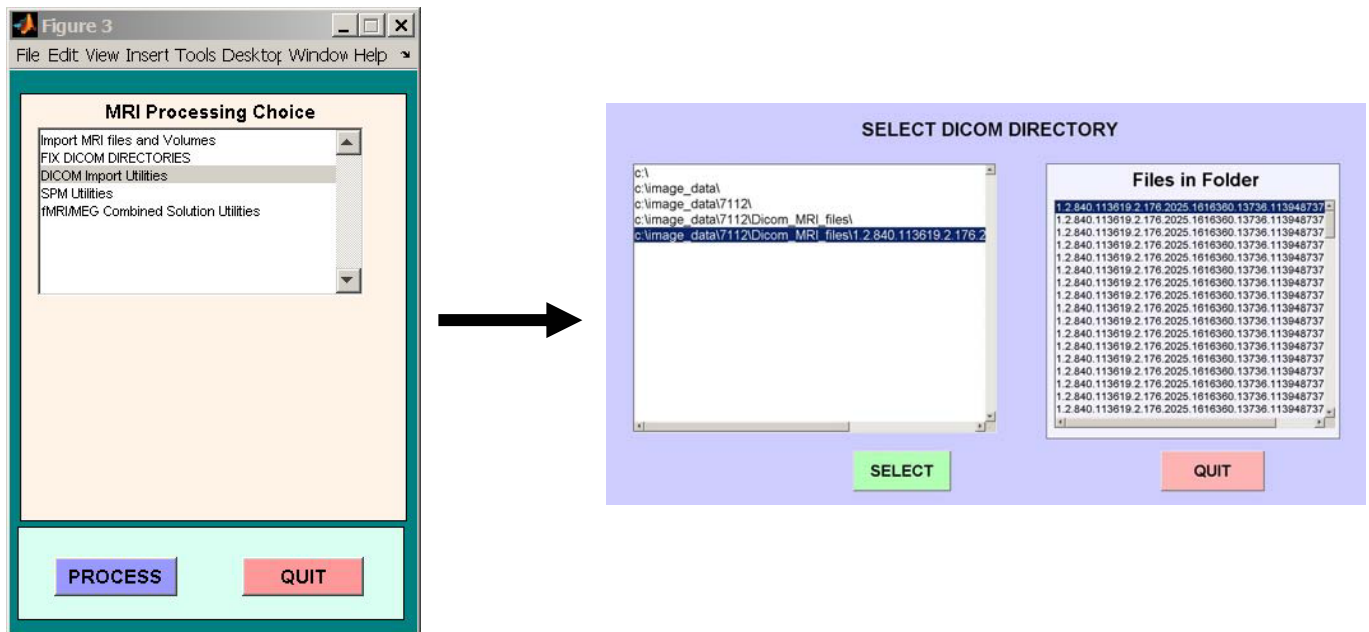


DICOM IMPORT

On the Main MEG_TOOLS MENU press  this will bring up the menu below.

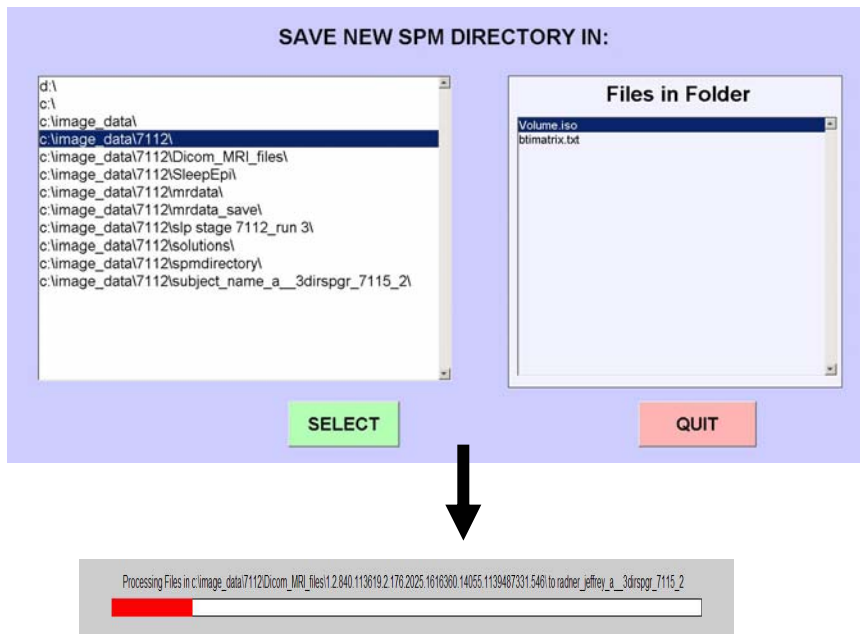
Chose the Dicom Import Utilities



Select the directory that contains the DICOM files. If you choose a directory that contains sub-directories, each containing a different MRI study, then the program will allow you the option to import all of them. However, each MRI study will be imported into a separate directory in analyze format and a separate MEG coregistration file. IF you have one study or multiple studies that are mixed in one directory or across multiple directories, choose the FIX DICOM Utilities option. This will sort all studies from the import directories and put each separate MRI study in a separate directory as DICOM FILES. Then you can use the DICOM Import Utilities to import one or more of the these studies in as analyze formatted volume files. (NOTE: The fMRI imaging package, SPM, uses analyze format directly and can use the output of this import program. Therefore, DICOM Import Utilities can be used to preprocess fMRI data for SPM or other programs that support or require analyze format.). After pressing the SELECT button above, the program will scan the directory and all subdirectories for all DICOM files (It opens the file and checks for the DICOM Identifier in the header structure).

(IF THE PROGRAM CRASHES WHEN ATTEMPTING TO IMPORT DICOM FILES OR OTHERWISE DOES NOT FUNCTION. CONTACT John Moran (moran@neursis.neuro.hfh.edu). IF POSSIBLE ATTACH ONE OF THE DICOM FILES.

You will then be presented with a menu that allows you to select where you will put the directories that contain the imported analyze format MRI files. Usually, it is good to put these in the subject/patient main directory (<drive:\image_data\patient_directory>). See menu below.

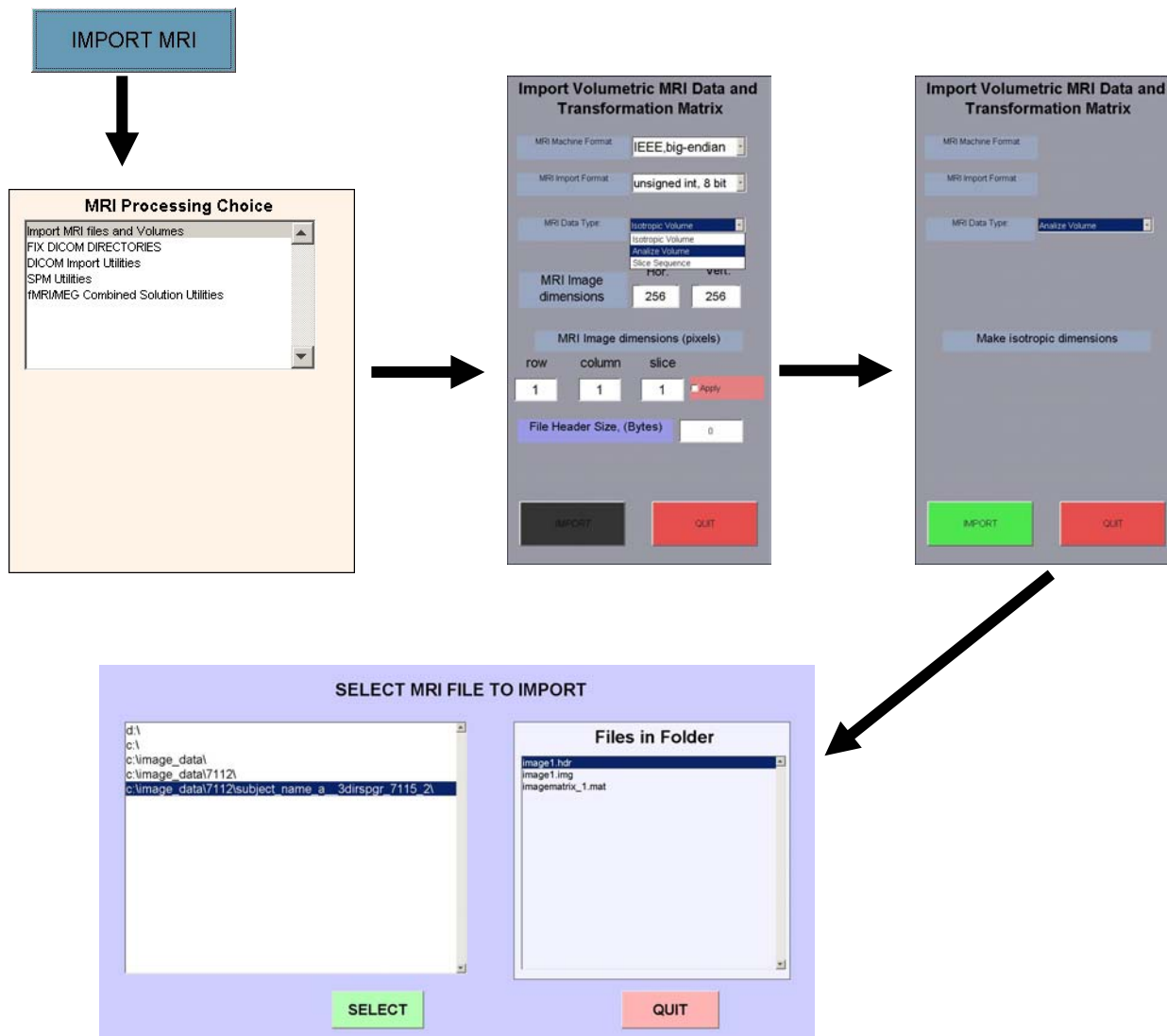


After pushing the <SELECT> button, the import will begin. The displayed message will inform you which DICOM directory is being IMPORTED and what the SPM directory name is assigned to the output. You can use Microsoft Windows Explorer to navigate to these SPM directories after the import is complete and rename if desired.

At this point the MRI images from the DICOM files will be imported into an analyze formatted volume file (image1.img) and an analyze format header file (image1.hdr) and a preliminary MEG coregistration matrix (imagematrix_1.mat) that contains the orientation of the head in MRI machine coordinates, such that MEG_Tools will know up from down and left from right. If fMRI data are imported, then each set of scan through the head will have a separate set of 3 files such as (image1.img, image1.hdr, imagematrix_1.mat, ..., image10.img, image10.hdr, imagematrix_10.mat). The final coregistration will be performed when the analyze format file is imported into MEG_Tools. Therefore, the next step, is to again go the main MEG_Tools Window and press

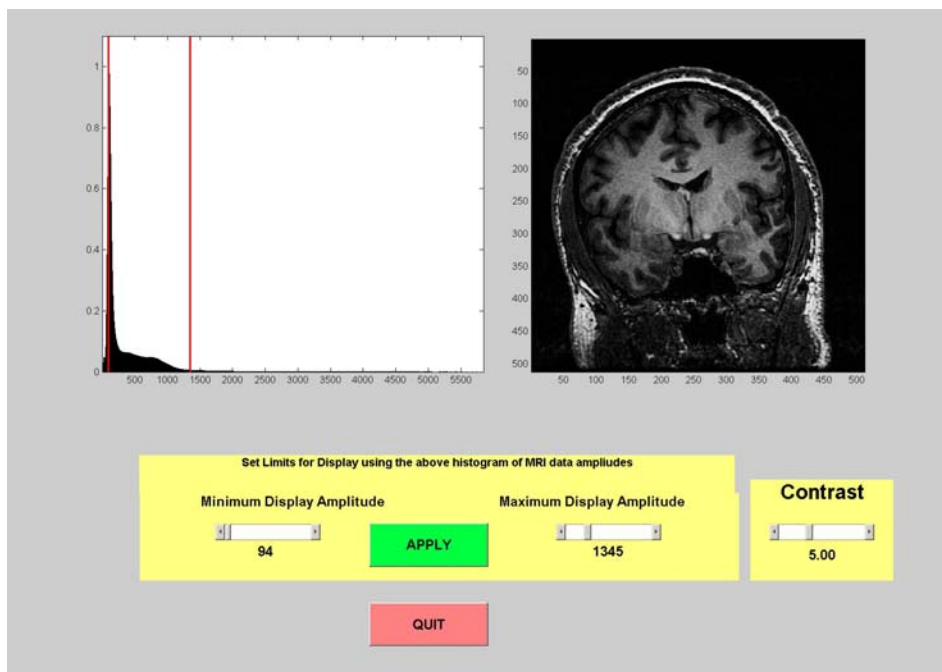
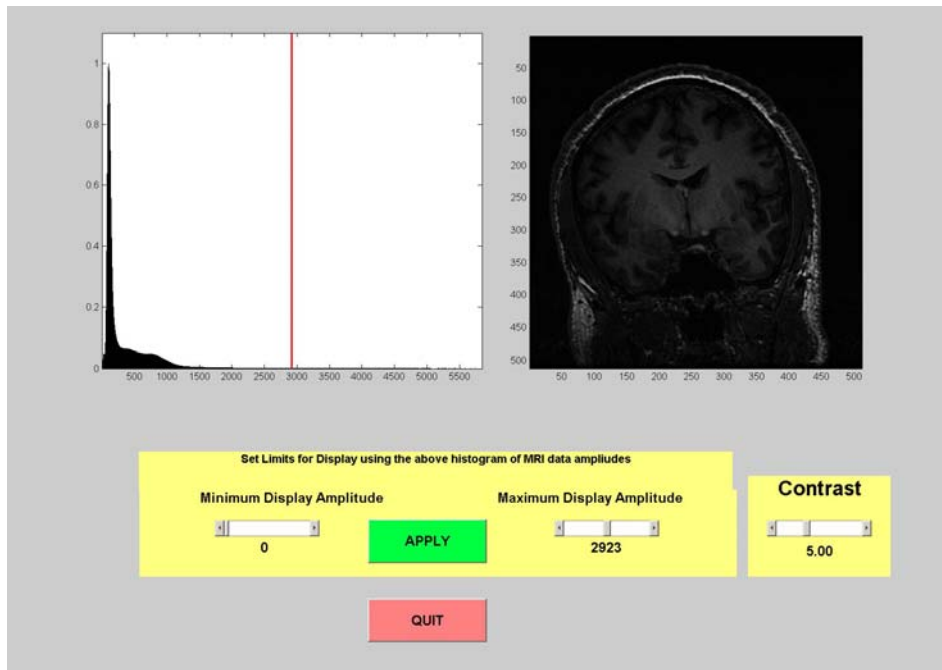


MRI IMPORT (ANALYZE FORMAT FILES)

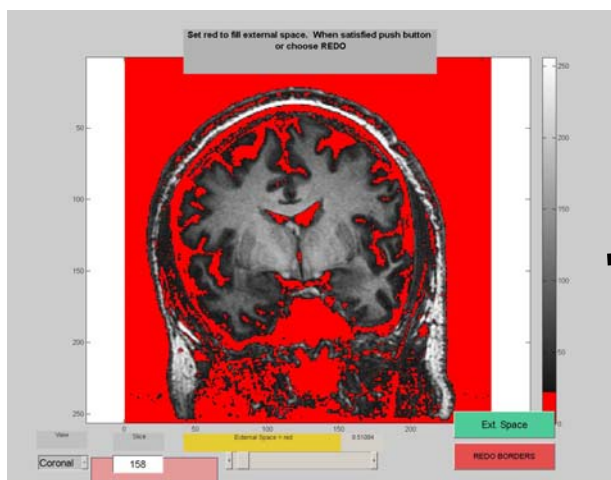
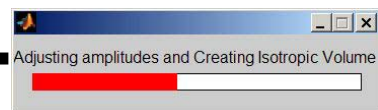
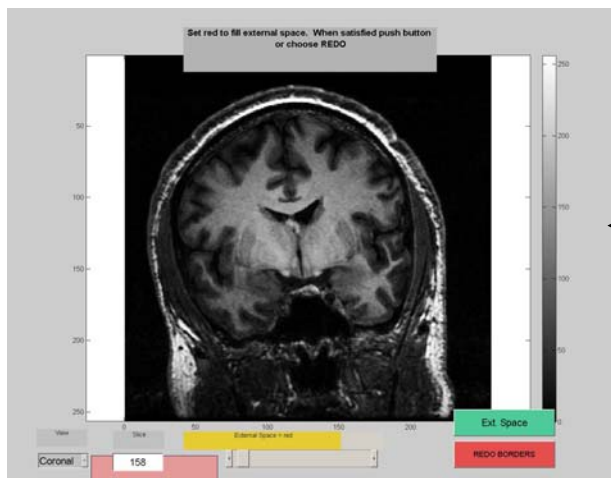


Using <MRI IMPORT> of the MEG_TOOLS main menu will bring up the first import menu above. CHOOSE the <Import MRI files and Volumes> option. On the middle menu above in the MRI data type box choose <analyze volume>. Then press the <IMPORT> button to obtain a MRI import selection window. Navigate to the analyze file to be imported (You can select either of the 2 files (image1.img, or image1.hdr).

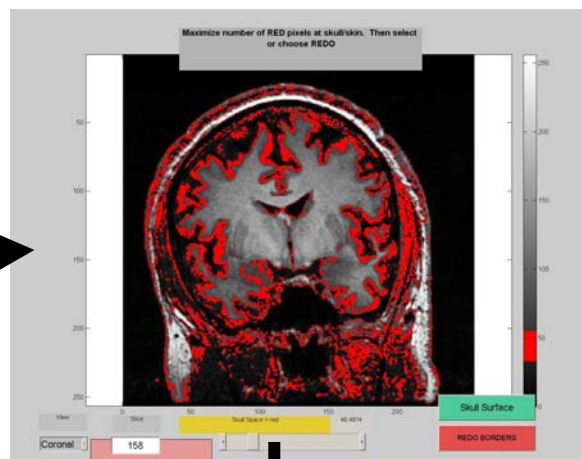
The program will first scan the slices in image1.img to find the range of amplitudes and the statistical distribution of amplitudes. These amplitudes must be mapped into an 8 bit format used by MEG_TOOLS. Therefore, the next menu, displays the distribution of amplitudes and shows you a picture that demonstrates how the mapped amplitudes will appear in MEG_TOOLS imaging results.



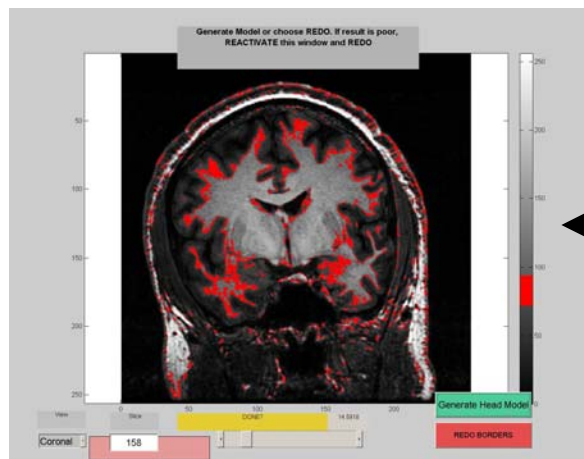
Usually set the MINIMUM DISPLAY AMPLITUDE such that the red line marker is at the corresponds to the peak of exterior pixel amplitudes and the MAXIMUM DISPLAY AMPLITUDE is at the bottom of the taper of the distribution taper. Contrast can also be adjusted. (Your chance to be artist). When you are happy with the way the MRI slice appears press the <APPLY> button. Next you will identify (approximately) 4 tissue types.



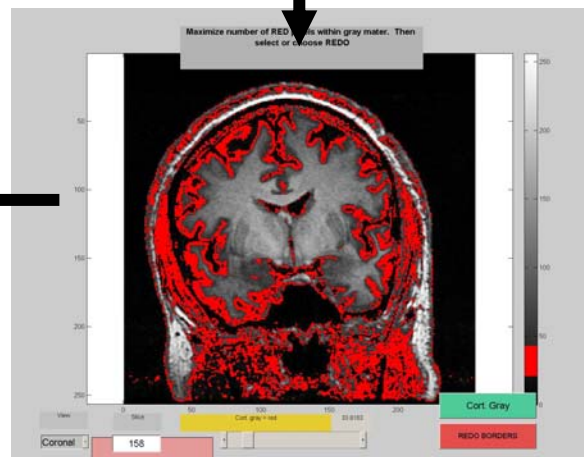
(1)



(2)



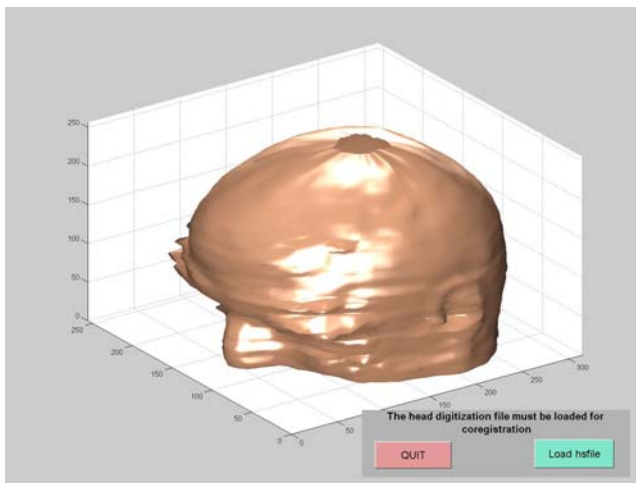
(4)



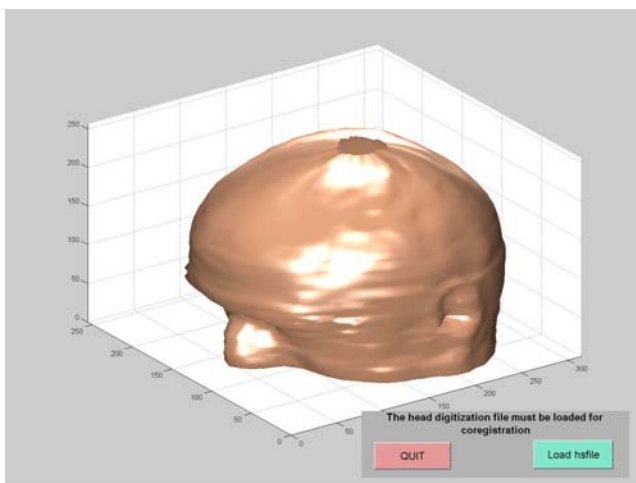
(3)

Adjust the slider control at the bottom to identify (1) Exterior Space; (2) Skull Surface, this is the most difficult one because MRI does not capture bone well. Get as many red pixels along edge as possible. It is likely that red pixels will be somewhat sparse. Do not be concerned if other tissue types are also selected; (3) Gray matter; (4) White matter. Try to highlight the white matter at the border with gray matter.

Press the adjust the Edge detection sensitivity lower if MRI is very good quality high resolution with little artifact in exterior space. Alternatively, set the Edge sensitivity higher if the MRI is poor and has significant artifact in the external space. The next selection is to generate the MRI 3D head model. If the results are poor or can be improved, press <QUIT> on the generated figure window (SEE figure with distortion due to external artifact below). Reset the edge sensitivity up or down as necessary and press the <Generate Head model> button again.



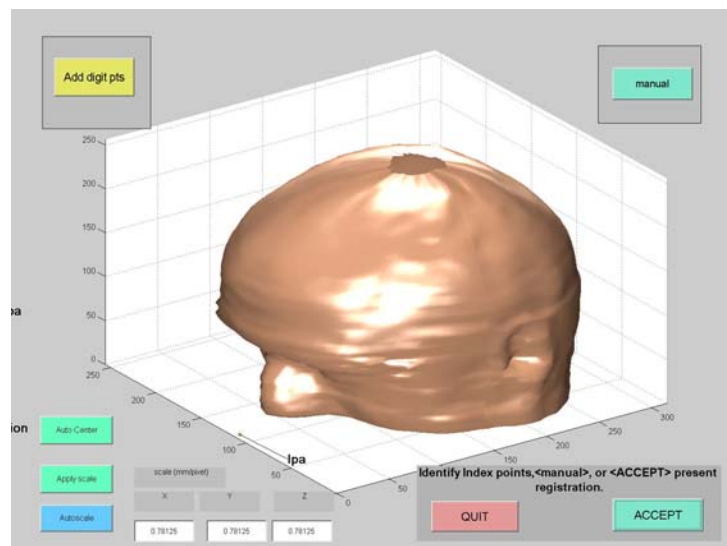
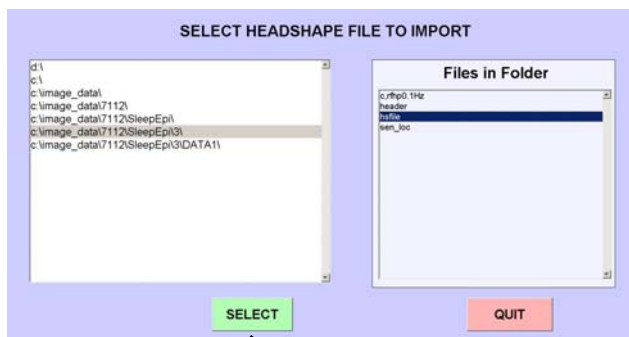
Head model with first EDGE sensitivity setting



Good result with second EDGE sensitivity setting

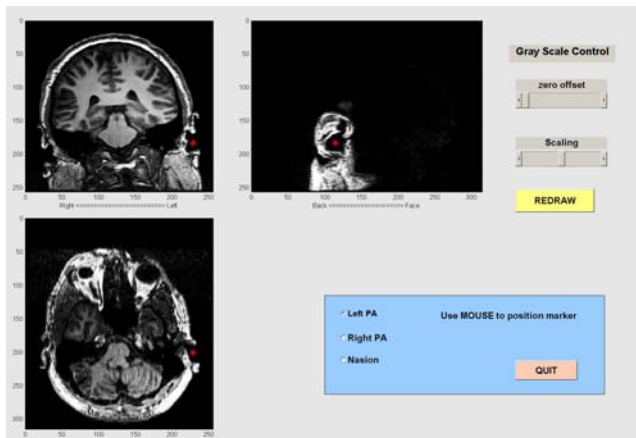
Now the “hsfile” must be loaded so that you can coregister the MRI with the corresponding points that were gathered during head digitization of the MEG study. Press the <Load hsfile> button. The “hsfile” is one of the three files generated by the “Get_MEG_Tools_info” utility that was installed in the 4DNeuroImaging Software protocols directory.

A hsfile file selection menu will appear. Navigate to the directory containing the hsfile file of the subject/patient. Highlight and select the hsfile file. This will display in the window the present coordinated of the LPA, RPA, and NASION. They may be very far from the proper location, as in the figure below. If they are close to correct press the <AUTO CENTER > button. Then, press the <DISPLAY DIGIT POINTS> button. The X,Y,Z scaling should not be changed if the original source of the MRI data was DICOM and the MRI data corresponds to this subject. If using an MRI from one person for MEG data of another subject, then once alignment is close use the <AUTO SCALE> to alter the X,Y,Z coregistration scaling to such that the digit points match the skull surface.

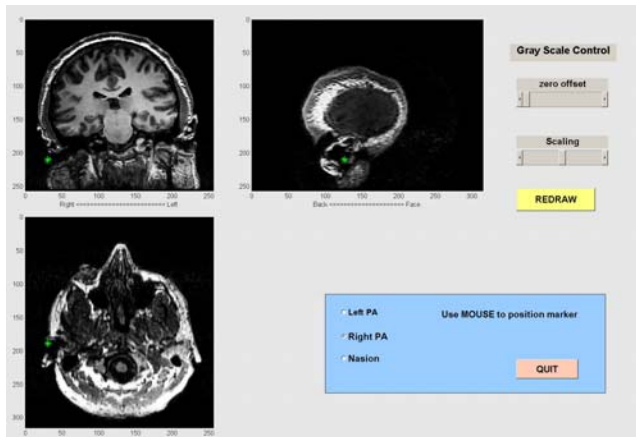


If they are very far away, (such as above) press the <MANUAL> registration button. This will display axial, coronal, and sagittal slices through the head and a RED STAR when LPA is toggled on, GREEN STAR when RPA is toggled on, BLUE STAR when NASION is toggled on. The location of the star is changed by clicking on an MRI VIEW in an appropriate place (or dragging the star by holding down the left mouse button while dragging). Once you have navigated the star to the optimum location, toggle to the next. (THERE IS NO SAVE

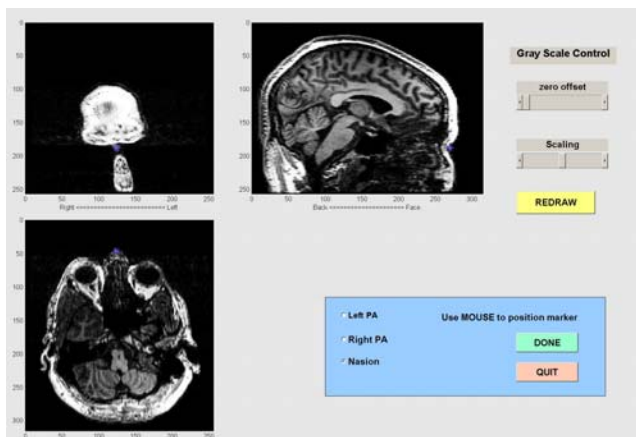
LOCATION BUTTON. The last location of the RED STAR will be the recorded location of the LPA, etc.)



LPA is marked with RED STAR
(toggle to RPA without altering location)



RPA is marked with GREEN STAR
(toggle to NASION without altering location)

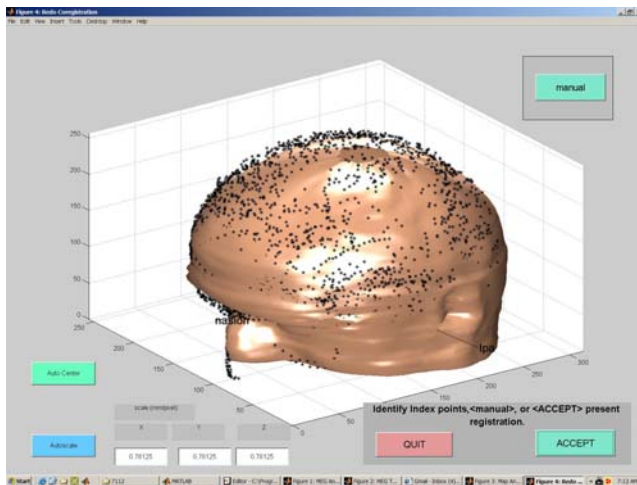


NASION is marked with BLUE STAR

All 3 sites are marked and <DONE> appears.
They can be identified in any order.

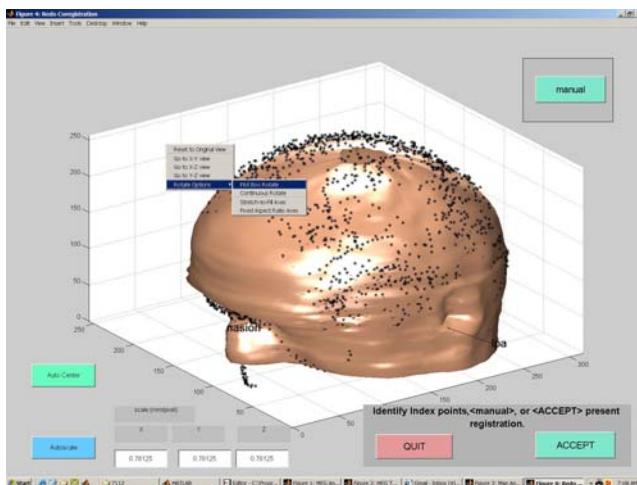
Press the <DONE> button to return to the HEAD VIEW. Unfortunately, I have not had time to have the program redisplay the <ADD DIGIT POINTS> button. You can get this button to appear without causing problem by adding a zero to end of one of the manual scaling numbers. Then the ENTER key of your KEYBOARD. After the digit points are added. You can judge if the coregistration points and digit point match the head properly. Use < AUTOCENTER> if some

adjustment remains. Only use AUTOSCALE if: (1) fitting MEG subject A to MRI of subject B or (2) the original MRI orientation matrix came from STA_R, such that scale factor is missing. MRI data from DICOM to ANALYZE will have the correct X,Y,Z scaling as shown in the manual scale input windows.

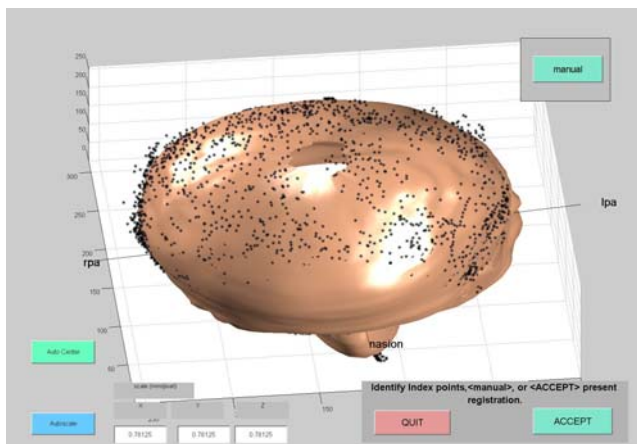


Fit of data after manual scaling

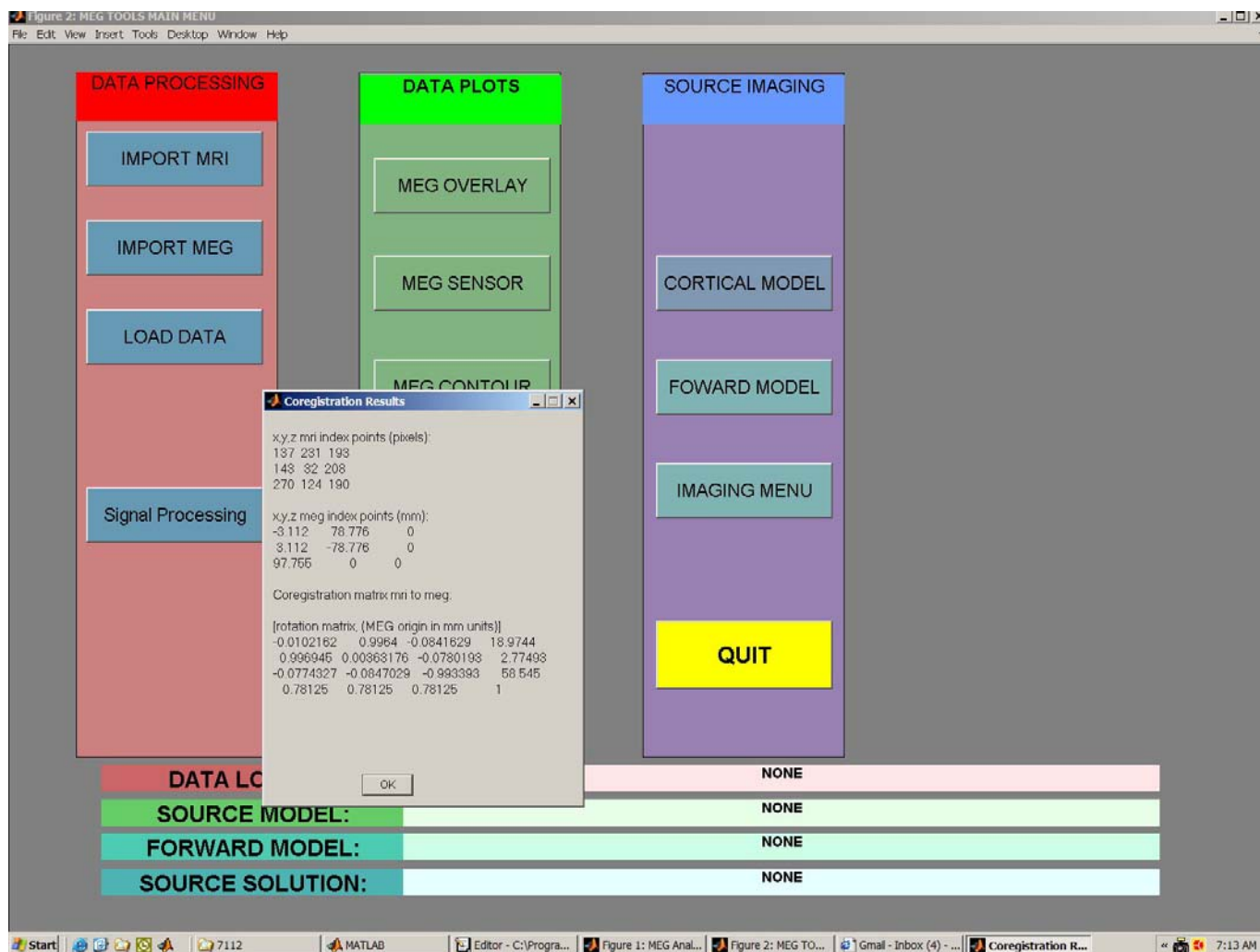
Using the MATLAB toolbar **TOOLS** → **Rotate 3D**, you can rotate the head to check the fit. However, change the default rotation to **PLOT BOX ROTATE** (right click on figure that is to be rotated to get option box) as shown in the figure below.



Right click to get options, choose plot box rotate.



Rotate to check fit MEG head shape points, LPA,RPA, and NASION to MRI head.
If good, press <ACCEPT>



After pressing <ACCEPT> the coregistration matrix results are displayed.

You can now move to the <CORTICAL MODEL> utility to construct a model of the subject/patient brain that matches the gray mater distribution of the MRI data that you have just imported and coregistered with the MEG head coordinates.