GARDEL USER MANUAL

GARDEL



GUI for Automatic Registration and Deep Electrodes Localization

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Introduction

GARDEL “GUI for Automatic Registration and Depth Electrode Localization” is a MATLAB tool that permits to register an MRI image into a CT space, to automatically segment the electrodes on the CT image, to visualize them on MRI or CT images or in a 3D rendering and to label each contact according to an Atlas. This document pretends to describe the usage of the tool.

Installation instructions

- Matlab runtime 9.5 v2018b required

Image format

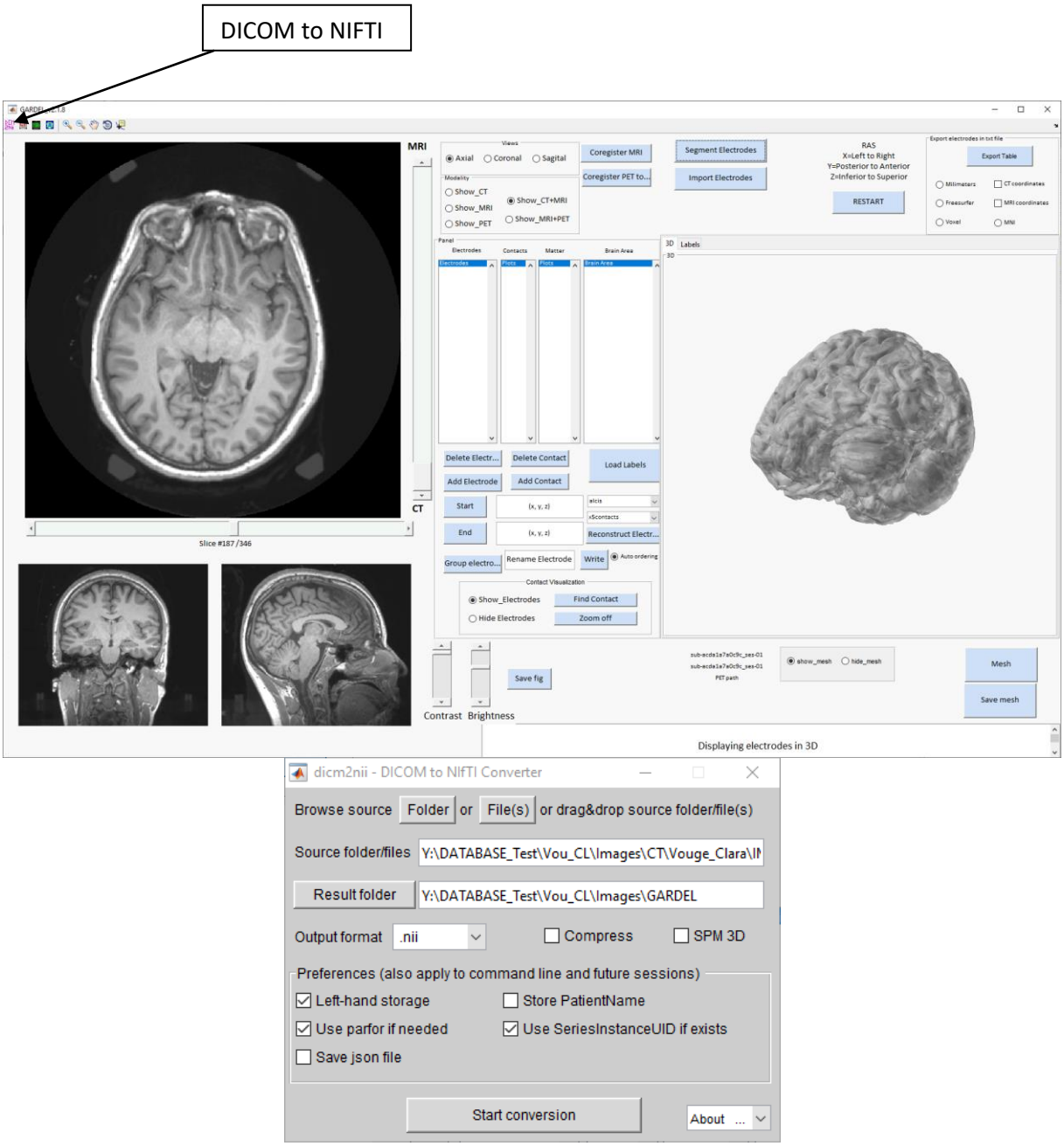
DICOM: The Digital Imaging and Communications in Medicine format (.dcm) is the international standard for medical images and related information (ISO 12052). It defines the formats for medical images that can be exchanged with the data and quality necessary for clinical use.

Analyze 7.5: Analyze is a software package developed by the Biomedical Imaging Resource (BIR) at Mayo Clinic for multi-dimensional display, processing, and measurement of multi-modality biomedical images. It is a commercial package. They proposed the Analyze 7.5 file format that consists of two files: one file with the actual data in a binary format with the .img extension and another file (*header* with extension .hdr) with information about the data such as voxel size and number of voxels in each dimension.

NIfTI: Neuroimaging Informatics Technology Initiative (.nii) is a new Analyze-style data format, which combines both files of Analyze 7.5 format (.img/.hdr) into a single file (.nii). This is the standard format used in neuroimaging nowadays.

DICOM to NIFTI

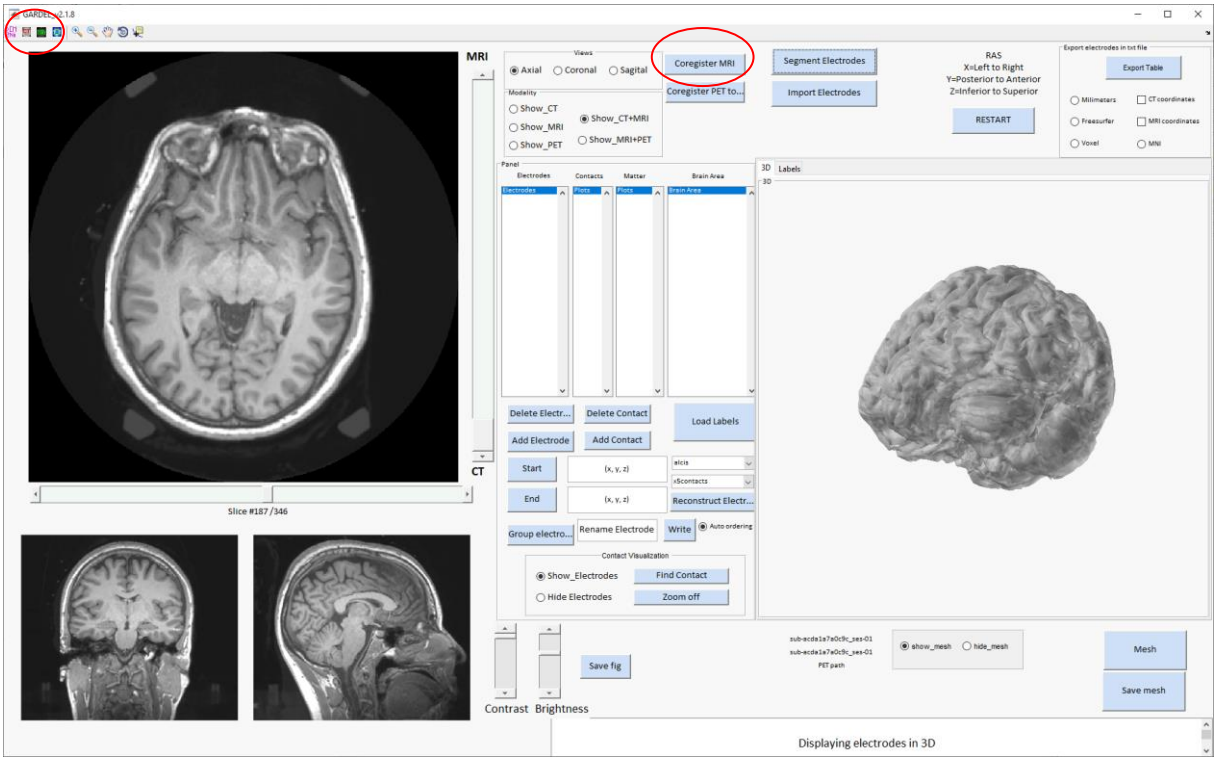
In general, the format obtained from the MRI or CT scan is DICOM, and the specified format that GARDEL uses is NIfTI. So the first step is to transform the image format for both MRI and CT images. For that purpose, use the DCM to NII module. This task can be done before with other software, but there is no guarantee that the image will be in the right orientation. By doing it with the module introduced in GARDEL images will be well oriented.



Choose in “Source folder” the folder where the DICOM images are located and in “Result folder” the folder where the NIFTI image will be stored. Do this for both the MRI and CT.

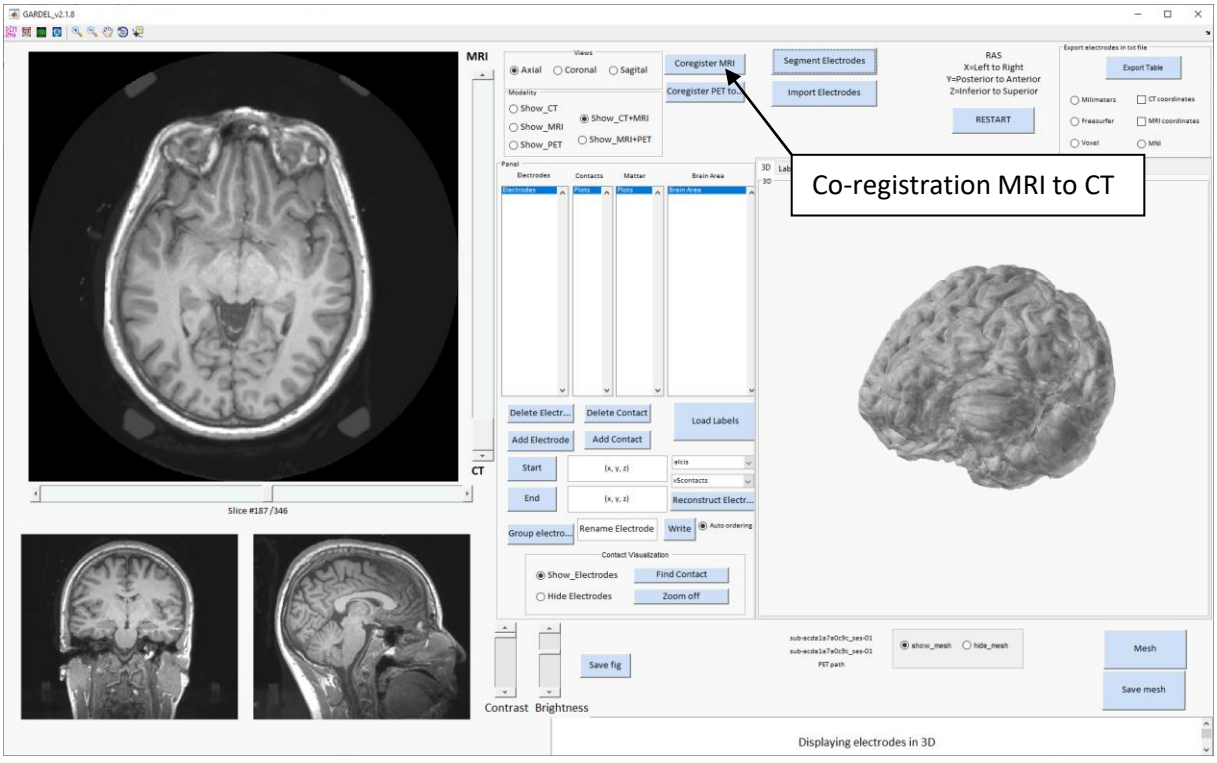
Load Images

Once images have been converted, they can be loaded by clicking on “Load CT” and “Load MRI”. If images are not registered, then they can be displayed by clicking on “Show CT” or “Show MRI”, but as they are not coregistered they cannot be visualized at the same time. Clicking on “Show both” will display an error message.



MRI to CT registration

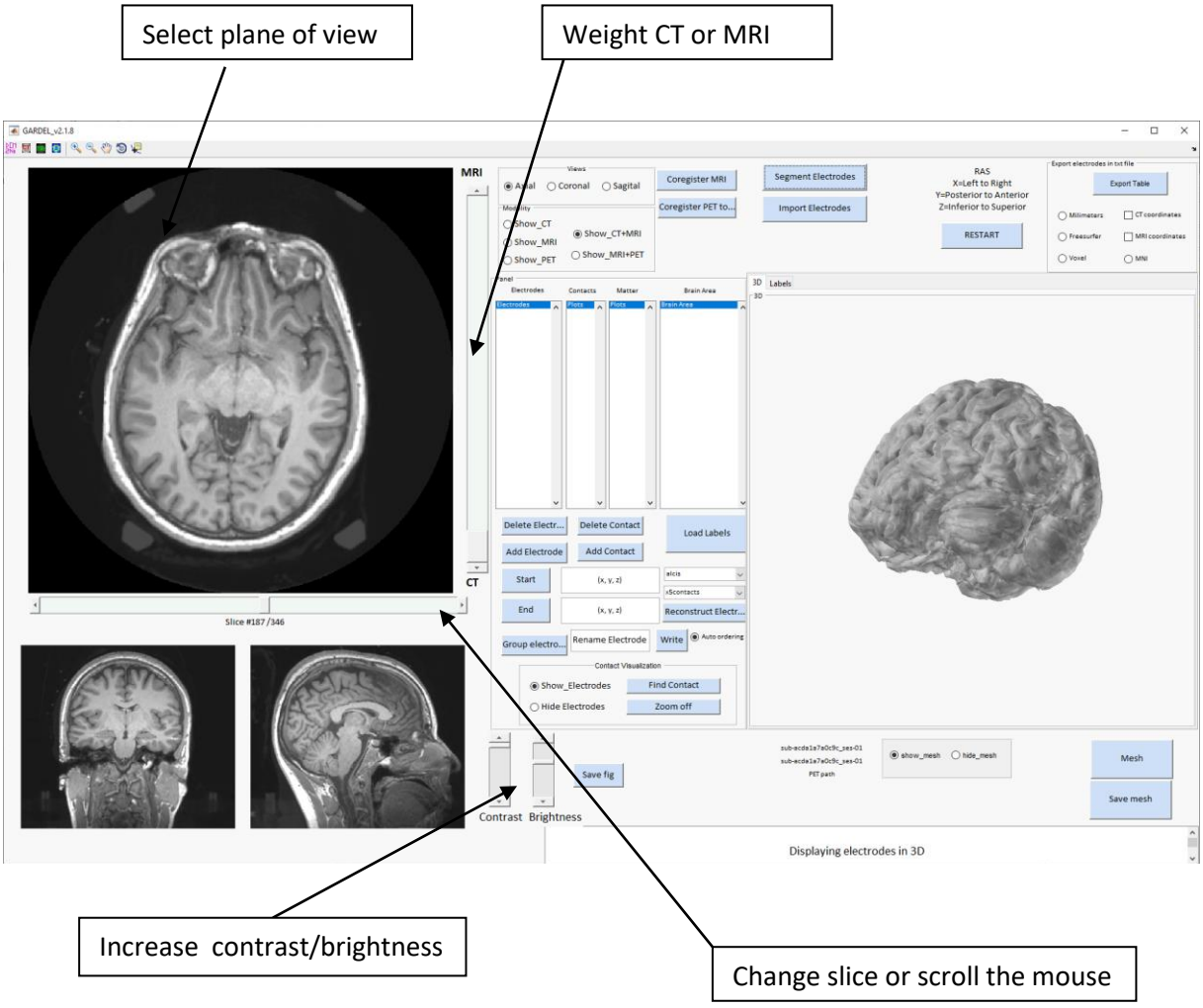
GARDEL performs MRI to CT registration using SPM8. Once images are loaded, click on "Coregister". This step may take a few seconds.



The registration step will create a *.nii file named *coreg_*name of MRI*.nii* in the same folder than the MRI scan. It will be loaded automatically at the end of the registration. If images are already co-registered, then this step is not done. This button will load automatically the registered file. It creates also a .mat file that contains transformation matrix from MRI coordinate system into CT coordinate system.

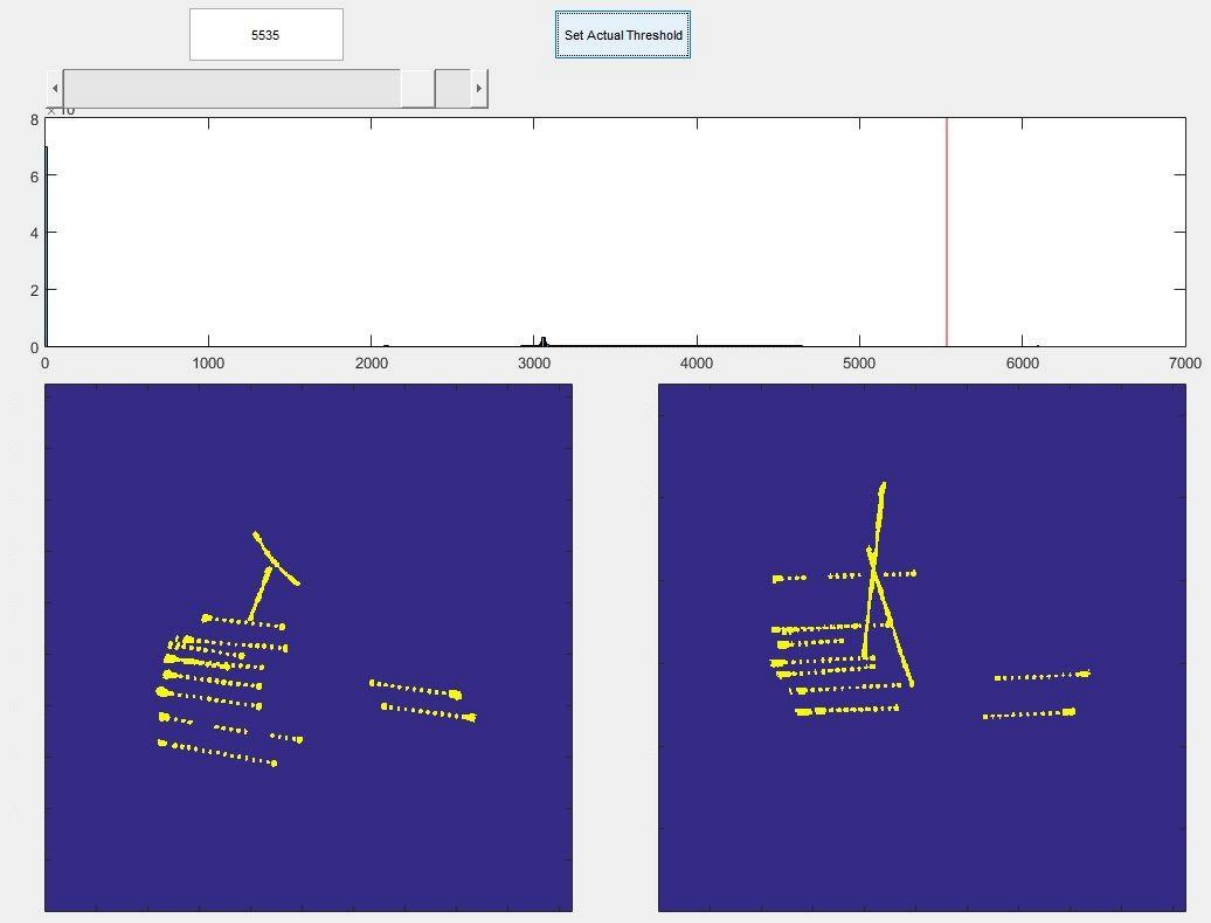
Image tools

With both images co-registered, they can be visualized and different tools can be used.

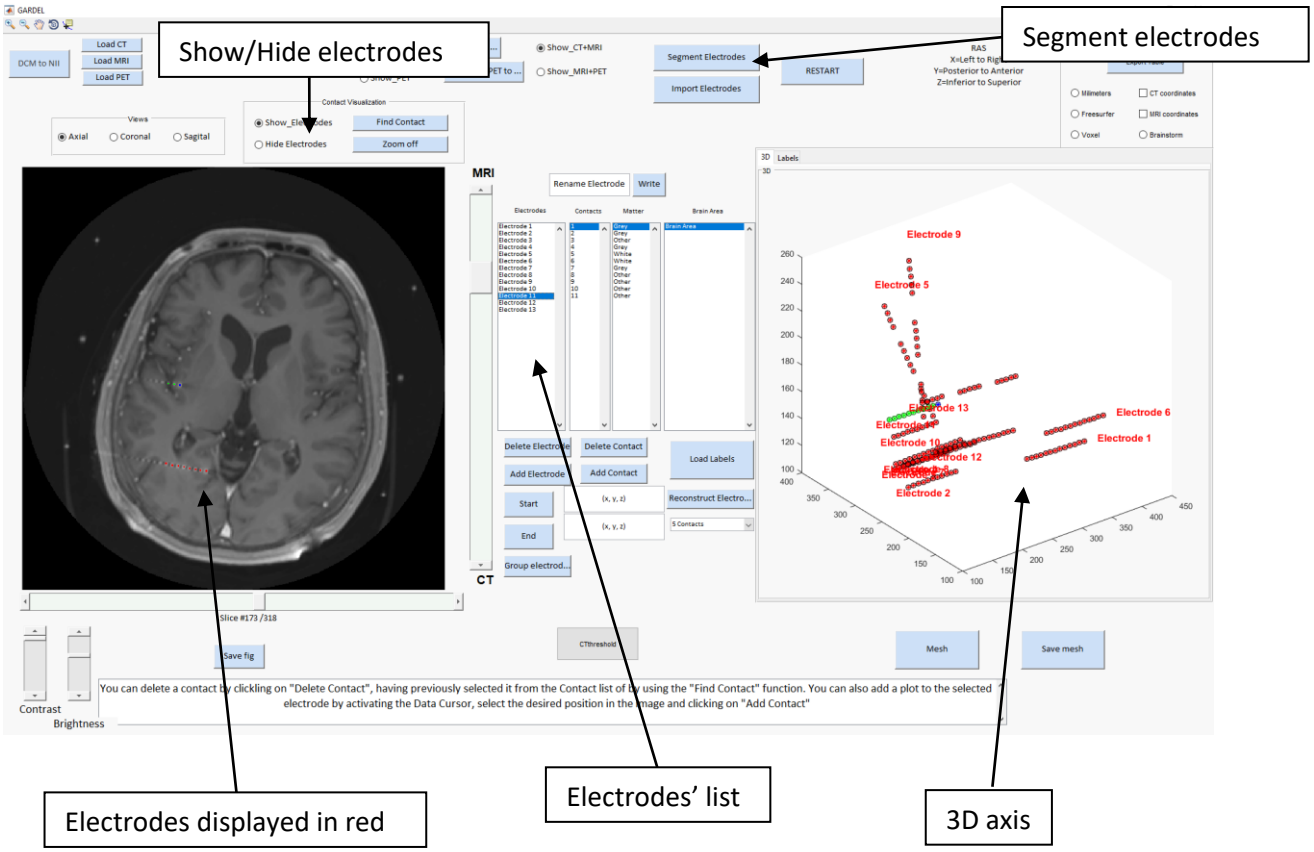


Electrode segmentation

With both images co-registered, electrodes can be segmented. This step may take a few minutes.
Firstly, a window enables you to set a threshold on CT values.



This can be used to adjust the threshold for a better segmenation.
Then, the automatic segmentation starts. It takes around 10-15 minutes.
Finnaly, at the end of the segmentation, electrodes will be displayed in the 3D axis, and a list of all electrodes detected will also be displayed as well as the anatomical structure associated to each contact. These electrodes will be displayed on the MRI/CT image. The centroids of all contacts detected will be plotted in red. They could be hidden or displayed clicking on "Hide Electrodes" from the panel above the CT/MRI image.

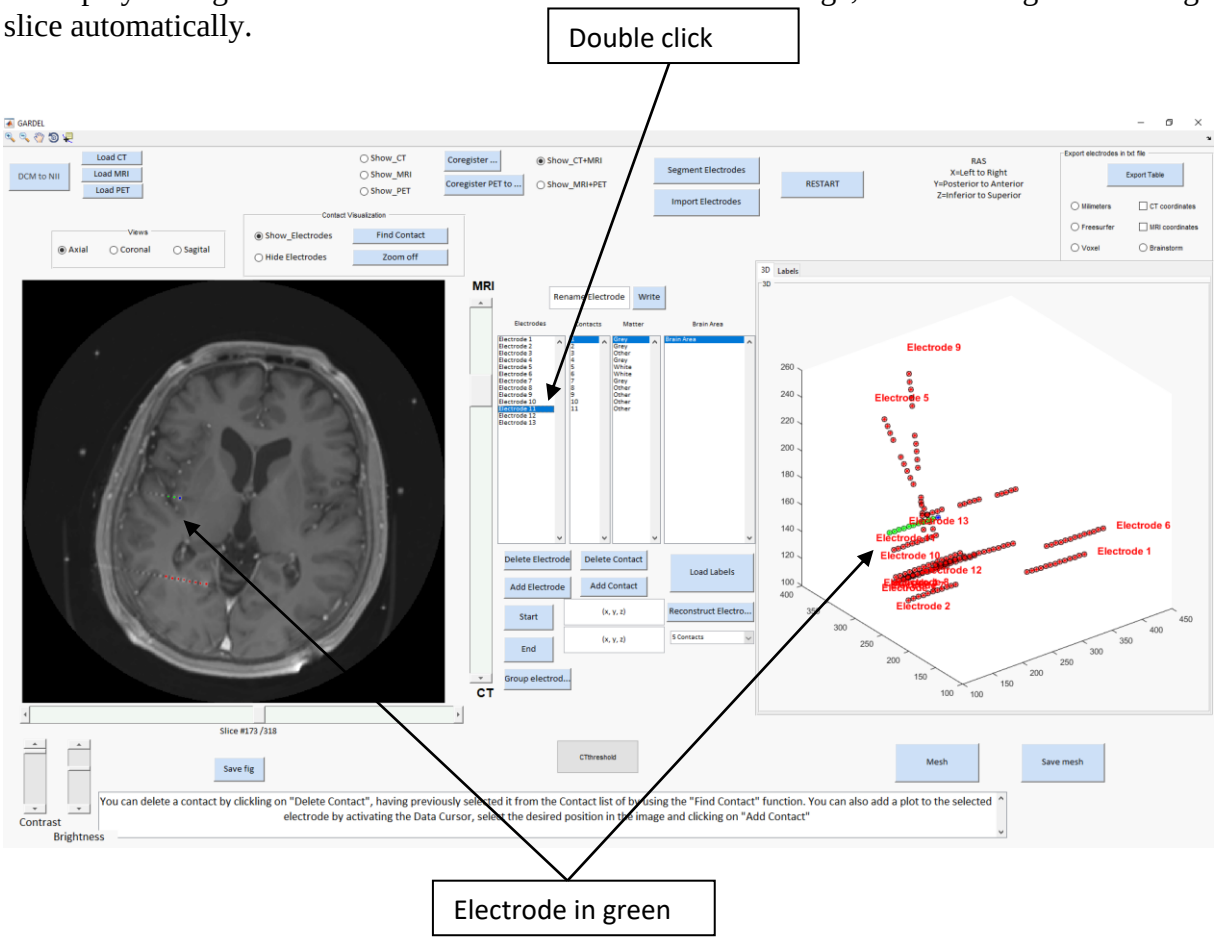

Show/Hide electrodes
Segment electrodes
Electrodes displayed in red
Electrodes' list
3D axis
Load CT
Load MRI
Load PET
DCM to Nii
Segment Electrodes
Import Electrodes
RESTART
Find Contact
Zoom off
Rename Electrode
Write
Delete Electrode
Delete Contact
Add Electrode
Add Contact
Load Labels
Start
End
Reconstruct Electro...
Group electrod...
Save fig
Mesh
Save mesh
MRI
CT
Contrast
Brightness
Electrode 9
Electrode 5
Electrode 13
Electrode 6
Electrode 1
Electrode 12
Electrode 2

Display Electrodes

In order to visually check if electrodes have been correctly segmented, the visualization tools can be used.

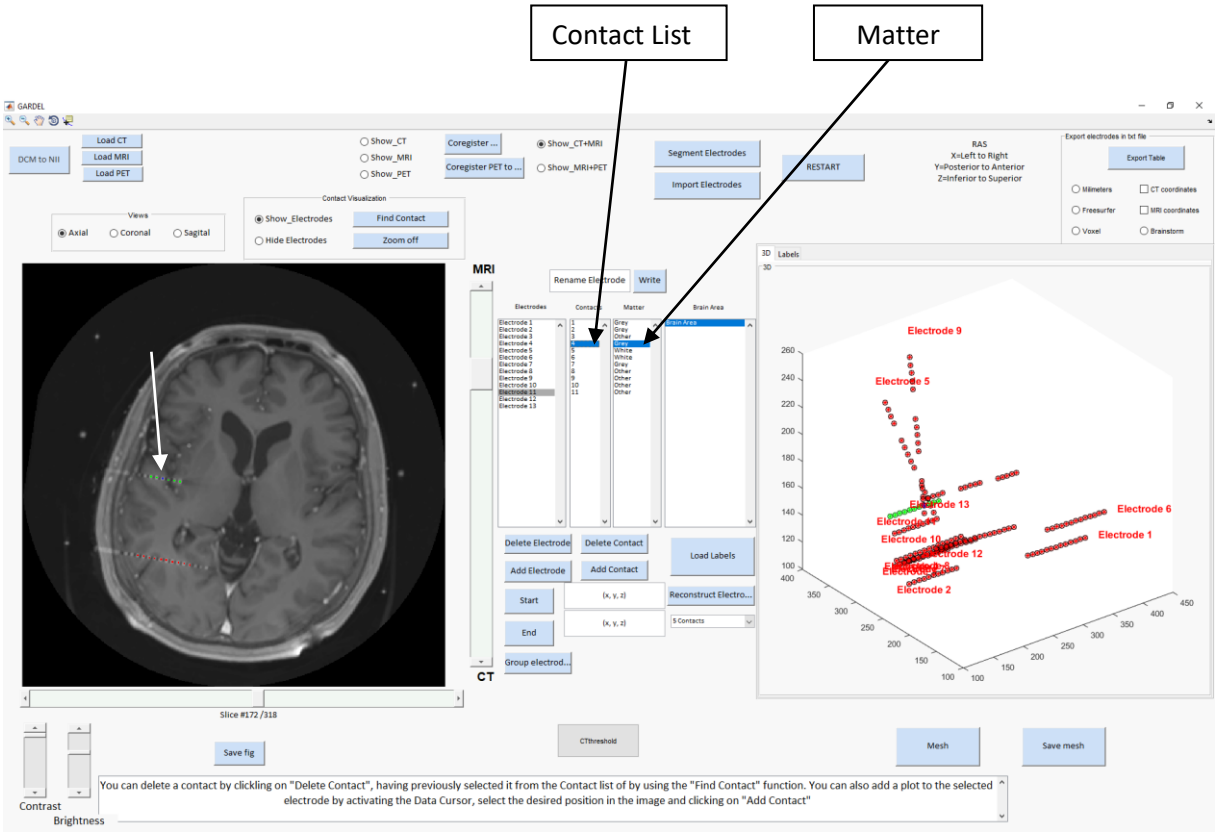
Electrodes' List

Double clicking on each electrode from the Electrodes' List, the selected electrode will be displayed in green in both the 3D axis and the CT/MR image, and the image will change slice automatically.



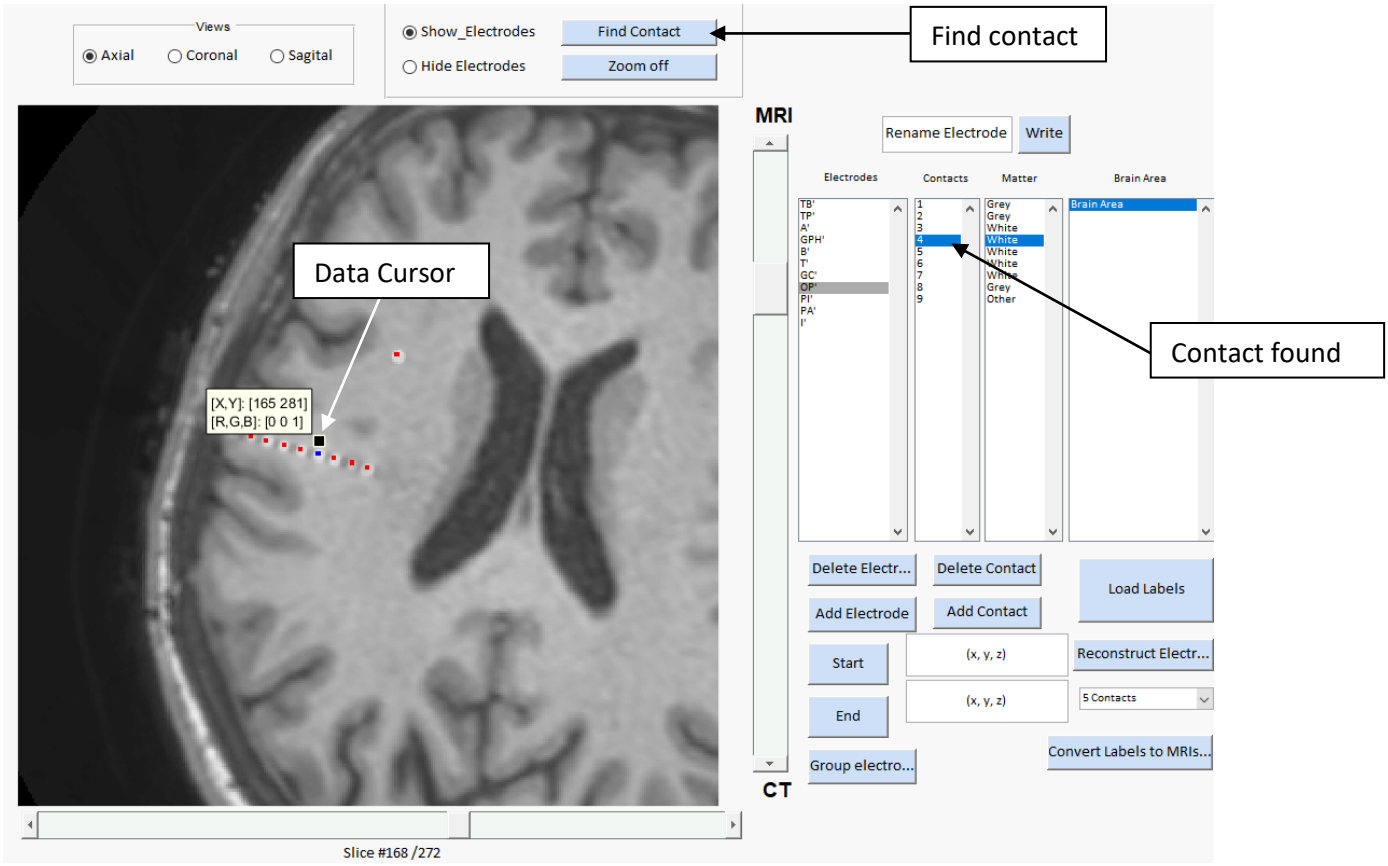
Contacts' List

When selecting an electrode, the contacts list will be filled with the number of contacts of the current electrode. Contacts are ordered from the deepest in the brain to the most superficial. Double clicking on one contact will display it in blue.



Find Contact

You can find a contact by selecting a pixel in the image with the data cursor and then clicking on “Find Contact”. This will display the contact in blue and the respective contact will be selected in the contacts’ list.



Correct electrode segmentation

Using the visualization tools it is possible to manually correct the segmentation if electrodes are eventually badly segmented.

Delete electrode

Choosing an electrode from the electrodes’ list and clicking on “Delete Electrode” will completely remove the electrode.

Delete Contact

Idem for contacts.

Add Contact

In order to add a contact to the current electrode, use the data cursor to select the point in the image that corresponds to the contact. Then click on "Add Contact" and it will be added to the current electrode.

Add electrode

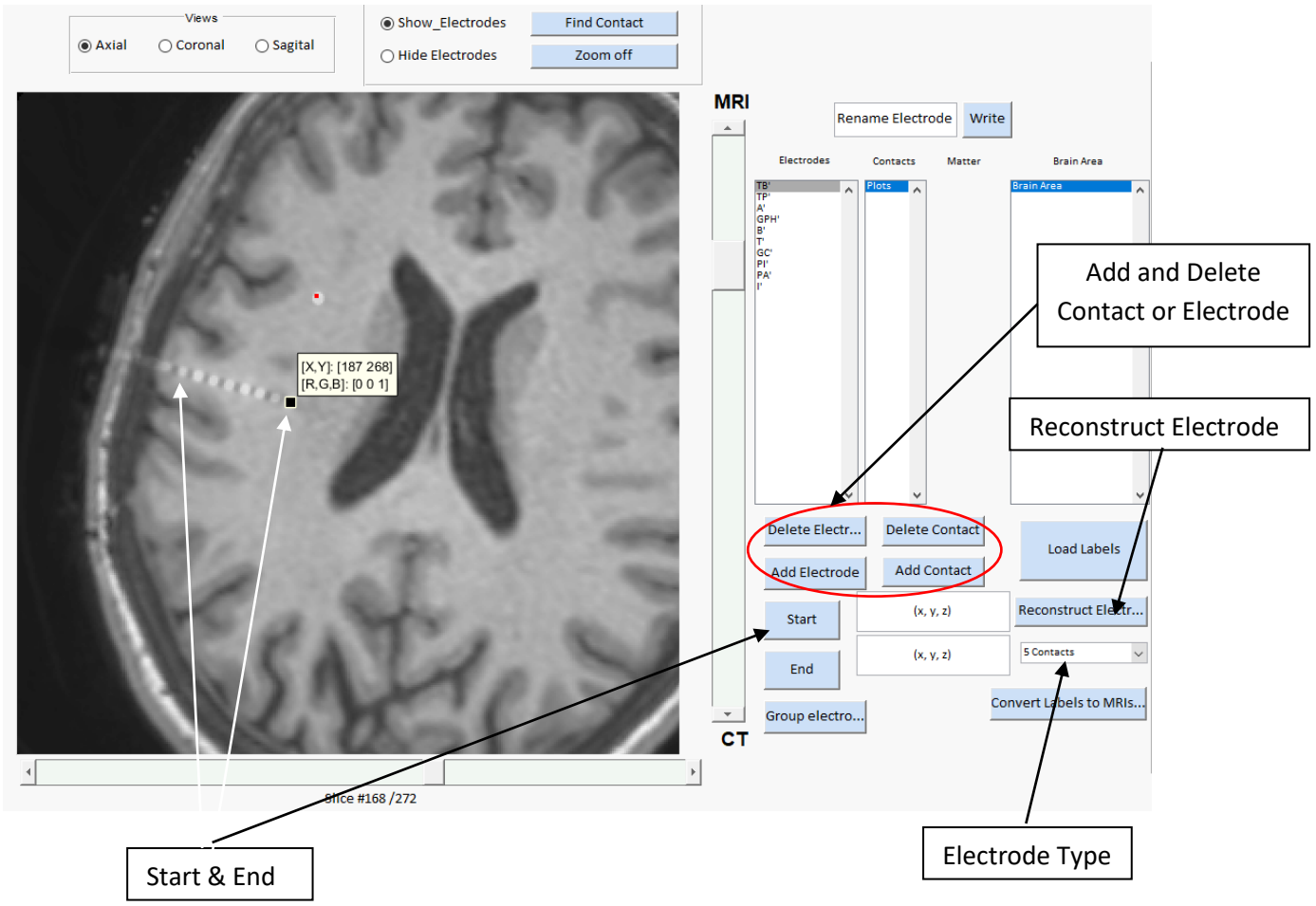
Electrodes can also be added entirely. First click on "Add Electrode". A new electrode will be added to the "Electrodes' List" but its contact list will be empty. To reconstruct the position of the contacts, two different tools can be used:

Add each contact separately

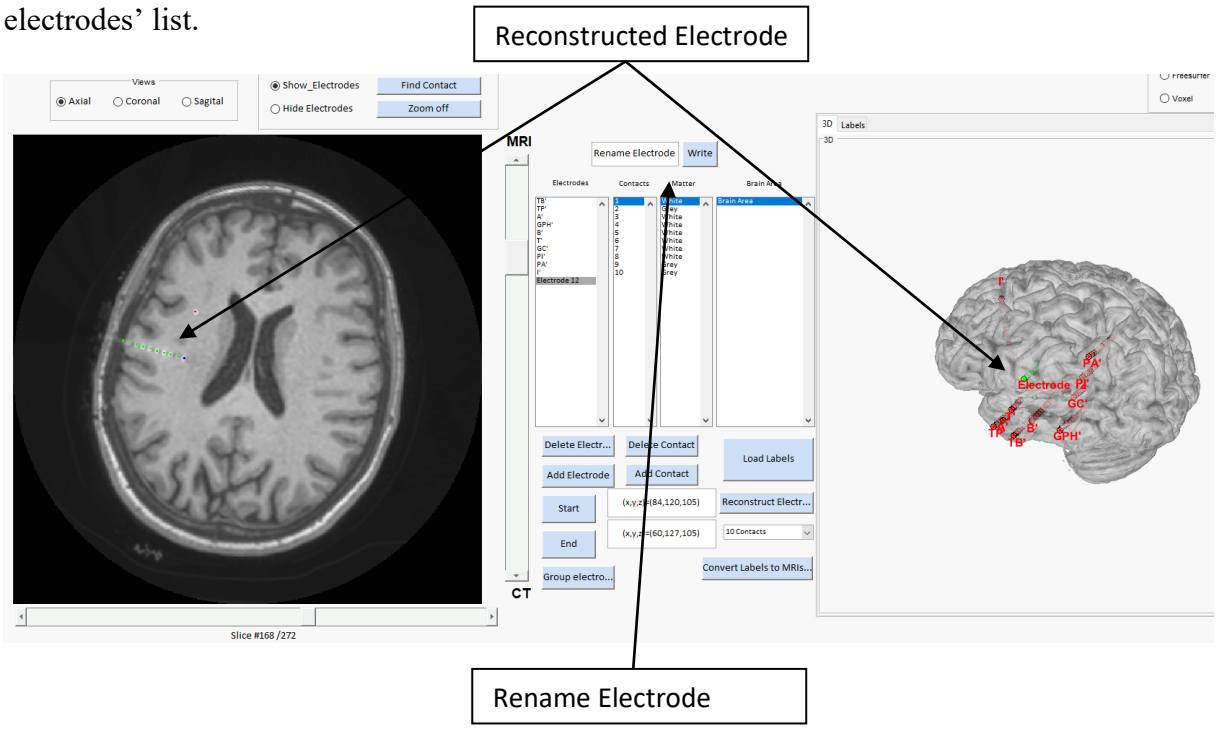
Using the "Add Contact" module described above, contacts can be added one by one.

Choose entry and target point

Use the data cursor to point the start contact (deepest) and click on "Start". Do the same with the end contact (most superficial). Then choose the electrode type from the list on the right and click on "Reconstruct Electrodes"



Once the electrode is reconstructed, it will be displayed in the 3D axis. In order to display it over the CT/MRI click on “Show Electrodes” or double click on the electrode from the electrodes’ list.



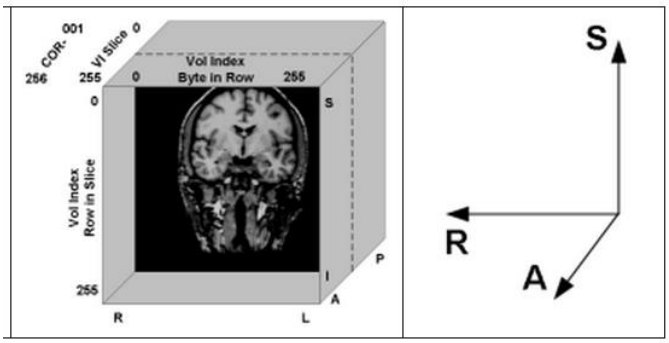
Rename electrodes

Electrodes will be named by default by “Electrode 1”, “Electrode 2”, …, “Electrode *n*”. In order to rename them, just choose them from the electrodes’ list, write the name in the textbox above and click on “Write”.

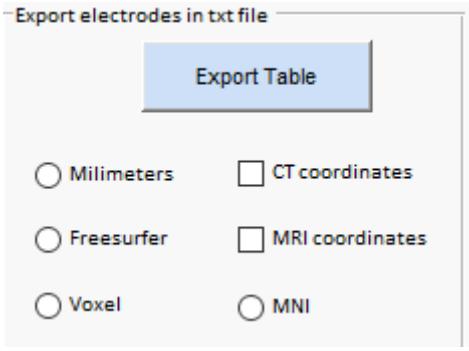
Export electrodes' coordinates

Once electrodes are correctly segmented, the coordinates of each contact can be saved in a text file. The coordinate system chosen is RAS. RAS stands for Right-Anterior-Superior. This means that the "x" axis will increase from left to right, "y" from posterior to anterior and "z" from inferior to superior. However, this is not enough to define the coordinates, because other 2 parameters have to be defined: the voxel size and the origin.

Voxel can adopt 2 sizes: the actual voxel size of the image provided by the MRI or CT scan or considering isotropic voxels of *1mmx1mmx1mm*.



The user will be asked to choose the appropriate coordinate system voxel/millimeters/freesurfer and CT/MRI.



Voxel/Millimeters/FreeSurfer

Voxel: Origin: Left, posterior and inferior edge of the original image, and the coordinates are in the original voxel size of the image (CT or MRI).

Millimeters: Origin: Left, posterior and inferior edge of the original image, and the coordinates are in millimeters.

FreeSurfer: Voxels are converted to millimeters and the image will be fitted to a *256x256x256* image with a voxel size of *1mmx1mmx1mm.* The origin is placed at the center of the image *(128,128,128)* and the directions of the axis are in RAS.

CT/MRI space

If MRI space is chosen, then the inverse transformation will be applied to the set of points corresponding to the contacts.

The resulting text file will indicate at the end of the file the coordinate system chosen. Each column is separated by tabulation.

NOTE :

- To be reused in GARDEL, electrodes have to be saved in CT millimeters, it will also create a file ElectrodesAllCoordinates.txt that can be reopen in GARDEL
- To be used in the 3Dviewer, electrodes have to be saved in MRI FreeSurfer coordinates.

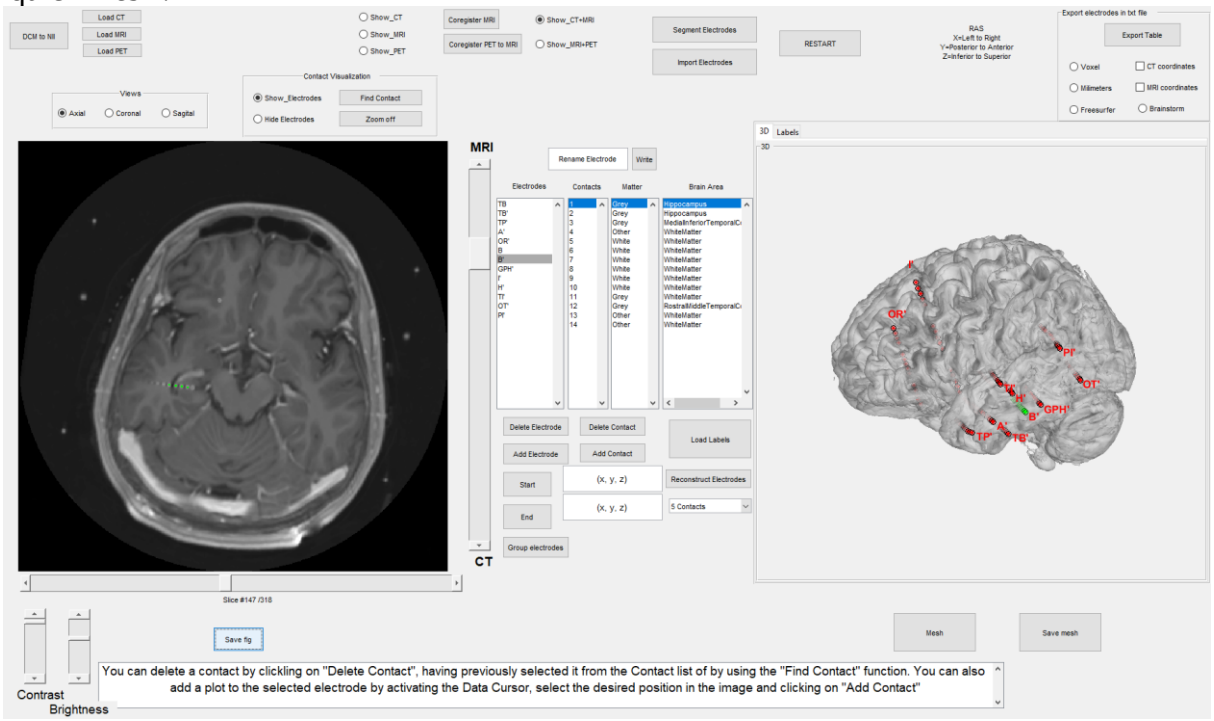
Electrode	Contact	x	y	z	isgrey	iswhite		
CU'	1	104.730281456338	53.1088837198623	85.0921199672915	2	2		
CU'	2	101.248075757839	52.7682478494382	85.1827327540197	1	1		
CU'	3	97.7658700593392	52.427611979014	85.2733455407478	2	2		
CU'	4	94.2836643608398	52.0869761085899	85.363958327476	2	2		
CU'	5	90.8014586623404	51.7463402381658	85.4545711142041	2	2		
CU'	6	87.3192529638409	51.4057043677417	85.5451839009323	2	2		
CU'	7	83.8370472653415	51.0650684973176	85.6357966876604	2	2		
CU'	8	80.3548415668421	50.7244326268935	85.7264094743886	2	2		
CU'	9	76.8726358683427	50.3837967564694	85.8170222611167	2	2		
CU'	10	73.3904301698433	50.0431608860452	85.9076350478449	1	1		
CU'	11	69.9082244713439	49.7025250156211	85.9982478345731	1	1		
CU'	12	66.4260187728445	49.361889145197	86.0888606213012	3	3		
CU'	13	62.9438130743451	49.0212532747729	86.1794734080294	3	3		
CU'	14	59.4616073758457	48.6806174043488	86.2700861947575	3	3		
PI'	1	103.014947749403	78.3507397651304	103.866899775196	2	2		
PI'	2	99.5363082023229	77.9729163960875	103.946375578388	2	2		
PI'	3	96.0576686552425	77.5950930270445	104.02585138158	2	2		
PI'	4	92.579029108162	77.2172696580016	104.105327184772	2	2		
PI'	5	89.1003895610816	76.8394462889586	104.184802987964	2	2		
PI'	6	85.6217500140012	76.4616229199157	104.264278791156	2	2		
PI'	7	82.1431104669207	76.0837995508727	104.343754594348	2	2		
PI'	8	78.6644709198403	75.7059761818298	104.42323039754	2	2		
PI'	9	75.1858313727598	75.3281528127868	104.502706200732	1	1		
PI'	10	71.7071918256794	74.9503294437438	104.582182003924	2	2		
PI'	11	68.2285522785989	74.5725060747009	104.661657807116	2	2		
PI'	12	64.7499127315185	74.1946827056579	104.741133610308	1	1		
PI'	13	61.271273184438	73.816859336615	104.820609413499	1	1		
PI'	14	57.7926336373576	73.439035967572	104.900085216691	3	3		
PC'	1	104.987870786437	89.3402879844747	107.33665606853	1	1		
PC'	2	101.498504851801	89.0808730278774	107.420496717979	2	2		
PC'	3	98.0091389171659	88.8214580712802	107.504337367427	2	2		
PC'	4	94.5197729825305	88.562043114683	107.588178016876	2	2		
PC'	5	91.0304070478952	88.3026281580857	107.672018666324	2	2		
PC'	6	87.5410411132598	88.0432132014885	107.755859315773	1	1		
PC'	7	84.0516751786245	87.7837982448912	107.839699965221	1	1		
PC'	8	80.5623092439891	87.524383288294	107.92354061467	1	1		
PC'	9	77.0729433093537	87.2649683316968	108.007381264118	1	1		
PC'	10	73.5835773747184	87.0055533750995	108.091221913567	2	2		
PC'	11	70.094211440083	86.7461384185023	108.175062563015	2	2		
PC'	12	66.6048455054476	86.486723461905	108.258903212464	1	1		
PC'	13	63.1154795708123	86.2273085053078	108.342743861912	1	1		
PC'	14	59.6261136361769	85.9678935487106	108.426584511361	3	3		
PC'	15	56.1367477015416	85.7084785921133	108.510425160809	3	3		
FeF'	1	103.050989441147	125.217007688971	112.397097272947	1	1		
FeF'	2	99.5593471000624	124.987725075652	112.473669103118	1	1		
FeF'	3	96.067704758978	124.758442462333	112.550240933289	2	2		
FeF'	4	92.5760624178935	124.529159849014	112.62681276346	2	2		
FeF'	5	89.084420076809	124.299877235694	112.703384593631	2	2		
FeF'	6	85.5927777357246	124.070594622375	112.779956423801	2	2		
FeF'	7	82.1011353946401	123.841312009056	112.856528253972	2	2		
FeF'	8	78.6094930535556	123.612029395737	112.933100084143	2	2		
FeF'	9	75.1178507124712	123.382746782418	113.009671914314	2	2		
FeF'	10	71.6262083713867	123.153464169098	113.086243744485	1	1		
FeF'	11	68.1345660303022	122.924181555779	113.162815574656	1	1		
FeF'	12	64.6429236892178	122.69489894246	113.239387404826	3	3		
FeF'	13	61.1512813481333	122.465616329141	113.315959234997	3	3		

Import electrodes

In order to save the work and reload the electrodes' coordinates, use the button "Import Electrodes", choose the text file of electrodes' coordinates previously saved. IMPORTANT: The file loaded must be the electrodes in the ElectrodesAllCoordinates.txt or CT space in millimeters.

Construct a rapid mesh using SPM and visualization

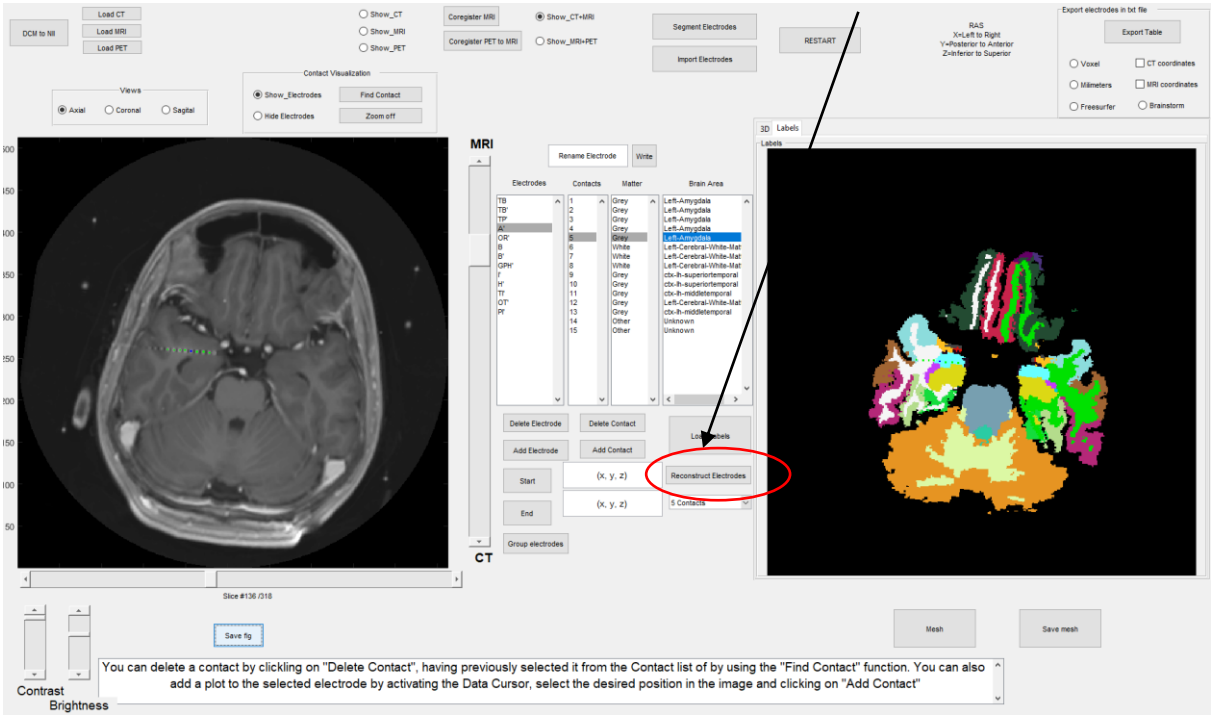
It's also possible to see these electrodes in a 3D representation of the MRI. Starting from it and using SPM, a mesh is constructed and Electrodes are display inside it simply clicking on 'quick mesh'.



Clicking on “Save Mesh” button, the mesh is saved in a .mat file that could be used for another study. For example to represent values or connectivity data using the 3DViewer.

Contacts labelling by Atlas

Load labels image



It’s possible to import Atlases in order to label automatically contacts to their anatomic areas. We worked with FreeSurfer, MarsAtlas and VEP atlases. They have to be in original MRI space obtained using Freesurfer own function to give atlas to native MRI space :
Cd $SUBJECTS_DIR/<subjid>/mri
mri_label2vol --seg aseg.mgz --temp rawavg.mgz --o aseg-in-rawavg.mgz --regheader aseg.mgz

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Contact

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