BEM me up

The manual below currently comprises Segmentation with BrainVISA, Normalizing the MRI with SPM8, Preparing NutMEG, running the BEM-skript.
(Version 0.1 (13.March 2012): Guide is complete, but needs spell-checking, formatting ...)
Author E-Mail: andreas.halbleib@uni-konstanz.de

The Preparations Menace (Necessary Programs)

SPM8

- Go and get SPM8 if it is not installed already:
http://www.fil.ion.ucl.ac.uk/spm/software/spm8/

BrainVISA

Download BrainVISA (for free) and make it run under Win7
In case you want to use WIN 7:
- Create a new folder in windows explorer in any location. This will be your BrainVISA installation folder, so give it a name e.g: BrainVISA.
- Download BrainVisa 4.2.1 from http://brainvisa.info/downloadpage.html
- The name of the file: brainvisa-Windows-XP-i686-4.2.1-2012_02_17.zip
- Open this .zip in e.g. WinRAR. You will see a single folder.
- Double-click on the folder, to see its contents
- Select the entire content of this folder and extract it to the folder you created previously (e.g.:BrainVISA).
- No installation is required, just the copying

For Win7: Don't use BrainVISA 4.1.0, since ..well it's buggy, 4.0.2 is too old..

Adding a special plug-in (Conductivity Modeler)
- Open the bv-bentools.zip-file
- In the folder you find a README-file, open it (e.g. editor).
- copy the three '.py'-files according to the README into the BrainVISA-structure:
    bem_modeler_ssd.py -> ~/.brainvisa/processes
    meeg_types.py -> ~/.brainvisa/types
    meeg_hierarchy.py -> ~/.brainvisa/hierarchies/brainvisa-*/
- If ~/brainvisa/processes does not exist (Win Version!), copy the file 'bem_modeler_ssd.py' into : ~/brainvisa/toolboxes/tools/processes

First Start:
- Go to the folder where you copied all the files.
- Start the Batch-file 'BrainVISA'
- Never close the command-line window unless you want to terminate BrainVISA
- BrainVISA will ask you to create a database folder
- Open the Preferences Window (Fig1):

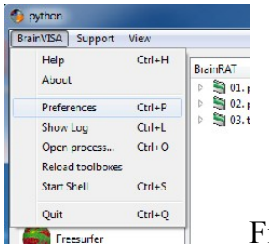

Fig1

A new Window will open (see Fig 2). It is the configuration-GUI.

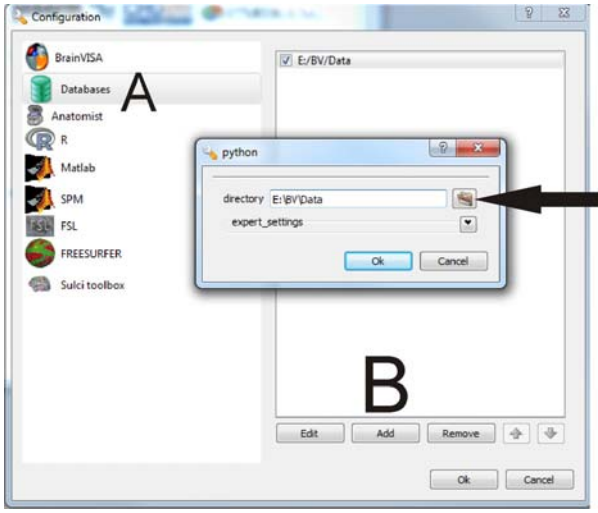

Fig2

- In this window (Fig2) click on (A) Databases
- Click ‘Add’ (B)
- A small window opens. Here you can choose a Database directory, by browsing (necessary button indicated by arrow). The Example is E.\BV\Data. You’ll need space…
- Click ‘OK’ , you will return to the configuration-GUI
- Now click the ‘BrainVISA entry to the left.
- Set user level to ‘Expert’.
- Since you are an expert now: figure out how to set the orientation of the MR-Image to the NEUROLOGICAL orientation.

Hint: there are two ways of presenting the image:
- Anatomic left on image left (neurologic)
- Anatomic left on image right (radiologic),

So you might want to uncheck an option…

OpenMEEG:

Download and install: http://www-sop.inria.fr/athena/software/OpenMEEG/
In Windows: install it into a path without whitespaces. Make sure to let the installer set the path-environment.

iso2mesh:
http://iso2mesh.sourceforge.net/cgi-bin/index.cgi?Download

Setting paths in MatLab

Add the BrainVISA, iso2mesh, NutMEG, SPM8 to the Matlab path!

Attack of the Meshes (Segmentation in BrainVISA)

T1-MRI

Importing

First you need to im port the MRI-scan. The best way to do this is via the 'Im port T1 MRI'-option BrainVISA main GUI (see Fig3).

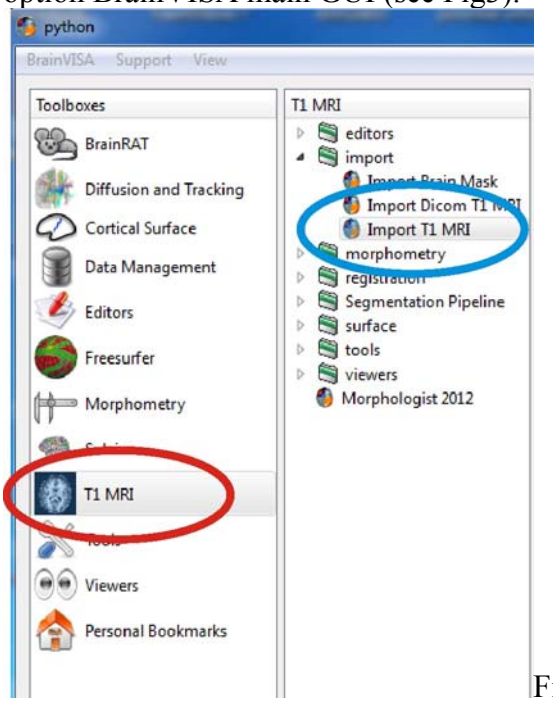

Fig3

- On the left side choose the item 'T1 MRI' (marked in Fig3 as red circle). The list to right changes and should list the items you see to the right in Fig3.
- Choose the second item from the top labelled 'import' and double-click 'import T1 MRI' (blue circle in Fig3)

A new window opens (Fig4). Here you will select the input MRI-file and 'fill' the database.

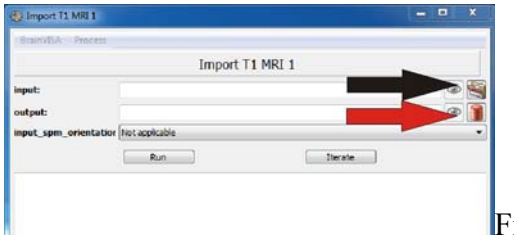

Fig4

The black arrow (see Fig4) indicates the button which allows you to browse your computer for the MRI-file.
Pushing the button indicated by the red (in Fig 4) arrow opens the window you see in Fig 5, which allows you to set various import parameters.

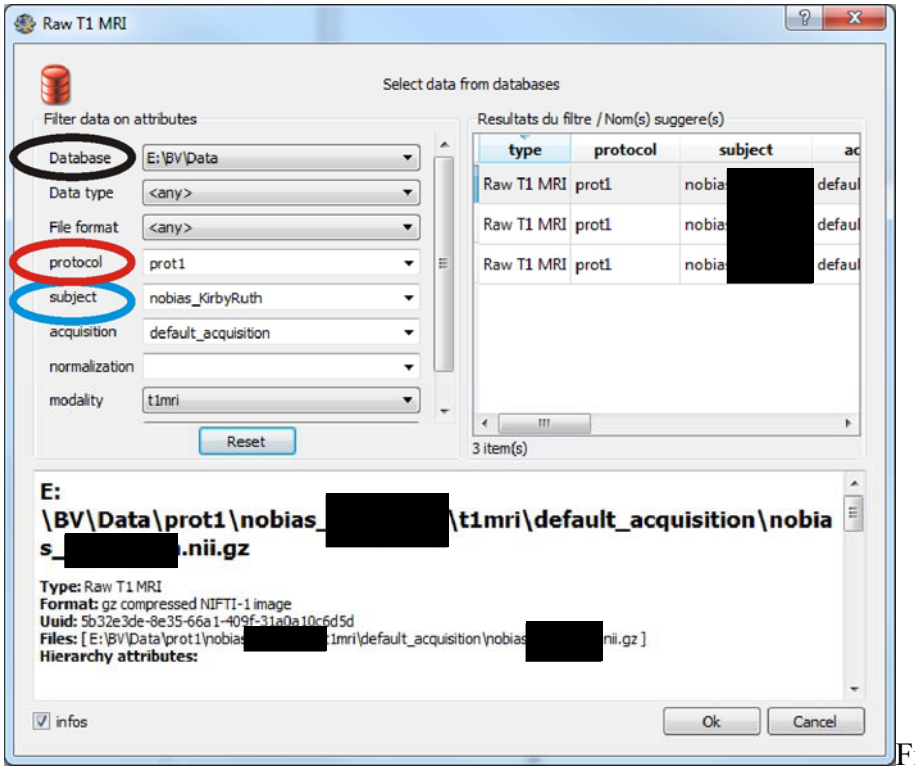

Fig5

- Select your Database folder (black circle Fig5) in the adjacent drop-down box
- Create a new protocol (red circle) by clicking in the adjacent box and typing a name for you protocol. A folder with the same will be created. Here BrainVISA stores all information you create in the whole segmentation process.
- The subject should be filled in automatically (blue circle).
- Click OK and return to the window you see in Fig4 or Fig6, now ‘input’ and ‘output’ should contain path information.

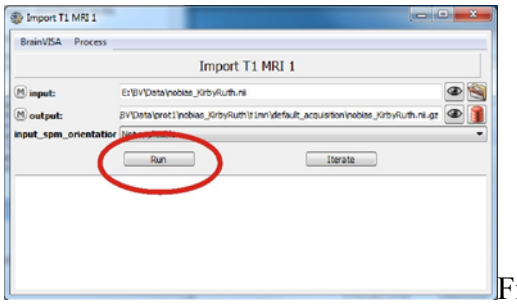

Fig6

- Click run (red circle Fig6)
- This should take several seconds, when it is done (The animation in the top right corner of Fig 6 has stopped) you can close the window. Don’t worry everything is saved to the database.

No differentiation between left and right, so ne left grey mask etc (morphometry)
No need for Talairach normalization

Thus the next step is preparing the subject for the anatomical pipeline.

Prepare Subject for Anatomical Pipeline

Now you prepare the subject for the anatomical pipeline.

- In the BrainVISA main GUI select ‘T1 MRI’ (black circle, Fig7).
- Select ‘Segmentation Pipeline/Components’ (blue circle, Fig7)
- Double-click on ‘Prepare Subject for Anatomical Pipeline (red circle Fig7)

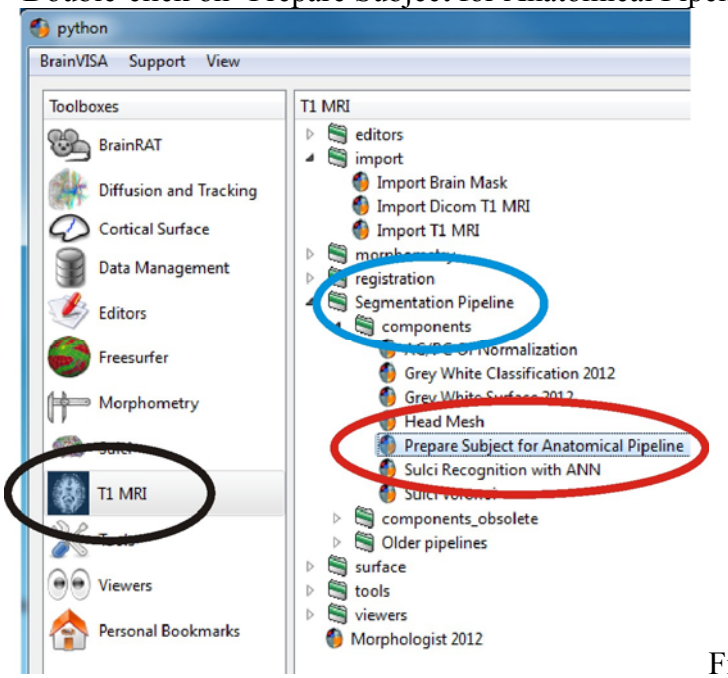

Fig7

Now the ‘Prepare Subject for Anatom ical Pipeline’-GUI opens (Fig 8). Now you can select the MRI-Data of subject of you choice by clicking on the green symbol in the top right corner (green circle Fig8).

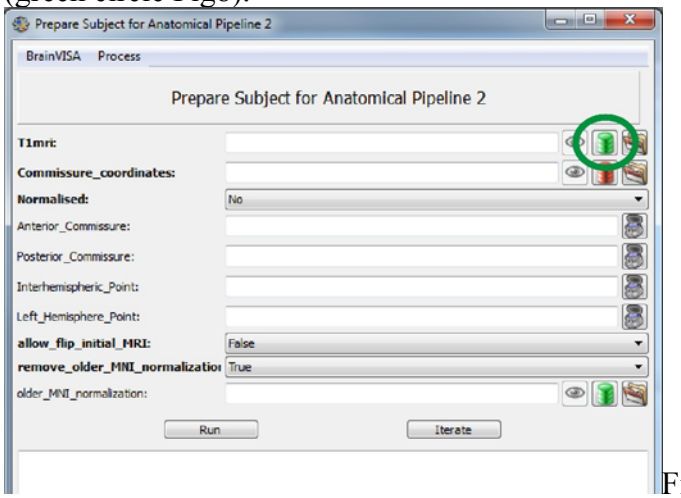

Fig 8

A new GUI opens (Fig9), which allows you for importing Data from the Database you set up before. Simply click on the on the dataset of you choice (black circle in Fig9).

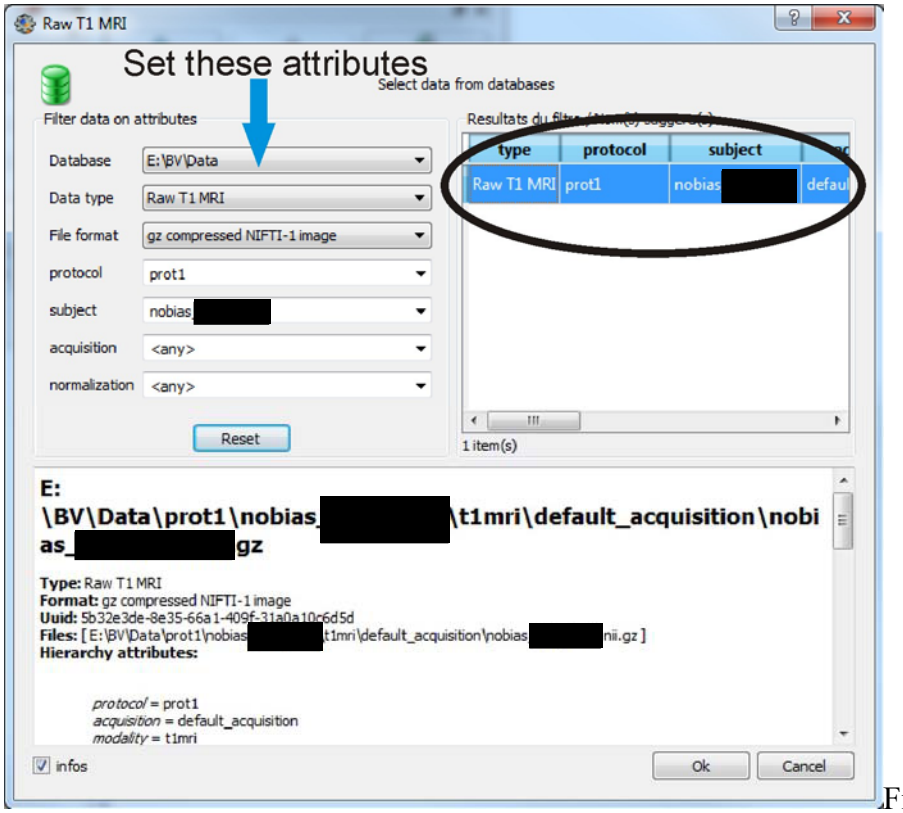

Fig9

The options on the left side of the GUI (blue arrow) need to be filled in
- Choose the database..
- Datatype: ‘Raw T1 MRI’
- Fileformat:..NIFTI (?)
- Protocol: Your choice, put something meaningful. A folder containing all future results will be created according to that name
- Subject name: well…
- Acquisition and normalization: <any>
- Click ‘OK’.

You are back at the ‘Prepare Subject for Anat omical Pipeline’-GUI (Fig 10). As you can see, the Locatio n for the saved ‘Commisure_coo rdinates:’ (b lack box Fig10) has been filled in automatically. In the drop down box indicate d by the blue box (Fig10), you can select a normalization method. Set ‘no’

<u>Defining Anatomical points</u>
Now you must define the ‘Anterior’ and ‘P osterior Comm issure’ as well as the ‘Interhemispherical Poin t’ and the ‘ Left Hem issphere Point’ . This is do ne in the ‘ Prepare Subject for Anatom ical Pipeline’-GUI (Fig 10). Clic k, one-by –one of cour se, on the buttons marked by the red circle.

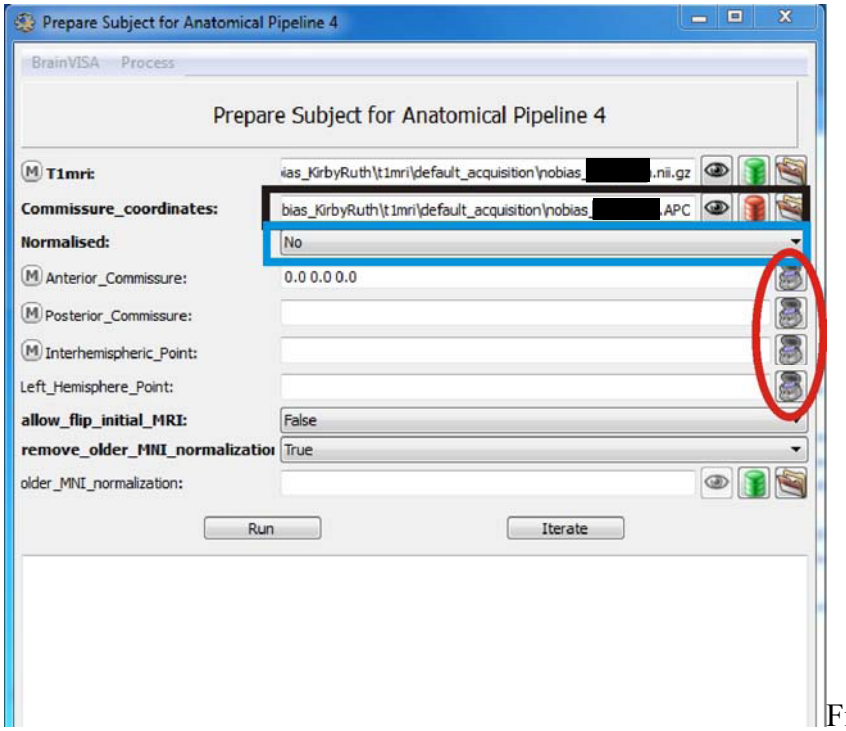

Fig 10

Anterior Commisure

First step is defining the 'Anterior Commissure'. Click on the according button to the right. Two new GUIs open: the Anatomist-GUI and a window displaying the MR-Image (see Fig 11).

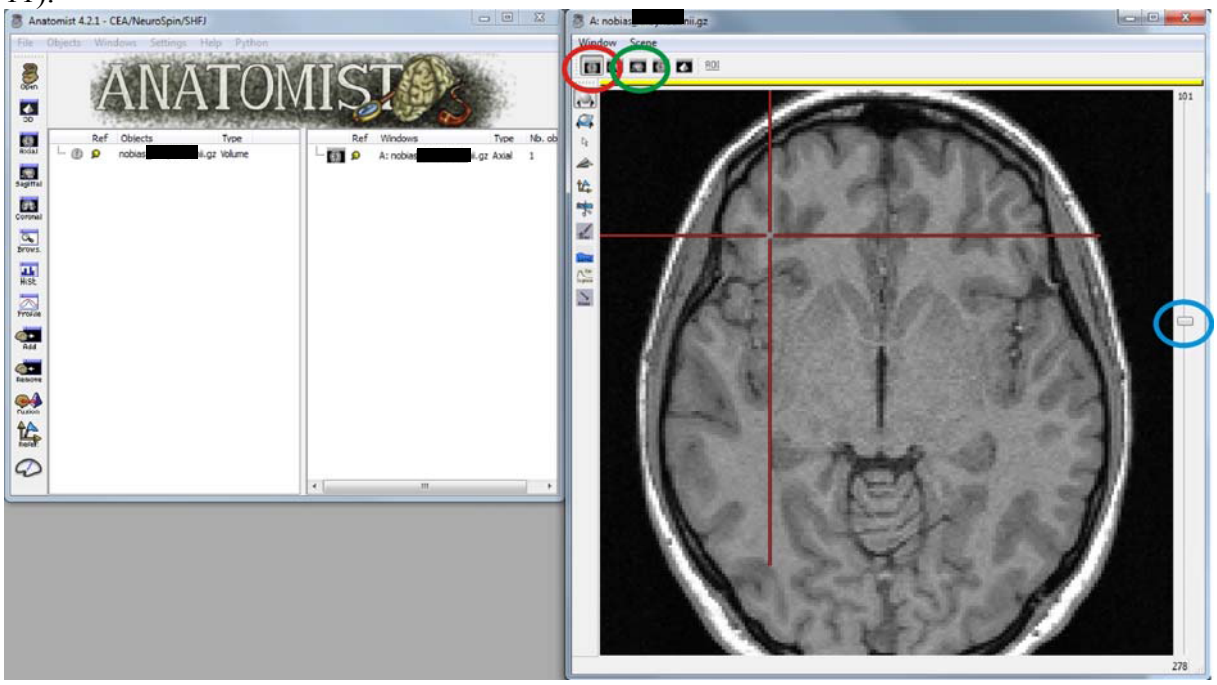

Fig 11

- Switch to Axial view (Red circle Fig 11)
- Slide through the slices (Blue circle Fig 11)
- You are looking for fibres connection the two hemispheres (structure highlighted blue in Fig 12) You should also see the Posterior Commissure (highlighted blue)

- Resize the Anatomy-window if necessary
- Switch to sagittal view (button right of the coronal view button you just used)
- Check the position of the cross hair. (Compare position to the anatomical table in Figures 13 and 14)
- If the Ant. Commissure is visible in more than one slice, position the crosshair in the topmost slice.

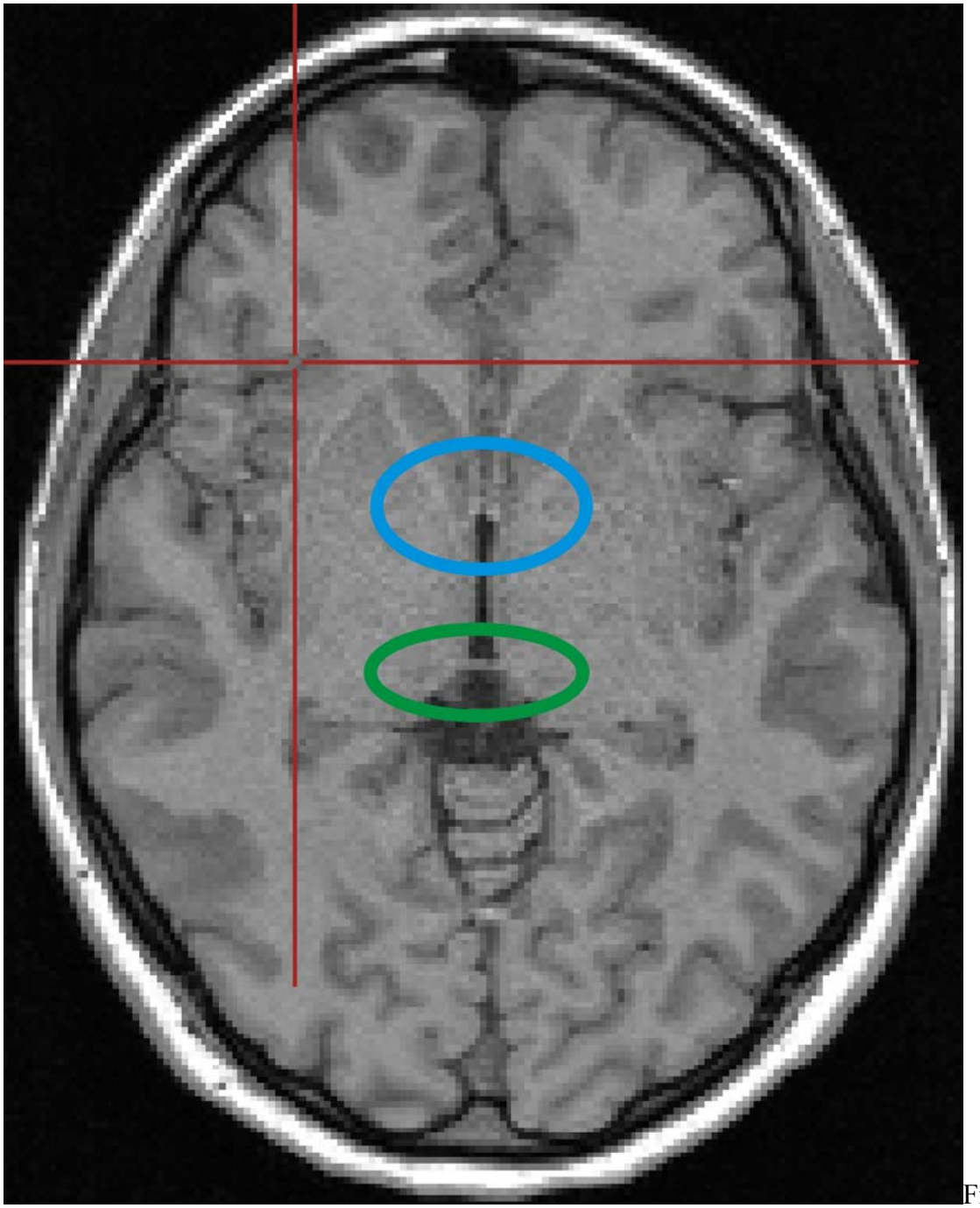
Fig 12

Attention: Don't use the optic chiasm! This structure looks ra ther similar, also connects both hemispheres but is located more caudal (lower).

When you have positioned the cr osshair on the comm issure, swit ch back to the 'Prepare Subject for Anatom ical Pipeline'-GUI and click on the button you used to open the

Anatomist-GUI (Red Circle Fig 10). Now the c oordinates should be visi ble in the according text box.

Now, what's the Anterior Commisure:
Well, it is a bundle of nerve fibres, thus forming a connection between the two hemispheres. It is not the corpus callosum, but below. Gray Table 744 shows its location in the coronal view (blue circle Fig 13). The red circle in Fig 13 is the optic chia sm. You don't want to confuse them…

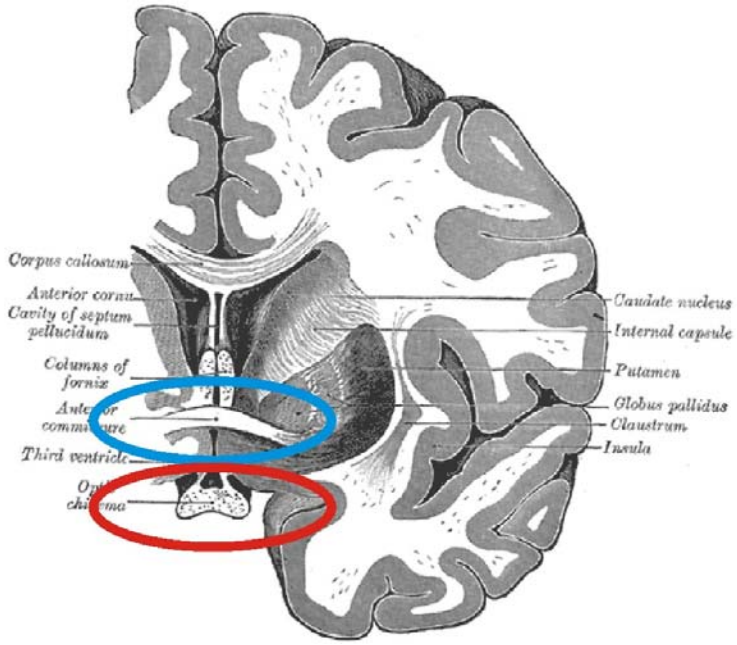

Fig13

And now for the sagittal view in Gray Table 720 (see Fig 14). The white circular structure in the blue circle is the an terior commisure. The green circle is the posterio r Commissure. The red circle is the optic chiasm and a no-go area for the crosshairs.

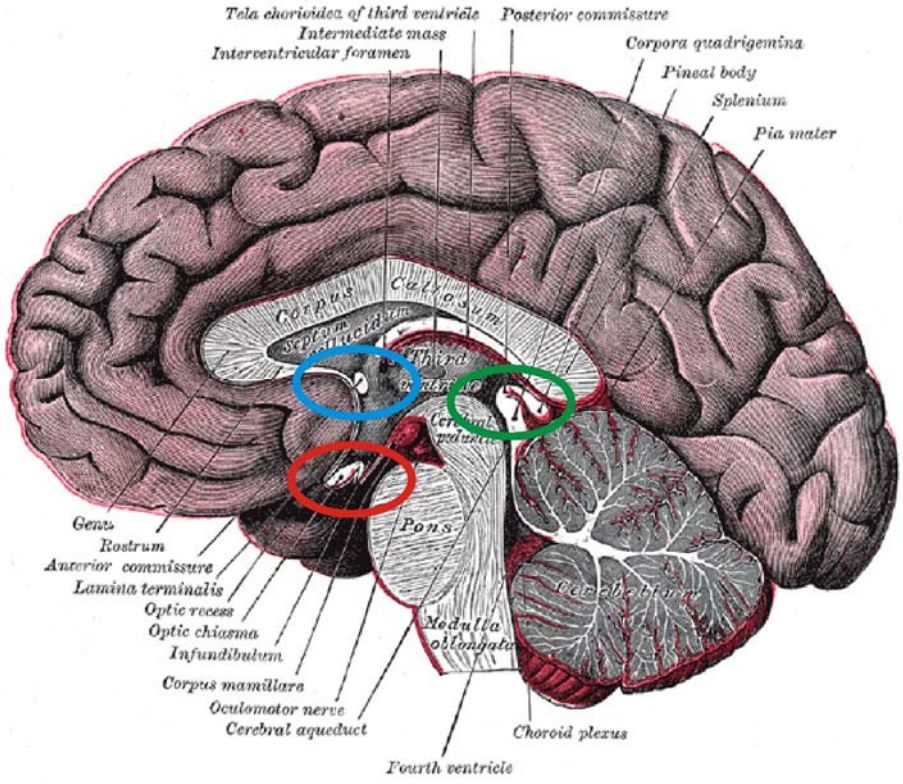

Fig 14

Posterior Commissure

Now that you've successfully located the Anterior Commissure, you will find the Posterior Commissure several centimetres dorsal (towards the back of the head). The position of the Posterior Commissure is highlighted in the green circle of Fig14.

- Go to the MR Image.
- Switch to the axial view.
- Position the crosshair on the structure seen in the green circle in Fig 12.
- Slide through the slices (blue circle in Fig 11) until you can see the desired structure
- If it is visible in more than one slice, position the crosshair on the lowest one.
- Verify the position in the sagittal view (Example Fig 15)
- Go to the click the according button in the 'Prepare Subject for Anatomical Pipeline'-GUI (Fig 10). Now the coordinates should be transferred to the GUI.

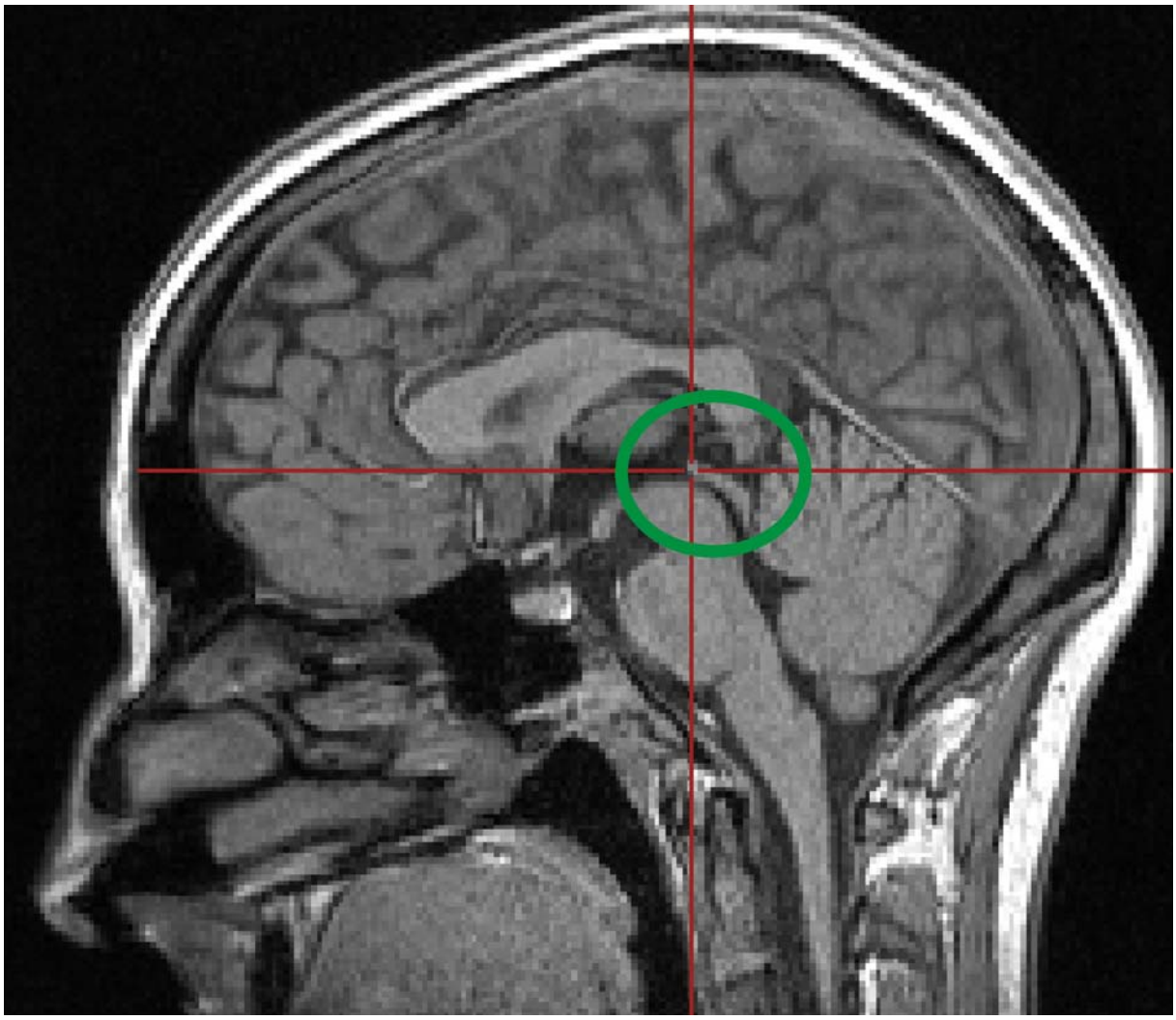

Fig15

The Interhemispheric Point

- Go back to the anatomic view
- Use the coronal view
- Pick any point between the two hemispheres. Optimal position would be towards the top of the head but not to far away from the commissures (Example: Fig 16, Left: Coronal, Right: Sagittal)
- Transfer the coordinates to the 'Prepare Subject for Anatomical Pipeline'-GUI

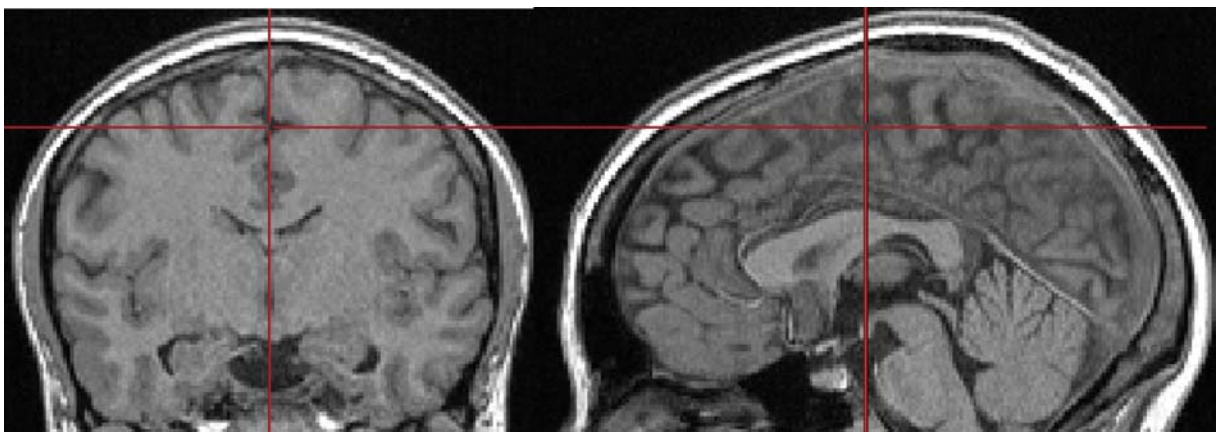

Fig 16

Left_Hemisphere_Point:
- Go back to the anatomic view
- Choose axial view
- Position the crosshair in the left hemisphere (depends on the view you have: neurological view: left is left; radiological view: left is right)
- Choose a point that is not on the same slice(s) as the inter-hemispheric point.
- Transfer coordinates to the 'Prepare Subject for Anatomical Pipeline'-GUI

Run the 'Prepare Subject for Anatomical Pipeline'-GUI

After a successful positioning of the anatom ical points the 'Prepare Subject for Anatom ical Pipeline'-GUI should look as in Fig 17:

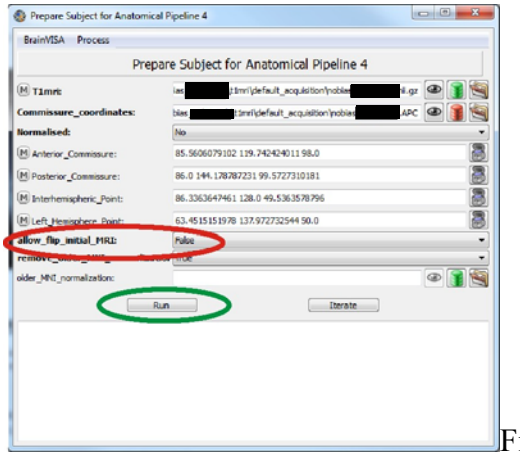

Fig 17

You may want to allow for flipping of the MR-Image (red circle Fig 17). Hit the 'Run' button (green circle Fig 17) and wait several seconds. In the Top right corner a little anim ation of a rotating runs while BrianVISA computes. W hen the process has ende d without error you can close the 'P repare Subject for Anatom ical Pi peline'-GUI, all data have been saved. (Don't bother to close the 'Anatomist GUI')

Segmentation via Morphologist 2012

Now let's segment the brain. The tool of c hoice is 'Morphologist 2012' from the BrainVISA package. Open it by double-clicking on its sym bol in the BrainVISA m ain GUI (red circle in Fig 18).

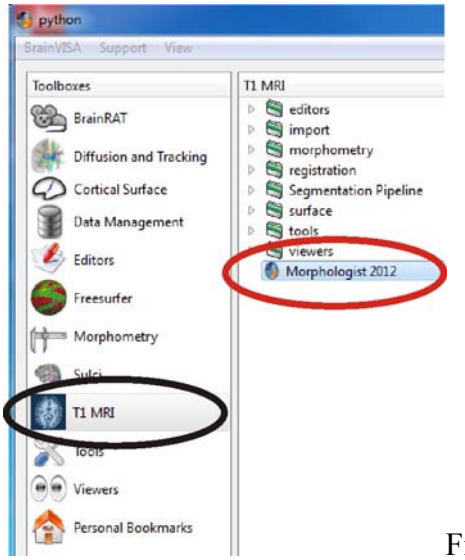

Fig18

In the Morphologist-GUI (left hand side Fig 19) you can import the dataset from the database by clicking on the green sym bol indicated by the green arrow in Fig19. Then the window on the right hand side of Fig 19 opens. Select th e desired dataset from the database by double-clicking (blue arrow Fig 19).

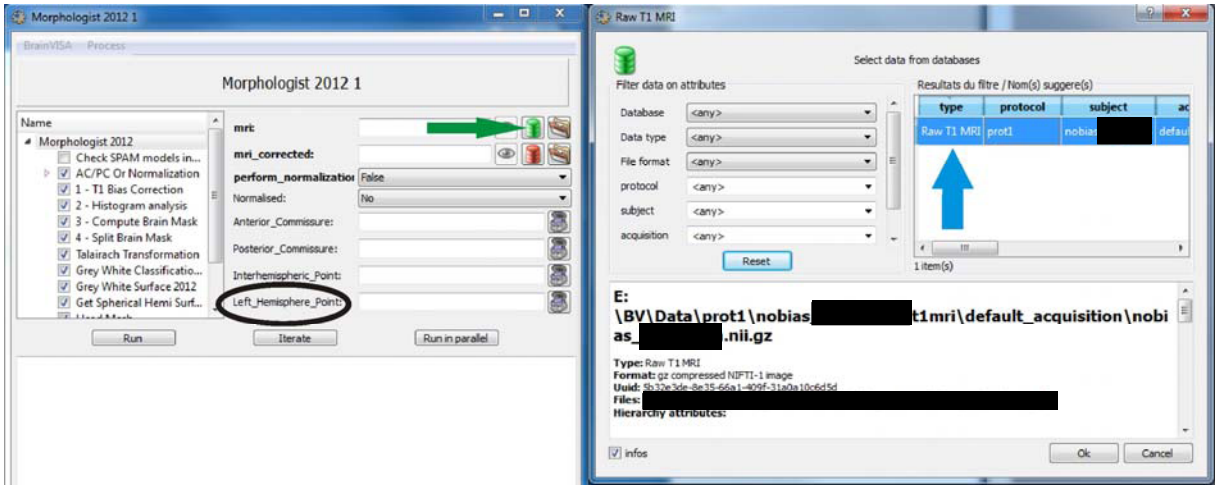

Fig19

The data are loaded automatically into the ‘Morphologist 2012-GUI’. Also the coordinates of the comm issures you defined previously are im ported. If e.g. the ‘left_hem isphere-Point’ (black circle Fig 19) is not imported correctly, proceed as described above.

Fig 20 shows the filled in ‘Morph ologist 2012’ GUI. Set ‘perform _normalisation’ to ‘false’ (red circle Fig 20. For the top level-entry (black circle) there are several options which need to be checked/unchecked. Leave the o ptions marked green an d blue checked. Uncheck the red options.

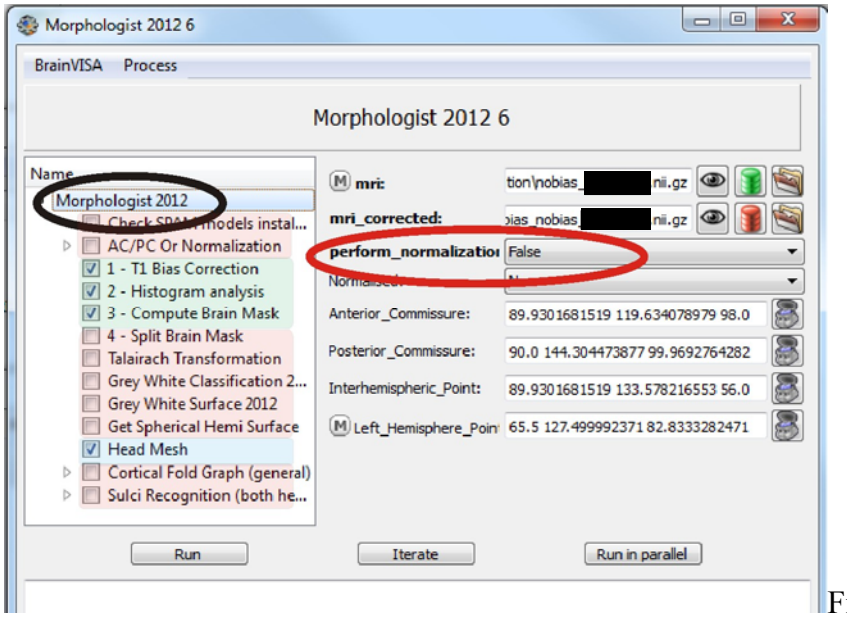

Fig 20

Click on the blue option labelled ‘Head Mesh ’. The ‘Morphologist 2012’ GUI changes on the right hand side (Fig 21). **Set the option ‘keep_head_mesh’ to ‘true’ (red circle Fig 21).**

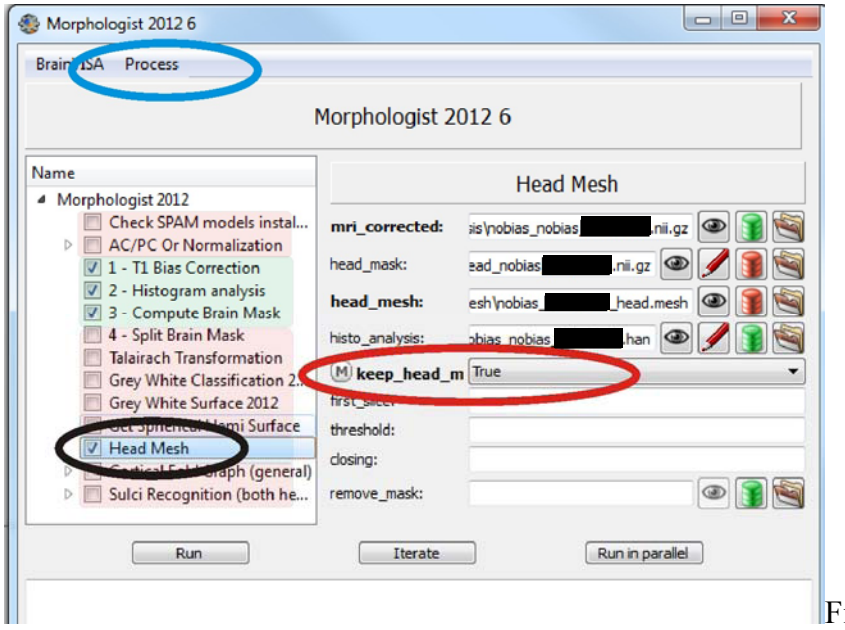

Fig21

Press the ‘Run-Button’. This might take some minutes. Again there is an animation in the top right corner. When it stops, the procedure is completed. Save the process via the GUI-Menu (blue circle in Fig 21). You can close the GUI.

Creating BEM meshes for skin, skull and brain

- Select the option tools in BrainVISA main GUI (black circle Fig22)
- Double-click on the item ’Conductivity_BEM_modeler’ (blue circle Fig22)

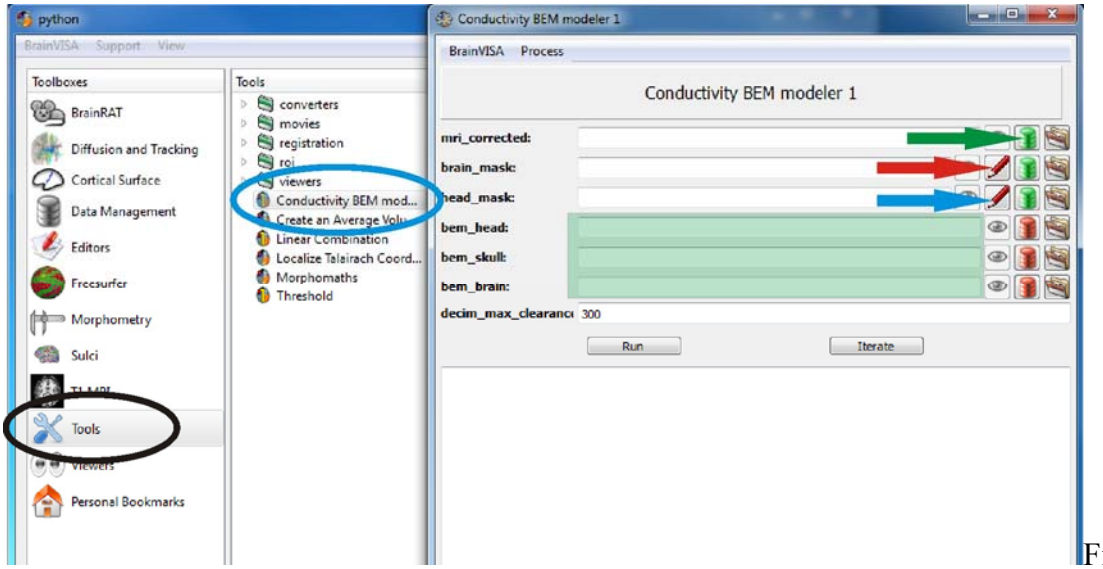

Fig22

The double click opens the 'Conductivity_BEM_m odeler'-GUI, which is shown in the right hand side of Fig22. Click on the green button for 'mri_corrected' (green arrow Fig22). A GUI opens, in which you choose the dataset to im port. This import-procedure is identical to the one described above.
Unfortunately, the nam es of the output-files are not written autom atically (Might be a bug in the W indows version of BrainVISA, It works perfectly on the MAC). The output has to be defined manually in the boxes highlighted in green in Fig 22.

Bem_head: Brain-mask Path + \mesh\ + Subjectname + '_BEM_head.mesh'
Bem_skull: Brain-mask Path + \mesh\ + Subjectname + '_BEM_skull.mesh'
Bem_brain Brain-mask Path + \mesh\ + Subjectname + '_BEM_brain.mesh'

Copy/Paste the Brain-mask Path from path given in the 'Conductivity_BEM_modeler'-GUI. Don't forget " \ ". Use these paths, they are expected later in the modelling chain.

!! DON'T HIT 'RUN' YET !!

<u>Check and edit the Segmentation</u>

The segmented Data have to be checked for er rors. Thus you need to edit the brain_m ask and the head_mask manually, step by step. First, you might want to edit the brain-mask. You open the editing GUI by clicking on the accord ing 'Pencil-Button' as indicated by the red arrow in Fig22. After editing the brain mask you should check the head-m ask, you open the according by clicking on the 'pencil-button' indicated by a blue arrow in Fig22.

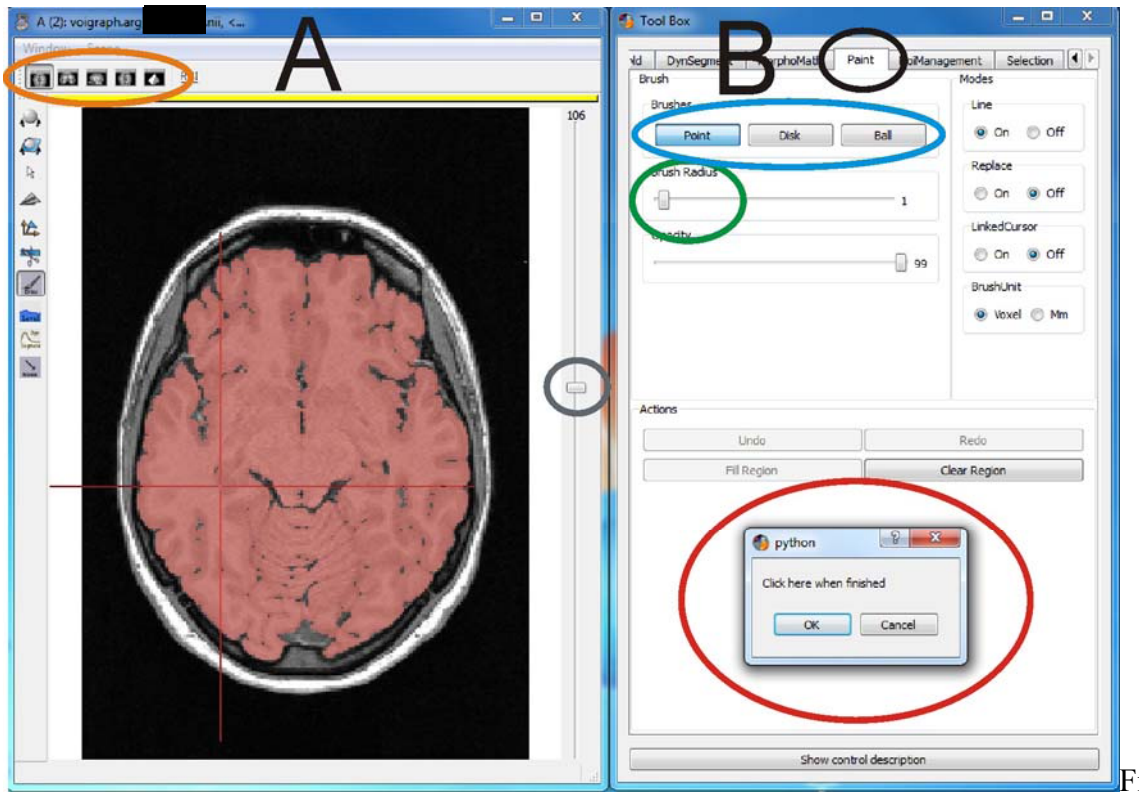

Fig23

What you are looking for:

Brain-mask: Delete the Medulla Oblongata and Spinal Cord
Check if there are bone structures identified / highlighted as brain (delete)
Eventually delete the lower part of the Pons
Eventually you might have to delete the lower part of the Cerebellum

Head-mask: Check if the head structure shows gaps that reach from the outside to the brain.
Don't worry about holes that have highlighted structure all around.
Check if the outer rim of the head mask is somewhere inside the brain (fill up)

The editing process is described for the brain-mask. The head-mask is edited the same way.

Careful:

After you've pushed the 'pencil-button', wait a little and several windows open. This includes the 'Anatomist 2012-GUI', the visual repres entation (Subfigure A in Fig23), a 'T ool-Box'-GUI (Subfigure B in Fig23) and m ost importantly a small Ok/Cancel Message-box it usually is covered by the other windows (example brought to the front: red circle in Fig23).

!!!!!!!

Don't forget this message box: only clicking 'OK' will save the results!

!!!!!!!

How to edit:
- Select the 'Paint' category as shown by the black circle in Fig23 Subfigure B.
- Choose a brush type in the blue circle (Fig23 Subfigure B).
    > 1D-brush: a Point. For very small errors only
    > 2D-Brush: a Disk. For editing in *one* slice only
    > 3D-Brush: a Ball. For simultaneous editing in more slices

- Change the size of the 2D and 3D brush via the green circle (Fig23 Subfigure B).
- Select the view via the orange circle (Figure 23 Subfigure A)
- Choose the slices by moving the slider (Grey circle, Figure 23 SubfigureA)
- Think 3D
- Add something to the highlighted area by clicking at the desired location.
- Delete from the highlighted area by 'Strg-Clicking'
- Click Undo if something went wrong.
- When you think that you are finished: Hit 'OK' in the mentioned Ok/Cancel Message-box!

!!!!!!!
Running the segmentation again will overwrite the edited version! Be careful!
!!!!!!!

Running the Conductivity Modeller

After clicking the OK-button as descri bed above you have returned to the 'Conductivity_BEM_modeler'-GUI (Fig22). Now, check again the filenam es you entered before. Hit 'Run' and wait until the process has finished. When the process has finished check if the desired files have been created (Exp lorer…). 6 files should have been created, 3 '.mesh'-files and 3 '.mesh.minf'-files. Save the process.

Revenge of SPM8 (Normalizing the MRI)

Normalising:

Now we have to norm alize the MRI with SP8. Start Ma tlab, and type SPM in the Matlab command window. The GUI seen in Fig24 opens. Click on 'fMRI' (black circle in Fig24)

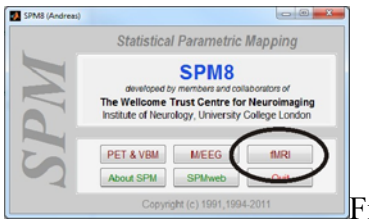

Fig24

From the fMRI-GUI (Fig25) chose the 'normalise (Est&Wri)' option from the dropdown-box (see black circle in Fig25).

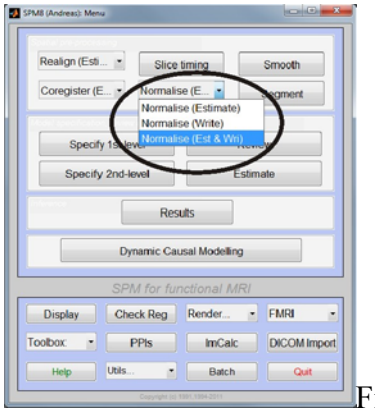

Fig25

The 'Batch-Editor-GUI' (see F ig26) opens, double- click on "Data" (Yello w circle in Figure 26). You are going to use the three options hi ghlighted black, red and blue in Figure 26 ("Source image", "Im age to write" and "Tem plate Im age"). Beside th e "Batch-Editor-GUI" two m ore windows open, they will become relevant later on: see Figure 30 for the SPM(name): Graphics.

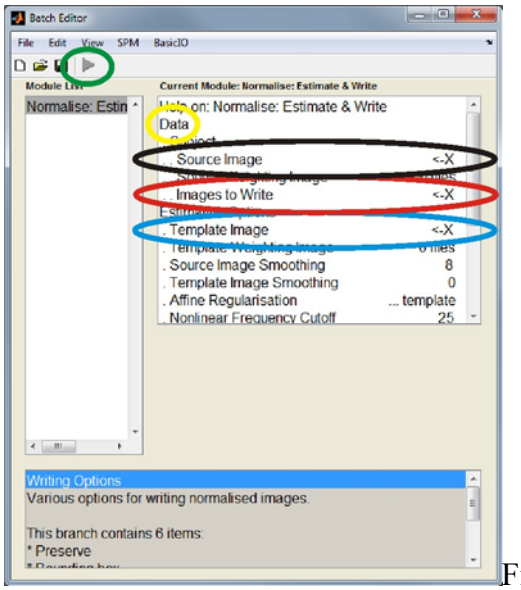

Fig26

Double-Click on the option highlighted black in Fig 26 ("Source image") and the 'Source-Image-GUI opens (Fig27). Navigate your way to where the desired MRI-file is, by clicking in the box highlighted green in Fig 27 ("..." brings you up one step in the folder hierarchy). Once you have located the file (suitable files are listed in the box highlighted yellow in Fig27) click on it. Its name will now be shown in the box at the bottom of the GUI (red-ish in Fig27). Click on 'Done' (black circle in Fig27) and you will return to the 'Batch-Editor-GUI'.

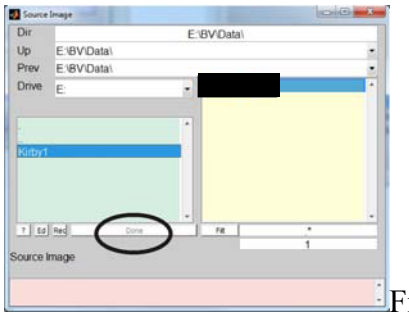

Fig27

Now double-click on the option marked by the red circle in Fig 26 "Images to Write". The "Images to Write-GUI" opens (Fig28). Navigate to the file you specified in the step before (the box marked green in Fig28). Now comes the scary part: select the same image-file as you did in the previous step (yellow area) and don't worry because a new file with a similar name (just a "w" is added at the beginning of the filename) is created although the name will appear unchanged in the box marked red in Fig28. Click 'Done' (black circle Fig28) and you will return to the 'Batch-Editor-GUI'.

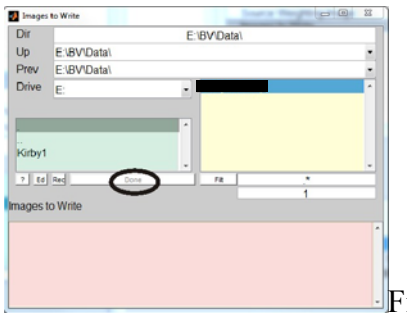

Fig28

Double-click on "Template Image", blue circle in Figure 26. The "Template-Image-GUI" (Figure29) will open. Here you select the template you normalize your MRI to. Do this by clicking on "T1.nii,1" (highlighted yellow in Fig29). Its name should appear in the red-ish box of Fig29. Click "Done" (black circle Fig29) and you will return to the 'Batch-Editor-GUI'.

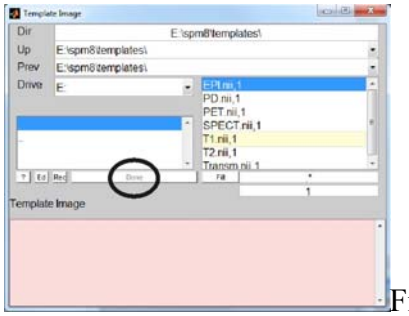

Fig29

In the ‘Batch-Editor-GUI’ click the green triangle below the menu. This button is highlighted in Figure 26 by the green circle.

Checking the normalisation:

SPM will announce in Matlab Command-window when it has finished the normalization. Also the “SPM8 (name): Graphics”-GUI, which was mentioned earlier, now contains graphical output. The relevant parts are shown in Figure 30. The left hand side in Figure 30 shows the T1-weigthed template, the right hand side shows the normalised MRI-scan. The fit has to be checked visually.

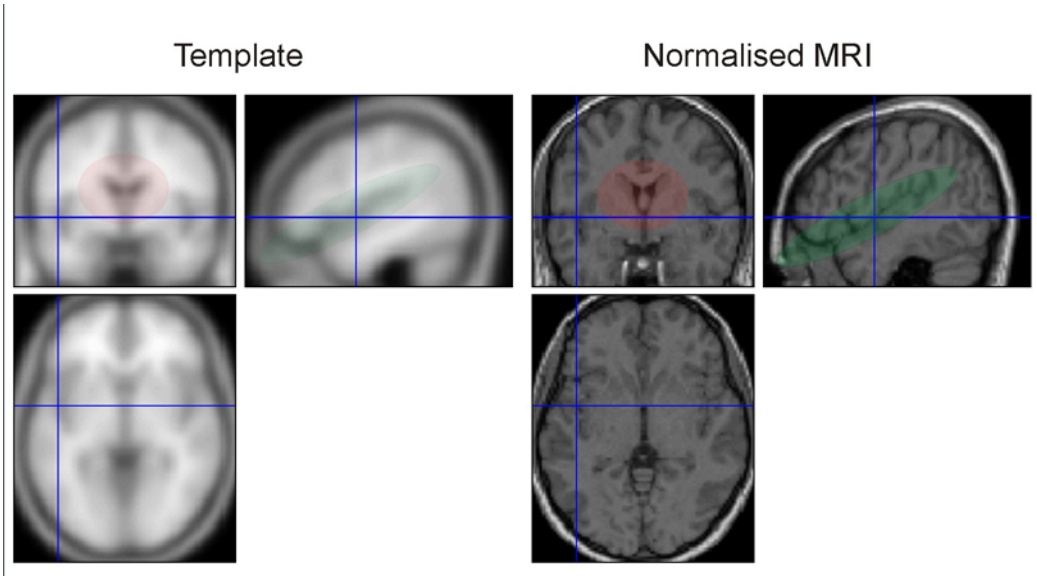

Fig30 SPM(name) Graphics

The fit is checked by e.g. two parameters:

1) Lateral Sulcus (green areas in Figure 30)
2) Ventricles (red areas in Figure 30)

To check the similarity, simply drag the blue crosshair in either one of the (interactive) images. The other crosshairs will assume the equivalent positioning. If the matching ‘looks good’ you can close the SPM8 by clicking on the “Quit” button in the fMRI-GUI (Fig25).

A NutMEG hope (creating the BEM)

Preparing NutMEG

Now you should switch to MAC, since the BEM-creation script works so far only there. (Note on the Win version: if you get the error "0xc000007b", then you are using a 32-Bit "*.dll" for a 64-Bit application..)

You need to build a structure with necessary information for the remaining BEM-steps. Simplest way is import functional data as well as anatomical data of the subject in to NutMEG. At the MatLab-command Window type "nm". If the path is set correctly NutMEG starts. Wait a few seconds until it is done initialising. You should see the NutMEG main-GUI as depicted in Figure 31 and a modified SPM8 GUI titled "SPM8 (name): Graphics" (partially in Figure 33).

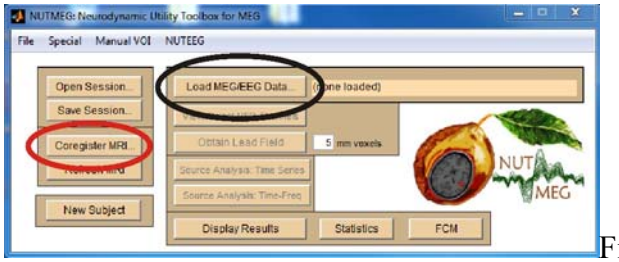

Fig31

The necessary steps are as follows:
- Import functional data via the "Load MEG/EEG Data…" button in the NutMEEG-GUI (black circle Figure 31). A new GUI opens which lets you select the filetype/importtype. Choose the appropriate (?import CTF?) type, a select-file- GUI appears. Choose your file and click "open"
- Start the MRI import by clicking on the "Coregister MRI.."-Button in the NutMEG main GUI. (red circle Figure 31). The "Coregistration Tool"-GUI opens (Figure 32). Open a MRI via the "Select MRI"-button (black circle in Figure 32). After you've successfully imported the MRI, it should be displayed in NutMEG "SPM8(name):graphics"-GUI. Now open the normalised MRI via the "Select Normed MRI"-button (red circle Figure 32). This file was created in a previous step via SPM. The name is the filename of the original MRI plus a "w" at the beginning.
- Don't close the "Coregistration Tool"-GUI yet.

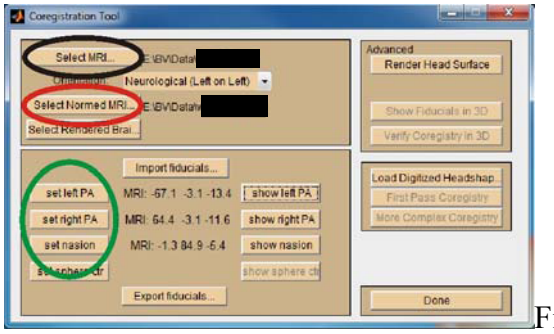

Fig 32

In Figure 32 the fiducials are already set. Most likely you need to set them yourself…which is easy. You need to set left PA right PA and Nasion. The sphere centre is not relevant for BEMs.

- Get th e coordinates for the e.g. “left PA” by position ing the crossh airs in the “SPM8(name):graphics”-GUI (Figure 33) to the anatomical positions.
- Click “se t lef t PA” in the Coregistr ation Tool”-GUI (green circle in Figure 32). The coordinates appear.
- Repeat this for the remaining fiducials.
- Feel free to export the coordinates
- Click “Done” in the “Coregistration Tool”-GUI.
- Don’t close MatLab or NutMEG

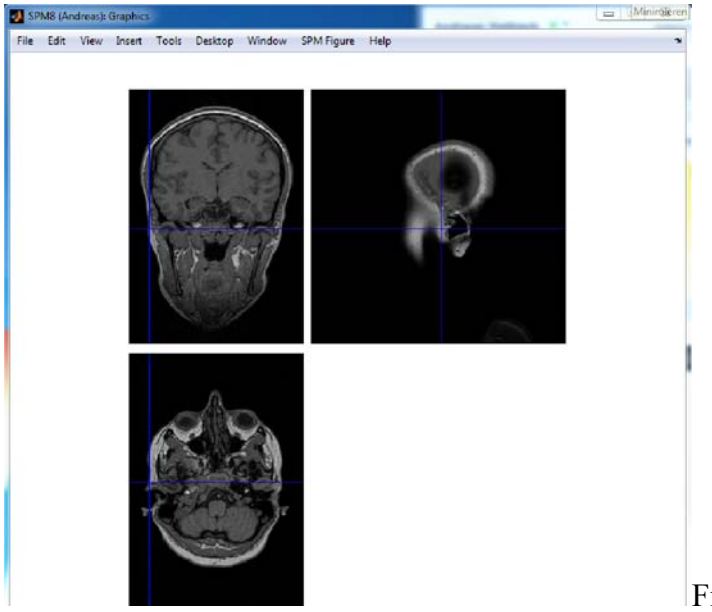

Fig33

About fiducials that you are looking for:

- PA: is the pre auricular point, m eaning it li es in front of the ear betw een the ear’s opening and the cheek (of course on the left and right side of the head) shown in the green box in Figure 34).
- Nasion: Point where som e bones at the upper end of the node intersect (red box in Figure 34).

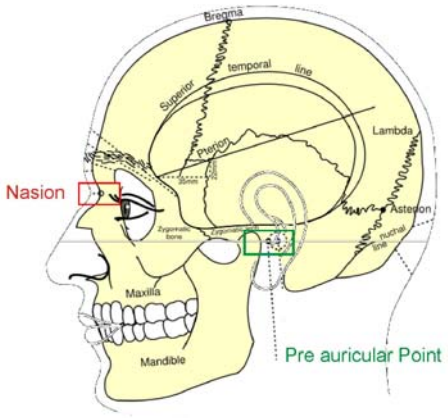

Fig34

The actual BEM calculation:

First: depending on the computer: this might take a while. Don't close MatLab or NutMEG for the duration of the operation.

Define the following variables:
Nuts: The GLOBAL nutMEEG structure
Subjpath: The base path (BrainVisa Database path ;-)
Subjname: Name of the Subject as given in the MRI-file(e.g:"surname/name.nii")
BVprotocol: Actually the folder in Subjpath, which was created by BrainVISA

Then type in the MatLab-Command window:

[BEMpath, Subjname] = nut_openMEEG_chain(nuts,Subjpath,Subjname,BVprotocol)

"Everything" (BEM) will be imported into the NutMEG structure. In the NutMEG main GUI the buttons "Source Analysis: time series" and "Source Analysis: Time-Freq" are enabled and ready to use. You might want to save the session, this way you don't need to run the importing/creation chain again.

<u>The following folder structure is assumed:</u>

"Subjpath" is the basepath (identical to the BrainVISA Database path) and includes:

Subjpath/openMEEG_BEM → that's where all output files go. Will be created!
Subjpath/BVprotocol → BVprotocolname is name you gave in BrainVISA and thus also a folder
Subjpath/BVprotocol/t1mri/default_acquisition/default_analysis/segmentation/mesh/
→ that's where all the meshes for brain skull head are put by the BEM_conductivity modeler in BrainVISA (or should have been put..)