

# *iEEGview's User Guide V1.0*

## Contents

1	Introduction.....	2
2	Requirements .....	2
3	Installation.....	3
3.1	Installation Instructions .....	3
3.2	Running iEEGview .....	3
3.3	Uninstallation .....	3
4	Use of iEEGview .....	3
4.1	Configuration Panel .....	4
4.1.1	Functions Panel .....	4
4.1.2	Graph Panel .....	4
4.1.3	Display Panel .....	5
4.1.4	Status Monitor Panel .....	5
4.2	Electrode localization.....	5
4.2.1	Segmentation.....	5
4.2.2	Coregistration.....	6
4.2.3	Electrode Selection.....	8
4.2.4	Localization Results Display.....	11
4.3	Native Brain Space Related Analysis .....	14
4.3.1	Anatomical Label Identification.....	14
4.3.2	View in MRI Brain Volume.....	15
4.3.3	Activation Map Visualization.....	17
4.4	Common Brain Space Operations .....	17
4.4.1	Mapping into Standard Brain Template for Single Subject.....	17
4.4.2	Mapping into Standard Brain Template for Multiple Subjects.....	19
4.4.3	Activations Map Visualization on Standard Brain Template.....	20
4.5	Data Files Saved in Subject Path.....	21
5	Summary .....	22

## 1 Introduction

iEEGview is a Matlab GUI based toolbox designed for the localization and visualization of intracranial electrodes. The toolbox is compatible for the scenarios of implanting either depth electrodes/subdural electrodes solely or the both. The toolbox provides four main functions including: 1) localizing the 3D coordinates of iEEG electrodes within each individual brain; 2) identifying the anatomical information for iEEG electrodes for that brain; 3) visualizing brain activation using iEEG recordings; 4) mapping electrodes from different individual subjects into a common standard brain. In details, from the GUI of the toolbox, users can simply run the full localization pipeline including brain segmentation, images co-registration, electrodes extraction, anatomical information identification, activation map generation and electrodes projection from a native brain space into a common brain space for group analysis. In addition, iEEGview implement methods for brain shift correction and provide visual inspection function for the automatically identified anatomical information of each electrode by reconstructing electrodes on the original MRI slices. In this manual, we introduce the installation of iEEGview and show how to use iEEGview in details with a sample subject implanting depth and subdural electrodes together.

## 2 Requirements

- 1) iEEGview is designed for Mac systems. The macOS version is suggested to be macOS 10.10 or higher.
- 2) Matlab should be installed and the version is suggested to be R2017b or higher.
- 3) FreeSurfer needs to be installed before the usage of iEEGview. The installation instruction can be found in the following link. XQuartz may needs to be installed as well so that the Freesurfer can work properly. <http://surfer.nmr.mgh.harvard.edu/fswiki/MacOsInstall>

### (Key Notes:

1: To make a better usage experience, please be sure that the environment variable is correctly set up.

“If you use Freesurfer frequently and want to avoid typing the above lines of code every time you open a terminal window, you can create a file called .profile in your home directory which contains those two lines. This will cause the terminal window to automatically source Freesurfer every time it is opened”, this needs the operations from terminal)

2: After the Freesurfer is properly installed, please also change the permission of the Freesurfer installation directory (generally, ‘applications/freesurfer’) to be “Read and Write” for all users and apply this setting to all the subfolders under this path.

- 4) The SPM needs to be installed before the successful usage of iEEGview and the version is suggested to be SPM12 or higher. It should be noted that the XCode should also be installed to compile the SPM functions. The installation instruction can be found in the following link. The instruction can also be found in the attachment files.

[https://en.wikibooks.org/wiki/SPM/Installation\\_on\\_64bit\\_Mac\\_OS\\_\(Intel\)#Installation](https://en.wikibooks.org/wiki/SPM/Installation_on_64bit_Mac_OS_(Intel)#Installation)

### **Key notes:**

- 1: Please be sure that the SPM12 MEX files are compiled following the instructions above. Because iEEGview uses some functions that need compilation. This may need the installation of X-Code (See above link).
- 2: After this installation, please also be sure that no previous repeated SPM12 or SPM8 files are in your Matlab path. Additional SPM12 files in the Matlab path without correct compilation may lead to the failure of iEEGview.

Till now, you should be able to go ahead with the successful usage of iEEGview.

## **3 Installation**

iEEGView is available as open-source Matlab code. It is distributed under the Aladdin Free Public License, which gives anyone the right to use, copy and modify the code, but not to sell it.

### **3.1 Installation Instructions**

- 1) Unzip the file iEEGview.zip.
- 2) Move the iEEGview folder to whichever directory you want it to reside in.
- 3) Run Matlab.
- 4) In Matlab, HOME>>Set Path>>Add with Subfolders, select the iEEGview folder and click Save.

### **3.2 Running iEEGview**

To run iEEGview, type ‘iEEGview’ in the Matlab command window.

### **3.3 Uninstallation**

Delete the path in Matlab and delete the iEEGview folders.

## **4 Use of iEEGview**

iEEGView runs with a Matlab GUI window, which is divided into five panels (Fig. 4.1). The iEEGview includes four main functions which are introduced in 4.2-4.4 respectively (The figures shown in this manual is produced here is for demonstration purpose only).

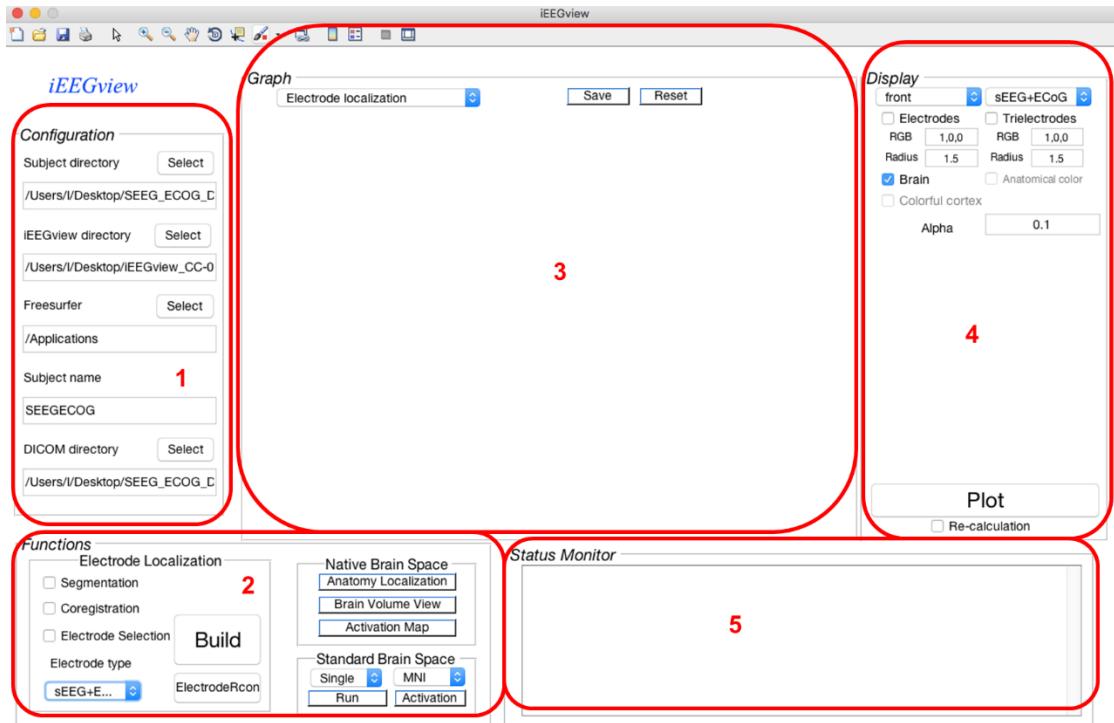


Fig. 4.1 The GUI of iEEGview

## 4.1 Configuration Panel

The configuration panel is at the top left of the GUI (Fig. 4.1). In this panel, directories and subject name needed for the following analysis can be set by users.

- Subject directory is the directory to save analysis results in the following steps. This directory should be created before the launch of iEEGview and should contain the DICOM files.
- iEEGview directory is the iEEGview installation directory.
- FreeSurfer directory is the FreeSurfer installation directory.
- Subject name can be edited by users.
- DICOM directory is the directory includes MRI files or CT files. The default directory is under the subject directory.

Users can click the ‘Select’ button to select the directory or input the directory path directly in the text field. The directories are automatically generated depending on the current directory of Matlab, but should be checked manually.

### 4.1.1 Functions Panel

The function panel contains three sub-panels, electrode localization, native brain space analysis and standard brain space, which correspond to the functional modules introduced in the following sections (Fig. 4.1).

### 4.1.2 Graph Panel

The graph panel is used for the visualization of results (Fig. 4.1). Functions of all components in this panel are described as following.

- Combo box. Switch between different function modules of iEEGview. e.g. show the electrode localization results, show the anatomical information of each electrode and segmented brain, show the activation map or standard brain mapping results.
- ‘Save’ button. Save the figure. Multiple formats are available (fig, png, bmp, jpg, eps).
- ‘Reset’ button. Clear the figure.
- ‘View’ setting panel. Adjust the view of the figure and the direction of light to be applied on brain surface.

#### 4.1.3 Display Panel

- The ‘Display’ panel is used to set the parameters for displaying (Fig. 4.1). Users can select the components (electrode, electrode projection points on cortical surface (trielectrode), color the brain surface (colorful cortex) and color each electrode with its anatomical information (anatomical color), assign each electrode/trielectrode with specific RGB value (RGB) or radius (Radius)).
- If you want to see the activation map, select the item ‘Activations’ in ‘Graph’ panel. Then import activation data by clicking the ‘Import data’, parameters used for rendering the activation map can be adjusted within the ‘activation parameter’ panel.
- After setting up the activation parameters, click ‘Plot’ to display the analysis results. If the ‘Re-calculation’ is selected, the calculation in the brain model will be always performed, otherwise, the calculation will only be performed in the first time of displaying and the results are displayed depending on the previous calculation results.

#### 4.1.4 Status Monitor Panel

The ‘Status Monitor’ panel shows the processing status for the functions of iEEGview (Fig. 4.1). The whole recording of processing procedure and status can be found in the file ‘ProcessState\_xx.txt’, where ‘xx’ represents the time point when the iEEGview is launched.

### 4.2 Electrode localization

This function module aims to localize electrodes (SEEG/Depth, ECoG/Subdural or the both). The module contains three functions. Users can select the functions to perform (either single function or multiple functions). When electrode selection is selected, the electrode type that you are going to localize should also be checked, where SEEG is in default three options in total, SEEG, ECoG, SEEG+ECoG). The operation steps are explained as following.

Before localization, a subject folder should be created. The folder name should be the subject whose data are going to be analyzed in the following step (the name set in the panel Configuration). In the subject folder, a folder called DICOM should be created before running the function of iEEGview, the DICOM folder should contain two subfolders called MRI and CT, where the MRI and CT ‘dicom’ format files are placed. After the correct placing of images files, brain segmentation and electrodes reconstruction can be realized through below steps.

#### 4.2.1 Segmentation

This function is used to run the brain reconstruction and segmentation. To do this, select the checkbox ‘Segmentation’ and click ‘Build’. Then the FreeSurfer will start automatically to segment

the brain. This step may take about 8-24 hours. A clock will appear showing the time cost. If this step is finished, the ‘Status Monitor’ panel will appear ‘Segmentation completed!’. If there are some errors appeared during this process, the ‘Status Monitor’ panel will show the error and the reasons. Please be sure to prevent your computer from sleeping or shutting down during this process.

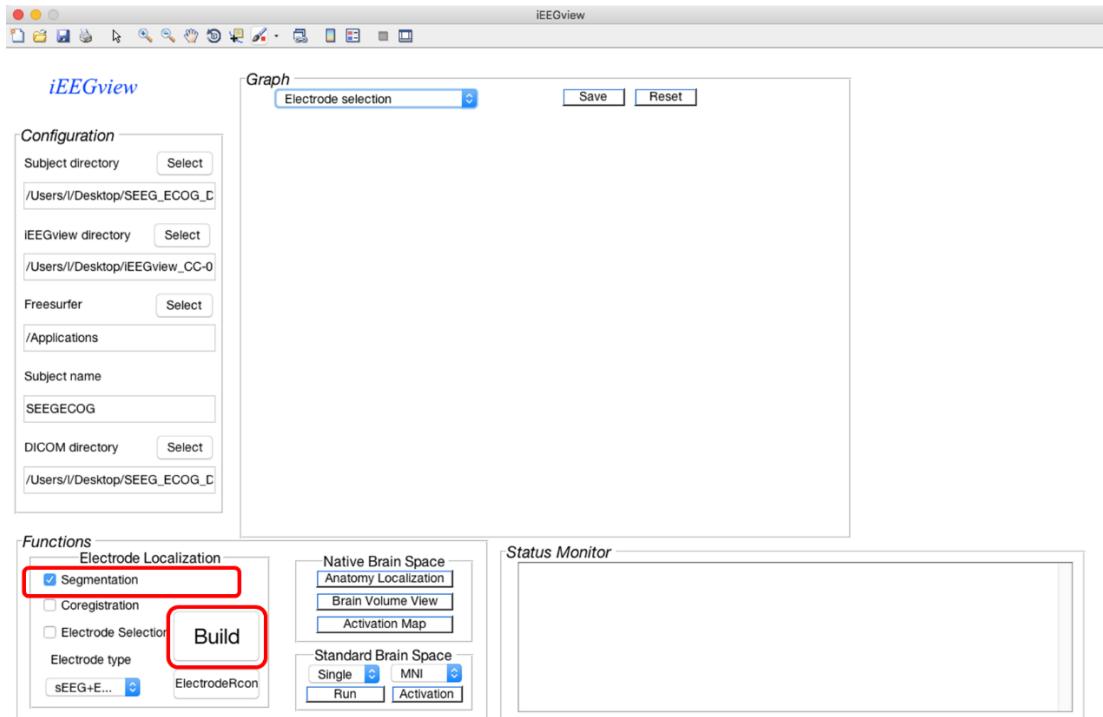


Fig. 4.2 The operations for brain segmentation

When the segmentation is completed successfully, the segmentation results will be saved in the FreeSurfer directory, named with the subject name. Then these files will be moved to subject directory that set in the iEEGview and placed in the subfolder called ‘Segmentation’ (Fig. 4.3).

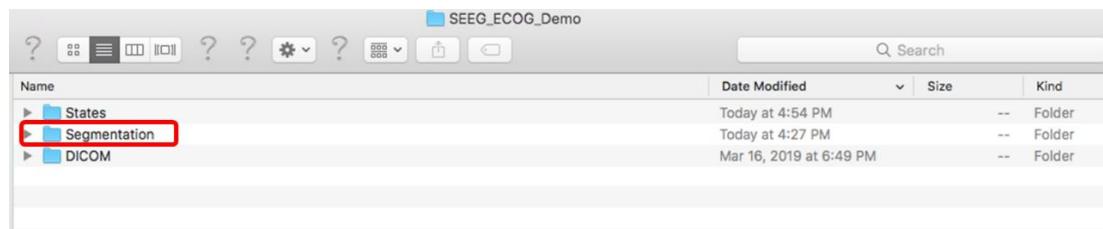


Fig. 4.3 The segmentations results folder in FreeSurfer directory.

#### 4.2.2 Coregistration

This function aims to coregister the post-implant CT with pre-implant MRI images. To do this, select the checkbox ‘Coregistration’ and click ‘Build’ (Fig. 4.4). This process runs the SPM built-in Matlab functions automatically to do the coregistration. Once this process is finished, the Freeview will be invoked automatically (Fig. 4.5, by clicking ‘yes’ on the pop-up window). Within the Freeview, coregistered CT and MRI image are shown. Then you can check the coregistration result by adjusting the opacity of MRI or CT images in Freeview to see if there are aligned correctly. Once you have confirmed that a good coregistration has been made, then please remove the MRI volumes leaving only the CT volume in the Freeview. For the CT volume, select the checkbox “show as

isosurface in 3D view" (Fig. 4.5), and after this, select the checkbox "Extract all regions", by adjusting the threshold (e.g. low threshold and high threshold), you can extract the surface of all the electrodes to be localized. After this, click the "save" button below the checkbox in Freeview and saved the surface as 'vtk' files in the 'Electrodes' folder located in the subject directory. Then close the Freeview. Once finishing this step successfully, the State panel will appear 'Coregistration completed!'. If there are some errors appeared during this process, the State panel will appear the error and the reasons (Notice, sometime coregistration may fail because the origin of CT images and MRI images are too far away from each other. If this happens, you can solve this problem by moving the origin of CT images close to the MRI images with the help of other software packages, such as SPM, 3D slicer and so on).

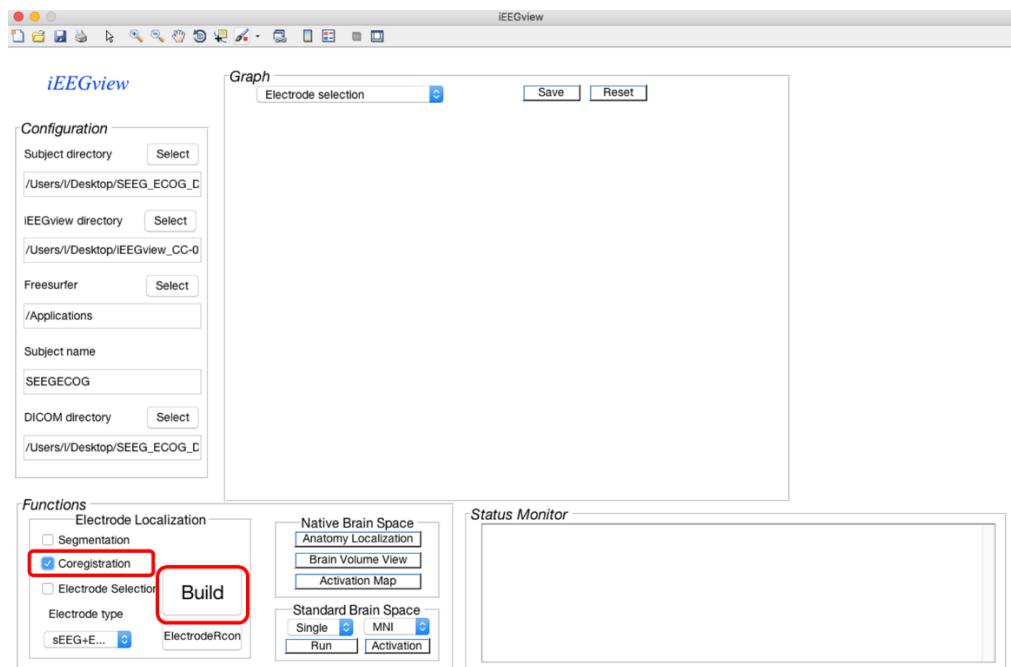


Fig. 4.4 The operation for coregistration

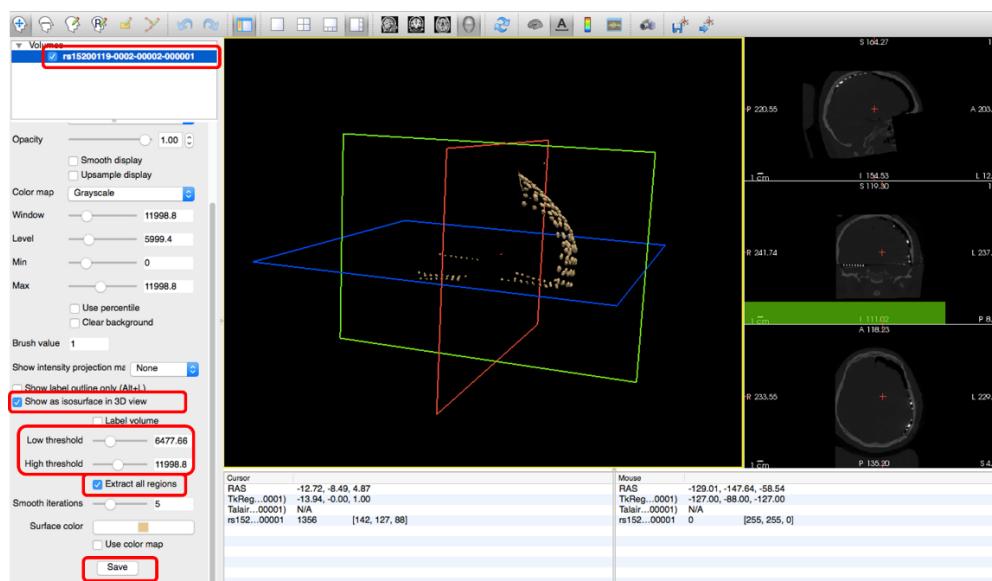


Fig. 4.5 The electrode extraction in Freeview

### 4.2.3 Electrode Selection

This part aims to label all the electrodes that are going to be localized.

- 1) Select the checkbox ‘Electrode Selection’, select the which electrode type is going to be localized, and click ‘Build’ (Fig. 4.6). Then a figure with multiple pins will appear which can be zoomed in/out and rotated.

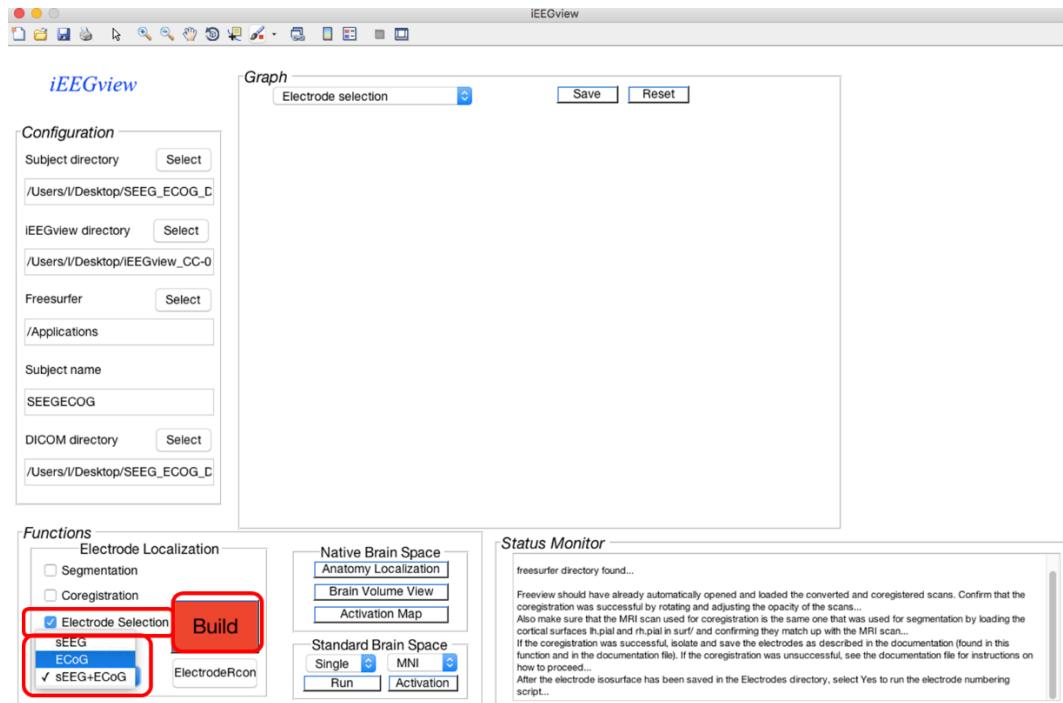


Fig. 4.6 The operations for electrode selection.

- 2) When you choose the SEEG/SEEG+ECoG, a dialog will appear and input each time one SEEG electrode shaft name (e.g. ‘A’) which is going to be localized in the next step (Fig. 4.7). For ECoG, there no such step.

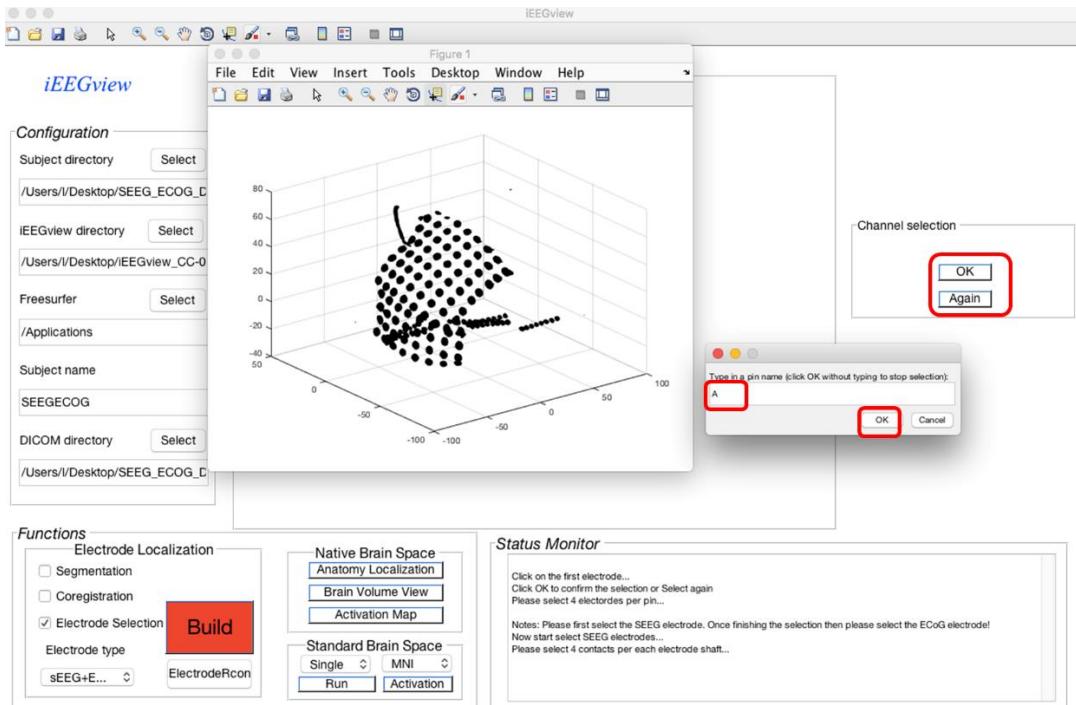


Fig. 4.7 The operations for naming the depth electrodes.

- 3) For SEEG/SEEG+ECoG, first select 4 points in electrode shaft A (Fig. 4.8). Users should confirm for each selection. A re-select operation (button ‘Again’) is available if the point is selected at the wrong position. For ECoG, just directly label each electrode until all the electrodes are selected properly. The ECoG electrodes will be named with Arabic numbers based on the sequence of labelling automatically. After all selections, click ‘Stop’ to end this step. While for the scenario of SEEG+ECoG, iEEGview lets users to label all SEEG electrodes first and then label all the ECoG electrodes (See step 2 of this section).

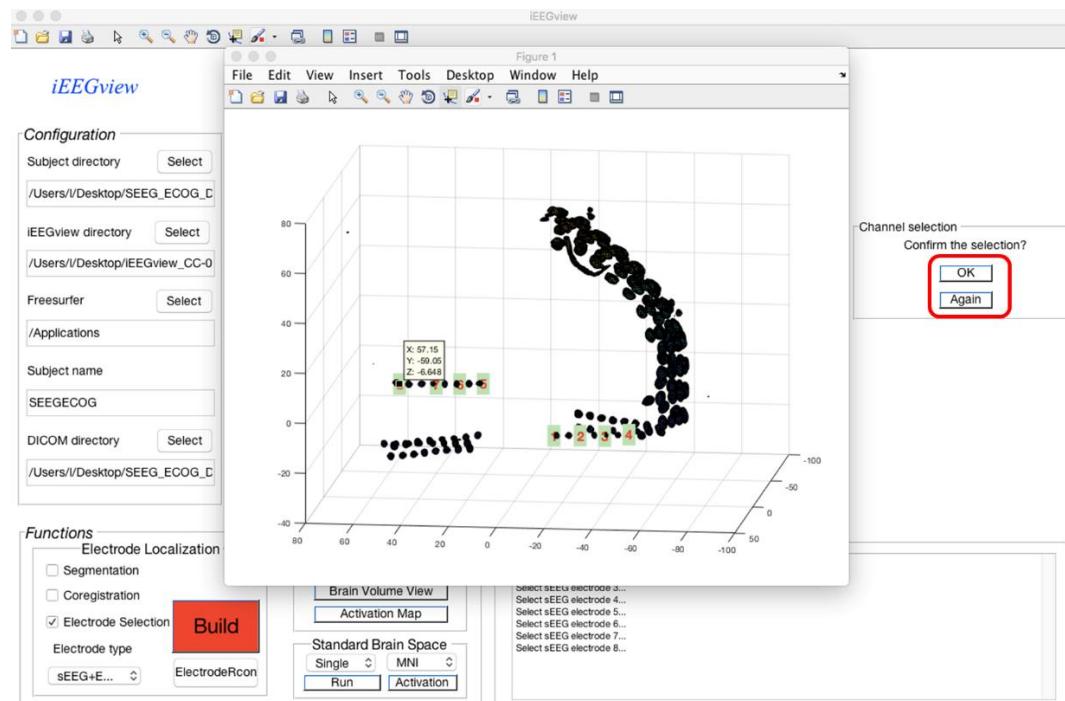


Fig. 4.8 Operations for electrode labelling in one shaft of depth electrodes.

- 4) If there are still electrodes to localize, repeat step 2) and 3). If not, click the ‘OK’ directly without input anything in the popup dialog of step 2) (Fig. 4.9) to finish the electrode selection for SEEG. Then for ECoG electrodes, click ‘Stop’ to finish all the electrode selection.



Fig. 4.9 Operations to finish electrode selection for depth electrodes and subdural electrodes.

- 5) When all the electrodes are selected, then for SEEG/SEEG+ECoG, users then need to input the electrode number for each SEEG electrode shaft. The sequence of number should be consistent with the sequence of electrode shaft selection. Also, in the GUI, the sequence of electrode shafts will appear to remind users (Fig. 4.10). For ECoG, there is no such step.

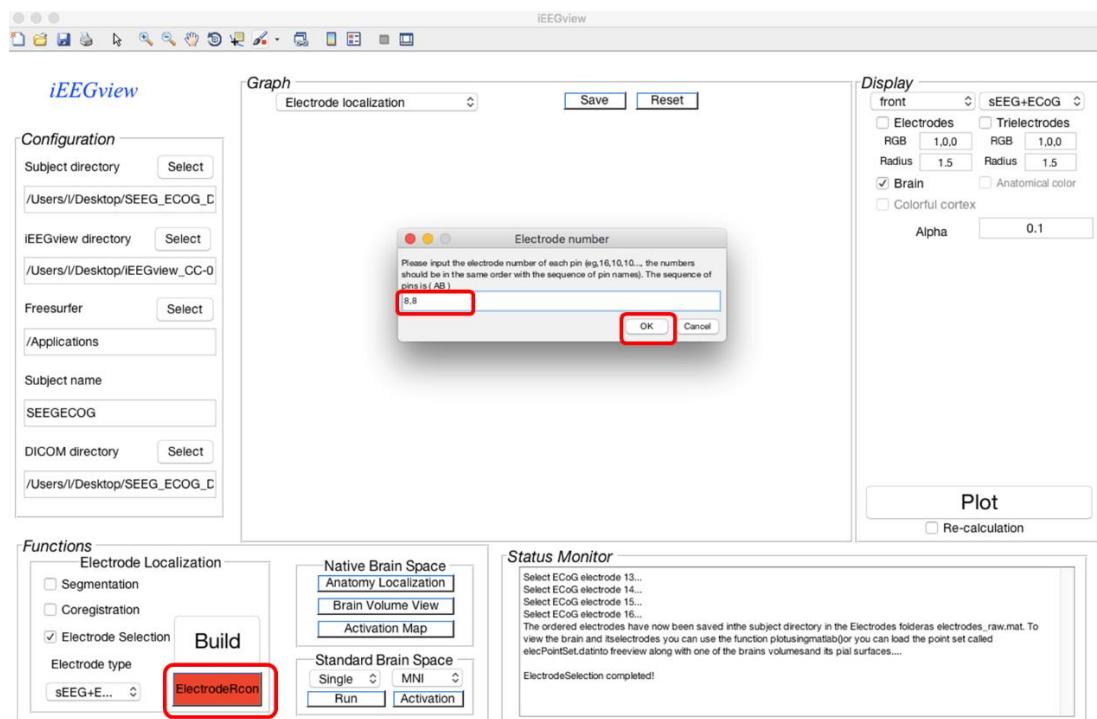


Fig. 4.10 Numbering the contacts for each of the depth electrodes.

- 6) If SEEG/SEEG+ECoG is selected, then another GUI that is used to configure each depth electrode shaft type will come out (Fig. 4.11). iEEGview provides three type of electrodes for the localization (Normal/ 8+8,70mm/10+6,80mm) considering that there are some special depth electrode shafts which only have contacts in the tips and bottom of each electrode shaft. Among these three type of depth electrode, normal type means the general used SEEG electrodes with equal spacing, “8+8,70mm” means there are 8 contacts in the tips and 8 in the bottom, totally length is 70mm. “10+6,80mm” means there are 10 contacts in the tips and 6 in the bottom, totally length is 80mm. In this step, first select the corresponding type of each SEEG electrode shaft. Additionally, considering that other parameters of depth electrodes including contact length, center-to-center contact distance and diameter of electrode shaft may be not always the same. So in this GUI, iEEGview enable users to type in these three additional parameters for an accurate localization process. After all the parameters are input properly, click ‘OK’ to finish. This step is only applicable if there are SEEG electrodes for localization.

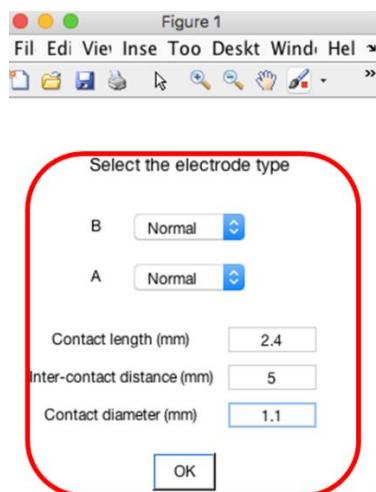


Fig. 4.11 Interface of configuring each depth electrode shaft

The ‘Status Monitor’ panel will appear ‘ElectrodeSelection completed!’ if this function is performed successfully.

#### 4.2.4 Localization Results Display

- 1) Select the ‘Electrode localization’ in the ‘Graph’ panel.

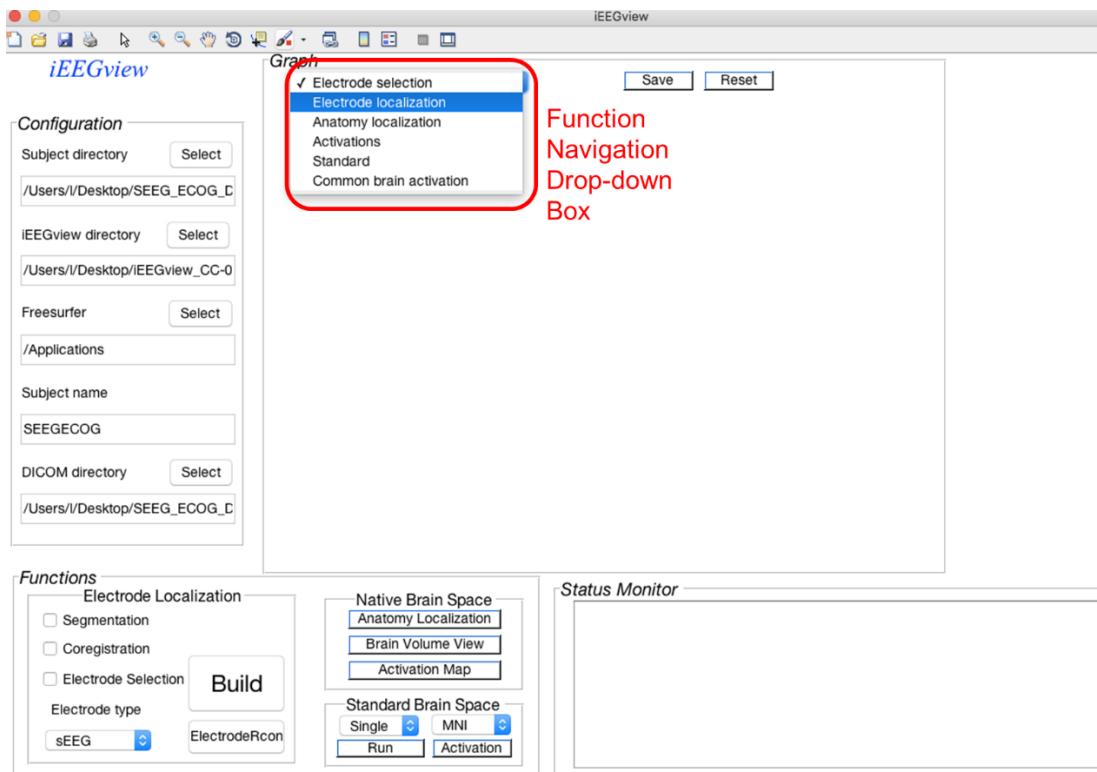


Fig. 4.12 The functions to be displayed in the Graph panel.

- 2) Select the side of brain you want to view in the top left drop-down box. For the electrode type of SEEG+ECOG, you can also select which type of electrode you want to view (SEEG only, ECoG only or the both (SEEG+ECOG)) in the top right drop-down box (Fig. 4.13).

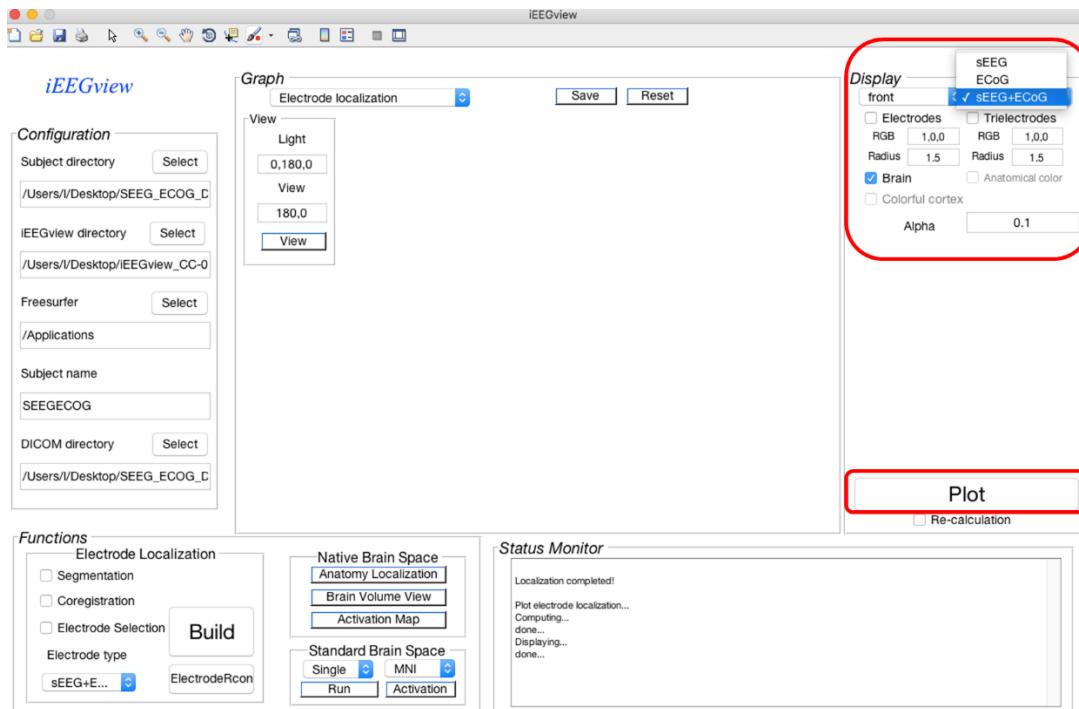


Fig. 4.13 The interface of the 'Display' panel for electrode localization .

- 3) Select the electrodes modules to plot (electrodes, trielectrodes or both). The brain is selected in default. Then you can adjust the radius and color of electrodes to be shown by change the value in the column Radius/RGB (Fig. 4.13). Besides, the transparency of the cortical surface can be adjusted based on needs by changing the alpha value from ‘Display’ panel.
- 4) Click ‘Plot’ to see the electrode localization results (Fig. 4.14). The calculation states are shown in the ‘Status Monitor’ panel.

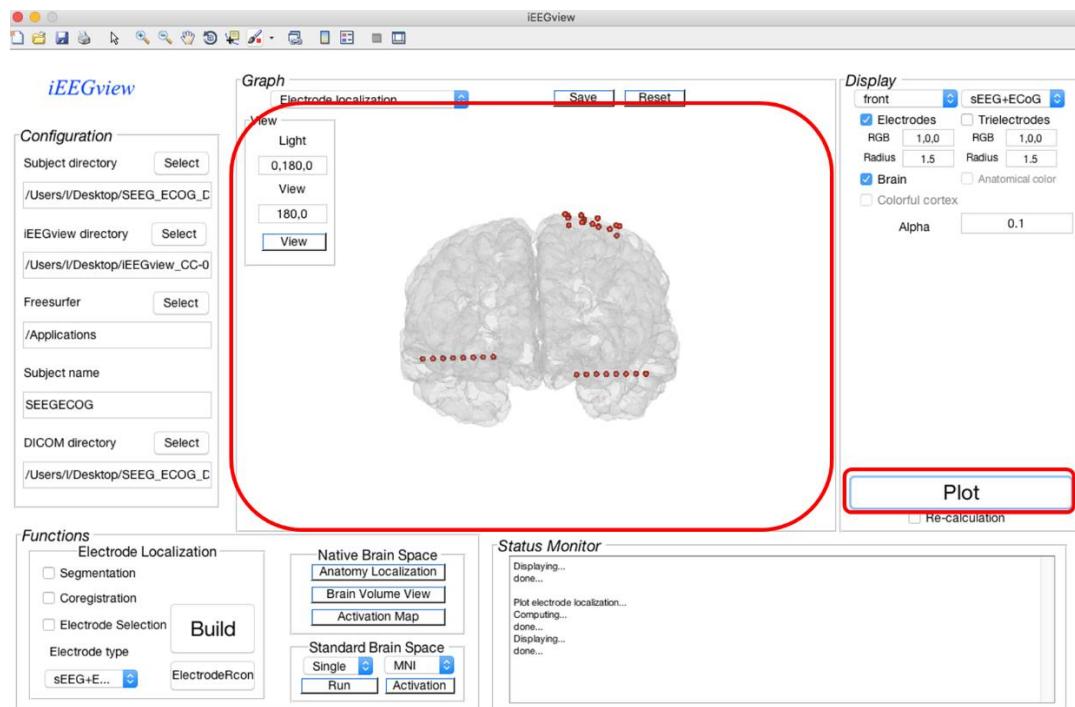


Fig. 4.14 Plotting results of electrode localization.

- 5) The figure can be rotated, saved or cleared (Fig. 4.15).

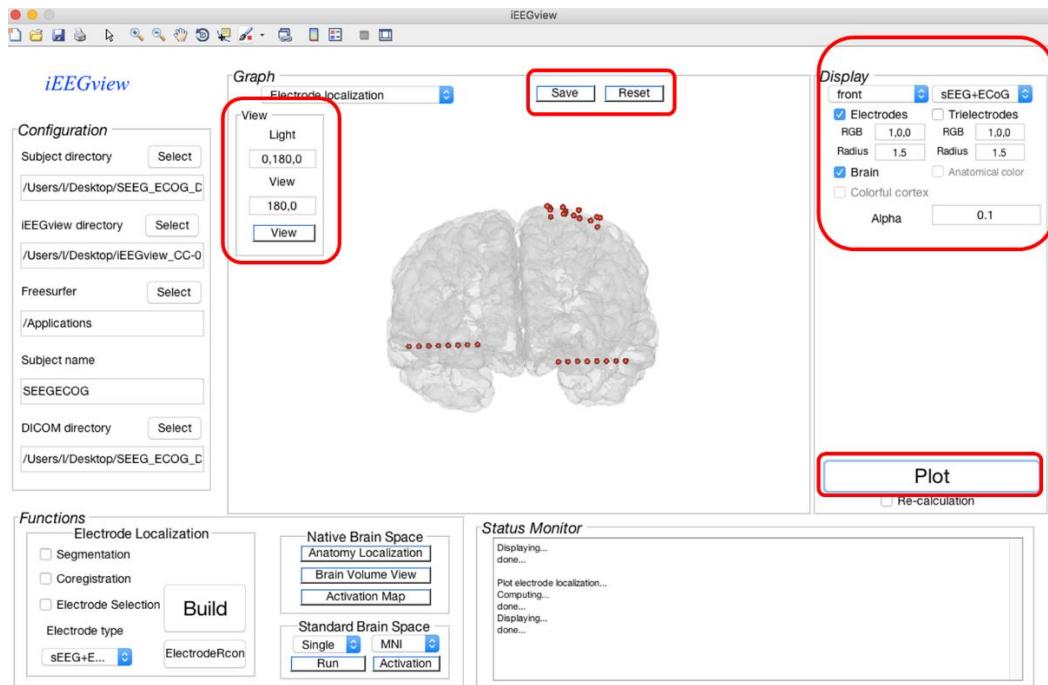


Fig. 4.15 Post operations for the figure.

## 4.3 Native Brain Space Related Analysis

### 4.3.1 Anatomical Label Identification

- 1) To get the anatomical label for each electrode, click the ‘Anatomy Localization’. iEEGview will automatically start to calculate this. And a popup window will appear to ask users to select one of the three Atlas to use. Once this process is finished successfully, the State panel will appear ‘AnatomyModel completed!’.
- 2) In this step, if you want to color the electrodes differently based on their anatomical locations, select the checkbox ‘Anatomical color’ and ‘Plot’ to present the anatomical information identification results (Fig. 4.16). Besides, users can also select the electrodes types and electrode modules to be shown (Sec.4.2.4).
- 6) Additionally, if you want to color the different cortical regions, select the checkbox ‘Colorful cortex’, then you can input the specific cortical region number in the column ‘ROI’ (e.g. 17,18 for single region, or 17:25 for multiple regions, default is the whole cortex areas). Similar with Sec.4.2.4, the transparency of the cortical surface can be adjusted as well based on needs by changing the alpha value from ‘Display’ panel.
- 3) Click ‘Plot’ to see the results (Fig. 4.16).

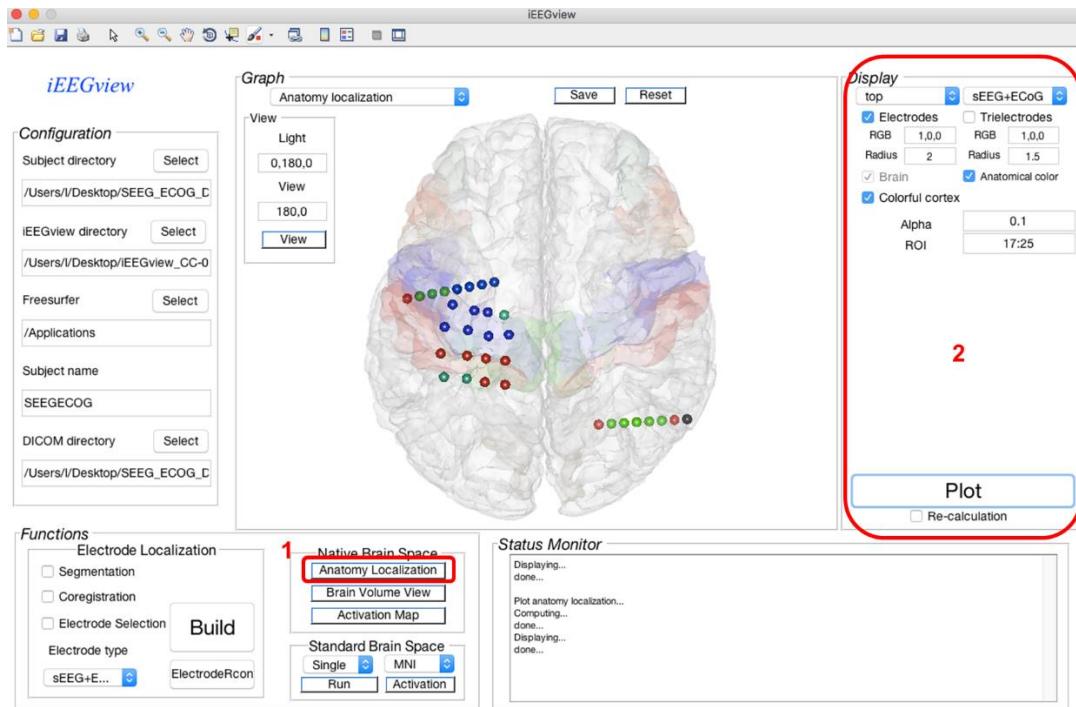


Fig. 4.16 Operations for identifying the anatomical information for each electrode.

### 4.3.2 View in MRI Brain Volume

- 1) Click ‘Brain Volume View’ and a new GUI window for this function will come out (Fig. 4.17).
- 2) In this new interface (Fig. 4.17), the original MRI and segmented brain images (Atlas) are shown in the bottom right side. In the top right is the scroll bars showing the current slice number of each view (sagittal/axial/coronal in total). The users can adjust the slice number in three dimensions by either click or scroll the wheels from the mouse. The anatomical labels for the electrode that existed in the MRI slices are shown in the top right. The 3D view of the current slice position is shown as a red cross in the bottom left. The view can be adjusted by using the drop-down box below the 3D brain. The checkbox ‘Electrode Name’ is used to turn on/off the displaying of electrodes name on the MRI slices.

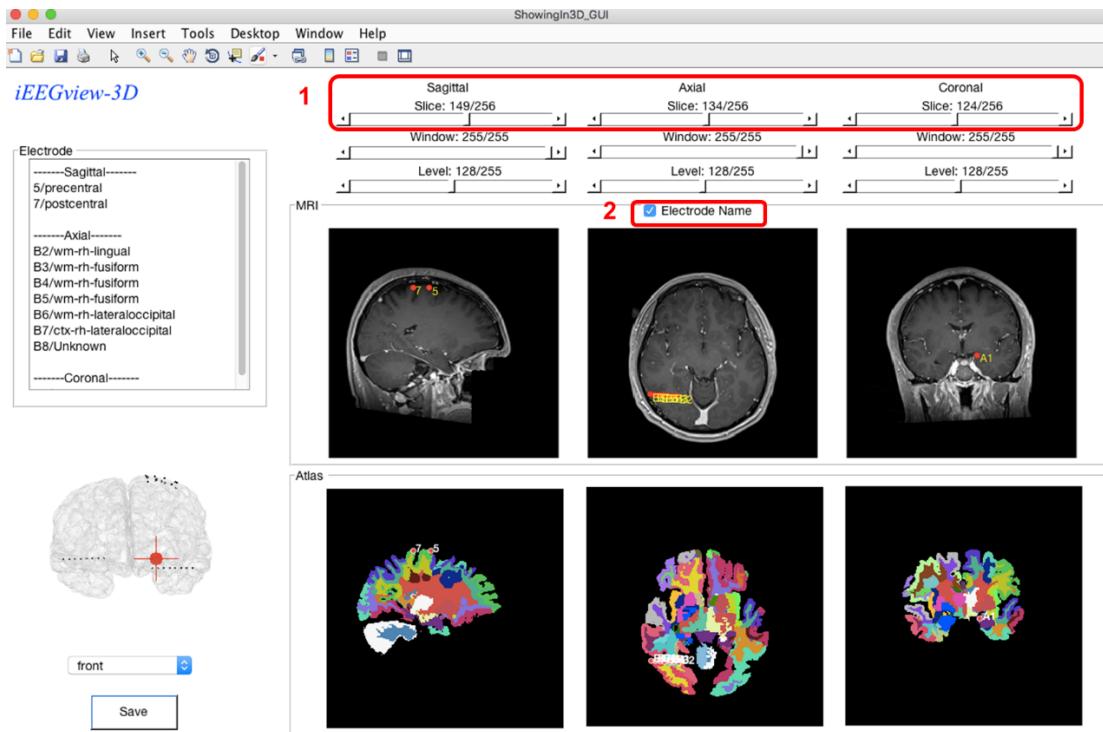


Fig. 4.17 The interface of ‘Brain Volume View’ function

- 3) If you want to save the figures, click ‘Save’, then an interface to come out let you to choose which figures you are going to save. Select the figures and then click ‘OK’, the figures will be saved (Fig. 4.18).

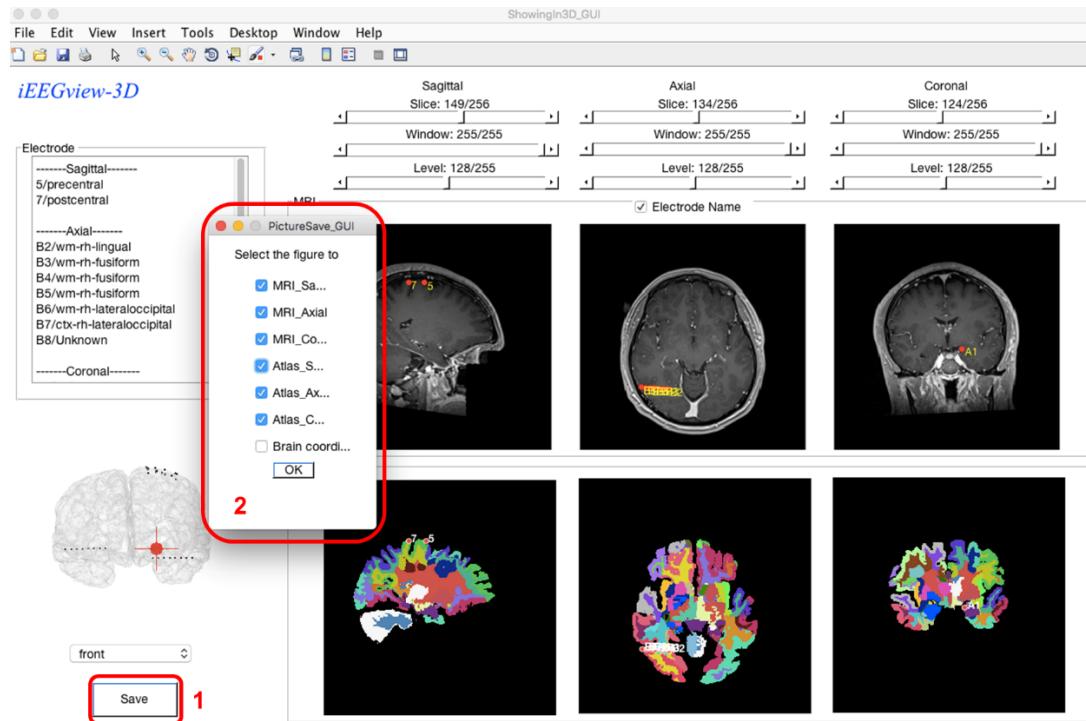


Fig. 4.18 Operations for saving figures.

### 4.3.3 Activation Map Visualization

- 1) If the users want to render the activation map using intracranial recording, click ‘Activation Map’ in the panel ‘Native Brain Space’ (Fig. 4.19).
- 2) Import activation data by clicking the icon ‘Import data’ and set the activation parameters in the ‘Display’ panel. The activation data can be either a component related with neural activation status or a statistical indicator of neural recordings. Please be noted that the activation data should be the same length with the electrodes and should be calculated and saved before this step by users.
- 3) Click ‘Plot’ to plot activation map.

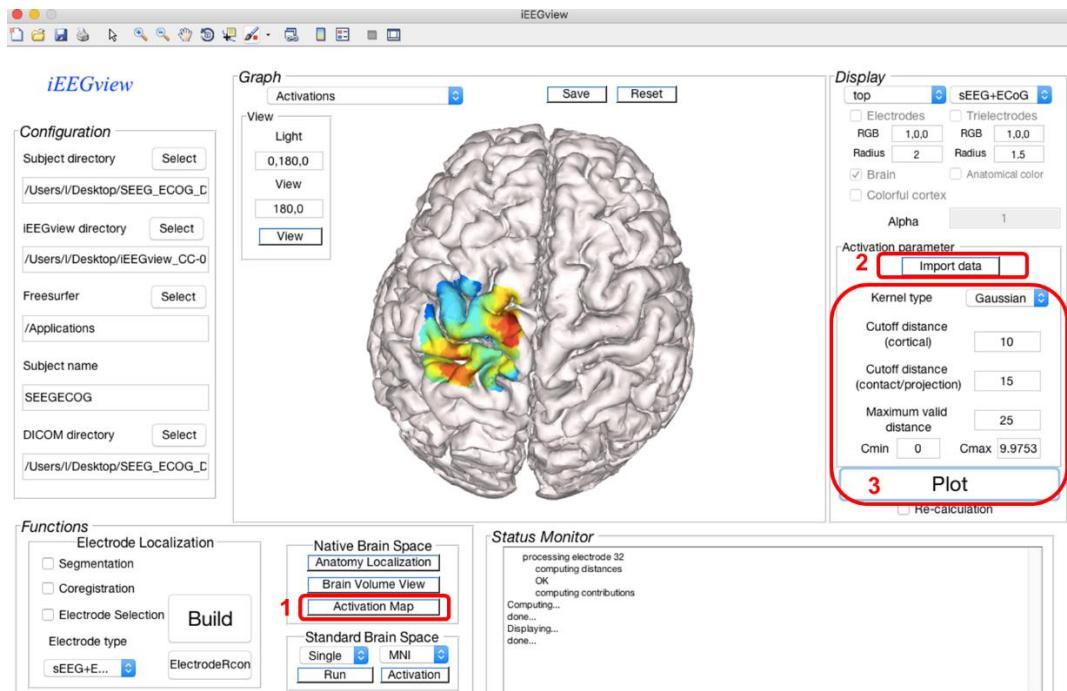


Fig. 4.19 Operations for plotting activation map.

## 4.4 Common Brain Space Operations

### 4.4.1 Mapping into Standard Brain Template for Single Subject

- 1) This function is used to transfer the electrodes in native brain space into common brain space. iEEGview provides two standard brain templates (one is Montreal Neurological Institute (MNI) brain template which is normalized to MNI152 space, the brain is known as ‘Colin27’; the other one is Freesurfer average brain, known as ‘Fsaverage’) for the mapping of both SEEG and ECoG electrodes. For the SEEG electrodes, iEEGview maps the electrodes using two methods on these two brain templates separately. For SEEG (depth electrodes), one is nonlinear (volumetric registration) transformation which is implemented on MNI brain template, the other one is linear transformation which is implemented on ‘Fsaverage’ brain. For ECoG electrodes, iEEGview uses volumetric /surface-based registration for the mapping, implemented on MNI/‘Fsaverage’ brain template separately.
- 2) To start the mapping of electrodes from single subject, select ‘Single’ in the ‘Standard

'Brain Space' panel (Fig. 4.20-4.21).

- 3) Select which standard brain model you want to view (MNI (Fig. 4.20) or 'Fsaverage' (Fig. 4.21)). iEEGview computes the coordinates of each electrode under these two brain templates, so this option is used for the display purpose.
- 4) Click 'Run', iEEGview will run the transformation of electrodes coordinates from native brain space to common brain space. Once finished, the standard brain mapping results are saved in the file 'electrodes\_Final\_Norm.mat' in the folder 'Electrodes' located in the subject directory.
- 5) Click 'Plot' in the 'Display' panel to see the electrode locations in the standard brain template. For electrodes, you can also change the color and radius of the electrodes in the Display Panel. For brain, you can color the specific standard brain based on needs in the Display Panel as well (Same with Sec.4.3.1).

Key notes: For the standard brain mapping of depth electrodes into the Freesurfer average brain template (Fsaverage), iEEGview runs the space translation directly (<http://surfer.nmr.mgh.harvard.edu/fswiki/CoordinateSystems>), therefore, this step needs the accurate Talairach registration (talairach.xfm) from Talairach to MNI atlas by Freesufer. You can check and fix the Talairach registration following the link if it's necessary: ([http://ftp.nmr.mgh.harvard.edu/fswiki/FsTutorial/Talairach\\_freeview](http://ftp.nmr.mgh.harvard.edu/fswiki/FsTutorial/Talairach_freeview)).

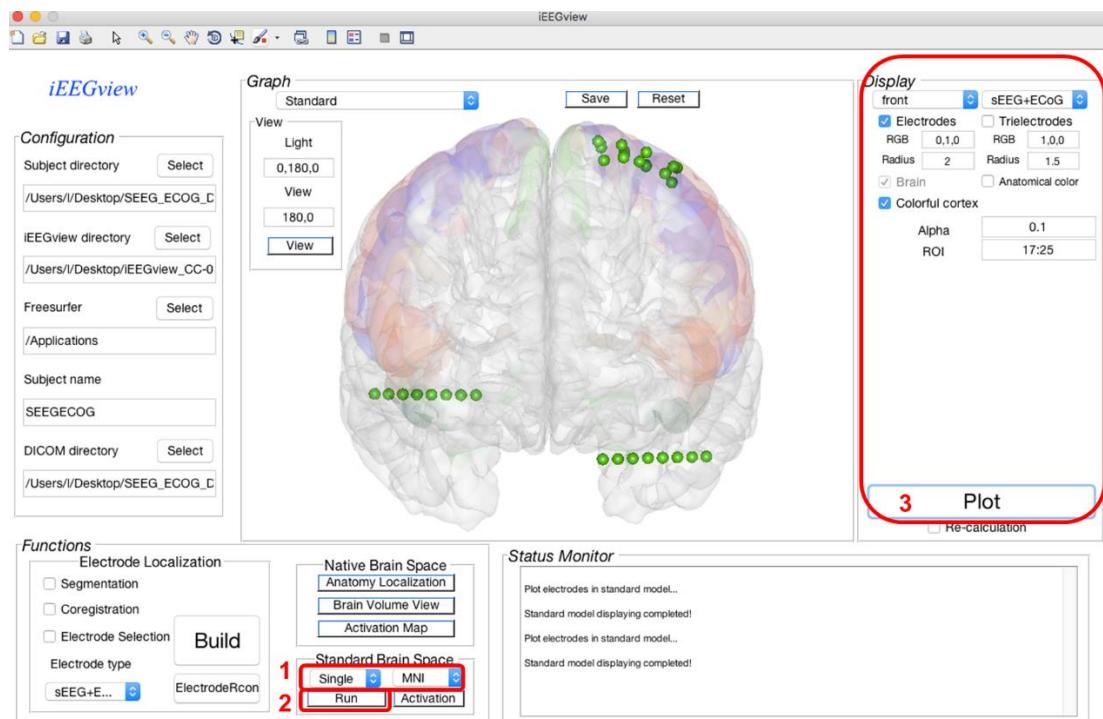


Fig. 4.20 Operations for standard brain (MNI) mapping of single subject.

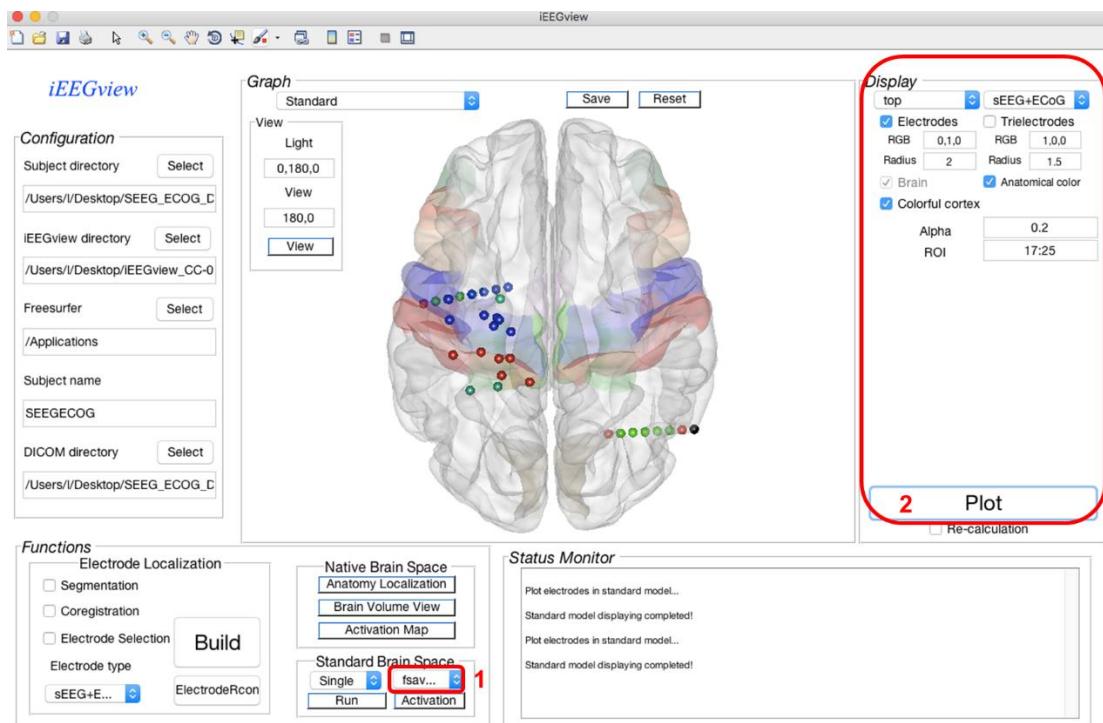


Fig. 4.21 Operations for standard brain ('Fsaverage') mapping of single subject.

#### 4.4.2 Mapping into Standard Brain Template for Multiple Subjects

- 1) Select 'Multiple' in the 'Standard Brain Space' panel to see the standard brain mapping results of electrodes when having multiple subjects.
- 2) Select which standard model for display.
- 3) Click 'Run' and select translation results of all subjects needed (Fig. 4.22). The translation results of other subjects should be calculated and saved before this step.

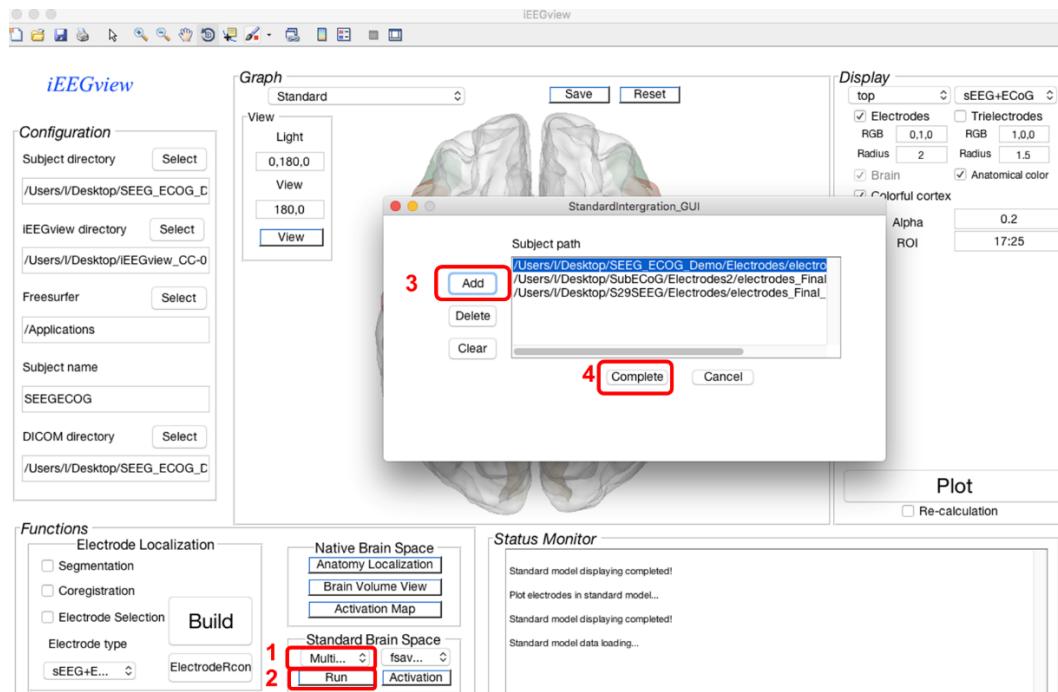


Fig. 4.22 Adding electrodes information from multiple subjects.

- 4) Click ‘Plot’ in the ‘Display’ panel to see the final results (Fig. 4.23). For electrodes, users can also change the color and radius of the electrodes in the ‘Display’ panel. When ‘trielelectrodes’ option is checked, the projection points on the cortical surface for each electrode will be shown. For the brain, users can color the specific standard brain based on needs in the ‘Display’ panel as well (Same with Sec.4.3.1).

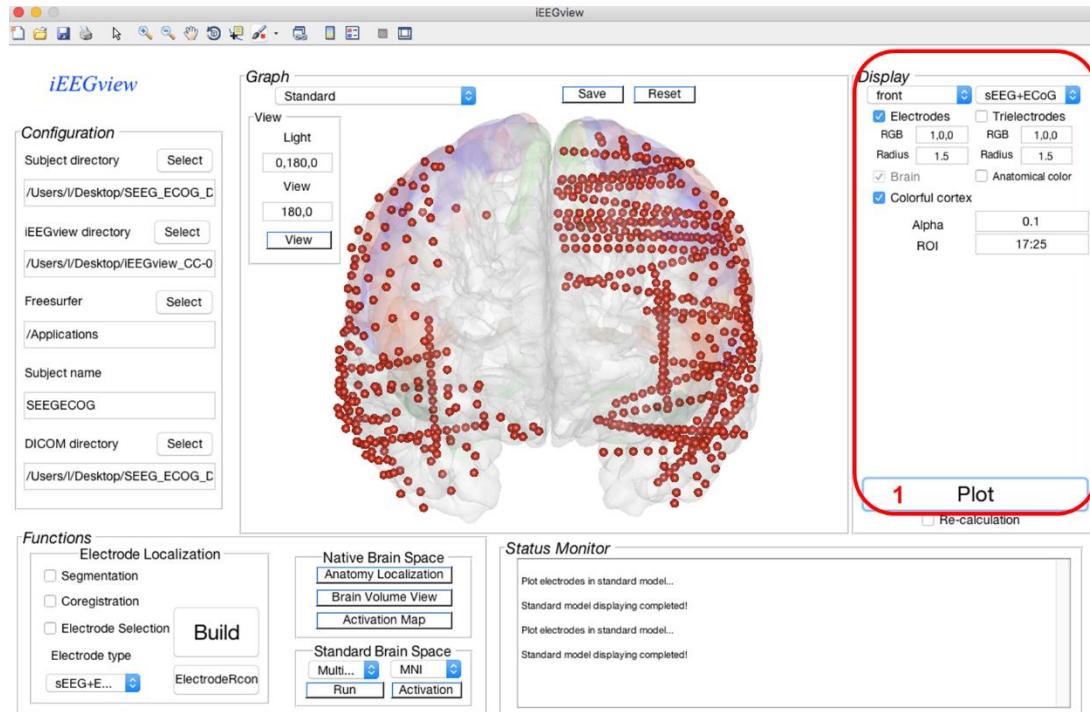


Fig. 4.23 Standard brain mapping results from multiple subjects on the MNI brain

#### 4.4.3 Activations Map Visualization on Standard Brain Template

- 1) This function is designed for calculating the activation map on standard brain template.
- 2) First select the brain template on which you want to produce the activation map. Then click ‘Activation’ in the panel ‘Standard Brain Space’ (Fig. 4.24).
- 3) The activation map can be either for a single subject or multiple subjects. Click ‘Import data’ in the sub-panel ‘Activation parameter’ to import the activation data for the loaded electrodes. The activation value should be in correspondence with the loaded electrodes. Then, confirm the activation parameters within this panel.
- 4) Click ‘Plot’ for the calculation and visualization of activation map in common brain space (Fig. 4.24). If the users want to see the activation map on another standard brain template, change the standard brain template first and then click the ‘Plot’ icon, the activation map will be re-generated on the specified brain template.

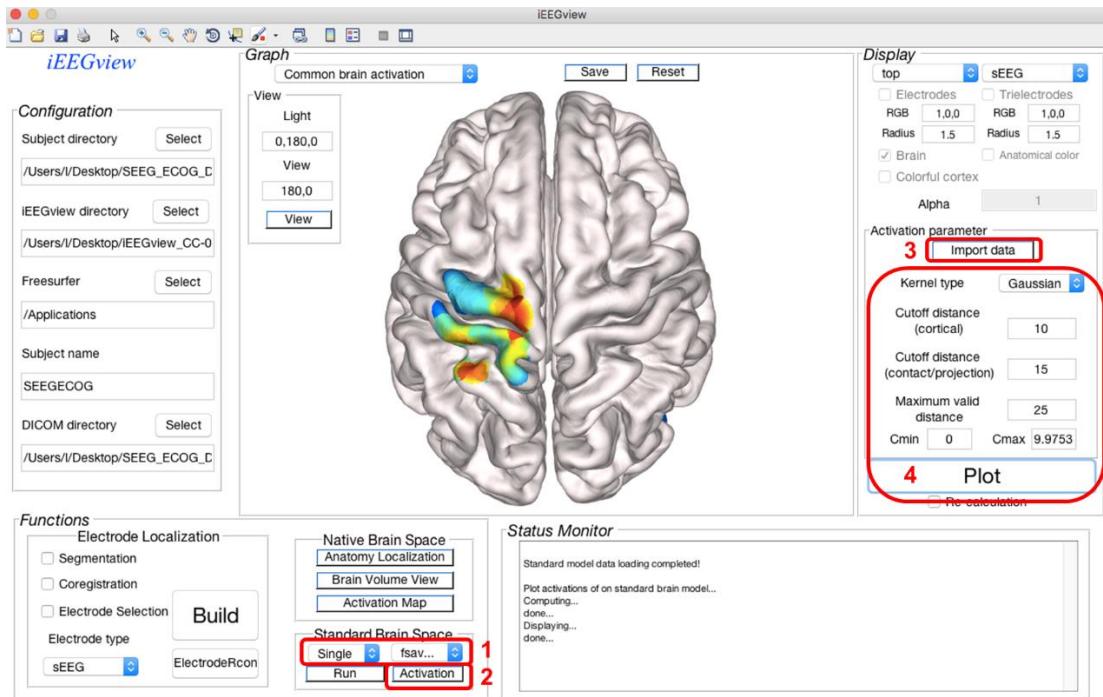


Fig. 4.24 Operations of plotting activation map on the standard brain.

For all above introduced functions of iEEGview (e.g. electrode localization, anatomical information identification, activation map and standard brain operations), if the results for each function have been calculated, users can directly go to the specific function by selecting the corresponding items in the drop-down box of ‘Graph’ panel, this will be convenient and can avoid repeated calculations.

## 4.5 Data Files Saved in Subject Path

After all above steps, iEEGview will generate several folders within each subject path folder (Fig. 4.25), where all the electrodes localization information are saved in the subfolder ‘Electrodes’; the extracted brain model information are saved in the subfolder ‘MATLAB’; the ‘Figure’ subfolder contains the saved figures during the operation process; ‘NIfTI’ is the converted CT and MRI images in volume format; ‘Segmentation’ subfolder contains brain reconstruction results from Freesurfer; ‘States’ subfolder save the log file during the operation. ‘DICOM’ subfolder is the original CT and MRI dicom images. Within the ‘Electrodes’ folder, ‘electrodes\_Final\_Norm.mat’ save the final electrodes information, including the coordinates in native brain space and common brain space, the anatomical information, electrodes name, electrode type and PTD index, etc. Within the ‘MATLAB’ folder, ‘WholeCortex.mat’ saves the original brain surface and smoothed brain surface that deprives the sulci of left/right/both hemisphere. Three surface cortical atlas are saved in the Cortex\_Center\_aparc/aparc2009/DKT40.mat. Users can find all the detailed data information from the folder and iEEGview scripts.

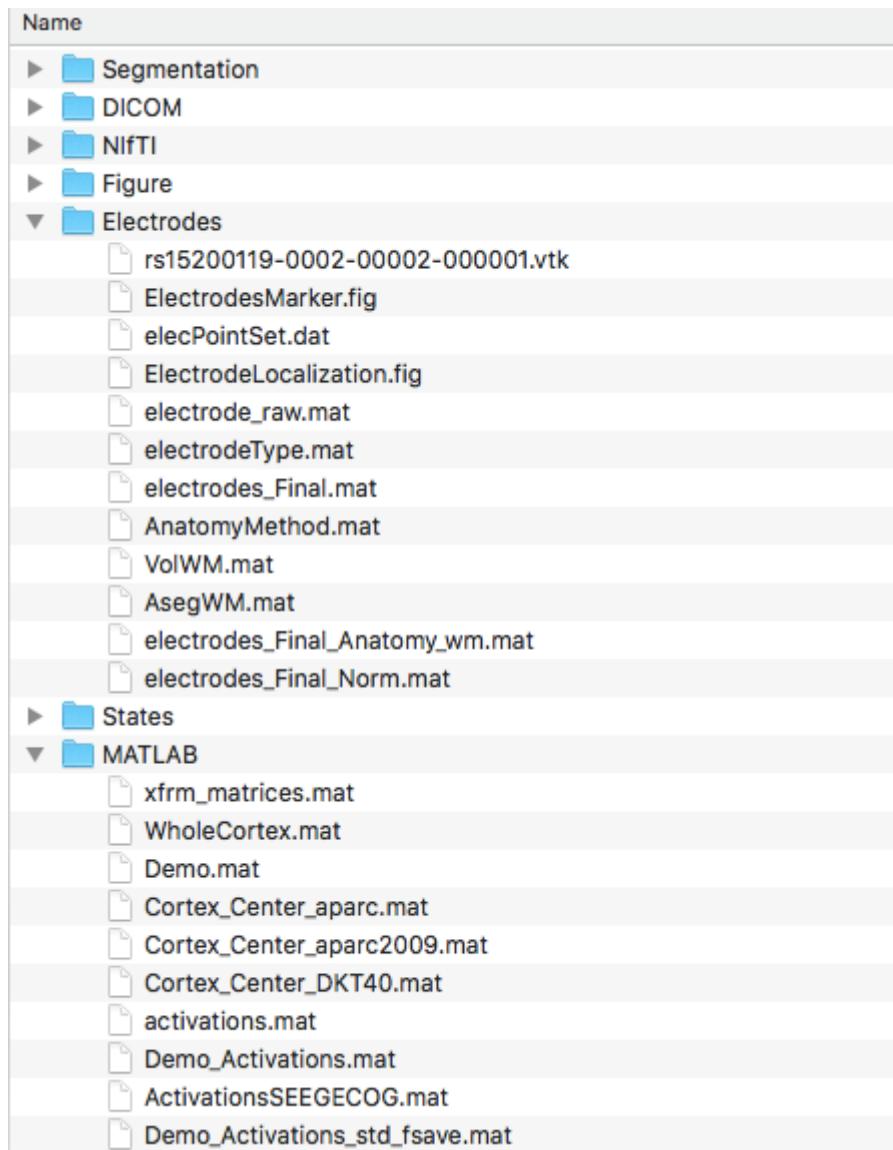


Fig. 4.25 Electrodes localization results data

## 5 Summary

We introduced how to use the iEEGview in this manual. The toolbox runs under a Mac OS system and needs the correct installation of Freesurfer and SPM. As a Matlab GUI based software packages, this toolbox can be easily used to the localize and visualize intracranial electrodes through one full pipeline for research and clinical purpose. This toolbox also provides more than one choice in some functions to fulfill potential various needs in this field. Even though lots of necessary functions are provided within this toolbox, we understand that more functions may be in need. Even though we have tested toolbox and tried to make the toolbox robust, we believe there are still space for improvements. Therefore, we welcome the field researchers to contribute on this toolbox to facilitate the intracranial EEG related studies together.