

Brain Explorer for Connectomic Analysis (BECA) Software Manual

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1. Launch the application

Double click on the BECA icon as shown in Figure 1.

If nothing shows up, you may need to launch it in compatible mode by following steps shown in Figure 2:

- Right click on the BECA icon and select 'Properties'
- Select 'Compatibility' tab
- Check 'Run this program in compatibility mode for' and then select 'Windows 7' in the combo box below.
- Click the 'OK' button and try to run it again.



Figure 1. BECA application icon

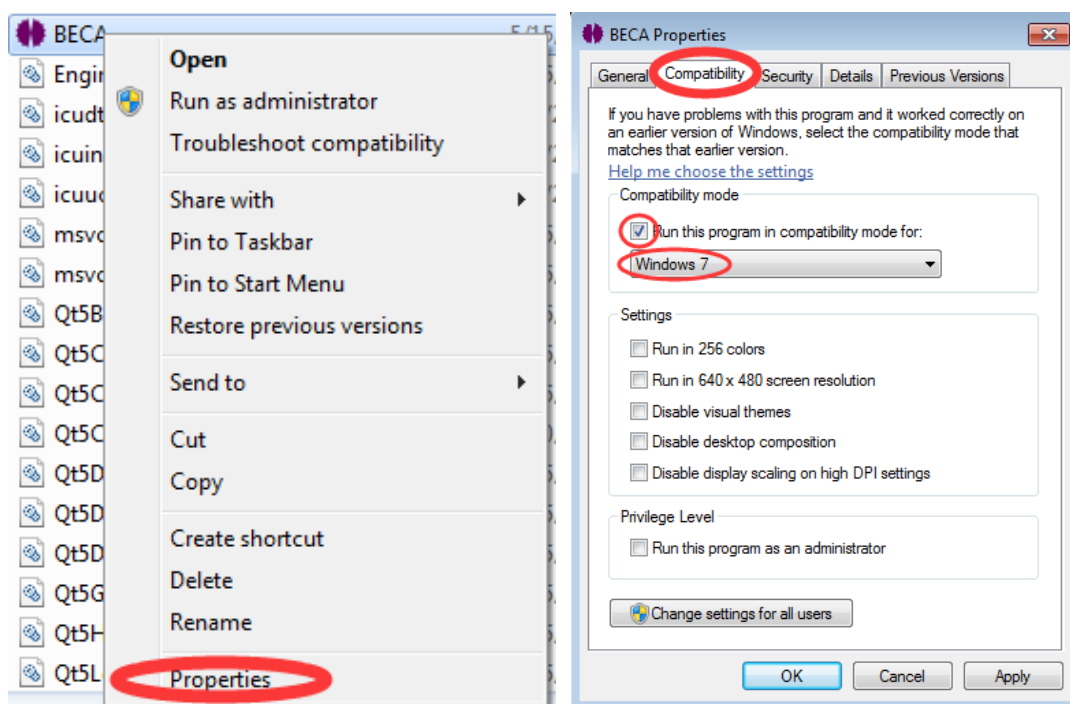


Figure 2. Run it in compatible mode

2. Tractography Visualization

Click the button in Fig. 1. Choose a track file (with .trk as filename extension). You may use the fiber.trk in the example data folder.

The track file format is defined here <http://www.trackvis.org/docs/?subsect=fileformat>

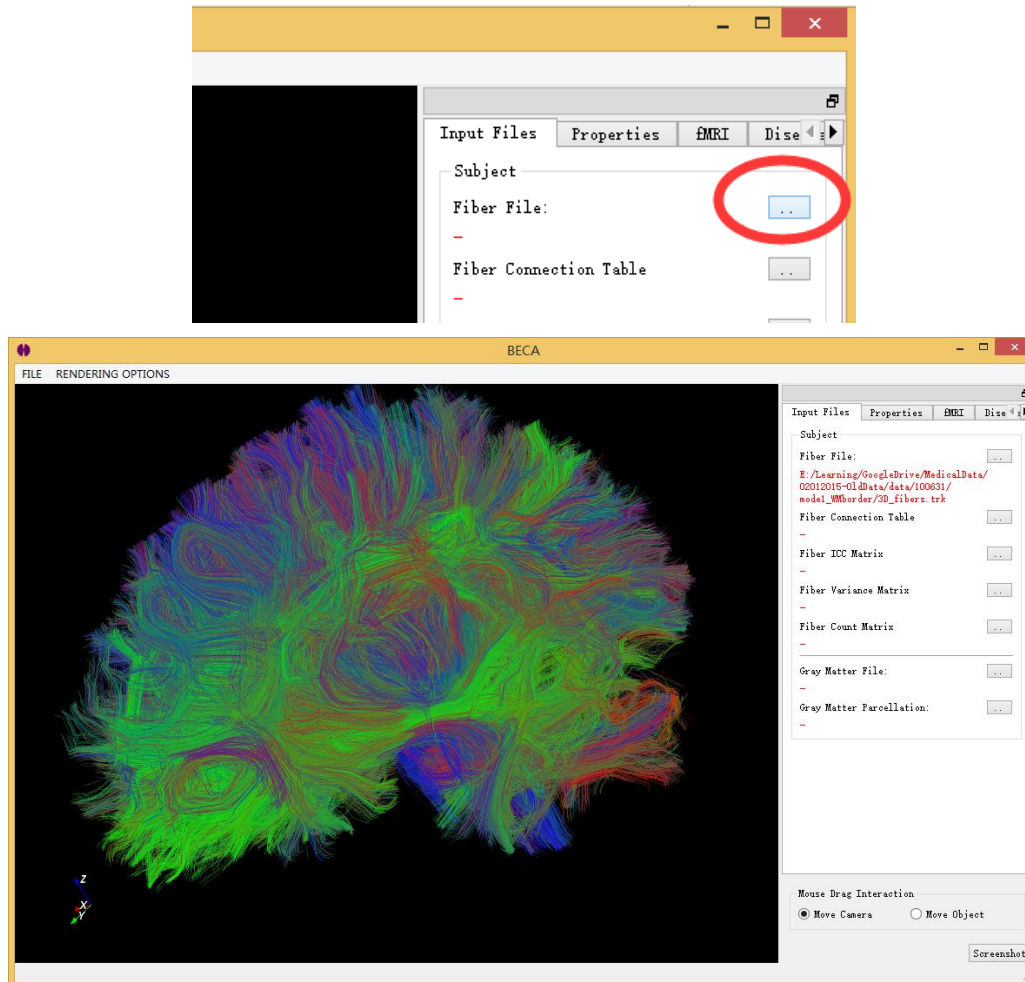


Figure 1. Open a track (*.trk) file

Use the scroll wheel on the mouse to zoom in/out.

Hold the left button to rotate.

The color of each fiber depends on its direction. X, Y and Z directions are encoded with R, G and B colors, respectively.

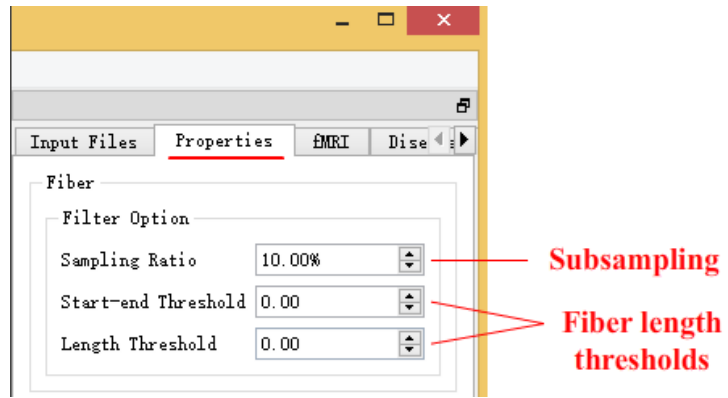


Figure 4. Filter parameter for fibers

As shown in Figure 4. There are some parameters to control the fiber filter:

- a. Sampling Ratio: ratio for random uniform sampling.
- b. Start-end Threshold: filter out the fibers whose endpoints distances are less than the threshold.
It can be used to filter out the U-shaped fibers.
- c. Length Threshold: filter out the fibers whose

3. Gray Matter Visualization

You can open the gray matter image and the parcellation using the buttons highlighted in Fig. 2. Both of them should be in Nifti (*.nii) format. In the example data folder, you may load the gray_matter.nii and parcellation.nii.

When parcellation is loaded, you may click on each ROI, the label and name will be shown in the highlighted combo box in Fig. 4. **(The window will freeze when loading the parcellation, and it takes about 30 seconds.)**

If you want to visualize the fiber and gray matter at the same time. It is recommended to adjust the opacity of the gray matter to 0.35, which is shown in Fig. 5.

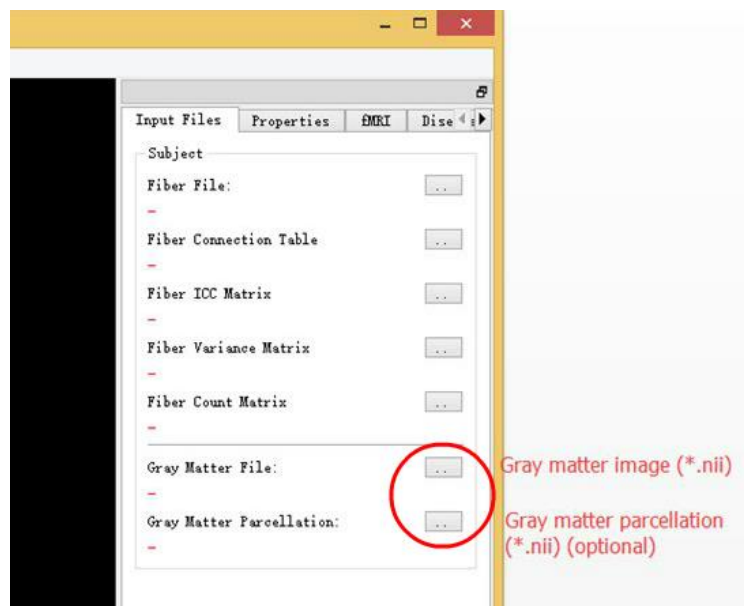


Figure 2. Open the gray matter image and its parcellation

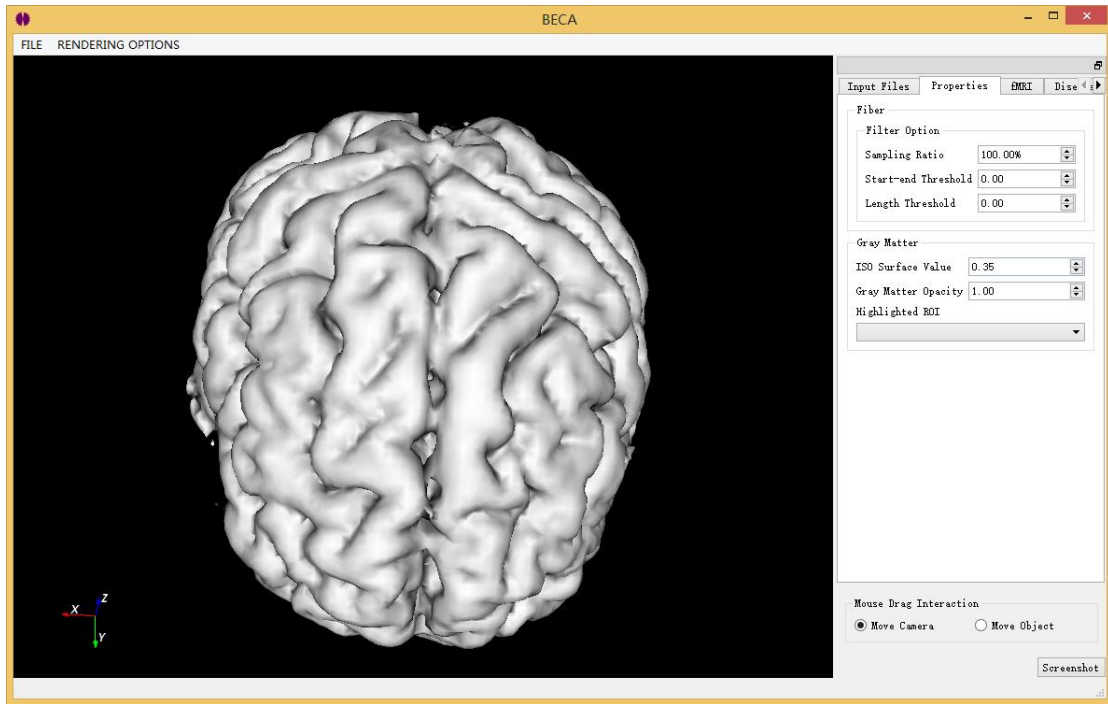


Figure 3. Gray matter image without parcellation

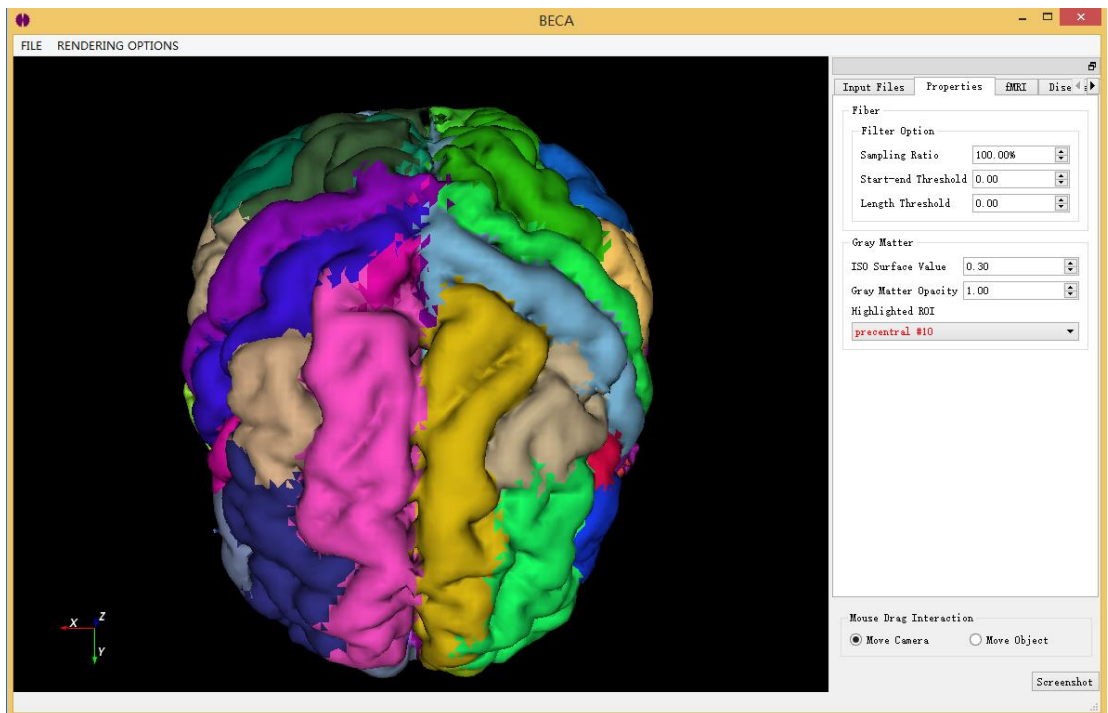


Figure 4. Gray matter with parcellation

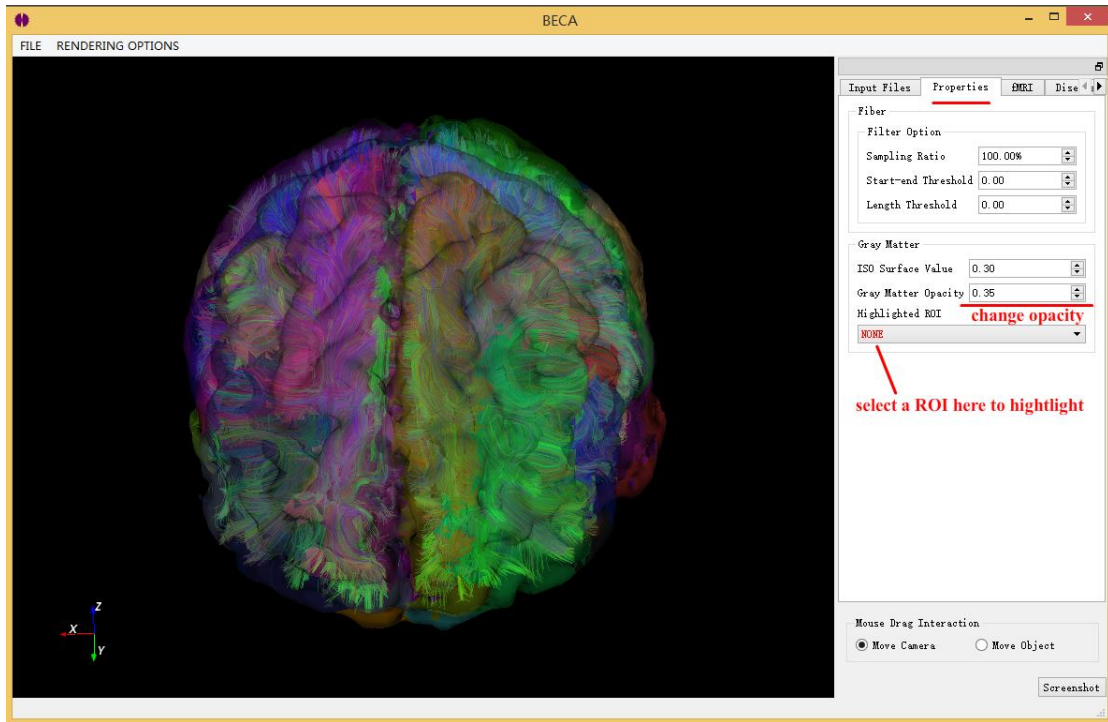


Figure 5. Visualize gray matter and fibers together

4. Fiber classification (Under Development)

We can classify fibers into 3 categories: reproducible, backbone and noise.

We need to load following files for the classification.

Fiber: *.trk (fiber.trk in example folder)

Gray matter image: *.nii (gray_matter.nii in example data folder)

Gray matter parcellation: *.nii (parcellation.nii in example data folder)

Fiber connection table: *.csv (connection_table.csv in example data folder)

Every row contains two integer which indicates the connected ROIs by the fiber. For example, if the first row is 1, 5, then it means the first fiber in the trk file connects the ROI 1 and 5.

ICC Matrix: *.csv (icc_matrix.csv in example data folder)

If we have 83 ROIs, then it is an 83x83 matrix in CSV format: there are 83 rows, and each row has 83 elements separated by comma.

Variance Matrix: *.csv (var_matrix.csv in example data folder)

If we have 83 ROIs, then it is an 83x83 matrix in CSV format: there are 83 rows, and each row has 83 elements separated by comma.

Count Matrix: *.csv (count_matrix.csv in example data folder)

If we have 83 ROIs, then it is an 83x83 matrix in CSV format: there are 83 rows, and each row has 83 elements separated by comma.

As shown in Fig. 7, after loading the above files, you can change the thresholds and display different fiber categories.

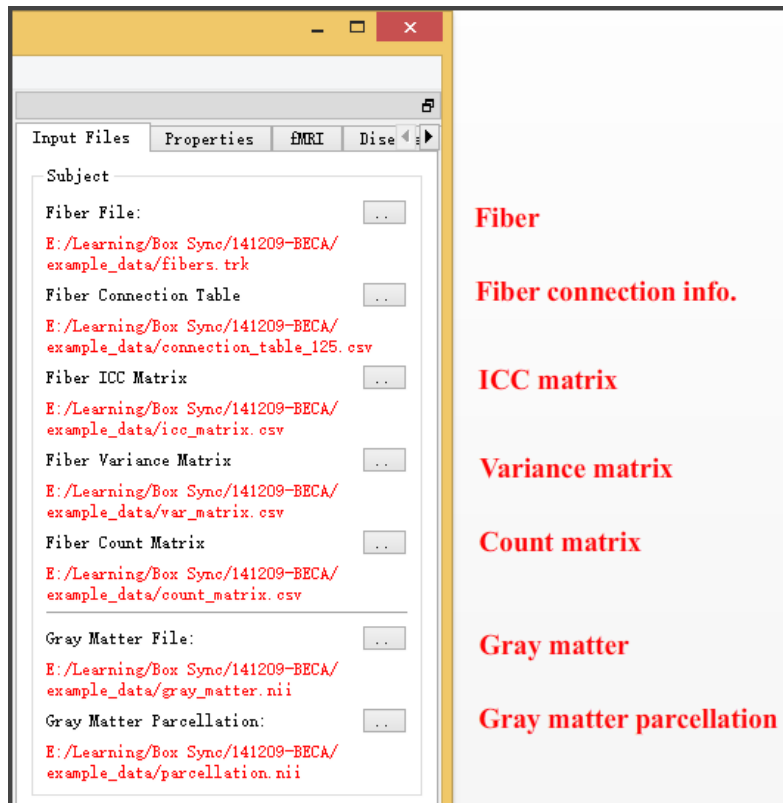


Figure 6. Load files for fiber classification

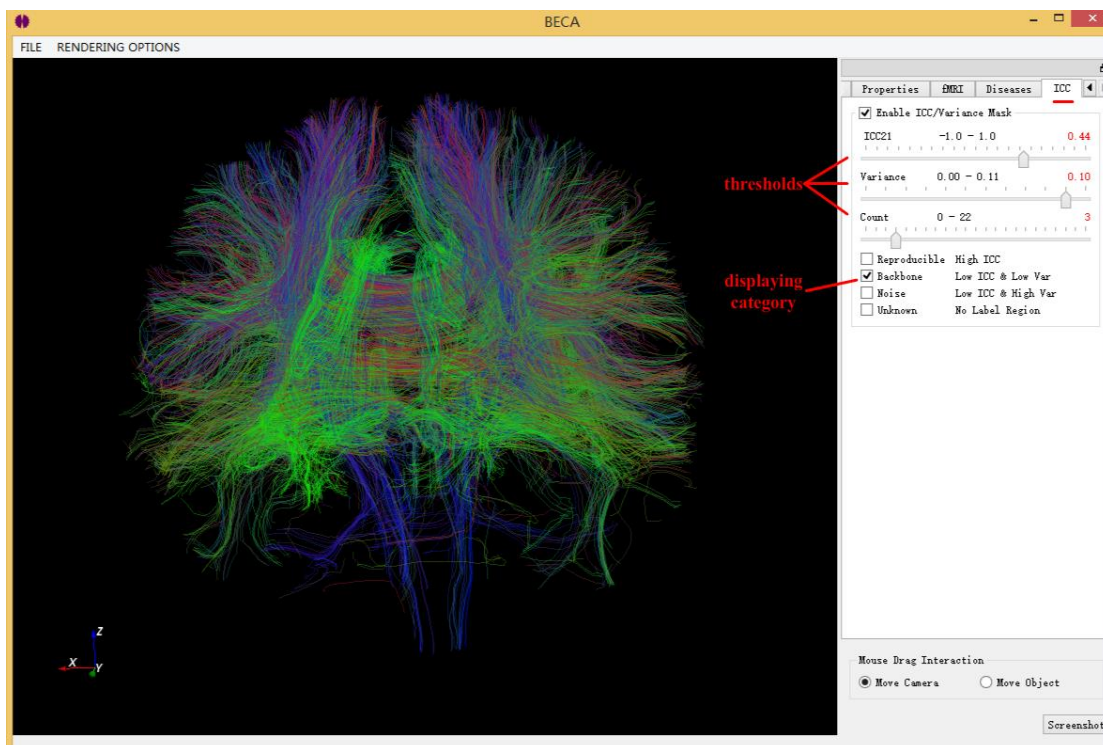


Figure 7. Change thresholds and displaying categories

5. fMRI Data Visualization

For fMRI visualization, we need to load following 3 files.

Gray matter image: *.nii (gray_matter.nii in example data folder)

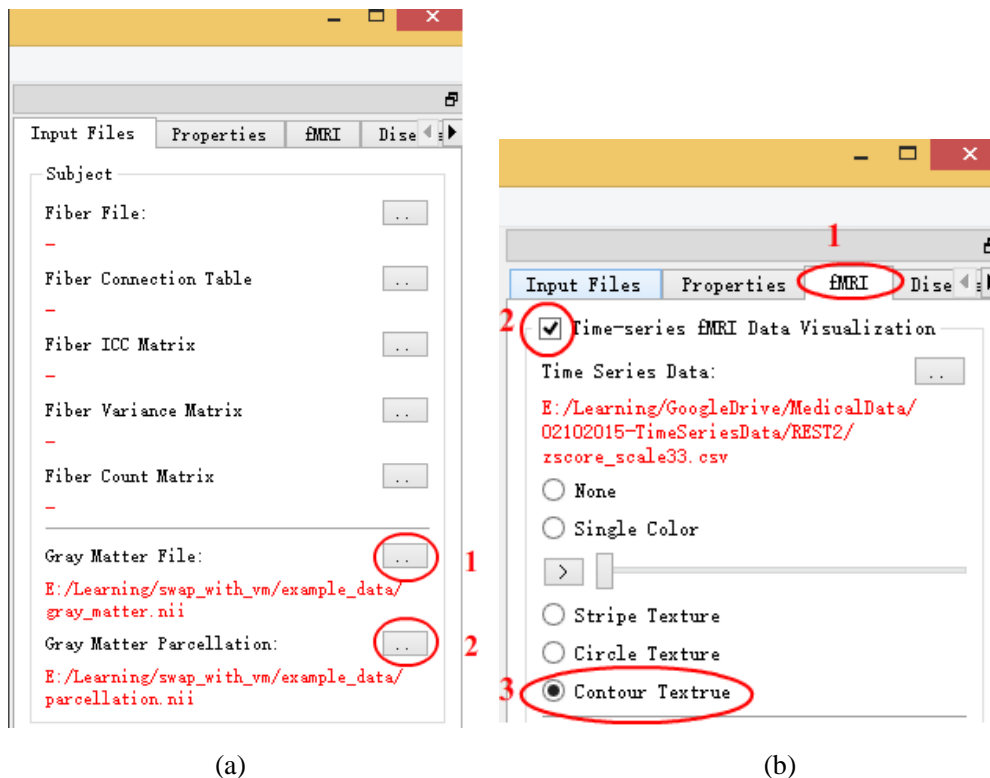
See step 1 in Figure 8(a).

Gray matter parcellation: *.nii (parcellation.nii in example data folder)

See step 2 in Figure 8(a).

Time Series Data: *.csv (fmri-data/fmri-data.csv in example data folder)

It is the fMRI data we want to visualize. If there are 83 ROIs in the gray matter and 632 time points, then this csv file should represent an 83x600 matrix. There should be 83 lines and every line consist of 632 elements separated by comma. The i^{th} row of the matrix represents the i^{th} ROI according to the gray matter parcellation. We can load the csv file, as shown in Figure 8(b), by switching to the 'fMRI' tab.



(a) Open the gray matter and its parcellation.
(b) Load and visualize the fMRI data

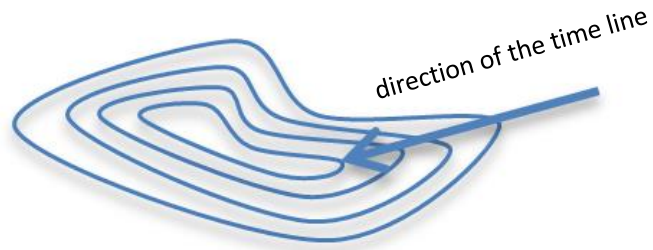


Figure 9. We use the offset contours to represent the fMRI (time series) data.

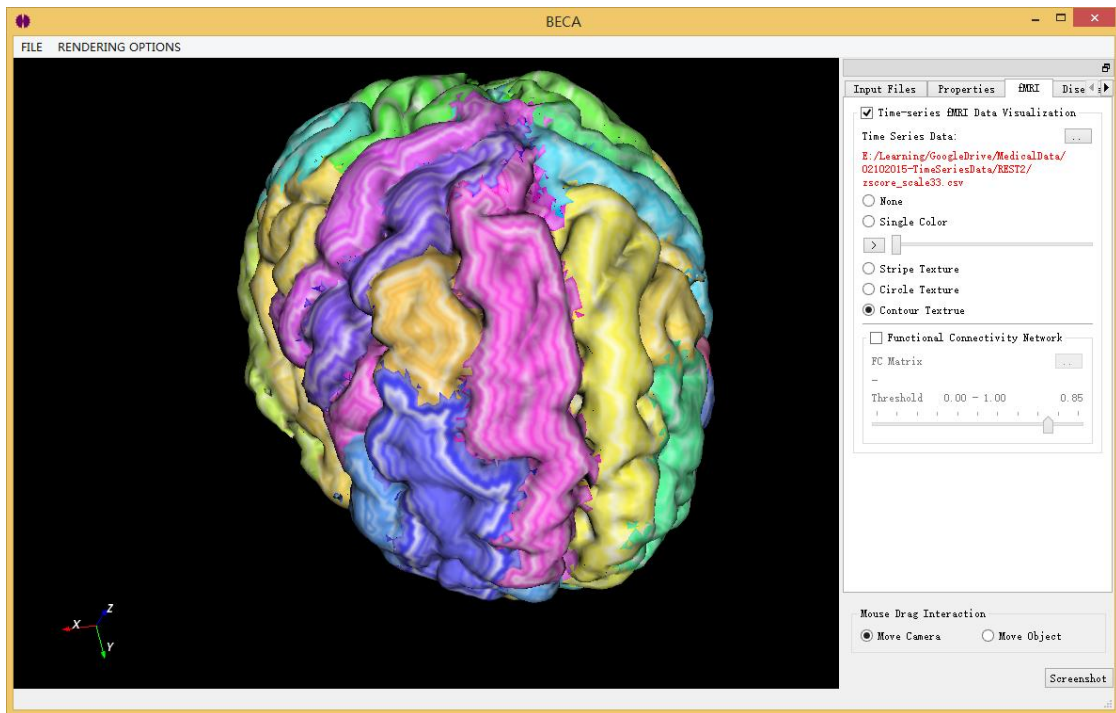


Figure 10. Applying the offset contour textures for representing the fMRI data.