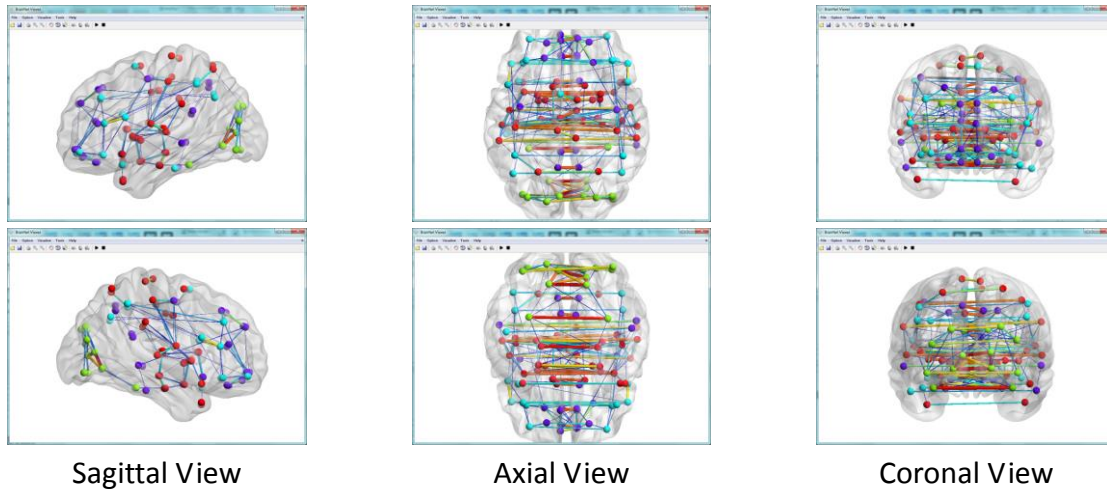
| Sagittal View | Axial View | Coronal View |

Fig. 24 Standard views

7.5 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 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.

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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/

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