Caret5 Tutorial
Segmentation, Flattening, and Registration

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About This Document

This document is designed to serve as a tutorial on how to segment and flatten surfaces using Caret5.

Conventions in this Document

• All tutorial steps are identified by bullets.
• Actions the user should take are in italics.
• User-interface components are in BOLD.

Bug Reporting or Questions About Caret5 Software

Please use either the Caret users’ mailing list (http://brainmap.wustl.edu/resources/caretnew.html#Help) or send an email to caret@brainmap.wustl.edu. Suggestions are also welcome.

Downloading and Installing Caret5

Please see the document Caret 5.5 Tutorial – Introduction, Installation, and Visualization.

Data Set for Use With This Tutorial

The data set for use with this tutorial is available in “zip” format from our SuMS database. Follow the link http://sumsdb.wustl.edu:8081/sums/archivelist.do?archive_id=6588227. On the SuMS web page, there is column named name containing the file name: caret_5.5_segment_flatten_register_tutorial.zip. To the left of this name in the action column is a control. Select this control, which will popup a menu, and select download to automatically start downloading the archive (set of files).

After downloading the data set, the archive needs to be uncompressed. Linux and Macintosh users should run the command unzip caret_5.5_segment_flatten_register_tutorial.zip. Windows XP users should place the mouse over the downloaded file and press the right mouse button. From the popup menu, choose Extract All and follow the prompts. Windows XP users may also extract the file from the command line window by running caret_unzip.
`caret_5.5_segment_flatten_register_tutorial.zip` provided the caret/bin directory is in the user’s PATH environment variable.

**Prerequisites**

This document assumes the reader has some familiarity with Caret5 such as the ability to view surfaces and volumes, use the Display Control Dialog, and manipulate borders. Please see one of the other tutorials if you are not familiar with viewing data in Caret5.

**Volume File Types Supported by Caret5**

Volume files of type AFNI, NIFTI, SPM, and Washington University’s “.ifh” format are read using the **Open Data File** item on the **File Menu**. These volumes have sufficient metadata that specifies the orientation and stereotaxic coordinates. If a volume of one of these types is used, some of the steps in this tutorial will not be necessary.

Volume files of type Analyze, MINC, and VTK are read using the **Import File** menu item on the **File Menu**. These file types rarely have sufficient metadata and it will usually be necessary to set some of the volume’s attributes using Caret5 prior to segmenting the volume. While most MINC volumes contain the required metadata, those MINC volumes written by SureFit (used for segmentation and distributed by our lab prior to this release of Caret5), do not contain the required metadata.

In this tutorial, an Analyze format volume file will be used that will require the setting of attributes in Caret5.

**Set the Current (Working) Directory**

Prior to starting Caret5, place the anatomical volume (tutorial data set files) into a directory containing no other files. Start Caret5 using the appropriate method for your operating system. If you do not start Caret5 from a terminal window with the current directory set to the directory containing the anatomical volume, perform the following steps to set the current directory:

- **Select Set Current Directory** from the **File Menu** to launch the **Choose Directory Dialog**.
- Using the **Choose Directory Dialog**, navigate to the directory containing the anatomical volume as shown in Figure 1 and press the **OK** button.
Figure 1 - Choose Current Directory Dialog

Read the Anatomical Volume

Import the Analyze Volume by performing the following steps:

• *Select Import File* from the *File Menu*.
• In the *Import Data File Dialog*, verify that the *File type* control is set to *Analyze Volume File (*.hdr)* and that the *Volume Type* in the *Import Selections* section is set to *Anatomy*.
• In the *Import Data File Dialog*, *highlight* the file named Human.case9.LR.711-2C.hdr as shown in Figure 2 and *press* the *Open* button to load the file.
Anatomical Volume Requirements

A volume must meet several requirements to be segmented in Caret5. These requirements are:

1) The volume must be standard T1-weighted MRI scans taken in vivo, in which white matter is bright, gray matter is darker, and CSF is even darker.
2) The intensities should be consistent throughout the volume. For instance, in Figure 3, the frontal lobes are much brighter than the remainder of the brain. This volume would not be segmented correctly.
3) The volume must be in an LPI orientation. That is, the negative X is left, negative Y is posterior, and negative Z is inferior.
4) The voxels must be 1mm cubic voxels (0.5mm for monkeys).
5) The volume’s stereotaxic coordinates must be set so that the coordinate (0, 0, 0) is at the anterior commissure.
6) The volume must contain only a single hemisphere or part of a single hemisphere.
7) The voxels must be in the range 0 to 255.
Figure 3 - Volume with Intensity Problems

Set the Volume’s Orientation

We know that the anatomical volume used in this tutorial is already in an LPI orientation but this information was not in the header file. Set the volume’s orientation by following these steps:

- Select Edit Volume Attributes from the Volume Menu to display the Volume Attributes Editor Dialog.
- In the Volume Attributes section, select the Orientation Tab by clicking it with the mouse. The current orientation is set to X-Unknown, Y-Unknown, and Z-Unknown.
- Press the mouse over the X-Unknown item and a menu will pop up listing the available choices. Change the X-Unknown to X-Left to Right. Perform the same operation on the Y-Unknown and Z-Unknown items so that they read Y-Posterior to Anterior and Z-Inferior to Superior respectively as shown in Figure 4.
- Press the Apply button to apply these changes to the volume.
Figure 4 - Volume Attributes Editor Dialog

If you use a volume type that has sufficient metadata that describes the volume’s orientation (such as an AFNI volume) Caret5 will automatically convert the volume to an LPI orientation. Otherwise, the Flip About X Screen Axis, Flip About Y Screen Axis, and Rotate Clockwise buttons in the Orientation section of the Volume Attributes Editor can be used to bring the volume into an LPI orientation.

**Set the Volume’s Stereotaxic Coordinates**

Now that the volume’s orientation has been set, the volume’s stereotaxic coordinates need to be established. The voxel sizes are already set to 1.0 mm for each dimension. The origin values are the coordinates of the voxel that is the most left, posterior, inferior voxel. To set the origin, we will find the anterior commissure and inform Caret5 of its location. Caret5 will then use the voxel sizes along with the anterior commissure...
position to determine the origin. Locate the Anterior Commissure so that it is under the
crosshairs in the Main Window by performing the following steps:

- In the **Main Window** **hold down** the shift key, **hold down** the left mouse button,
  and **drag** the volume to that the entire volume slice is visible.
- **Click** the mouse near the bottom of the anterior set of ventricles as shown in
  Figure 5.
- **Switch** to a parasagittal view by **pressing** the mouse over the **Volume Axis**
  **Viewing Control** in the toolbar (currently labeled **H(XY)**) and **selecting** **P(YZ)**.
- **Click** the mouse over the anterior commissure as shown in Figure 6.
- **Switch** to a coronal view by **changing** the **Volume Axis Viewing Control** to
  **C(XZ)** to view the crosshairs relation to the anterior commissure.
- **Switch** back to a horizontal view. The selected slices should now read 88, 122,
  73. If they do not, adjust them using the arrows in the **Toolbar** as shown in
  Figure 7.

![Figure 5 - Crosshairs Near Ventricle](image-url)
Now that the crosshairs are over the anterior commissure, the volume’s stereotaxic coordinates are established by performing the following steps:

- On the Volume Attributes Editor Dialog, press the Coordinates Tab.
- Press the Use Main Window Crosshairs as AC Location to Determine Origin push button. After doing so, you will see the origin values set to –88.0, -122.0, and –73.0.
- Press the Apply button so that the volume’s origin is updated.
• Press the R (Reset) button on the Main Window’s Toolbar to set the view of the volume to the default view with the (0.0, 0.0, 0.0) stereotaxic coordinate at the center of the window.

Setting the Voxel Range to 0 to 255

• On the Volume Attributes Editor, press the Data Tab.
• Press the Rescale Voxel Values button.
• Change the Output Range values to 0 and 255 (or press the Set button in the Output Range row and selection the top item, Byte – Unsigned).
• Press the Close button on the Volume Attributes Editor Dialog.

Saving the Anatomical Volume

With the volume’s attributes properly set, the volume should be saved by following these steps:

• Select Save Data File from the File Menu to display the Save Data File Dialog.
• Set the File Type to Volume File – NIFTI (*.nii *.nii.gz).
• In the Comment section add a comment stating that the volume is now an AC centered coordinate system volume.
• Leave the Write Data File As set to Other.
• Verify that the Volume Type is set to Anatomy.
• Verify that the Volume File is set to Human.case9.LR.711-2C.hdr (the Analyze volume that was imported).
• Change the File name to Human.case9.LR.711-2B_AC_ORIGIN+orig.nii so that the Save Data File Dialog appears as shown in Figure 8.
• Press the Save button on the Save Data File Dialog to save the volume file.
• When asked “Would you like to create a Spec File ?”, click the Yes push button.
• In the Create Spec File Dialog, set the Species to Human by selecting the Species push button and selecting human.
• Set the Subject to case9.
• Set the Hemisphere to Right (Note: even though we are saving a full volume, in this tutorial we are going to segment the right hemisphere).
• Select the Space push button and set the space to 711-2B-111 (which is the stereotaxic space of the anatomy volume). This value is just for informational purposes.
• Select the Category push button and set the category to INDIVIDUAL.
• Press the OK button on the Create Spec File Dialog. As new files are created in Caret5, the information from the Create Spec File Dialog will be used for default file names.
• In the Spec File Name Dialog, the name of the spec file that will be created (Human.case9.R.spec) using the information on the Create Spec File Dialog is shown. Accept this name by pressing the OK button.
Cropping the Anatomical Volume to a Single Hemisphere

Caret5’s segmentation algorithm requires that the input volume contain only a single hemisphere. In the next steps, the anatomical volume will be cropped so that it contains just the right hemisphere.

- **Select Resize Underlay Volume from the Volume Menu.**
- **Press the Reset button on the Resize Volume if the cropping boundary lines are not displayed on the volume in the Main Window.**
- **Press the Up Arrow for the X Min parameter so that it is set to 85 (or just enter 85 in the box).**
- **Press the Down Arrow for the X Max parameter so that it is set to 163.**
- **Press the Up Arrow for the Y Min parameter so that it is set to 15.**
- **Press the Down Arrow for the Y Max parameter so that it is set to 197 so that the volume cropping boundary lines appear as shown in Figure 9.**
• Change to a Parasagittal view of the volume so that the Z cropping parameters can be set by using the Volume View Axis Control in the Main Window Toolbar.

• Press the Up Arrow for the Z Min parameter so that it is set to 30.

• Press the Down Arrow for the Z Max parameter so that it is set to 158 so that the volume cropping boundary lines appear as shown in Figure 10. Use a coronal view to assist in verifying that the inferior part of the temporal lobe does not get cut off.

• Press the OK push button on the Resize Volume Dialog to crop the anatomical volume.

• Press the R button in the Main Window Toolbar to center the view of the cropped right hemisphere. Note that the volume crosshairs center on the Anterior Commissure.

• The cropped volume in a horizontal view should appear as shown in Figure 11.

Figure 9 - Cropping Right Hemisphere Horizontal View

Figure 10 - Cropping Right Hemisphere Parasagittal View
Figure 11 - Cropped Right Hemisphere

The cropped right hemisphere should be saved by performing the following steps:

- **Select** **Save Data File** from the **File Menu**.
- **Change** the **File name** to **Human.case9.R.RIGHT_HEM+orig.nii**.
- **Update** the **comment** to indicate that it is a cropped right hemisphere so that the **Save Data File Dialog** appears as shown in Figure 12.
- **Press** the **Save** push button to save the file.
Segmenting an Anatomical Volume

Now that you have a single hemisphere that is AC-centered, in LPI orientation, with 1.0 mm cubic voxels, it is now time to start the segmentation process.

- *Select SureFit Operations (Segmentation) from the Volume Menu.*
- The first page of the Surefit Segmentation Operation Dialog is Change/Verify Current Directory page. The directory already be set to the directory containing the volume files as shown in .
The second page of the **SureFit Segmentation Operations Dialog** is the **Subject Information Page** as shown in Figure 14. This information is what was entered on the **Create Spec File Dialog**. **Press** the **Next** push button.
The Spec File Selection Page shows the Spec File that will be updated as new data files are created during the segmentation process as shown in Figure 15. If you had not created a spec file, the name for the new spec file would be entered on this page. Press the Next push button to continue.
The **Volume Selection Page** allows selection of the volume that will be processed by the SureFit segmentation algorithm as shown in Figure 16. *Press* the **Next** push button to continue.
The Volume Attributes Page describes requirements for the volume that is to be processed by the SureFit segmentation algorithm as shown in Figure 17. These requirements were met during previous steps of this tutorial. Press the Next push button to continue.
The _Set Gray and White Matter Peaks_ page is used to provide information about the distribution of gray and white matter in the volume. On the left side of page is a histogram showing the distribution of voxels in the anatomical volume. On the right side of the page are controls for adjusting the gray and white matter peaks. Selecting the round or diamond shaped button to the left of _Gray Peak Control_ or the _White Peak Control_ colors all voxels exceeding that peak in green. Caret5 will attempt to identify the gray and white peaks but they normally will need some adjustment.

For additional information on drawing peaks visit the web page [http://brainvis.wustl.edu/help/peak_tweaking/index.html](http://brainvis.wustl.edu/help/peak_tweaking/index.html).

- *Use* the **Y-Max** slider to control the display of the histogram so that the peaks are easily visible.
- *Press* the arrows in the **Gray Peak Control** so that the gray peak is set to about 57 (to the left of the actual gray peak).
- *Press* the arrows in the **White Peak Control** so that the white peak is set to about 106 (just to the left of the white peak)
- The _Set Gray and White Matter Peaks Page_ should appear as in Figure 18. *Press* the **Next** push button.
The **Segmentation Operations Page** allows the user to choose the operations that are to be carried out during the segmentation process. While the SureFit algorithm attempts to identify and correct all topological defects (handles), there are usually a few handles that the algorithm is unable to correct. So, to save a little time, **deselect the Generate Very Inflated Surface, Generate Ellipsoid Surface** (used for Flattening) and **Create Curvature, Depth, and Paint Attributes** check boxes so that the **Segmentation Operations Page** appears as in Figure 19. **Press the Next** push button.
An **Information Dialog** will appear informing you that any previously generated surface files will be removed from the spec file and deleted due to the fact they will be incompatible with the newly generated surfaces produced by the segmentation process. *Press the OK button and the segmentation process will begin.* This may take up to several hours depending upon the speed of your computer. A progress dialog will be displayed during the segmentation process indicating the step that is being performed. *The Automatic Error Correction step will take the longest amount of time.*

At the conclusion of the SureFit Algorithm the **Segmentation Complete Page** will appear as shown in Figure 20. It will list the execution time and, if a surface was generated, the number of topological defects (handles) still remaining in the surface. *Press the Close push button on the SureFit Segmentation Operations Dialog.*
Manual Error Correction

In most cases, there will be handles remaining after the initial segmentation. In addition, the SureFit algorithm may classify non-cortical material near the eye or in the midbrain as cortex. Arteries and blood vessels may also get segmented and are usually very bright in the anatomical volume. As a result, manual error correction must be performed. At times, this may be an iterative process in which multiple cycles of manual correction of the segmentation volume and surface generation are performed.

- Use the Model Selection Control to display VOLUME in the Main Window.
- Press the D/C button in the Main Window Toolbar to show the Display Control Dialog.
- Set the Display Control Dialog’s Page Selection so that the Overlay/Underlay Volume page is shown.
- Set the Underlay to Anatomy. Set the Primary Overlay to the newest segmentation volume, most likely one with “Error_Corrected” in its name.
- Select Viewing Window 2 from the Window Menu.
- In Viewing Window 2, display the FIDUCIAL surface.
- Press M in the Viewing Window 2’s Toolbar to place the surface in a medial view. Look for non-cortical material that may appear as shown in FIGURE???
and is shown by a green symbol. *Click* on the non-cortical material that is part of the fiducial surface and you will see the volume slice and **crosshairs** in the **Main Window** relocate to the non-cortical material.

- The problems near the eye are found in horizontal slice 14.

Figure 21 - Segmentation

Figure 22 - Segmentation Near Eye
Figure 23 - Segmentation Near Eye Corrected

- *Switch* to a coronal view. Check for erroneous segmentation in midbrain structures as in Figure 24. This part of the segmentation will need to be removed.
- To edit segmentation voxels select Edit Voxels from the Volume Menu’s Segmentation submenu.
- On the Segmentation Volume Editor, set the Editing Mode to Turn Voxels Off.
- Set the Brush Size to 3x3 (or larger). Press the Apply push button.
- Place the mouse over the midbrain structure and hold down the left mouse button. The mouse will act as an eraser. Continue moving the mouse around, with the left mouse button held down, until all of the segmentation voxels that overlay the midbrain structures have been removed. Use the middle slice control in the toolbar to correct other slices that contain segmentation voxels over the midbrain structures. Check slices ranging from about 90 to 140.

In some cases, it may not be necessary to remove all of voxels on the midbrain structures. Instead, just make sure that the voxels overlaying the midbrain structures no longer connect to the voxels overlaying the white and gray matter. Once you believe the segmentation voxels overlaying the two structures are no longer connected, select Remove Islands form the Volume Menu’s Segmentation submenu. You might want to save the segmentation volume prior to using this option.
Now that the voxels overlaying the midbrain structure have been removed it is time to look for handles (topological defects).

- Select **Find Handles** from the **Segmentation** sub-menu on the **Volume Menu**.
- In the **Volume Handle Finder Dialog**, check the box next to **Y Axis (Coronal)** in the **Search** section.
- Press the **Search For Handles** push button in the Search section of the dialog. This will require a few minutes to search the volume for handles. When complete, the **Volume Handle Finder Dialog** will appear similar to that in Figure 26 with possibly different handles listed. Voxels that make up the “hole” of the handle are colored in purple by creating an RGB Volume and displaying it as the Secondary Overlay. For each handle found, the dialog will list the slice indices of one voxel in the handle, the number of slices along the search axis that the handle is within, and the total number of “hole” voxels in the handle.
Figure 26 - Segmentation Volume Handle Finder Dialog

- Select Window 2 from the Window Menu.
- Use the Model Selection Control in the Viewing Window 2 to show the INFLATED surface. Notice that surface nodes around handles are colored in purple. It may be necessary to switch to a medial or ventral view.
- In the Handles section of the Volume Handle Finder Dialog, click one of the listed handles with the mouse. The volume slices should jump to the handle with the “inside” of the handle shown in purple. Sometimes it is necessary to adjust the viewed slice by one slice.

When correcting errors in the volume it is sometimes helpful to turn off the segmentation and the RGB coloring that shows the handles to view the underlying segmentation to help determine the type of correction necessary.

Error Correction Example
This example is not from this tutorial’s segmentation. Here is an instance where the segmentation has jumped across the banks of a sulcus in the occipital lobe. Figure 27 shows the segmentation with the handle in purple, Figure 28 shows the segmentation, Figure 29 shows just the anatomical volume, Figure 30 shows the segmentation with the voxels that should be removed in a black encircled region, and Figure 31 shows the handle on the inflated surface.

Figure 27 - Handle Voxels Highlighted In Purple

Figure 28 - Handle Voxels Without Highlighting

Figure 29 - Anatomical Volume in Handle Region
The following steps are taken to correct this handle.

- Set the **Primary Overlay** to the **Segmentation Volume**.
- Set the **Secondary Overlay** to **No Coloring** (Removes purple coloring of voxels inside the handle).
- Set the **Underlay** to **Anatomy**.
- Select **Edit Voxels** from the **Segmentation** sub-menu on the **Volume Menu**.
- On the **Segmentation Volume Editor Dialog**, set the **Editing Mode** to **Turn Voxels Off** (In this mode, the mouse pointer functions like an eraser removing segmentation voxels).
- Set the **Brush Size** to 3x3. This means that when the mouse is clicked or dragged (moved with the left mouse button held down) over a voxel, the voxel and its eight surrounding neighbors in the slice will be affected by the segmentation editing operation. Leave the **Brush Thickness** set at **Current Slice Only** so that only segmentation voxels in the current slice will be modified. The **Segmentation Volume Editor** should appear as shown in Figure 32.
- Press the **Apply** push button on the **Segmentation Volume Editor Dialog**.
• *Place* the mouse over a segmentation voxel that is fusing the banks of the sulcus together. *Hold down* the left mouse button and *drag* the mouse over the voxels that are causing the problem. When the offending voxels are removed, *release* the mouse button.

![Figure 32 - Segmentation Volume Editor Dialog](image)

Correcting handles involves adding voxels to the segmentation or removing voxels from the segmentation. When voxels need to be removed from the segmentation, set the *Editing Mode* of the *Segmentation Volume Editor* to *Turn Voxels Off*. When voxels need to be added, set the editing mode of the *Segmentation Volume Editor* to *Turn Voxels On*. The mouse will function as an eraser or a paint brush. After making any changes to the *Segmentation Volume Editor Dialog*, press the dialog’s *Apply* push button. In the *Main Window* with the segmentation volume displayed, just move the mouse with the left mouse button held down to change the status of segmentation voxels. If there is a hole in a slice that needs to be filled, set the *Editing Mode to Flood Fill 2D*. Clicking the mouse on a voxel that is not part of the segmentation will fill all connected voxels that are not part of the segmentation. If at any time a mistake is made while editing the surface, pressing the *Undo* push button will restore the values of voxels that were just changed. It may be necessary to press the *Undo* push button several times to back out changes.

When using the *Volume Handle Finder* to locate and correct handles, correct handles along one axis at a time. When you think the listed handles have been fixed, press the *Search For Handles* push button again to verify that no new handles were created and handles were corrected. Once no handles are reported for an axis, search along a different axis and correct the handles found. The *Volume Handle Finder Dialog* is not guaranteed to find all handles so it may be necessary to inspect a surface, such as the inflated surface, for handles.
Save Corrected Segmentation Volume

Once all of the handles have been corrected, the segmentation volume should be saved.

- Select **Save Data File** from the **File Menu**.
- Set the **File type** to **Volume File – AFNI (*.HEAD)**.
- In the bottom of the **Save Parameters Dialog**, set the **Volume Type** to **Segmentation**.
- Set the **Volume File** to the “ErrorCorrected” segmentation volume that was just edited.
- In the **Comment** section, add information that errors were corrected.
- Change the name of the volume file from Human.case9.R.Segment_ErrorCorrected.<date>.HEAD to Human.case9.R.Segment_ErrorCorrected_fix1.<date>+orig.HEAD.
- Press the **Save** push button to save the error corrected segmentation volume file.

Generating Final Surface and Surfaces For Flattening

Since the segmentation volume has been modified to correct topological errors, the surface needs to be regenerated.

- Select **SureFit Operations (Segmentation)** from the **Volume Menu**.
- On the **Subject Information Page**, just press the **Next** push button since the subject information is already loaded into the page.
- On the **Spec File Selection Page**, just press the **Next** push button since the spec file is already set.
- On the **Volume Selection Page**, set the **Volume Type to Segmentation** and the **Volume File** to the **Segmentation Volume File** that was just edited and saved so that the **Volume Selection Page** appears like that in Figure 33. Press the **Next** push button.
On the Volume Attributes Page, just press the Next push button.

The Segmentation Operations Page has some of its operations disabled (in a light shade of gray and not responsive to the mouse). These options are disabled since we are starting with a segmentation volume instead of an anatomical volume. Deselect Automatic Error Correction since that process has already been performed. Verify that Generate Raw and Fiducial Surfaces, Generated Inflated Surface, Generate Very Inflated Surface, Generate Ellipsoid Surface, Create Curvature, Depth, and Paint Attributes, and Auto Save Generated Data Files are selected as shown in Figure 34. Press the Next push button to generate all of the surface and the surface attribute files. Select OK on the Information Dialog informing you that previously generated surfaces and related files will be deleted. In the Partial Hemisphere Padding Dialog, leave all options deselected and press the OK button. If you were to segment a partial hemisphere, selections are made in the Partial Hemisphere Padding Dialog to inform the surface generation algorithm where the hemisphere was cut. Generating the surfaces and related files may take a half hour or more depending upon your computer’s speed.
Figure 34 - Segmentation Operations Page (Final Surfaces)

- Press the Close push button on the SureFit Segmentation Operations dialog.
- Press the D/C button in the Main Window’s Toolbar to display the Display Control Dialog.
- Set the Display Control Dialog to display the Overlay/Underlay – Surface page.
- Set the Underlay to Shape with Depth as the selected column.
- View the different surfaces in the Main Window.
- Set the selected Shape column to Folding (Mean Curvature).
- View different surfaces with curvature shading the surface.

Surface Flattening

Now that the ellipsoid surface has been generated it is time to flatten the surface.

- Set the Main Window so that it displays the Ellipsoid Surface.
- Select Flatten Full or Partial Hemisphere from the Surface Menu.
- On the Flatten Full or Partial Hemisphere Dialog, set the Flattening Type to Full Hemisphere (Ellipsoid) and Morph Sphere.
• Since Caret5 starts with a volume whose origin is at the anterior commissure and Caret5 produces surface with the origin at the anterior commissure, the Anterior Commissure Position should be set to (0, 0, 0).
• Set the Border Template Cuts to Human Right Standard Cuts.
• The Flatten Full or Partial Hemisphere Dialog should appear as in Figure 35. Press the OK button to start the flattening process. A dialog will pop up asking you to confirm that the anterior commissure is at the origin. Press the Yes, Continue Flattening push button.

![Flatten Full or Partial Hemisphere Dialog](image)

**Figure 35 - Flatten Full Hemisphere Dialog**

**Correct Template Medial Wall Boundary and Calcarine Cut Borders**


After a short time the “compressed medial wall” surface will appear with a red border somewhat enclosing the medial wall region and blue borders showing where cuts will be made. See Figure 36.
Figure 36 - Template Cuts on Compressed Medial Wall Surface

- Drag the Continue Flattening Full Hemisphere Dialog to the side.
- Select Viewing Window 2 from the Window Menu.
- Use the Model Selection Control in Viewing Window 2 to view the INFLATED surface. It may also be helpful to enlarge Viewing Window 2.
- Switch to a medial View in Viewing Window 2 by pressing the M button in the Toolbar.
- Press the View button in the Main Window Toolbar to make sure that Caret is in View Mode.
- Click the mouse (perform Node Identification operations) around the boundary of the inflated surface’s medial wall. The green node identification symbols will appear on both the inflated and compressed medial wall surface.
- After identifying the boundary of the medial wall, identify the calcarine sulcus so that the inflated surface appears as in Figure 37 and the compressed medial wall surface appears as in Figure 38.
Select **Delete Border With Mouse** from the **Borders** sub-menu of the **Layers Menu**. Click the mouse over the existing medial wall and calcarine borders to delete them.

Select **Draw Border** from the **Borders** sub-menu of the **Layers Menu** to display the **Draw Borders Dialog**.

Press the **Select** push button and in the **Name Selection Dialog** highlight **MEDIAL.WALL** with the mouse and press the **OK** push button.

Press the **Apply** push button on the **Draw Borders Dialog**.
• In the Main Window, move the mouse over one of the green symbols around the medial wall. Hold down the left mouse button and follow the green symbols to trace out the medial wall. When the mouse gets near the start of the new border, release the left mouse button, hold down the shift key, and click the left mouse button to tell Caret5 that you are done drawing the medial wall border.

• In the Draw Border Dialog, press the Select push button. In the Name Selection Dialog highlight Calcarine Cut and press the OK push button.

• Press the Apply push button on the Draw Border Dialog. Now use the mouse to draw a border along the calcarine sulcus. Be sure that the border denoting the calcarine sulcus crosses the medial wall boundary. So, start drawing the border inside the medial wall and continue to the posterior part of the calcarine sulcus. The new medial wall and calcarine sulcus borders should appear similar to that in Figure 39.

• Press the Close push button on the Draw Borders Dialog.
• Press the Close push button on Viewing Window 2.
• Press the Continue Flattening push button on the Continue Flattening Full Hemisphere Dialog. This next process will take several minutes.

![Figure 39 - Corrected Medial Wall and Calcarine Cut on Compressed Medial Wall Surface](image)

The initial flat surface will appear similar to that in Figure 40. The green symbols may be removed by selecting Clear Node Identify Symbols from the Identify sub-menu of the Surface Menu or by pressing the CID button in the Identify Window’s Toolbar. If there are any large regions of crossovers (shown in red), indicating handles that are still present in the surface, it may be necessary to go back and edit the segmentation volume to correct the handles. If the handles are found the edge of the flat surface they can be removed by following the instructions in the Initial Flattening Dialog.
Continue the flattening process by pressing the **Continue Flattening** push button on the **Initial Flattening Dialog**.

**Multi-Resolution Morphing (Surface Distortion Reduction)**

- The **Multiresolution Morphing – Flat Dialog** will appear. This dialog contains the parameters that will be used by the multi-resolution morphing algorithm. This algorithm will reduce distortions in the flat surface caused by flattening. It rarely necessary to alter these parameters so just press the **OK** push button.
- The **Multiresolution Morphing – Sphere Dialog** will appear. This contains parameters for the reducing the distortion in the spherical surface. Press the **OK** push button to continue. The multi-resolution morphing of the flat and spherical surfaces will take a half-hour or longer to complete.

**Aligning the Surfaces to Standard Orientation**

When the multi-resolution morphing process is complete, several dialogs will pop up.
- Drag the **Align Surfaces Dialog** to the side.
- The **Spherical Morphing Measurements Dialog** displays measurement information collected during spherical morphing. Press the **Close** push button to remove it.
- The **Flat Morphing Measurements Dialog** displays measurement information collected during flat morphing. Press the **Close** push button to remove it.
- Press the D/C button in the **Main Window Toolbar** to display the **Display Control Dialog**.
- Change to the **Overlay/Underlay – Surface Page**.
- Set the **Underlay** to **Shape**.
• *Set* the **Shape** column to **Folding (Mean Curvature)**.
• *Set* the **Primary** and **Secondary Overlays** to **No Coloring**.
• *Press* the **Close** push button on the **Display Control Dialog** to remove it.
• *Place* the **Align Surface(s) to Standard Orientation Dialog** to the side of the **Main Window**.
• *Press* the **Reset** push button on the **Align Surface(s) to Standard Orientation Dialog**.
• In the **Main Window**, *click* the mouse on the ventral tip of the Central Sulcus (near the middle of the surface). The ventral tip is shown by the green square in near the center of Figure 41.

![Figure 41 - Unaligned Flat Surface](image)

• *Hold down* the Shift Key and *click* the mouse on the dorsal-medial tip of the Central Sulcus (opposite end of the Central Sulcus from click made in last step). You should see X and Y values for the **Ventral** and **Dorsal-Medial Tips** of the Central Sulcus in the **Align Surface(s) to Standard Orientation Dialog**.
• In the **Spherical Surface** section of the **Align Surface(s) to Standard Orientation Dialog**, *check* the box to the left of **Align Sphere**.
• *Press* the **Apply** push button on the **Align Surface(s) to Standard Orientation Dialog**. After a short time the flat surface should appear similar to Figure 42.
• *Press* the **Close** push button on the **Align Surface(s) to Standard Orientation Dialog**.
Since data files (flat coordinate, spherical coordinate, and latitude longitude) have been modified by the alignment process, they need to be saved.

**Saving the Aligned Surface Files**

- Select **Save Data File** from the **File Menu**.
- Set the **File type** to **Coordinate Files (*.coord)**.
- Near the bottom of the dialog verify that **Coord File** is the CYCLE5_OVERLAP_SMOOTH coordinate file.
- Set the **Coord Frame** to **Cartesian Standard**.
- Set the **Orientation** to **Left, Posterior, Inferior**.
- Add information about alignment to standard orientation to the **Comment** section.
- Change the **File name** to Human.case9.R.FLAT_ALIGNED.<date>.<#nodes>.coord so that the dialog is similar to that in Figure 43.
Figure 43 - Save Aligned Flat Coordinate File

- Press the Save push button to save the file.
- Select Save Data File from the File Menu.
- Near the bottom of the dialog set the Coord File to the SPHERE_CYCLE4 coordinate file.
- Set the Coord Frame to Spherical Standard.
- Set the Orientation to Left, Posterior, Inferior.
- Change the File name to Human.case9.R.SPHERE_ALIGNED.<date>.<#nodes>.coord.
- Press the Save push button to save the file.
- Select Save Data File from the File Menu.
- Set the File type to Latitude Longitude Files (*latlon).
• *Change* the **File name** to Human.case9.R.LAT_LON.<date>.<#nodes>.latlon.
• *Press* the **Save** push button to save the file.

At this point you are done.
* *Select Exit* from the **File Menu** (*Quit* from the **Caret Menu** for Macintosh users).
Spherical Registration

Caret5 provides two registration methods, flat and spherical, for bringing one surface into register with another using landmarks to constrain the deformation. The landmarks consist of borders that identify regions identified on both surfaces such as the medial wall boundary and various sulci. There are several advantages of spherical registration over flat registration. First, the spherical surfaces are closed (contain no cuts), eliminating the requirement for landmarks along the surface perimeter in flat registration. Secondly, spherical registration requires six landmarks, two along the medial wall boundary, and one each on the calcarine sulcus, the central sulcus, the sylvian fissure, and the superior temporal gyrus.

The first step in performing a spherical registration is to draw the needed registration landmarks (borders) on both the individual and atlas surfaces. For good quality registration, six registration landmarks are needed. Fortunately, three of the six required registration landmarks are automatically created during the flattening of a full hemisphere. You may recall drawing the medial wall and calcarine cuts during the flatten full hemisphere process. The medial wall cut becomes two of the registration landmarks by splitting it into two pieces where it intersects both the frontal and calcarine cuts. The calcarine cut becomes the third registration landmark. You will need to draw the other three required registration landmarks that denote the central sulcus, the sylvian fissure, and the superior temporal gyrus.

For a very thorough description of drawing the borders for registration (and flattening) visit the web page http://brainvis.wustl.edu/help/landmarks_core6/landmarks_core6.html.

There are two other very important considerations regarding the landmark borders. First, both the individual and atlas landmarks must consist of the same number of borders with a one-to-one correspondence in the border names. Secondly, each of the corresponding landmark borders must be oriented in the same manner. In other words, each of the corresponding borders must begin and end in corresponding anatomical locations.

- **Exit** out of any Caret5 programs that are running.
- **Change** into the tutorial’s registration/INDIVIDUAL.1582.L directory.
- **Start** Caret5.
- **Open** the Human.1582.L REGISTER-with-ATLAS.03-05.65950.spec specification file.
- In the spec file dialog **press** the Select All button, deselect both of the border projection files, and **press** the Load button to load the files.
- In the Main Window, use the Model Selection Control to select the FLAT surface.
- **Press** the Toolbar:D/C button to launch the Display Control Dialog.
- On the Overlay/Underlay – Surface panel, set Shape to Folding – Fiducial – 1582L to see the folding (mean curvature) on the flat surface.
- **Select** Layers: Borders: Draw Border to launch the Draw Border Dialog.
• **Press** the Select button in the Draw Borders Dialog’s Attributes frame.
• **Select** the name LANDMARK.CentralSulcus and **press** the OK button in the Name Selection Dialog.
• **Set** the Resampling to 4.0.
• Verify that the **Type** is set to Open.
• **Press** the Apply in the Draw Borders Dialog.
• **Draw** a border that follows the fundus of the central sulcus. Be sure to start at the bottom of the central sulcus near the middle of the window and draw upwards to the other end of the central sulcus (yellow border in Figure 45). If you do not know how to draw a border, see the borders section of this document.
• **Press** the Select button in the Draw Borders Dialog.
• In the Name Selection Dialog, **choose** the LANDMARK.SylvianFissure item and **press** the OK button to close the Name Selection Dialog.
• **Draw** a border that follows the sylvian fissure. Start at the end of the sylvian fissure near the middle of the surface and draw left and down as show in Figure 45.
• **Use** the Main Window’s Model Selection Control to view the INFLATED surface.
• **Press** the Main Window Toolbar’s View button to place the mouse back into view mode.
• **Use** the ID Node function to identify (click the mouse) along the anterior portion of the superior temporal gyrus.

![Figure 44 - Node Identified Along Superior Temporal Gyrus](image)

• **Use** the Main Window’s Model Selection Control to return to viewing the FLAT surface.
• **Press** the Selection button in the Draw Borders Dialog.
• In the Name Selection Dialog, **choose** the LANDMARK.SF_STSant item and **press** the OK button to close the Name Selection Dialog.
• *Press* the Draw Borders Dialog’s Close button.
• Starting at the top of the identified nodes, *draw* superior temporal gyrus border.
• *Switch* the Display Control Dialog to the Border panel.
• In the *Main* tab, *select* Show First Link Red. You will see the beginning of each border in red as in Figure 45.

![Figure 45 - Central Sulcus, Superior Temporal Gyrus, and Sylvian Fissure Landmarks](image)

• *Select* Layers: Borders: Project Borders. Leave the Projection Method set to Nearest Tile and *press* the OK button in the Border Projection Dialog. This will project the three borders that you have just drawn to all of the other surfaces.
• *Use* the Model Selection Control to *view* the SPHERICAL surface in the Main Window. *Rotate* the surface to view the Central Sulcus landmark (in yellow) and the Sylvian Fissure landmark (in cyan).
• *Press* the Spec button in the Main Window Toolbar.
• *Press* the Open button to the left of the border projection file Human.1582.L.Full.LANDMARKS.FromFlattening.65960.borderproj. In the Append or Replace Dialog, *choose* Append. This loads the landmarks that were automatically created when the hemisphere was flattened.
• In the Main Window’s Toolbar, *press* the M button to get a medial view of the spherical surface. You will see additional landmarks around the medial wall and along the calcarine sulcus (Figure 46).
Choose File: Save Data File.
- In the Save Data File Dialog, set the File Type to Border Projection Files.
- In the File Name text box, change the name to Human.1582.L.Full.LANDMARKS.ForSphericalRegistration.65950.borderproj.
- Press the Save button to save the border projection file.
- Exit out of this Caret program. You will be informed about unsaved border files that were created during the border projection process. We do not need these since the border projection file was saved, so, quit without saving.

The INDIVIDUAL surface now has the landmarks required for registration. The ATLAS surface already has its needed landmarks so it is now time to execute the registration process.

- Change up one directory level so that you are in the tutorial’s REGISTER_SPHERE directory.
• **Start** Caret5.
• **Select** Surface: Deformation: Run Spherical Surface Deformation to launch the Spherical Surface Deformation Dialog.
• **Press** the Individual Tab.
• **Press** the Spec File button.
• In the **Choose Spec File Dialog**, go into the INDIVIDUAL.1582.L directory, **select** the Human.1582.L.REGISTER-with-ATLAS.03-05.65950.spec specification file, and **press** the Open button. This results in the remaining fields of the dialog being set.
• **Press** the Border File button. Make sure the selected border file is set to Human.1582.L.Full.LANDMARKS.ForSphericalRegistration.65950.borderproj.
• **Press** the Atlas tab.
• **Press** the Spec File button.
• In the **Choose Spec File Dialog**, go into the ATLAS_LEFT_HEM directory, **select** the Human.colin.L.REGISTER-to-INDIVIDUAL.03-05.71785.spec specification file, and **press** the Open button.
• **Press** the Spherical Parameters tab.
• **Press** the Select Standard Parameters button (near the bottom of the dialog).
• In the **Choose Registration Parameters Dialog**, **press** the Human to Human radio button and **press** the OK button.
• **Press** the OK button on the Spherical Surface Deformation Dialog to start the deformation. This will take 10 to 20 minutes depending upon the speed of the computer.
• Part way through the deformation process, you might get a dialog reporting that crossovers (spherical surface tangles) were encountered. If the number is small (i.e. less than 12) choose to continue the deformation process. If the number is larger, it is possible that one of the landmarks, central sulcus, or sylvian fissure was drawn in the wrong orientation. Verify that the landmarks are correct.

**Viewing Registration Results**

• **Press** the OK button on the Deformation Completed Dialog. **Exit** out of this Caret5.
• **Change** into the REGISTER_SPHERE/ATLAS_LEFT_HEM directory.
• **Start** Caret5.
• In the **Open Spec File Dialog** are two spec files. **Choose** the deformation_Human.1582.L.REGISTER-with-ATLAS.03-05.71785.spec which contains the individual’s data (1582.L) registered to the atlas surface.
• In the **Spec File Dialog**, in addition to the default files, **select** either of the Area Color Files, either of the Border Color Files, the deformed_Human.1582.L.CartesianGrid.71785 Border Projection file, the deformed_1582.L.Eye-movements-attention.71785.metric Metric file, and both of the Paint files. **Deselect** the deformed_Human.1582.L.COMPOSITE.71785.surface_shape Surface Shape file and **select** the Human.colin.L.COMPOSITE.71785.surface Shape file. **Press** the Load button to load the files.
In the Main Window, use the Model Selection Control to view the FLAT surface. The Cartesian grid borders provide feedback on the surface deformation.

Press the ToolBar:D/C button to launch the Display Control Window.

Press the Borders button near the bottom to turn off the borders.

Set the Primary Overlay to Paint and select the Paint column Geography – 1582.L to see the individual’s sulcal pattern deformed to the atlas.

Switch the Paint to Geography – Human.colin.L to view the atlas’ geography and contrast it with the individual’s geography.

Set the Primary Overlay to Metric to view the individual’s functional data deformed to the atlas.

Exit this Caret5.
Command Line Segmentation

To segment at the command line, the volume must be in an LPI orientation with its origin set so that the (0, 0, 0) stereotaxic coordinate is at the anterior commissure. The gray and white peaks must also be known.

VOLUME SEGMENTATION

caret_command -volume-segment <operation_code>\ 
   <f-gray-peak> <f-white-peak>\ 
   <padding-code> <structure> <spec-file-name> 
   <anat-or-segment-volume>

Operation_Code characters
 Specify each with either a "Y" or "N".
 All characters must be specified.
Character   Operation Description
         --------   ---------------------
         1   Disconnect Eye and Skull
         2   Disconnect Hindbrain
         3   Use High Threshold for Hindbrain disconnection
         4   Cut Corpus Callosum
         5   Generate Segmentation
         6   Fill Ventricles
         7   Automatic Error Correction
         8   Generate Raw and Fiducial Surfaces
         9   Generate Inflated Surface
        10   Generate Very Inflated Surface
        11   Generate Ellipsoid Surface (For Flattening)
        12   Generate Hull Surface
        13   Generate Curvature, Depth, and Paint Attributes

gray-peak specifies the intensity of the gray matter peak in the anatomy volume.

white-peak specifies the intensity of the white matter peak in the anatomy volume.

padding-code
 Specify padding for any cut faces when segmenting a partial hemisphere.
 Specify each with either a "Y" for padding or "N" for no padding.
 All characters must be specified.
Character   Padding Description
         --------   -------------------
structure  Specifies the brain structure.
    Acceptable values are RIGHT or LEFT

spec-file-name  Name of specification file.

anat-or-segment-volume  Name of input volume.
    The volume must be in a Left-Posterior-Inferior orientation and
    its stereotaxic coordinates must be set so that the origin is
    at the anterior commissure.