

FreeSurfer Manual

FreeSurfer is a set of semi-automated tools for reconstruction of the brain's cortical surface and overlay of functional data onto the reconstructed surface.

csurf is a graphical interface to those reconstruction and functional overlay tools.

The purpose of this tutorial is to provide the user with an in-depth guide to using the csurf tools

The general steps in the reconstruction process are:

- 1) Conversion of the MRI data into 256 coronal slices with 256 x 256 in-plane voxels (i.e. 1 mm x 1 mm x 1 mm voxels)
- 2) Intensity normalization of the MRI volume to remove variations in intensity due to magnetic susceptibility artifacts and RF-field inhomogeneities
- 3) Removal of extrameningeal tissues.
- 4) Segmentation of white matter with minimal manual editing to remove any topological defects
- 5) Tessellation, smoothing and inflation for each cortical hemisphere
- 6) Cutting of the cortical surface
- 7) Flattening of the cortical surface
- 8) Morphing of the cortical surface into a sphere

A more technical description of the reconstruction process can be found in Dale, Fischl and Sereno. Cortical Surface-Based Analysis: I. Segmentation and Surface Reconstruction. *NeuroImage* (9): pp. 179-194. 1999. A more technical description of the cortical surface inflation, flattening, and surface-based coordinate system can be found in Fischl, Sereno, and Dale. Cortical Surface-Based Analysis: II. Inflation, Flattening, and a Surface-Based Coordinate System. *NeuroImage* (9): pp. 195-207. 1999.

This manual can be found on the Web at:

<http://www.nmr.mgh.harvard.edu/freesurfer>

<http://www.cortechs.net/>

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Installation

FreeSurfer (Version 0.8) is being distributed with executables for both Linux/Intel and SGI/Irix. This is a beta release.

To install FreeSurfer

- 1) `cp -rp <CD-ROM drive location> <destination directory>`
- 2) `cd <destination directory>`
- 3) edit `FreeSurferDefs.csh` and change the following line
 `setenv CSURF_DIR XXXXXXXX # CHANGE THIS DEFINITION`
CSURF_DIR should be defined as the directory which contains the installation (this is usually the FS_DIST directory). It should be possible to run the installation as a demo directly from the CD-ROM.
- 4) Make sure that you are running `csh` or `tcsh`, and then source the `FreeSurferDefs.csh` file.
- 5) Type `csurf` at the prompt.

Note: you will need a license file to run FreeSurfer. Register at **www.cortechs.net** to receive the license file.

MRI Parameters

Structural (or anatomical) images from an MRI scanner are required for the reconstruction. The reconstruction process creates surfaces (ex: inflated, spherical, flattened) of the brain using the volume information obtained from the scanner.

Using the 1.5T General Electric (GE) as an example, three structural sequences are obtained, motion corrected and averaged. The resulting image is used to create the surface. The exact parameters for the GE sequence are:

TR:24	Bandwidth: 10.42
Flip Angle: 30	Slice Thickness: 1.3
# of Scan Locs: 124	FOV: 25

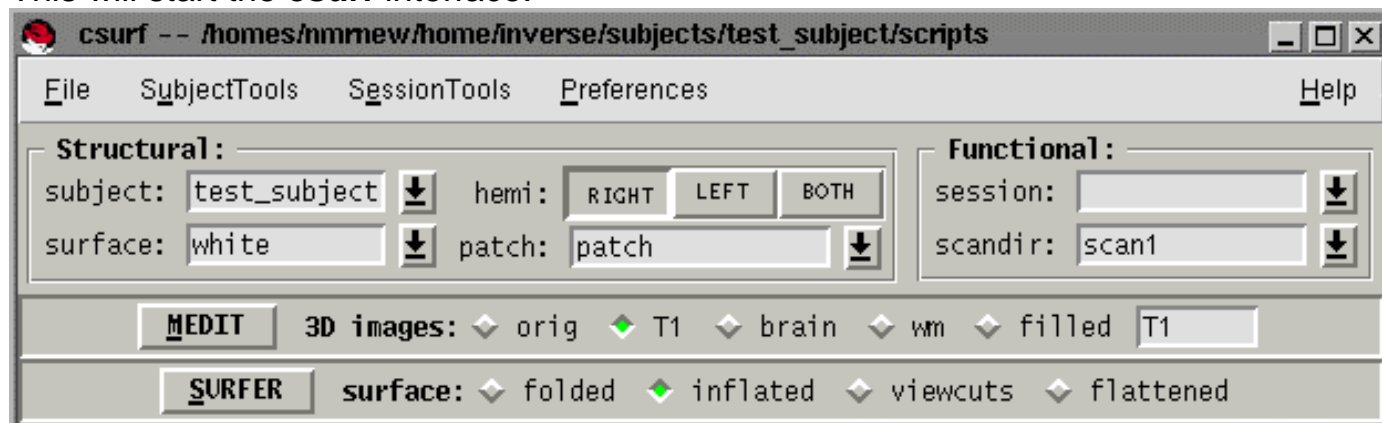
The sequence starts with an axial localizer (16 secs.) and is followed by 3 sagittal SPGR runs (each run, 9:53 minutes).

The first step is to copy the data and then transfer it to the appropriate subdirectory in the subject's directory. But before this, a new directory needs to be created for the subject in **csurf**.

Starting csurf

At the prompt, type:
csurf

This will start the **csurf** interface.

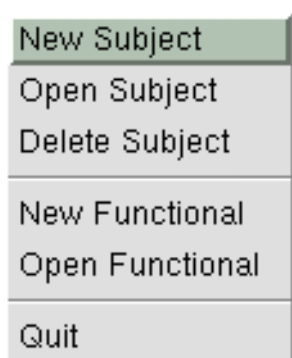


There are four pull down menus: **File**, **SubjectTools**, **SessionTools**, and **Preferences**

Below the pull down menus are two boxes labeled **Structural** and **Functional**.

For the following examples, the subject to be created is named “test_subject” This subject’s data will be used throughout the rest of the tutorial.

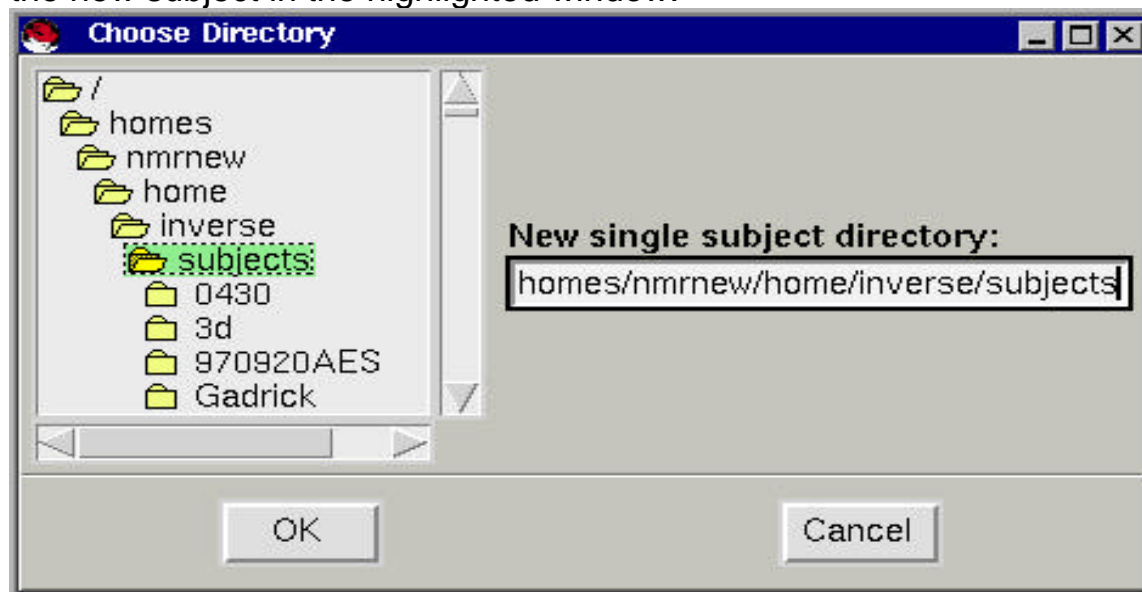
File Menu



The File pull down menu can also be accessed by pressing **Alt-F**.

New Subject

Creates the necessary directories for a subject’s structural data. Specify the name of the new subject in the highlighted window.

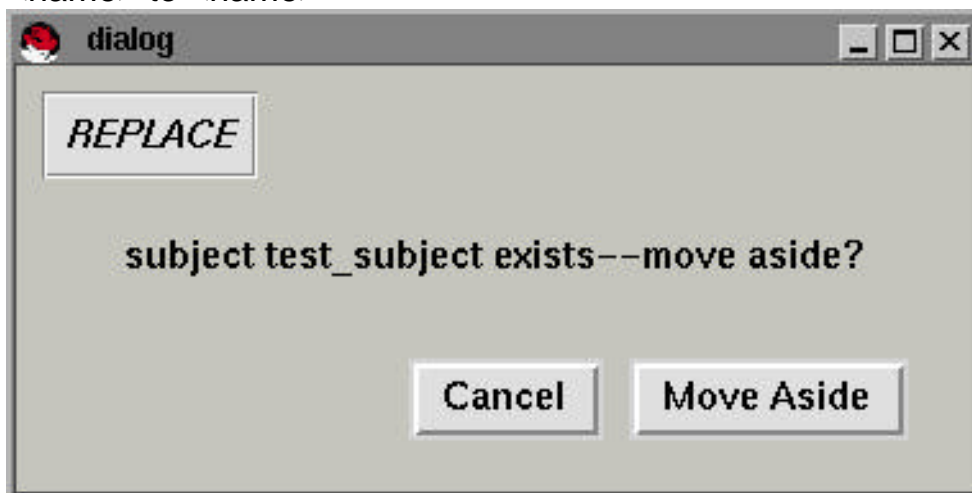


When a new subject is created, the following directories required for the structural data will be made:

```
<name>
  bem
  label
  morph
  mpg
  mri
    T1
    brain
    filled
    orig
    tmp
    transforms
    wm
  rgb
  scripts
  surf
  tiff
  tmp
```

NOTE: Two of the important directories are the **mri** directory, which contains the subject's volume information, and the **surf** directory, which shows the surfaces that have been created for the subject.

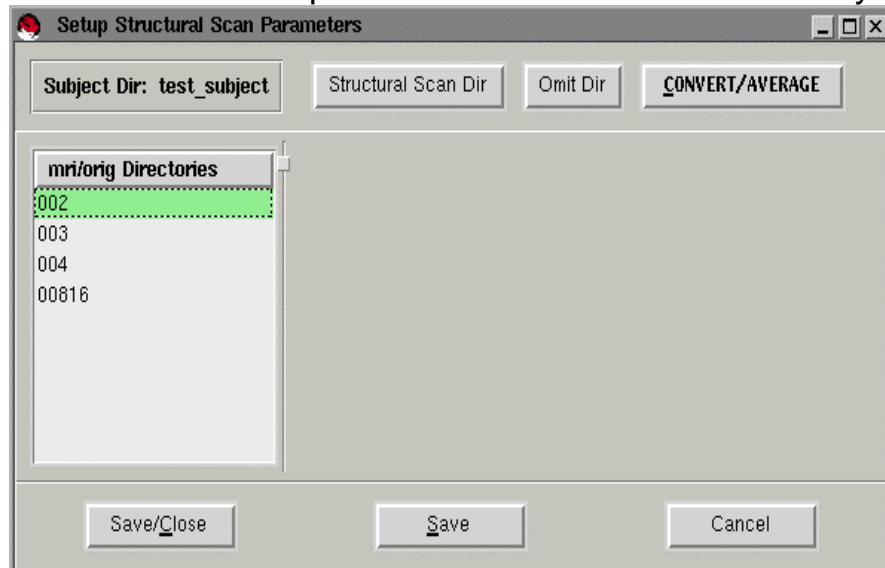
If the subject does exist, you will be asked if you want to move the current subject from <name> to <name>



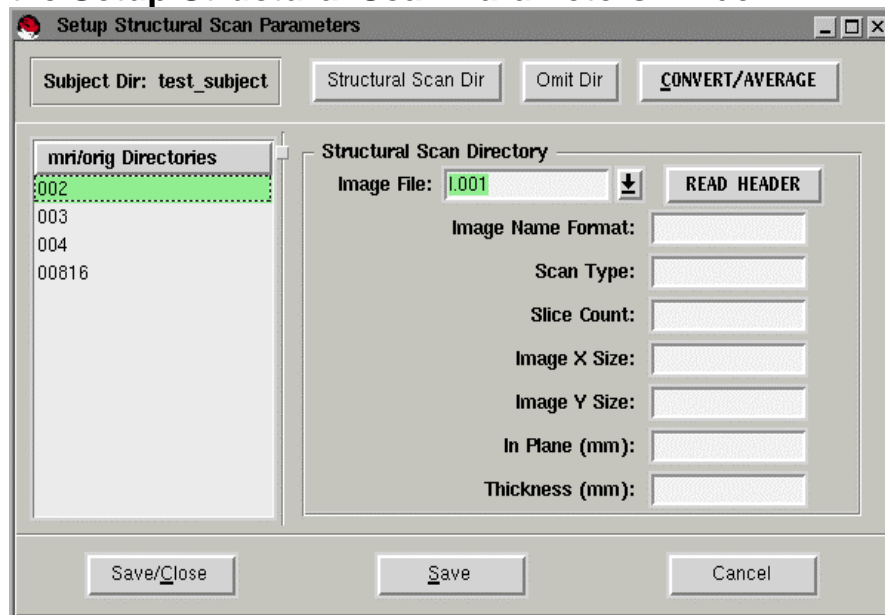
Setup Structural Scan(s)

This step converts (and averages if there are multiple acquisitions) the MRI data into the 256 coronal slices, 256 x 256 voxels in plane with 1 mm³ resolution. Currently supported formats are: SPM/analyze, AFNI, Siemens, and GE.

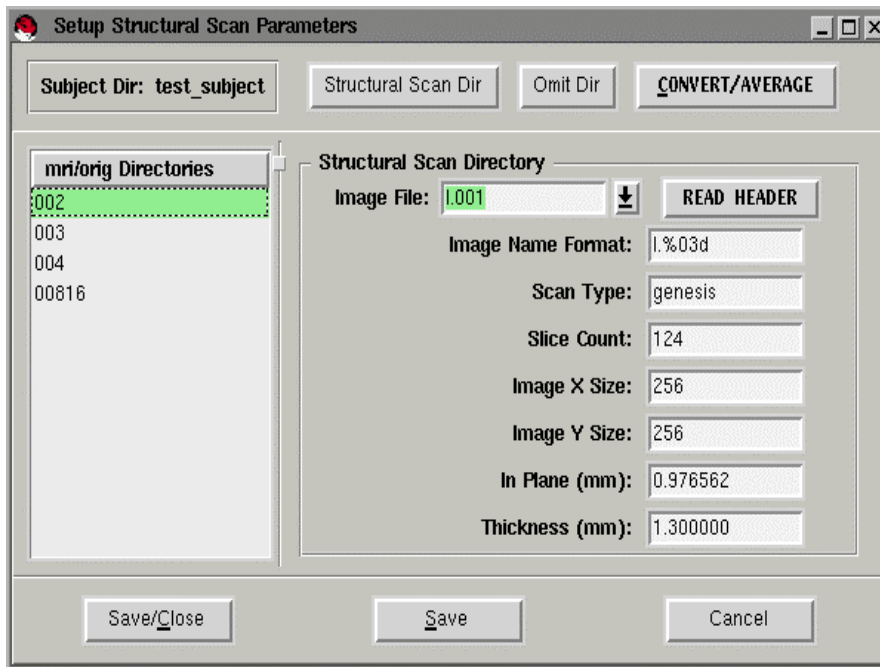
Each structural acquisition must be in its own directory in the **mri/orig** directory.



Select the first structural acquisition and press **Structural Scan Dir**. This will expand the **Setup Structural Scan Parameters** window:



Select the first image file in the **Image File** field and press **READ HEADER** to automatically determine the scan parameters. If there are any errors, manually enter them in the field.



For each structural acquisition, repeat the process of selecting the acquisition on the left window, pressing **Structural Scan Dir**, and then pressing **READ HEADER** .

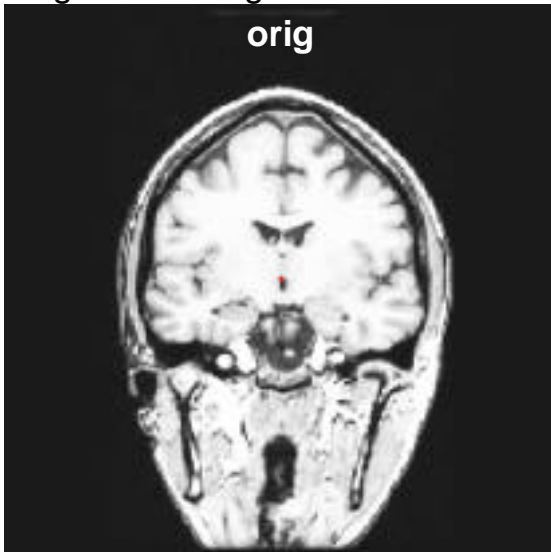
If you want to omit an acquisition that was previously selected, reselect the directory and press **Omit Dir**.

Press **Convert/Average** to average the acquisitions and convert the MRI volume in the 256 coronal slices.

The output files of the setup are:

images: \$SUBJECTS_DIR/\$name/mri/orig/COR-???

Original T1 weighted MRI volume (orig volume)



Motion Correction

If multiple structural scans are acquired, they need to be corrected for motion before reconstruction. The motion correction is done using **AFNI** binaries. The multiple acquisitions are averaged together to generate one image that is free of motion. The **AFNI** utilities are the copyright and work of Robert Cox, PhD at the Medical College of Wisconsin. For more info see <http://varda.biophysics.mcw.edu/~cox/>.

I. Data Conversion

The structural data first needs to be converted into COR format and this is done using a binary called **mri_convert**.

To convert raw MR data into COR files

To convert, first go into the mri/orig directory. This is where the raw MR data should reside. Then, type:

```
mri_convert <nameofstructuralrun>/<firstMRacquisition>
```

Example:

```
mri_convert 002/l.001
```


Repeat this step for all the structural runs that need to be motion corrected and averaged.

II. Motion Correction

Use the register.csh script with the following command line:

```
register.csh dir1 dir2 #dir3
```

dir1 is the base set of COR files

dir2 is the new set. It is rotated to match dir1.

#is the scaling factor that the registration program uses. A value of 1 means no rescaling. 2 scales the images down by a factor of two and is less memory intensive than a factor of 1.

dir3 is where the finished product goes

Repeat this step for all the structural runs that need to be motion corrected.

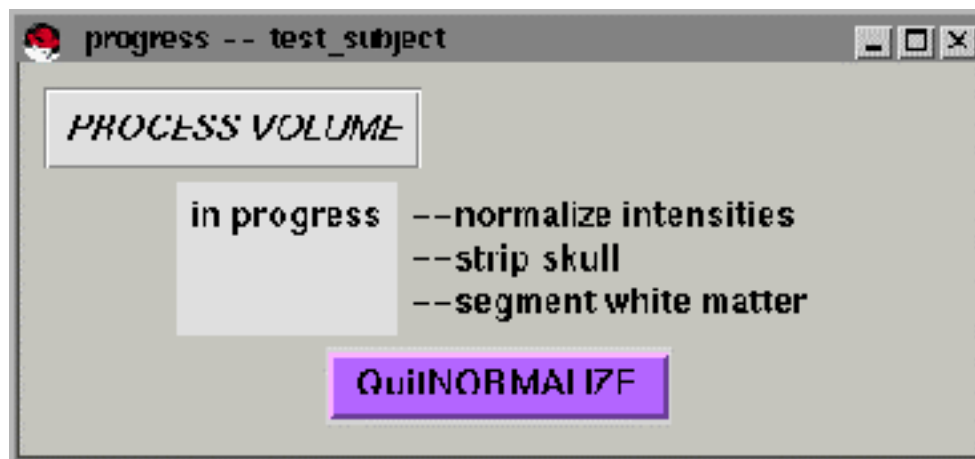
III. Averaging motion corrected images

Use mri_average to average the rotated images with their base to produce the final target. If more than two runs need to be motion corrected, you may need to average the averaged outputs of two individual runs.

Process Volume

Once the data has been motion corrected and averaged, this process should be run. **Process Volume** starts a three-part background process to prepare the 3-D MRI data to make a surface. While the volume is being processed, the csurf interface can still be accessed. The process can be canceled by pressing the **Quit** button that is highlighted in purple. This process should only be run once for each subject and takes approximately 1 hour to run to completion.

Part 1: Normalize Intensities

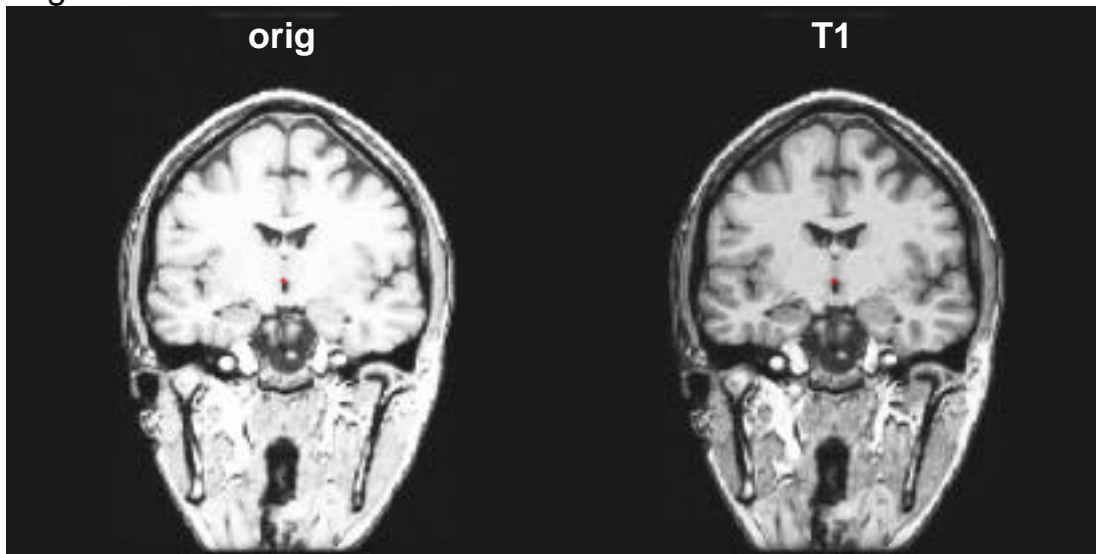


The intensity normalization procedure removes variations in intensity due to magnetic susceptibility artifacts and RF-field inhomogeneities

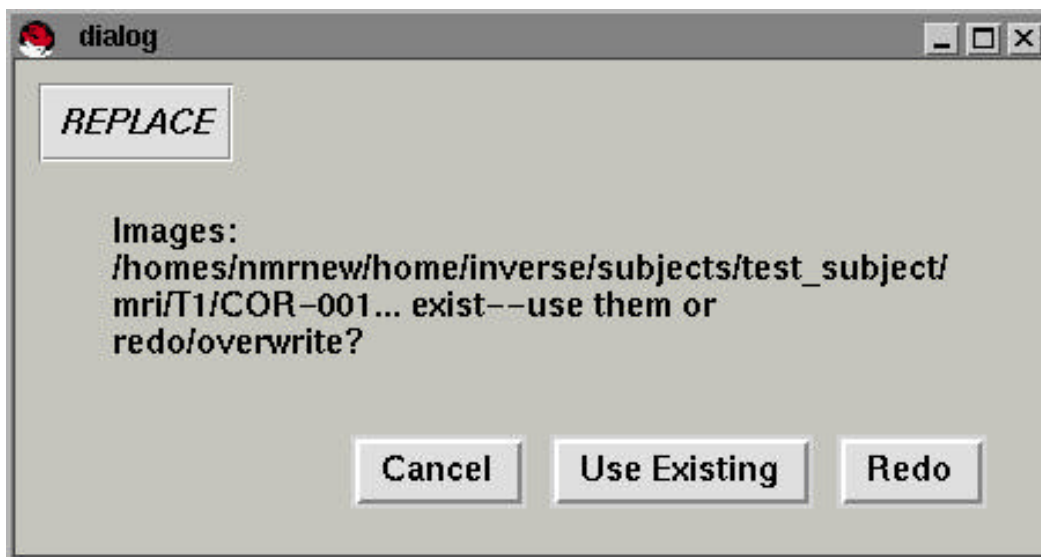
The output files written by the normalization procedure are:

images: \$SUBJECTS_DIR/\$name/mri/T1/COR-???

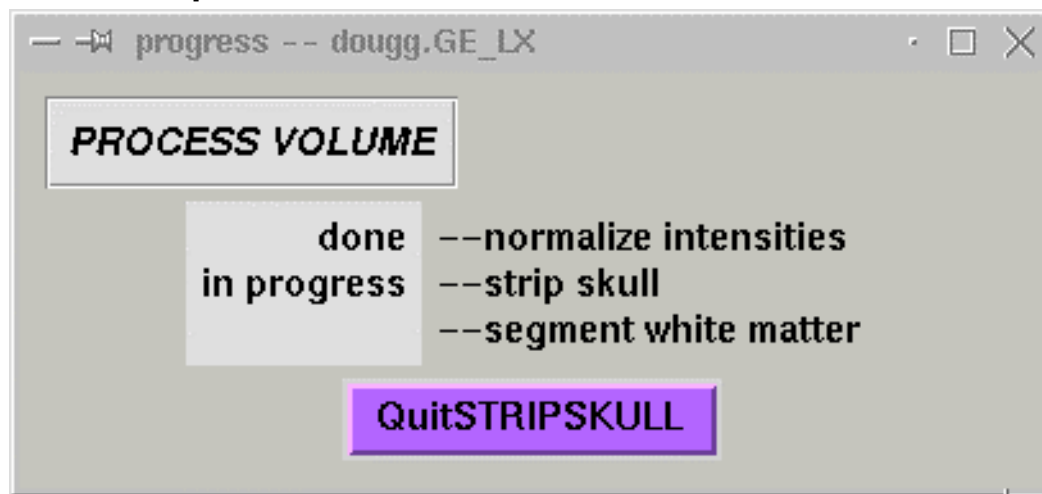
orig and T1 volume



NOTE: If **Don't Ask Overwrite** (under the **Preferences** menu) is clicked, the intensity normalization is automatically redone. This button should only be pressed if some or all of the processes need to be redone.



Part 2: Strip Skull

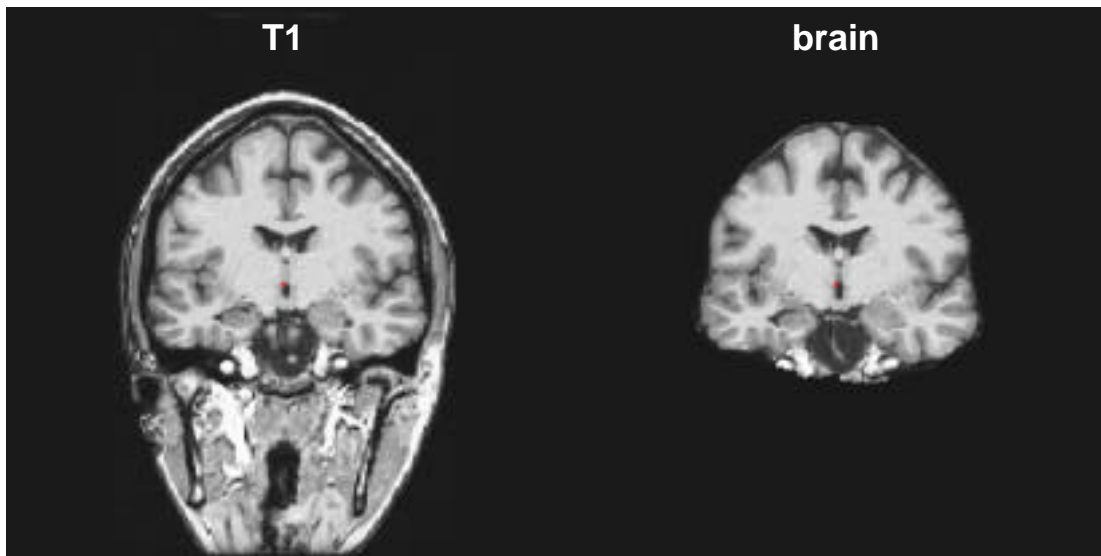


A supertessellated icosahedron is shrunk onto the normalized data set. At each point on the surface a 'core sample' is used to search for the black laminae that correspond to the inner and outer tables of bone in a T1-weighted scan, while at the same time, preserving neighbor relations. Once this surface is found, it is used to strip the skull off the T1 data set.

The output files written by this procedure are:

```
shrinksurface: $SUBJECTS_DIR/$name/bem/brain.tri
images: $SUBJECTS_DIR/$name/mri/brain/COR-???
```

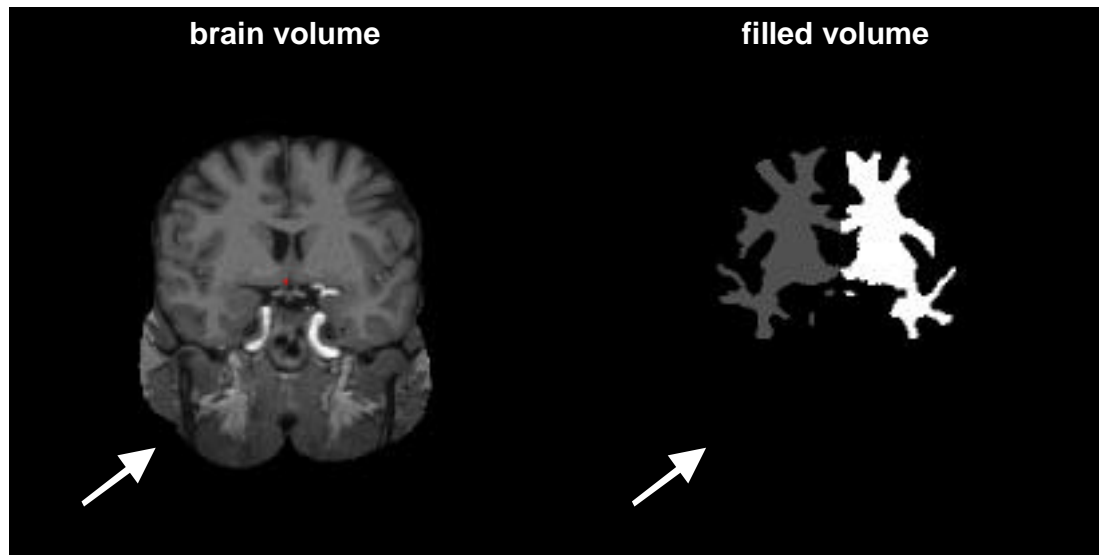
T1 and brain volume



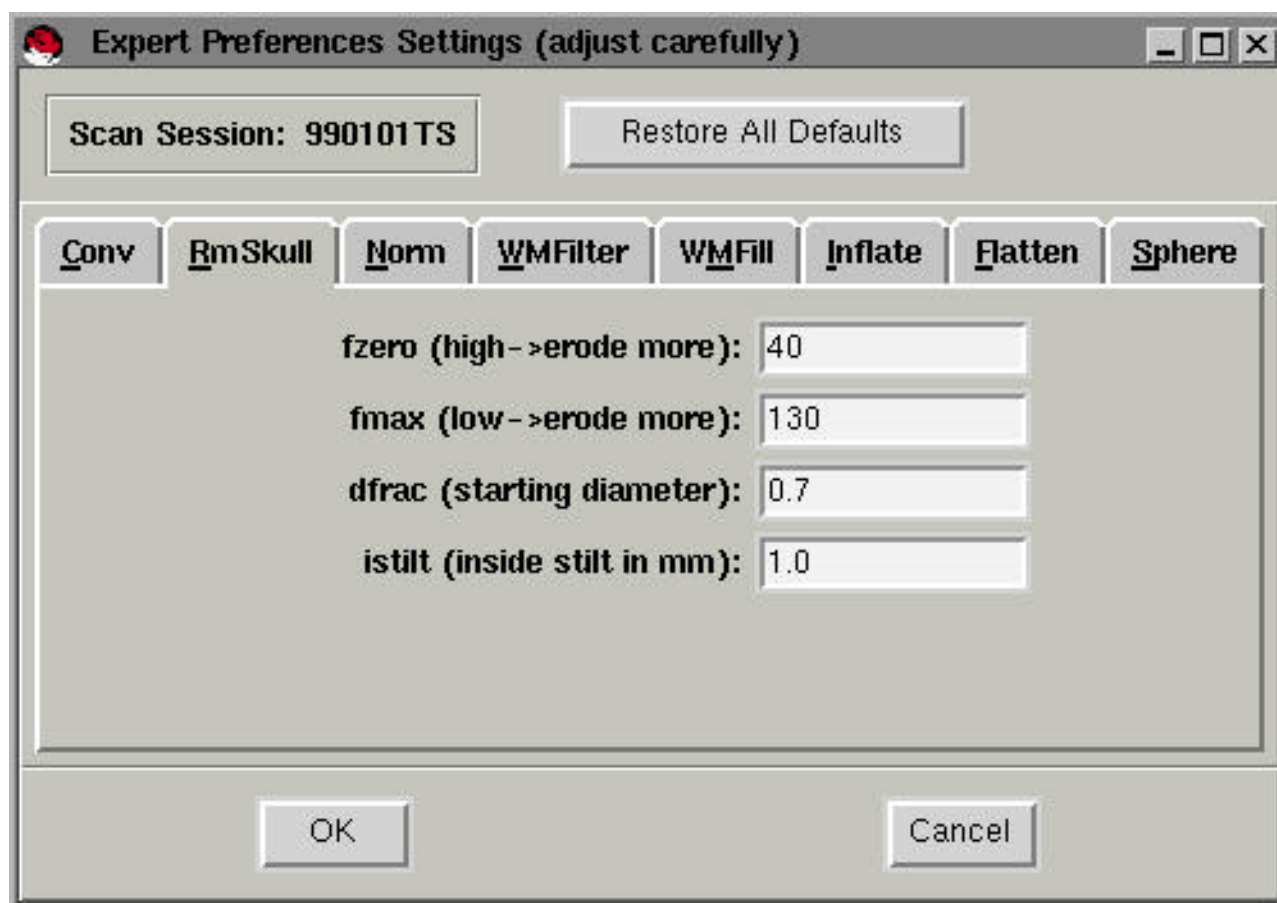
If the brain volume (brain/COR-??? files) already exists, you can either use the existing files (**Use Existing** button) and continue with the process, or redo the intensity normalization (**Redo** button).

Failure of the skull stripping

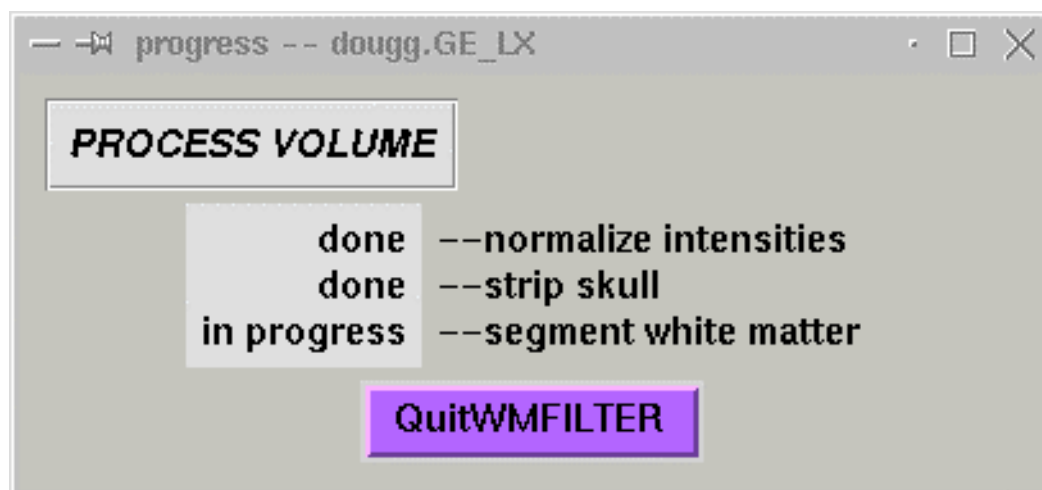
In rare cases, the skull stripping either removes too little skull or removes some of the brain parenchyma. First, examine the **filled** volume. In some cases where the skull stripping has left a substantial amount of neck, the subsequent segmentation and filling has removed the extra neck.



If the filled volume has unwanted skull and neck structures, or actual brain has been removed, select **Expert Preferences** under the **Preferences** menu. Select the **Stripskull** tab. If there are extra structures (e.g. unwanted skull and neck) in the filled volume, increase the **fzero** parameter and decrease the **fmax** parameter in small increments (5 is good choice). If brain has been removed, decrease the **fzero** parameter and increase the **fmax** parameter in small increments (5 is good choice). Rerun **Process Volume** from the **Tools** menu. You do not have to redo the intensity normalization (i.e. select **Use Existing**).



Part 3: White Matter Filter

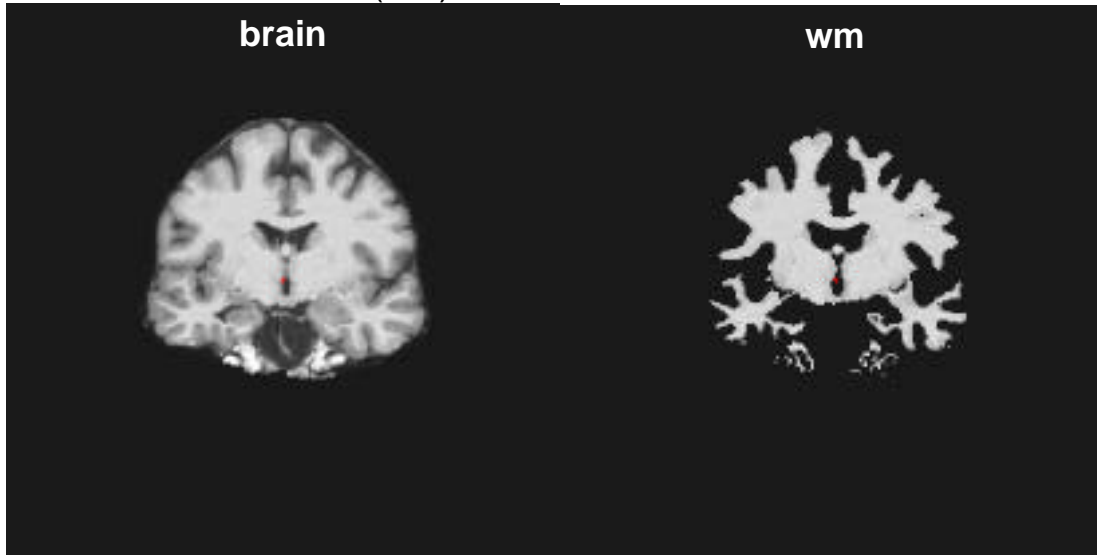


The white matter segmentation uses intensity information as well as geometric information to segment the white matter voxels.

The output files written by this procedure are:

images: \$SUBJECTS_DIR/\$name/mri/wm/COR-???

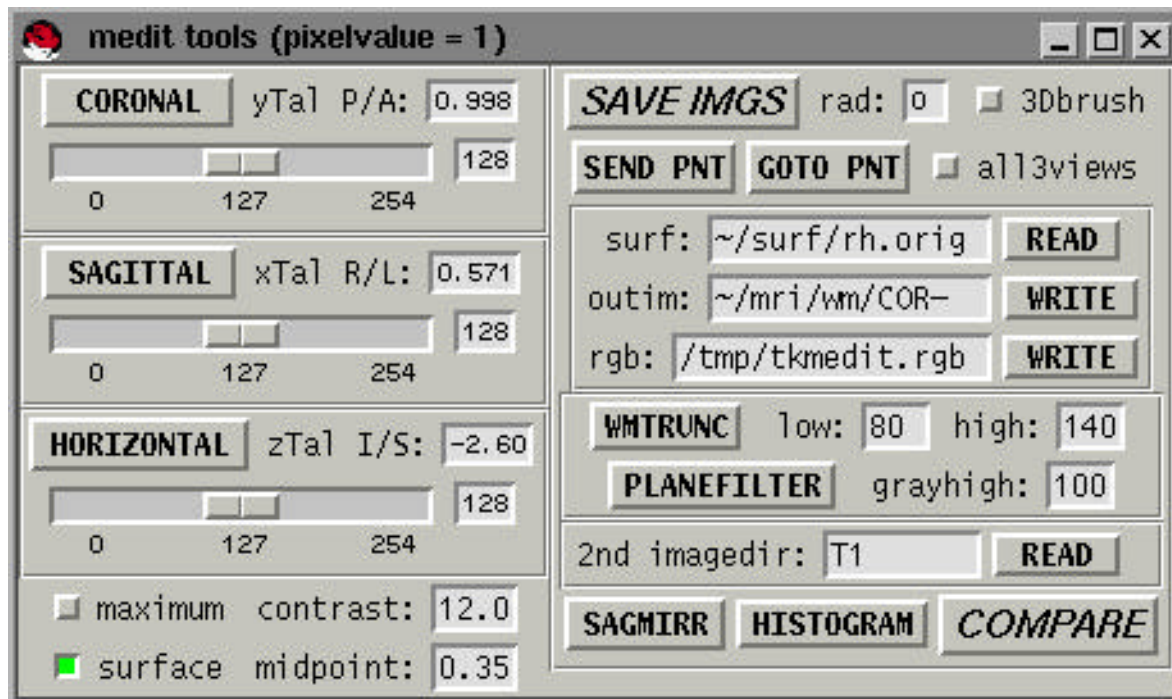
brain and white matter (wm) volume



If the white matter volume (wm/COR-??? files) already exists, you can either use the existing files (**Use Existing** button) and continue with the process, or redo the intensity normalization (**Redo** button).

Viewing with Medit

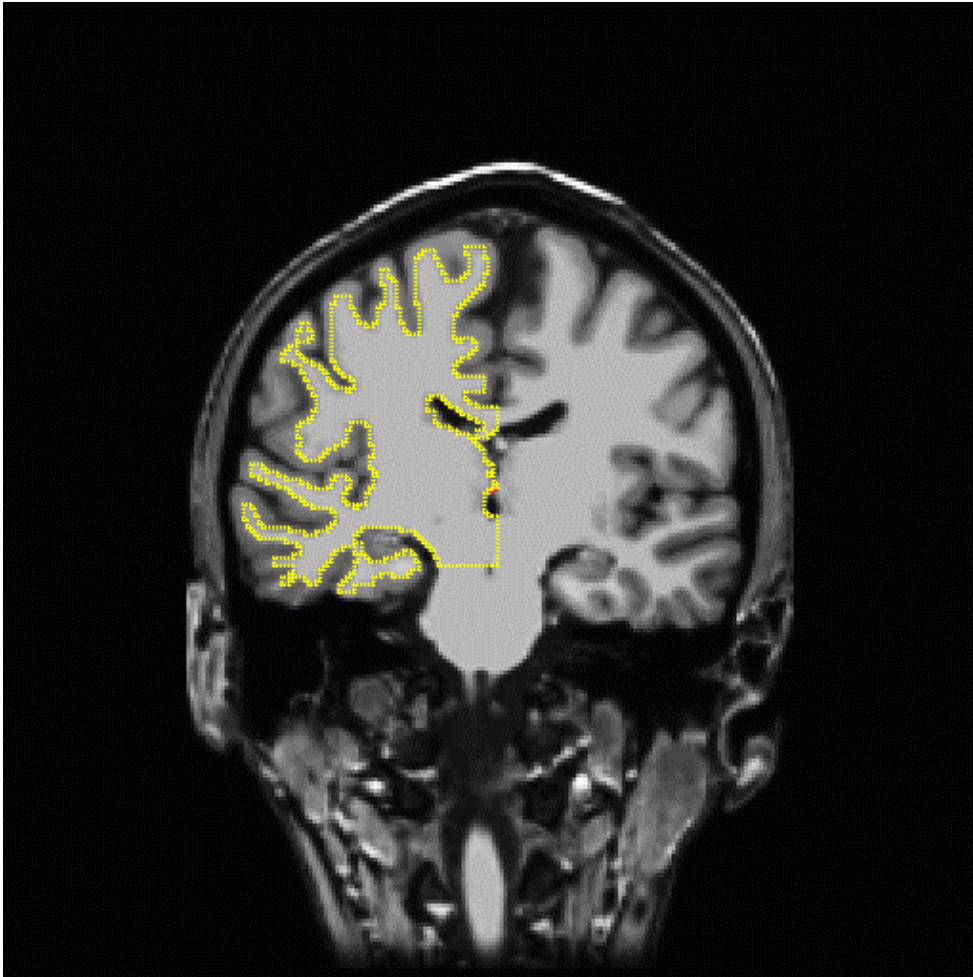
Medit allows for viewing of the volumes. On the csurf interface, click the button labeled **Medit**



Medit reads one or two volumes and displays them in coronal, sagittal, horizontal, or all 3 planes. The images in the first (edit) buffer can be edited and saved. Images read into the second buffer cannot be edited. Edits applied while viewing the second buffer affect the first buffer (useful when edit buffer has segmented white matter and second buffer has original full T1 images). Note that next to the button named **Medit** on csurf, there are options for viewing the desired volume (ex: **T1**, **orig**, **brain**, etc..)

Medit can also read in a surface and display the intersection of the surface with the current slice.

T1 IMAGE WITH SURFACE OVERLAY IN YELLOW



Viewing orientation

CORONAL button:	switch to coronal view
slider :	change coronal slice
field :	enter coronal slice number
SAGITTAL button:	switch to sagittal view
slider :	change sagittal slice
field :	enter sagittal slice number
HORIZONTAL button:	switch to horizontal view
slider :	change horizontal slice
field :	enter horizontal slice number
all3views radiobutton:	displays all three views with a maximum intensity projection

Display parameters

maximum radiobutton:	maximum intensity projection
surface radiobutton:	toggle surface overlay
contrast field:	contrast
midpoint field:	midpoint of intensity range
SAGMIRROR button:	Mirror volume about sagittal plane (left-right mirror)

Read/Write

SAVE IMGS button:	save images (COR files) in volume specified by outim , used after having made edits to the volume
surf field:	surface for overlay
outim field:	volume to save with SAVE IMGS button
rgb field:	name of rgb to save currently viewed slice

Editing in Medit (see **Editing Defects** for more details)

MIDDLE-CLICK	draw (set intensity to 255)
RIGHT-CLICK	erase (set intensity to 1)
rad field:	radius of editing brush
3Dbrush radiobutton:	toggle 3D/2D brush (2D brush only edits viewed slice)
SEND PNT button	save location of cursor for surfer
GOTO PNT button	goto location of point saved by surfer
2nd imagedir field:	name of 2 nd volume to read in
READ button:	read in 2 nd volume
COMPARE button:	toggle between two volumes (must first read in 2 nd imagedir)

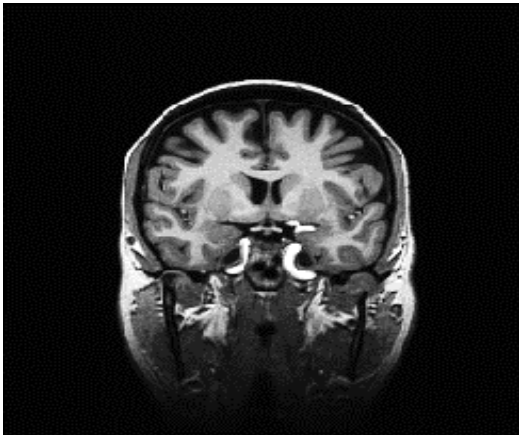
Unsupported

WMTRUNC button
PLANEFILTER button
low field
high field
grayhigh field
HISTOGRAM button

Process Volume Summary

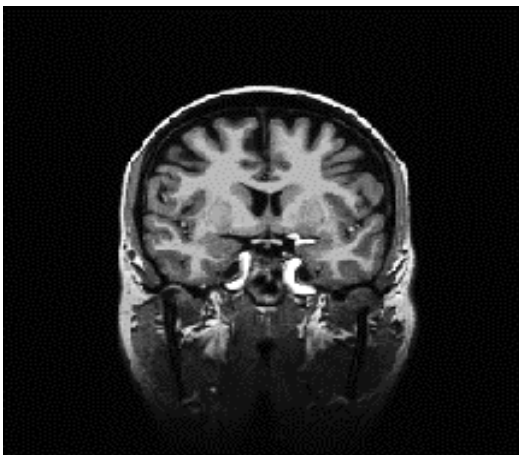
The following images should be available for viewing after certain steps of the Process Volume procedure have been run to completion:

- 1) After having motion corrected the data, the **ORIG** image is generated and can be viewed



ORIG IMAGE

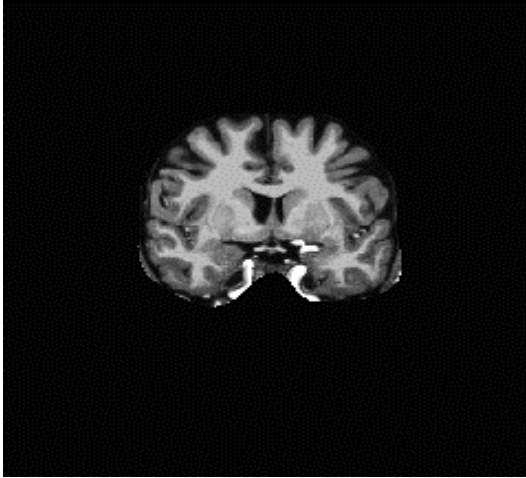
- 2) After the intensity normalization procedure has run to completion, the **T1** image is generated and is available for viewing. This image is the **ORIG** after the intensities have been normalized.



T1 IMAGE

ORIG IMAGE

- 3) After the skull stripping procedure has run to completion, the **brain** image is generated and is available for viewing. This is the skull stripped **T1** image



BRAIN IMAGE

T1 IMAGE

- 4) After the white matter has been segmented, the **wm** image is generated and is available for viewing.

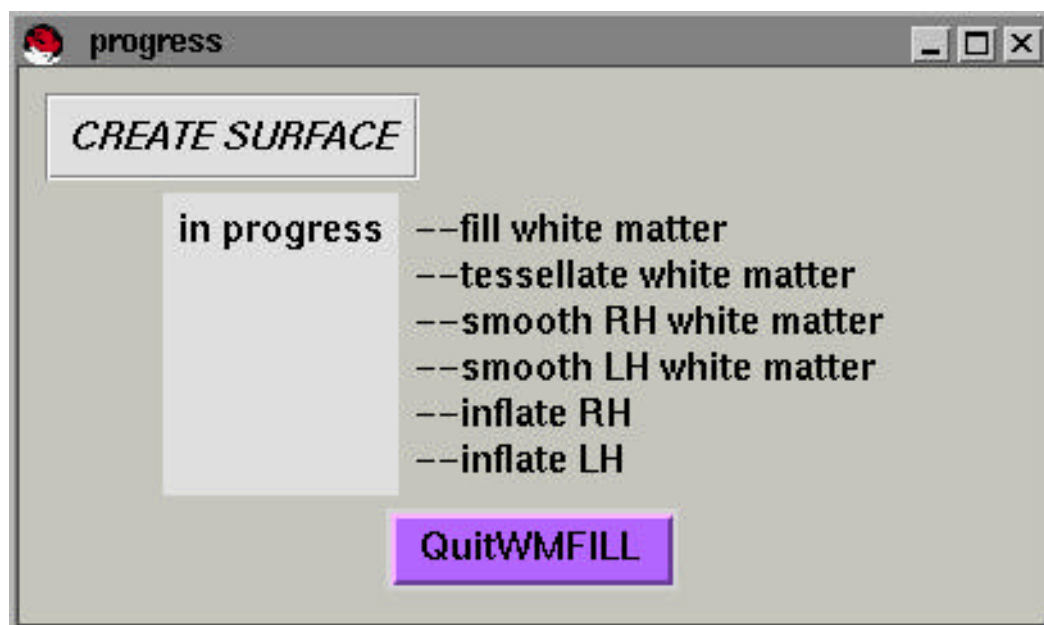


WM IMAGE

Create Surface

Once the process volume step has run to completion, the surface is created using the **Create Surface** process. The Create Surface procedure starts a six-part background process to create the left and right hemisphere cortical surfaces. If necessary, you can create the left or right hemispheres alone. While the surface is being generated, the csurf interface can still be accessed. The process can be canceled by pressing the **Quit** button that is highlighted in purple. Unlike the Process Volume step, this process requires multiple iterations in order to have a surface free of topological defects (see **Editing Defects** section for more information). This is a fully automated process that takes approximately 30 minutes to run to completion.

Part 1: Fill White Matter



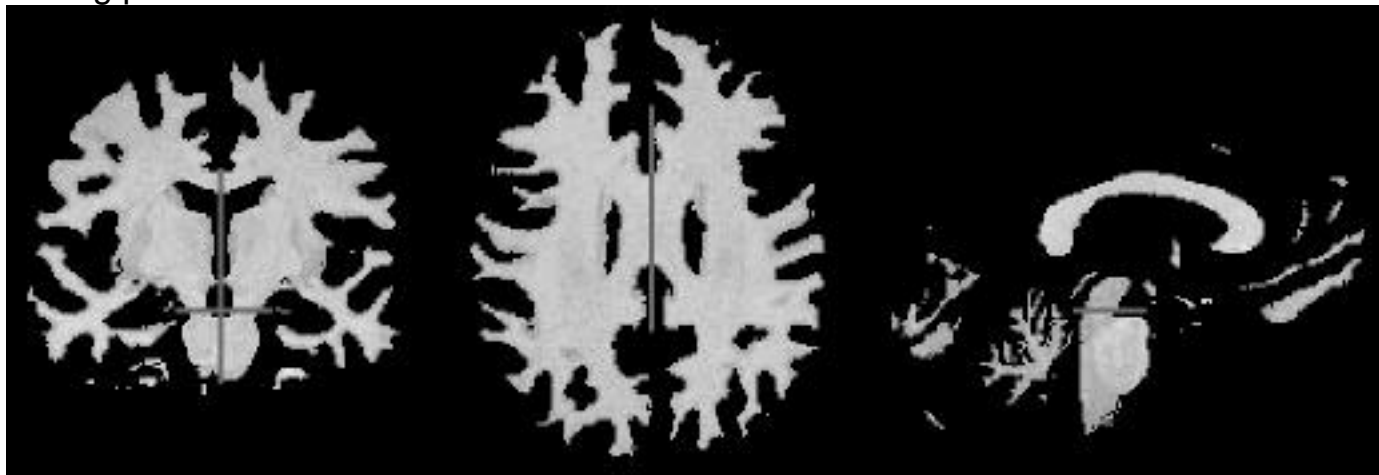
First, the cutting planes are automatically found to 1) separate the left and right hemispheres and 2) prevent the surface from going down into the brain stem. Then, starts a 3-D region growing process from a starting point within the white matter in order to generate the starting point for a surface.

Right hemisphere voxels are assigned a value of 80 (gray). Left hemisphere voxels are assigned a value of 255 (white).

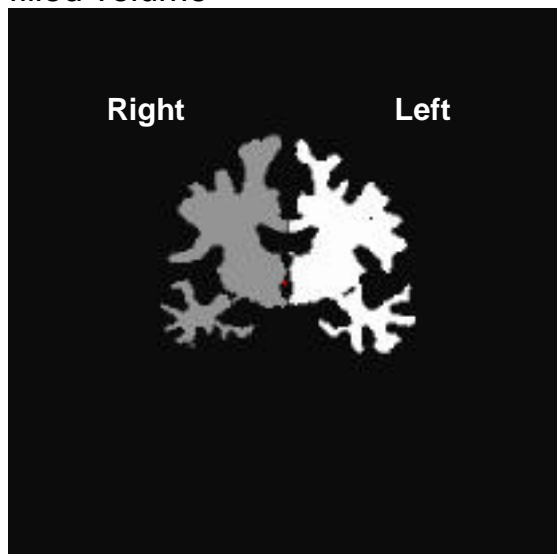
The output files written by this procedure are:

images: \$SUBJECTS_DIR/\$name/mri/filled/COR-???

cutting planes

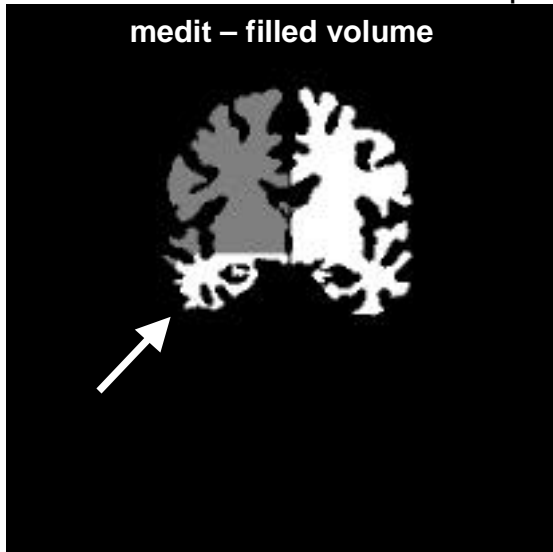


filled volume

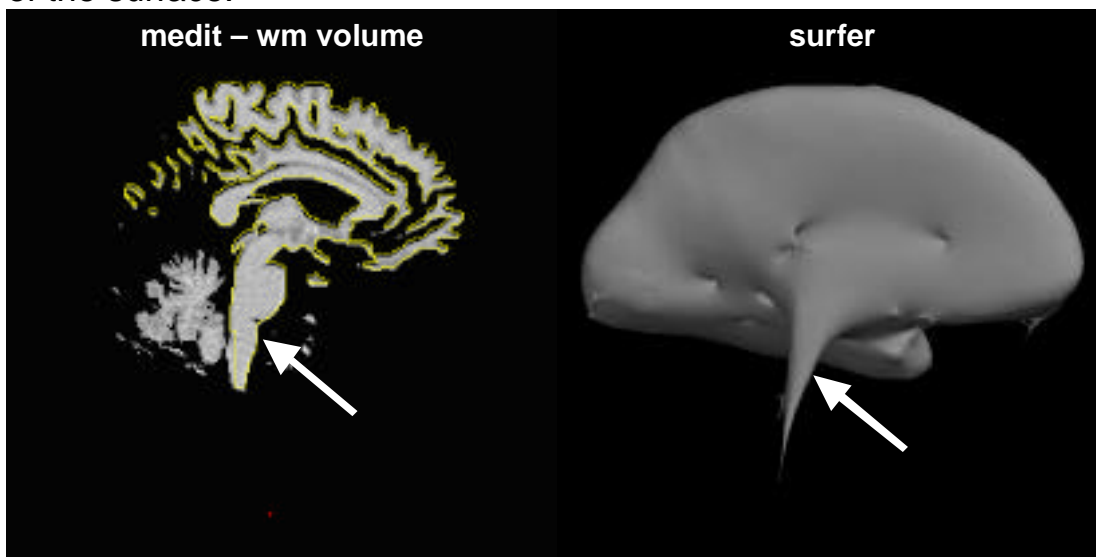


Failure of the automatic cutting planes:

In some cases, the cutting planes are not found correctly. This can be seen in **medit** as incorrectly colored voxels, e.g. some voxels in the right hemisphere are white (255) or some voxels in the left hemisphere are gray (80).



This can also be seen in **surfer** as a large protrusion in the center of the medial aspect of the surface.

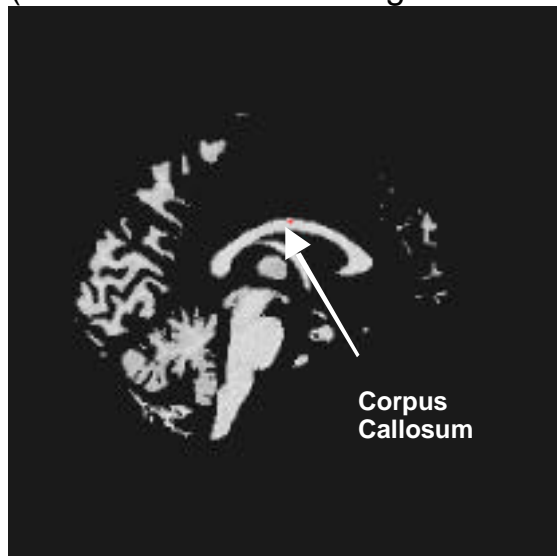


Manually defined cutting planes

The following instructions describe how to manually define the two cutting planes.

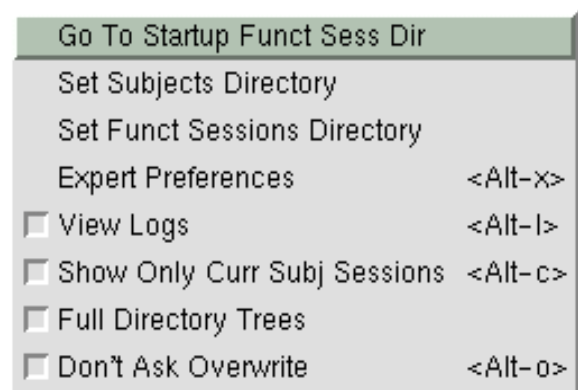
Left-Right Hemisphere separation (Corpus Callosum)

Using **medit**, find a sagittal slice in the **wm** volume in which the corpus callosum is disconnected. This slice should be near the mid-line. If you cannot find a slice with the corpus callosum disconnected, manually erase voxels to separate the corpus callosum (erase voxels with the right mouse button in **medit**).

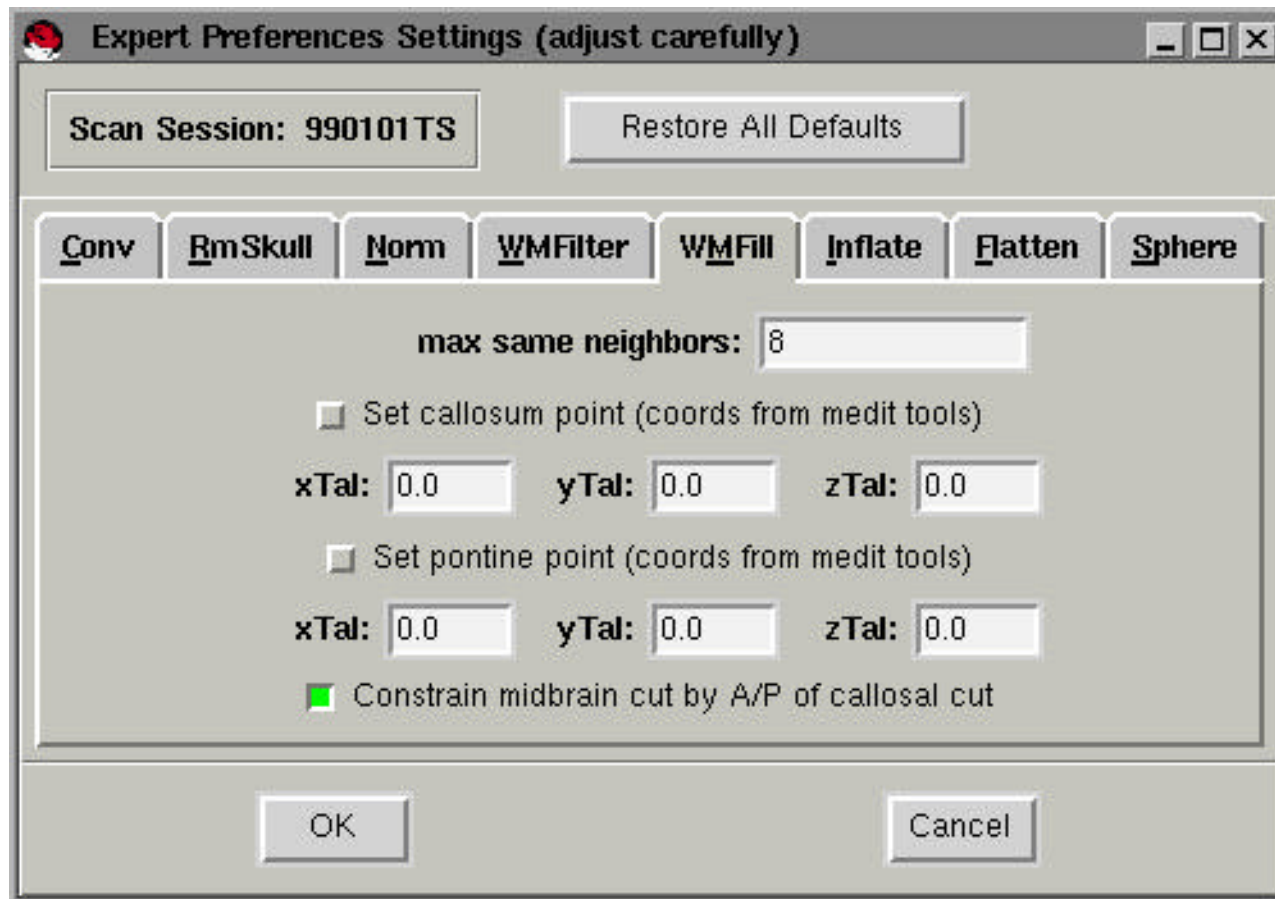


Select a point (left mouse button) in the corpus callosum to get the Talairach coordinates. Be sure that **View Logs** is selected. The Talairach coordinates will be printed in the **csurf** window under the **medit** bar.

Select **Expert Preferences** from the **Preferences** menu.



In the **Expert Preferences** window, select the **WMFill** tab.



Enter the Talairach coordinates of the corpus callosum into the **WMFill** window and press the button next to "**Set callosum point.**" If the Talairach transformation matrix is not available, enter the x, y, and z locations output by **medit**.

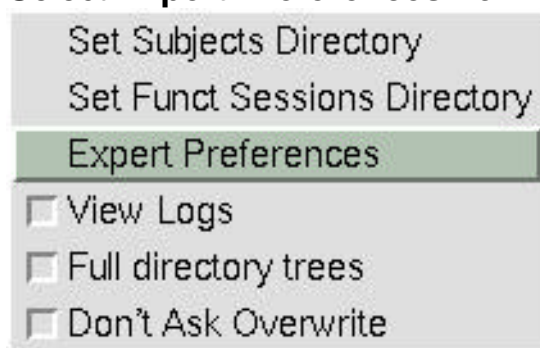
Pons:

Using **medit**, find a horizontal slice in the **wm** volume in which the brainstem is disconnected from the rest of the brain. This slice should be near the top of the pons. If you cannot find a slice with the mid-brain disconnected, manually erase voxels to separate the mid-brain (erase voxels with the right mouse button in medit).

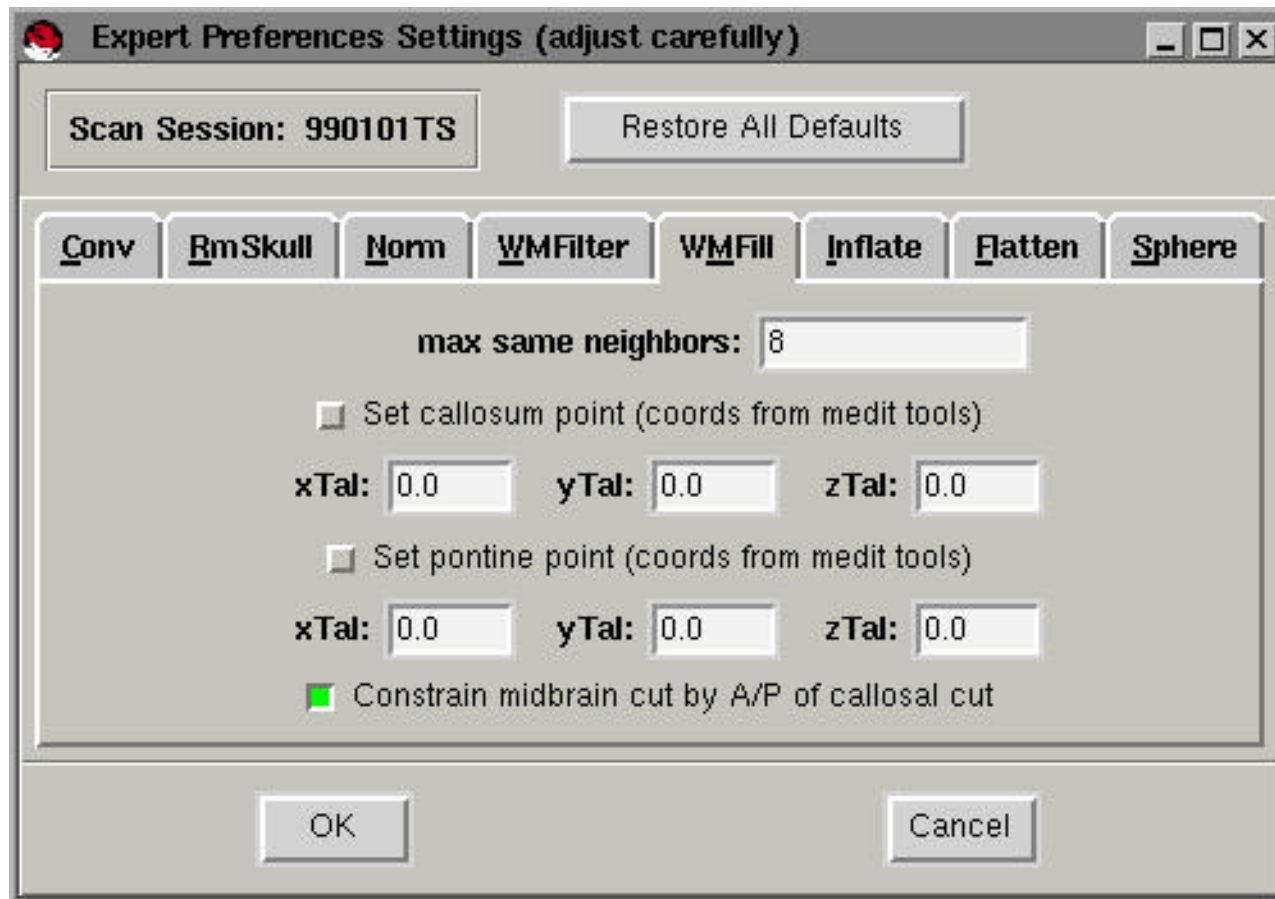


Select a point (left mouse button) in the brainstem to get the Talairach coordinates. Be sure that **View Logs** is selected. The Talairach coordinates will be printed in the **csurf** window under the **medit** bar.

Select **Expert Preferences** from the **Preferences** menu.

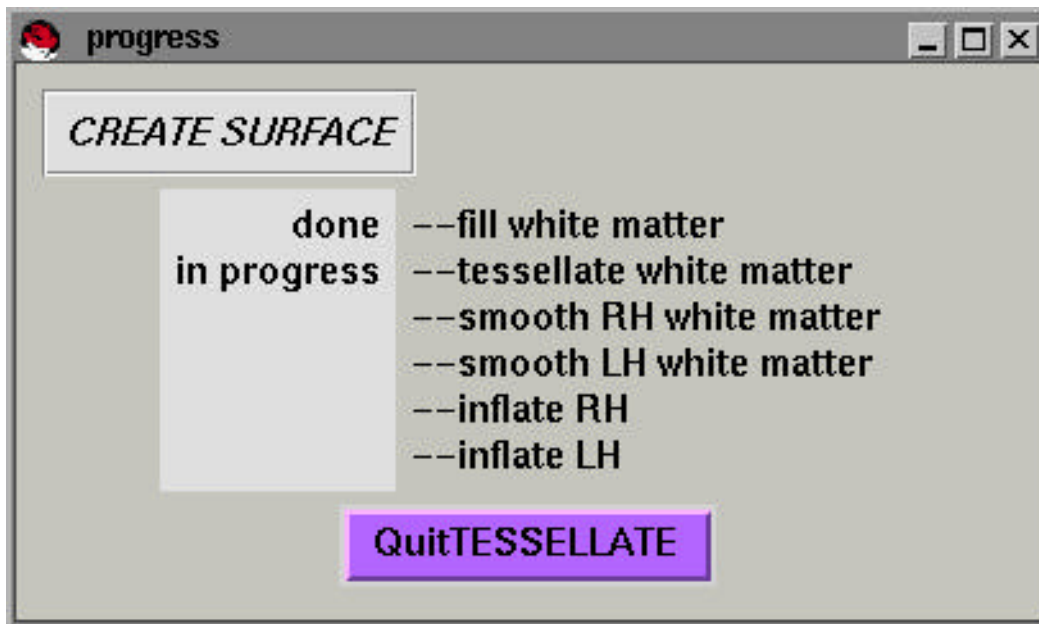


In the **Expert Preferences** window, select the **WMFill** tab.



Enter the Talairach coordinates of the pons into the **WMFill** window and press the button next to "**Set pontine point.**" If the Talairach transformation matrix is not available, enter the x, y, and z locations output by **medit**.

Part 2: Tessellate White Matter



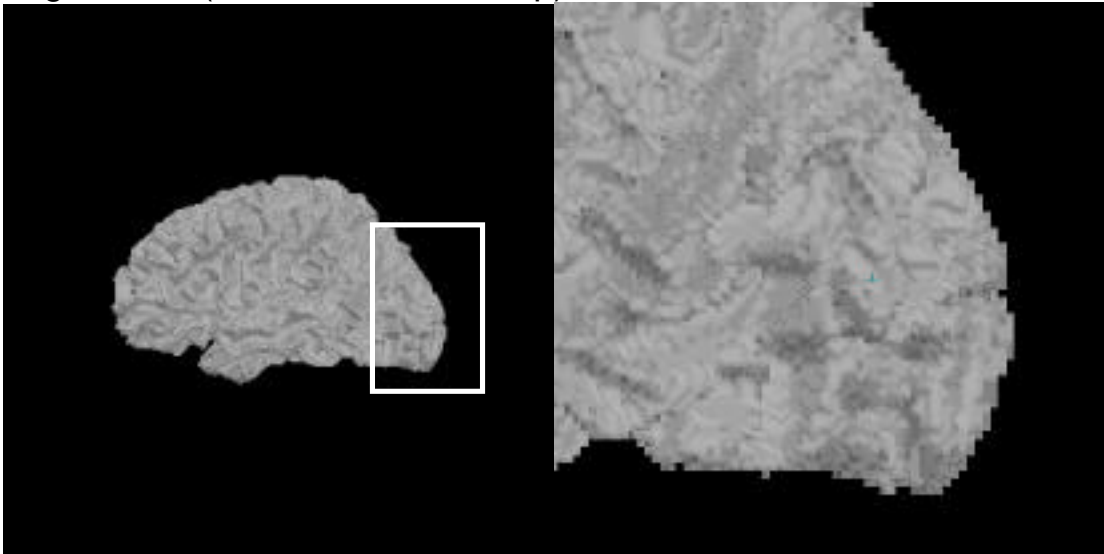
Connects the surfaces of the filled white matter voxels into a continuous surface.

The output files written by this procedure are:

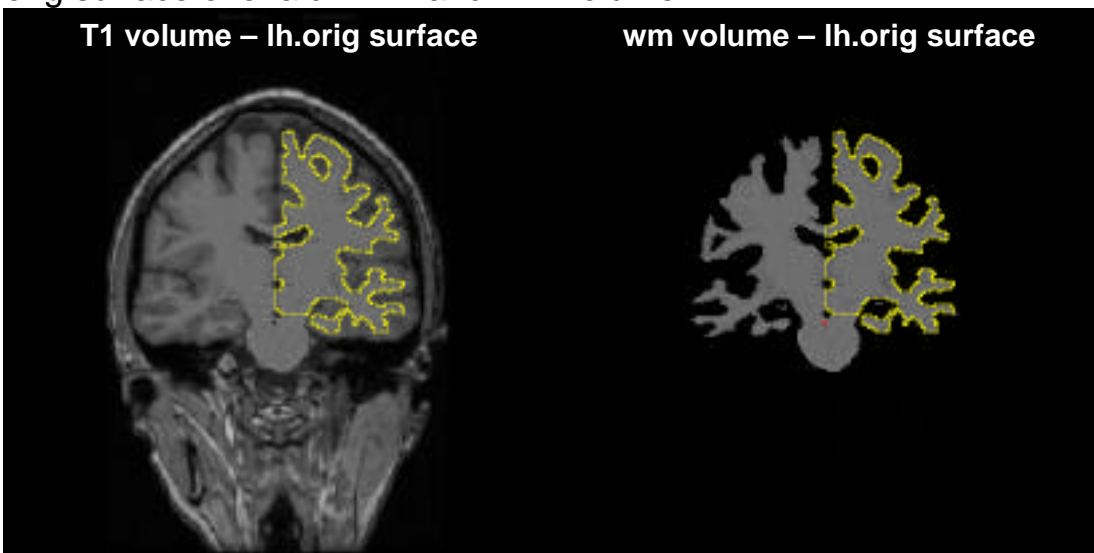
surface: \$SUBJECTS_DIR/\$name/surf/rh.orig

surface: \$SUBJECTS_DIR/\$name/surf/lh.orig

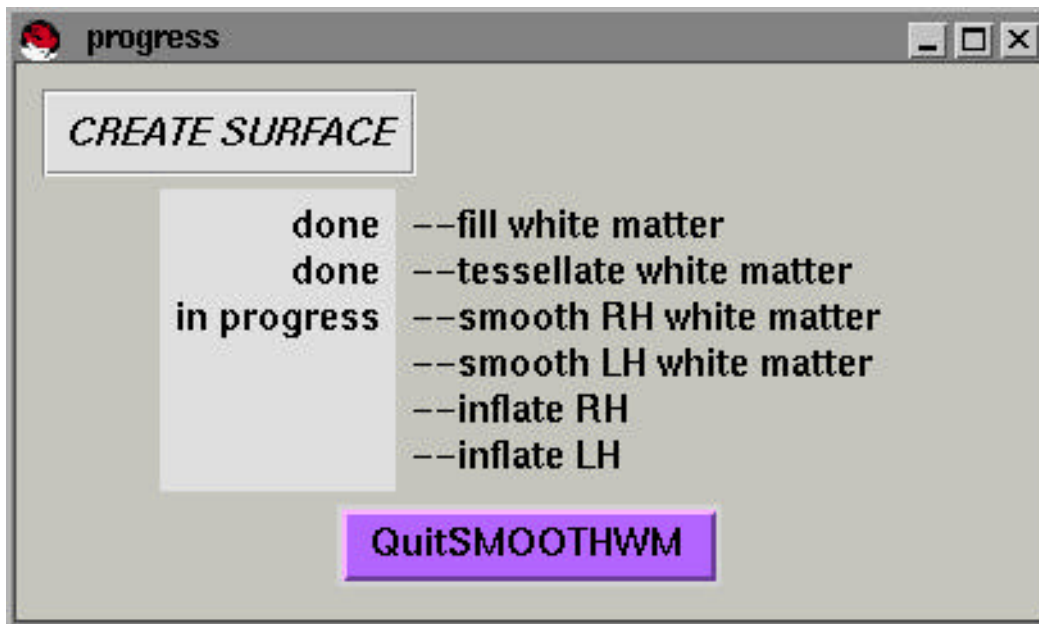
orig surface (full view and close up)



orig surface overlaid in T1 and wm volume



Part 3: Smooth Right Hemisphere White Matter



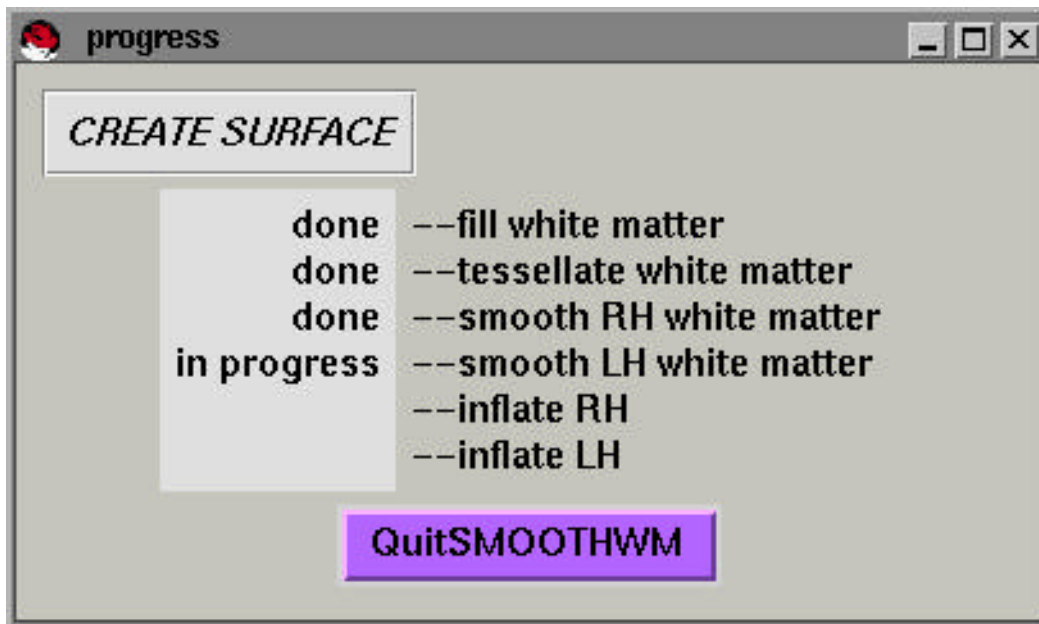
The reconstructed white matter surface of the right hemisphere (rh.orig) is smoothed. The mean curvature is computed from the smooth surface.

The output files written by this procedure are:

surface: \$SUBJECTS_DIR/\$name/surf/rh.smoothwm

curv: \$SUBJECTS_DIR/\$name/surf/rh.curv

Part 4: Smooth Left Hemisphere White Matter



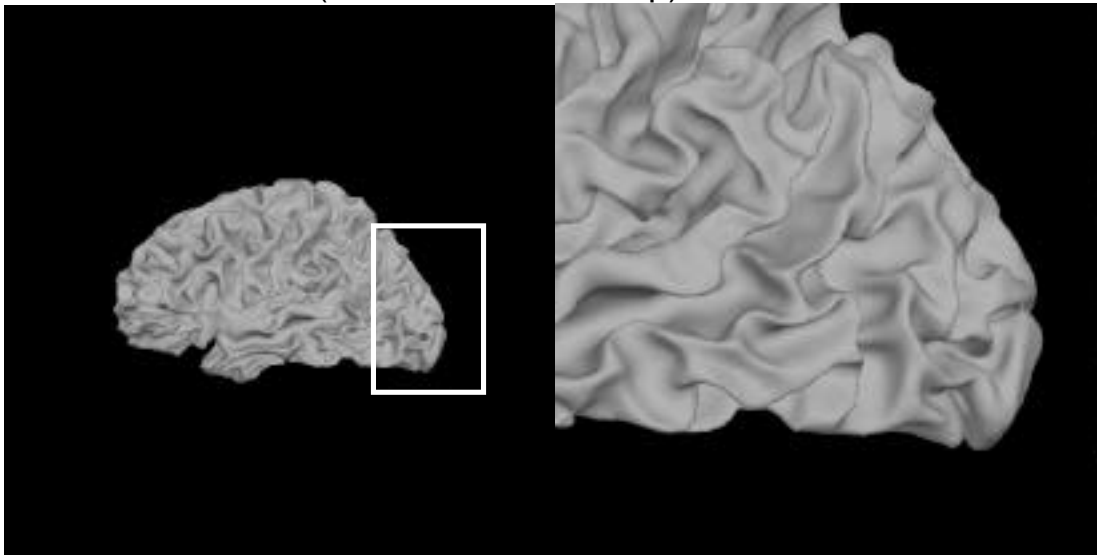
The reconstructed white matter surface of the left hemispheres (lh.orig) is smoothed. The mean curvature is computed from the smooth surface.

The output files written by this procedure are:

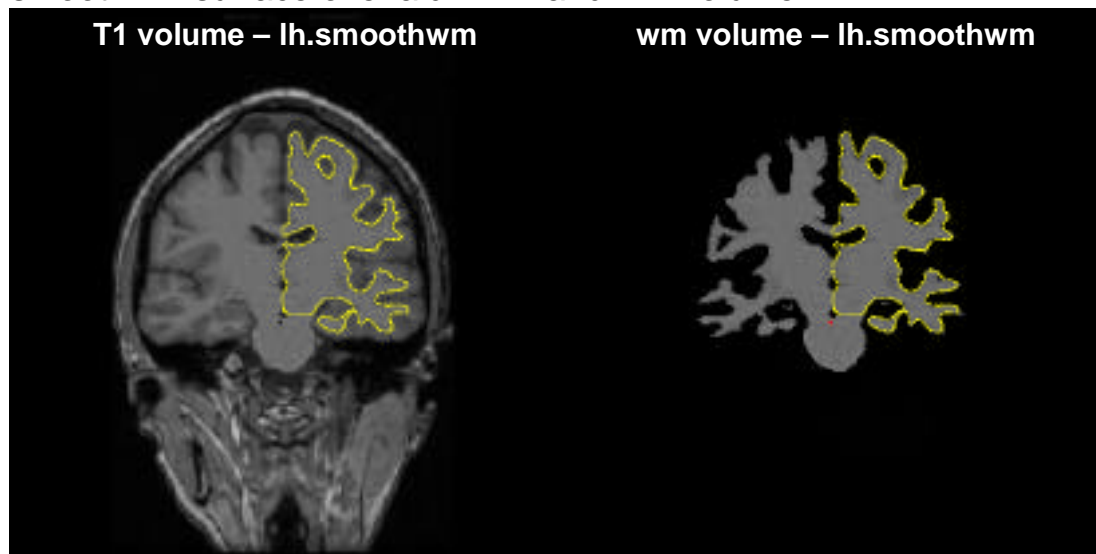
surface: \$SUBJECTS_DIR/\$name/surf/lh.smoothwm

curv: \$SUBJECTS_DIR/\$name/surf/lh.curv

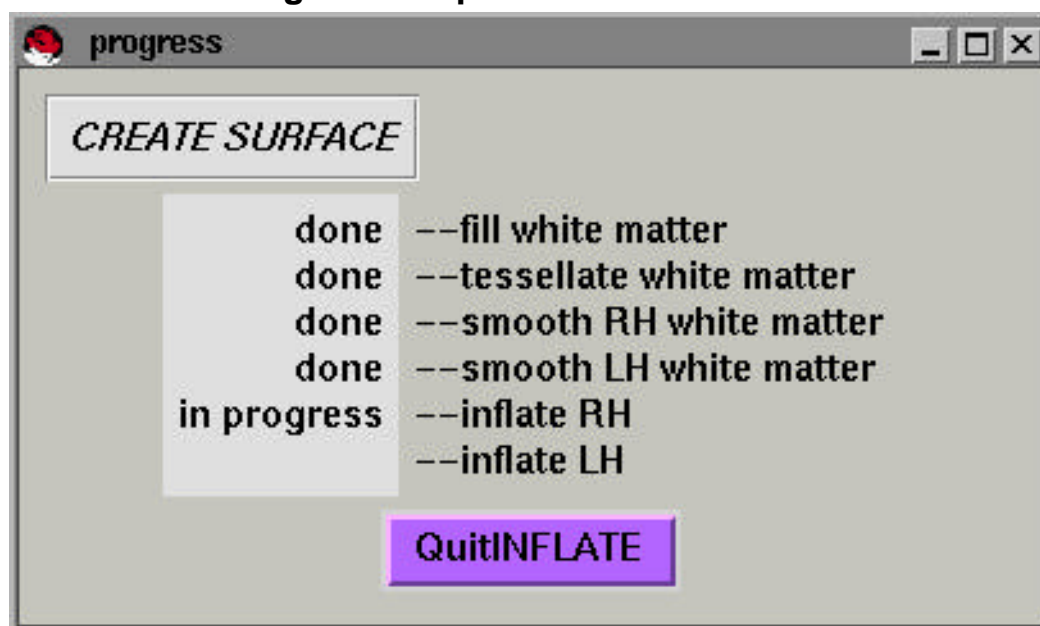
smoothwm surface (full view and close up)



smoothwm surface overlaid in T1 and wm volume



Part 5: Inflate Right Hemisphere

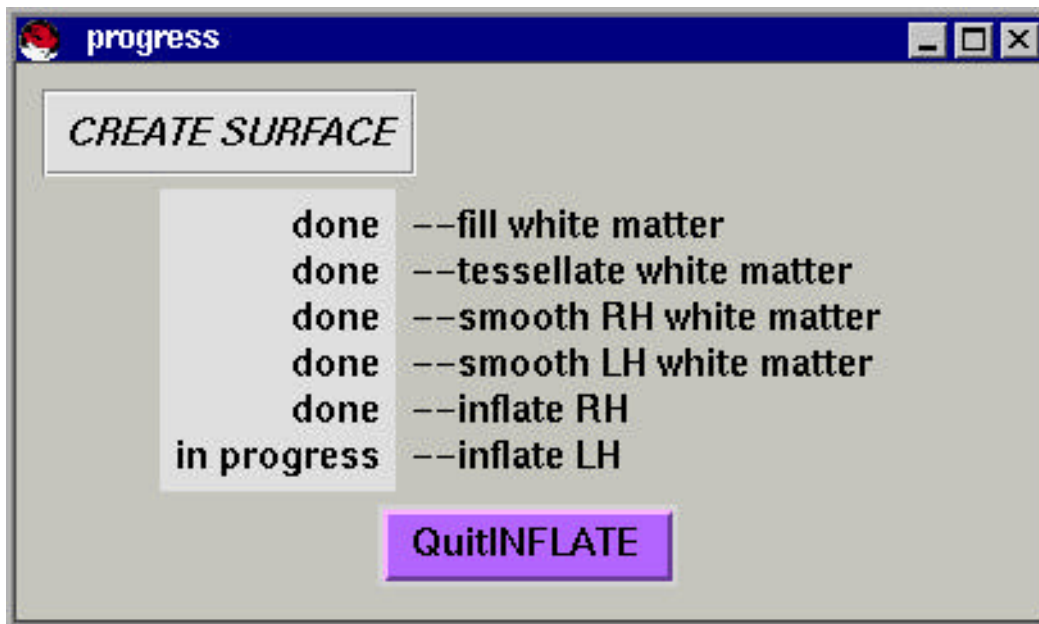


Inflates the right hemisphere surface (rh.smoothwm) while attempting to minimize metric distortion.

The output file written by this procedure is:

surface: \$SUBJECTS_DIR/\$name/surf/rh.inflated

Part 6: Inflate Left Hemisphere

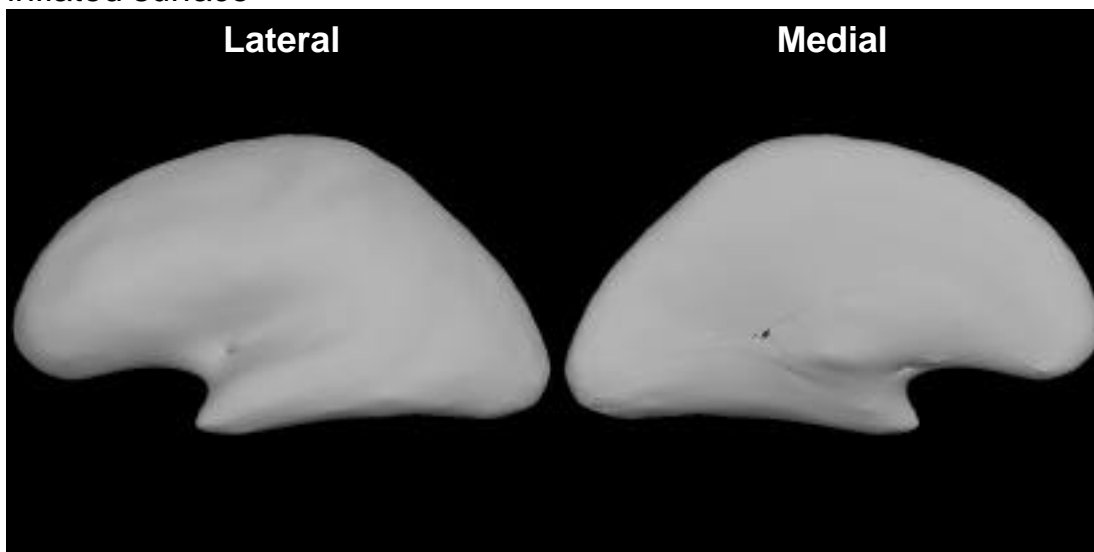


Inflates the left hemisphere surface (lh.smoothwm) while attempting to minimize metric distortion.

The output file written by this procedure is:

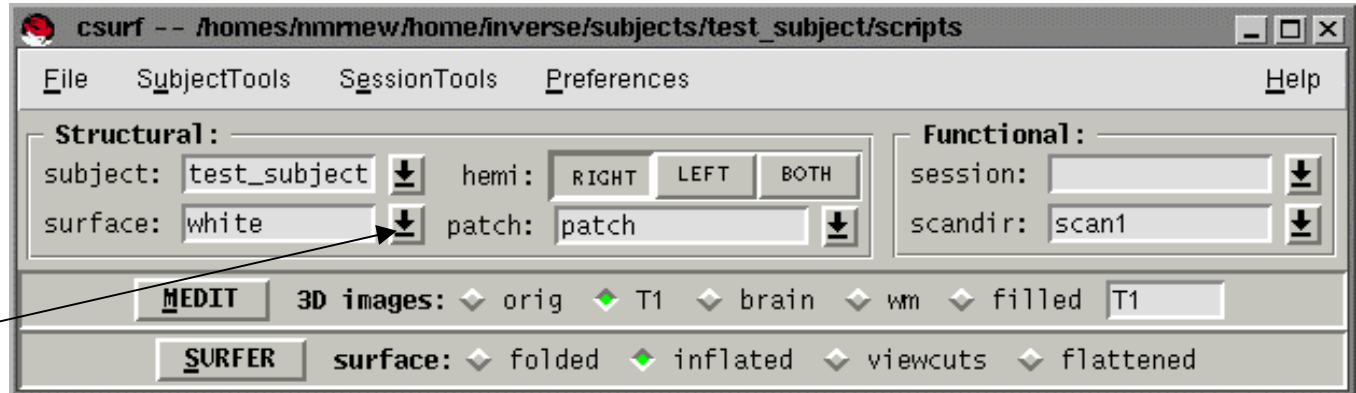
surface: \$SUBJECTS_DIR/\$name/surf/lh.inflated

inflated surface



Create Surface Summary

Different surfaces can be selected by clicking onto the surface button

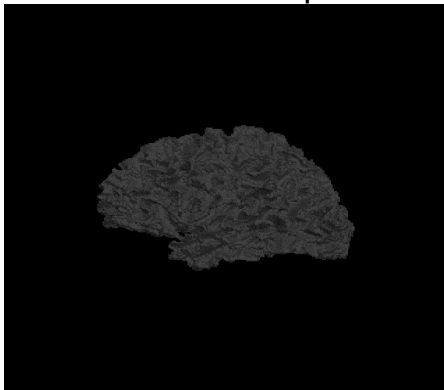


- 1) After the white matter has been filled and the cutting planes have been found, the wm volume is available for viewing



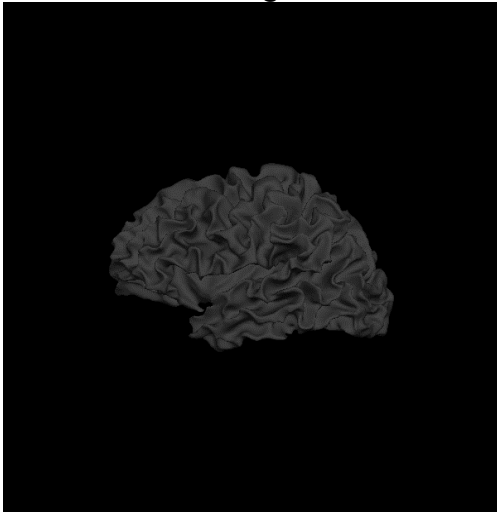
filled image

- 2) After the tessellation procedure, the **orig** image is available for viewing



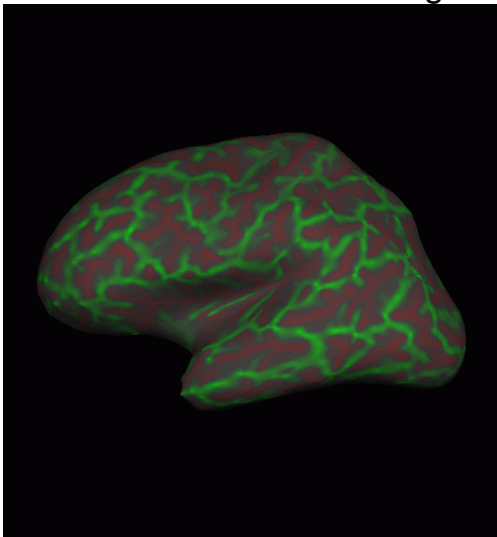
orig surface

- 3) After the white matter surface has been smoothed, the **smoothwm** surface is available for viewing



smoothwm surface

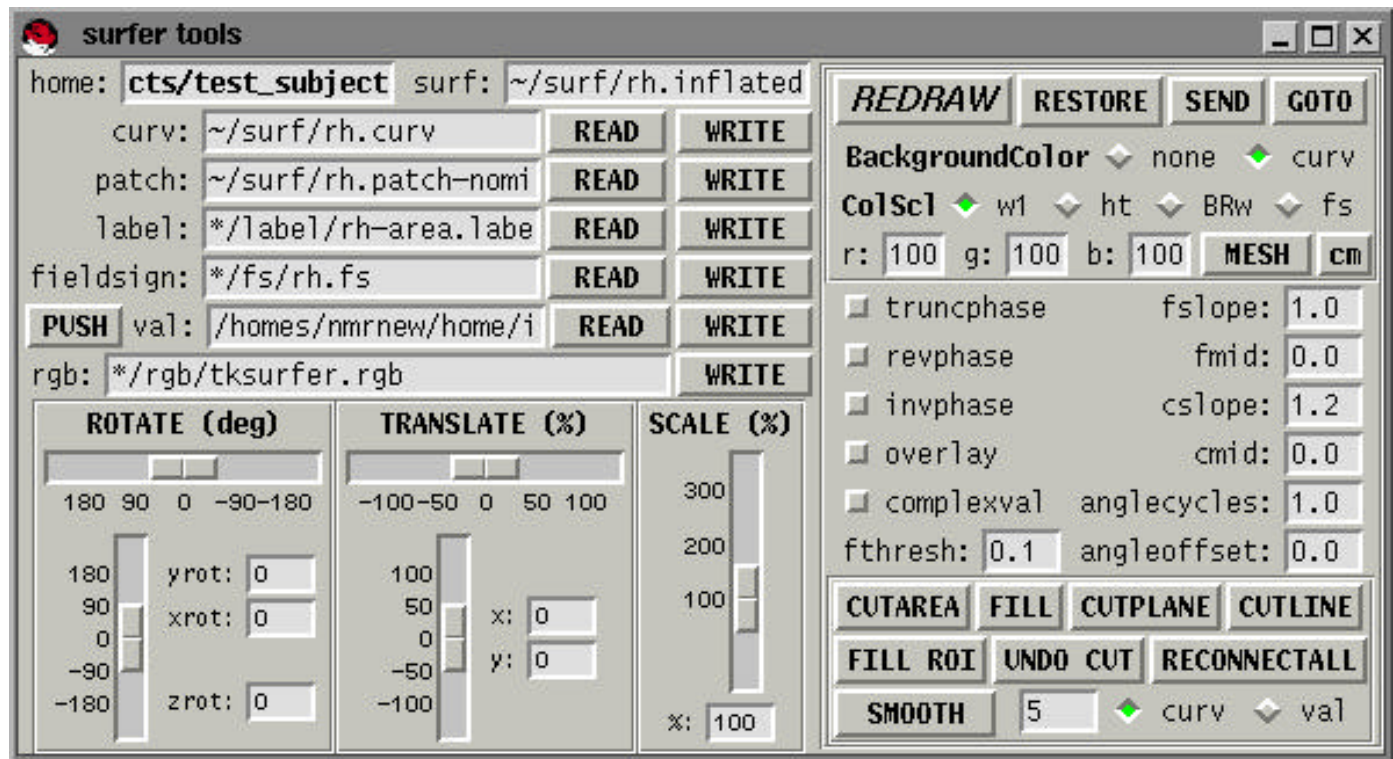
- 4) Following the smoothing procedure, once the surface has been inflated, the **inflated** surface is available for viewing



inflated surface

Viewing with Surfer

Surfer allows viewing of surfaces. Click the button labeled **Surfer** on csurf



Surfer reads a surface file, and optionally, functional data, and then renders a view of the surface.

home field: subject directory
surf field: surface that is displayed. To view a different surface, enter the surface and press **RETURN**

READ/WRITE

curv field:	cortical curvature file
READ	read curvature file
WRITE	write curvature file
patch field:	cortical patch file
READ	read cortical patch
WRITE	write cortical patch
label field:	not supported - future functionality
READ	
WRITE	
fieldsign field:	Not supported. Future functionality
READ	
WRITE	
val field:	val file – same format as *.w files
READ	read val file
WRITE	write val file
rgb field:	rgb file
WRITE	write rgb file of current surfer window.

Viewing orientation

REDRAW	redraw screen – redraw is not always automatic
RESTORE	restore original viewing orientation
ROTATE	
slider (horizontal)	rotate view around vertical axis
slider (vertical)	rotate view around left-right axis
yrot field	rotate around y axis
xrot field	rotate around x axis
zrot field	rotate around z axis
TRANSLATE	
slider (horizontal)	translate left-right, to view translation, translate and then redraw
slider (vertical)	translate up-down
x field	translate in x axis
y field	translate in y axis
SCALE	
slider (vertical)	scale larger-smaller
% field	scale in percent

Surface Display

BackgroundColor

none radiobutton

curv radiobutton

MESH button

r, g, b fields

cm button

do not display curvature information (uniformly gray brain)

display curvature information (specified in **curv** field)

display actual vertices and mesh

set color of mesh

display scale bars (size scale bar = 1cm)

Functional Display

ColSci

w1 radiobutton

ht radiobutton

BRw radiobutton

fs radiobutton

truncphase

revphase

invphase

overlay

complexval

fthresh field

fslope field

fmid field

cslope

cmid

anglecycles

angleoffset

SMOOTH button

field

curv

val

color scale of functional data

not supported - future functionality

yellow/red for positive values, blue/green for negative values

not supported - future functionality

not supported - future functionality

only display positive values (red/yellow).

not supported - future functionality

reverses positive and negative values

displays functional data when checked

not supported - future functionality

statistical threshold (for values below the threshold, the underlying curvature is displayed). This is equivalent to

Stat Hard Thresh in **Setup Rendering Parameters**

color slope from **fmid** (red/blue) to the maximum color (yellow/green). Maximum color (yellow, green)

represents a statistical value of **fmid** + 1/ **fslope**. This is equivalent to **Stat Color Contrast**.

statistical value for full red/blue. Equivalent to **Stat Color Midpoint**

contrast of curvature

mid-point of curvature colorscale

not supported - future functionality

not supported - future functionality

smooth curvature or values (functional data)

number of smooth iterations

smooth curvature

smooth values (functional data)

Cutting Surface

CUTAREA

cuts a close line from selected **LEFT-CLICKs**

FILL

fills in a region from a selected **LEFT-CLICK** defined by cuts

CUTPLANE

planar cut. First 3 **LEFT-CLICKs** define plane, 4th

CUTLINE

LEFT-CLICK defines surface to keep

FILL ROI

cuts an open line from selected **LEFT-CLICKs**

UNDO CUT

fills in a region defined by statistical values

RECONNECTALL

undoes the most recent cut

undoes all cuts

Zoom Function

Control Key and Left Mouse Button

allows zooming in

Control Key and Right Mouse Button

allows zooming out

The zoom function is particularly useful when correcting defects

NOTE: To view any changes or modifications made by selecting any keys, need to click **REDRAW**

Editing Defects

This procedure follows the **Create Surface** step, once the surface has finished inflating. This is the only manual step of the whole reconstruction process and requires a few iterations. There are two major types of defects: a) large, anatomical defects and b) small, topological defects. The topological defects can be fixed using the automated topology fixer but before this process can be run, the larger anatomical defects have to be fixed manually.

The major anatomical defects are:

- 1) Fornix
- 2) Basal Ganglia
- 3) Lateral Ventricle
- 4) Temporal Lobe
- 5) Optic Nerve

How to correct defects:

In **medit**, read in the **T1** volume into the second volume:

- 1) Enter "**T1**" into the field **2nd imagedir**
- 2) Press **READ** to read in the **T1** volume into the second volume
- 3) To change volumes displayed, use the **COMPARE** button. This will allow you to compare the segmented volume (**wm**) with the original MRI volume (**T1**) to determine how the defect needs to be fixed.

Select a point (**LEFT-CLICK**) on the cortical surface (in **surfer**) near the topological defect.

1. Save the location of the point with **SEND** in the **surfer** window
2. Go to the point in the volume with **GOTO PNT** in the **medit** window

Medit commands:

Fill voxels – **MIDDLE-CLICK**

Erase voxels – **RIGHT-CLICK**

Increase/Decrease the brush size for filling/erasing – **rad** field

For small defects use **rad** = 0, For most others **rad** = 1 is good.

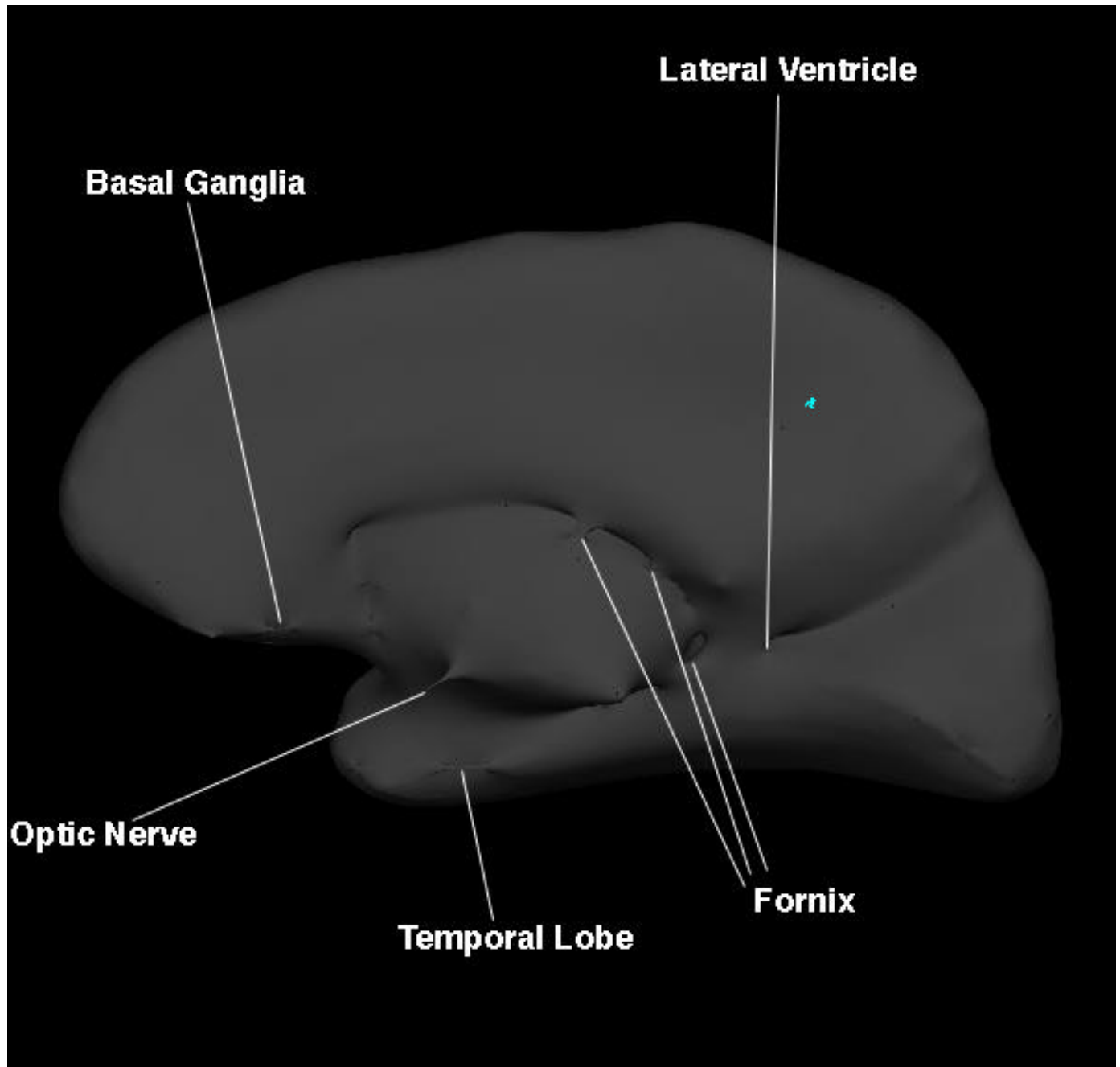
Use 3D brush (edits out of visible plane) – **3Dbrush** radiobutton

Use care with the 3D brush because you are editing pixels you can't see

Save volume after changes are made – **SAVEIMG**

Toggle surface overlay – **surface**

Overlay of Defects



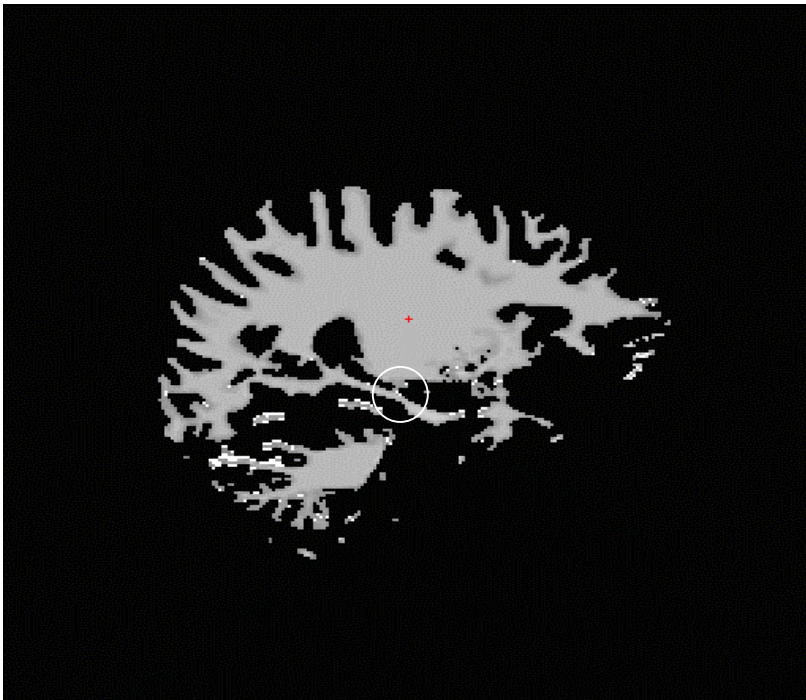
Now a detailed analysis of how to fix these defects.

The Specific Defects:

Fornix

The fornix needs to be erased. The erasing process is best done in the sagittal view using a brush of radius 1. The images below serve as a guide to erasing the fornix (in one hemisphere) and show where to start erasing and where to finish. Note that the fornix (like many defects) needs to be corrected for in both hemispheres. The regions requiring correction are indicated by a white circle.

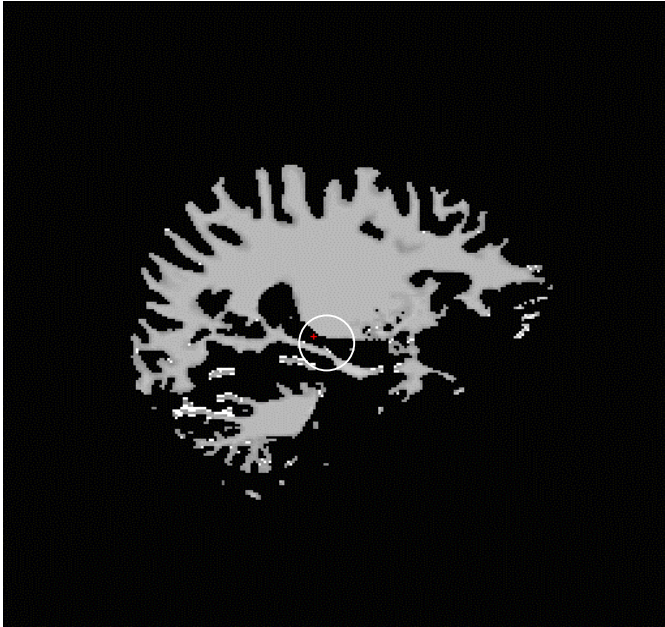
BEFORE CORRECTION-IMAGE 1



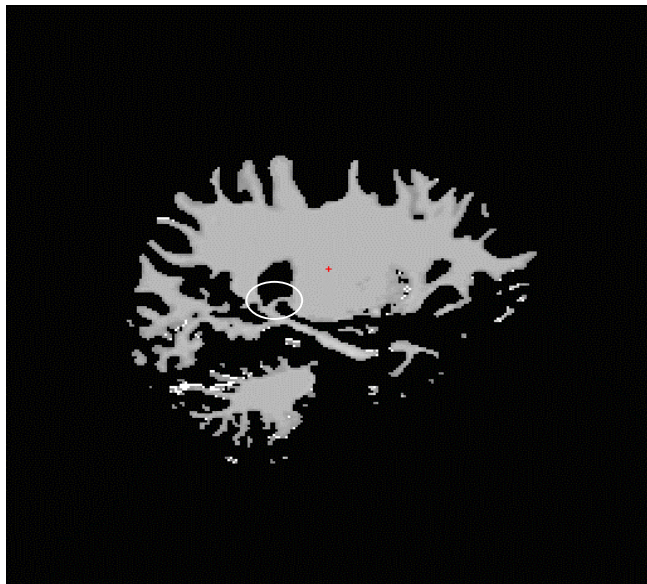
In this slice, the connection between the hippocampus and the subcortical structures needs to be erased.

AFTER CORRECTION-IMAGE 1

As can be seen from the corrected sagittal image below, the fornix has been removed. To start erasing the fornix, find the first slice where the fornix connects the temporal strand to the subcortical structures and erase that connection. Apply the same erasing procedure to all subsequent slices where the fornix connects the temporal strand and the subcortical structures.

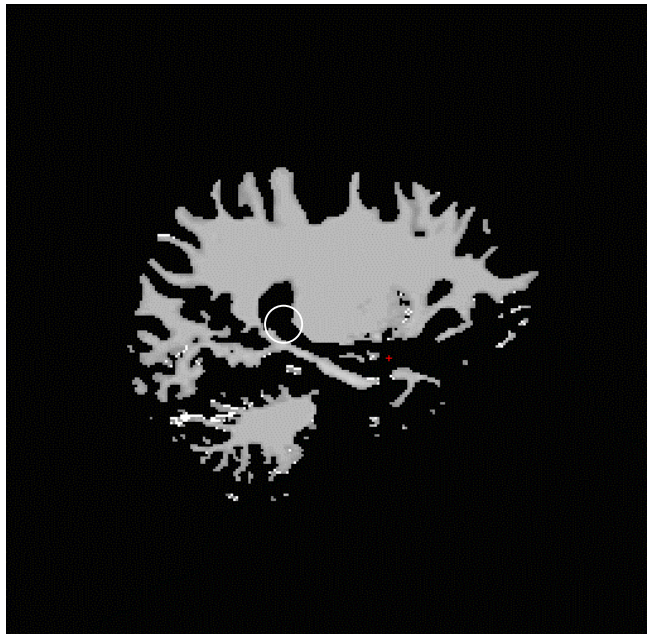


BEFORE CORRECTION- IMAGE 2

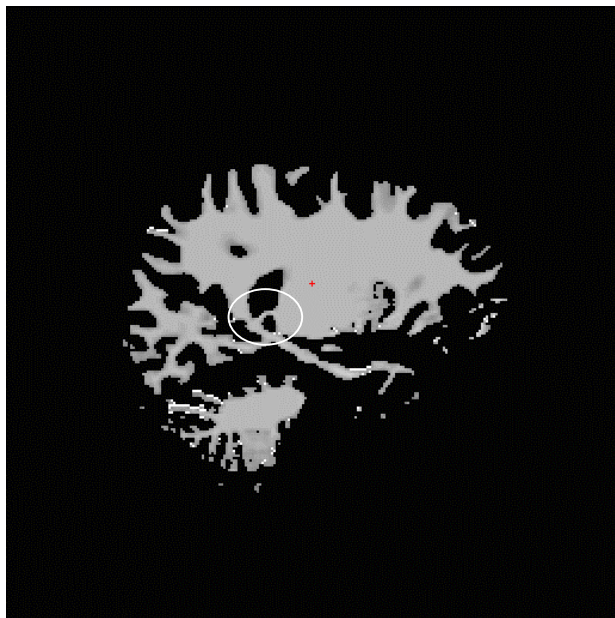


In this slice, the fornix is present and needs to be erased

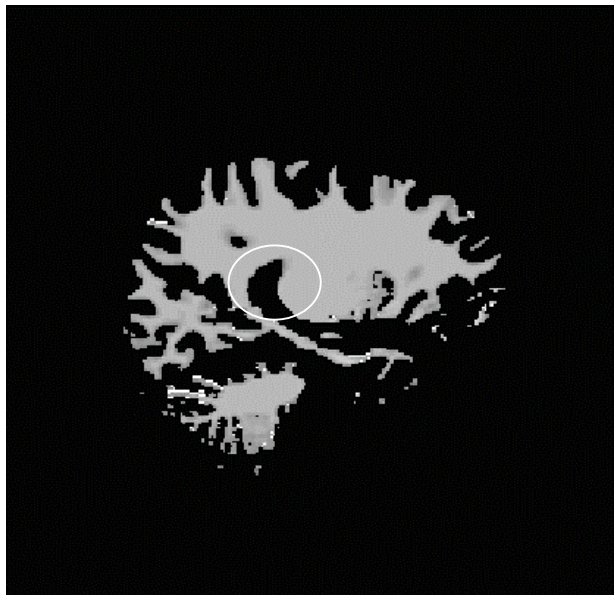
AFTER CORRECTION-IMAGE 2



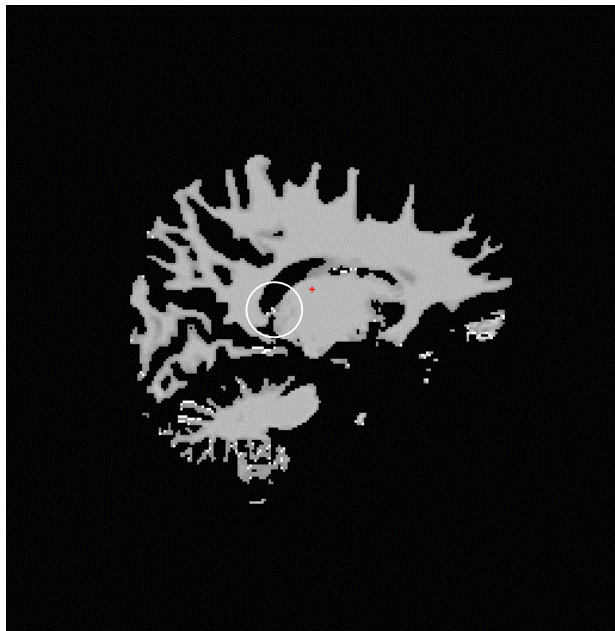
BEFORE CORRECTION-IMAGE 3



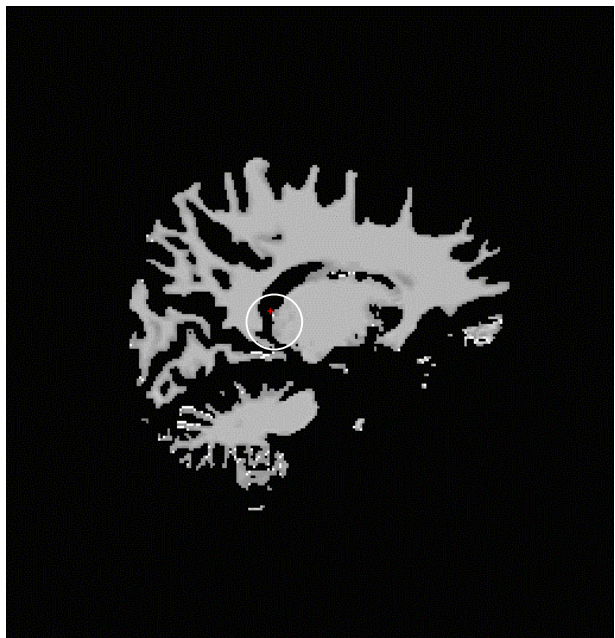
AFTER CORRECTION-IMAGE 3



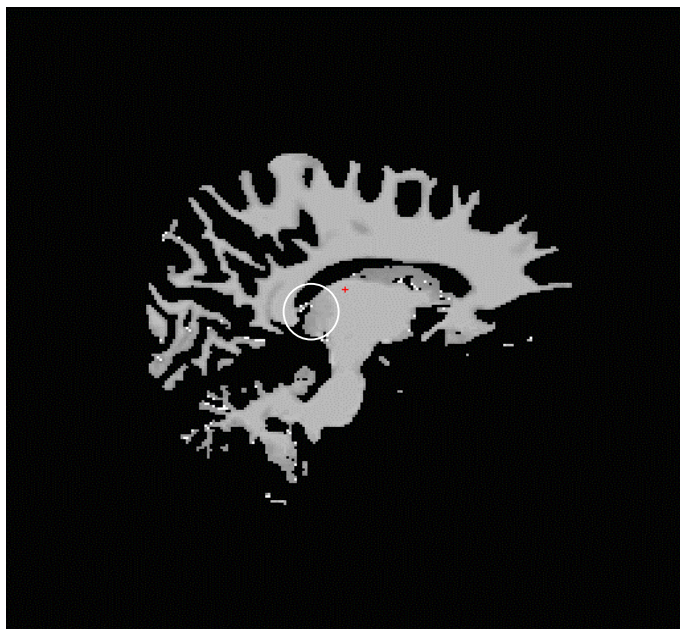
BEFORE CORRECTION-IMAGE 4



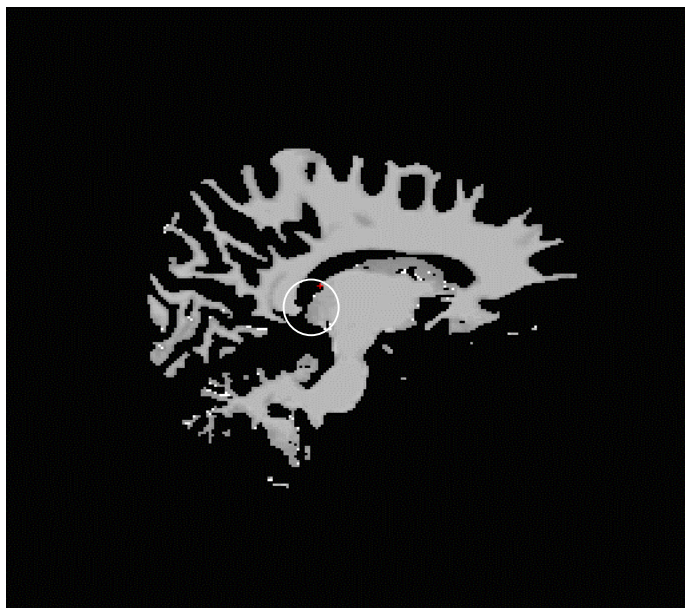
AFTER CORRECTION-IMAGE 4



BEFORE CORRECTION-IMAGE 5



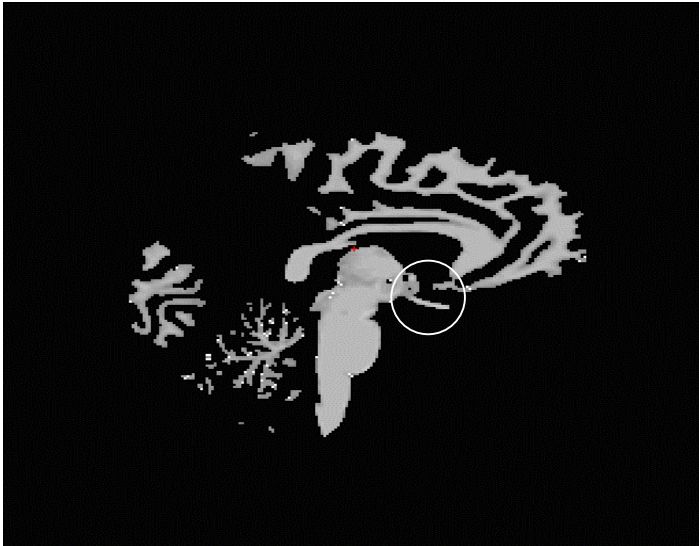
AFTER CORRECTION-IMAGE 5



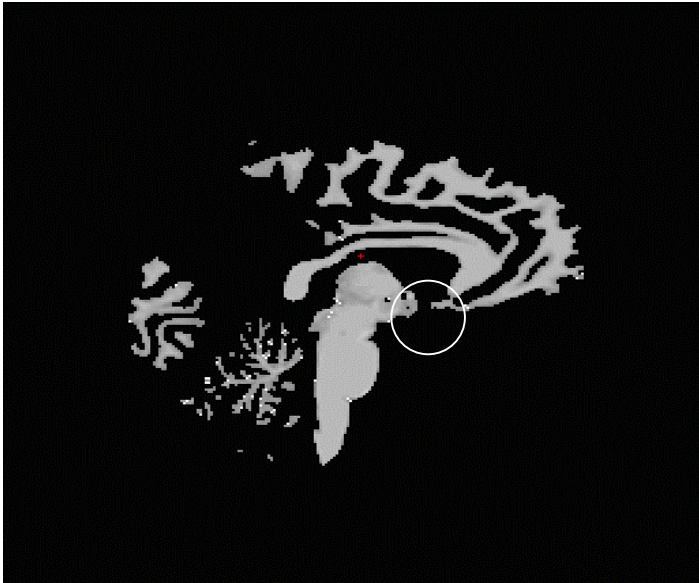
Once all the fornix has been erased, continue on to the optic nerve.

Optic Nerve

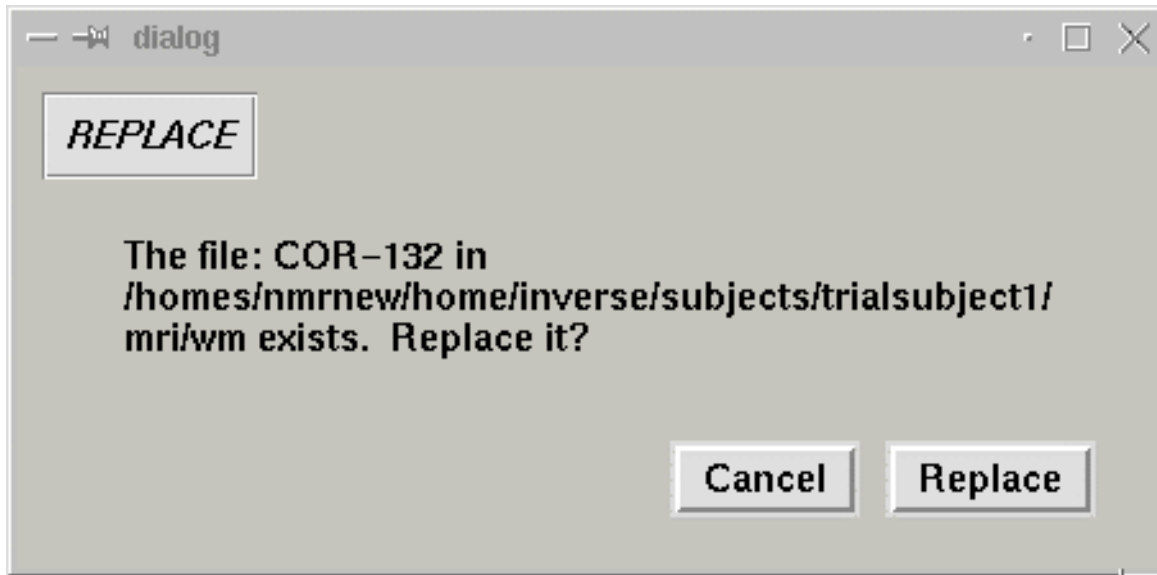
BEFORE CORRECTION-IMAGE 1



AFTER CORRECTION-IMAGE 2



After editing, save the changes made by clicking the **SAVEIMGS** button in Medit and choose **Replace** once the dialog box comes on

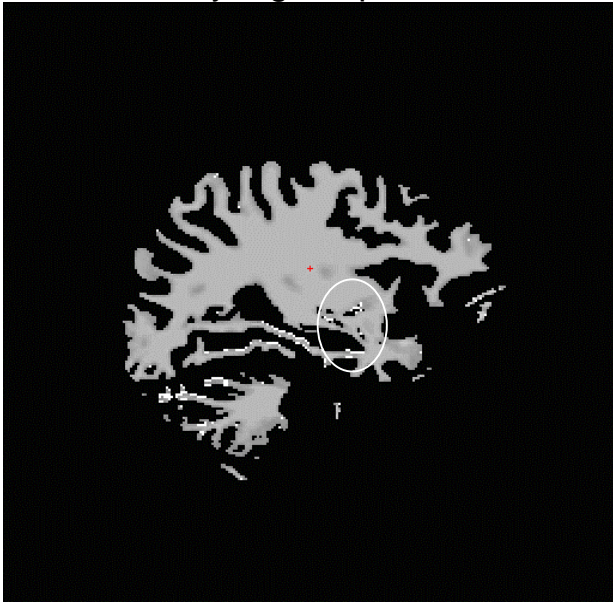


Basal Ganglia (Caudate, Putamen)

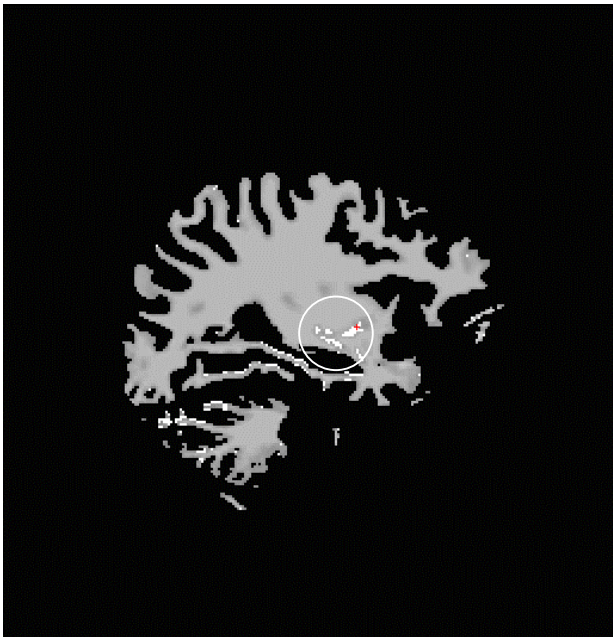
The basal ganglia needs to be filled in. Use the images below as a guide to filling in the basal ganglia. Like the fornix, corrections are best made in the sagittal view (though they can be made in the horizontal or coronal view as well) and the optimum brush size is of radius 1. To start the edits, find the first slice where the basal ganglia is not filled in, start filling and stop the edits once the basal ganglia becomes fully separated from the rest of cortex. The regions requiring correction are labeled by a white circle.

BEFORE CORRECTION-IMAGE 1

Here the claustrum, an area between the basal ganglia and the insula, requires filling. This is usually a good place to start correcting defects for the basal ganglia area.

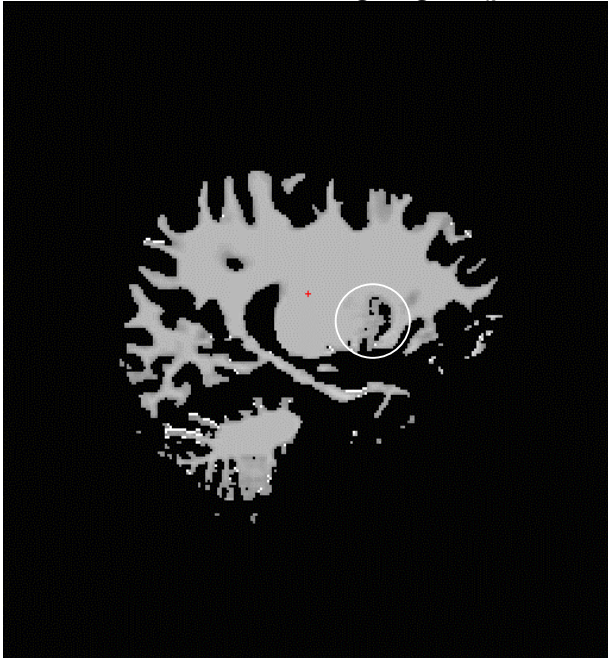


AFTER CORRECTION-IMAGE 2

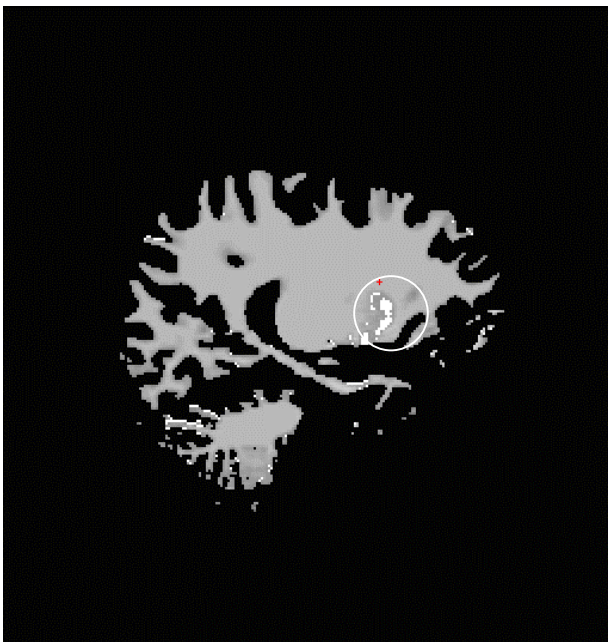


BEFORE CORRECTION-IMAGE 2

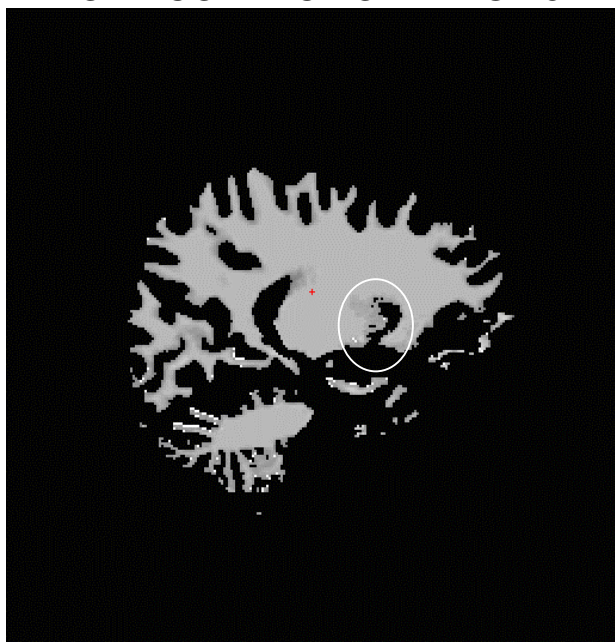
Here the actual basal ganglia (putamen) defects arise and need to be filled in.



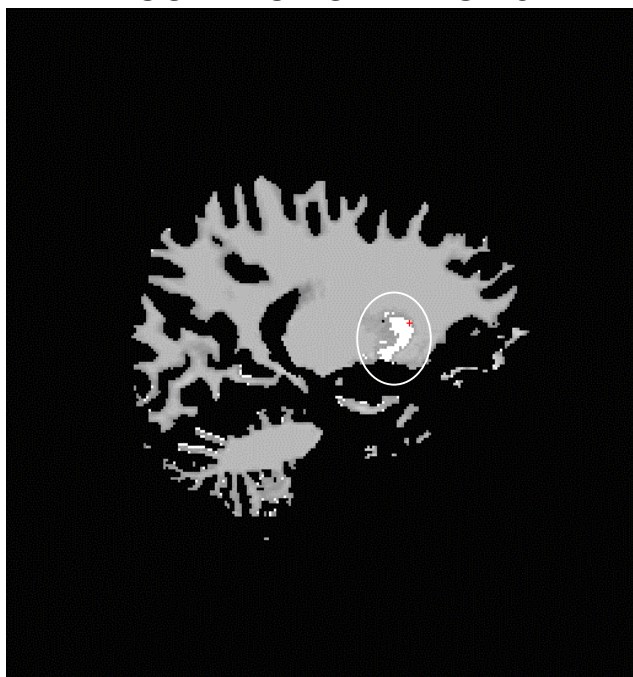
AFTER CORRECTION-IMAGE 2



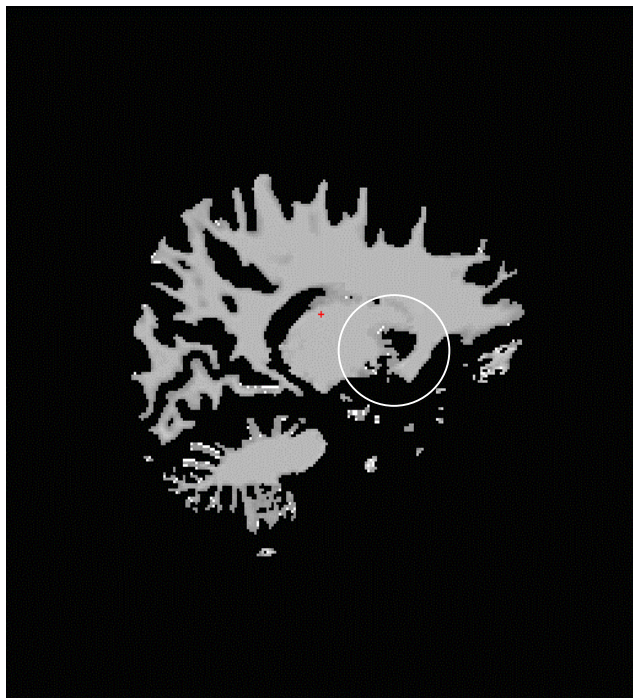
BEFORE CORRECTION-IMAGE 3



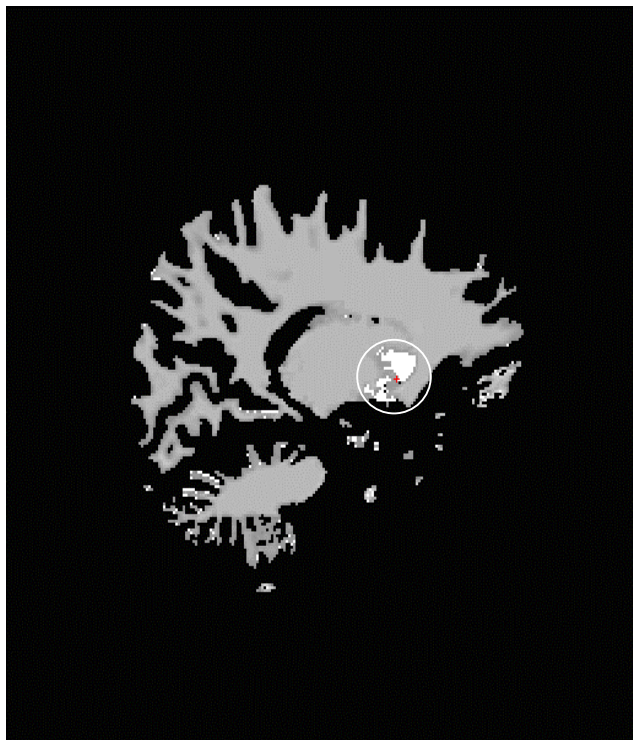
AFTER CORRECTION-IMAGE 3



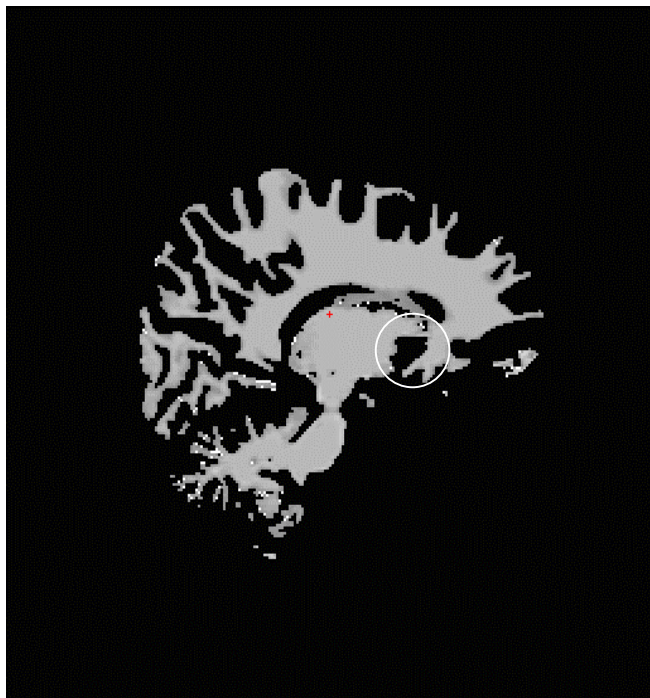
BEFORE CORRECTION-IMAGE 4



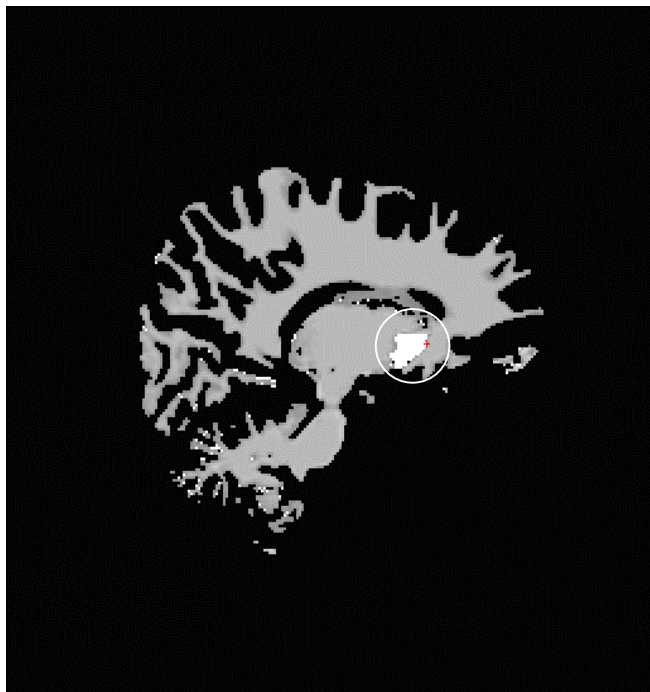
AFTER CORRECTION-IMAGE 4



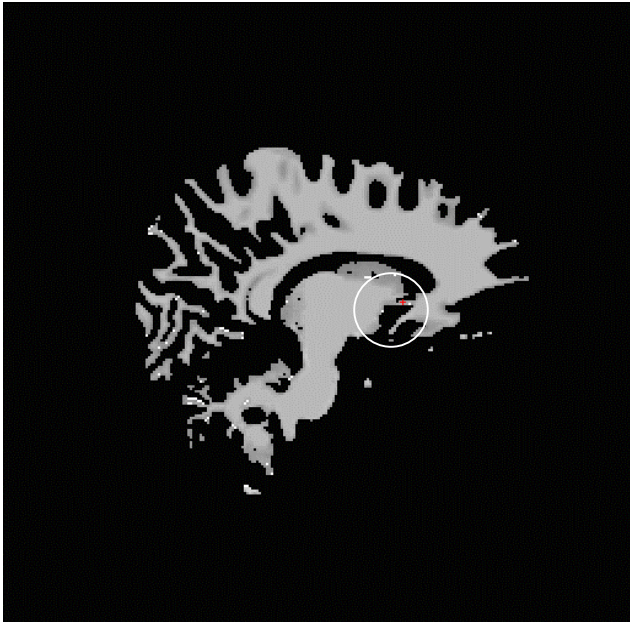
BEFORE CORRECTION-IMAGE 5



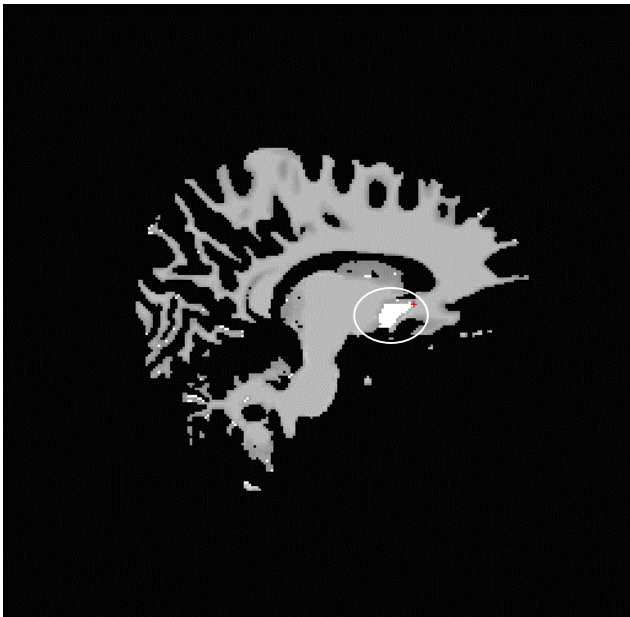
AFTER CORRECTION-IMAGE 5



BEFORE CORRECTION-IMAGE 6



AFTER CORRECTION-IMAGE 6

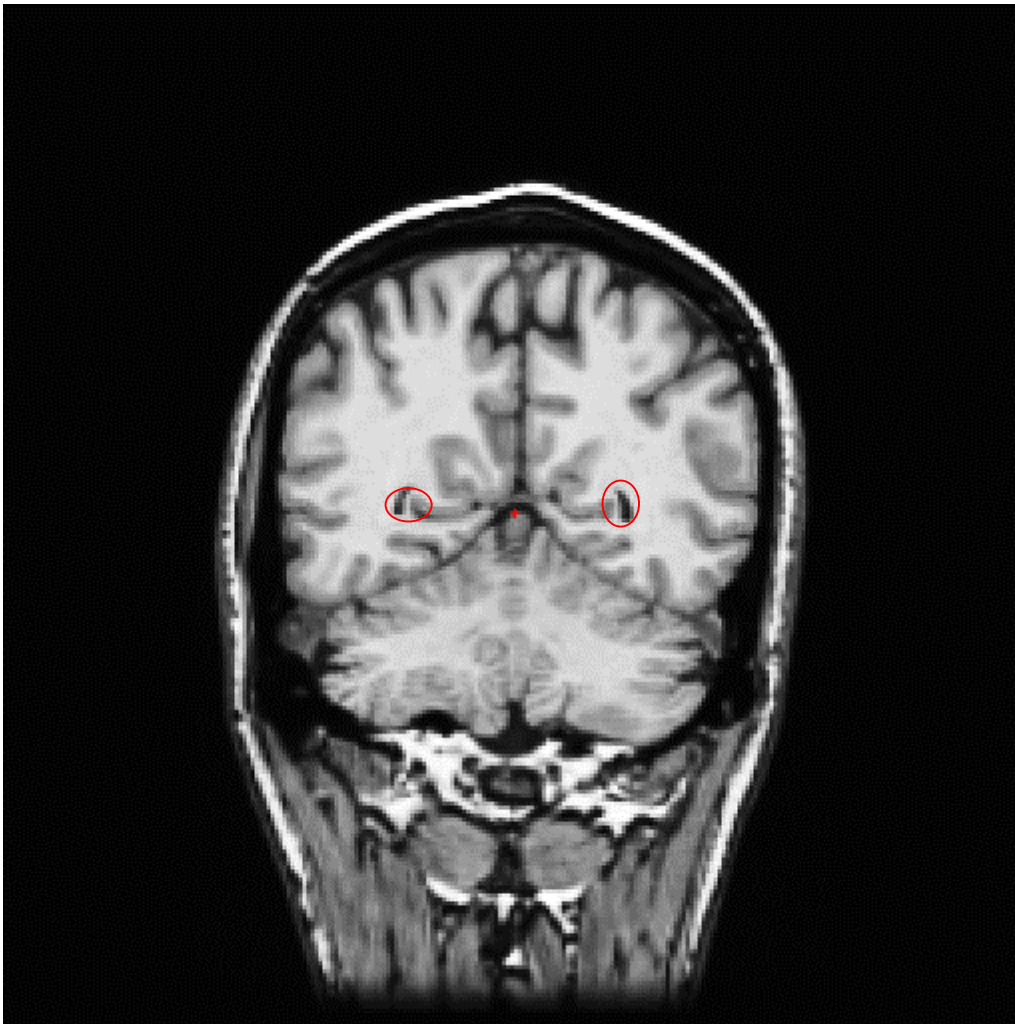


This is usually a good place to stop the edits since the basal ganglia separates off from the cortex in the proceeding slice.

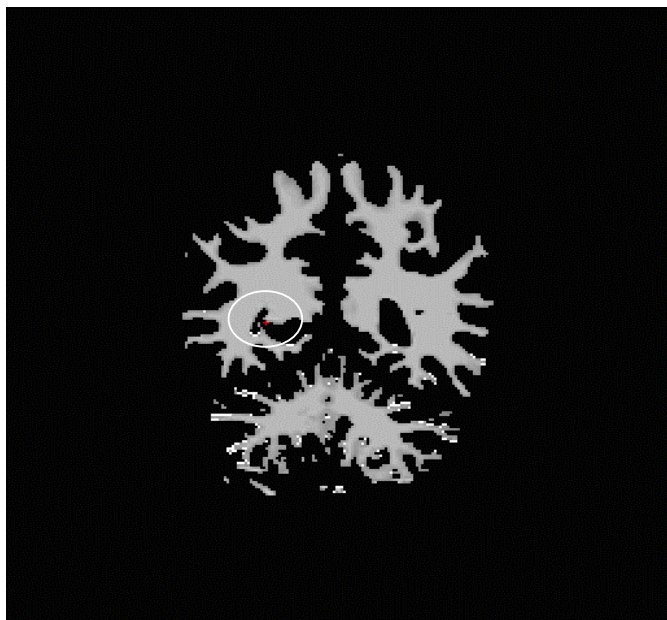
Lateral Ventricle

The lateral ventricle is a tube-like structure that requires filling. The occipital horn of the lateral ventricle is very thin and thus does not get segmented as white matter. The coronal view and a brush of radius 1 are best for correcting lateral ventricle defects. Note that the lateral ventricle needs to be filled in both hemispheres and can be done so simultaneously in the coronal views. The images below serve as a guide to editing the lateral ventricle defects: start filling in when the ventricle appears, keep filling the ventricle until it breaks off on its own. The region requiring correction is labeled by a white circle.

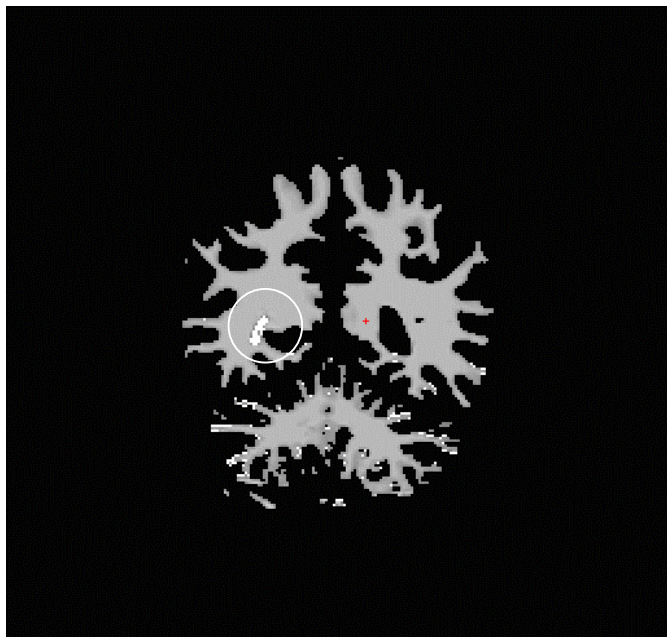
T1 IMAGE-LATERAL VENTRICLE



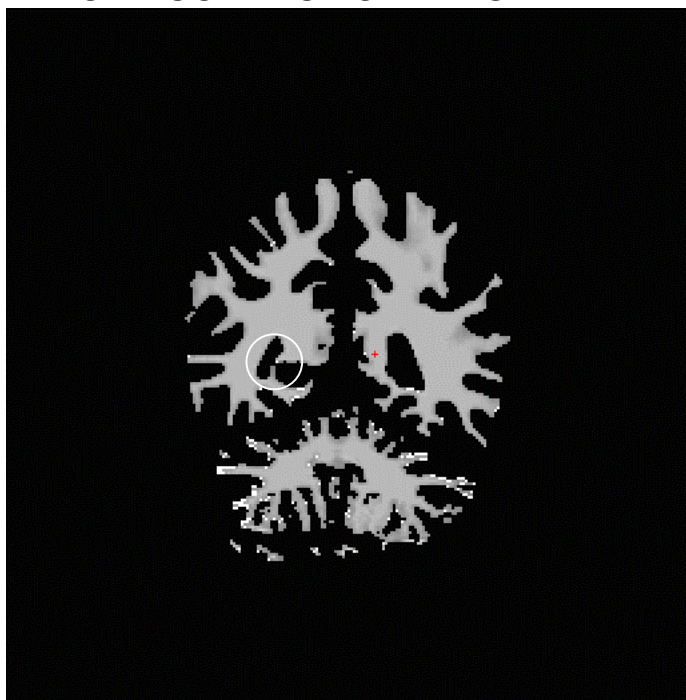
BEFORE CORRECTION-IMAGE 1



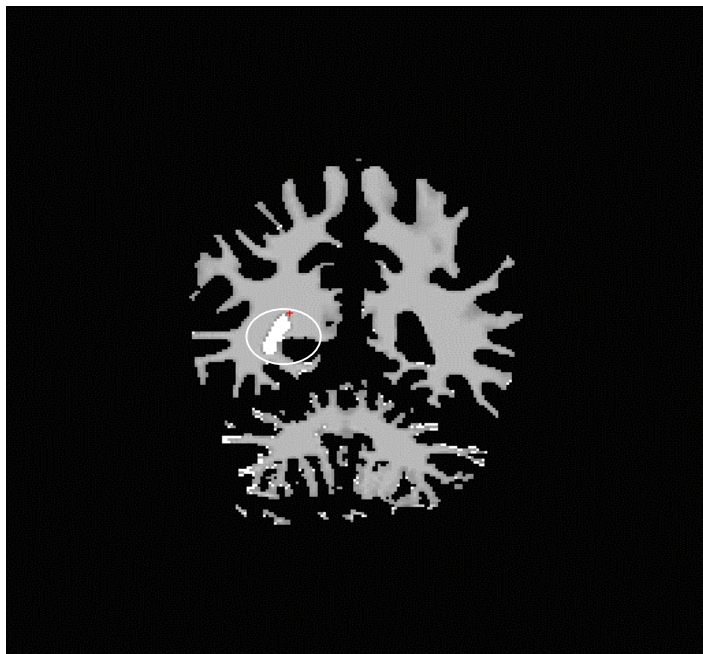
AFTER CORRECTION-IMAGE 1



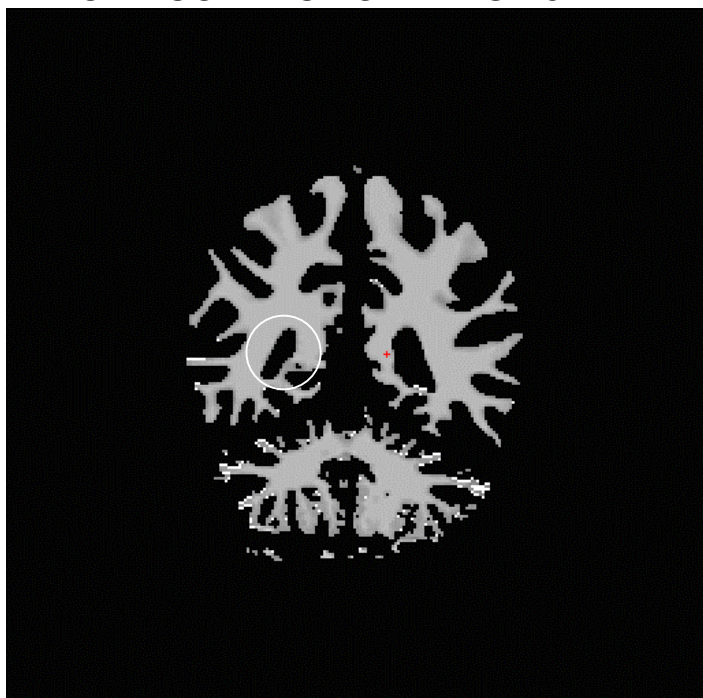
BEFORE CORRECTION-IMAGE 2



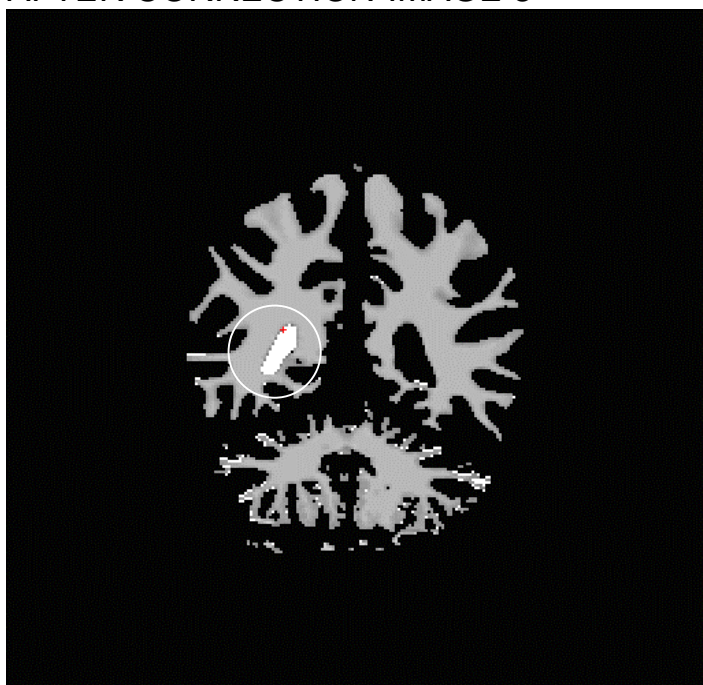
AFTER CORRECTION-IMAGE 2



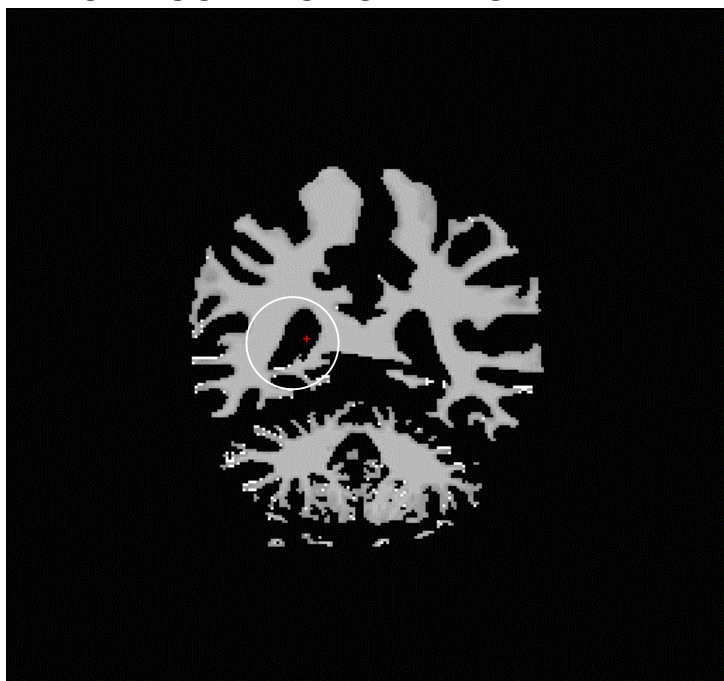
BEFORE CORRECTION-IMAGE 3



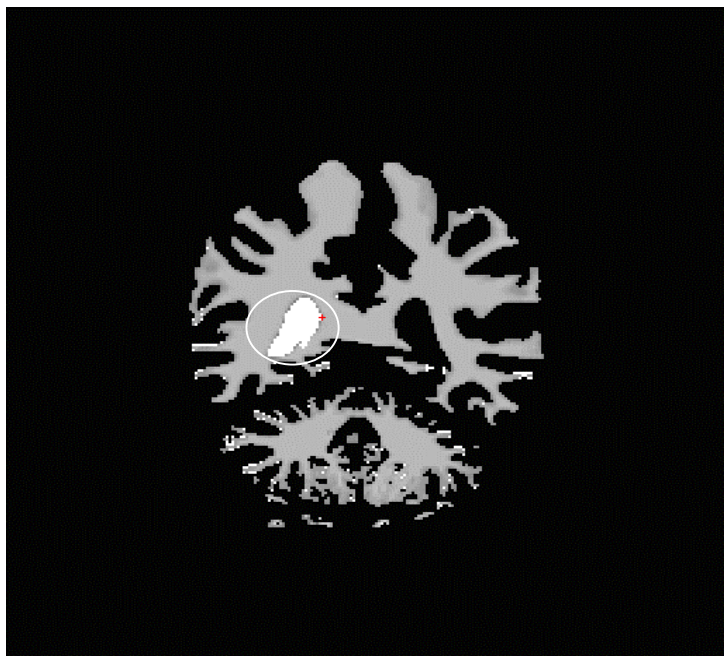
AFTER CORRECTION-IMAGE 3



BEFORE CORRECTION-IMAGE 4



AFTER CORRECTION-IMAGE 4



BEFORE CORRECTION-IMAGE 5



AFTER CORRECTION-IMAGE 5

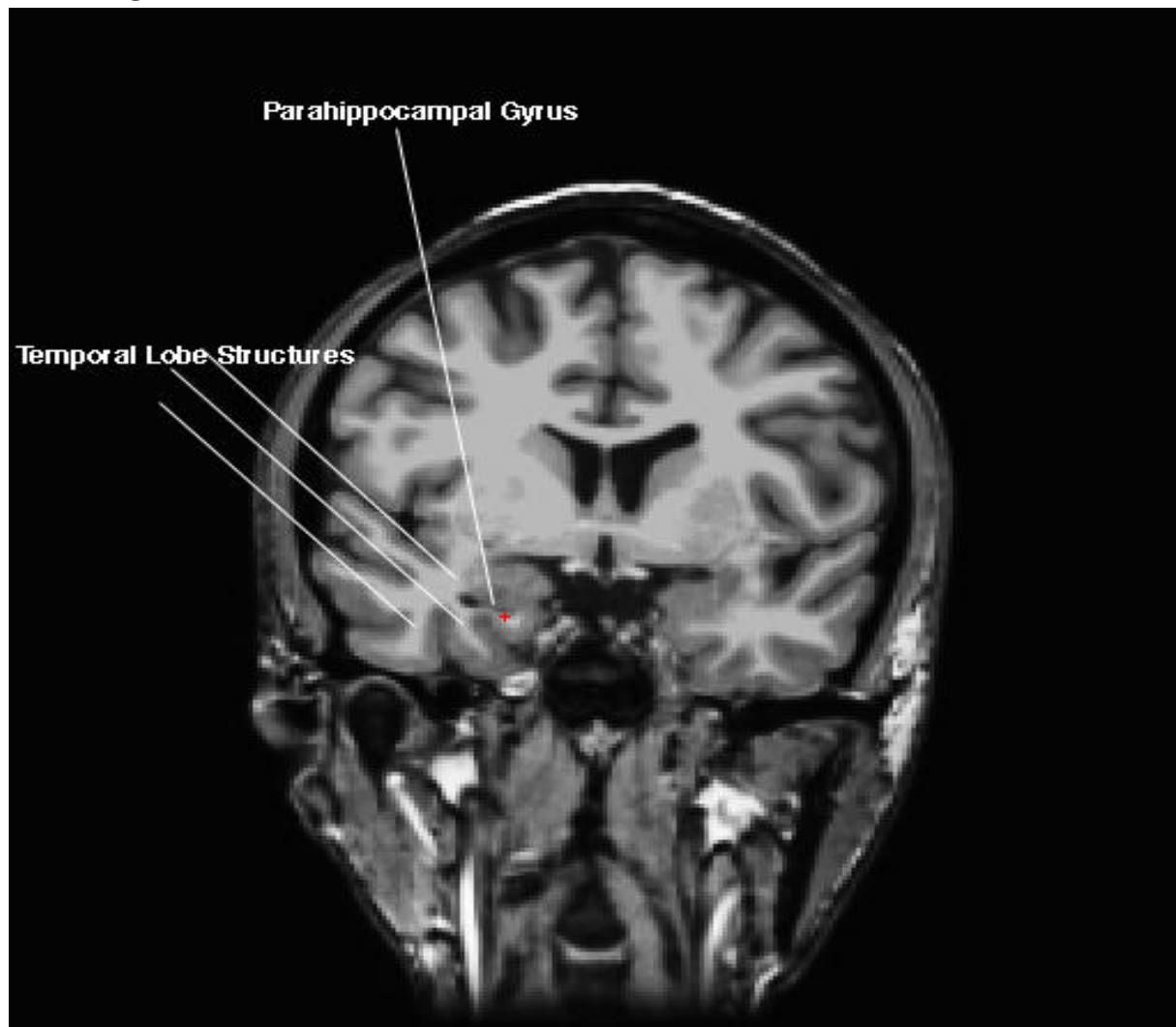


This is the last slice where the lateral ventricle needs to be filled in. In proceeding slices, the ventricle breaks off.

Temporal Lobe

The defects arising due to the temporal lobe are the most difficult to fix. Most of the time with the temporal defects, the parahippocampal gyrus is broken or very thin and thus either needs to be filled in or thickened up. Below are a set of images meant to serve as a guide for correcting temporal lobe defects. The coronal view and a brush size of radius 0 are optimal for editing temporal defects. The region requiring correction is labeled by a white circle.

T1 IMAGE



BEFORE CORRECTION-IMAGE 1



Here the parahippocampal gyrus is very thin and needs to be thickened up.

AFTER CORRECTION-IMAGE 1

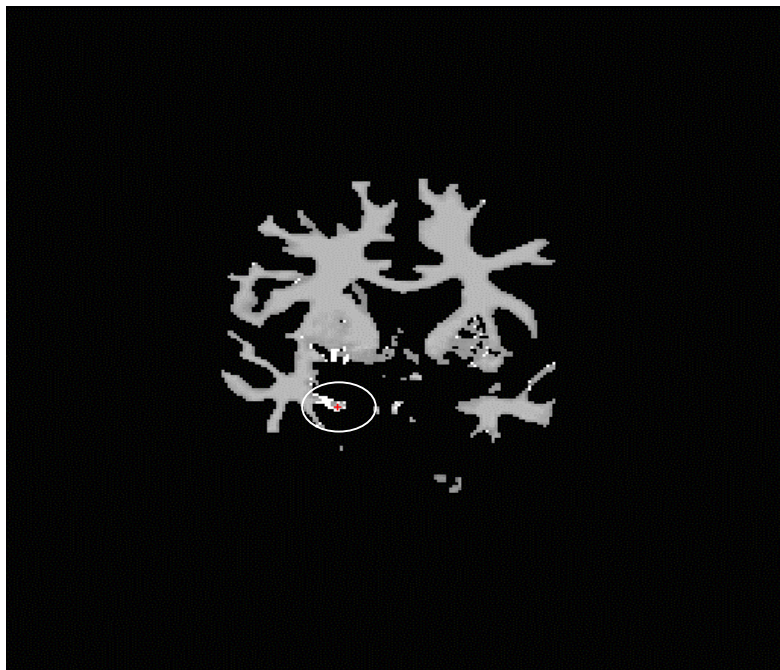


BEFORE CORRECTION-IMAGE 2

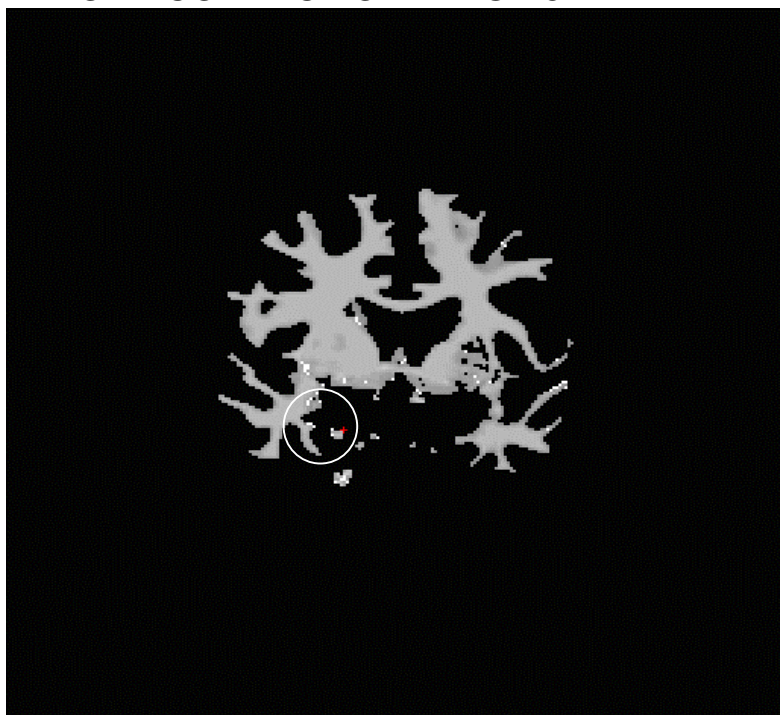


In this subsequent image, the parahippocampal gyrus actually breaks off and needs to be filled in.

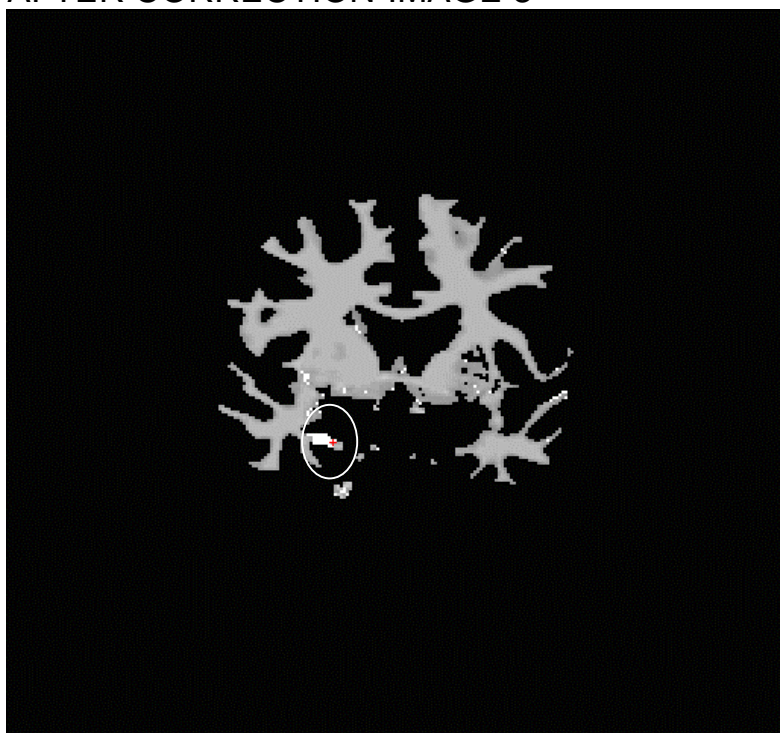
AFTER CORRECTION-IMAGE 2



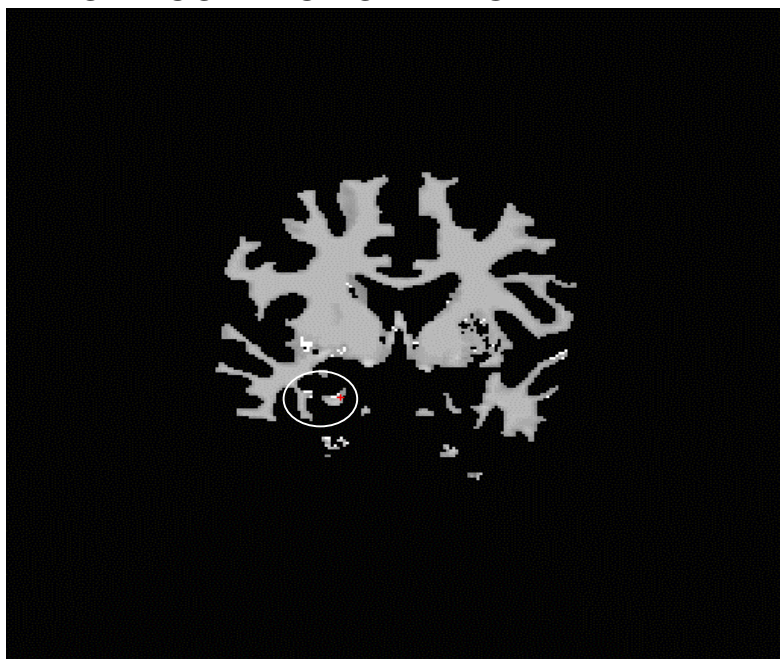
BEFORE CORRECTION-IMAGE 3



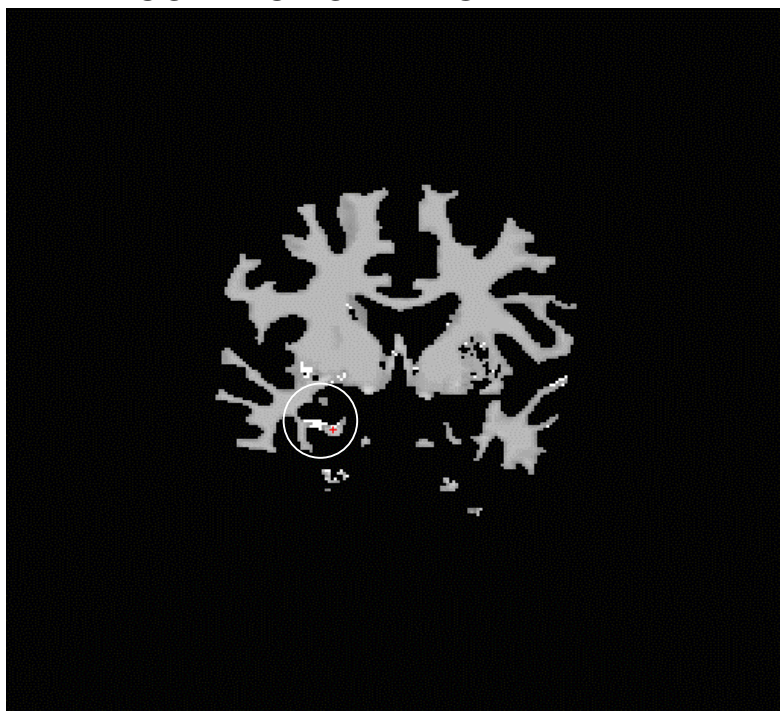
AFTER CORRECTION-IMAGE 3



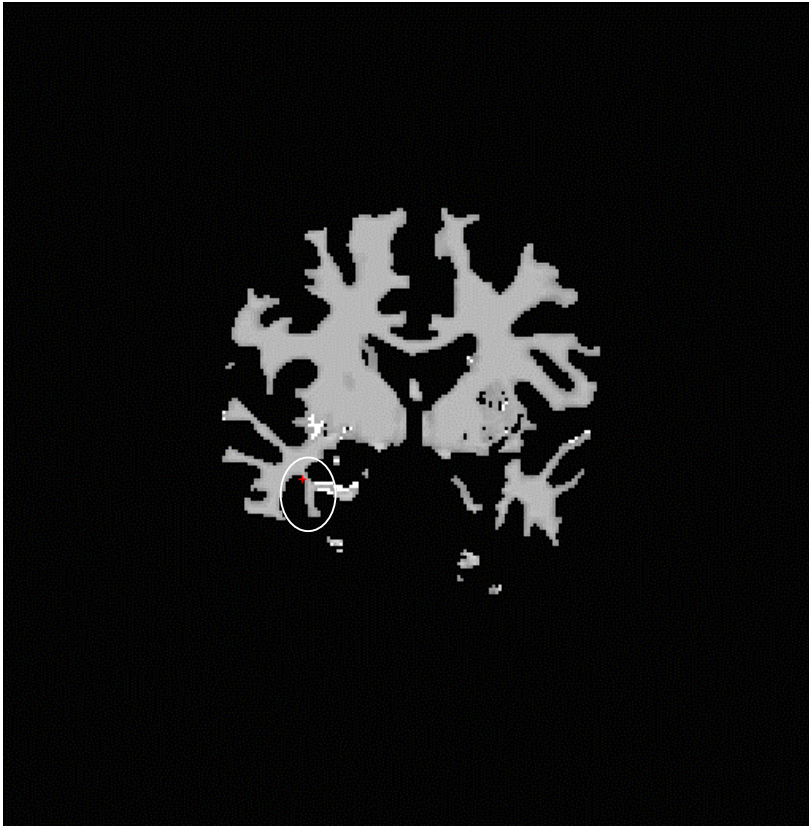
BEFORE CORRECTION-IMAGE 4



AFTER CORRECTION-IMAGE 4



PROBLEMATIC TEMPORAL AREA



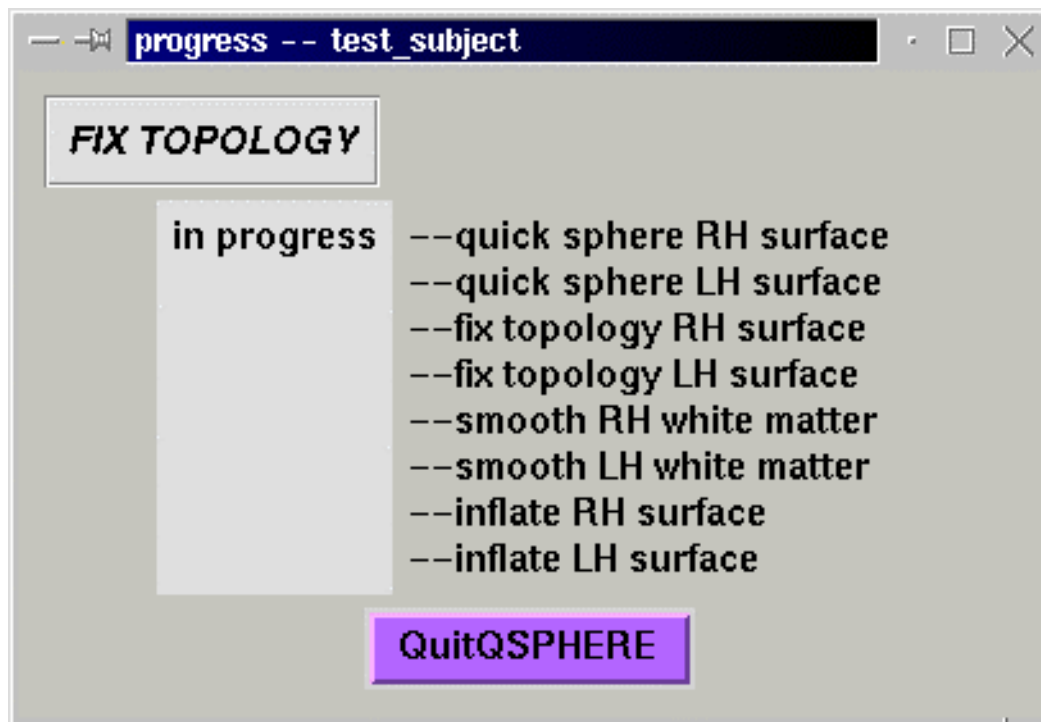
The temporal area near the cross in the figure above is particularly problematic and causes surface defects. Usually it is either broken, in which case it needs to be filled in or very thin, in which case it needs to be thickened up.

NOTE: The above described anatomical defects may require several iterations before they are completely fixed. Once edits are made to the wm volume when correcting defects and saved, the **Create Surface** step needs to be re-run in order for the changes to appear.

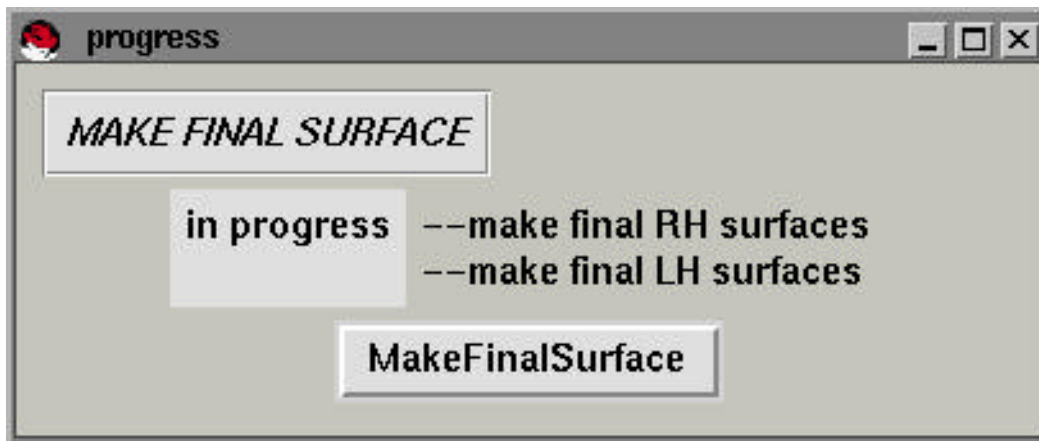
Topology Fixing

Once the surface is free of anatomical defects, the automated topology fixer can be used to remove the smaller, topological defects.

Under the SubjectTools menu, select **Fix Surface Topology**



Make Final Surfaces



This is the next step after the defect free surfaces are available. This automated step starts a two-part background process to create the final left and right hemisphere cortical surfaces. **Make Final Surface** should only be run once the surface editing is complete (i.e. the surface is topologically correct).

Part 1: Make Final Right Hemisphere Surfaces

The output files written by this procedure are:

- surface: \$SUBJECTS_DIR/\$name/surf/rh.white
- surface: \$SUBJECTS_DIR/\$name/surf/rh.pial

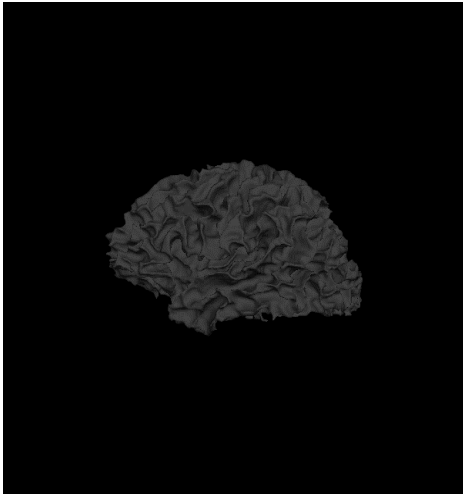
Part 2: Make Final Left Hemisphere Surfaces

The output files written by this procedure are:

- surface: \$SUBJECTS_DIR/\$name/surf/lh.white
- surface: \$SUBJECTS_DIR/\$name/surf/lh.pial

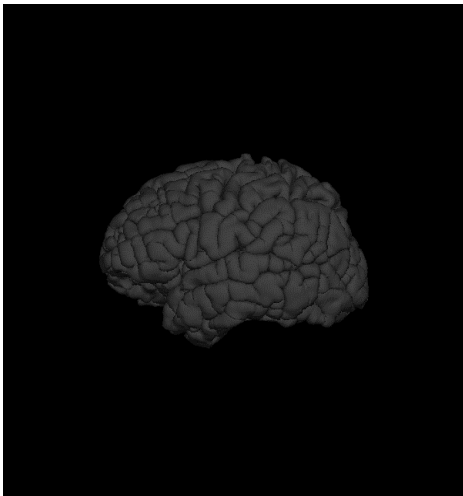
The Make Final Surface generates two additional surfaces:

1. The **white** surface



white surface

2.The **pial** surface



pial surface

Cutting Surfaces

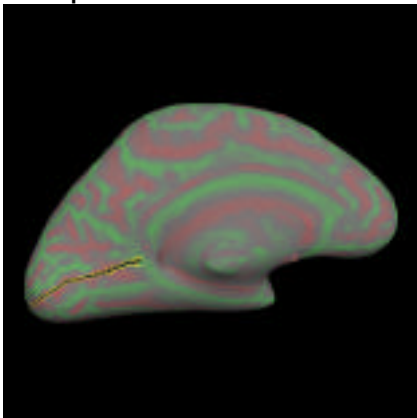
This process is optional and provides the user with flattened images of the whole brain or select parts (ex. occipital lobe) of the brain.

Cutting the Occiput Surface

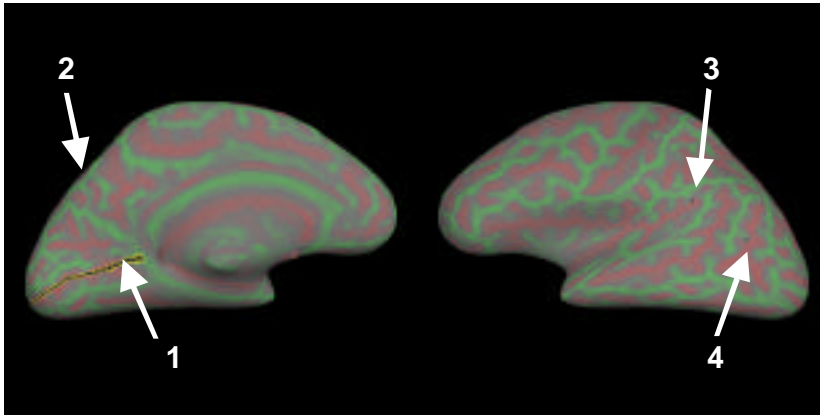
The occiput patch represents the occipital pole with a cut down the calcarine fissure. This step is particularly useful in experiments designed to study visual stimuli.

The procedure is as follows:

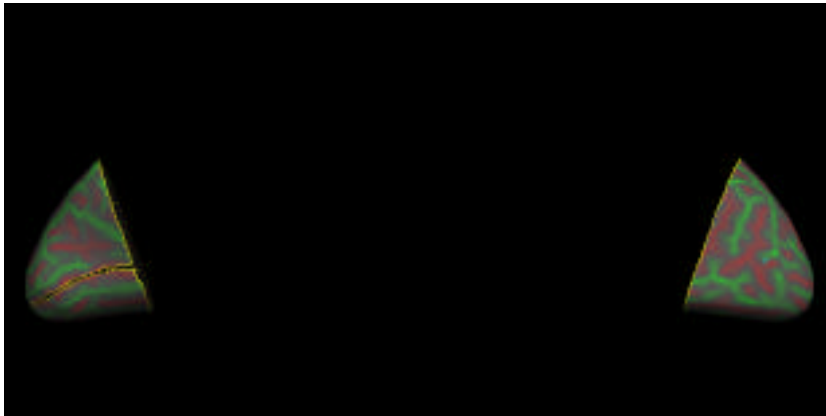
1. make calcarine sulcus relaxation cut
select points (**LEFT-CLICK**) along the calcarine fissure beginning at the occipital pole and moving anterior.
open-line cut with **CUTLINE**



2. specify cutting plane
select three points (labeled 1, 2, and 3 below) to define the cutting plane, and a fourth point (labeled 4 below) to specify which portion of the surface to keep (**LEFT-CLICK**)



3. make the planar cut
CUTPLANE button

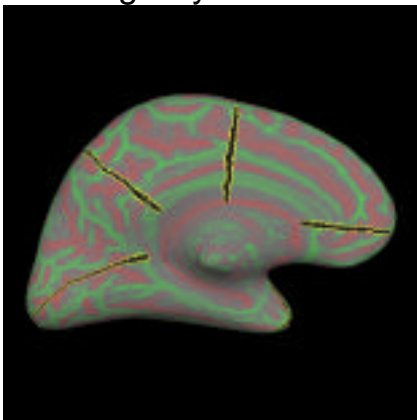


4. save patch
specify the patch name in the **patch** field and press **WRITE**
The default names for the occiput cortical surfaces are:
rh.full.patch.3d
lh.full.patch.3d

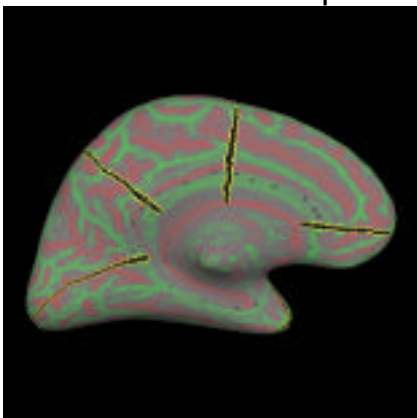
Cutting the Full Surface

The full surface represents an entire hemisphere without the mid-brain (middle of the medial surface).

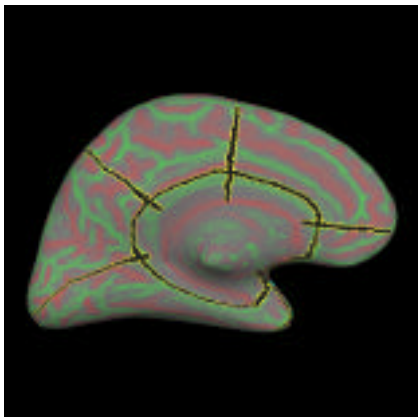
1. Make 5 relaxation cuts.
For each cut, select the points (**LEFT-CLICK**) and then press **LINE**.
a cut down the calcarine (same cut as for the occiput surface)
three equally spaced radial cuts on the medial surface
a sagittally oriented cut around the temporal pole



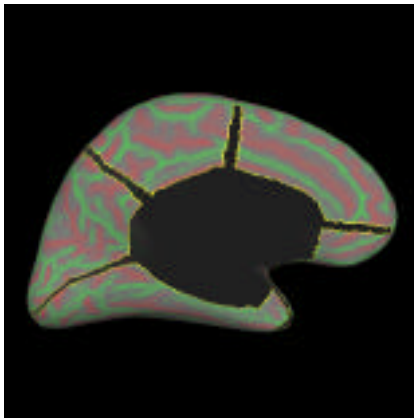
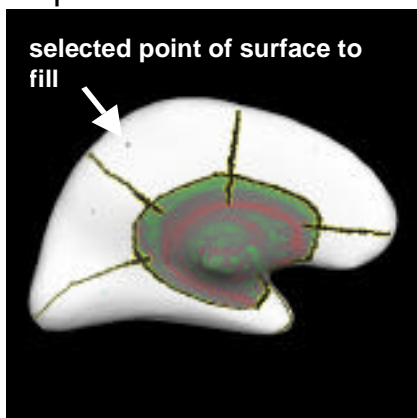
- (1) encircle midline region (corpus callosum and mid-brain structures) to remove:
LEFT-CLICK sequence



- (2) make closed-line cut
CUTAREA button

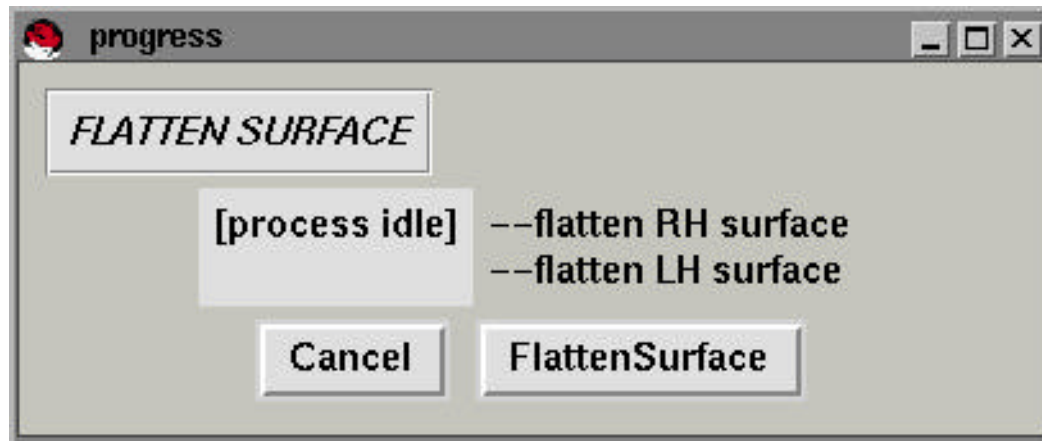


- (3) mark and fill region to save
single **LEFT-CLICK** in region to save
press **FILL** button



- (8) save patch
specify the patch name in the **patch** field and press **WRITE**
The default names for the full cortical surfaces with the midline removed are:
rh.full.patch.3d
lh.full.patch.3d

Flatten Surface



This step is run once the various cuts (occiput and full surface) have been made. This automated step starts a two-part background process to create the flattened left and right hemisphere cortical surfaces (or surface portions). (16-30 hours per full surface, 12 hours for the occiput surface).

Part 1: Flatten Right Hemisphere Surfaces

The output file written by this procedure is:

surface: \$SUBJECTS_DIR/\$name/surf/rh.*.patch.flat

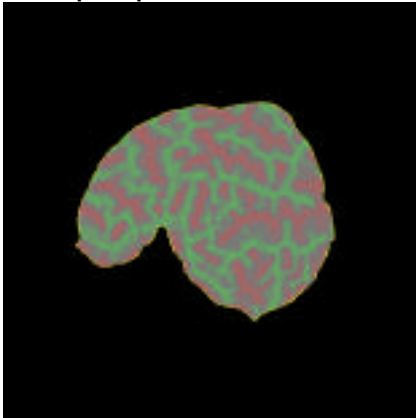
Part 2: Flatten Left Hemisphere Surfaces

The output file written by this procedure is:

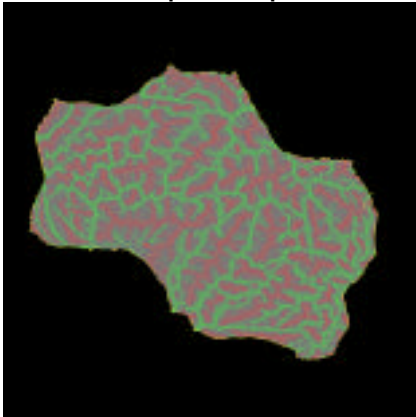
surface: \$SUBJECTS_DIR/\$name/surf/lh.*.patch.flat

Typical flattened patches:

Occiput patch



Full hemisphere patch



Sphere Surface

Starts a four-part background process to create the spherical left and right hemisphere cortical surfaces and then registers them with an average spherical cortical surface representation.

Part 1: Sphere Right Hemisphere Surface

The output file written by this procedure is:

surface: \$SUBJECTS_DIR/\$name/surf/rh.sphere

Part 2: Sphere Left Hemisphere Surface

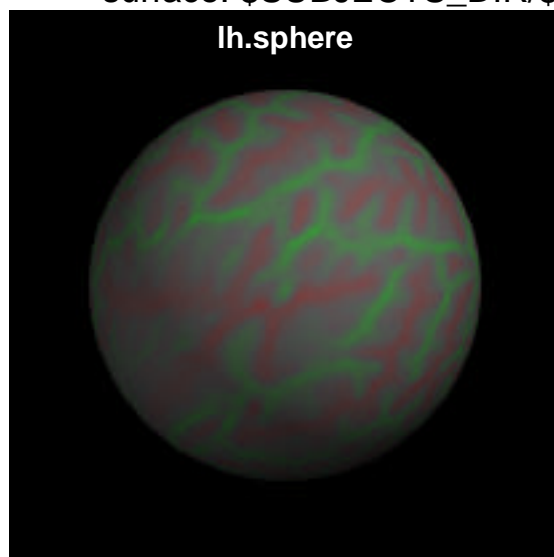
The output file written by this procedure is:

surface: \$SUBJECTS_DIR/\$name/surf/lh.sphere

Part 3: Register Right Hemisphere Surface

The output file written by this procedure is:

surface: \$SUBJECTS_DIR/\$name/surf/rh.sphere.reg



Part 4: Register Sphere Left Hemisphere Surface

The output file written by this procedure is:

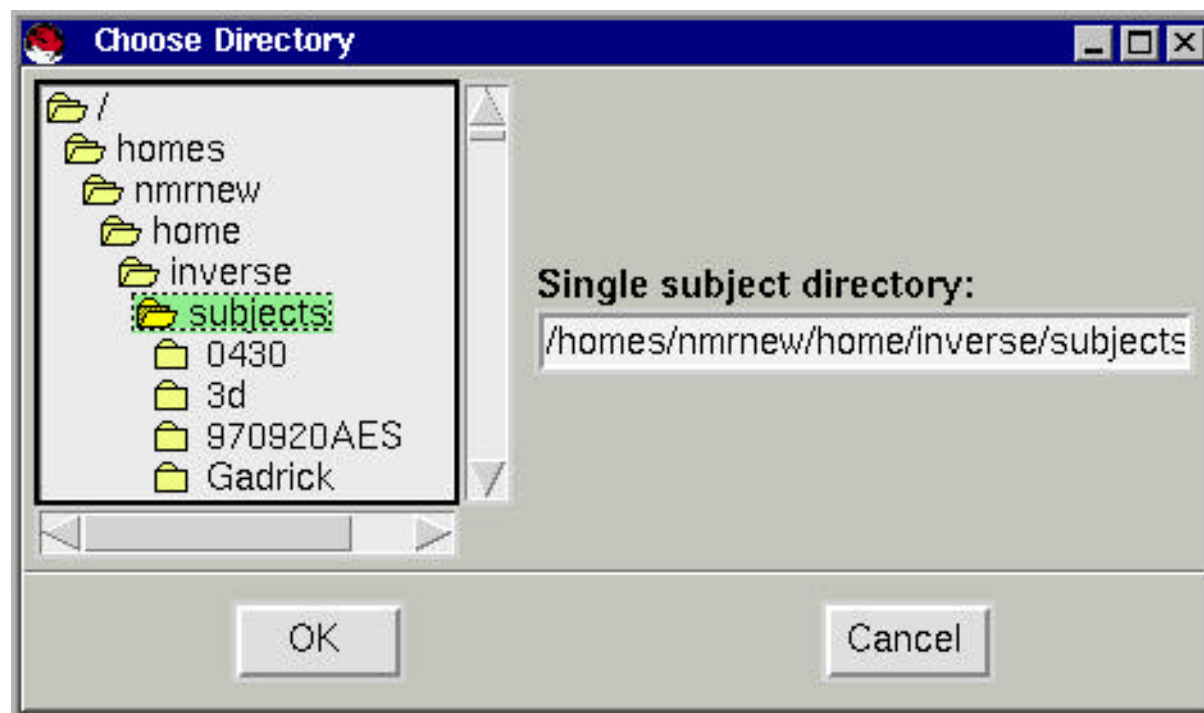
surface: \$SUBJECTS_DIR/\$name/surf/lh.sphere.reg

Additional Commands in Csurf

File Menu

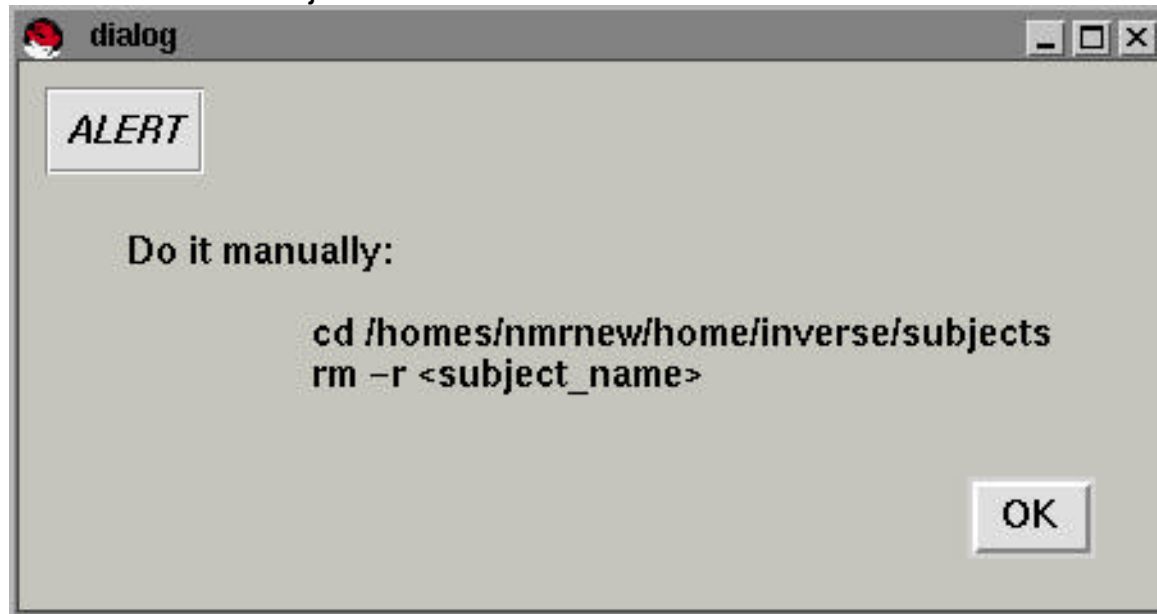
Open Subject

Opens an existing subject. Either select the subject directory on the left or enter the subject directly into the field on the right.

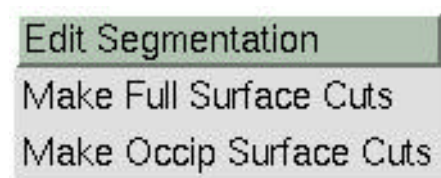


Delete Subject

Deletion of the subject is manual.



Edit Menu



Edit Segmentation

Starts both medit (to edit the white matter volume) and surfer (to view the inflated cortical surface). Medit reads in the wm (white matter) volume with the orig surface overlaid and surfer reads in the inflated surface.

For a detailed description of how to fix topological defects, see the section titled **“Editing Defects”**

Make Full Surface Cuts

Starts surfer using the inflated surface

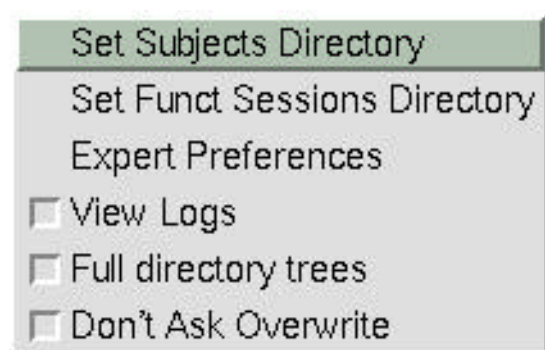
For a detailed description of how to make the full surface cuts, see the section titled **“Cutting the Full Surface.”**

Make Occiput Surface Cuts

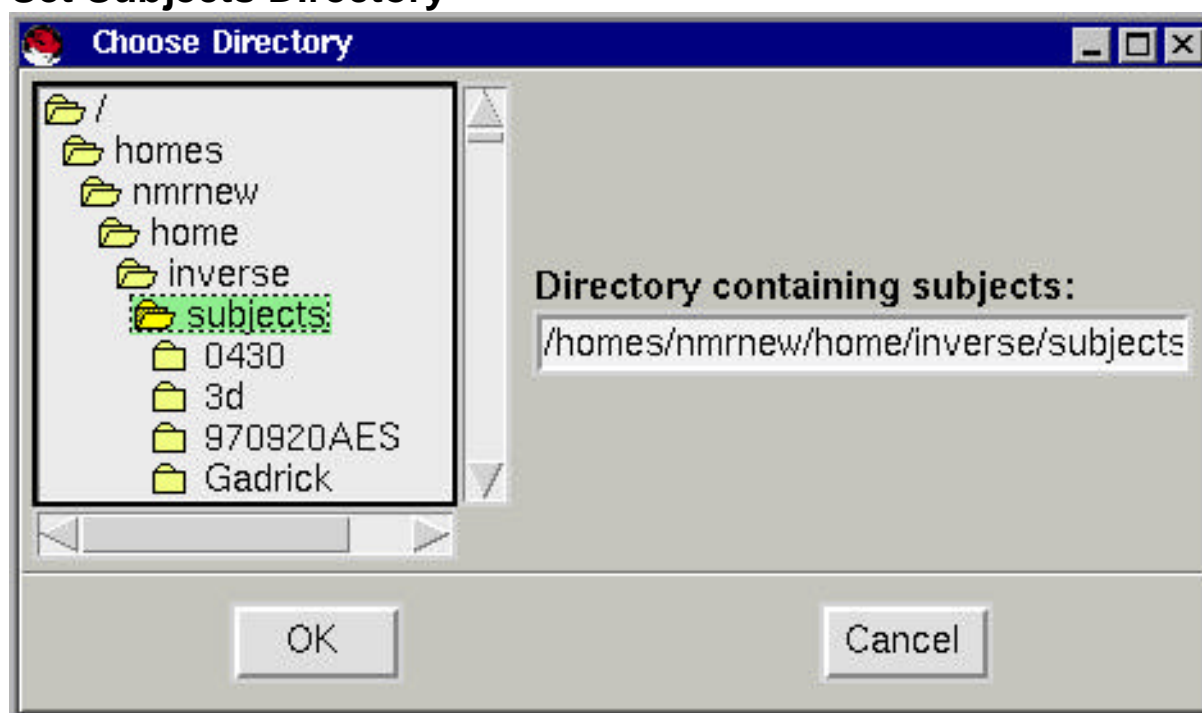
Starts surfer using the inflated surface

For a detailed description of how to make the occiput surface cuts, see the section titled **“Cutting the Occiput Surface.”**

Preferences



Set Subjects Directory

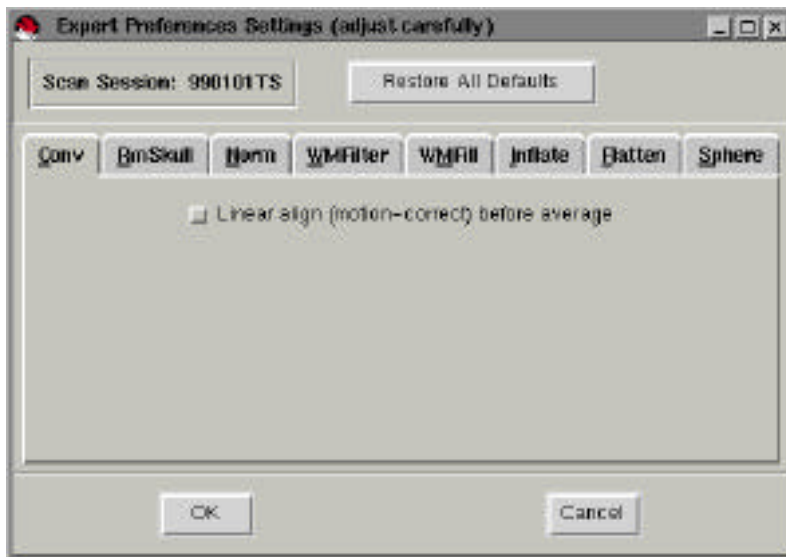


Sets the default directory for the subjects' structural data, volumes and surfaces.

Expert Preferences

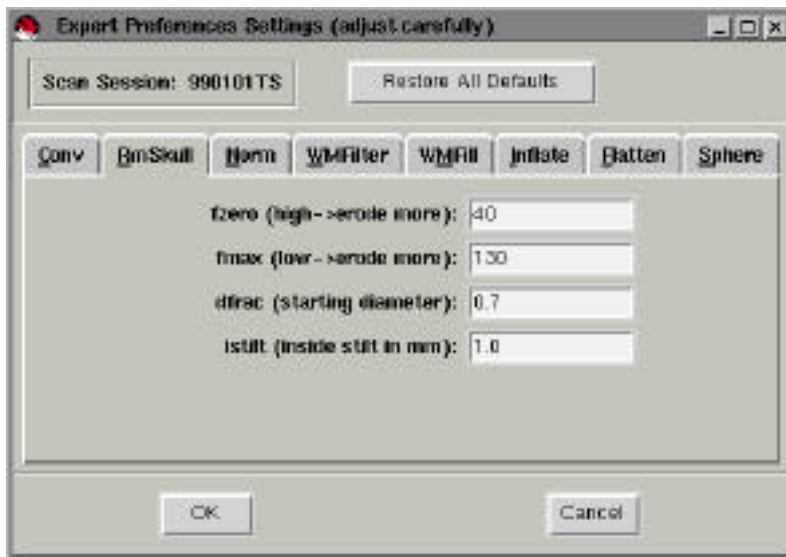
Provides additional parameters which can be adjusted if necessary.
To return to the original parameters, press **Restore All Defaults**.

Conv



Not supported. Do not modify.

Rmskull



These parameters are used in the skull stripping part of **Process Volume**.

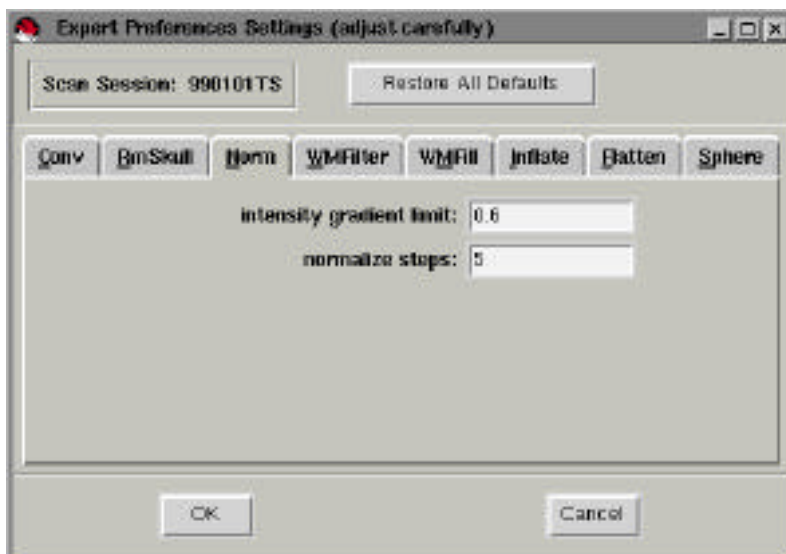
fzero: Minimum value while estimating outer brain surface. Larger values will strip more.

fmax: Maximum value for while estimating outer brain surface. Smaller values will strip more.

dfrac: Initial size of estimated outer brain surface.

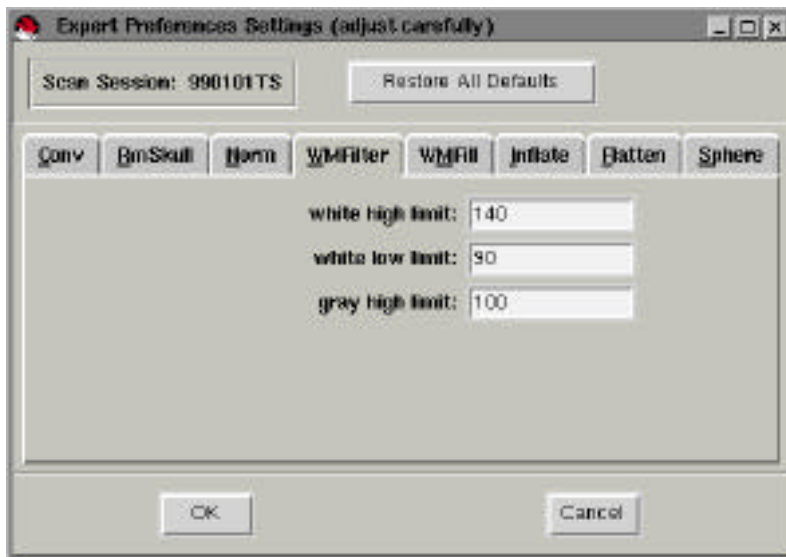
lstill: Minimum distance of outer brain surface from outer brain.

Normalize



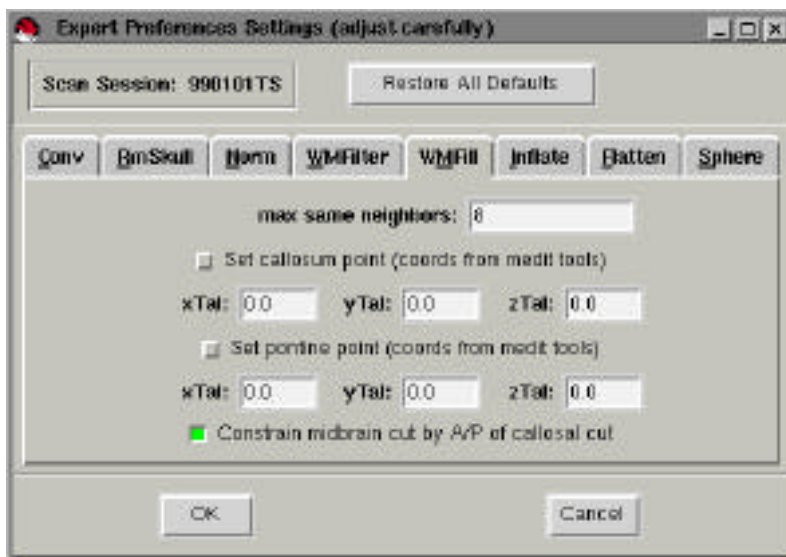
Not supported. Do not modify.

WMFilter



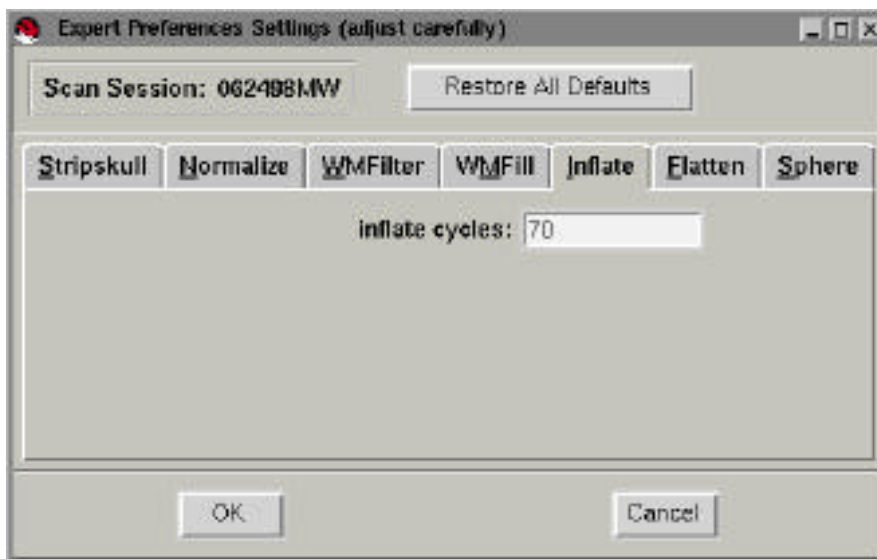
Not supported. Do not modify.

WMFill



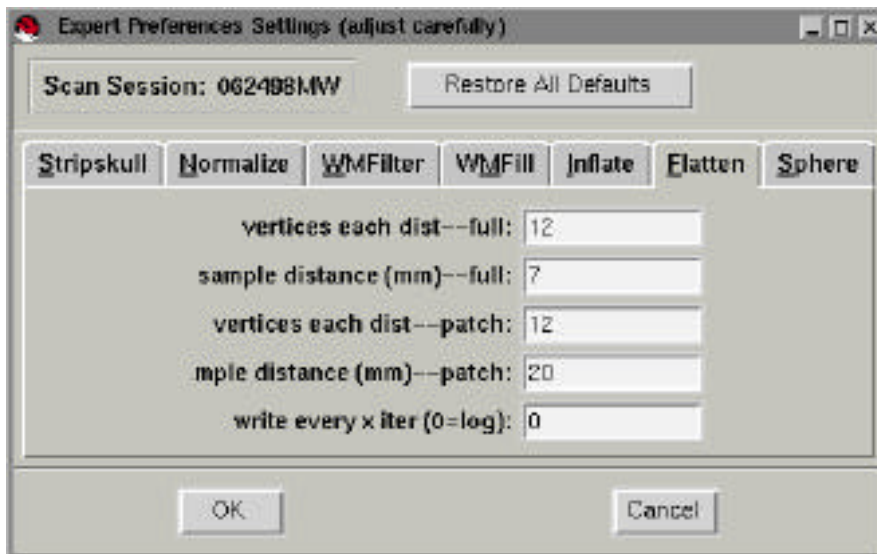
The coordinates specified here are used in **Part 1: Fill White Matter of Create Surface**. If the cutting planes fail, enter the Talairach coordinates of the corpus callosum or pons into the **WMFill** window and press the button next to “**Set callosum point**” or “**Set pontine point.**” If the Talairach transformation matrix is not available, enter the x, y, and z locations output by **medit**.

Inflate



This parameter is used during the cortical surface inflation in **Create Surface**. Fewer **inflate cycles** will result in a less smooth surface.

Flatten



These parameters are used during the flattening of the cortical surface in **Flatten Surface**.

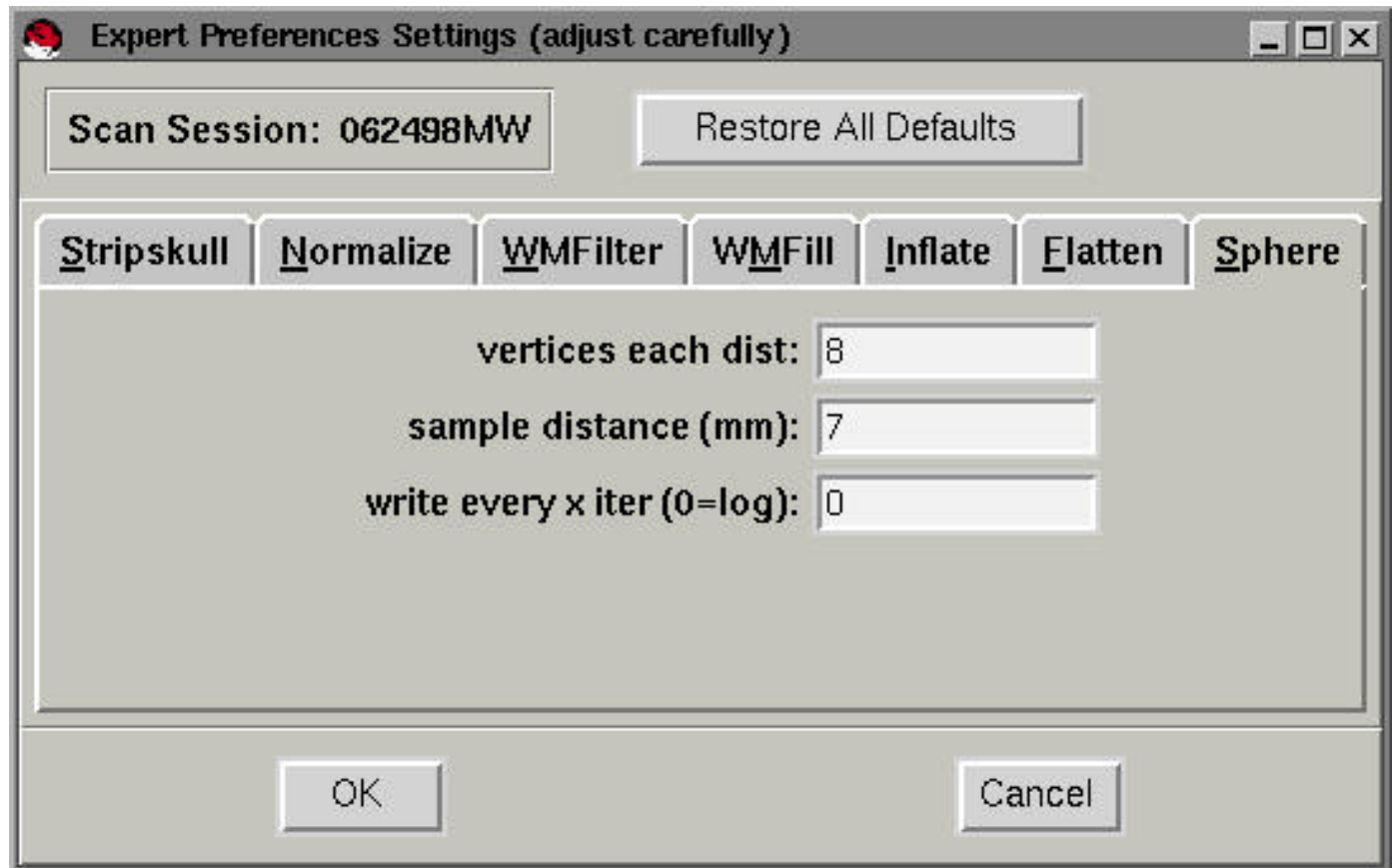
vertices each dist: number of vertices to examine

sample distance: distance limit to sample vertices.

write every x iter: writes out an intermediate surface at each **x** iterations

Fewer vertices and smaller sample distances will result in more metric distortion, but will require less memory and run faster.

Sphere



These parameters are used during the spherical morphing of the cortical surface inflation in **Sphere Surface**.

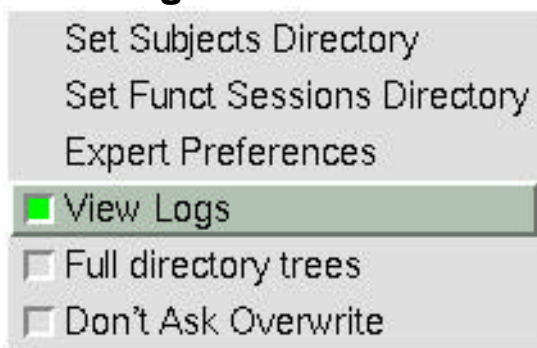
vertices each dist: number of vertices to examine

sample distance: distance limit to sample vertices.

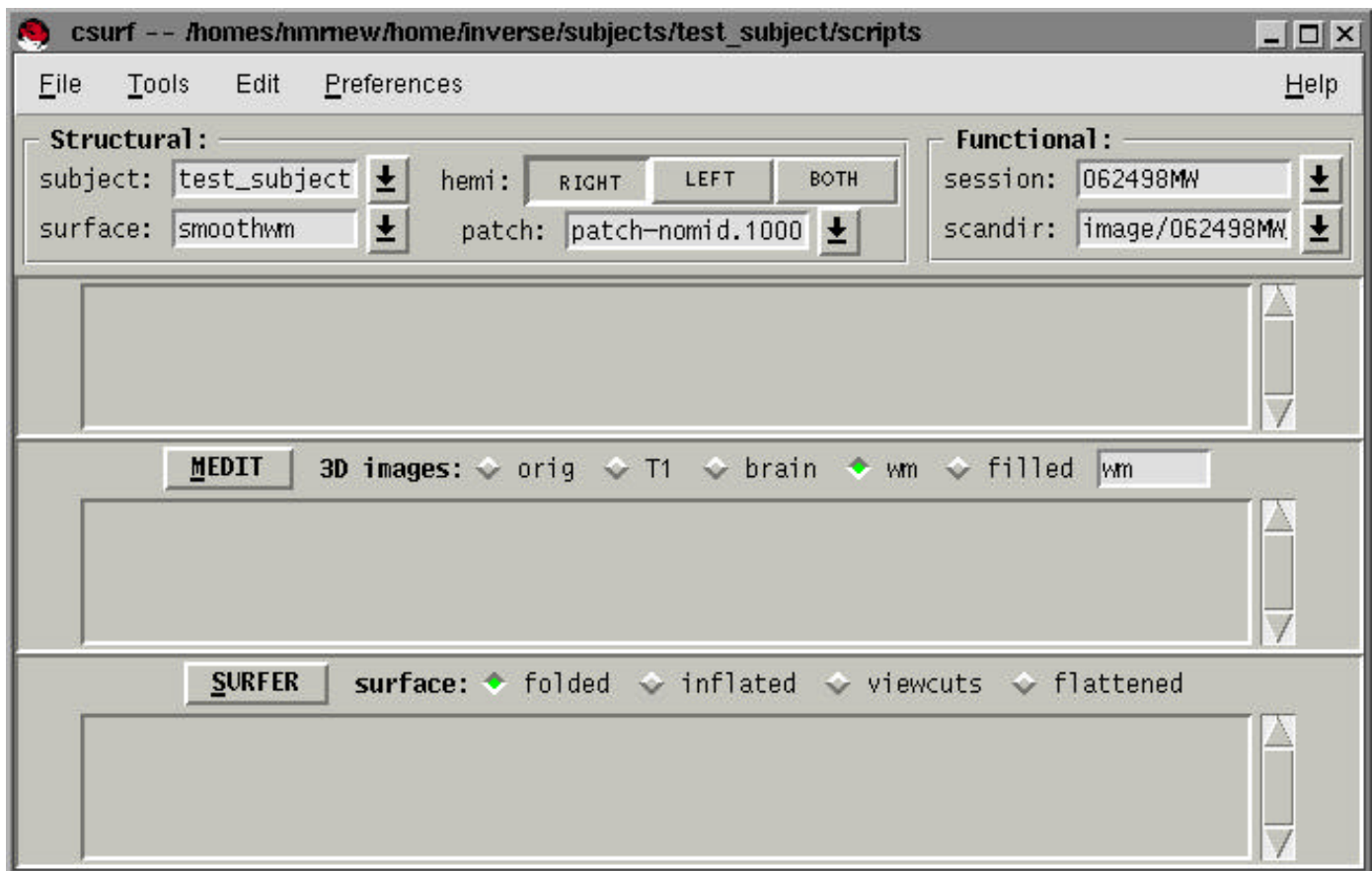
write every x iter: writes out an intermediate surface at each of the specified iterations

Fewer vertices and smaller sample distances will result in more metric distortion, but will require less memory and run faster.

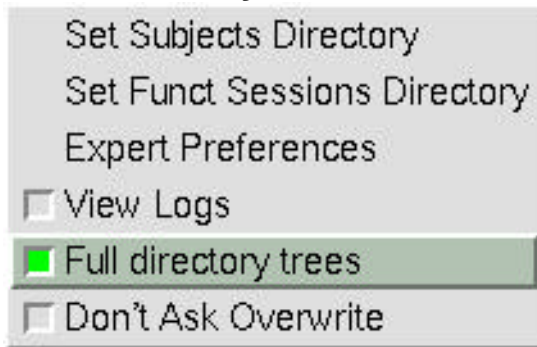
View Logs



Enlarges the main **csurf** window to display 3 additional log windows. The top window shows the text output of processes run through the **csurf** interface (except for **medit** and **surfer**). For example, output for the various steps in **Process Volume** are displayed in the top window. Text output for **medit** and **surfer** are shown in the middle and lower windows, respectively. For example, the coordinates of a selected point (MRI and Talairach coordinates, when available) are displayed in these windows.

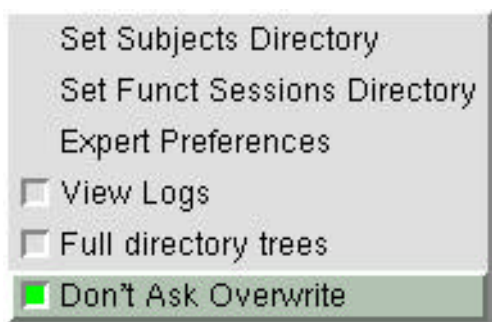


Full directory trees



When selecting directories, displays entire directory trees. This option can be quite slow for large file systems.

Don't Ask Overwrite



Automatically regenerates the volumes and surfaces created by the selections under the **Tools** menu. This is equivalent to selecting **Redo** in the Replace dialog window.

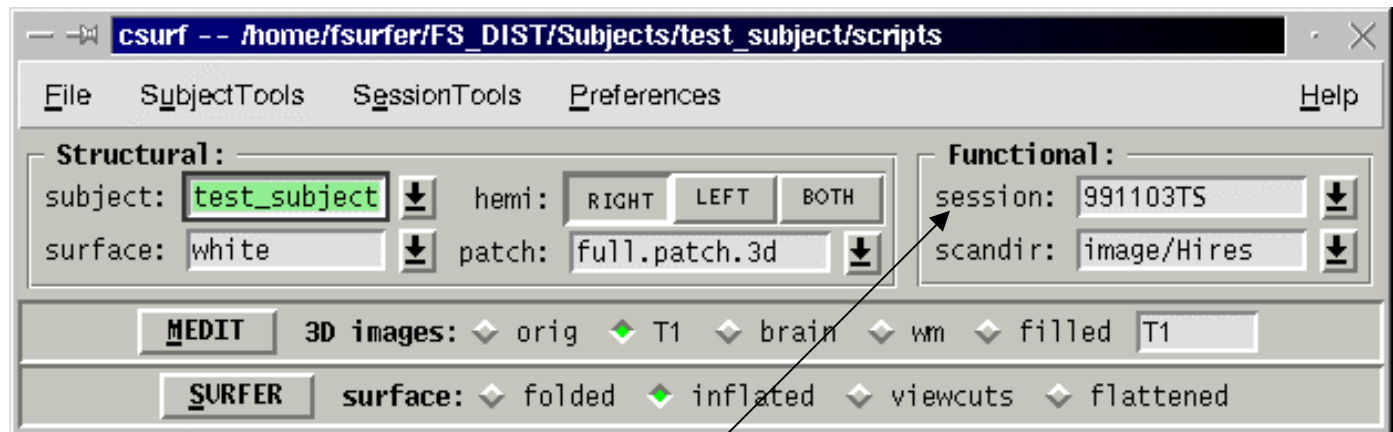
Summary of a Typical Surface Reconstruction

This is a menu step by menu step summary of a typical reconstruction including cutting flattened cortical patches. For more detail refer to the specific sections in the manual.

- 1) Under **File**, select **New Subject**
- 2) Under **Tools**, select **Setup Structural Scans**
- 3) Under **Tools**, select **Process Volume**
- 4) Under **Tools**, select **Create Surface**
- 5) Under **Edit**, select **Edit Segmentation**
- 6) Manually fix topologic defects using **medit** and **surfer**
- 7) Repeat steps 5-7 until all defects are fixed
- 8) Under **Tools**, select **Make Final Surface**
- 9) Under **Edit**, select **Make Full Surface Cuts**
- 10) Make and save full patch
- 11) Under **Edit**, select **Make Occip Surface Cuts**
- 12) Make and save occiput patch
- 13) Under **Tools**, select **Flatten Surface** for each patch that was cut
- 14) Under **Tools**, select **Sphere Surface**

FUNCTIONAL OVERLAY

The following section describes in detail how to overlay functional data on both the volume and the surface.

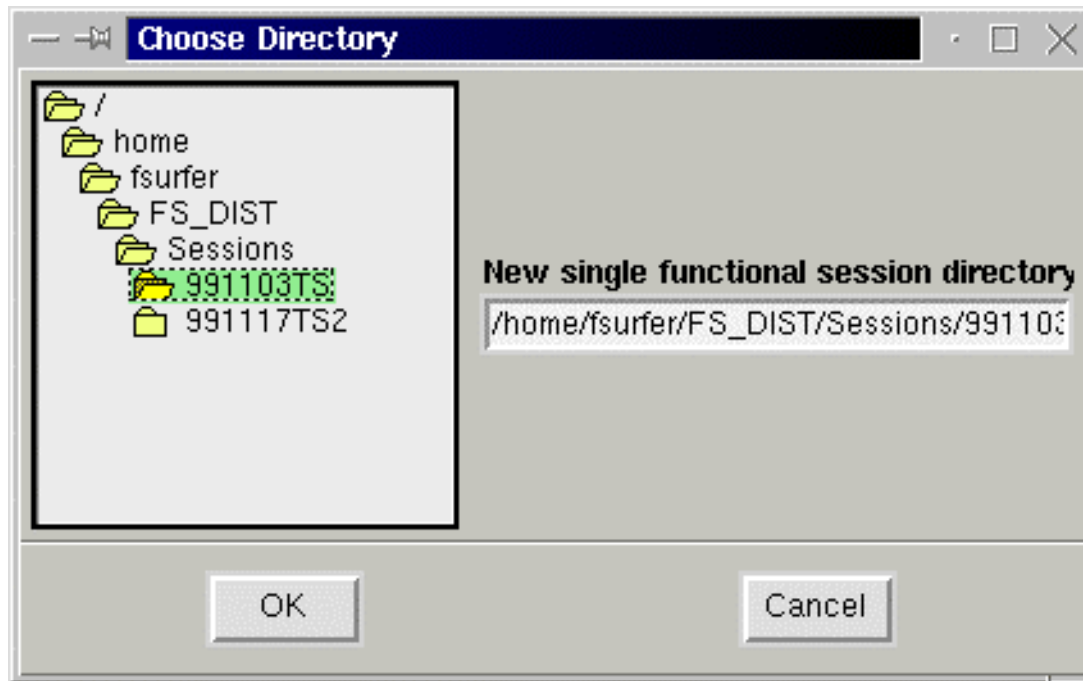


All functional data should be in the Sessions directory. This directory can be viewed in Csurf. But before placing the functional data in the Sessions directory, a new functional directory must be created for the subject.

Under the **File** Menu

New Functional

Creates the necessary directories for a new functional scan. Specify the name of the new functional directory in the highlighted window. The suggested naming convention is <2year><2month><2day><2-3initial>.



Then, select the subject that corresponds to the new functional scan.

The following directories are created

<functional scan>

image

mpg

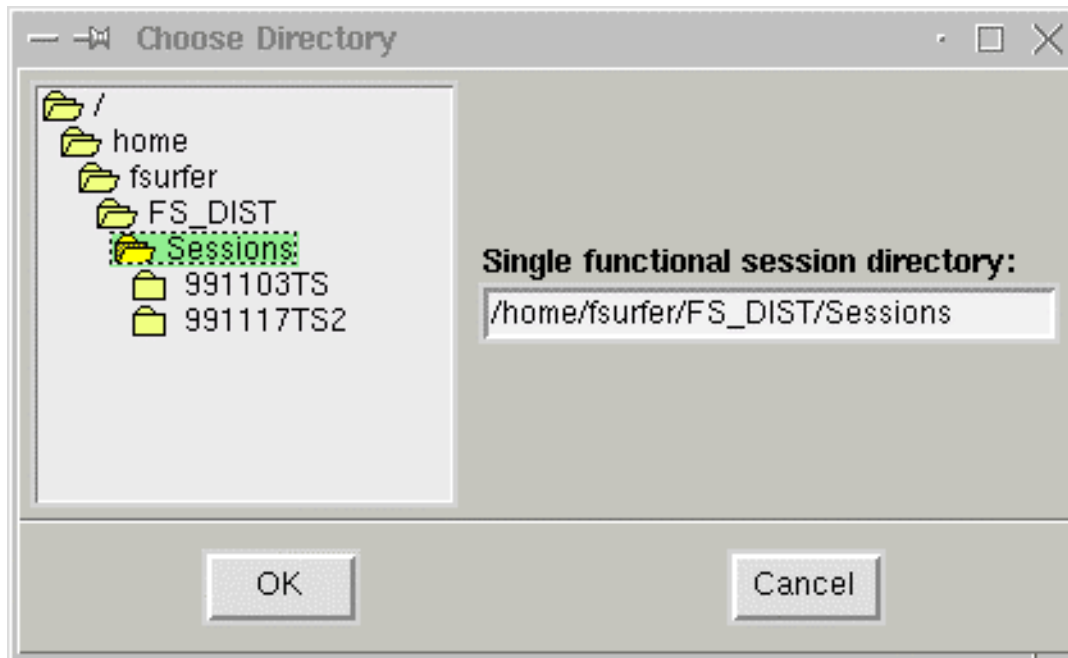
rgb

scripts

In addition the file "name" is created in the new functional directory and contains the name of the subject.

Open Functional

Opens an existing functional scan. Either select the functional directory on the left or enter the functional directory directly into the field on the right.



Registration

For successful overlay of functional data, the structural Hires-T1 images need to be registered with the functional Hires-EPI images. This process is done in SPM and is described below in three parts.

Conversion

Both the structural and the functional data sets need to be converted into a format that SPM can use.

For the structural data, this is done using a script called **mri_convert** which converts –COR files to .img files that can then be processed by SPM.

To convert, go into the subjects' mri directory and type:

`mri_convert <nameofdirectorywhereCORfilesare> <nameof.imgfile>`

Note: the COR files should be in the **orig** directory and the user has to specify a name for the .img file.

Example: `mri_convert orig hires.img`

For the functional data, the original Hires-EPI data first needs to be converted into **analyze** (.img) format. For EPI images in **bshort** format a script called **bshort_to_analyze** is used to convert into SPM format.

To convert the bshort data, type:

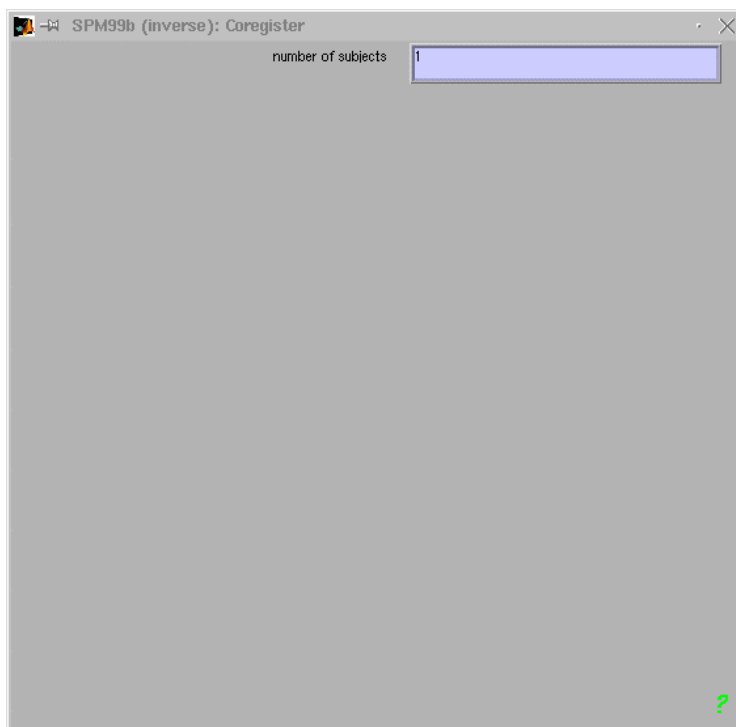
```
bshort_to_analyze xsize ysize zsize bshort_format first_bshort_index  
last_bshort_index analyze_format
```

Co-Registration in SPM

Open SPM and click the button labeled Check Register. This serves to ensure that both the structural and the functional images are in the correct orientation.

Once both sets of images are in the correct orientation, click the button labeled

Co-Register



Pick “1” for number of subjects



Pick “Coregister only”



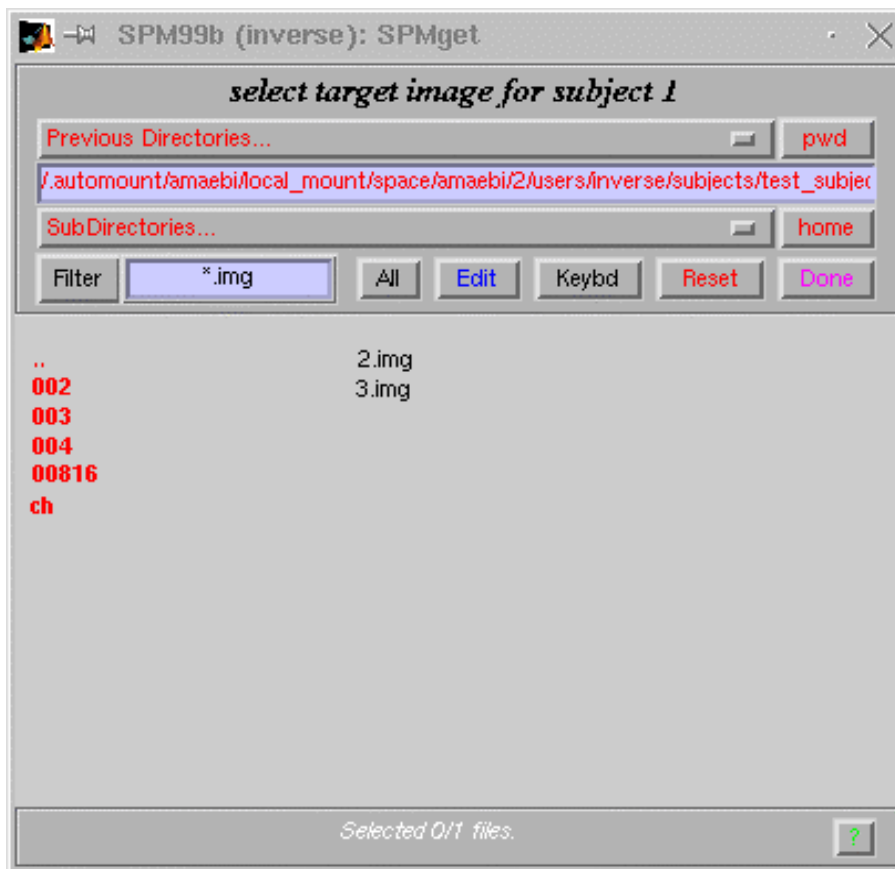
Pick “target-T1 MRI” as the modality of the first target image



Modality of first object image?...

- object - PET
- +object - T1 MRI
- object - T2 MRI
- object - PD MRI
- object - EPI
- object - Transm

Pick “object-T1 MRI” as the modality of the object image



Pick the functional EPI to be the target image and the structural T1 image to be the object image. Click Done after picking the target and the object images.

Generation of register.dat

Once the images have been registered in SPM, a transformation matrix needs to be generated that allows painting of functional data onto the structural images. This transformation matrix is called **register.dat** and is created by a script called **spmrat2register**.

To generate a register.dat, type:

```
spmrat2register -svol <structuralvolumename> -fvol <functionalvolumename> -
subject <subjectname>
```

Note: the register.dat file should be placed in the same directory where the functional data exists

Example:

```
spmrat2register -svol hires -fvol epi -subject test_subject
```

Registering functional data using register

This is a manual registration process done using the program **tkregister**. Currently, **tkregister** is only available for IRIX platforms. This process can be used in addition to the SPM and spm2register.

Note: This step currently only works for IRIX

Each set of functional data needs to include a T1-weighted sequence in the same slice prescription as the functional data. I will refer to the T1 volume used to generate the cortical surface as the “structural T1” and the T1 volume collected during the functional scan as the “functional T1.”

First, two data files must be in the directory with the T1 images:
analyse.dat and **register.dat**

For the examples, assume the subject name is “Al” (must match the name chosen during the cortical surface reconstruction process), the T1-weighted sequence had 16 slices, 128 x 128 voxels in plane (1.5625 mm resolution), and 4 mm slice thickness.

The names of the T1-weighted files are:

```
970123AL_03004_00002_00002_00001_001_000.bshort
970123AL_03004_00002_00002_00001_001_000.hdr
970123AL_03004_00002_00002_00001_001_001.bshort
970123AL_03004_00002_00002_00001_001_001.hdr
.....
970123AL_03004_00002_00002_00001_001_014.bshort
970123AL_03004_00002_00002_00001_001_014.hdr
970123AL_03004_00002_00002_00001_001_015.bshort
970123AL_03004_00002_00002_00001_001_015.hdr
```


analyse.dat

```
path_to_T1_directory
filename_descriptor
number_of_slices images_per_slice
x_dimension(in_voxels) y_dimension(in_voxels)
```

Example

```
.
970123AL_03004_00002_00002_00001_001_%03d.bshort
16 1
128 128
```

register.dat

```
name_of_subject
in_plane_resolution(mm)
slice_thickness(mm)
brightness
transformation_matrix
```

Example

```
al
1.562500
4.000000
0.088888
1 0 0 0
0 1 0 0
0 0 1 0
0 0 0 1
```

The brightness parameter changes the display brightness of the functional T1 relative to the structural T1. A larger number will make the functional T1 brighter in the registration program. Ideally, you should chose a brightness parameter that makes the functional T1 approximately as bright as structural T1. This will make the manual registration process easier. This parameter can be changed during the registration (change the **fepi** field).

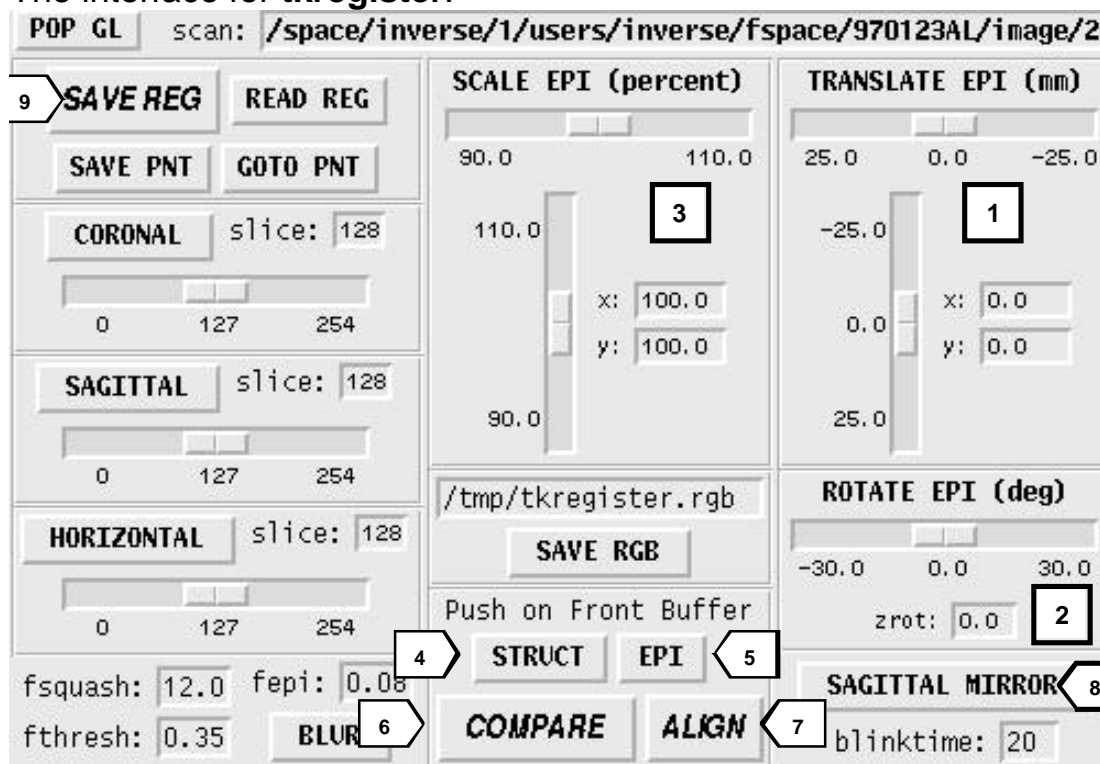
In the example, the transformation matrix was set to the identity matrix (i.e. no transformation between the two coordinate systems). If the subject has been scanned before using the same slice prescription, copy the transformation matrix. This will usually provide a better starting point for registration.

To perform the registration, change directories to the functional T1 directory:

tkregister 2

The registration program allows translation, rotation and linear scaling (i.e. stretching/shrinking).

The interface for **tkregister**:

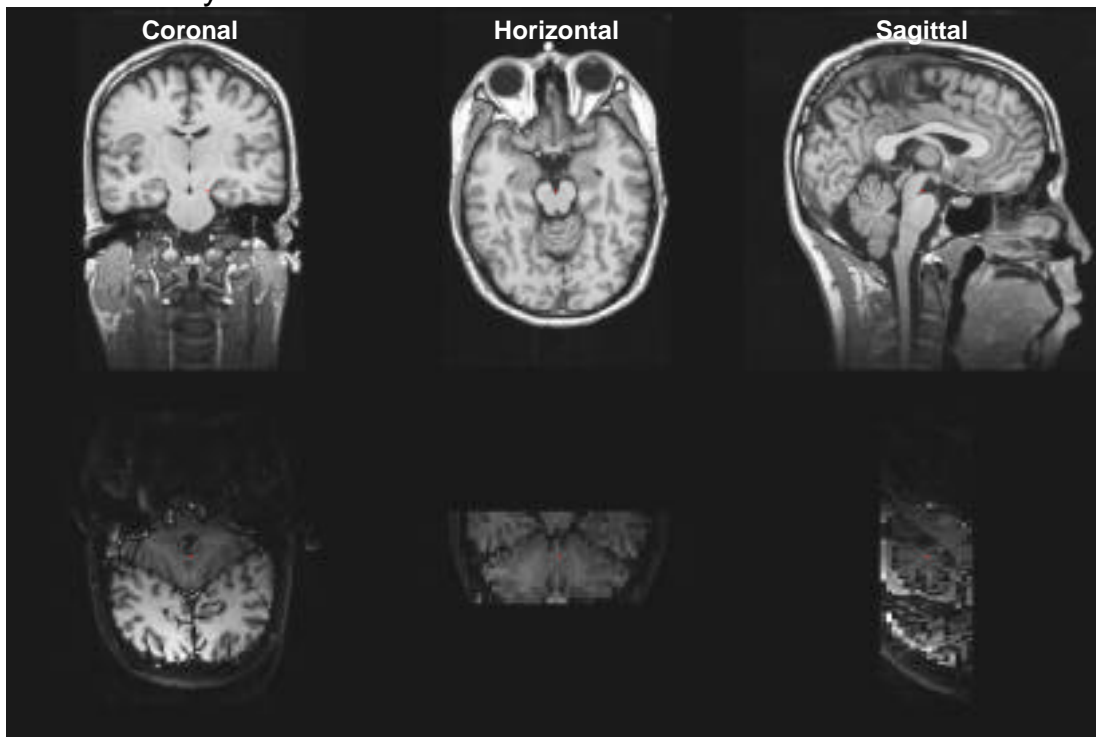


1. Translate EPI (functional) volume left/right and up/down as defined in the viewing plane
2. Rotate EPI (functional) volume around selected point (red crosshair)
3. Scale EPI (functional) volume left/right and up/down as defined in the viewing plane
4. Display structural volume (structural T1 used to construct the cortical surface)
5. Display EPI (functional) volume

6. Switch display between last two volumes displayed. NOTE: Any changes made to the volume result in that changed volume becoming the last volume. In other words, if you display the structural volume, then display the EPI volume and then select a new point in the EPI volume, the two most recent volumes are the two EPI volumes with the different points selected, NOT the structural and EPI volumes.
7. Aligns the EPI and structural volume based on a point selected in the EPI volume and a point selected in the structural volume. The point in the EPI volume must be selected first.
8. Left-right reverse (along the sagittal plane) the EPI volume
9. Write the transformation matrix defined by the translations, rotations and scaling into **register.dat**

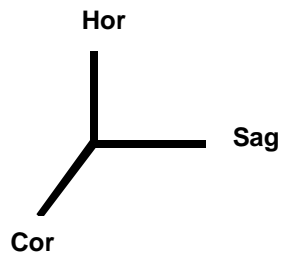
Here is an example of the manual registration process.

Examining all three orientations we see that the coronal and horizontal orientations are switched between the structural and the functional volumes. Note: the orientations are defined based on the structural T1 coordinate system.

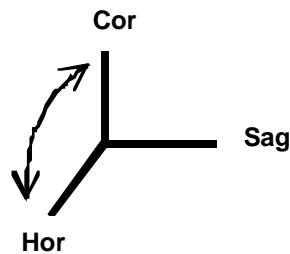


Therefore we want to rotate in the sagittal orientation

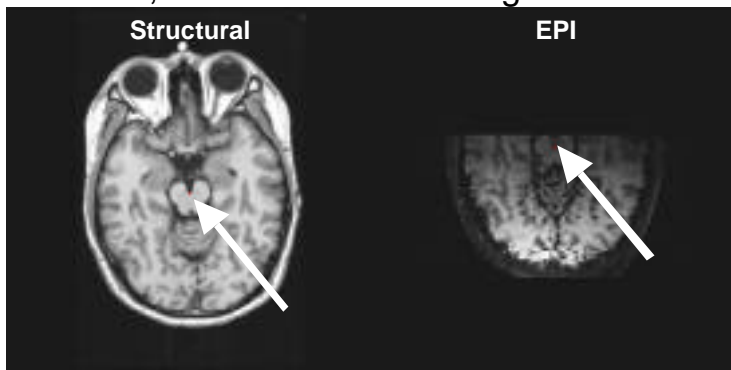
Structural Orientation



EPI (Functional) Orientation

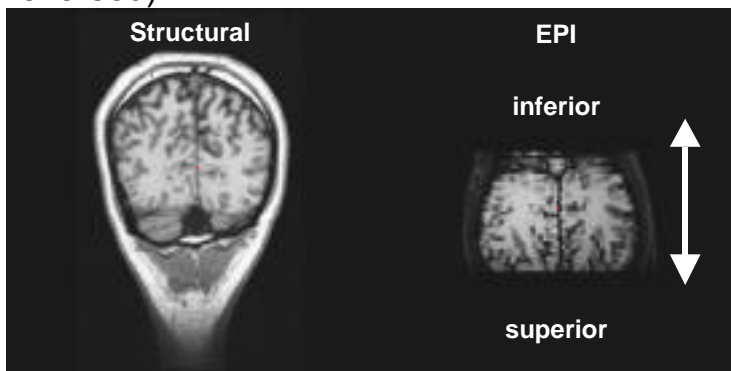


After rotating +50 degrees in the sagittal orientation, examine some other views. In this case, the brainstem is recognizable in the horizontal view.

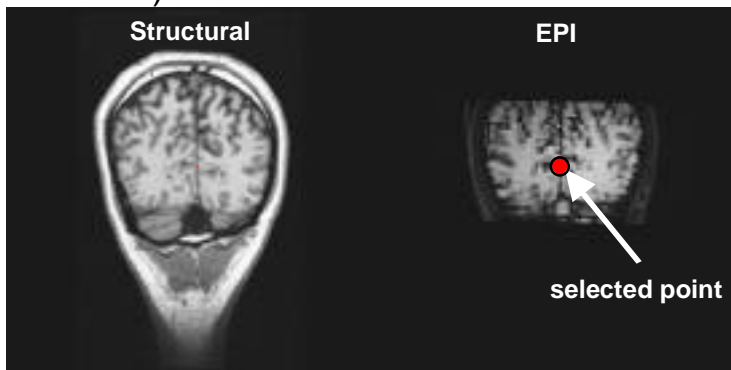


Select a easily identifiable point in the EPI volume. Then press **STRUCT** (4) and select the corresponding point in the structural volume. Press **ALIGN** (7) to align the two points. Note: Typically, it is easier to align the two volumes (using **ALIGN**) than using the translation sliders (1).

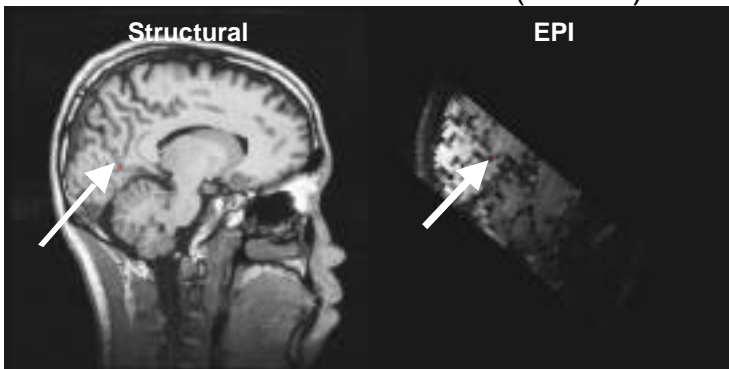
Repeat the alignment in the coronal view. Now we see that the functional image is upside down relative to the structural image in the coronal view (superior-inferior are reversed).



Using the rotation sliders (2), rotate the EPI volume 180 degrees. The rotation of the EPI volume is around the selected point (shown as a red circle in the figure below for ease of visualization – in the tkregister display window, the selected point is a red crosshair).

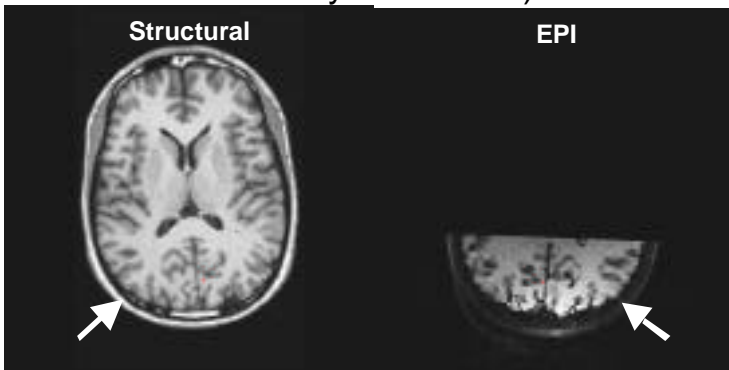


Now in the sagittal view, slightly off the midline we look for landmarks that we can identify in the functional buffer. Here we can see the intersection of two sulci (arrows).

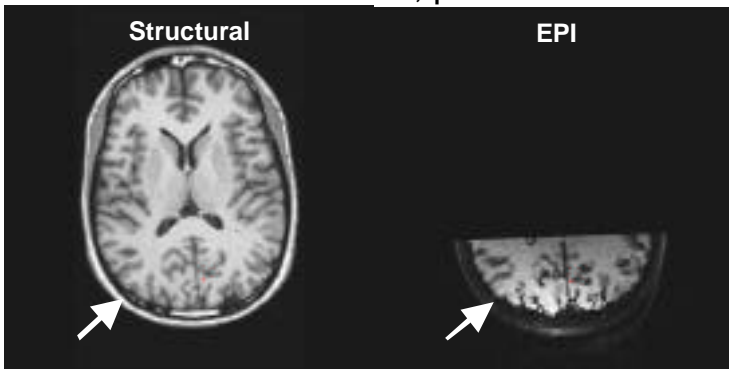


Select the intersection of the two sulci in the EPI volume, and then select the intersection in the structural volume. Press **ALIGN** to align the two selected points.

Now we can also see that the functional volume is left-right reversed (Note the structure indicated by the arrows).



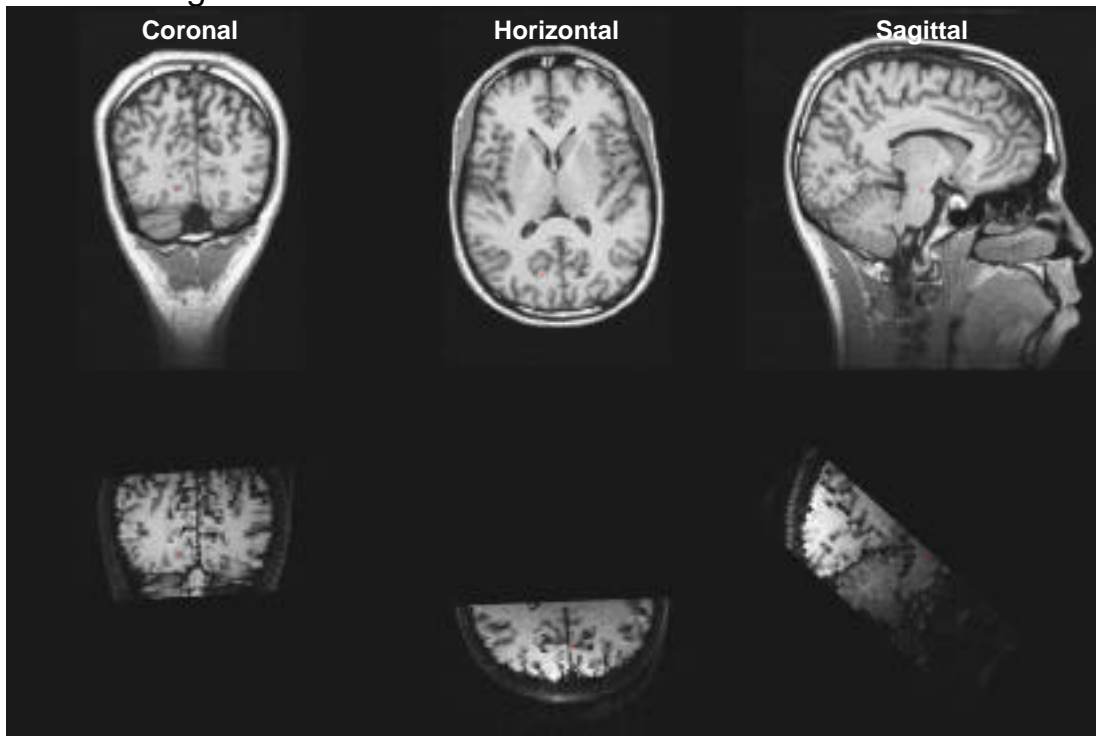
To reverse the orientation, press **SAGGITAL MIRROR** (8)



The registration process continues by repeating these steps:

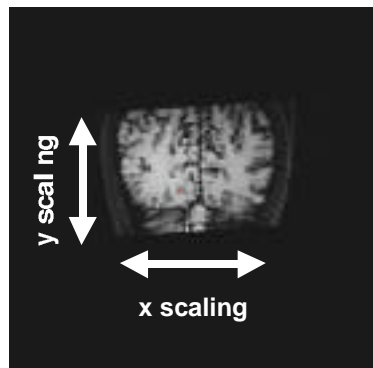
1. align the two volumes
 - select point in **EPI** volume
 - select point in **STRUCT** volume
 - ALIGN** (7)
2. rotate
 - use rotation sliders (2)
3. go to another view
4. repeat steps 1 and 2

The final registered volume looks like:



If after rotation and translation, the two volumes are still not is registration, the EPI volume may need to be scaled using the scaling sliders (3). That will scale the EPI volume based on the current viewing orientation.

For example, if the viewing orientation is coronal, the x and y scaling directions are shown below



Once the structural and functional volumes have been registered, press **SAVE REG** to write out new transformation matrix into **register.dat**.

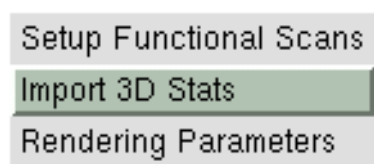
register.dat

```
al
1.562500
4.000000
0.088888
9.988024e-01 -3.736436e-02 -3.161692e-02 1.835571e+00
4.849941e-02 6.684349e-01 7.421880e-01 2.726025e+01
6.597552e-03 7.428333e-01 -6.694470e-01 1.334711e+01
0.000000e+00 0.000000e+00 0.000000e+00 1.000000e+00
```

Functional Painting in Csurf

Once the structural and the functional datasets have been registered and functional analysis has been performed, the functional data can be painted on any generated surface and/or the volume.

Under the SessionTools menu in Csurf,

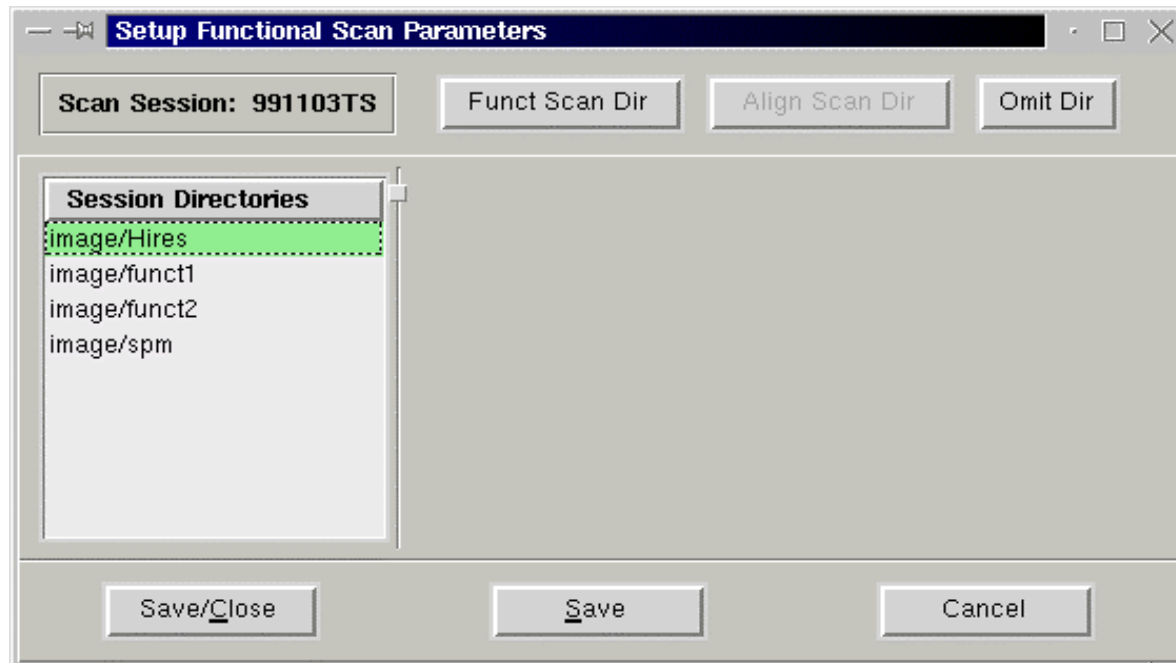


select **Setup Functional Scans**

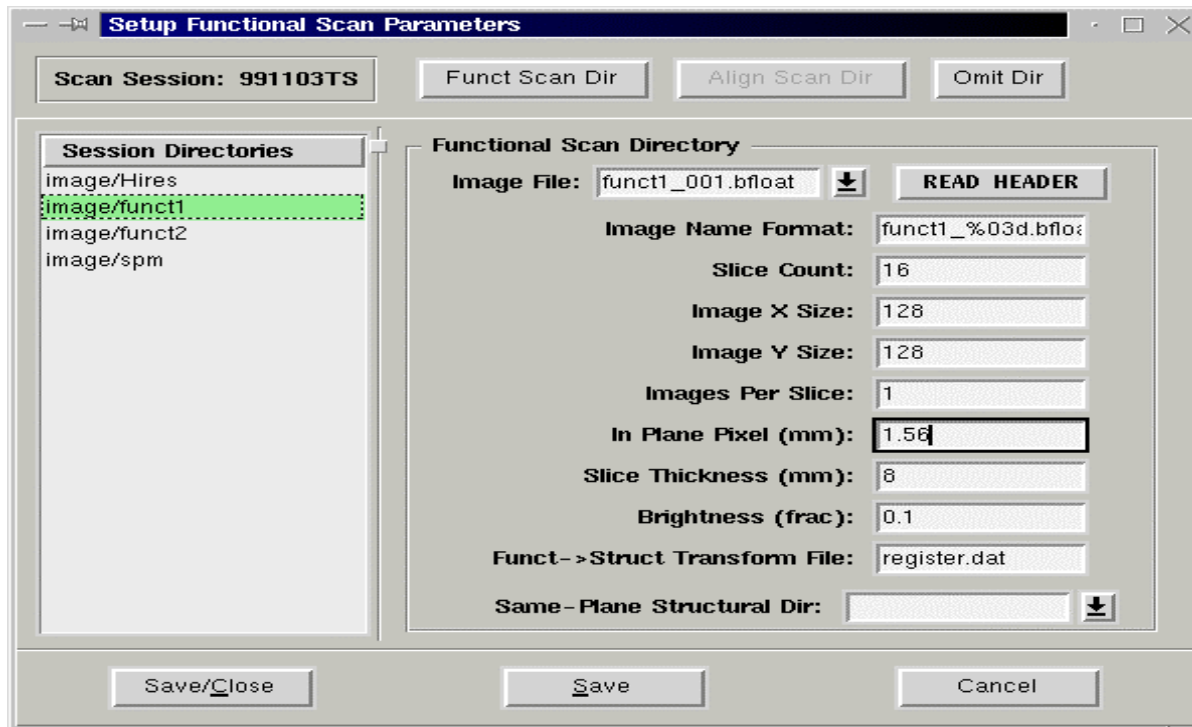
Setup Functional Scans

Selects the functional directories and determines the resolution of the scans. Currently supported formats are: SPM/analyze, AFNI, and bfloat

Each functional acquisition must be in its own directory in the **image** directory. Within each functional directory there must be a file **register.dat**.

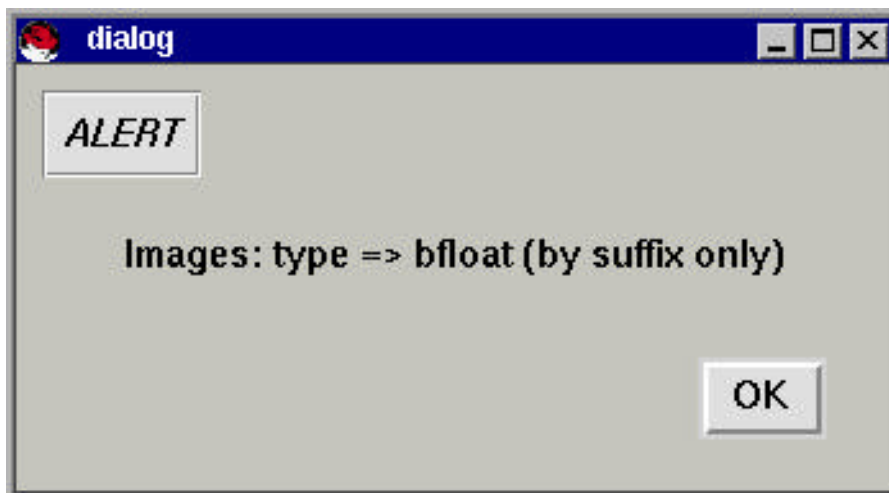


Select the first functional scan in the window on the left and press **Funct Scan Dir**.



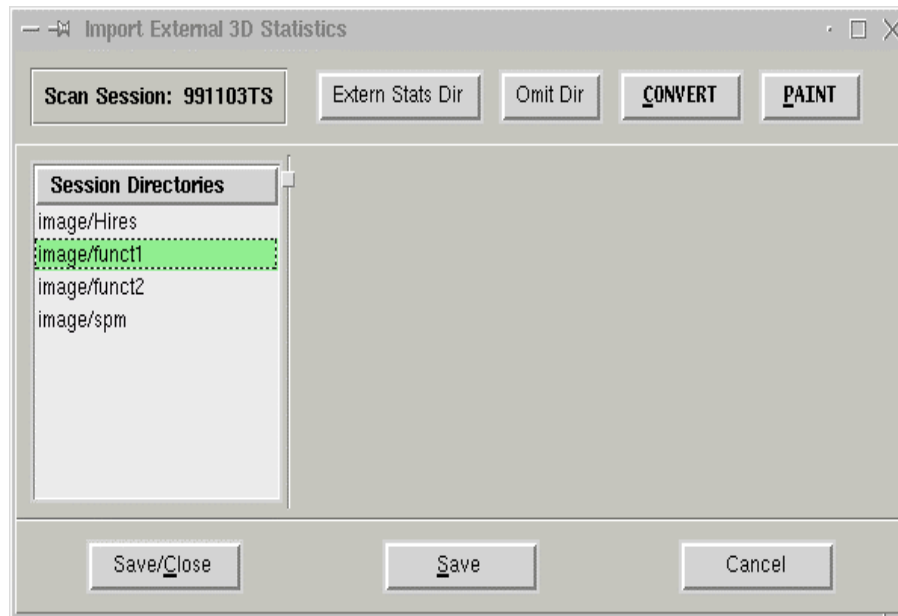
Manually correct any fields that were not correctly determined. If you want to omit a functional scan that was previously selected, reselect the directory and press **Omit Dir**.

The **READ SUFFIX** button simply determines the type of the scan based on the suffix.

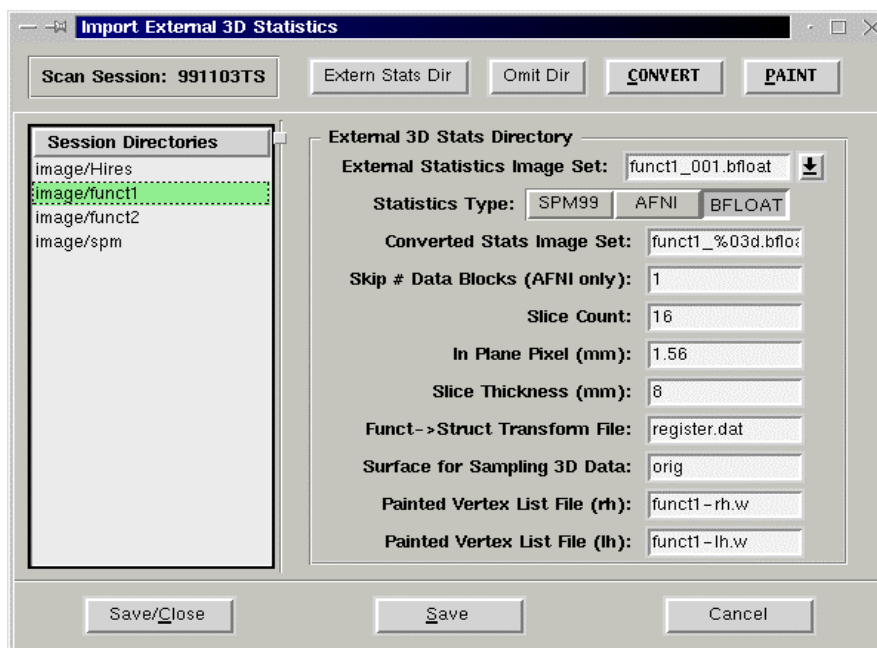


Setup Import Stats

Determines the filename structure for the imported statistical volume, converts the data to bshorts (if necessary), and samples the statistical volume using the **smoothwm** surface.



Select the external statistics directory in the left window and press **Extern Stats Dir**.



Description of each field:

Statistics Type: Select the type of statistical volume (either **SPM**, **AFNI**, or **BFLOAT**) with the appropriate button. If the statistic type is either SPM or AFNI, press **CONVERT** to convert to bshorts.

Skip # Data Blocks (AFNI only): For AFNI data, enter the number of data blocks to skip.

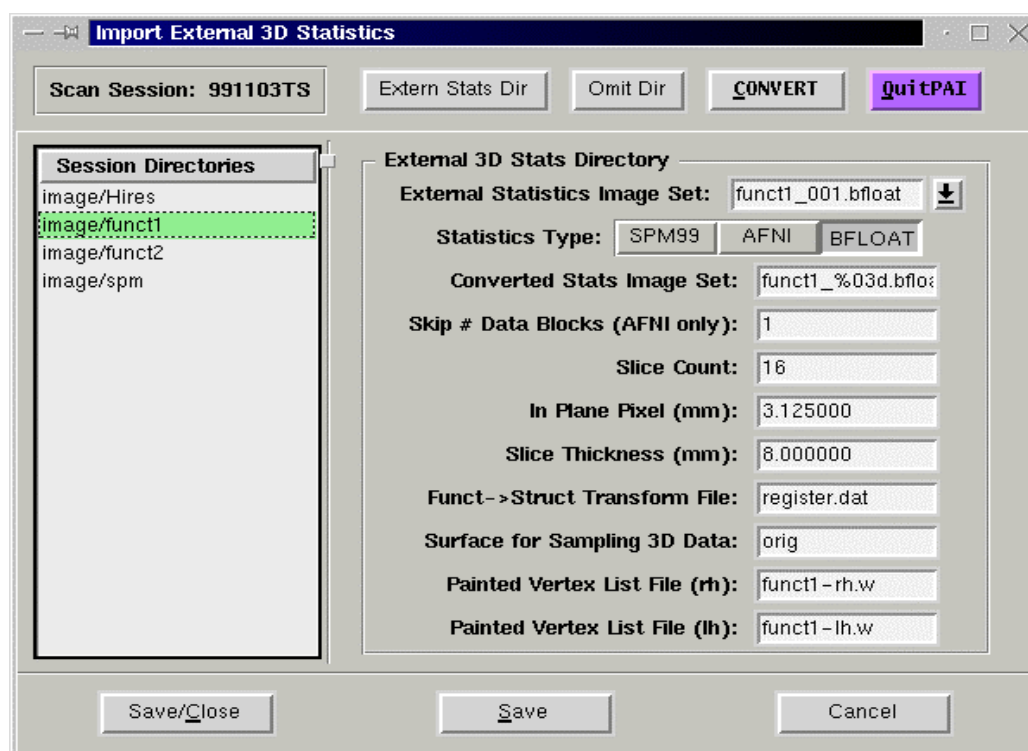
Converted Stats Image Set: Format string to describe the functional data

Funct->Struct Transform File: Default is **register.dat**. Do not edit.

Painted Vertex List File (rh): Defaults to <stem of the functional data>-rh.w

Painted Vertex List File (lh): Defaults to <stem of the functional data>-lh.w

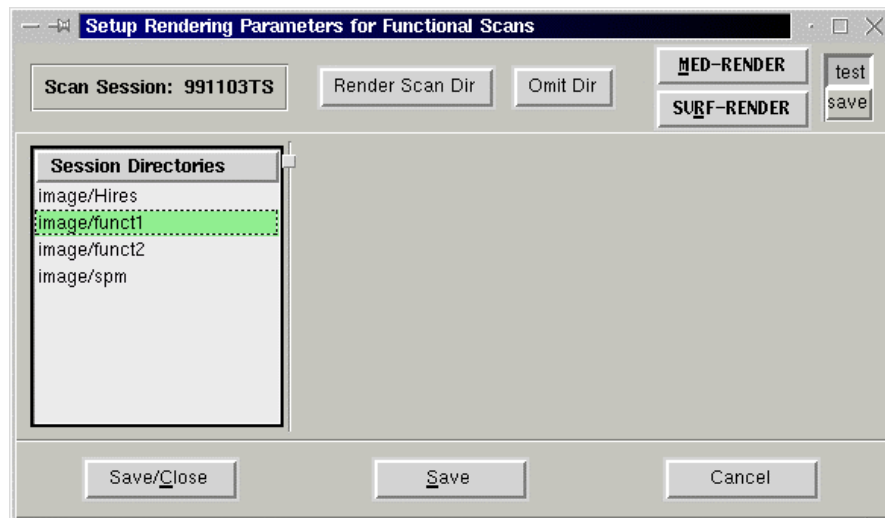
To generate the statistical surface overlay (values only), press **PAINT**. This creates a list of vertices and the associated statistic sampled from the volume.



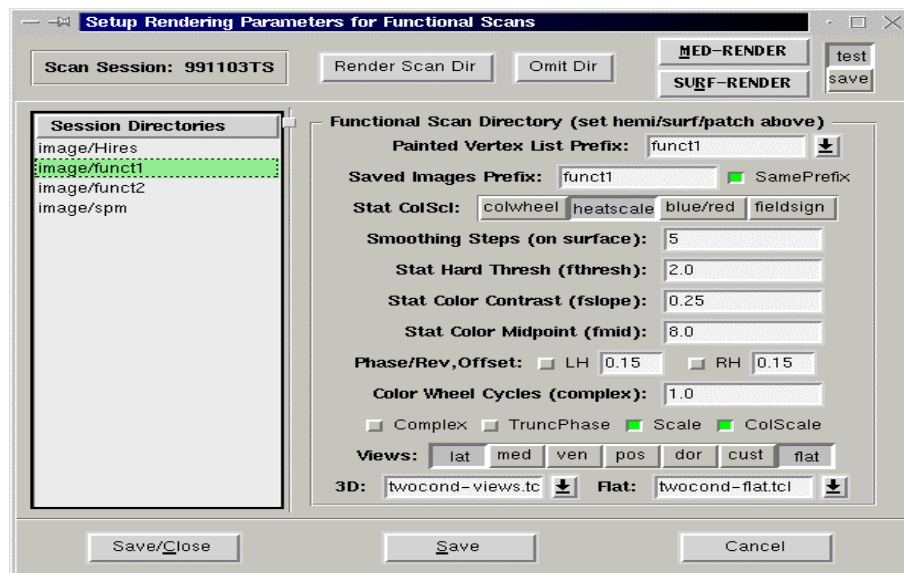
Repeat for each functional directory. If you want to omit a functional scan that was previously selected, reselect the directory and press **Omit Dir**.

Setup Rendering Parameters

Specify the rendering parameters for the overlaid statistical volume (previously selected using **Setup Import Statistics**). Provides both a volume overlay (using **medit**) and a surface overlay (using **surfer**).



Select the functional directory in the left window and press **Render Scan Dir**. Be sure that the functional directory that is selected in the left window matches the functional directory in the **scandir** field in the **csurf** window.



Description of each field:

Saved Images Prefix: Specifies the prefix for any saved images (rgb format). Images are saved in the **rgb** directory. Image are saved only if the **Save** button is depressed. Default filename is <prefix>-<hemi>-<surface>.rgb.

Painted Vertex List Prefix: Must match the prefix specified in **Setup Import External Statistics**.

Stat ColScl: heatscale displays positive statistics in red and yellow and negative statistics in blue and green. **Colwheel**, **blue/red**, and **fieldsign** are currently unsupported (future functionality).

Stat Hard Thresh (fthresh): Statistical threshold (for values below the threshold, the underlying curvature is displayed).

Stat Color Contrast (fslope): Color slope from **Stat Color Midpoint (fmid)** (red/blue) to the maximum color (yellow/green). Maximum color (yellow, green) represents a statistical value of **Stat Color Midpoint + 1/ Stat Color Contrast**.

Stat Color Midpoint (fmid): Statistical value for full red/blue.

Phase/Rev, Offset: Currently unsupported (future functionality).

Color Wheel Cycles: Currently unsupported (future functionality).

Radiobuttons:

Complex: : Currently unsupported (future functionality).

TruncPhase: Only display positive values (red/yellow).

Scale: Display scale bar (1 cm).

ColScale: Display color scale bar.

Pushbuttons:

Views: Specify which viewing orientations should be generated and saved. Can specify multiple orientations.

lat: lateral

med: medial

pos: posterior

dor: dorsal

cus: custom

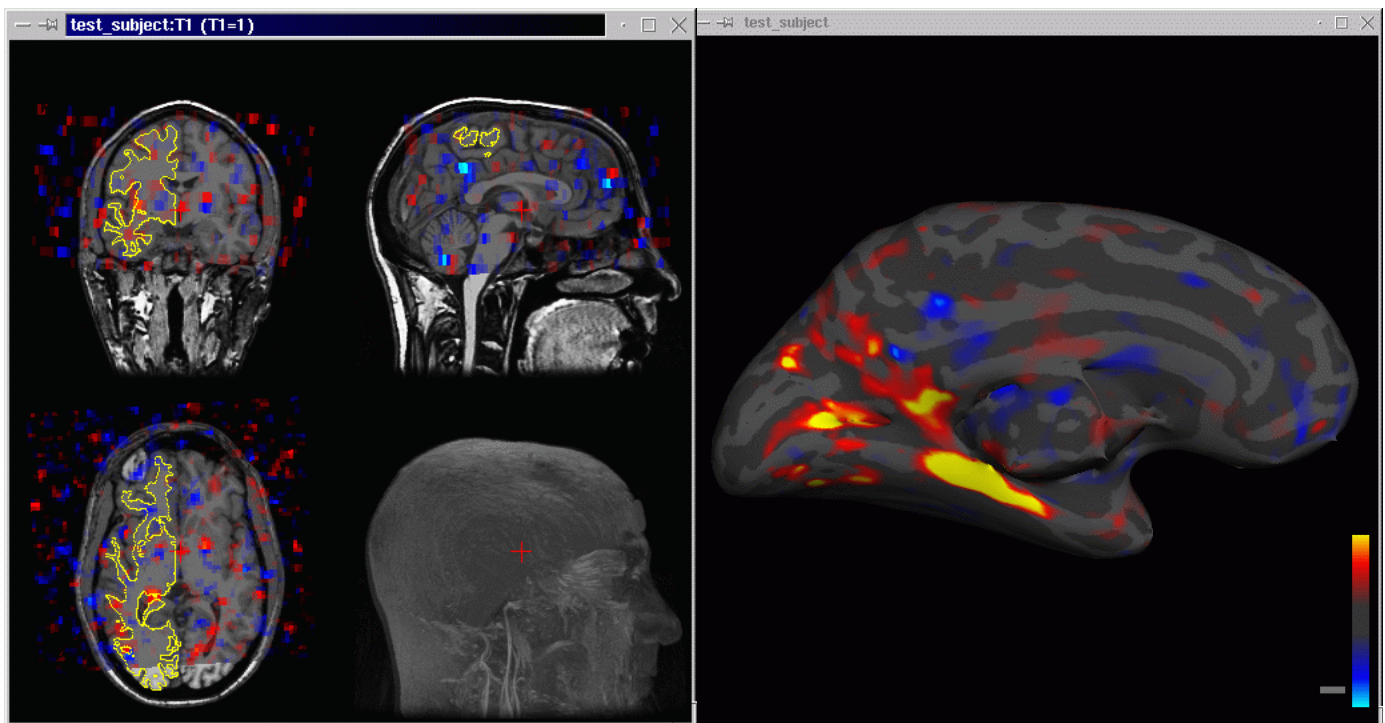
flat: flattened patch

Repeat for the setup each functional directory. If you want to omit a functional scan that was previously selected, reselect the directory and press **Omit Dir**.

If you begin to experience errors with the rendering, exit **Setup Rendering Parameters** and begin again. Also be sure that the functional scan that you are rendering is also correctly listed in the **scandir** field in the **csurf** window.

To view the statistical volume overlaid into the T1 volume, press **MED-RENDER**. To view the statistical volume painted onto a surface or flattened patch, press **SURF-RENDER**. Select the surface or patch in the **csurf** window (**surface** or **patch** field). To save the images generated by **SURF-RENDER**, press the **save** button. To view (without saving) the images generated by **SURF-RENDER**, press the **test** button.

An example of the statistical overlay in the volume in 3 views (left) and the corresponding surface overlay (right) are shown below:



MEDIT

SURFER

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c) You must cause the whole of the work to be licensed at no charge to all third parties under the terms of this License.

d) If a facility in the modified Library refers to a function or a table of data to be supplied by an application program that uses the facility, other than as an argument passed when the facility is invoked, then you must make a good faith effort to ensure that, in the event an application does not supply such function or table, the facility still operates, and performs whatever part of its purpose remains meaningful.

(For example, a function in a library to compute square roots has a purpose that is entirely well-defined independent of the application. Therefore, Subsection 2d requires that any application-supplied function or table used by this function must be optional: if the application does not supply it, the square root function must still compute square roots.)

These requirements apply to the modified work as a whole. If identifiable sections of that work are not derived from the Library, and can be reasonably considered

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Thus, it is not the intent of this section to claim rights or contest your rights to work written entirely by you; rather, the intent is to exercise the right to control the distribution of derivative or collective works based on the Library.

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This option is useful when you wish to copy part of the code of the Library into a program that is not a library.

4. You may copy and distribute the Library (or a portion or derivative of it, under Section 2) in object code or executable form under the terms of Sections 1 and 2 above provided that you accompany it with the complete corresponding machine-readable source code, which must be distributed under the terms of Sections 1 and 2 above on a medium customarily used for software interchange.

If distribution of object code is made by offering access to copy from a designated place, then offering equivalent access to copy the source code from the same place satisfies the requirement to distribute the source code, even though third parties are not compelled to copy the source along with the object code.

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If such an object file uses only numerical parameters, data structure layouts and accessors, and small macros and small inline functions (ten lines or less in length),

then the use of the object file is unrestricted, regardless of whether it is legally a derivative work. (Executables containing this object code plus portions of the Library will still fall under Section 6.)

Otherwise, if the work is a derivative of the Library, you may distribute the object code for the work under the terms of Section 6. Any executables containing that work also fall under Section 6, whether or not they are linked directly with the Library itself.

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b) Accompany the work with a written offer, valid for at least three years, to give the same user the materials specified in Subsection 6a, above, for a charge no more than the cost of performing this distribution.

c) If distribution of the work is made by offering access to copy from a designated place, offer equivalent access to copy the above specified materials from the same place.

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It may happen that this requirement contradicts the license restrictions of other proprietary libraries that do not normally accompany the operating system. Such a contradiction means you cannot use both them and the Library together in an executable that you distribute.

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a) Accompany the combined library with a copy of the same work based on the Library, uncombined with any other library facilities. This must be distributed under the terms of the Sections above.

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END OF TERMS AND CONDITIONS

Appendix: How to Apply These Terms to Your New Libraries

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<one line to give the library's name and a brief idea of what it does.>

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That's all there is to it!