

User Documentation :

IntrAnat Electrodes (https://gin11-web.ujf-grenoble.fr/?page_id=228) is a software in development, based on Brainvisa 4.5 (<http://brainvisa.info/web/index.html>). It uses some of brainvisa's toolbox such as morphologist (<http://brainvisa.info/web/morphologist.html>) and cortical surface analysis (http://brainvisa.info/web/cortical_surface.html).

It's using ANTs (<http://stnava.github.io/ANTs/>) and SPM as well (<http://www.fil.ion.ucl.ac.uk/spm/software/spm12/>) for multimodality coregistration and estimation of the deformation field « patient space » to « MNI space ».

IntrAnat Electrodes is not certified for medical usage !!!!

Its goal is to visualize all « imaging » data recorded for neurology patients either in a patient-specific space, or in the MNI space for group studies.

Imaging modalities managed by the software are :

- MRI images : T1, T2, FLAIR, fMRI results, FGATIR. (fMRI results are the statistics from the analysis on top of an anatomic MRI).
- CT
- PET
- HomeMade (possibility to load any images calculated in the same referential as the T1)

You can precise three « stages » for the images.

Pre (before any surgery), Post (when the patient has electrodes whitin the head), PostOp (when the electrodes has been removed and the patient had a resection)

In developpment : Visualisating EEG and sEEG data.

The only requirement of the software is a 3DT1 (isotropic voxel, approximatly 1 mm³ resolution). All other images can be load or not, and be isotropic or not.

IntrAnat Electrodes in divided in three interfaces.

- ImageImport for data importation (importation of Nifti images, patient information, coregistering images, T1 segmentation and MarsAtlas parcels calculation)
- locateElecotrdes for patient data visualisation, electrodes positionning, « second step » processing (resection, ROIs, ...).
- groupDisplay for group studies (in the MNI space).

The image format used by IntrAnat Electrodes is NIFTI (.nii or .img and .hdr).

If your images are in dicom format, you have to convert the files. There is multiple software to do that, for example MRI Convert (<http://lcni.uoregon.edu/~jolinda/MRIconvert/>) or dcm2nii (<https://www.nitrc.org/plugins/mwiki/index.php/dcm2nii:MainPage>)

IntrAnat Electrodes was mainly developed for DBS and epilepsy electrodes visulization onto MRI, CT and PET images. This is what guided the GUI and functions of the software. Even if its use is not limited to that, it oriented the software developpement and may be less user friendly for others uses.

The software runs on Linux operating system (developped under ubuntu 14.04). Some libraries it uses do not run correctly on Windows and Mac OS X.

1 Running the software from a terminal :

open a terminal (or konsole, gnome-terminal...).

Go to the folder/IntrAnatElectrodes/epilepsie

Now there are two possibilities.

- Blind Mode :

If the .sh files have been configured (ImageImport.sh, locateElectrodes.sh and groupDisplay.sh) and you want to run it in « blind mode » (you won't have the display on the terminal of the comments of the different steps).

Then type ./ImageImport.sh or ./locateElectrodes.sh or ./groupDisplay.sh

To configure the .sh, open them using a text editor.

They have to contain the following text (please adapt the paths to Brainvisa and Intranat installation paths) :

ImageImport.sh :

```
#!/bin/bash
cd /brainvisa-4.5.0/bin/
./brainvisa-4.5.0/bin/bv_env.sh /brainvisa-4.5.0/
cd /home/b67-belledone/Desktop/IntrAnatElectrodes/epilepsie/
echo #####
>> intranat-imageImport-`whoami`.log
date >> intranat-imageImport-`whoami`.log
python ImageImport.py >> intranat-imageImport-`whoami`.log
```

#4.5.0

locateElectrodes.sh :

```
#!/bin/bash
cd /brainvisa-4.5.0/bin/
./brainvisa-4.5.0/bin/bv_env.sh /brainvisa-4.5.0/
cd /home/b67-belledone/Desktop/IntrAnatElectrodes/epilepsie/
echo #####
>> intranat-locateElectrodes-`whoami`.log
date >> intranat-locateElectrodes-`whoami`.log
python locateElectrodes.py >> intranat-locateElectrodes-`whoami`.log
```

groupDisplay.sh :

```
#!/bin/bash
cd /brainvisa-4.5.0/bin/
./brainvisa-4.5.0/bin/bv_env.sh /brainvisa-4.5.0/
cd /home/b67-belledone/Desktop/IntrAnatElectrodes/epilepsie/
echo #####
>> intranat-locateElectrodes-`whoami`.log
date >> intranat-locateElectrodes-`whoami`.log
```

```
python groupDisplay.py >> intranat-locateElectrodes-`whoami`.log
```

- Seeing Mode (**mandatory to run ANTs process**) (debug mode also)

once (once per terminal, it has to be done for each « new terminal » but only once per terminal) :
type in the terminal :

```
source /brainvisa-4.5.0/bin/bv_env.sh /brainvisa-4.5.0/
```

(of course replace [/brainvisa-4.5.0](#) with the path where you installed brainvisa 4.5)

and then type :

```
cd /home/b67-belledone/Desktop/IntrAnatElectrodes/epilepsie/
```

```
python ImageImport.py
```

```
python locateElectrodes.py
```

```
or python groupDisplay.py
```

you are then running the python code directly and it will show all « print » in the code ; if there is any problem it will be easier to find.

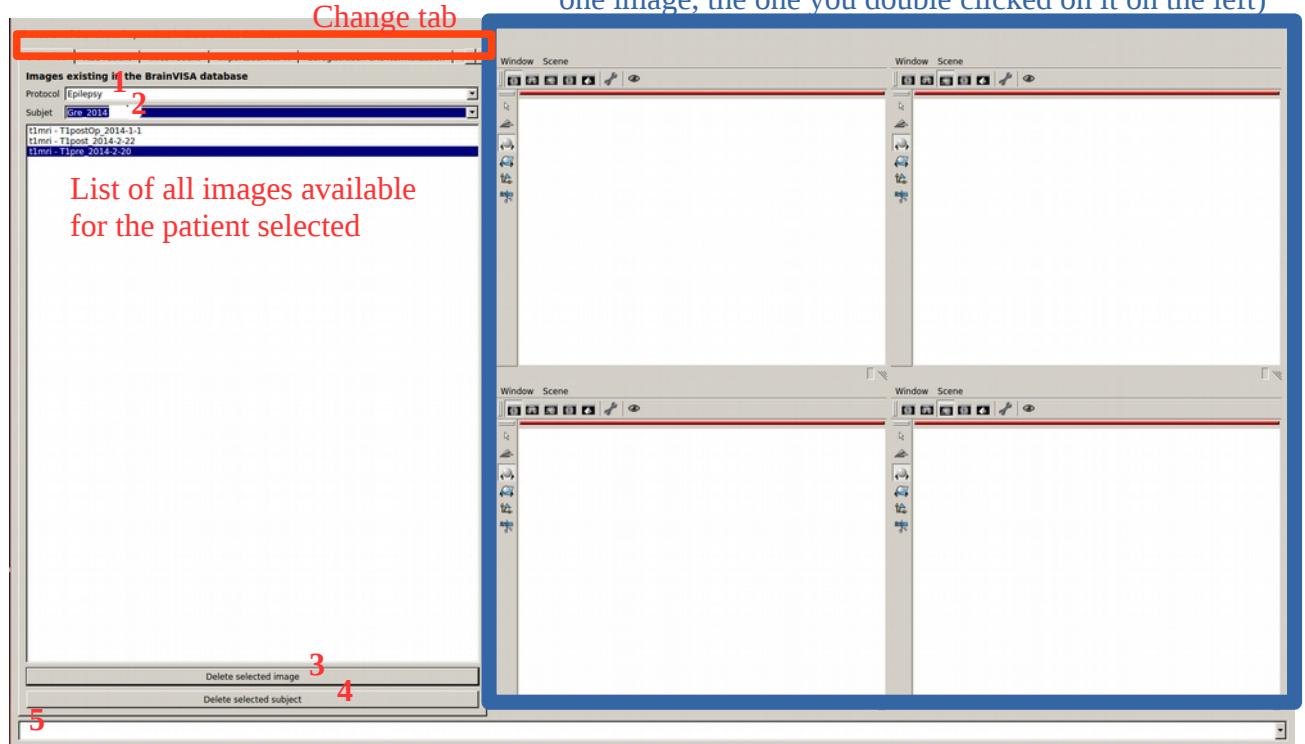
- Closing the gui

When you close the GUI you must also close the anatomist windows corresponding (look at the name of the images within the anatomist windows to recognize which anatomist windows is linked to which IntrAnatElectrodes gui).

2 ImageImport :

- When you open it you arrive on Tab 1 : delete images/patients from the database

Anatomist Windows (on Tab 1, the 4th are linked to one image, the one you double clicked on it on the left)



1 Select protocol (epilepsy, OCD, parkison, ...) correspond to folder made within the database

2 Select the patient (which has to be added using the Tab 2)

3 Delete the image selected (in this case : t1mri-T1pre-2014-2-20)

4 Delete the subject selected (in this case : Gre_2014_youwillnotknowwhobuthewasaniceguy)

5 Confirmation Bar. Sometimes, when we have done things right, it will inform you when a process is finished

Anatomist Windows :

Anatomist Windows are not made by IntrAnat Electrodes Developpers, you can find documentation online (http://brainvisa.info/anatomist-4.5/user_doc/anatomist_tutorial.html)

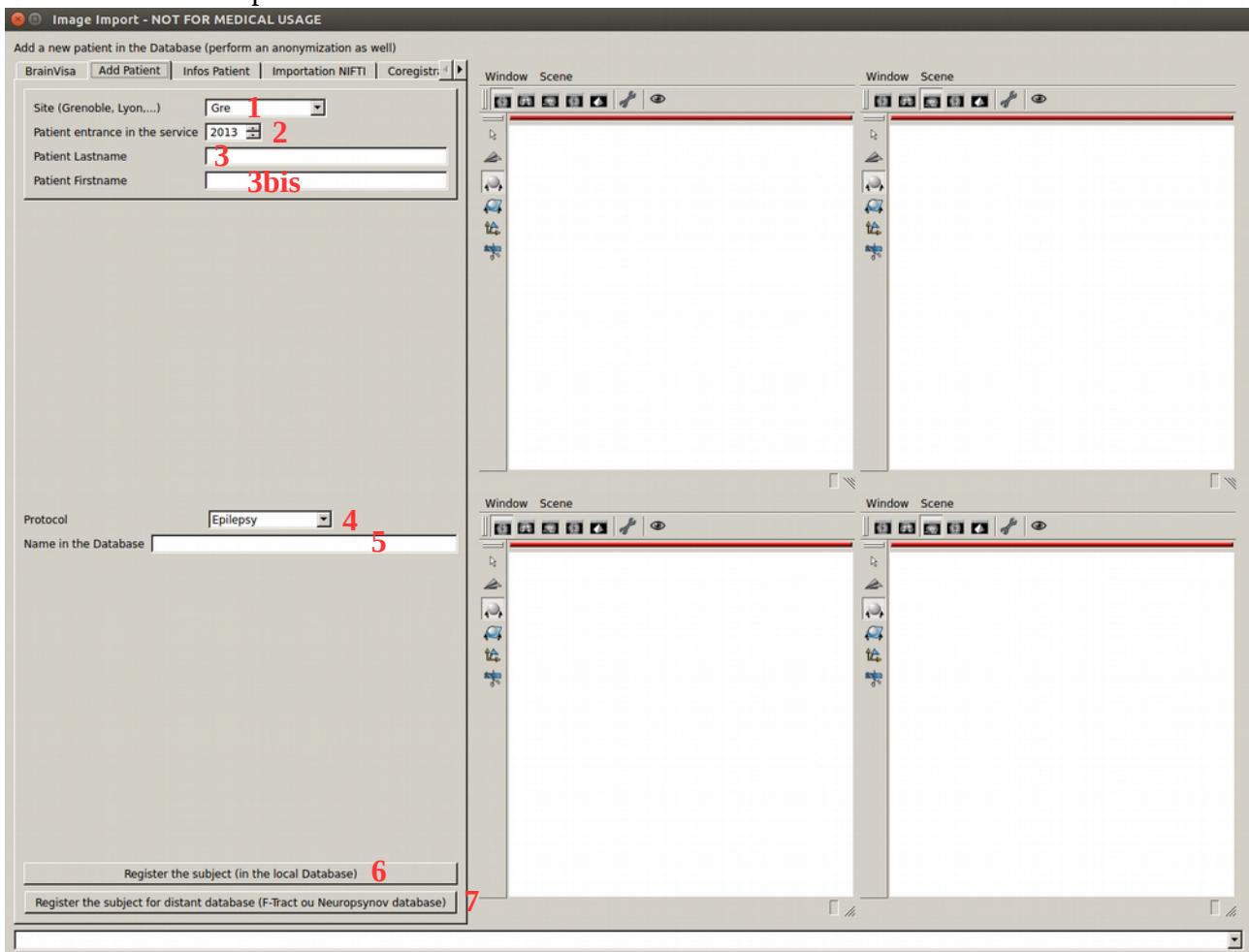
basically :

all windows are synchronized, this means that if you click at one point of the space in one, it will update the other windows to show the same position.

In the Windows menu, you can save the image currently displayed, save movies.

In the Scene menu, you have option to configure the display. In Scene->Tools, there is an option to enable/disable the cursor if you want to do screenshots for a presentation.

- Tab 2 : Add patient



- 1** Select the Center performing the patient surgery/treatment. This is editable, you can type a new one and it will be available in the list next time.
 - 2** Select the year when the patient started to be followed in the service (often we put the year of electrodes implantation when the patient is implanted)
 - 3 and 3bis** enter the patient lastname and firstname, they are used to compute the name in the database (different modes available, see preferences tab). You can always type directly the name that will be used in the database in **5**.
 - 4** Select the protocol (available protocols are folders created in the local Database, see the part on local Database organization)
 - 5** Name of the patient in the local Database (and then of the patient folder). It is editable in case you don't like the generated patient name (but in the preferences tab you have to select the appropriate « project »). Some projects required a specific patient name according an « anonymization » process.)
 - 6** Register the subject in the local Database (see the part on local Database organization)
In the confirmation bar you should have something like that :
- 13:27:17: Subject POUETGRE added to the database
- 7** (Useless for now, it is to push patient data on a network database by computing a new anonymization, but not done yet, will depend on the project selected in tab 6 : Preferences)

- Tab 3 : General Medical Information (only in french for now)

General information

today's date

birthdate

patient age

patient sexe

patient lateralization

Signature date of the consent

Research protocol inclusion

Date of the inclusion

Personal past history

Familial past history

Causal eurologic disease

MRI lesion

Right

Left

Neurologic exam

Comorbidity

Neurologic Comorbidity

Psychiatric Comorbidity

Other Comorbidity

Pathology Specific Information

Epilepsy crisis start

Aura

Seizure Type

Crisis frequency

Treatment tried

Actual treatment

Validation Button

Precise patient information (general and pathology specific)

BrainVisa | Add Patient | Infos Patient | Importation NIFTI | Coregistr.

Protocol: **Epilepsy**

Subjet: **POUETGRE**

Information générale:

Date:	16/08/2016
Date de Naissance:	01/01/1900
Age patient:	116
Sexe:	Inconnu
Latéralité manuelle:	Inconnu
Consentement Date Signature:	01/01/1900
Protocol:	
Date d'entrée dans le protocol:	01/01/1900
Antécédents Personnels:	
Antécédents Familiaux:	
Maladie neurologique causale:	
Lésion IRM:	
Droite:	T F P O Ins
Gauche:	T F P O Ins
Examen Neurologique:	Inconnu
Comorbidité:	<input type="checkbox"/> Aucune
comorbidité neurologique:	
comorbidité psychiatrique:	
comorbidité autre:	

Information spécifique pathologie:

Age du début des crises:	-1
Aura:	
Seizure Type:	Inconnu
Fréquence des crises:	Inconnu
Traitemen essayés (DCI):	
Traitemen actuel:	

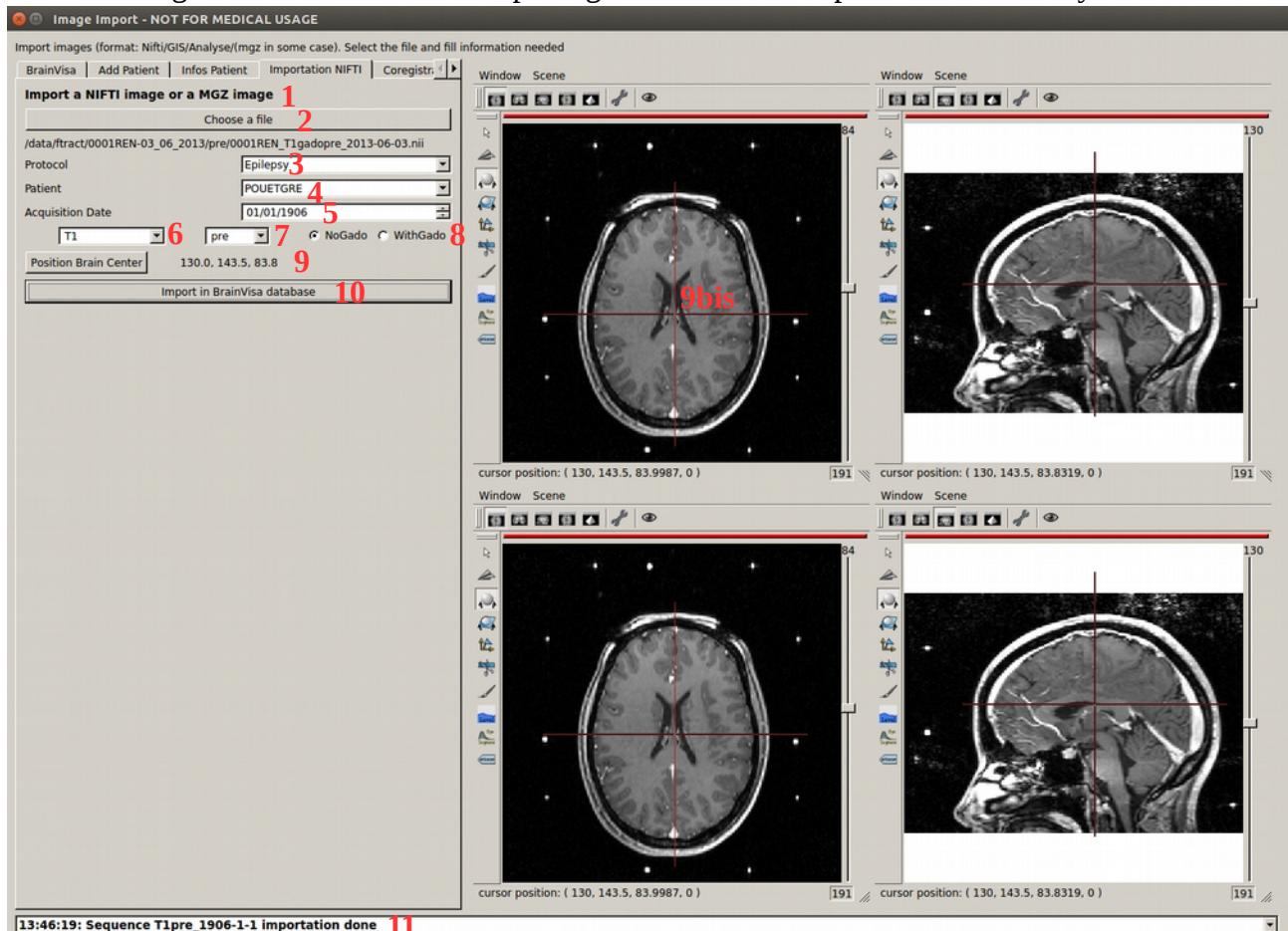
Validate Patient Information

Some of the fields are editable. Just type in whatever you want, press enter and it will be added to the list. In the database, there is a file containing all new entries, so once you have added one for a patient, the new entries will appear for the next patients.

All information is saved in a file in the database but for now they are not displayed when you reopen the patient (in progress).

- Tab 4 : Import Nifti file (it is also possible to import mgz freesurfer file, atlases).

Remember that for all patient, the only mandatory (but it is really mandatory) image is a 3DT1 (isotropic, around 1 mm, resolution) without electrodes (prior to electrode implantation). All images are then coregistered to this 3DT1. Morphologist and MarsAtlas processes are run by default on it.



1 software should accept all .nii and .img + .hdr images. It can accept mgz files from freesurfer but it is made only for the filetype fressurfer atlas and hippocamp freesurfer atlas. For freesurfer atlas, it is assumed that atlases have been calculated on the same 3DT1 as the 3DT1 pre **previously** imported on IntrAnat Electrodes for this patient. This is because freesurfer output images are always 256x256x256 so for the importation we resample the atlases on the 3DT1 pre previously imported.

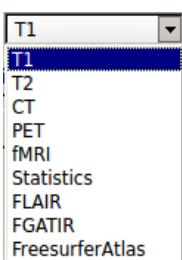
2 Select the file on your computer (once selected it should have reset the braincenter (**9**) if one was selected on a previous image loaded)

3 Select the protocol to which the patient belongs (it is a filter to not scroll on the full patient list)

4 Select the patient

5 Select the acquisition date of the image (won't accept the default date : 01/01/1900)

6 List of all accepted image types.



fMRI are results of fMRI, not the raw data. This means it is a RGB image, with in grayscale the anatomical MRI taken during the fMRI sessions with in RGB color the results of the fMRI (activated area, p-value, ...).

Statistics are whatever values (like p-values, t-value whatever, where they pass a threshold and zero everywhere else). These « maps » have to be calculated (or resampled) in the T1 pre referential because they will automatically be considered in the brainvisa database as having the same geometry as the T1 pre (matrix size and scanner-based to storage matrix transformation).

FreesurferAtlas is for example a file like the one generated for the Destrieux atlas aparc.a2009s+aseg.mgz

7 three stages period available. Pre, Post and postOp (as the software was made for epilepsy at the beginning). Pre is before implantation of the electrodes. Post is when the patient has the electrodes (for electrode localizations) and postOp is after the removal of electrodes, and after the resection of the epilepsia focus. For DBS patient, you need to load images only in pre and post stage period. Don't put anything as postOp.

8 option available only for T1. Morphologist and MarsAtlas don't run very well on T1 with gado. So if the T1pre is made with gado, it will use spm to segment grey and white matter, and run Morphologist and MarsAtlas on this segmentation. Results will be linked to the original t1, not the mask. (in development).

9 and 9bis BrainCenter. Some coregistration algorithms need a first step to align the brains of the images so that they overlap at least a little before starting the registration. Setting the Brain Center of all images allows to pre-align the images so that the brain matter of images overlap. This doesn't need to be precise (around 2 cm precision is more than enough). (example of position on the screenshot above). This step is necessary because the image center of images may be incorrectly set or the field of view of images is too different.

10 Validation button to import the image. Should make appear a confirmation as shown in **11**. or an error message if a problem happened.

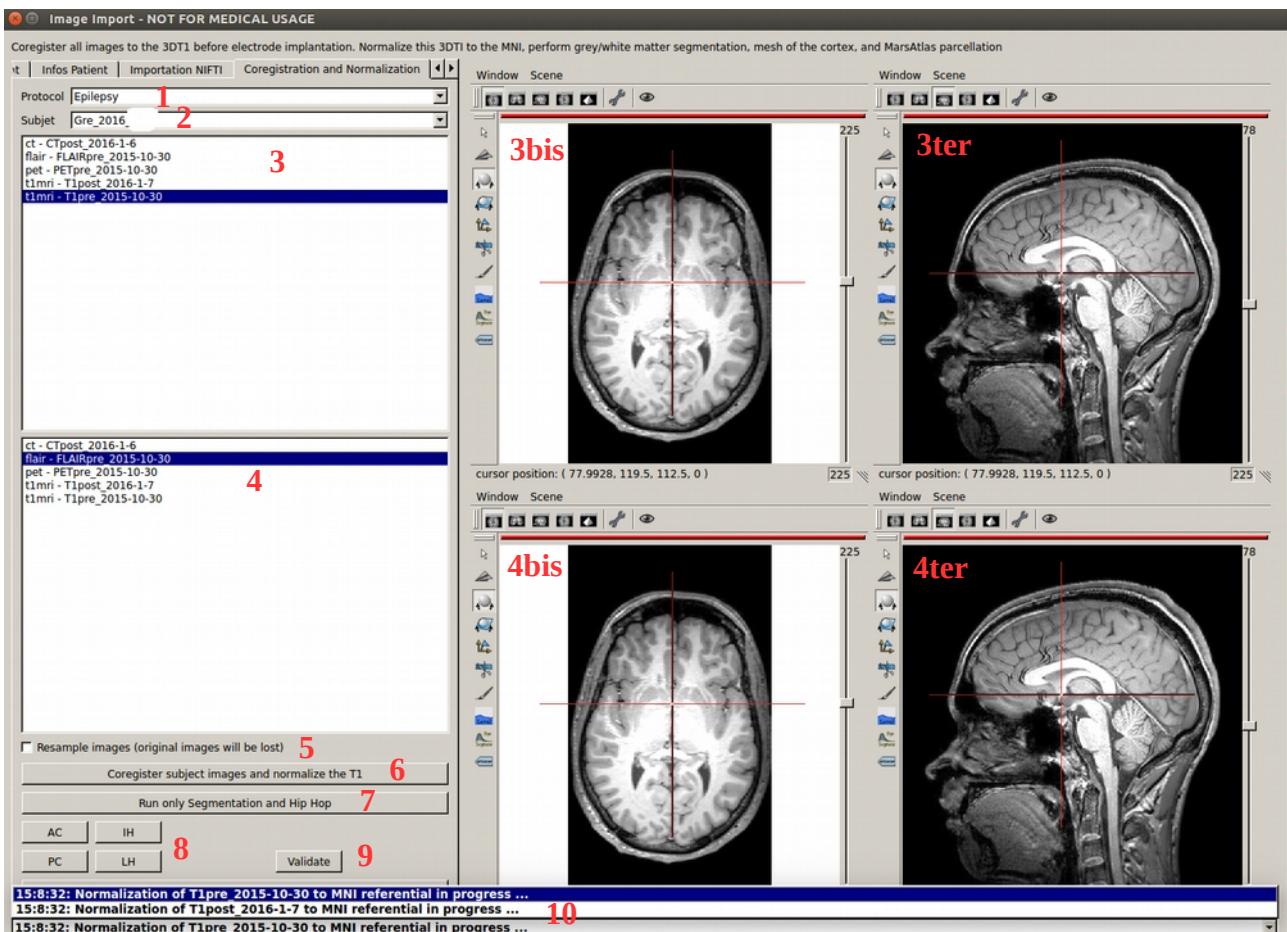
Be Careful !!

If you enter more than one 3DT1 pre. The software will be completely lost. Even if they have two different acquisition date.

You have to make sure that there is only one 3DT1 pre.

For all imaging types, except fMRI and statistics which accept more than one images (with the definition of a subfield), there should be only one image per type. The software for now doesn't « sort » images by acquisition date, it's only a user information field.

- Tab 5 : Coregistration, estimation of the deformation field for MNI normalization, running Morphologist and MarsAtlas processes



1 Select the protocol to which the patient belongs (it is a filter to not scroll on the full patient list)

2 Select the patient

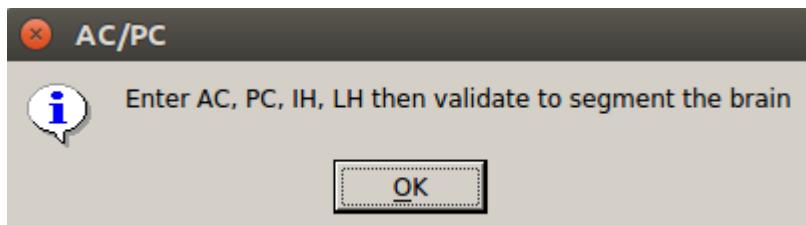
3, 3bis and 3ter : List of all available images. If you double click on one, it will show it on 3bis and 3ter anatomist windows. (http://brainvisa.info/anatomist-4.5/user_doc/anatomist_tutorial.html)

4, 4bis and 4ter : List of all available images. If you double click on one, it will show it on 4bis and 4ter anatomist windows. (http://brainvisa.info/anatomist-4.5/user_doc/anatomist_tutorial.html)

5 this option was « coregister and reslice » of spm. After coregistration of an image to the T1pre, it's resampling it on T1pre as well. The option was made when using spm8, it has not been updated to spm12. If needed ask IntrAnat developpers.

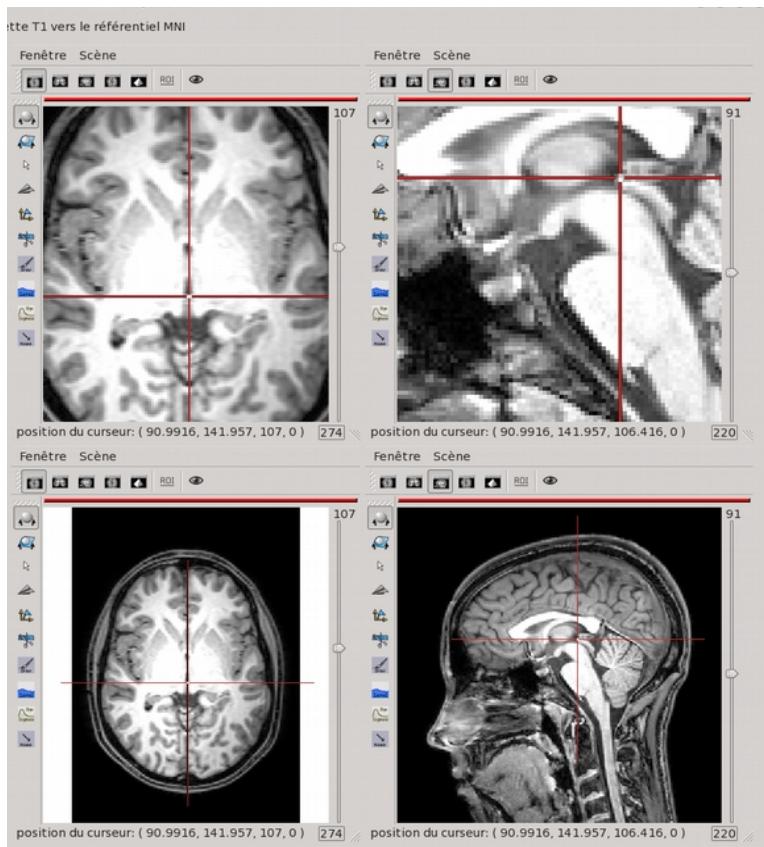
6 run all processes (on multiple threads) : Coregistration of all images on the T1pre Scanner Based, estimation of the deformation field for normalization into the MNI. Run morphologist and MarsAtlas. To run these two last processes, the software needs to know the position of AC (anterior commissure, PC (posterior commissure), IH (inter hemisphere) and LH (left hemisphere).

So it will shows automatically the 3DT1 pre on anatomist windows on the side and open this message box.



You have to click ok to close it. If you want to run Morphologist and MarsAtlas you then have to set these points.

You have to click on the position of one, for example PC as shown below



and then click on the button PC in **8**. this button will turn green. So you have to click on the position on the image, and then click on the corresponding button.

Once all buttons are green, you have to click on validate **9**.

Normaly the left hemisphere should be on the right side if importation worked well, to check.

Once Morphologist and MarsAtlas are done, in **10** the message HIP HOP : done will appear.

This mean that if you want to run only the coregistration of all images, you click on **6**, you click ok on the opening message box. But you don't precise AC, PC, IH and LH and of course you don't validate the positions as you haven't entered them. Only the coregistration will run in this case.

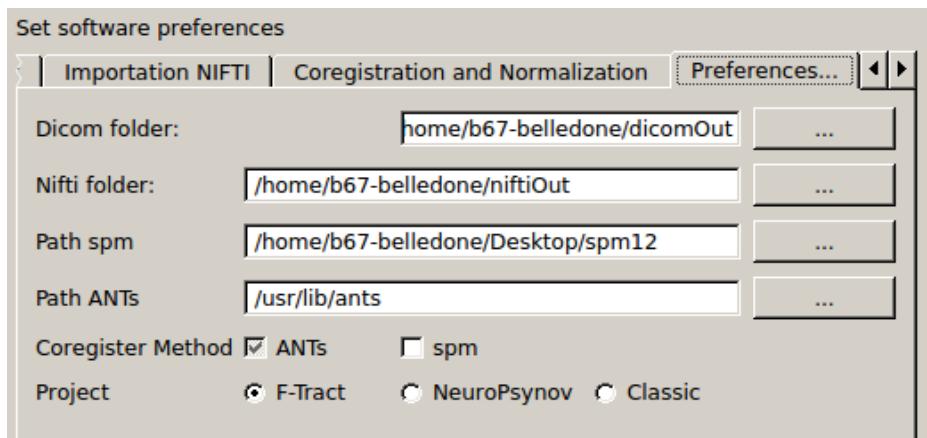
7 If you don't want to recalculate the coregistration matrix and normalization estimation, but want to run Morphologist and MarsAtlas. (if the coregistration was tricky it is nice). It will open the message box saying that you have to enter AC, PC, IH and LH, as in point **6**, and you have to proceed the same way.

8 button to precise AC/PC/IH and LH (see point **6** and **7**)

9 Validate the position of AC, PC, IH and LH that you entered to run Morphologist and MarsAtlas.

10 update of processes started and finished. Display for example when a coregistration finished. Display as well when morphologist and maratlas finished (message Hip Hop : done)

- Tab 6 : Preferences



Set the software preferences.

Dicom folder and Nifti folder are useless for now. The dicom importation is not finished yet.

Path SPM : set the path to the main folder of SPM12 (IntrAnat is compatible only with SPM12. Compatibility with SPM8 is not maintained due to lack of time). If not set, you can't run coregistration using SPM, compute the deformation field to the MNI, or compute MNI position of the electrode contacts etc ...

Path ANTs : set the path to the main folder of ANTs. If not set, can't run coregistration using ANTs.

Coregister Method : either ANTs or SPM. If ANTs is selected you have to run ImageImport in the Seeing Mode (see part one of the user documentation).

Project : it changes the Patient name in tab 2, object 5. Using project NeuroPsynov or Classic for example, the patient name is « Center »_« year »_« Three first letters of the lastname in capital »_« first letter of the firstname in lower case ».

for example a patient name John Smith, implanted in Grenoble in 2013, his patient name will be : Gre_2013_SMIj. And that will be the name of its folder in the database as well.
`(.../BrainVisaDatabaseFolder/Protocol/Gre_2013_SMIj)`.

- Tab 7 : SEEG data Importation (only in french for now, in development)

We open sEEG data using the python-neo toolbox : <https://github.com/NeuralEnsemble/python-neo> for now the only option available to users using sEEG data is for the groupDisplay. Instead of displaying all contacts of all electrodes, you can display only contacts which has been recorded. Other options using sEEG data are not available to users for now.



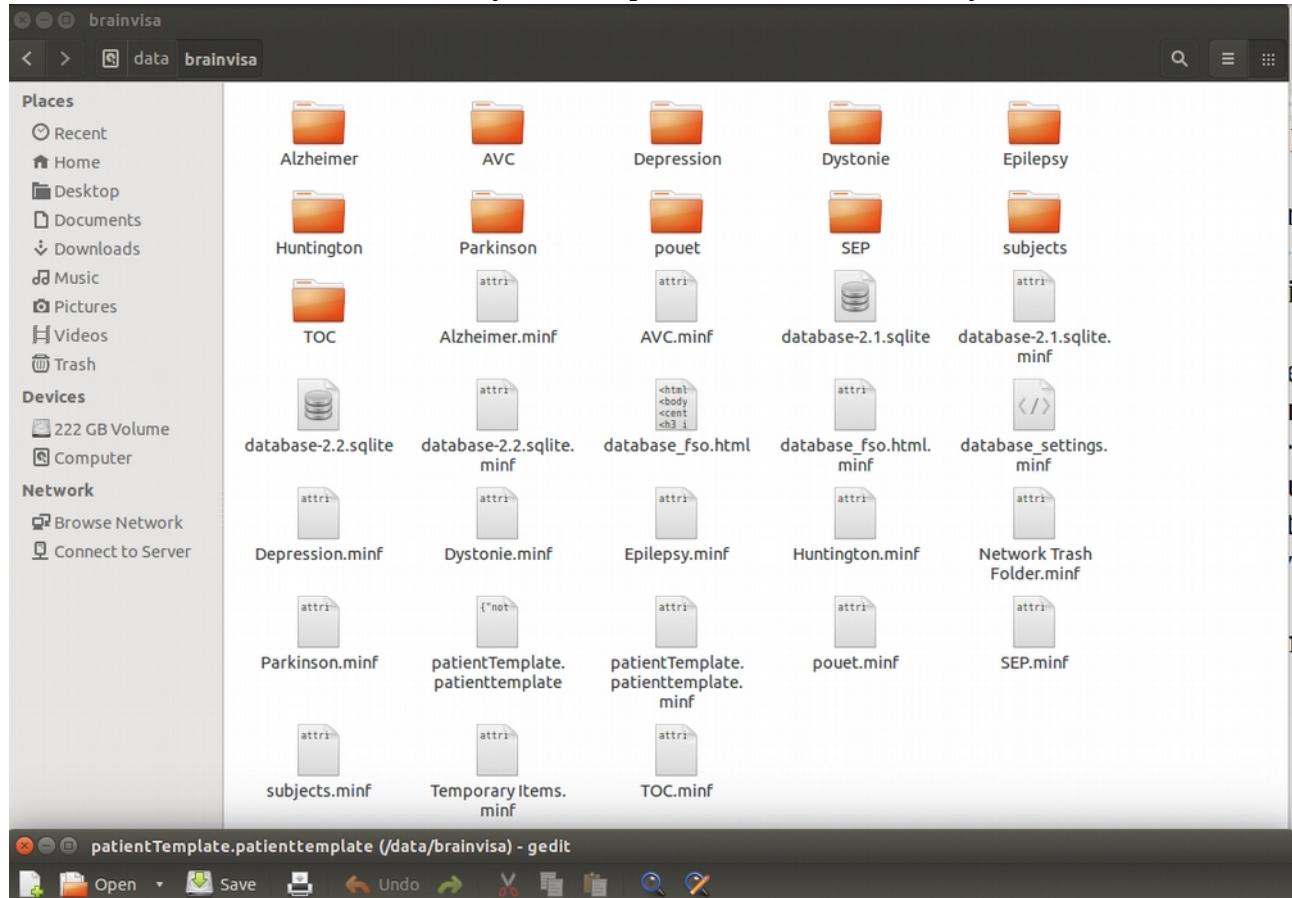
You have to select the patient, give an experiment name (in the example it's lec1), you can give a subexperiment name and an acquisition number but they are not mandatory. And then click on « importer dans brainvisa ». all others button are useless for now.

- File Organization from ImageImport

Remember, **NEVER DELETE anything in this folder and subfolders**. If you want to delete an image or a subject, use button dedicated to that in Tab 1.

If, for any reason, you delete something, you will have to run BrainVisa and perform an Update Database.

In the BrainVisa Database folder that you have specified at the installation you have this :



-To add a protocol, you create a folder in the BrainVisa Database Folder (for example Epilepsy, Parkinson,).

Then you start BrainVisa, and you perform an update database.

Once it's done, a file with the same name as the folder with a .minf extension has been created.

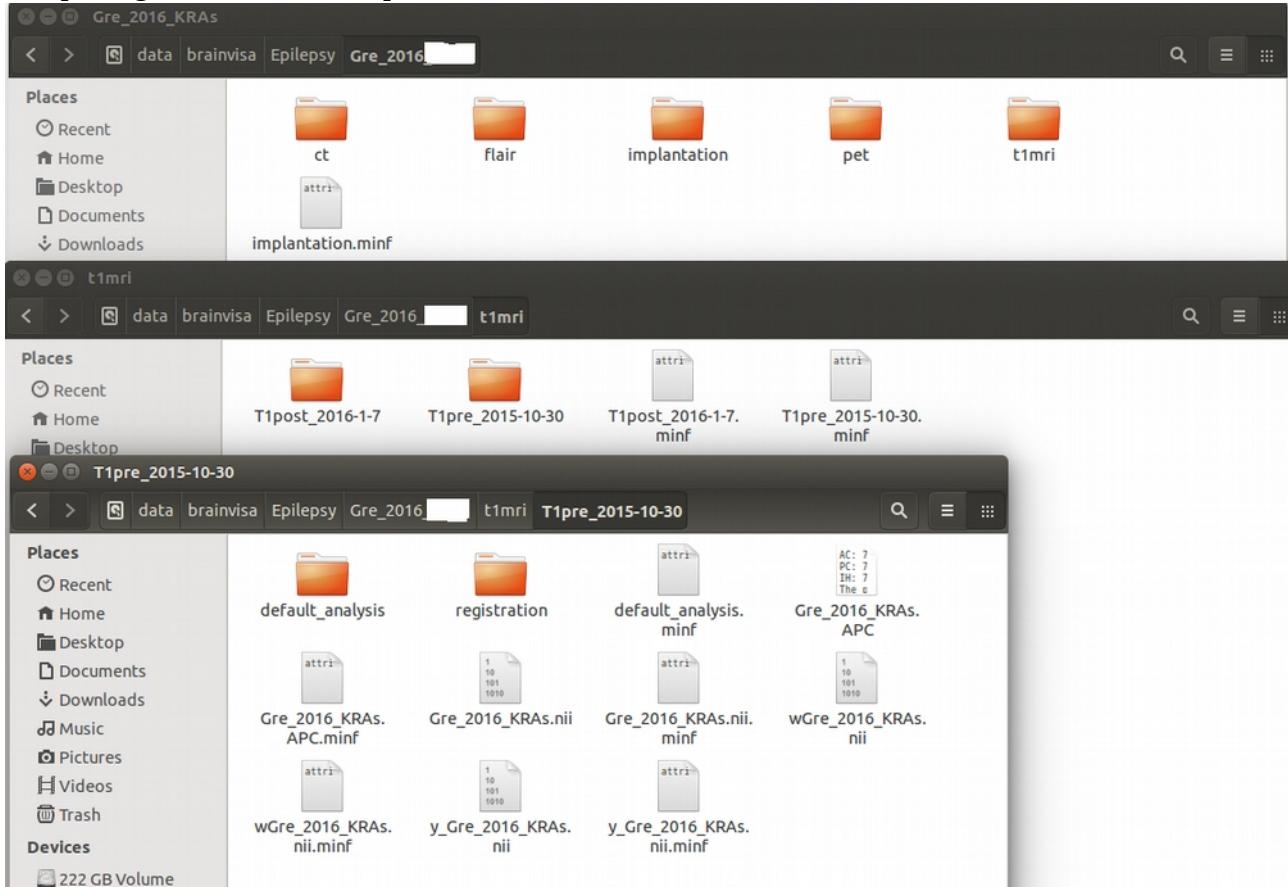
-you have a file named patientTemplate.patienttemplate (shown above).

This file is a json file containing a python dictionary. In this python dictionary there are all names set as patient general information and pathology specific information. This is the file that stores all new field types entered manually in Tab 3, and makes them available for the next patients

-In a patient folder, there is a folder for each modality (t1, ct...).

Inside it there is a folder for each acquisition period (pre, post or post op). The image and associated data is inside. There is also a registration folder containing the transformation matrices Scanner-Based to Native and Scanner-Based to T1pre Scanner Based.

If it is the folder of the T1pre, there is also the image normalized to MNI space, the deformation field from the T1pre to the MNI and a folder called « default_analysis » with all files created by the Morphologist and MarsAtlas processes.



(in this example there is an implantation folder, this one is generate by locateElectrodes, not by ImageImport. Will see about him in the locateElectrodes part).

3 LocateElectrodes

LocateElectrodes is the GUI to visualize all imaging data imported using ImageImport, fusion images etc ... You can set the position of the electrodes to visualize them on top of all images.

It allows as well :

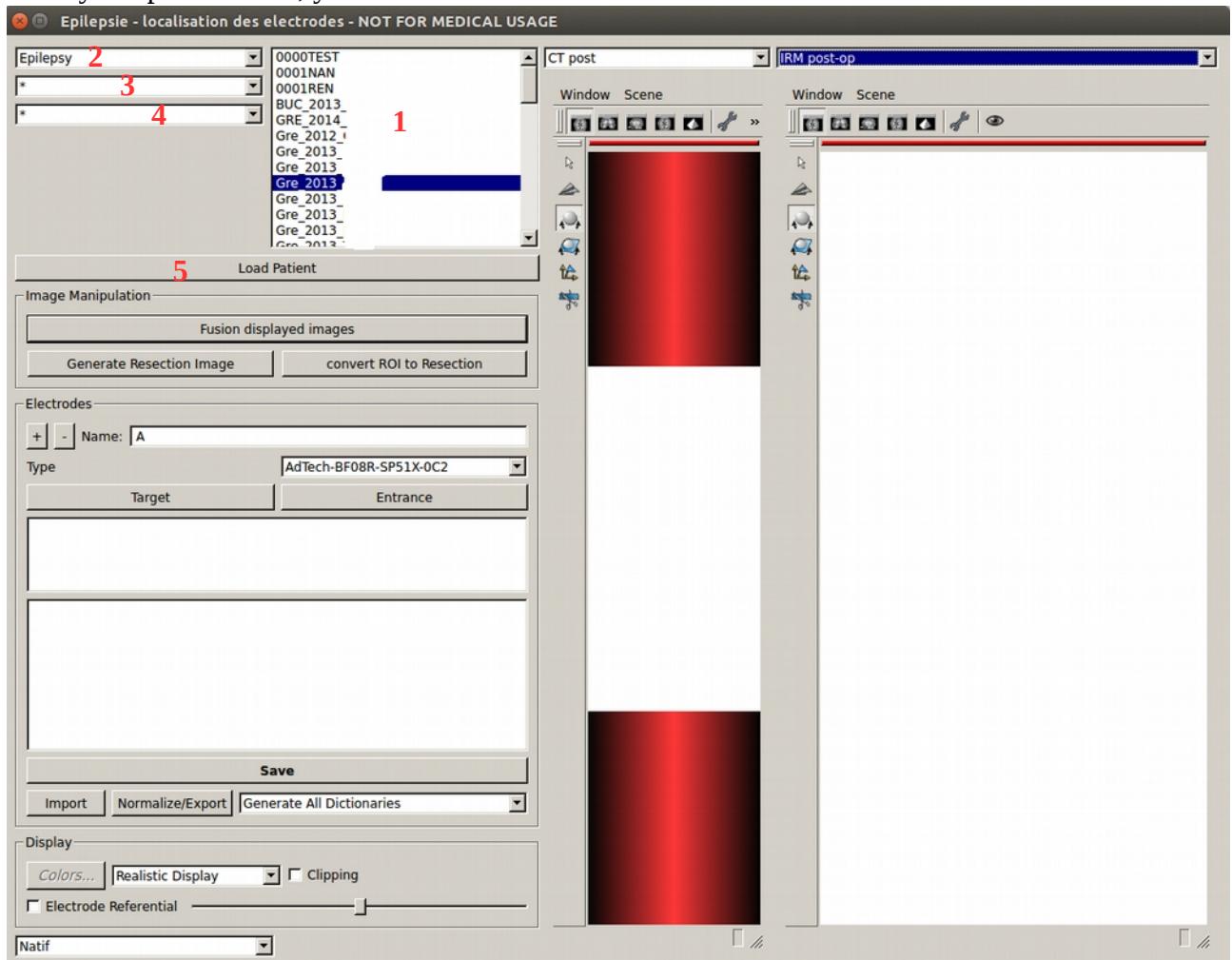
Semi-automatic estimation of the resection

Automatic exportation of « dictionaries » containing contacts position information (and center of bipole), their MNI position, mars atlas parcel in which they are (implantation of different atlas in progress) and if they are in the resection or not

Automatic exportation of dictionaries containing the total volume of the resection and percentage of MarsAtlas parcels which has been impacted by the resection (implantation of different atlas in progress - almost done: freesurfer atlases)

- Load a patient

Once you open the GUI, you see this :



1 List of all patients available, filtered by **2**, **3** and **4**

2 Select the protocol to which the patient belongs (it is a filter to not scroll on the full patient list)

3 Select the center to which the patient belongs (it is a filter to not scroll on the full patient list)

4 Select the year of patient implantation (it is a filter to not scroll on the full patient list)

for **3** and **4**, the symbol « * » means that you don't filter according to the center or year respectively.

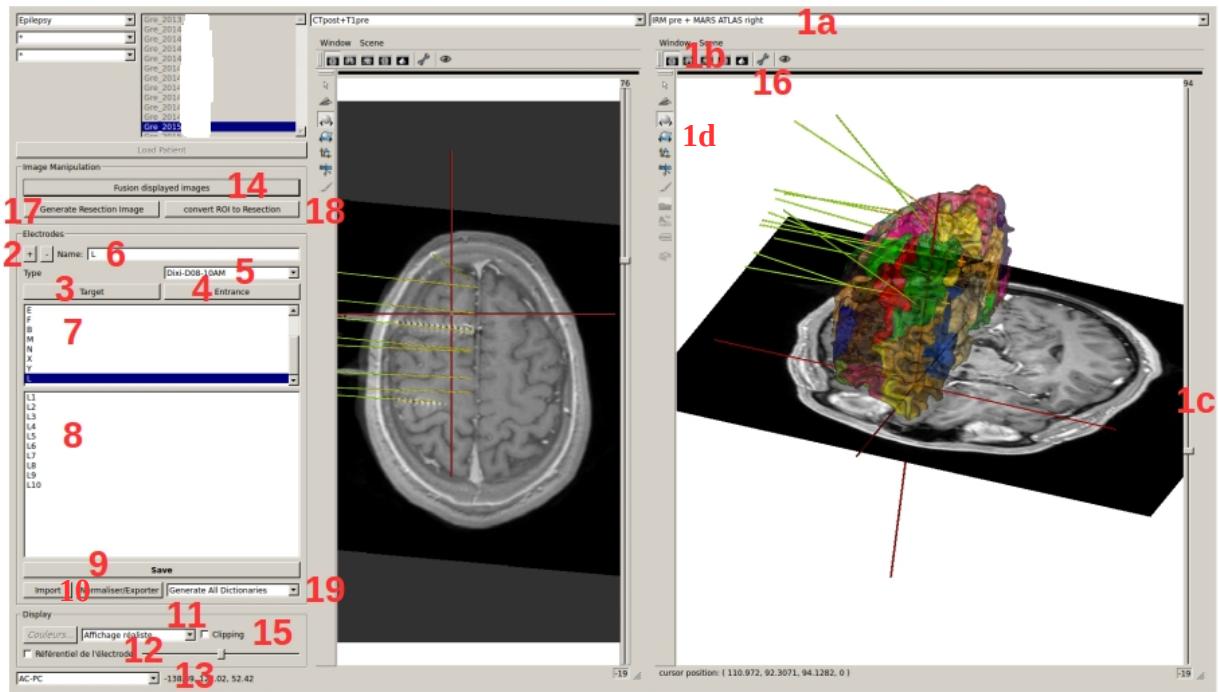
5 Load the patient selected (in blue in **1**, you can double click on the patient name in the list as well)

Once a patient is loaded, you cannot load another one.

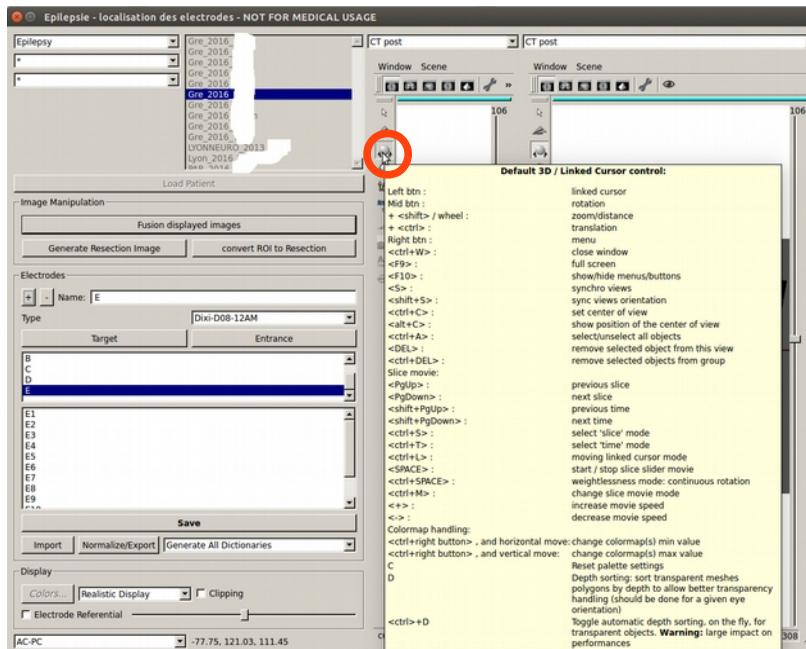
You have to close the GUI, and close the corresponding anatomist windows (see « closing the GUI » page 3).

- Once a patient is loaded

All images available will be selectable in image list such as **1a** below (one list for the left anatomist windows and one list for the right anatomist windows).



1a, 1b, 1c and 1d : Select an image to display in the anatomist windows below the image list (**1a**) and manage its display. Anatomist developpers made lot of documentation online (http://brainvisa.info/anatomist-4.5/user_doc/anatomist_tutorial.html). If you leave the mouse few seconds on an icon without clicking, it will display all commands available when you select the icon, for example :



Quickly :

1b allows you to change the orientation (axial, sagittal and coronal). The wrench icon allows to open the ROI GUI.

1c allows you to change the slice of the image displayed

1d lot of options. Allows you to rotate the image in 3D, to change the orientation the slice displayed, if you don't want to stay in axial, sagittal or coronal slice, you can rotate it to any orientation), to change the min and max of the colormap to increase or decrease contrast etc ...

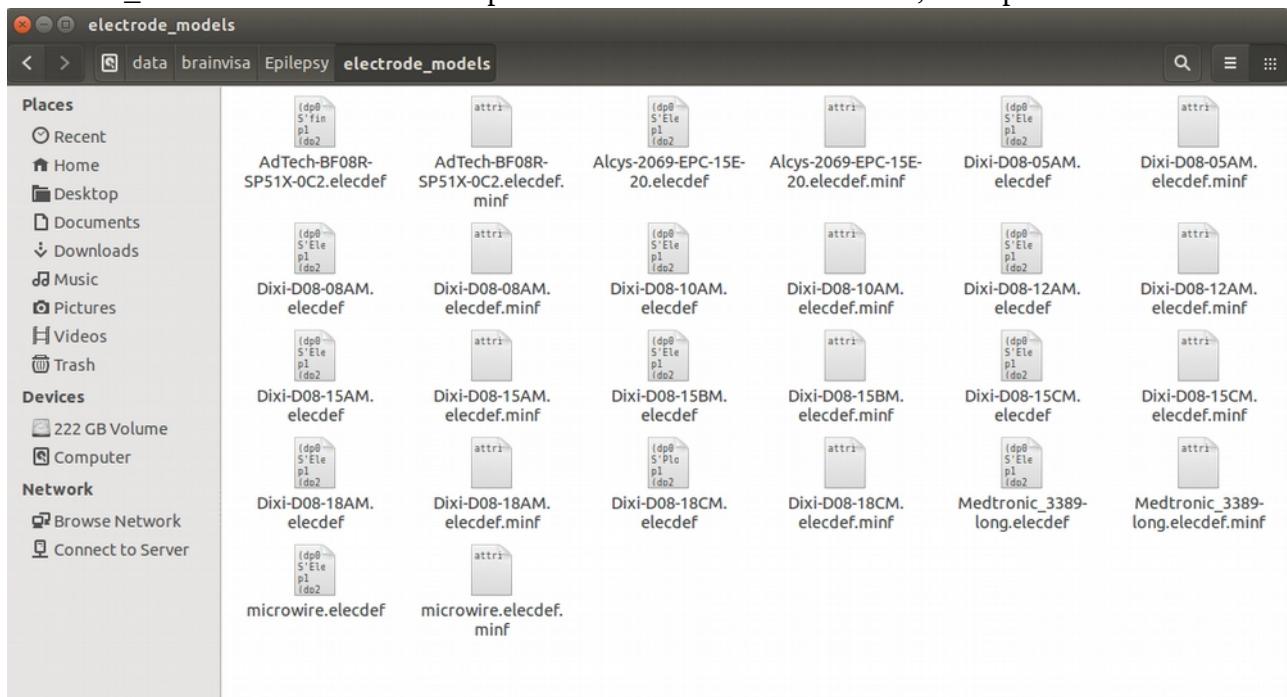
2 to 9 are made to generate the meshes of electrodes. You need of course to display in one of the anatomist windows an image in the « post » stage where you can see electrodes (CT or MRI post implantation) using image lists such as **1a**. To add an electrode, start by **2** and then do **3, 4, 5 and 6** (no order for these ones).

2 add (+) or remove (-) an electrode. When you add one, it will take the name of the next unused letter (alphabetical order). You can change it later using **6**.

3 validate the cursor position (click on the image to move the cursor) as the target position (deepest point of the electrode). Once clicked on it, it instantaneously updates the display of the electrode.

4 validate the cursor position as the entrance position (The software only uses this point for the direction, so as entrance point we often use the center of the screw as it's more precise to define an orientation when both points are far away, but you can set the entrance point anywhere on the trajectory). Once clicked on it, it instantaneously updates the display of the electrode.

5 Select the model of the electrode currently selected in **7** (background blue). Once changed, it instantaneously update the display. Models available are the models set in the folder `electrode_models` in the folder of the protocol in the database brainvisa, example below :



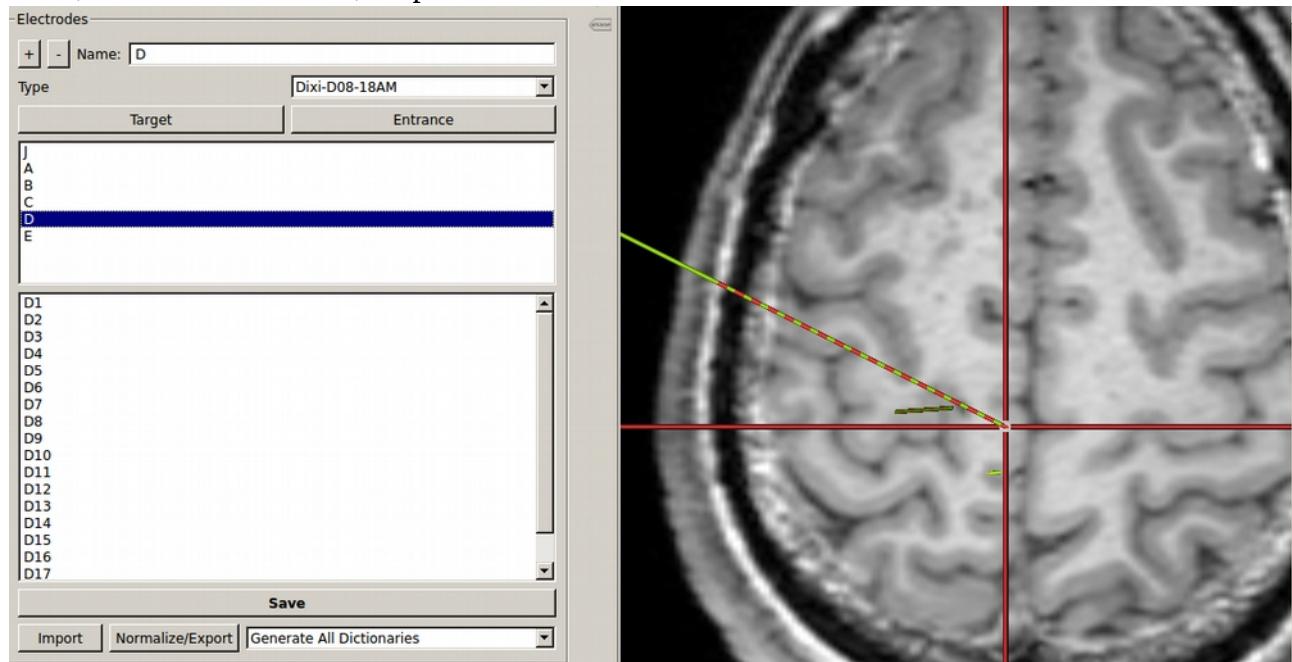
Models are made by IntrAnat Developpers, or now the GUI to make new ones is not very easy to use, you can try it (it comes with IntrAnat Electrodes) but better to ask to IntrAnat Developpers. If you don't have this folder in the database, you have to add it. Remember, to add something in the database, you need to run BrainVisa and perform an « update database » after adding files or directories (see page 13).

Models are referenced as name given by the company who built them.

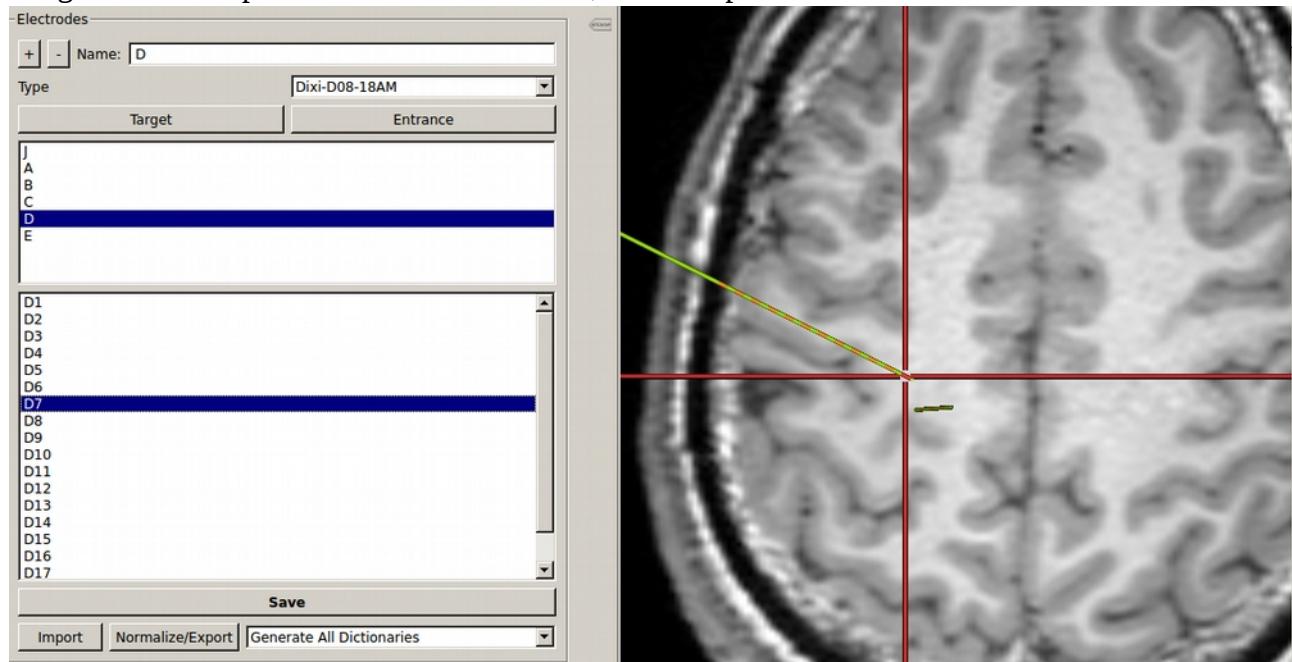
6 Name that you want to give to the electrode. Change it and when you click outside of the editable name it will update it (on the image for example).

7 List of all electrodes already set. If you click on one, it sets its background to blue and the contacts in the anatomist windows become red. If you double click on one, it sets its background to blue and the meshes of the contacts in the anatomist windows become red **AND** it moves the cursor to the

deepest contact of the electrode and updates the image slice (see example below). In both cases, click or double click, it updates the list of contacts in **8**.



8 list of contacts of the electrode selected in **7**. If you click on one, only the corresponding contact will be set in red, all others take back the « original color » (color when not selected, often it's orange). If you double click on one, it does the same as simple click **AND** it update the cursor and image slice to the position of selected contact, see example below :



9 Save electrodes. Once you have saved them, the next time to load this patient electrodes will be displayed automatically. It generates a folder « implantation » in patient folder in the database. This button save implantation in « patient space », not in the MNI space.

10 you can **import** an implantation. For example if the implantation has been generated on an other computer and you want to import it on this computer.

You can **normalize and export** : generate the MNI position of the electrodes (necessary for group

studies and the use of groupDisplay).

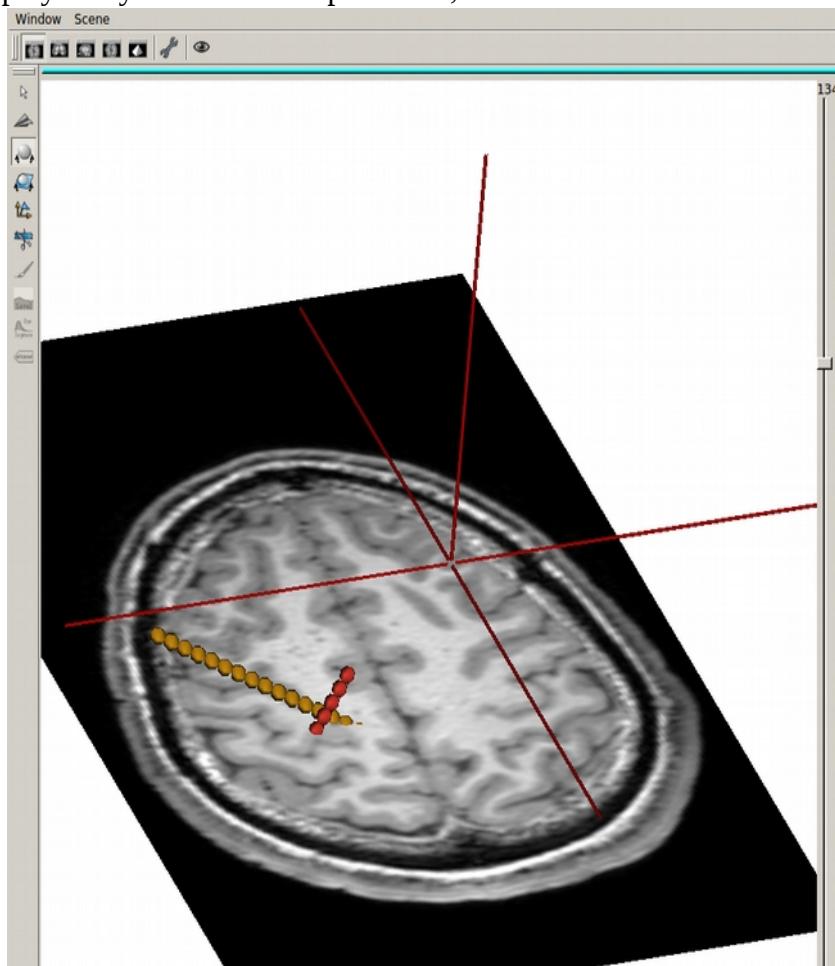
It generates as well PTS and TXT files with electrodes names and position (in patient space and in MNI space if normalization is available). The files will be in the implantation folder of the patient. Once the process is done the following message box is displayed :



11 Change the display of the contacts. Two types of display :

-realistic display : The whole electrode is represented (contacts and parts between the contacts, as in figure above).

-x mm sphere display. Only contacts are represented, as below :



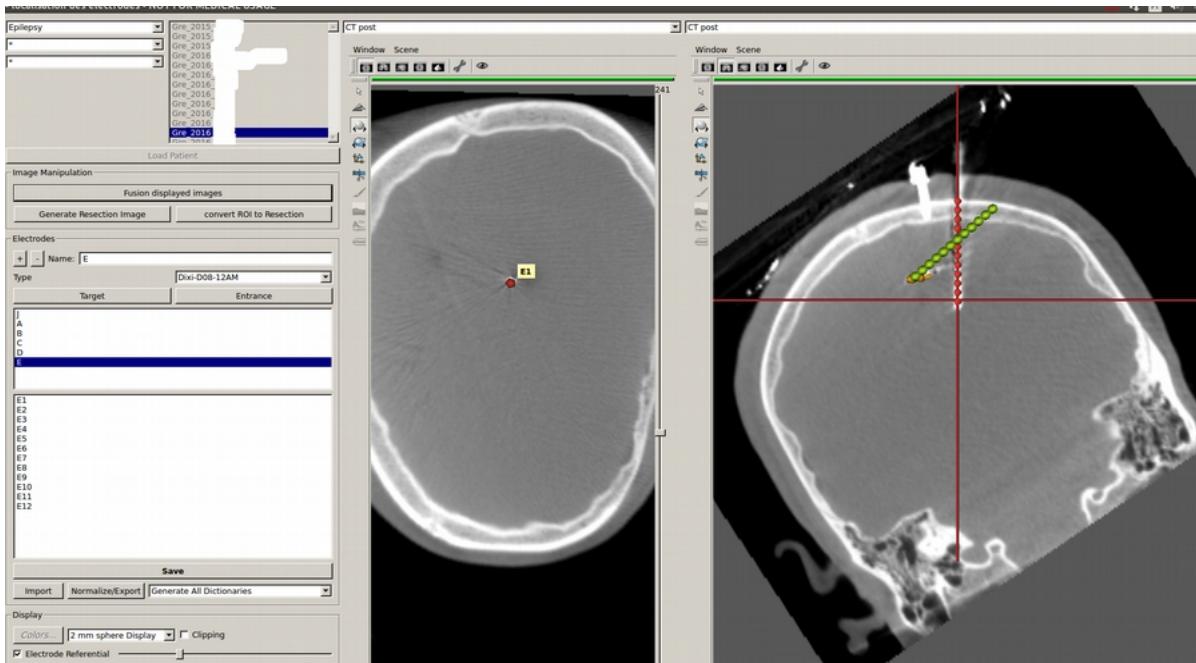
12 Change the referential. If unchecked you are in T1 pre Scanner-Based referential. If checked, the axial view is perpendicular to the electrode selected in **7**. At the position of the contact selected in **8** if any, if not, the position of the deepest contact.

The electrode will be coplanar with sagittal and coronal view.

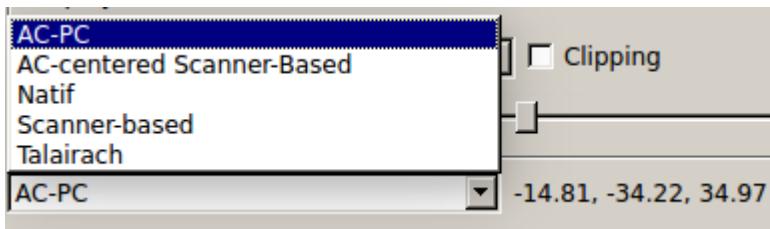
Example below :

the electrode selected is E, display mode is 2 mm sphere, no « contact » selected so by default it's has contact 1 is selected. The left anatomist window show a plan perpendicular to the electrode, crossing the electrode in contact E1. The right anatomist window, set in coronal mode, show a plan

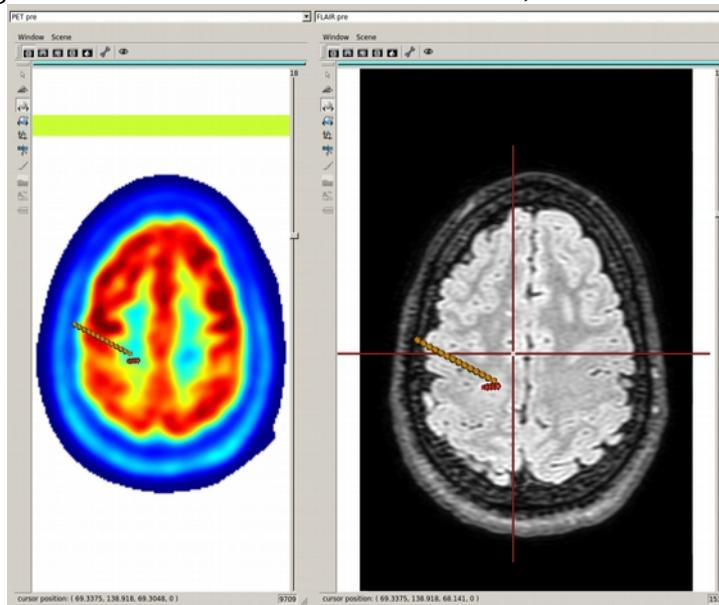
coplanar with the electrode (centered). The contacts of the electrode are red as it is selected in **7** and no contact is selected in **8**.



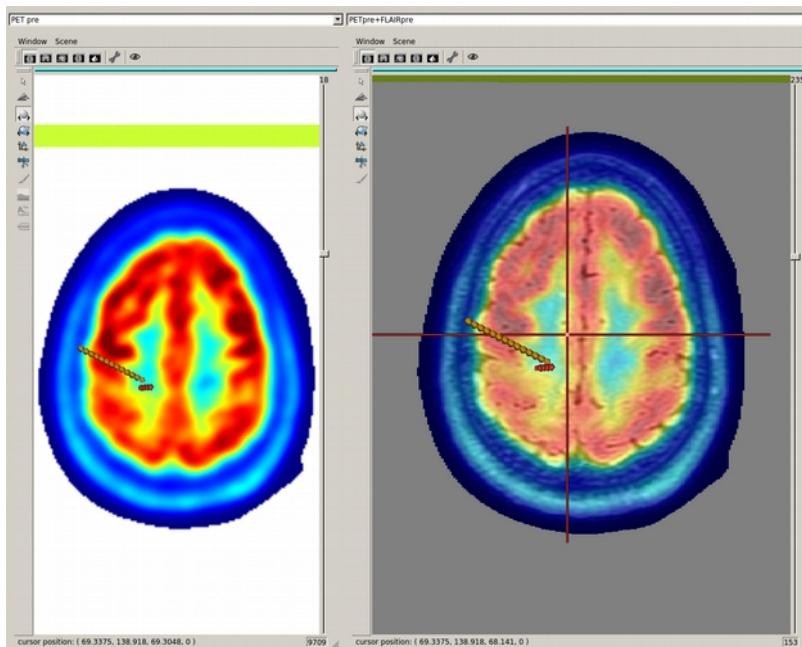
13 Change the referential in which the position of the cursor is given. Here the position of the cursor [-14,81 -34,22 34,97] is the position in the referential AC-PC.



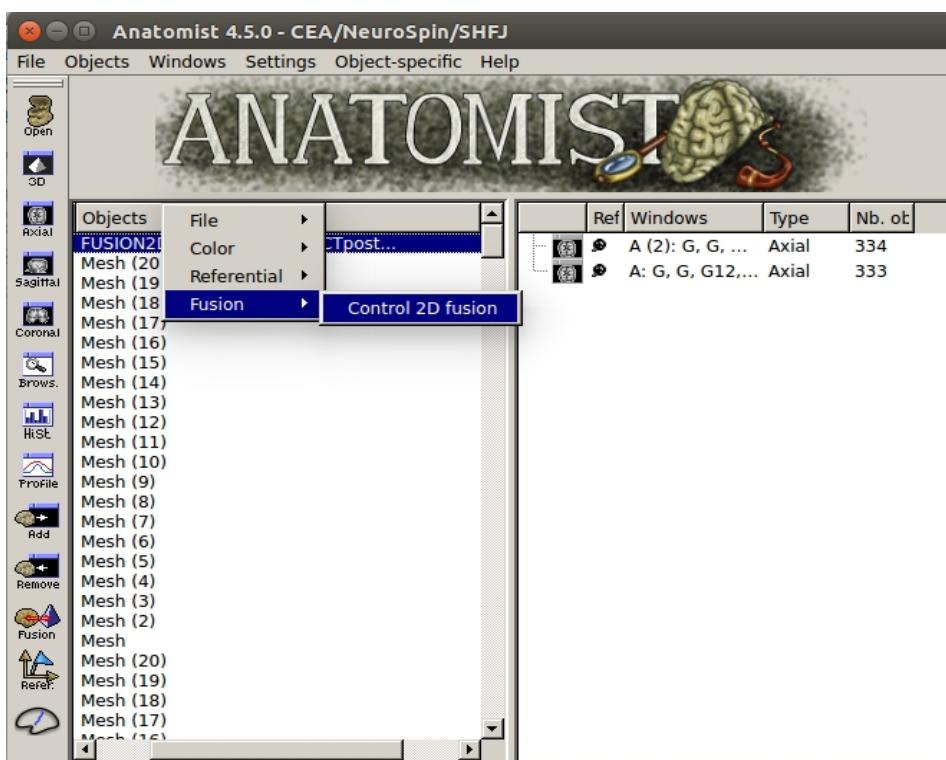
14 Perform the fusion between the two displayed images. If on the left anatomist window there is the PET and in the right anatomist window there is the FLAIR, as below :



and if you click and fusion displayed image, in the right anatomist window will be displayed the fusion as below:

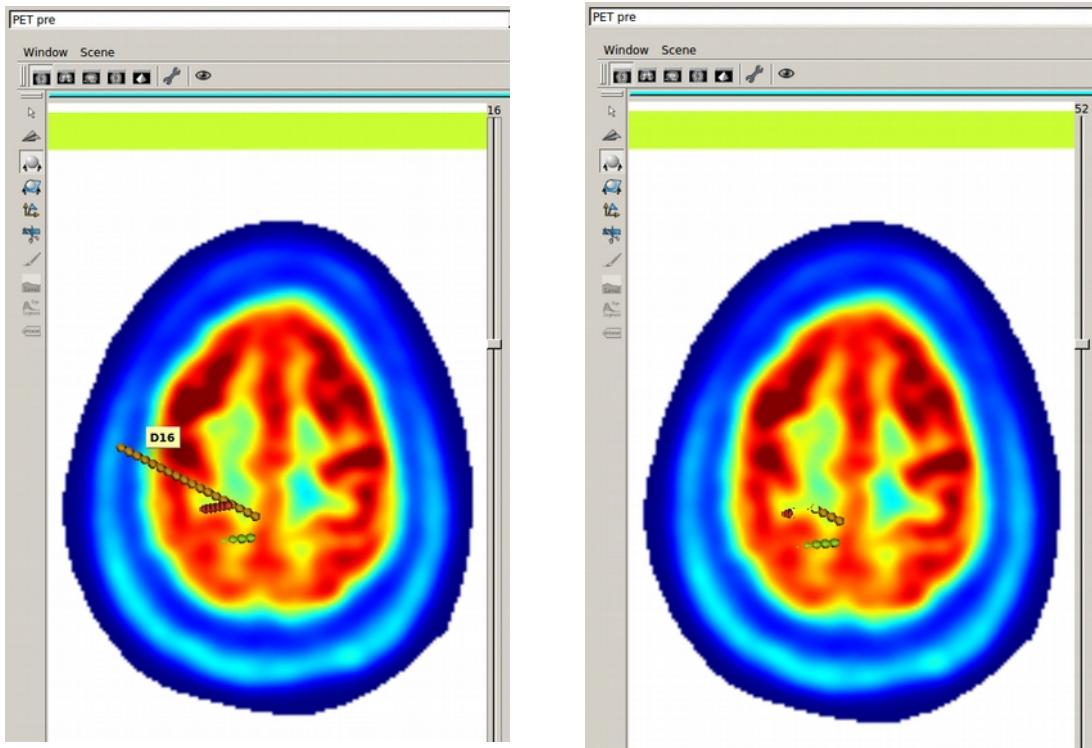


In the corresponding list of image appear « PET + FLAIR » (image which was on the left + image which was on the right). You can use this list change to another image and come back to this fusion. The fusion is not saved in database to allow computers having just « reading rights » and no « writing rights » on the database to perform the fusion. So if you close locateElectrodes, you'll have to perform the fusion again if wanted. To control the mixing rate between both images, you have to go in the anatomist GUI, right click on the object name FUSION2Dxxx and the click on Fusion->Control 2D fusion as shown below.

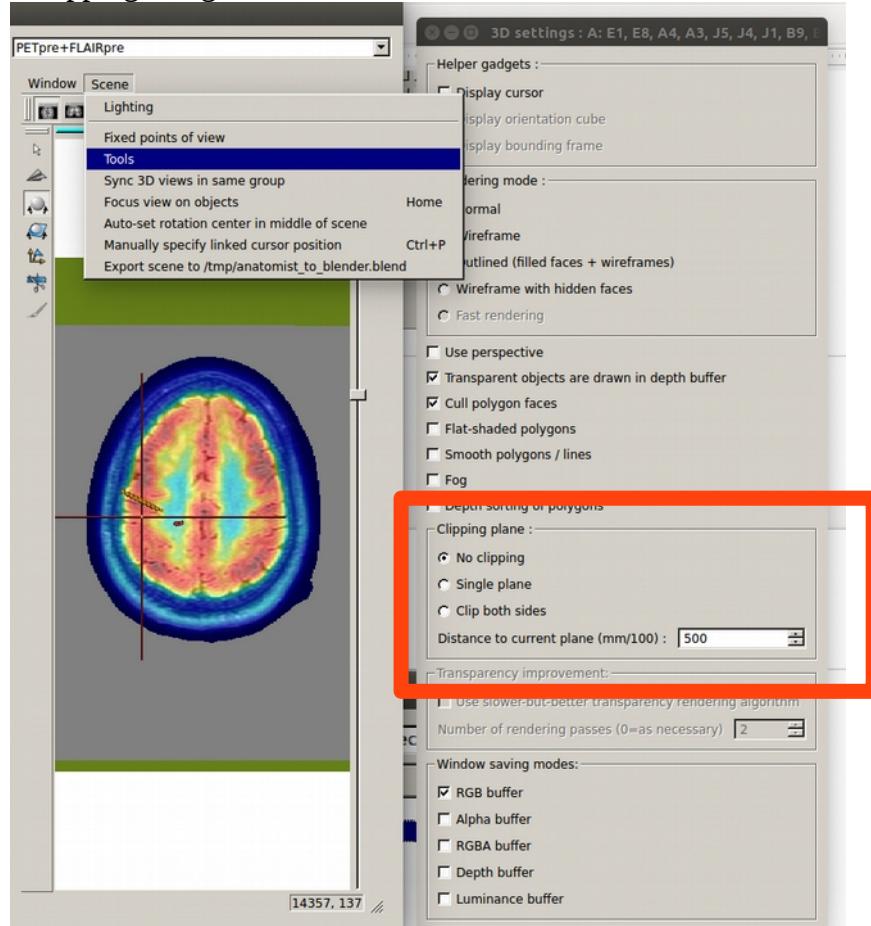


15 Clipping : does not display the meshes « too far » from the slice displayed (± 5 mm). Useful to avoid mistaking the position of a contact. For example in the case below, on the left there is no clipping, on the right there is. On the left, without the clipping, contact D16 could be « seen » as in hypoactivity, although it is far away from the displayed slice, it's corresponding to a slice way

lower. Meshes are 3D objects, slices 2D, please remember that.

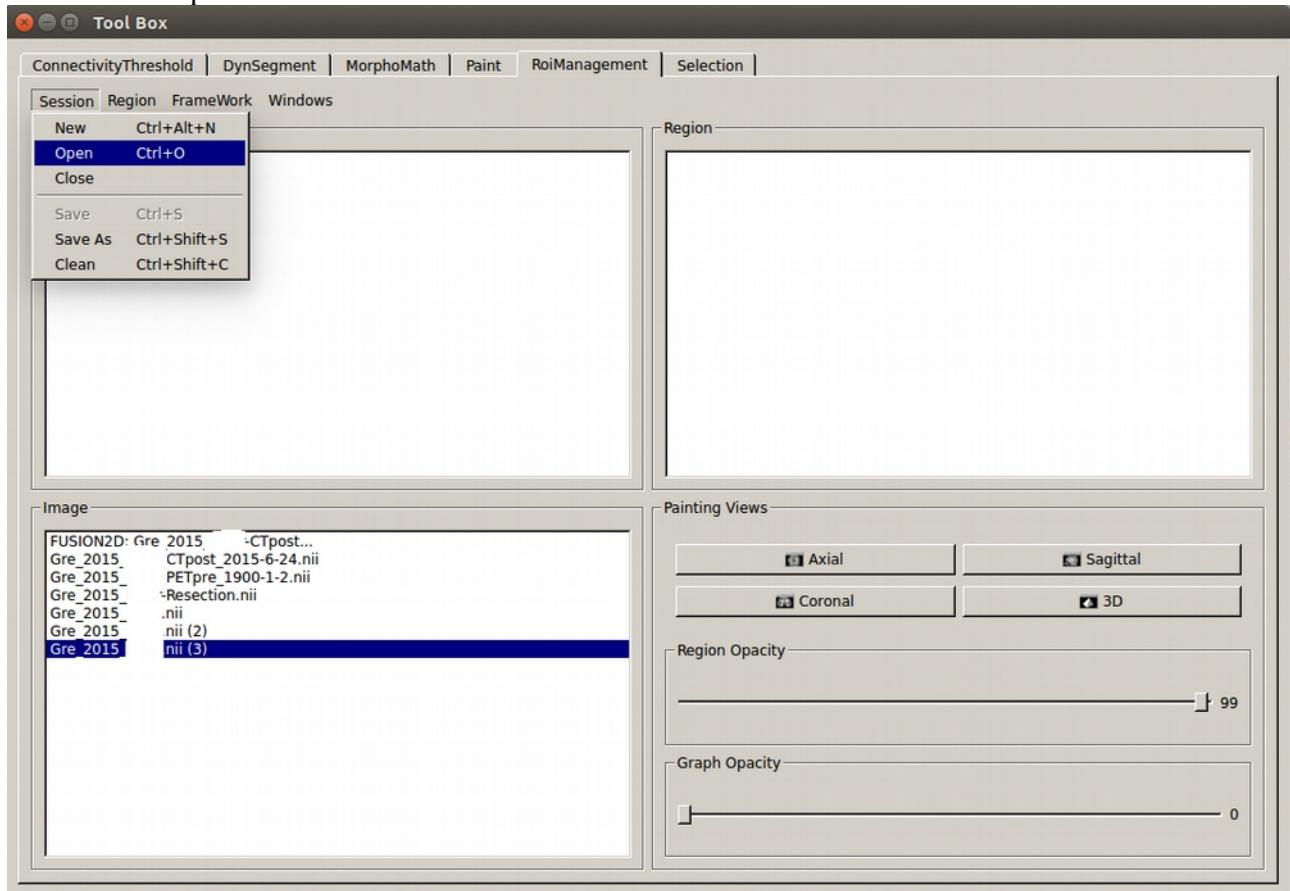


The clipping checkbox clips only meshes on the left anatomist window. But each anatomist window can be set with a clipping using the Scene->Tools menu as shown below :

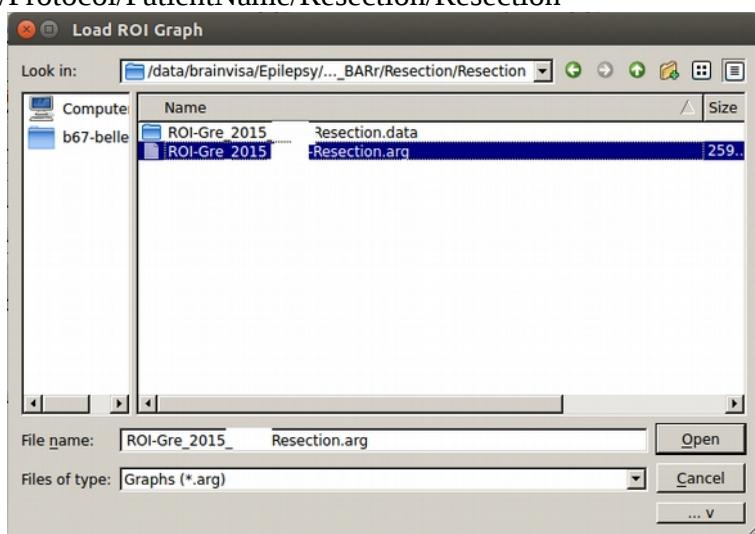


16 : BrainVisa ROI Toolbox. This toolbox is not made by IntrAnat Developpers but by Anatomist Developpers. You can find some information here :
http://brainvisa.info/anatomist/user_doc/anatomist_tutorial.html,
http://brainvisa.info/anatomist/user_doc/anatomist_manual2.html, and here :
<http://brainvisa.info/axon/en/processes/ROIDrawing.html>

It is useful for example when the Resection estimation didn't work very well and you have to perform manual correction. Once the resection algorithm has finished, if you want to correct the result, open the roi toolbox (wrench icon). The following GUI will open, with the list of available images for the current patient. You then have to open the ROI made by the resection algorithm, go to Session->Open

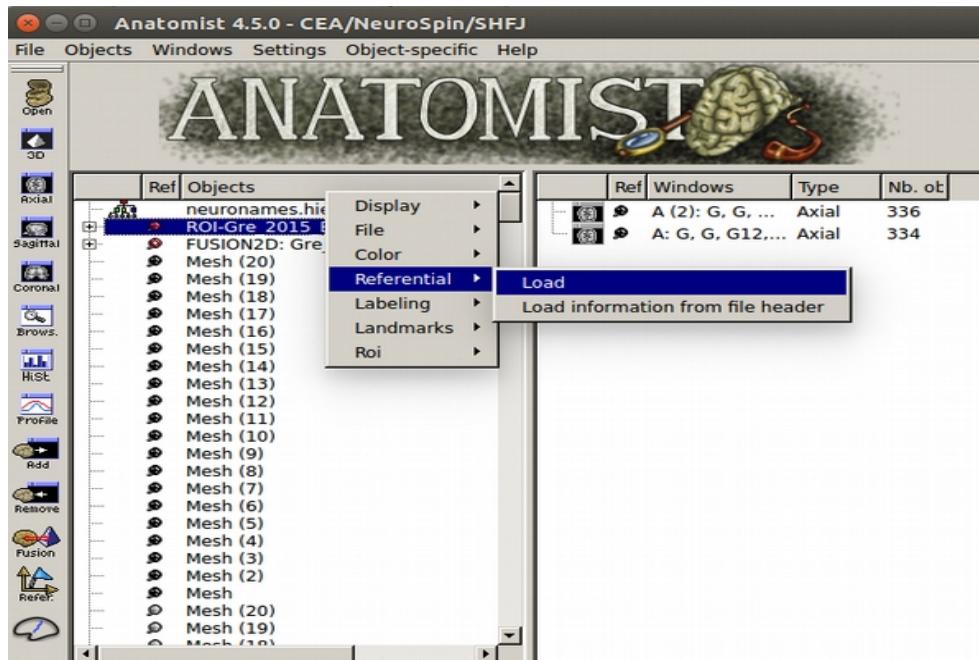


Then look for the file ROI-SubjectName-Resection.arg and open it. It will be in the /BrainVisaDatabase/Protocol/PatientName/Resection/Resection

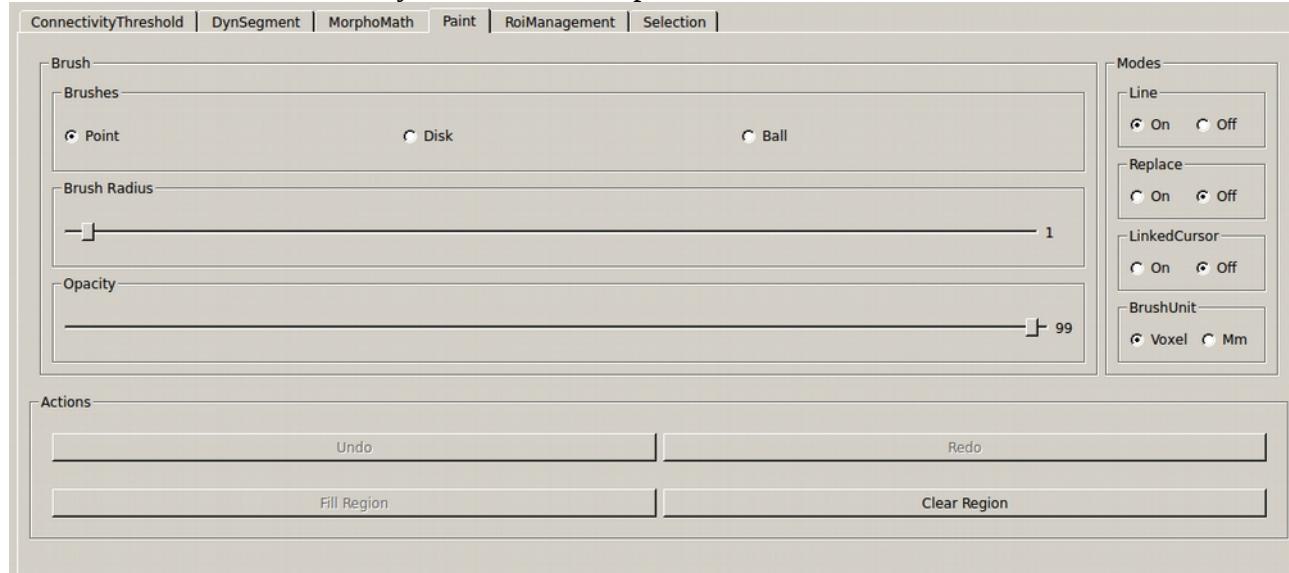


Once it has been loaded, you have to set the referential in which has been made the ROI. The referential is always T1pre native but it doesn't load this information by default.

In the anatomist GUI, right click on the ROI, then referential>Load. The name of the referential should be t1mri_t1pre....native. The referential in anatomist are identified by the color of the sphere on the left of the object name in the anatomist GUI. All object/images generated from the T1pre acquisition should have the same color (T1pre, Rhemi, Lhemi, ROI, Rwhite, Lwhite, etc), that should one of the most common color.



Then in the ROI toolbox GUI you can select the paint tab :



and modify the ROI. Left click to add area to the ROI, ctrl+left click to remove area from the ROI.

For the resection, once the modification done, you have to convert the ROI into an Image by clicking on **18**.

All calculation of resection volume, overlap of the resection with MarsAtlas or Freesurfer Atlas parcels are done on the Resection Image and not the Resection ROI. The ROI is there only to make manual correction. So DON'T FORGET TO CONVERT THE ROI INTO IMAGE !!!!

17 : Generate the resection image and ROI automaticaly by subtracting the brain mask of the T1postOp with the brain mask of the T1pre. If the T1postOp has not been imported, it doesn't do anything, but for now it doesn't display any error/warning message either. Once the resection calculation is done, it will automaticaly show the resection image in the right anatomist window. The resection is added in the patient folder

/BrainVisaDatabase/Protocol/PatientName/Resection/Resection

19 : Generate dictionnaries :



Generate All Dictionnaires will generate all « options » in the displayed order. Otherwise it will generate only the selected one.

For now you have to perform the Mars Atlas Contact Position to be able to perform the others. (will change « soon »).

These dictionaries are useful for group studies, in groupDisplay you can select all patients having a contact in xxx parcel, or having a resection in xxx parcel. See part on groupDisplay.

-Mars Atlas Contact Position and Resection Position generate json files containing python dictionaries.

For the contact position, in the patient folder, in Implantation, the file generated is PatientName.eleclabel. If you open it you will see a python dictionaries with different keys (for now plots_label and plots_label_bipolar).

For each contact or bipole center it says if it is in the Grey or White matter, in which MarsAtlas parcel, if the contact was in the part of the brain resected (for now. Soon destrieux atlas and hippocampus subfield atlas will be included as well)

example below :

```
{"plots_label": {"L09": {"MarsAtlas": [0, "not in a mars atlas parcel"], "GreyWhite": [0, "not in brain matter"], "Resection": [0, "not in resection"]}, "L08": {"MarsAtlas": [0, "not in a mars atlas parcel"], "GreyWhite": [255 "Whitematter"], "Resection": [0, "not in resection"]}, "L07": {"MarsAtlas": [127, "R_PMdm"], "GreyWhite": [100, "Greymatter"], "Resection": [1, "in resection"]}, "L06": {"MarsAtlas": [127, "R_PMdm"], "GreyWhite": [100, "Greymatter"], "Resection": [1, "in resection"]}, etc .....
```

Contact L09 is not in grey or white matter (possibly in the skull, ventricles, ...), not in a recognized MarsAtlas parcel, not in the resection.

Contact L06 is in the Greymatter, in the MarsAtlas parcel called R_Pmdm, and in the part of the brain which as been removed.

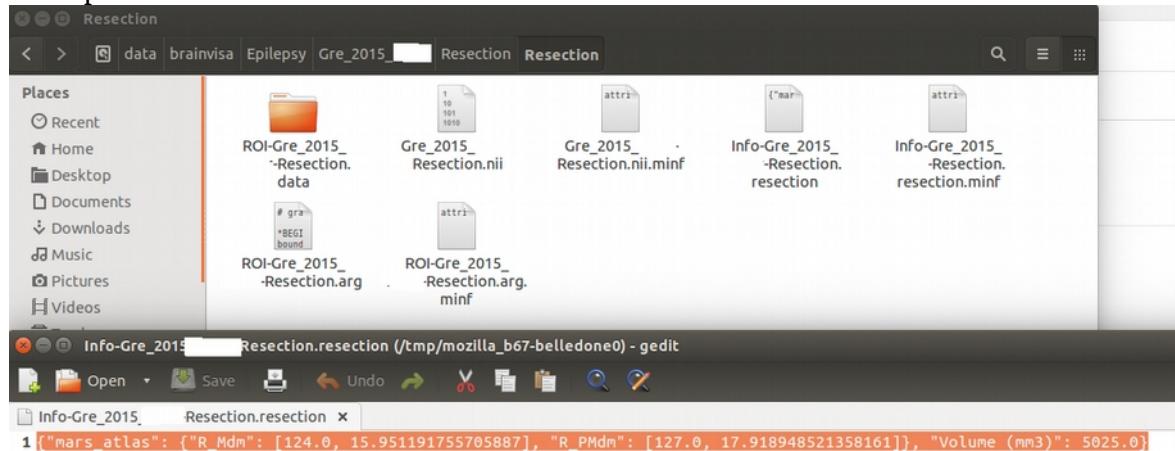
For the resection, n the patient folder in Resection/Resection, the file generated is Info-PatientName-Resection.resection. If you open it you will see a python dictionary with different keys (for now only mars_atlas and volume but soon Destrieux atlas and hippocampus subfield atlas as well).

Volume is the total volume of the resection in mm³.

In mars_atlas, you have the name of the parcel concerned by the resection, here R_Mdm and R_PMdm (see <http://www.ncbi.nlm.nih.gov/pubmed/26813563> for full name), the value of the index corresponding to the parcel on the nifti file of MarsAtlas parcels, and the percentage of the

parcel that has been resected. Careful it's a rough estimation of the percentage. We haven't yet performed an estimation of the accuracy of this percentage but it's a really rough approximation.

Example below :



-Export to csv convert the json files of contact position and resection position as a csv file (more readable for matlab and excel users for example). The file is located in database/protocol/patientname/implantation/patientname.csv

At the begining of the file there are information on contact, then on bipole center and then on the resection, as below :

Contacts Positions				
	MarsAtlas	GreyWhite	Resection	MNI
B01	R_Mdm	Greymatter	not in resection	[6.43560097615168, -7.752495549378427, 47.56618056351361]
B02	not in a mars atlas parcel	not in brain matter	not in resection	[9.915004777531387, -7.5571619963368475, 47.653462781808095]

•
•
•
•
•

B02 - B01	R_Mdm	Greymatter	not in resection	[8.17530288 -7.65482877 47.60982167]
B03 - B02	R_Mdm	not in brain matter	not in resection	[11.58570247 -7.52612616 47.65925306]

•
•
•
•

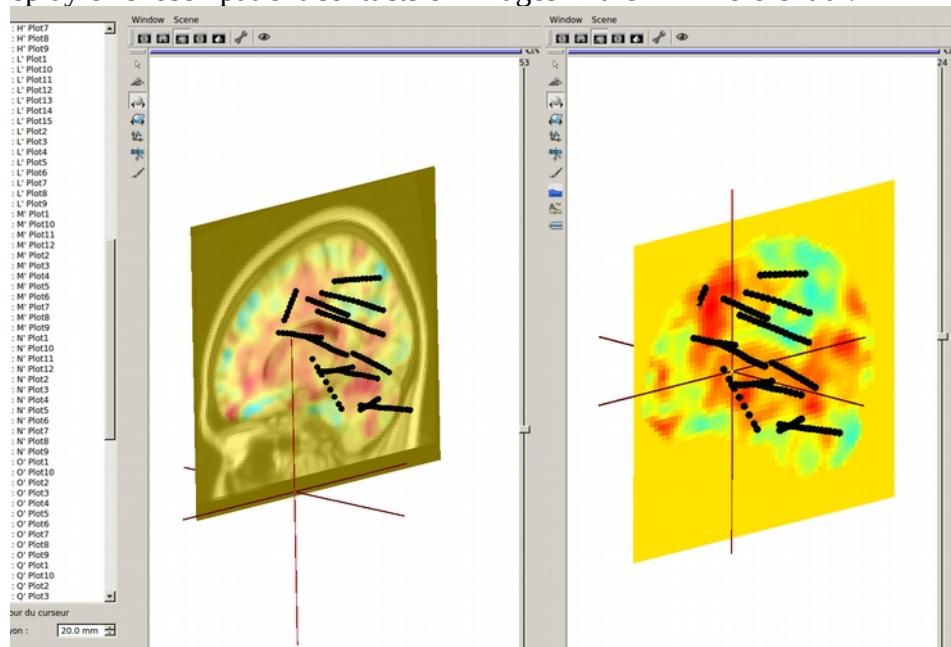
Resection Information				
mars_atlas				
R_Mdm				15.951191755705887
R_PMdm				17.91894852135816

-Generate mapping contact – hemi mesh generates a file containing, for all electrode contacts, the distance to every vertex of the cortex mesh. Useful when you want to project sEEG data/analysis on the cortex. For each contact you will be able to project the data on all vertex within x mm around the contact, give a weight of the data depending on the distance to the vertex etc ... and then generate a texture on the mesh to visualize all that on the software.

4 groupDisplay

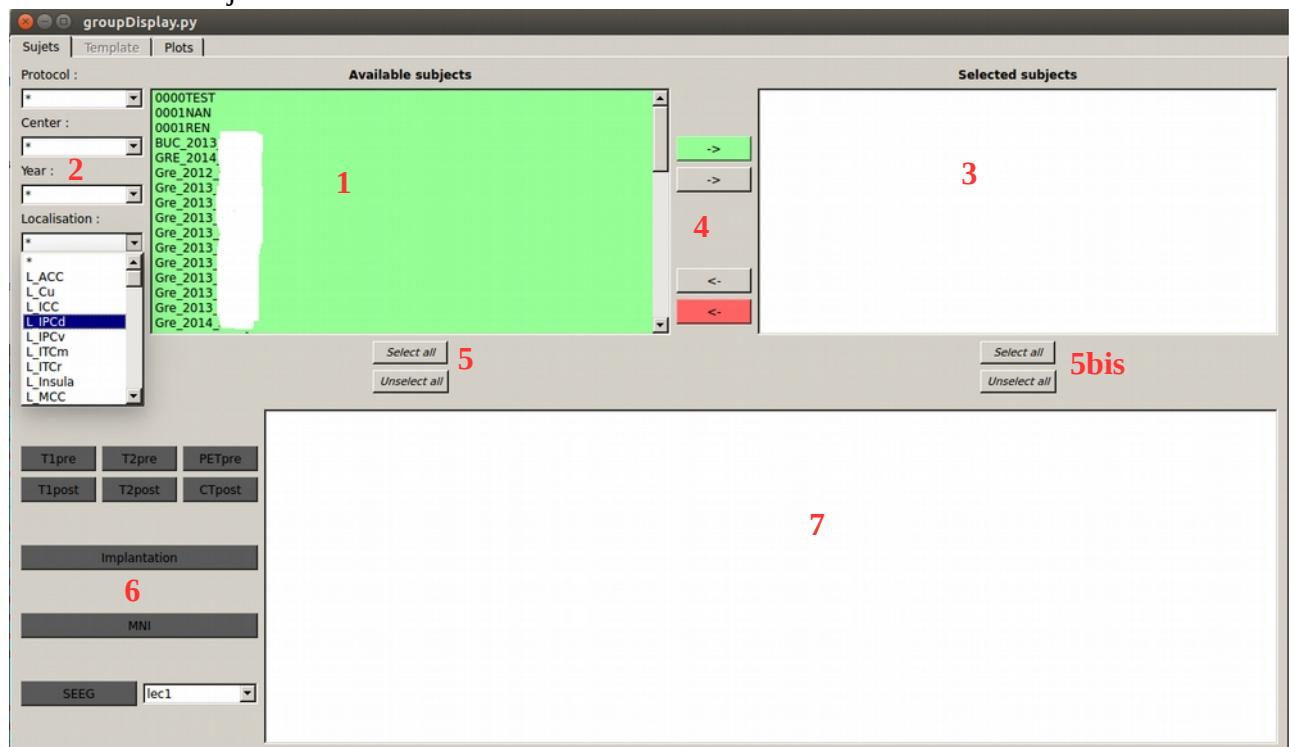
groupDisplay is the GUI to visualize all data in the MNI referential.
 This interface is evolving a lot so for now it can be a little tricky to use.
 There are two tabs, Subjects and Plots.

Subjects is a data filtering interface, to select only few patients on the whole database.
 Plots is the display of chosen patient contacts on images in the MNI referential.



For now its main use has been to show that implantation of subjects have covered correctly some structures. To compare with group study fMRI, when you have the fMRI results of a group study in the MNI, you can look for patients who had contacts where a statistical test on fMRI studies was significant.

- Tab : Subjects



1 List of all patients available according to the filter in 2 (Protocol, Center, Year, Localization, Cognition (in development), Resection)

2 Filters (to not scroll over the full list). In **1** there will be only :

-Protocol : patient who are included in the selected protocol (specified in ImageImport)

-Center : patient who have been affiliated to the selected center (on ImageImport)

-Year : patient who have been affiliated to the selected year (on ImageImport)

-Localization : patient who have at least one contact in the selected MarsAtlas parcel (in development, same with Destrieux parcels from Freesurfer)

-Cognition : patient who performed the selected cognitive task (in development)

-Resection : patient who had a resection including at least a part of the selected MarsAtlas parcel (in development, same with Destrieux parcels from freesurfer)

for all of them, the symbol « * » means that no filter is applied.

3 List of selected patients (patients who will be manageable once in the tab Plots). To move a patient from **1** to **3**, use **4**.

4 From the top to the bottom (if you leave the mouse on one of these buttons without clicking, explanation will appear, as on figure below) :

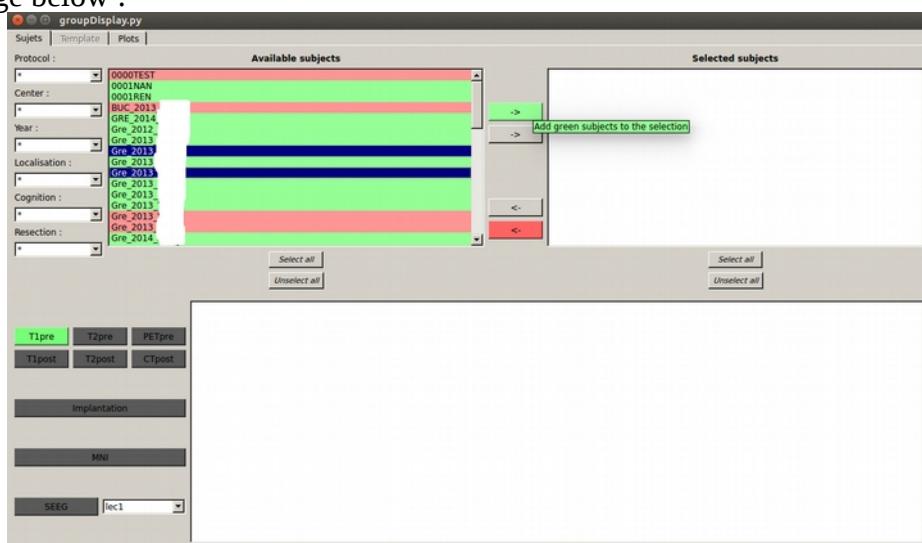
Arrow to the right, background green : add green subjects to the selection

Arrow to the right, background gray : add selected subjects to the selection

Arrow to the left, background gray : remove selected subjects from the selection

Arrow to the left, background red : remove red subjects from the selection

example image below :



subject with blue background will be transferred in the list of selected subjects using the arrow to the right, gray background.

Subject with green background will be transferred in the list of selected subjects using the arrow to the right, green background.

5 and 5bis : select and unselect all subjects of the list of available subjects and selected subjects respectively.

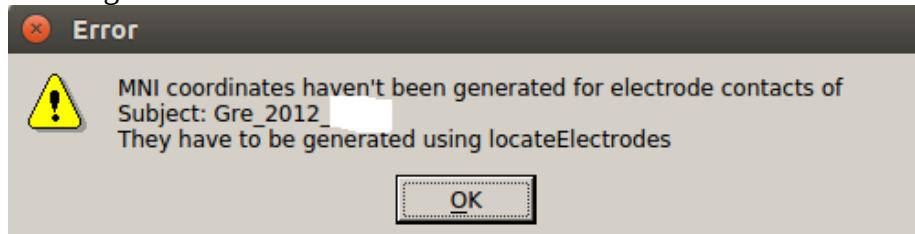
6 Highlight with green background all subjects having the selected item in the available list and selected list, with red background all subjects who haven't. In order to potentially transfert them in the selected list using the arrow to the right, green background. In the example above, all subjects having a T1pre are highlighted with green background.

It works as logical and operator, if you select T1pre and CTpost for example, only subjects having a T1pre **AND** a CTpost will be highlighted with a green background.

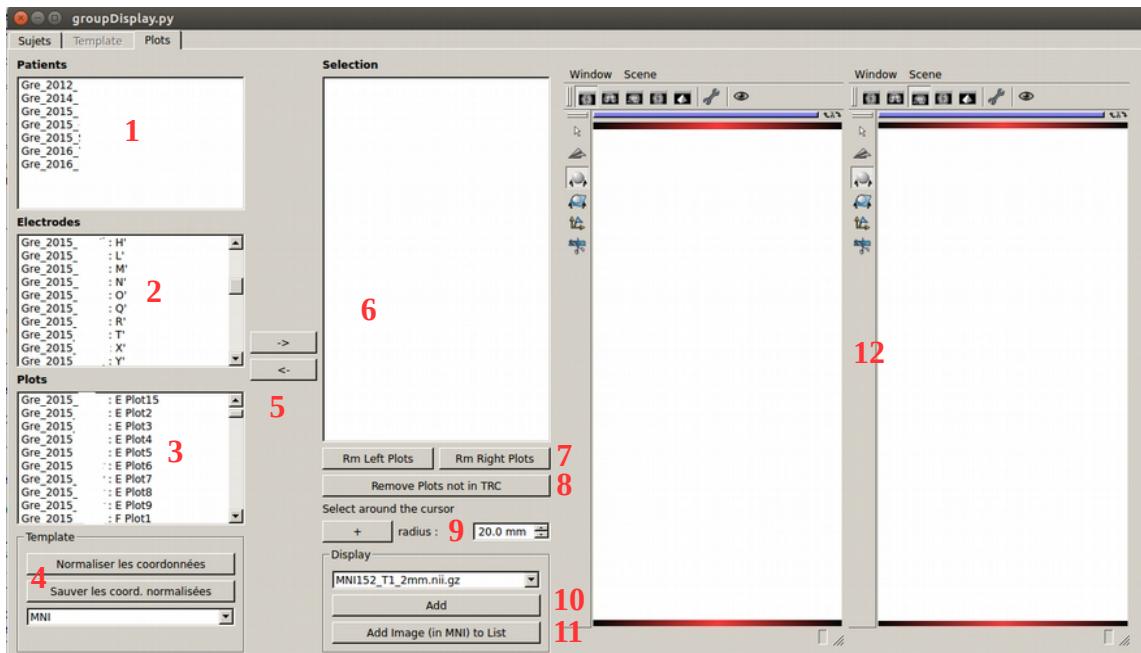
7 No idea what it is for.

- Tab : Plots

When you click on Plots, it will try to generate the mesh objects of each contacts of all patients, so it needs the MNI position. If the MNI position haven't been generated on locateElectrodes, it will show this error message :



It won't stop, it will continue to generate the mesh of the contacts of the other patients selected. It's just a warning that this patient won't be generated. (it stops the process until you click on ok).



- 1 List of patient selected in the Subjects tab (even if there was no MNI position for the contacts)
- 2 List of electrodes for all patients (so if you had an error message because the MNI position of the contacts were not calculated for a patient, they won't appear here)
- 3 List of all contacts for all patients (so if you had an error message because the MNI position of the contacts were not calculated for a patient, they won't appear here)
- 4 Useless for now. The buttons will allow to generate MNI position for patient for who it haven't been made in locateElectrodes.
- 5 Add or Remove selected items. If you select an electrode in 2, it will add all contacts of the electrode. If you select a patient in 1 it will add all contacts of all patients. If you select only one contact, it will add this contact.
- 6 List of all contacts displayed
- 7 Remove left or right plots (in MNI, negative or positive value in x)
- 8 Remove contacts which haven't been recorded on the sEEG for the corresponding patients, if SEEG was imported in ImageImport (for now it accepts only Micromed .TRC format, but we use the neo toolbox so it is easily adaptable to any format read by neo <https://github.com/NeuralEnsemble/python-neo>).
- 9 Select all plots in a sphere which has the cursor as center and of a radius of x mm (here 20 mm)
- 10 add the selected image (from the list, here it's MNI152_T1_2mm.nii) in the anatomist windows

in **12**. To be coregistered with plots, the image has to be in the MNI referential.

11 Add an image to the list, to be able to select and display it in the anatomist window. By default the list contains only the images in the MNI that contain the folder SPM12

12 anatomist windows (http://brainvisa.info/anatomist/user_doc/anatomist_manual1.html), see parts before (ImageImport or locateElectrodes).