# Register

# Introduction

## Image Registration

The goal of image registration is to determine a spatial transformation that will bring into alignment separately acquired images of the same object. When accurately registered, each separate image will have the same coordinate system and same voxel size, a voxel in one image will represent the same physical location as the corresponding voxel in the other image. The registration process interpolates the registered images as they are resampled and/or reformatted during the registration process. For example, registration of an axial PET data set to a sagittal MRI data set results in the PET data being transformed (resampled and reformatted) into the sagittal MRI space.
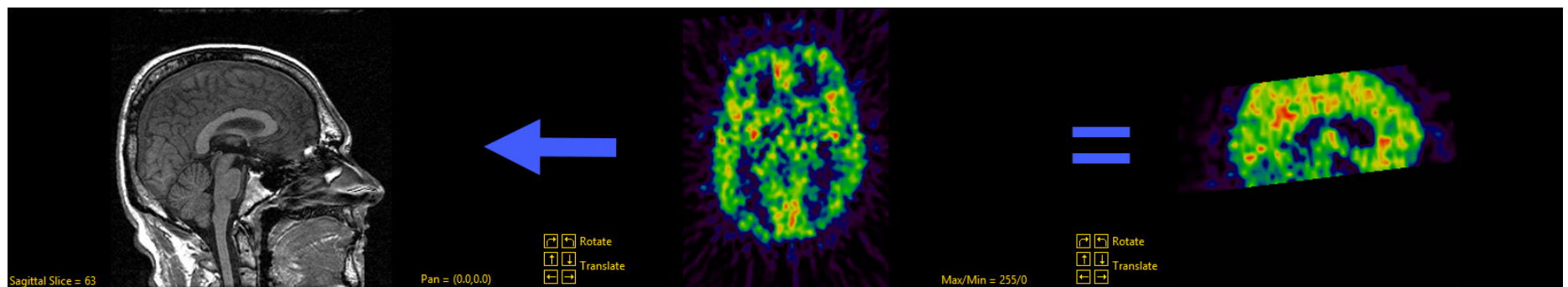


Registration is a prerequisite for several applications including; the display, segmentation, and analysis of structural and functional data, algebraic manipulation of image data (image addition, subtraction, multiplication, and division), the analysis of dynamic image data, and the fusion of data from multiple images.

# Introduction (continued)

## Image Fusion

Image fusion is the process of combining, into one image, the information from multiple registered images. For example, the registration of an axial PET to a sagittal MRI allows for the transformed PET image data to be superimposed upon the sagittal MRI and output as a single fused volume illustrating both structure and function.
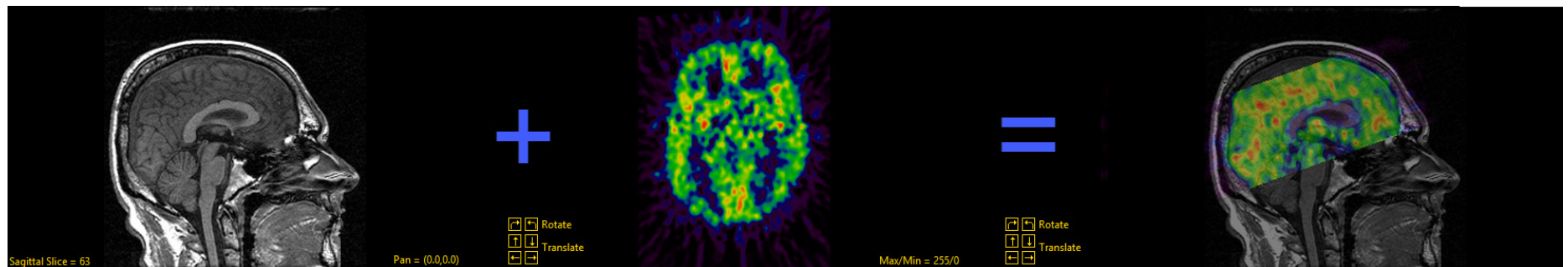


## Transformation

Transformation is the process of changing a match data set to align with the base data set using the parameters calculated during registration, these parameters include; translation, rotation, scaling, and shear.

**Translation:** A translation moves data to a different position. A 2D image can be moved left, right, up or down. A 3D volume can be moved left, right, up, down, backwards or forwards.

**Rotation:** Rotation rotates the data at a particular angle from its origin.

**Scaling:** Scaling changes the size of a data set. Scaling either expands or compresses the dimensions of the image data.

**Shear:** Shearing, sometimes referred to as skewing, is a transformation that slants the shape of the data.

# Register Module Interface

The register module is divided into several areas: 1) the menu, 2) tools, 3) the display area, and 4) the registration controls.

## Menu

**File:** The File menu allows users to load the base and match data, load and save transformed object maps, and save transformed match data. The File options include:

- **Input/Output:** Displays a Volume area at the bottom of the Register module window. This area facilitates the dragging and dropping of image data into the module and the reversing of inputs via the Swap Inputs button.
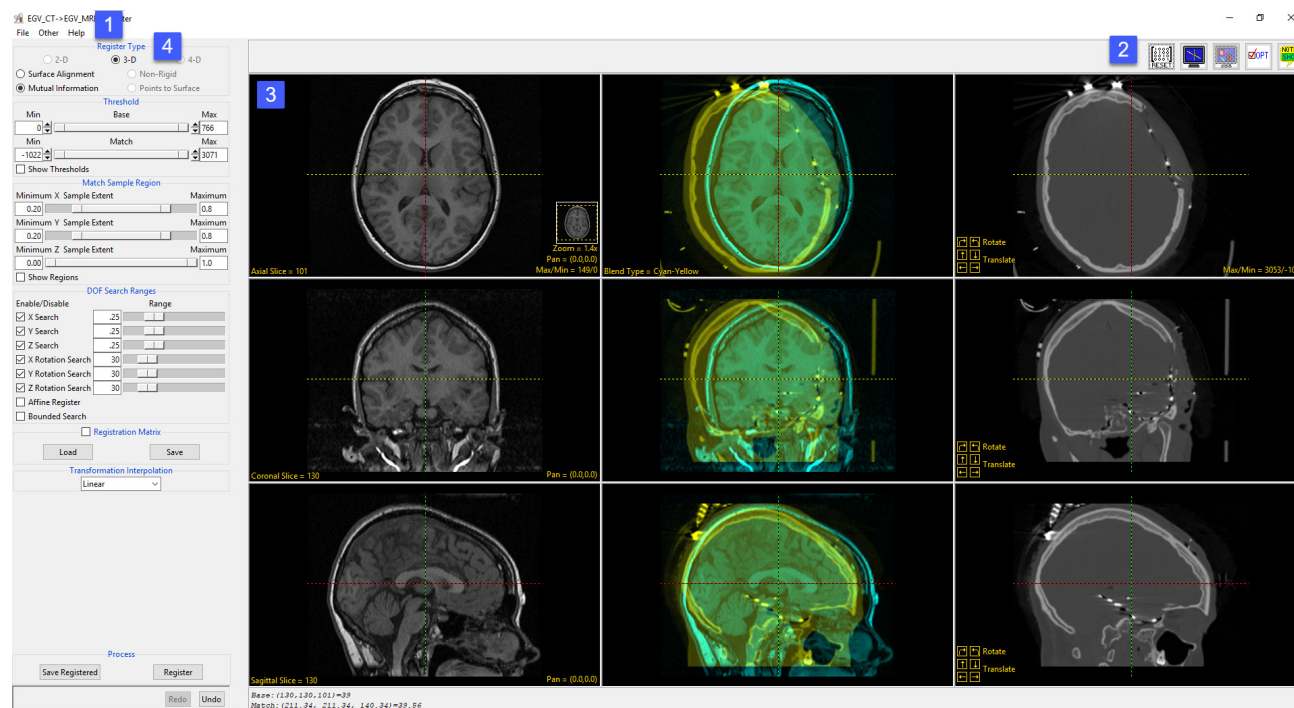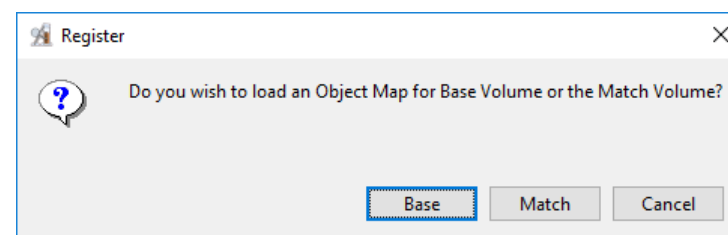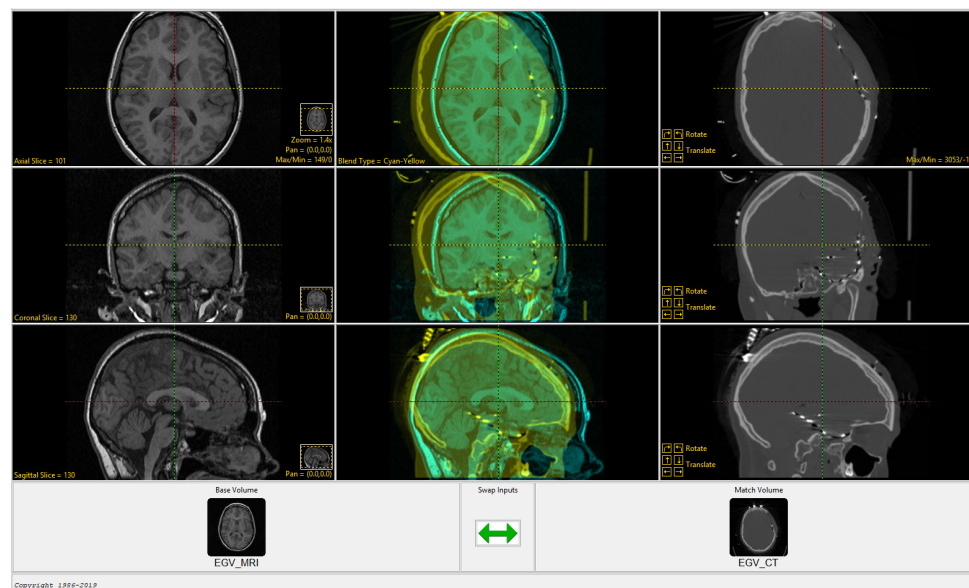
# Menu (Continued)

**File >Input/Output (continued):**

Tip: Swapping inputs is useful when you register a match data set to a base data but need the base data set transformed into the space of the match data set. This situation can arise when you are unable to register image A to image B, but are able to register image B to image A.

- **Load Object Map:** Allows users to load an object map for the Base and/or Match volume. When selected a window will be returned prompting the user to specify which volume the object map should be loaded for. There is also the option to cancel the object map load. Once Base or Match is selected a Load Object Map window will open allowing users to navigate to, select, and load an object map file. The following options are available:

  · **Current Directory:** Takes user to the current directory, the current directory is set by right-clicking in the main Analyze 14.0 window and then choosing Current Directory from the menu.
  · **Workspace Directory:** Takes user to the current Workspace directory.
  · **Home Directory:** Takes user to the user's Home directory.
  · **Cancel Load:** Cancels load of the object map.

# Menu (Continued)

**File (continued):**

- **Unload Object Map:** Allows users to unload the Base, Match, or both object maps. Users also have the option to cancel the object map unloading process.

- **Save Registered:** The Save Registered option allows users to save the transformed match data set, the fused image data, or the transformed match object map – only available if a match object map was loaded.

When the Save Object Map option is selected users will be prompted to save the object map or cancel the save. When Save Object Map is selected a new window will open providing users with the option to overwrite the loaded object map (Yes) or to save as a new object map (No, I want to specify a name and location).

- **Exit:** Closes the module

**Other:** The other menu provides access to the Options and Powerbar editor menus.

**Other > Options:** When selected opens the Options menu providing access to Module configuration options, including:

- **Intensities Linked:**  Allows users to enable or disable linked intensity adjustment. When linked any adjustment an images intensity display will be applied to all grayscale slices displayed. When disabled image intensities can be adjusted individually.

- **Linked Pan:** Allows users to enable (default) or disable linked image panning. Note that linked panning only applies to the current row of images. Disabling linked pan allows you to pan a single image at a time.
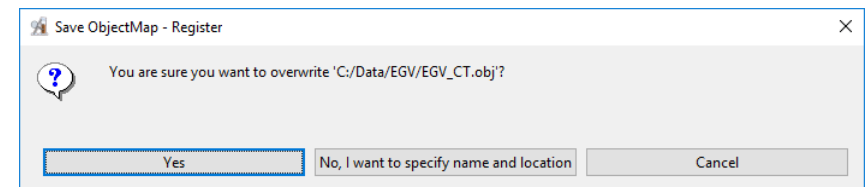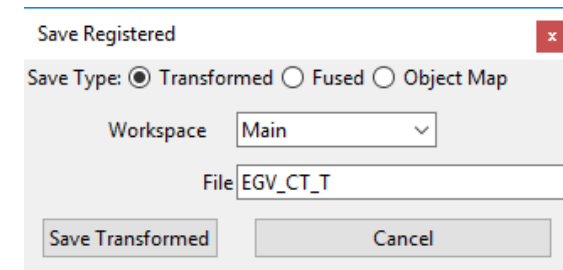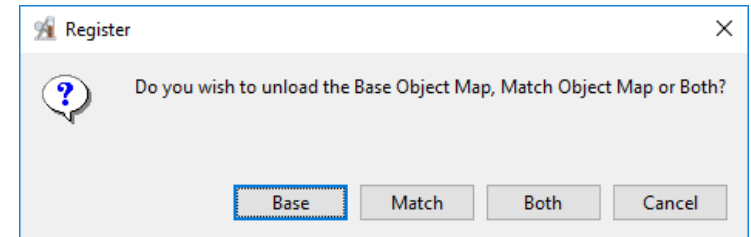
# Menu (Continued)

**Other > Options (continued):**

- **Linked Zoom:** Allows users to enable or disable linked zooming. The following options are available:

  · **Both:** Both is the default option, when selected any zoom in/out on an image is applied to all images for both input data sets.
  · **Row:** Allows zooming to be applied to the current row of images.
  · **Column:** Allows zooming to be applied to the current column of images.

- **Linked Blend:** The linked blend option allows for the enabling (default) and disabling of the same blend type to be applied to all fused images in the center column. Keep enabled if you wish to apply the same blend option to all fused images, disable if you wish to apply different blend options to the fused images.

- **Adjust Scale:** Allows users to enable or disable (default) the scale tool for the match data allowing for interactive image scaling.

- **Auto Note Update:** Allows the Auto Note Update option to be enabled or disabled.

- **Threads:** Allows users to specify the number of threads used in a multi-threaded rendering process. By default, the number of threads is set to the number of processors on the system.

**Other > Powerbar Editor:** Provides access to the Powerbar Editor allowing users to add and remove tools from the tools area. See the Powerbar Editor description in the Segment section for further information.

**Help:** The Help menu provides users with quick access to help resources including:

- **About:** View version, system and environment information.

- **Users Guide:** Opens the Analyze 14.0 User's Guide.

- **Get Help:** Opens the AnalyzeDirect Support Page.
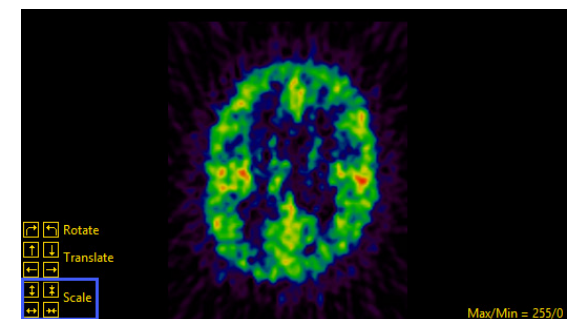
# Tools

The Tools options provide access to the Toggle Cursor Link, Toggle Region Display and the Set Note State tools. For further information on these tools please refer to section 2. Image Display, Controls and Customization.

- **Reset Matrix:** The reset matrix tool is unique to Register and allows users to reset the match data sets matrix at any time. To reset the match registration matrix simply click the Reset Matrix button.

# Display Area

The Register display area consists of; 1) the base image display, 2) the match image display, 3) the fused image display, 4) the linked cursor tool, 5) linked cursor coordinates, 6) slice display tool, 7) image display controls, 8) blend type options, and 9) manual registration tools.
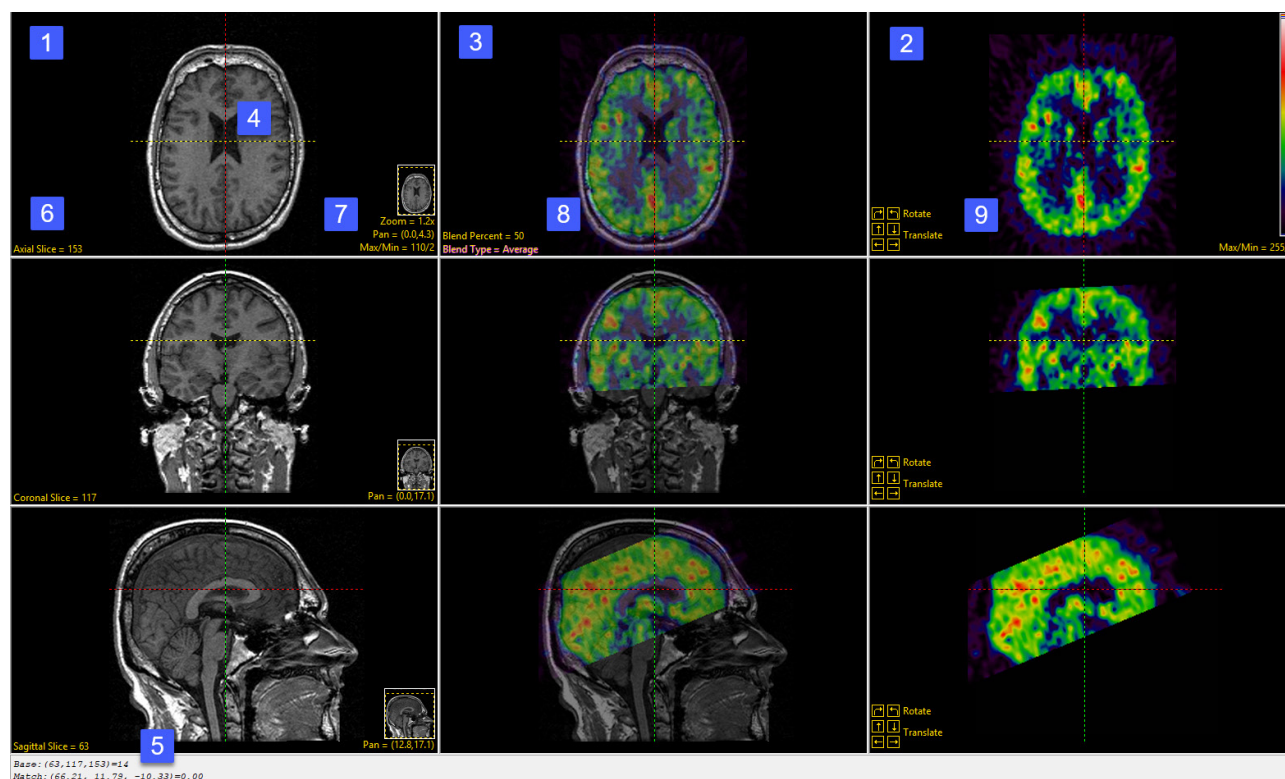
# Display Area (Continued)

**Display Area:** The Register module display area is a nine-panel display divided into three columns and three rows; each column displays a different data set while each row displays a different orientation.  The first column [1] displays the base data set, the third column [2] displays the match dataset, while the middle column [3] displays a fused image - a blended combination of the base and match data. The top row displays all three image data sets (base, fused, and match) in the axial orientation, the middle row displays all three data sets in the coronal orientation, and the bottom row displays all three data sets in the sagittal orientation.

**The Cursor Link:** The cursor link [4] allows users to interactively navigate through the input image data. The cursor linked tool can by adjusted in any of the nine display panels interactively updating all nine simultaneously. The linked cursor coordinates as well as the voxel intensity value for both the base and match volumes are displayed in the lower left-hand corner. [5] The cursor link can be enabled or disabled using the Toggle Cursor Link button.

**The Slice Tool:** Users can navigate through image slices using the slice tool. Click the yellow Slice text in the lower left-hand corner of the base axial, [6] coronal, or sagittal image display. An up/down slice cursor will appear. Hold down the left mouse button and slide the cursor upward to move to a higher slice number and downward to move to a lower slice.

Users can quickly navigate to the First, Middle and Last slice by right-clicking the yellow Slice text. A specific slice number can be chosen by double-clicking the yellow Slice text and typing in the desired slice number.

**Image Display Controls:** Register provides users with access to the Zoom, Pan, and Max/Min tools [7].

- **Zoom Tool:** Users can increase and decrease the display size of the data using the Zoom tool. Click on the yellow Zoom text in the bottom right corner of the image pane. A zoom cursor will be displayed. While clicking and holding the left mouse button, move the mouse upward to zoom in and downward to zoom out. Let go of the left mouse button when the desired zoom factor is reached. For a full description of the Zoom tool including right mouse menu options please refer to the Zoom tool in Section 2. Image Display, Controls and Customization.
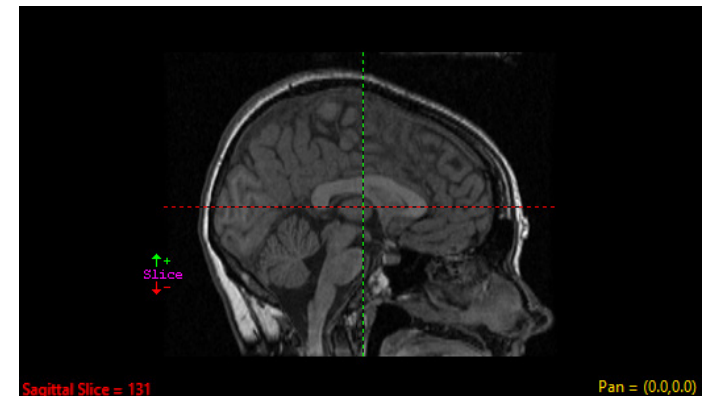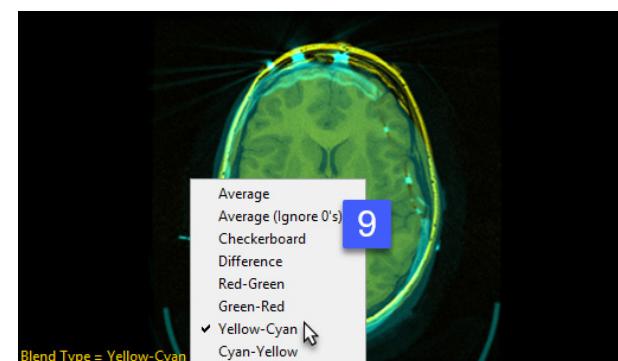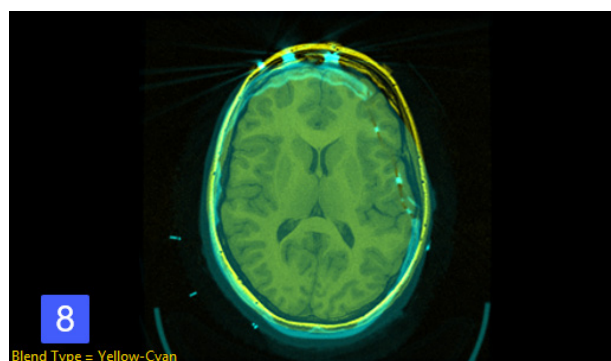
# Display Area (Continued)

**Image Display Controls > Zoom Tools (Continued):** Note: Linked Zooming can be disabled, enabled, or enabled for just columns or rows. See the Other > Options menu description above for additional information.

- **The Pan tool:** The Pan tool is automatically enabled in Register. Click on the yellow Pan text in the bottom right corner of the axial, sagittal, or coronal base images. A pan cursor will be displayed. While clicking and holding the move the cursor to pan the image. Panning is linked for the selected row, to pan the current image only disable Linked Pan in the Other > Options menu for additional information see the Other > Options menu description above.

- **Max/Min tool:** The Max and Min display intensities of the base data set can be changed by clicking on the yellow Max/Min Tool at the bottom right corner of the axial base image window. A cursor will return that allows the values to be manipulated. Hold down the left mouse button and move the mouse up/down or left/right to adjust the display. To change the intensity display of the match data, click on the yellow Max/Min Tool at the bottom right corner of the match image window. For a complete description on how to how values are changed with the Max/Min tool please Section 2. Image Display, Controls and Customization.
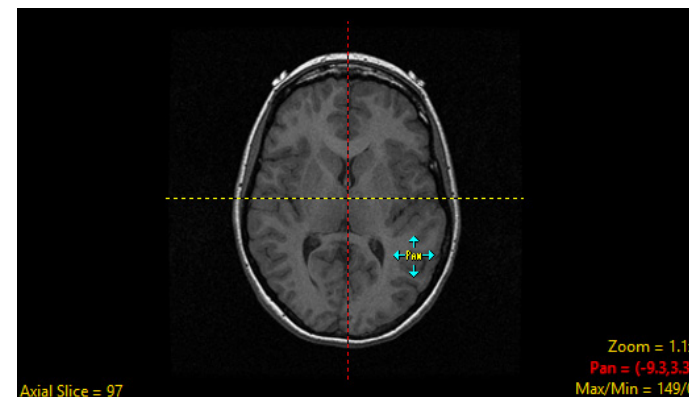
**Blend Type Options:** The blend type in the lower left-hand corner of the fused axial image [8] can be used to adjust the blended composition of the fused image. To adjust the blend type, left click on the yellow Blend Type text to toggle through the blend type options, alternately, right click on the yellow Blend Type text and choose a blend type from the menu [9].
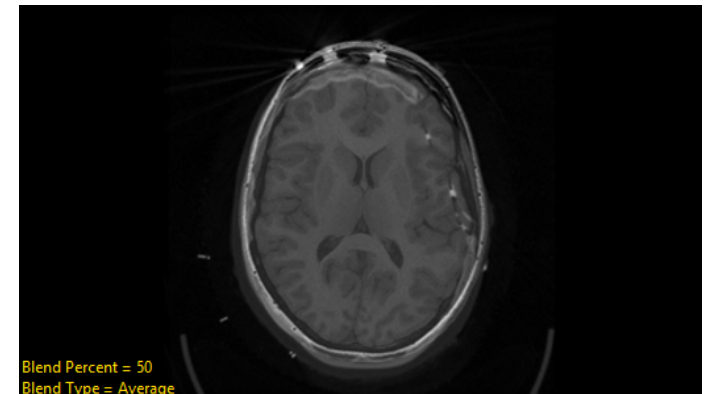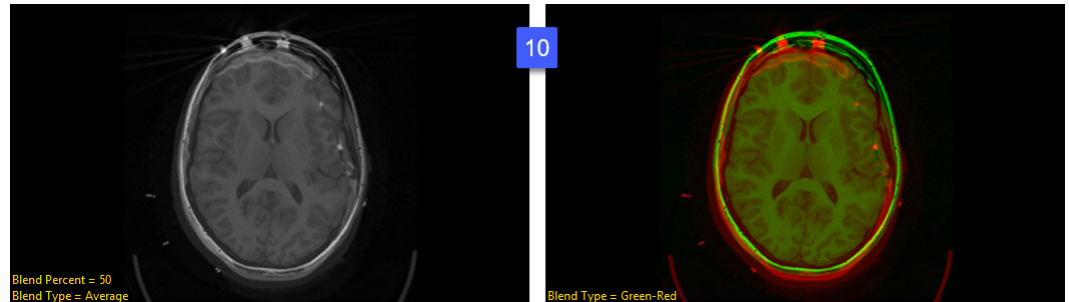
# Display Area (Continued)

**Blend Type Options (continued):**

Blend type adjustment is helpful for the visual assessment and verifications of registration, especially when the base and match images are both grayscale [10].



The following blend types are available:

- **Average:** The Average blend option linearly interpolates the base and match images to form the fused image.

  · **Blend Percent:** The blend percent option is available when the Average blend type option is selected. The blend percent allows users to adjust the percent of the Base image used in the interpolation to form the fused image. The default blend percent is 50, lowering the percentage will lower the amount the base image displayed in the fused image, higher the percentage will increase the amount of the base image displayed in the fused image. Double-click on the yellow Blend Percent text to enter a percent value or right-click and choose a value from the menu.



- **Average (Ignore 0's):** Like the Average blend option the Average (Ignore 0's) option linearly interpolates the base and match images to form the fused image, however, voxels with a value of 0 in the base image are not included when creating the fused image.

# Display Area (Continued)

**Blend Type Options > Average (Ignore 0's) (continued):**

In the example here, a rectangular region has been removed from the base image and the voxel values set to 0 [11]. Instead of a black rectangle appearing in the fused image, these voxels are ignored and the voxels from the match image are displayed [12].
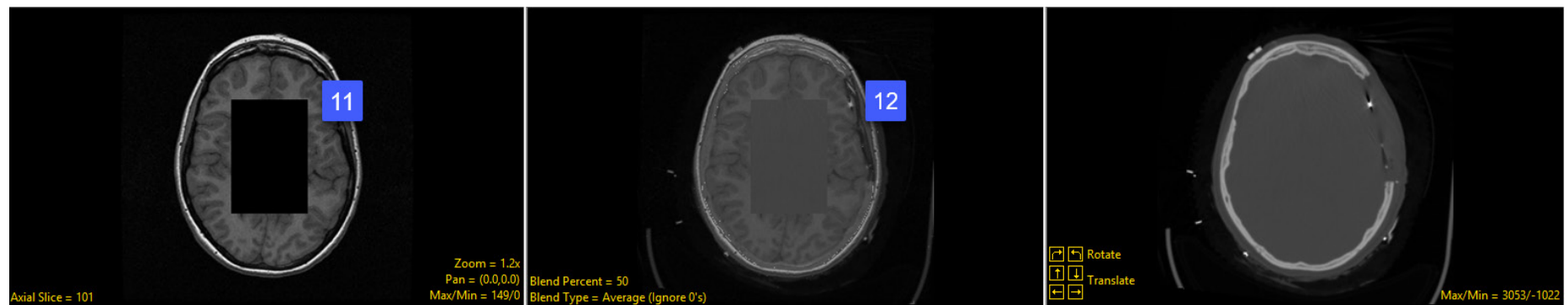


- · **Blend Percent:** The blend percent option for the Average (Ignore 0's) blend options works and functions the same as the blend percent option for the Average blend option.

- • **Checkerboard:** This function depicts the base and match volumes in a checkerboard pattern. The following options are available:

  - · **Grid Size:** Allows users to specify the size of squares used to create the checkerboard grid.
  - · **Toggle Grid:** Switches the base and match volume inputs for the checkerboard squares [13].

# Display Area (Continued)

**Blend Type Options (continued):**

- **Difference:** The difference option subtracts the base volume from the match, directly showing the difference between volumes [14].



Blend Type = Difference

- **Red-Green:** The red-green blend option applies a red color overlay to the base volume and green color overlay to the match volume. Color blending is useful when the two volumes are both grayscale or from the same modality.



Blend Type = Red-Green

- **Green-Red:** The green-red blend option applies a green color overlay to the base volume and red color overlay to the match volume.



Blend Type = Green-Red
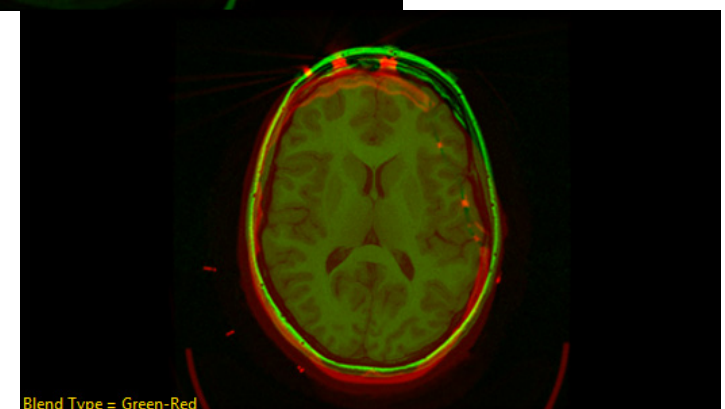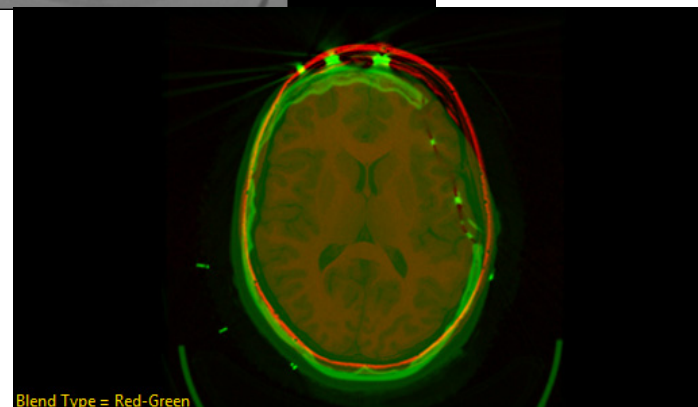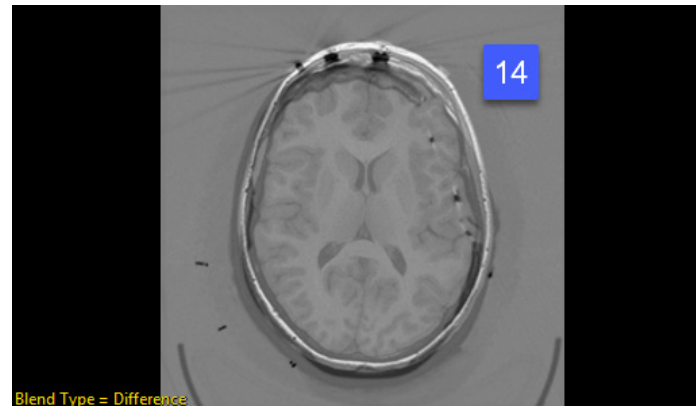
# Display Area (Continued)

**Blend Type Options (continued):**

- **Yellow-Cyan:** The yellow-cyan blend option applies a yellow color overlay to the base volume and cyan color overlay to the match volume.



Blend Type = Yellow-Cyan

- **Cyan-Yellow:** The cyan-yellow blend option applies a cyan color overlay to the base volume and yellow color overlay to the match volume.



Blend Type = Cyan-Yellow
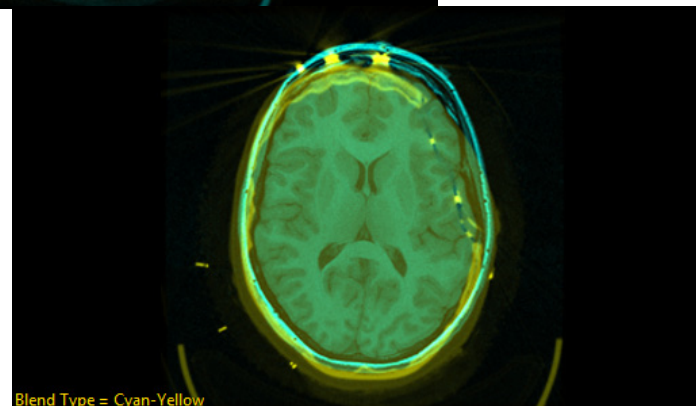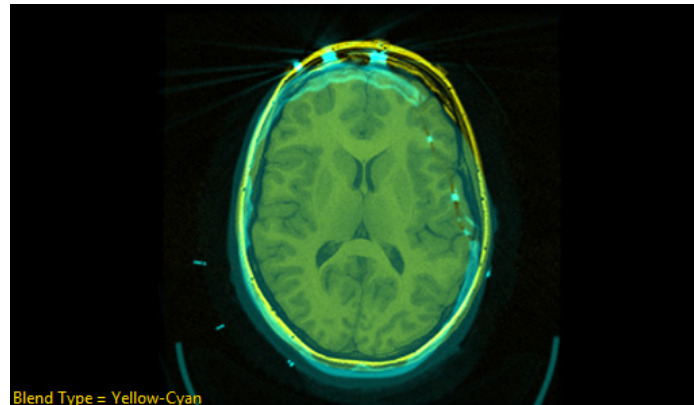
**Manual Registration Tools:** The manual registration tools [15] allow users to adjust the position of the match data set by translating or rotating the data in the axial, coronal, and sagittal orientations. When enabled users are also able to scale the match data manually in all orientations.
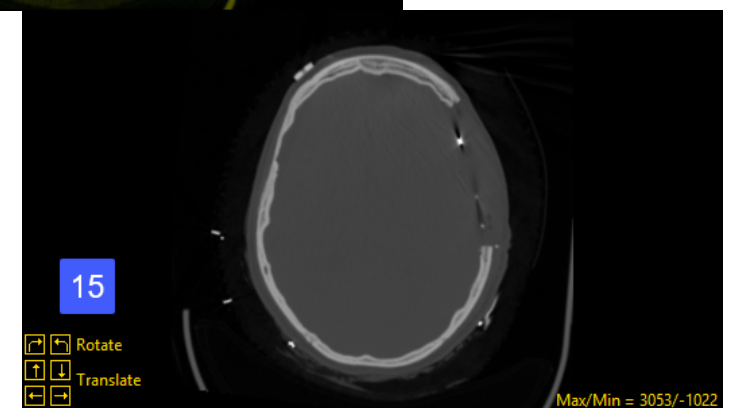
# Display Area (Continued)

**Manual Registration Tools (continued):**

- **Rotate:** The rotate buttons allow users to incrementally rotate the image data clockwise or counterclockwise relative to the selected orientation. Left click either rotate button to rotate the data in that direction.

  · **Rotate increment:** The default number of pixels rotated at a time is 10, to adjust the number of degrees for each rotation left click on the yellow Rotate text and then choose Rotation Increment and then select for the options available [16].

  · **Rotating with the mouse:** Left click on the yellow Rotate text and a Rotate cursor will be displayed. While clicking and holding the left mouse button, move the mouse upward to rotate clockwise [17] and downward to rotate counterclockwise [18].
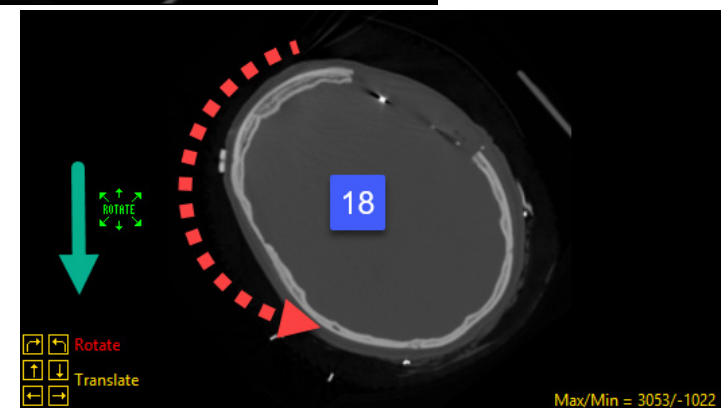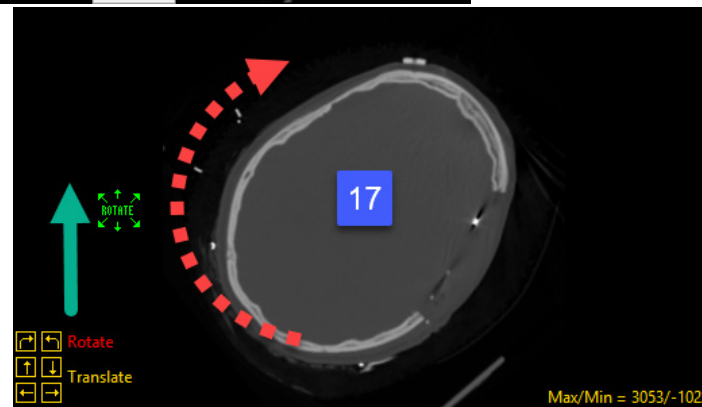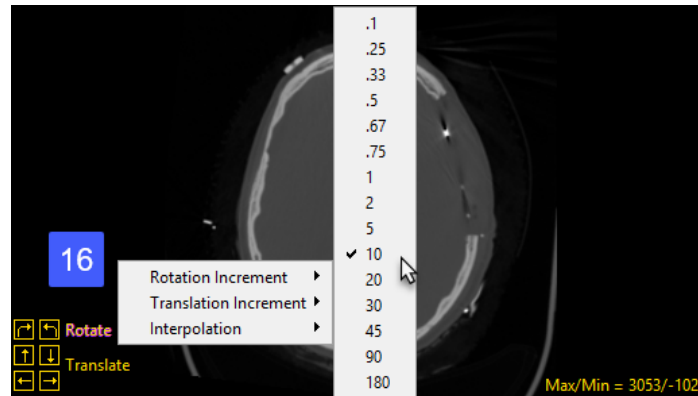
# Display Area (Continued)

**Manual Registration Tools (continued):**

- **Translate:** The translate buttons allow users to incrementally translate the image data up or down or to the left or right, relative to the selected orientation. Left click any of the four translate buttons to translate the data in that direction.

    - **Translate increment:** The default number of pixels translated at a time is 1. To adjust the number of pixels for each translation left click on the yellow Translate text and then choose Translation Increment and then select for the options available [19].

    - **Translating with the mouse:** Left click on the image or click on the yellow Translate text and a Translate cursor will be displayed. Translation will mimic the movement of the mouse: while clicking and holding the left mouse button, move the mouse forward to translate the image up, backwards to translate the image down, right to move the translate the image right, and left to translate the image left [20]. Note, translation from the left mouse button is enabled by default, allowing translation of the match image data by clicking on it and moving the cursor. To disable this option right click in any of the Match display windows and uncheck the Left Drag to Translate option.

- **Scale:** The scale tools are not enabled by default; they can be enabled from the Other > Options menu. The scale buttons [21] allow users to incrementally translate the image data up or down or to the left or right, relative to the selected orientation. Left click any of the four translate buttons to translate the data in that direction.
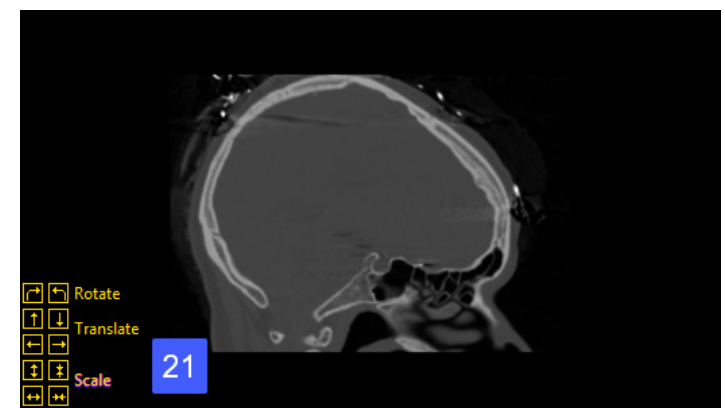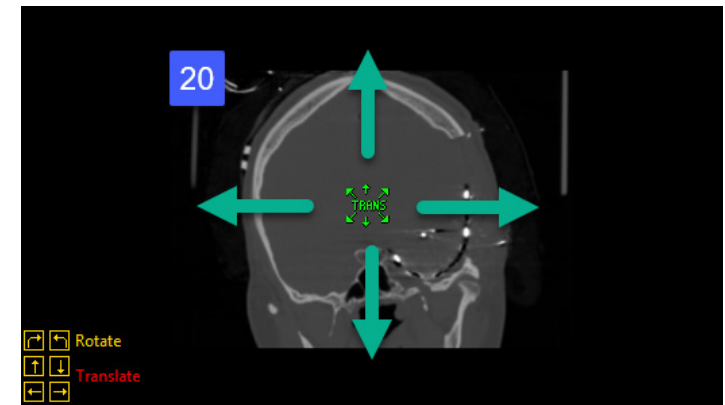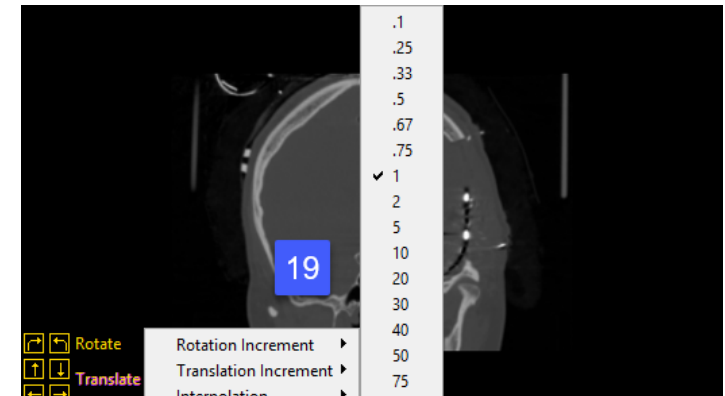
# Display Area (Continued)

**Manual Registration Tools > Scale (continued):**

- **Scale increment:** To adjust the scale increment left click on the yellow Scale text and then choose Scale Increment (only available when scale is enabled) and then select for the options available [22].

- **Scaling data with the mouse:** To scale using your mouse, left click on yellow Scale text and a Scale cursor will be displayed [23]. While clicking and holding the left mouse button, move the mouse forward to increase the vertical scale [24], move the mouse backwards to decrease the vertical scale [25].

  Move the cursor to the right to increase the horizontal scale [26], left to decrease the horizontal scale [27].
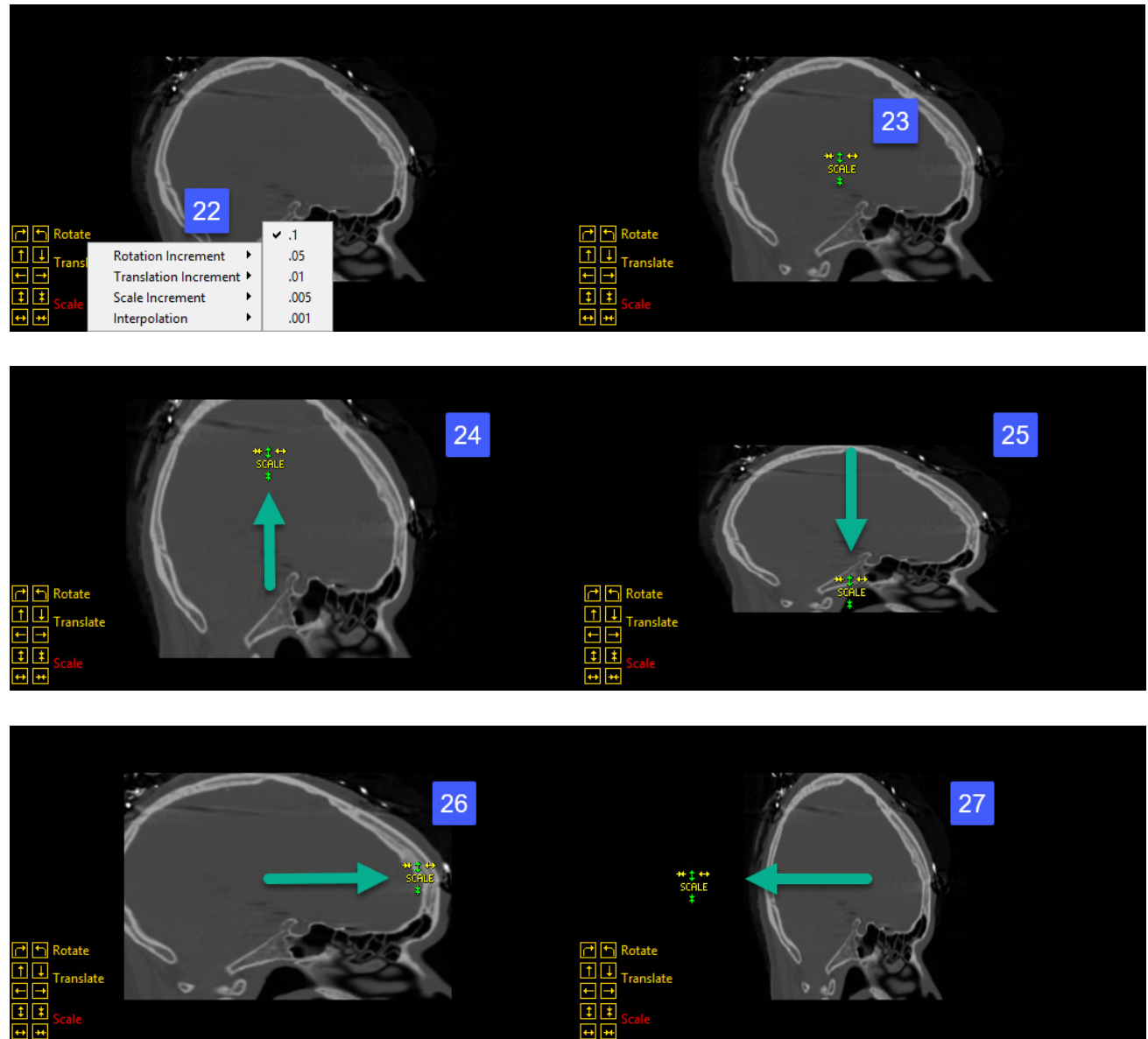
# Display Area (Continued)

**Manual Registration Tools Right Click Options:** Right clicking on the manual registration tools provides access to the Rotation, Translation, and Scale Increment adjustment options. The right menu also provides access to an Interpolation option allowing users to select the following interpolation options for manual manipulation of the data; Nearest Neighbor, Linear, Bicubic (default), and Windowed Sync.

**Display Area Right Mouse Options:** The following additional options are available from the right mouse menu in the Register display area. Note that the options available depend on the column selected (Base, Fused, Match). The options include:

- **Middle Button Action:** Sets the action of the middle mouse button.
- **Rotate @ Point:** Only available in the Register module, this option allows users to select a specific point to use to rotate the match input around.
- **Mouse While Action:** Sets the action of the middle mouse wheel.
- **Copy to Clipboard:** Copies the current slice display to memory.
- **Isotropic:** Active only for anisotropic data. Allows users to toggle between an isotropic or anisotropic display of the data.
- **Rotation Increment:** Allows users to adjust the rotation increment (see Rotate Increment).
- **Translate Increment:** Allows users to adjust the translation increment (see Translate Increment).
- **Scale Increment:** Available when Scale is enabled. Allows users to adjust the scale increment (see Scale Increment).
- **Matrix:** The matrix option allows users to: **Load** a matrix file (*.mat file) for the match data set; **Save** the current matrix file; or **Reset**: the matrix file, selecting from Axial, Coronal, or Sagittal.
- **Alignment Grid:** When selected a grid displays over the current image providing a reference aid for match data realignment [28].
- **Left Drag to Translate:** Translation from the left mouse button is enabled by default, allowing users to translate the match image data by clicking on it and moving the cursor. To disable uncheck the option.
- **Reset:** Resets all options to default. This option does not reset the matrix.
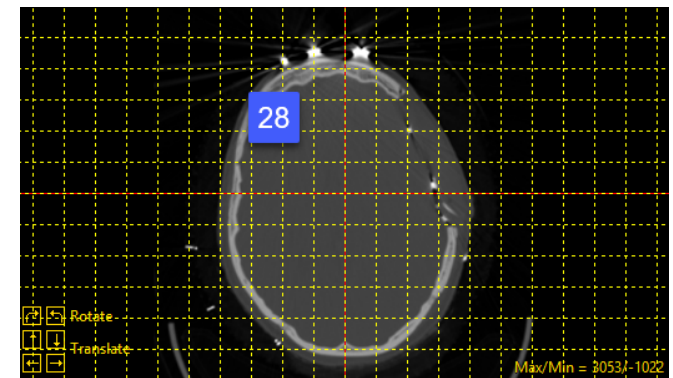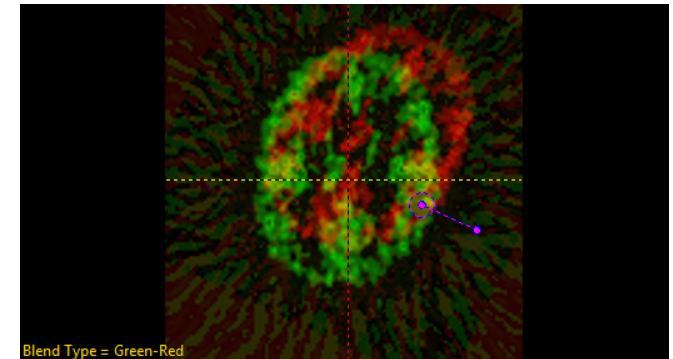
# Registration Controls

The Registration Controls are found in the left hand column of the Register Module Interface.

## Register Type

Register Type indicates the current dimensionality mode; 2-D, 3-D, or 4-D. This is set automatically by Register and is dependent upon the data selected. Choosing two single 2D slices or a single 3D volume will open the Register in 2-D mode, selecting two 3D volumes will open Register in 3-D mode. Note, if multivolumes are selected, additional volume controls became available under 3-D mode. See Volumes for additional information. The Register algorithm is selectable and users can choose between Surface Alignment or Mutual Information.

## Surface Alignment

Surface alignment, also referred to as surface matching, is a geometry-based registration method. Surface alignment is fast and robust, even in the presence of image noise and incomplete overlap of the input image volumes.

Surface alignment tries to maximize the overlap between corresponding surfaces extracted from two image inputs. To use surface alignment both input volumes must contain common objects which need be explicitly segmented from the grayscale image data, for example the brain from an MRI data set saved as either a grayscale or binary image prior to use in Register.

Alternatively, if the object is segmentable via thresholding (e.g. the brain from a SPECT image,) a surface can be defined interactively within Register using the threshold controls.
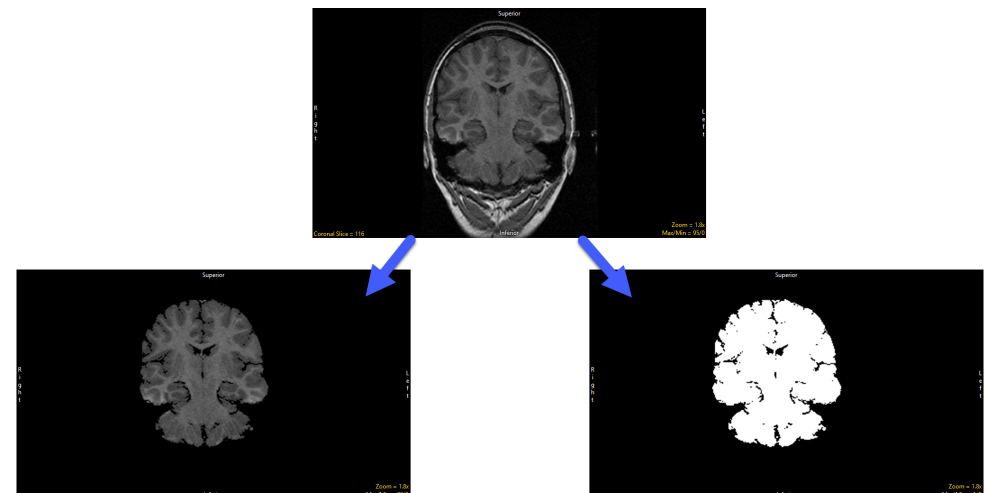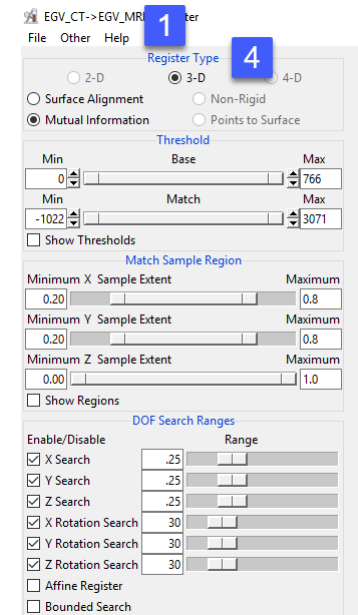
# Registration Controls (continued)

A surface is extracted from both the base object (base image) and the match object (match image). The base object is used to create a chamfer distance volume. This is a volume in which each voxel has a value equal to the number of single-voxel steps from that coordinate to the nearest point on the base surface. Surface points are defined as any non-zero-valued voxel with at least one zero-valued orthogonal neighbor in 3-D space.



For the match object surface points are defined as any non-zero-valued pixel with at least one zero-valued orthogonal neighbor within the same slice. To evaluate the error at any orientation, the coordinates of the selected 'match surface' points are transformed into the space of the base image, and the chamfer volume voxel values at those coordinates are summed. If all the match surface coordinates land on the base surface, the sum is zero. The minima search algorithm is a variant of simulated annealing which searches for minima at randomly determined multiple starting orientations, researching promising minima at successively higher resolution until a best minima is found.
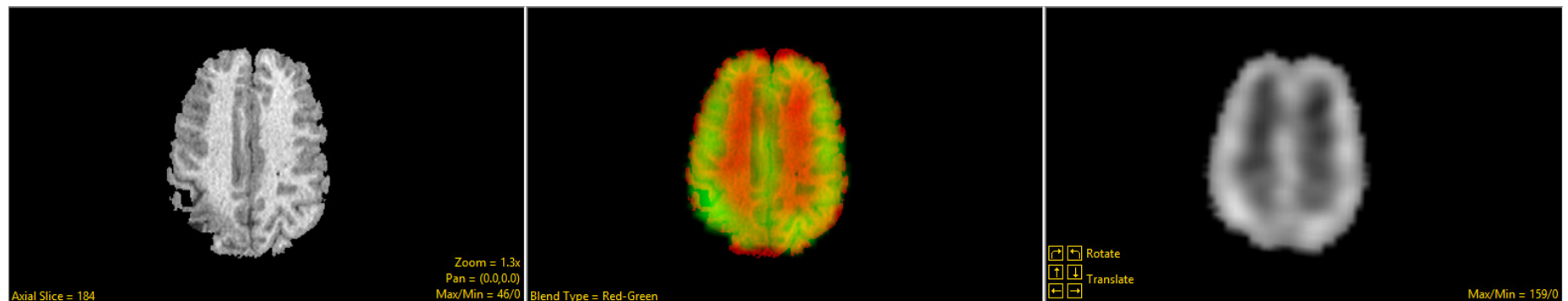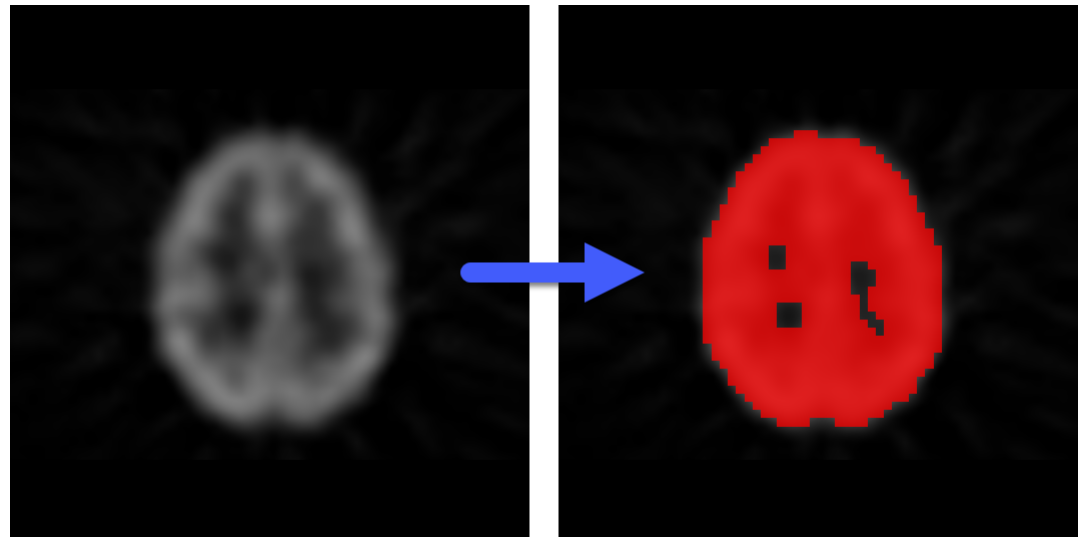
# Registration Controls (continued)

Mutual information registration is proven to be effective for registering image data from different modalities. Mutual information seeks to align voxels whose values have common probabilities of being present in their respective image sets.

There are two components of the registration paradigm in Analyze:

1. The cost function used as the metric to judge when the volumes are in register.

2. The multiresolution search strategy used to find the global optimum of the cost function.

The mutual Information cost function is based on the individual and joint entropy measured from the voxel values in the base and match volumes. There needs to be enough overlap and mutually shared signal from common structures for a relationship to be found between the two volumes and for them to be successfully co-registered.

The mutual information algorithm determines the geometric transformation parameters used to spatially register the input data. The transformation parameters include both translation and rotation and scaling and shearing if enabled. The parameters are output in a homogeneous 4x4 matrix file. Image registration is achieved by transforming a volume using the transformation matrix.
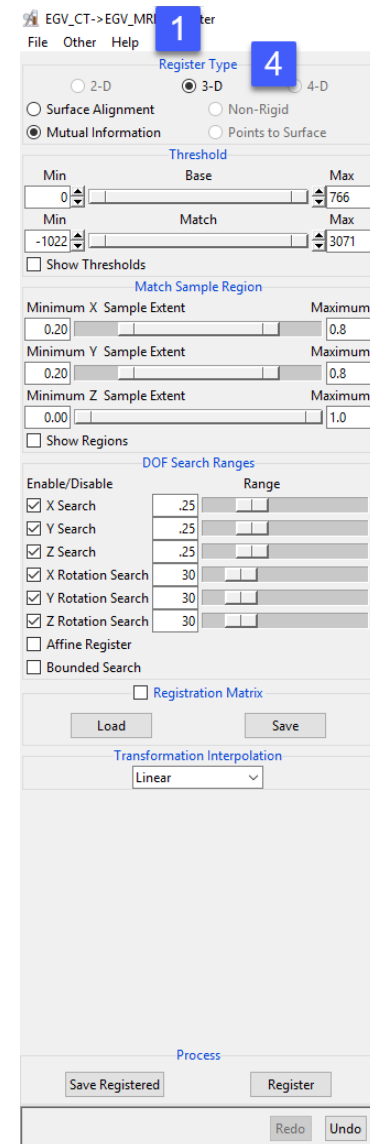
# Registration Controls > 2D

2D registration determines the geometric transformation parameters to be used to align 2D images, slice-by-slice or matching a series of slices to a single base slice.



Unregistered stack of 2D images        Registered stack of 2D images
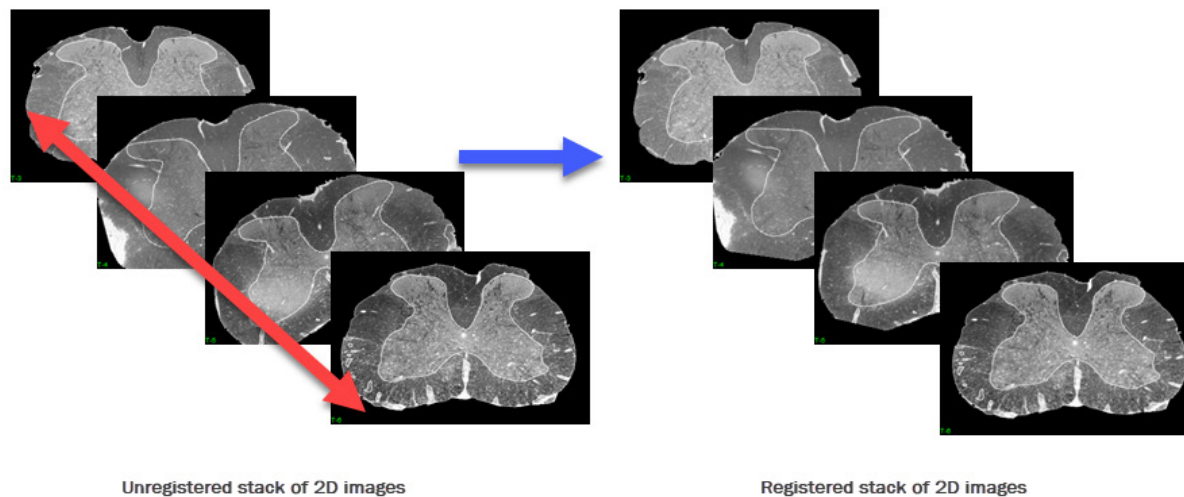
The following options are enabled/available with 2D registration:

**2-D:** The 2-D dimension mode is enabled when two 2D slices or a single 3D volume are loaded into Register.

**Surface Alignment:** Enables surface matching registration. The following options are available:

• **Threshold:** The Threshold double-ended slider bars for both the Base and Match data allows the end user to specify a range of threshold values to isolate common surfaces between the input images. Note, if common surfaces are not segmentable via thresholding the input data will need to be segmented prior to registration.

   · Base: The base threshold double-ended slider bar allows users to specify a range of threshold values using the minimum and maximum ends of the threshold slide for the base input data.

# Registration Controls > 2D (continued)

**2-D > Surface Alignment > Threshold (continued):**

· Match: The match threshold double-ended slider bar allows users to specify a range of threshold values using the minimum and maximum ends of the threshold slide for the match input data.

• **Show Thresholds:** When enabled displays a filled preview of the minimum/maximum threshold value set for base and match input data.

**Registration Matrix:** When enabled displays the 4 by 4 transformation matrix.

• **Load:** Load a matrix file (*.mat file) for the match data set.

• **Save:** Save the current matrix file.

**Transformation Interpolation:** The transformation interpolation option allows users to specify the interpolation type to be used when transforming the match data set. Users can choose from:

• **Nearest Neighbor:** Allows users to select the nearest neighbor option for interpolation. Nearest Neighbor works by selecting the value of the closest voxel to which the interpolation resampling maps. This interpolation option is generally the fastest of the four available interpolation options.

• **Linear:** Allows users to select the linear option for interpolation. The linear algorithm applies a linear interpolation of grayscale intensity based on the distance of neighboring voxels from the interpolated voxel.

• **Bicubic:** Bicubic is the default interpolation option. The Bicubic option uses a cubic spline function to determine interpolated value, resulting in a smoother image that preserves detail.

• **Windowed Sinc:** Allows users to select the Windowed Sinc option for interpolation. The algorithm uses the windowed sinc function $\sin(x)/x$ to determine the interpolated value.

# Registration Controls > 2D (continued)

**Slices:** This option is only available when a single 3D volume is selected for input for 2D registration. The slices sliders allow users to navigate through the base and match inputs.

- **Base:** The base slider controls the display of the base slice. This will also be the 2D slice used for registration.

- **Match:** The match slider controls the display of the match slice. This will be the slice registered to the base for single Matrix and Single Reference registration. See Process and Registration mode for information on other registration options.

**Process:** The process controls allow users to register and save registration result, the following options are available.

- **Save Registered:** Allows users to save the transformed match image, the fused image, or the transformed object map (if applicable). See File > Save Registered at the being of this module section for a full description of the save options.

- **Register:** Initiates the slice-to-slice registration.

- **Register Pairs:** Only available when a single 3D volume is loaded. The register pairs option registered the current match slice to the current base slice. To adjust the select of the base or match slice input use the Slices sliders.

- **Match Range:** Only available when a single 3D volume is loaded. The match range slider allows users to specify a range of 2D match images to be registered to the base image.

**Register Mode:** Only available when a single 3D volume is loaded. The registration mode allows users to select from the following options:

- **Single Matrix:** The single matrix option applies the transformation matrix created when registering the currently displayed match data set to the displayed base data to the range of match images selected using the match range slider. All images in the match range are transformed to the same single matrix.

# Registration Controls > 2D (continued)

**Register Mode > Single Matrix (continued):**
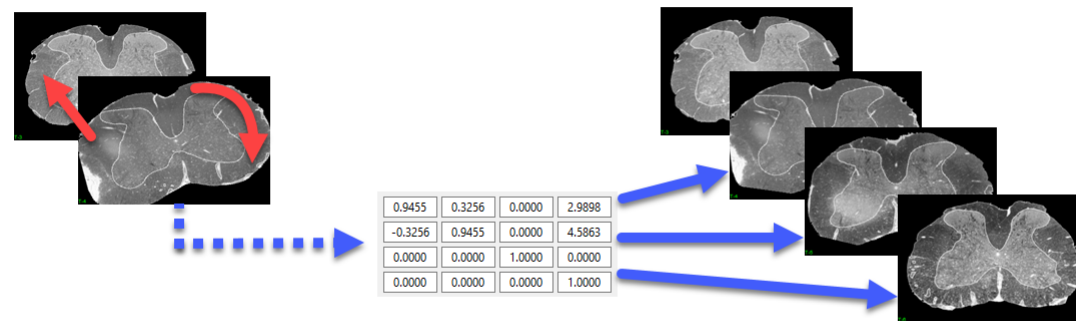


**Single Matrix** - the same transformation matrix is applied to all slices.

- **Single Reference:** The single reference option registers each of the match images specified in the match range, individually to the base image.
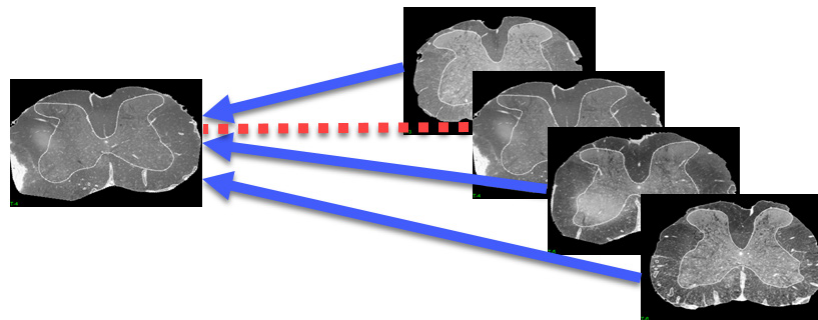


**Single Reference** - each slice is registered to a single base slice.

# Registration Controls > 2D (continued)

**Register Mode (continued):**

- **Sequential:** Performs a sequential match image to base image registration within the specified match range. For example, match image 2 to base image 1, then match image 3 to based image 2, etc.
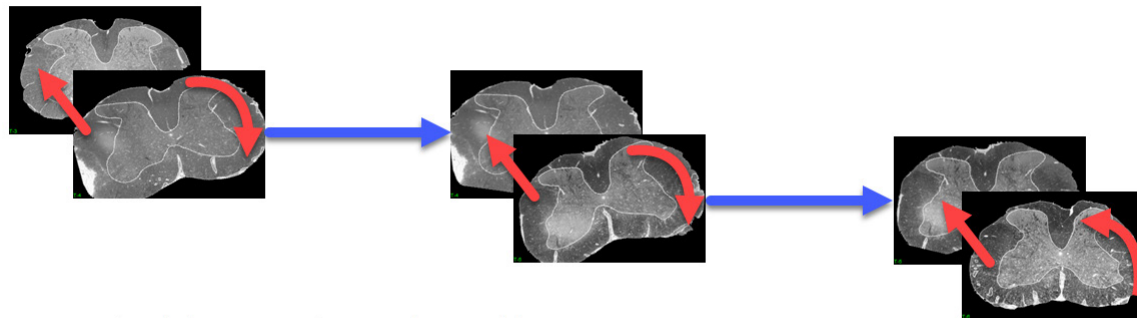


**Sequential** - each slice is registered sequential to its neighbor.

- **Register Sequence:** Only available for the single reference and sequential register modes. When selected initiates registration.

**Redo:** Reverses your last undo action. Redo is only available after using Undo.

**Undo:** Reverses you last action. Can reverse more than one action.

# Registration Controls > 2D (continued)

**Mutual Information** enables mutual information-based registration. The following options are available:

- **Threshold:** The Threshold double-ended slider bars for both the Base and Match data allows the end user to specify a range of threshold values to consider for registration. The use of thresholding with mutual information-based registration is normally to remove background noise, artifact from implants, or other ranges of greyscale values from the data that could interfere with registration.

  · Base: The base threshold double-ended slider bar allows users to specify a range of threshold values using the minimum and maximum ends of the threshold slide for the base input data.
  · Match: The match threshold double-ended slider bar allows users to specify a range of threshold values using the minimum and maximum ends of the threshold slide for the match input data.

- **Show Thresholds:** When enabled displays a filled preview of the minimum or maximum threshold value set for base and match input data.

**Match Sample Region:** The match sample region slides allow users to increase or decrease the sampling density in the X, Y, and Z (if applicable).

- **Minimum X Sample Extent:** Use the slider to specify the x sampling density. Decreasing the x minimum value and increasing the x maximum value will increase the minimum x sample range [1]. Increasing the x minimum value and decreasing the x maximum value will decrease the minimum x sample range [2].
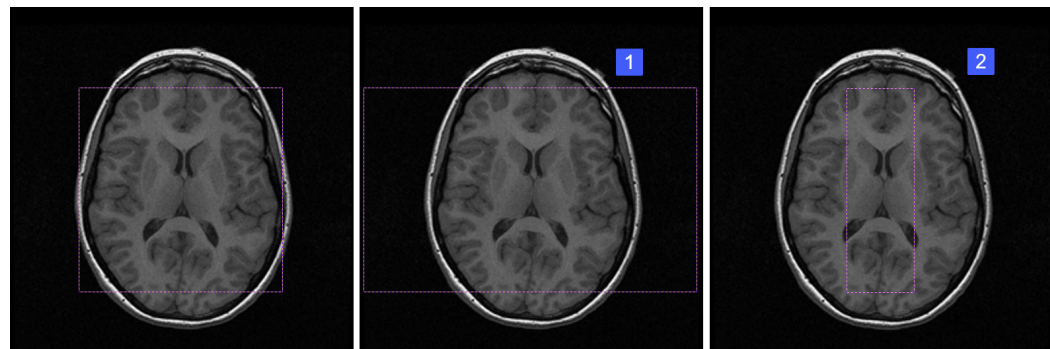
# Registration Controls > 2D (continued)

**Match Sample Region (continued):**

The minimum and maximum values can also be adjusted to select a specific x region or exclude a region that could interfere with registration [3].

- **Y Sample Extent:** As with the minimum X sample extent, users can use the minimum Y sample extent slider to specify the minimum y sampling density. Decreasing the y minimum value and increasing the y maximum value will increase the minimum y sample range [4]. Increasing the y minimum value and decreasing the y maximum value will decrease the minimum y sample range [5]. The minimum and maximum values can also be adjusted to select a specific y region or exclude a region that could interfere with registration.

- **Z Sample Extent:** Use the slider to specify the z sampling density.

- **Show Region:** Enables the display of the sample extent on the match image, showing the region as a purple and white dashed box.
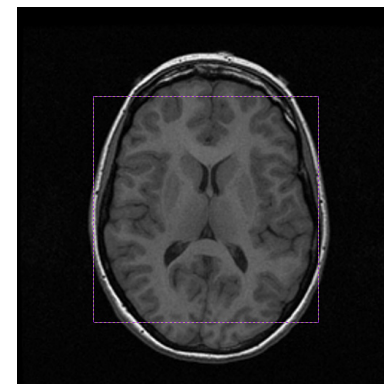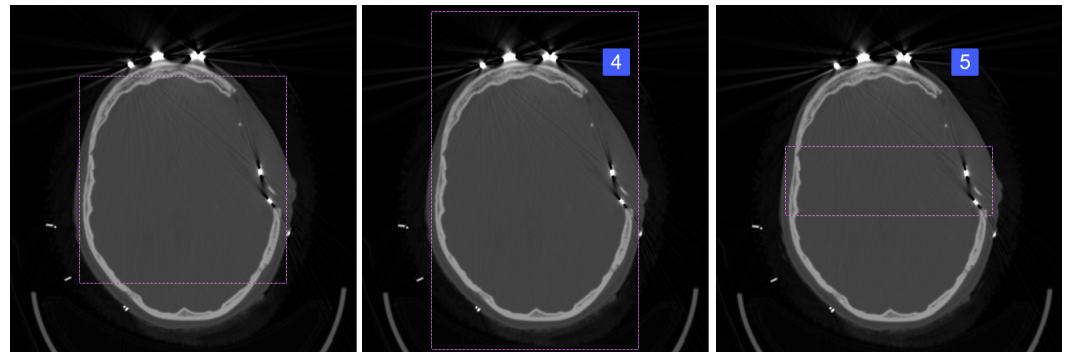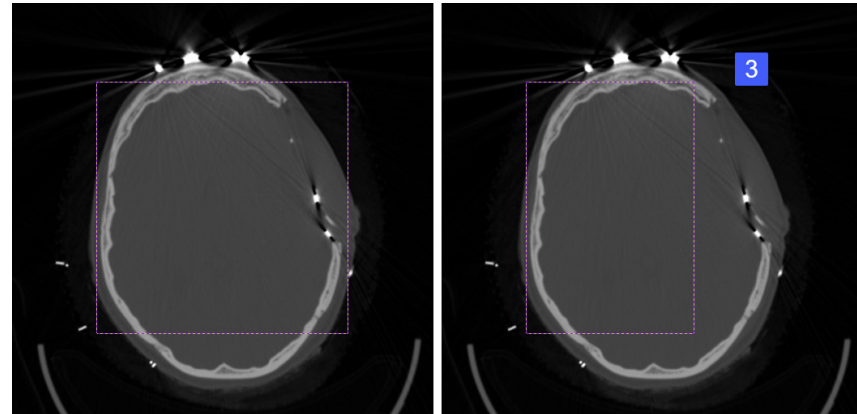
# Registration Controls > 2D (continued)

**DOF Search Ranges:** The Degrees Of Freedom (DOF) search range allows users to adjust the default parameters set for registration.

- **X Search:** Allows users to adjust the maximum expected horizontal displacement (in either direction) of the match image in pixels.

- **Y Search:** Allows users to adjust the maximum expected vertical displacement (in either direction) of the match image in pixels.

- **Z Rotation Search:** Allows users to adjust the maximum expected rotation of the match image in degrees.

- **Affine Register:** Allows users to enable affine registration providing access to X and Y scale and shear search options:

  · **X Scale Search:** Adjust the maximum expected horizontal scaling difference between the match and base images
  · **Y Scale Search:** Adjust the maximum expected vertical scaling difference between the match and base images
  · **X Shear in Y Search:** Adjust the level of x shear in the y search.
  · **Y Shear in X Search:** Adjust the level of y shear in the x search.

- **Bounded Search:** Limits the total number of search steps.  The registration algorithm, while robust in most cases, can fail to converge in extremely low-information situations. This option avoids program hang-up in those situations, and seldom significantly affects typical solutions.

**Registration Matrix:** When enabled displays the 4 by 4 transformation matrix.

  · **Load:** Load a matrix file (*.mat file) for the match data set.
  · **Save:** Save the current matrix file.

**Transformation Interpolation:** The transformation interpolation option allows users to specify the interpolation type to be used when transforming the match data set. Users can choose from:

  · **Nearest Neighbor:** Allows users to select the nearest neighbor option for interpolation. Nearest Neighbor works by selecting the value of the closest voxel to which the interpolation resampling maps. This interpolation option is generally the fastest of the four available interpolation options.

# Registration Controls > 2D (continued)

**Transformation Interpolation (continued):**

- **Linear:** Allows users to select the linear option for interpolation. The linear algorithm applies a linear interpolation of grayscale intensity based on the distance of neighboring voxels from the interpolated voxel.
- **Bicubic:** Bicubic is the default interpolation option. The Bicubic option uses a cubic spline function to determine interpolated value, resulting in a smoother image that preserves detail.
- **Windowed Sinc:** Allows users to select the Windowed Sinc option for interpolation. The algorithm uses the windowed sinc function sin(x)/x to determine the interpolated value.

**Slices:** This option is only available when a single 3D volume is selected for input for 2D registration. The slices sliders allow users to navigate through the base and match inputs.

- **Base:** The base slider controls the display of the base slice. This will also be the 2D slice used for registration.
- **Match:** The match slider controls the display of the match slice. This will be the slice registered to the base for single Matrix and Single Reference registration. See Process and Registration mode for information on other registration options.

**Process:** The process controls allow users to register and save registration result, the following options are available.

- **Save Registered:** Allows users to save the transformed match image, the fused image, or the transformed object map (if applicable). See File > Save Registered at the being of this module section for a full description of the save options.
- **Register:** Initiates the slice-to-slice registration.
- **Register Pairs:** Only available when a single 3D volume is loaded. The register pairs option registered the current match slice to the current base slice. To adjust the select of the base or match slice input use the Slices sliders.
- **Match Range:** Only available when a single 3D volume is loaded. The match range slider allows users to specify a range of 2D match images to be registered to the base image.

**Register Mode:** Only available when a single 3D volume is loaded. The registration mode allows users to select from the following options:

- **Single Matrix:** Applies the transformation matrix created when registering the displayed match data set to the displayed base data to the images selected using the match range slider. All images in the match range are transformed to the same single matrix.

# Registration Controls > 2D (continued)

**Register Mode (continued):**

- **Single Reference:** This option registers each of the match images specified in the match range, individually to the base image.
- **Sequential:** Performs a sequential match image to base image registration within the specified match range. For example, match image 2 to base image 1, then match image 3 to based image 2, etc.
- **Register Sequence:** Only available for the single reference and sequential register modes. When selected initiates registration.

**Redo:** Reverses your last undo action. Redo is only available after using Undo.

**Undo:** Reverses you last action. Can reverse more than one action.

# Registration Controls > 3D

The 3-D dimension mode is enabled when two 3D volumes or one or more multivolumes (4D data sets) are loaded into Register.

**Surface Alignment:** Enables 3D surface matching registration. The following options are available:

- **Threshold:** The Threshold double-ended slider bars for both the Base and Match data allows the end user to specify a range of threshold values to isolate common surfaces between the input images. Note, if common surfaces are not segmentable via thresholding the input data will need to be segmented prior to registration.

  - **Base:** The base threshold double-ended slider bar allows users to specify a range of threshold values using the minimum and maximum ends of the threshold slide for the base input data.
  - **Match:** The match threshold double-ended slider bar allows users to specify a range of threshold values using the minimum and maximum ends of the threshold slide for the match input data.

**Show Thresholds:** When enabled displays a filled preview of the minimum or maximum threshold value set for base and match input data.

# Registration Controls > 3D (continued)

**Registration Matrix:** When enabled displays the 4 by 4 transformation matrix.

- **Load:** Load a matrix file (*.mat file) for the match data set.
- **Save:** Save the current matrix file.

**Transformation Interpolation:** The transformation interpolation option allows users to specify the interpolation type to be used when transforming the match data set. Users can choose from:

- **Nearest Neighbor:** Allows users to select the nearest neighbor option for interpolation. Nearest Neighbor works by selecting the value of the closest voxel to which the interpolation resampling maps. This interpolation option is generally the fastest of the four available interpolation options.
- **Linear:** Allows users to select the linear option for interpolation. The linear algorithm applies a linear interpolation of grayscale intensity based on the distance of neighboring voxels from the interpolated voxel.
- **Bicubic:** Bicubic is the default interpolation option. The Bicubic option uses a cubic spline function to determine interpolated value, resulting in a smoother image that preserves detail.
- **Windowed Sinc:** Allows users to select the Windowed Sinc option for interpolation. The algorithm uses the windowed sinc function $sin(x)/x$ to determine the interpolated value.

**Process:** The process controls allow users to register and save registration result, the following options are available.

- **Save Registered:** Allows users to save the transformed match volume, fused volume, or the transformed object map (if applicable). See File > Save Registered at the being of this module section for a full description of the save options.
- **Register:** Initiates the 3D registration.
- **Register Pair:** Only available when the register mode is set to Single Reference or Sequential. Will initiate the registration of the current match volume to the current base volume.
- **Match Range:** Only available when one or more 4D multivolumes are loaded. The match range slider allows users to specify a range of 3D volumes in the 4D match multivolume to be registered to the base volume.

# Registration Controls > 3D (continued)

**Register Mode:** Only available when a single 4D volume is loaded. The registration mode allows users to select from the following options:

- **Single Matrix:** The single matrix option applies the transformation matrix created when registering the currently displayed match data set to the displayed base data to the range of match data sets selected using the match range slider. All volumes in the match range are transformed to the same single matrix.
- **Single Reference:** The single reference option registers each of the match volumes specified in the match range, individually to the base volume.
- **Sequential:** Performs a sequential match volume to base volume registration within the specified match range. For example, match volume 2 to base volume 1, then match volume 3 to based volume 2, etc.
- **Register Sequence:** Only available for the single reference and sequential register modes. When selected initiates sequential registration.

**Redo:** Reverses your last undo action. Redo is only available after using Undo.

**Undo:** Reverses you last action. Can reverse more than one action.

**Volumes:** This option is only available when one or more 4D multivolumes are selected for input for 3D registration. The Volume sliders allow users to navigate through the volumes in the match and/or base input multivolumes.

- **Base:** The base slider controls the display of the base volume. This will be the volume used for single matrix and single reference registration.
- **Match:** The match slider controls the display of the match volume. This will be the volume registered to the base for Single Matrix and Single Reference registration. See Process and Registration mode for information on other registration options.

**Mutual Information:** Enables 3D mutual information-based registration. The following options are available:

- **Threshold:** The Threshold double-ended slider bars for both Base and Match data allows specificiation of a range of threshold values to consider for registration. The use of thresholding with mutual information-based registration is normally to remove background noise, artifact from implants, or other ranges of greyscale values from the data that could interfere with registration.

# Registration Controls > 3D (continued)

**Mutual Information > Threshold (continued):** Enables 3D mutual information-based registration. The following options are available:

- **Base:** The base threshold double-ended slider bar allows users to specify a range of threshold values using the minimum and maximum ends of the threshold slide for the base input data.
- **Match:** The match threshold double-ended slider bar allows users to specify a range of threshold values using the minimum and maximum ends of the threshold slide for the match input data.

- **Show Thresholds:** When enabled displays a filled preview of the minimum or maximum threshold value set for base and match input data.

**Match Sample Region:** The match sample region slides allow users to increase or decrease the sampling density in the X, Y, and Z.

- **X Sample Extent:** Use the slider to specify the x sampling density. [1]
- **Y Sample Extent:** Use the slider to specify the Y sampling density. [2]
- **Z Sample Extent:** Use the slider to specify the Z sampling density. [3]
- **Show Region:** Enables the display of the sample extent on the match image. The region will be shown as a purple and white dashed box.

**DOF Search Ranges:** The Degrees Of Freedom (DOF) search range allows users to adjust the default parameters set for registration.

- **X Search:** Allows users to adjust the x translation search step.
- **Y Search:** Allows users to adjust the y translation search step.
- **Z Search:** Allows users to adjust the z translation search step.
- **X Rotation Search:** Allows users to adjust the rotation about the x search step.
- **Y Rotation Search:** Allows users to adjust the rotation about the y search step.
- **Z Rotation Search:** Allows users to adjust the rotation about the z search step.
- **Affine Register:** Allows users to enable affine registration providing access to X, Y, and Z scale and shear search options:
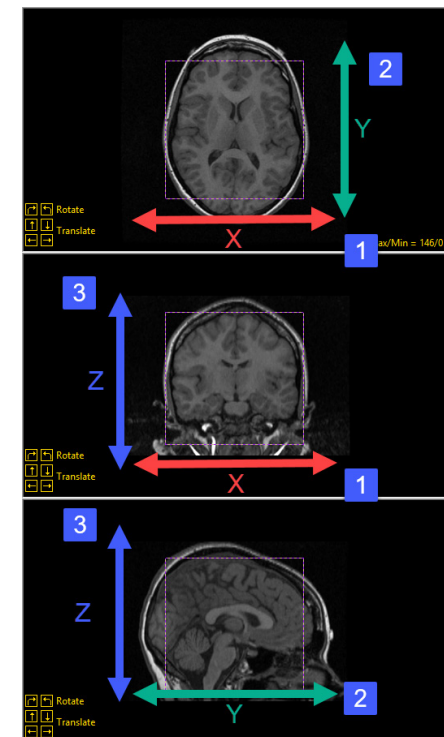
# Registration Controls > 3D (continued)

**DOF Search Ranges > Affine Register (continued):**

- **X Scale Search:** Allows users to adjust the X scaling search parameter.
- **Y Scale Search:** Allows users to adjust the Y scaling search parameter.
- **Z Scale Search:** Allows users to adjust the Z scaling search parameter.
- **X Shear in Z Search:** Allows users to adjust the level of x shear in the z search.
- **Y Shear in Z Search:** Allows users to adjust the level of y shear in the z search.
- **X Shear in Y Search:** Allows users to adjust the level of x shear in the y search.
- **Z Shear in Y Search:** Allows users to adjust the level of z shear in the y search.
- **Y Shear in X Search:** Allows users to adjust the level of y shear in the x search.
- **Z Shear in X Search:** Allows users to adjust the level of z shear in the x search.

- **Bounded Search:** Limits the total number of search steps.  The registration algorithm, while robust in most cases, can fail to converge in extremely low-information situations. This option avoids program hang-up in those situations, and seldom significantly affects typical solutions.

**Registration Matrix:** When enabled displays the 4 by 4 transformation matrix.

- **Load:** Load a matrix file (*.mat file) for the match data set.
- **Save:** Save the current matrix file.

**Transformation Interpolation:** The transformation interpolation option allows users to specify the interpolation type to be used when transforming the match data set. Users can choose from:

- **Nearest Neighbor:** Allows users to select the nearest neighbor option for interpolation. Nearest Neighbor works by selecting the value of the closest voxel to which the interpolation resampling maps. This interpolation option is generally the fastest of the four available interpolation options.
- **Linear:** Allows users to select the linear option for interpolation. The linear algorithm applies a linear interpolation of grayscale intensity based on the distance of neighboring voxels from the interpolated voxel.

# Registration Controls > 3D (continued)

**Transformation Interpolation (continued):**

- **Bicubic:** Bicubic is the default interpolation option. The Bicubic option uses a cubic spline function to determine interpolated value, resulting in a smoother image that preserves detail.
- **Windowed Sinc:** Allows users to select the Windowed Sinc option for interpolation. The algorithm uses the windowed sinc function sin(x)/x to determine the interpolated value.

**Process:** The process controls allow users to register and save registration result, the following options are available.

- **Save Registered:** Allows users to save the transformed match volume, fused volume, or the transformed object map (if applicable). See File > Save Registered at the being of this module section for a full description of the save options.
- **Register:** Initiates the 3D registration.
- **Register Pair:** Only available when the register mode is set to Single Reference or Sequential. Will initiate the registration of the current match volume to the current base volume.
- **Match Range:** Only available when one or more 4D multivolumes are loaded. The match range slider allows users to specify a range of 3D volumes in the 4D match multivolume to be registered to the base volume.

**Register Mode:** Only available when a single 4D volume is loaded. The registration mode allows users to select from the following options:

- **Single Matrix:** The single matrix option applies the transformation matrix created when registering the currently displayed match data set to the displayed base data to the range of match data sets selected using the match range slider. All volumes in the match range are transformed to the same single matrix.
- **Single Reference:** The single reference option registers each of the match volumes specified in the match range, individually to the base volume.
- **Sequential:** Performs a sequential match volume to base volume registration within the specified match range. For example, match volume 2 to base volume 1, then match volume 3 to based volume 2, etc.
- **Register Sequence:** Only available for the single reference and sequential register modes. When selected initiates sequential registration.

# Registration Controls > 3D (continued)

**Redo:** Reverses your last undo action. Redo is only available after using Undo.

**Undo:** Reverses you last action. Can reverse more than one action.

**Volumes:** This option is only available when one or more 4D multivolumes are selected for input for 3D registration. The Volume sliders allow users to navigate through the volumes in the match and/or base input multivolumes.

- **Base:** The base slider controls the display of the base volume. This will be the volume used for single matrix and single reference registration.

- **Match:** The match slider controls the display of the match volume. This will be the volume registered to the base for Single Matrix and Single Reference registration. See Process and Registration mode for information on other registration options.
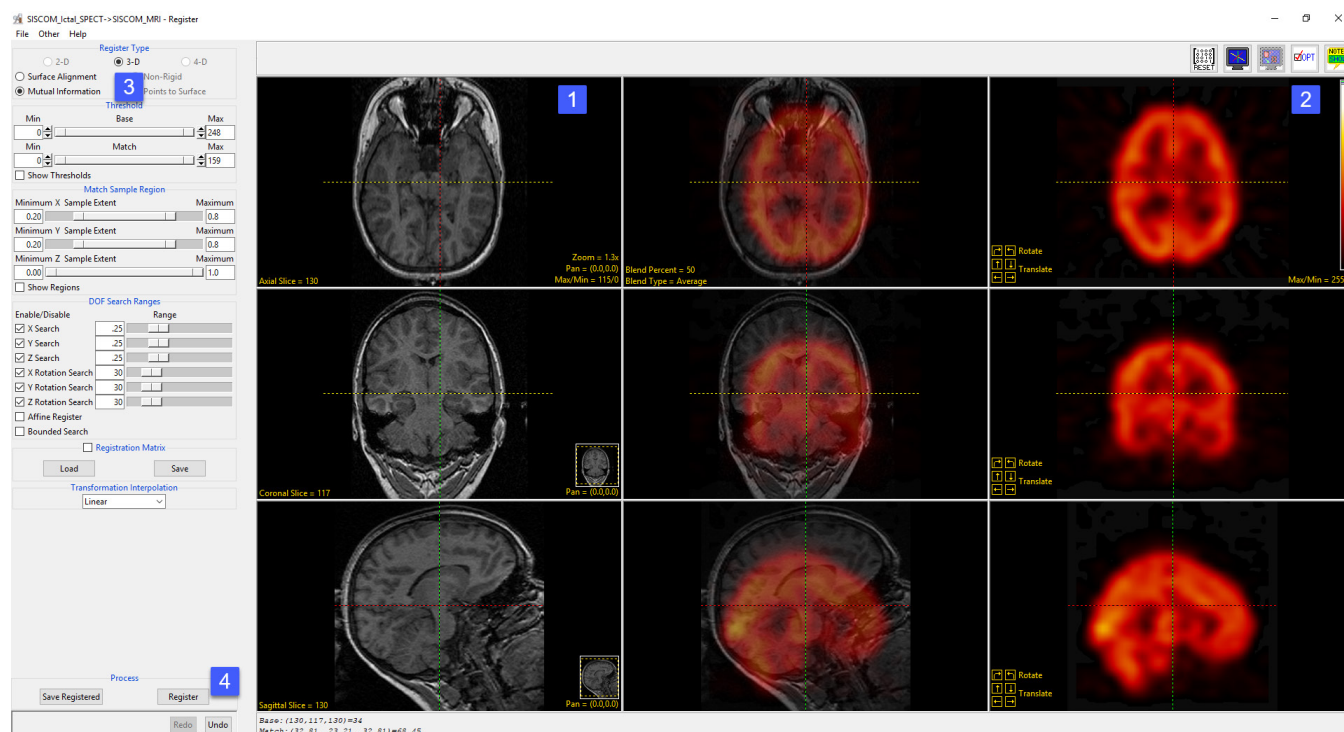
# 3D Registration - Surface Alignment

Surface alignment is used to register image data that does not have enough or any mutual information, for example a functional SPECT scan and structural MRI scan. This exercise will provide the steps necessary to correctly register a SPECT scan and an MRI scan of the brain. However, first we will observe what happens when we try to register the image data set using Mutual Information.

To follow along, download data sets SISCOM_MRI.avw and SISCOM_Ictal_SPECT.avw from analyzedirect.com/data

- Open Input/Output and load both the SISCOM_MRI.avw and SISCOM_Ictal_SPECT.avw data sets into Analyze.

- Once loaded select the SISCOM_MRI data set then press and hold the Ctrl button on your keyboard and select the SISCOM_Ictal_SPECT data set and open Register. Note the order in which the data is selected is important. The first data set selected will be loaded

- as the base data set, in this example the MRI [1], while the second data set will be the match data set, in this example the SPECT [2].

- Set the Register Type to Mutual Information [3] and then click Register [4].

## 3D Registration - Surface Alignment (continued)

Due to the lack of mutual information between these two modalities the registration will fail. Note the incorrectly positioned SPECT [5] with respect to the MRI.

In order to facilitate successful registration of the MRI and SPECT data we need to establish surfaces for common objects in both data sets, this means the explicit segmentation of the brain from the MRI and SPECT data sets.

- Close the Register module.
- From the main Analyze window select the SISCOM_MRI data set and then open Segment.
- From the Semi-Automatic tab [6] select Object Extractor [7].
- On Coronal slice 115 click in the white matter to set a seed point [8]. Adjust the threshold range [9] to define the brain, a minimum value of 21 and a maximum value of 47 works well for this data set.
- Click Extract Object [10].
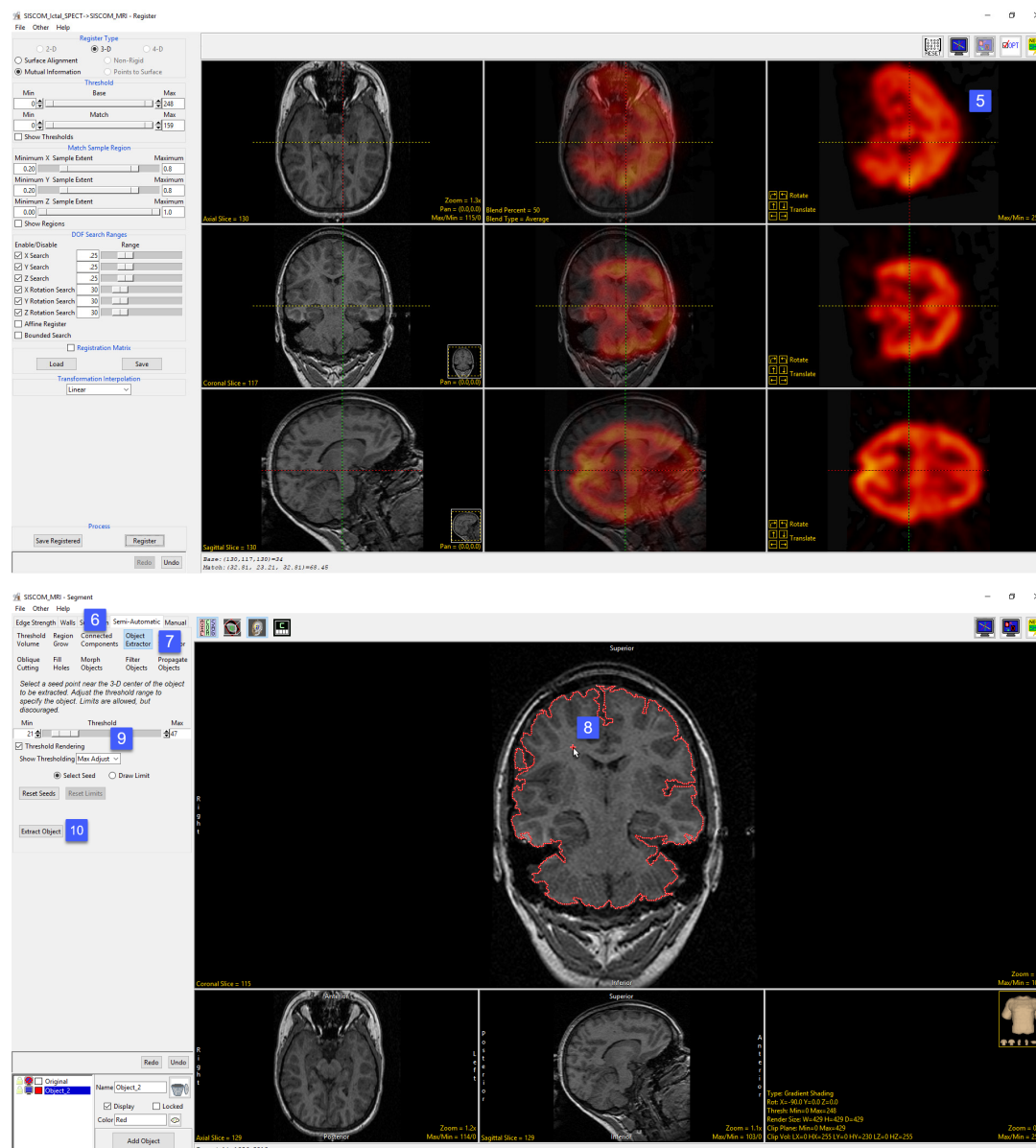
# 3D Registration - Surface Alignment (continued)



- After segmentation is complete notice that the brain object contains some minor holes. To correct for these holes, choose Fill Holes [11], set the Fill Type to 3-Pass [12], click on the brain object [13] to initiate the fill process.

- Once the fill process is complete the brain will no longer contain any holes. Right-click on the brain object in the object list and then choose Save Grayscale from the menu [14].

- In the Save Grayscale window retuned change the name of the output file to SISCOM_MRI_Brain [15] and click Save Grayscale [16]. A grayscale version of the segmented brain object will be saved to the workspace, this will provide the surface of the brain for surface alignment with the SPECT data set.

- Close Segment.

- As the brain surface in this SPECT data set can be easily isolated via thresholding in Register there is no need to segment the data set using Segment. However, if the SPECT image data contained extracranial signal that prevented a clear representation of the brain surface via thresholding the data set could be segmented to isolate the brain using Segment prior to use in Register.
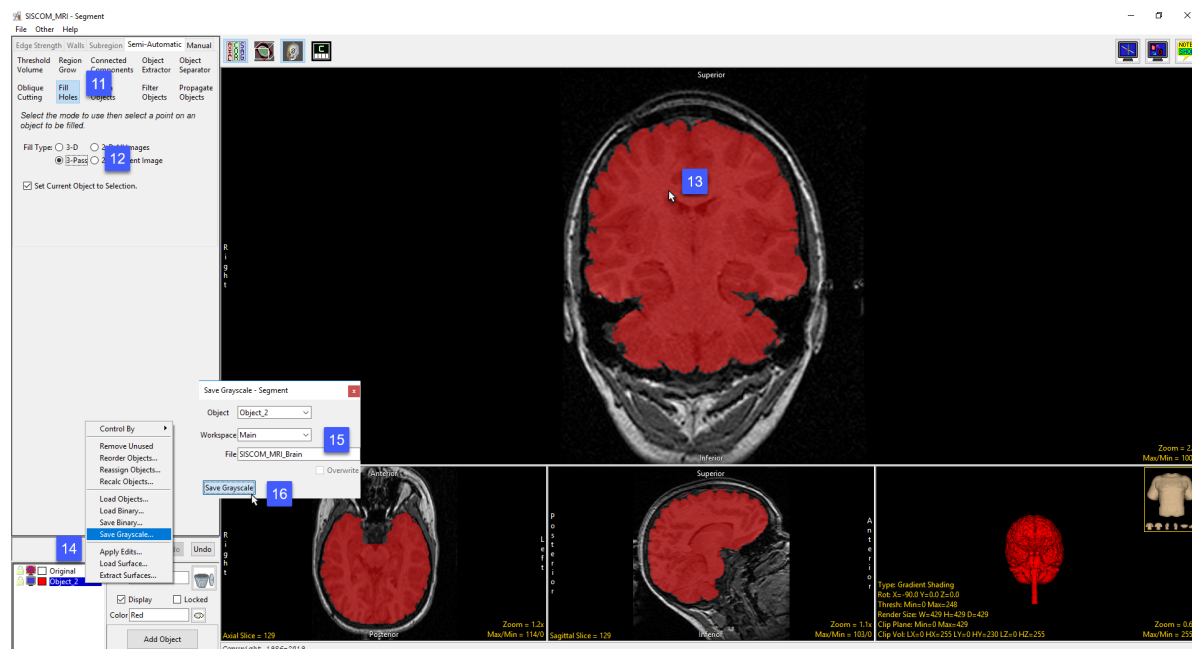
# 3D Registration - Surface Alignment (continued)

- Select the SISCOM_MRI_Brain data set then press and hold the Ctrl button on your keyboard now select the SISCOM_Ictal_SPECT data set and open Register.

- Set the Register Type to Surface Alignment [17].

- If desired modify the blend type [18].

- Next click the Show Threshold check box [19].



- Note that all voxels for both the base and match data sets are currently selected. To exclude the background voxels from the base volume set the Base minimum threshold level to 1 [20] by entering the value in the text field or by adjusting the slider. Note the update on the base display [21], only the voxels within the red mask will be considered for registration.

- Adjust the threshold range for the match data set to remove the background voxels and all non-brain voxels. Set the minimum threshold value to 20 [22] by entering the value in the text field or by adjusting the slider. Note the update on the match display [23], the voxels within the red mask represent the brain and will provide the match surface to facilitate a successful registration.

# 3D Registration - Surface Alignment (continued)

- Uncheck the Show Threshold option [24].

- To register the data click Register [25].

- After the registration is complete visually review the transformed and fused image data [26].

- Click Save Registered to save the Transformed SPECT data to the workspace and then close Register.
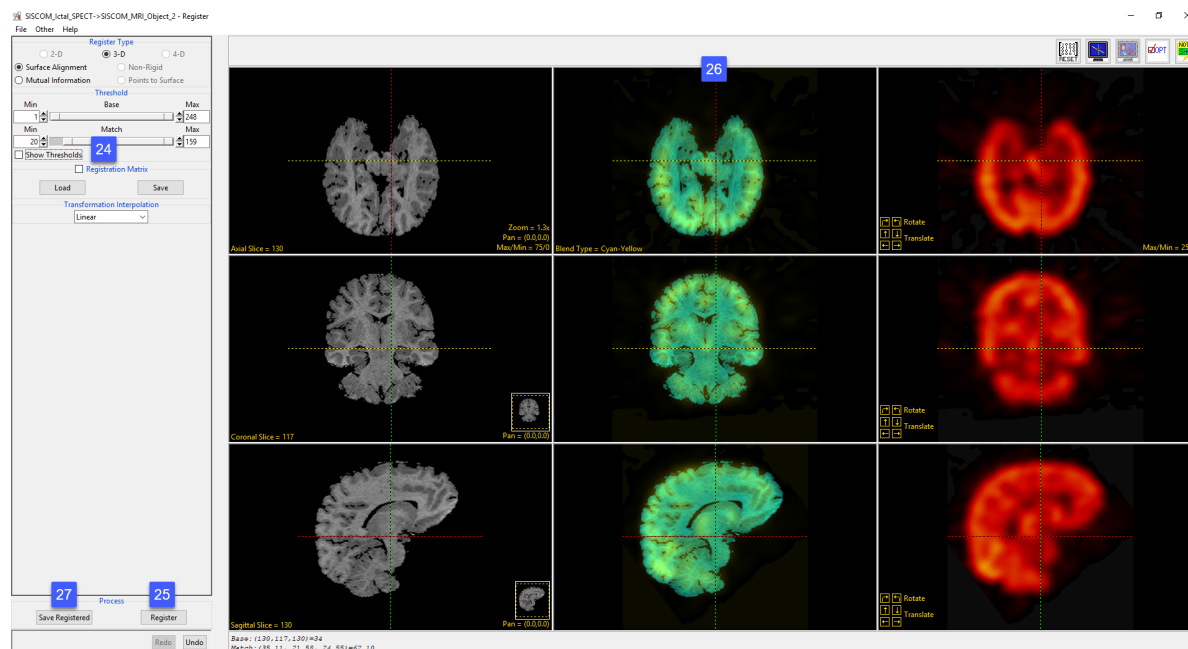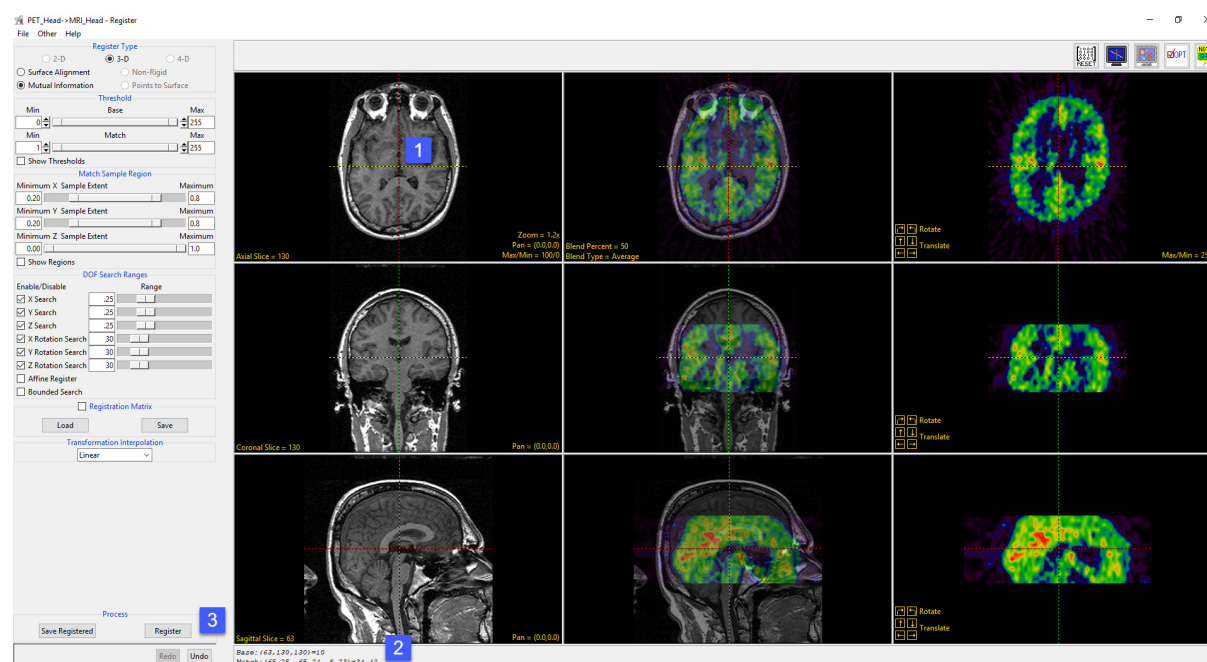
# 3D Registration - Mutual Information

The goal of this exercise is to demonstrate how to apply mutual information to registration of image data from two different modalities, MRI and PET. The MRI data set is sagittal acquisition anisotropic (non-cubic) data set, while the PET data set is an axial acquisition with isotropic voxels, so not only are the image data sets different modalities they also have different volume and voxel dimensions and were acquired in different orientations. To view this information right-click on the data once loaded into Analyze and then choose Info, review the volume metadata in the tab at the bottom of the Analyze window.  To follow along, download data sets MRI_Head and PET_ Head from analyzedirect.com/data. Open Input/Output and load both the MRI_Head and PET_ Head data sets into Analyze.

- Select the MRI_Head data set and while holding down the Ctrl key, select the PET_Head data set and then open Register.

- Select File > Input/Output Ports to view the input and output ports at the bottom of the Register window. Make sure that MRI_Head is the base volume, and PET_Head is the match volume. If the data was loaded incorrectly, click the Swap Inputs button to correct.

- The base MRI data set will display in the first column while the match PET data will display in the last column.

- At this point no registration has taken place, but the match data set has been correctly scaled to the base data set, displayed isotropically.

- The crosshair (linked cursor) [1] in each of the image display panes can be used to move through the volumes. When the crosshair is moved in any of the panes, the other panes automatically update. Note that the base and match coordinates are reported at the bottom of the window [2].

- Click the Register button [3].

# 3D Registration - Mutual Information (continued)

- After registration is complete, you will see that the PET volume has been scaled, rotated and translated to match the sagittal MRI [4].

- If desired right-click the Blend Type yellow text in the fused axial image (middle upper panel) [5] and change the blend type.

- To evaluate the registration, move the crosshair in any of the panes. Note, if moving the crosshair in fused or match data you can unintentionally translate the data. If you do this click Undo to reverse the last action. To prevent this from happening again either right-click in a fused or match image and uncheck the 'Left Drag to Translate' option or simply control the crosshair maneuvers from the base volume only.

- If the registration is not satisfactory, you can choose to undo the last action using the Undo button at the bottom of the left tool bar.

- If you want to reset the data back to the original matrix, use the Reset button in the top right of the register window [6].

- To view the current transformation matrix, select the Registration Matrix box [7] on the left tool bar. This gives the option to save the current matrix as an ASCII floating-point file or load a previously saved matrix.

- To save a copy of the transformed PET data set or fused MRI/PET data set, click Save Registered [8]. Select the Transformed Save Type, Workspace, File and then select Save Transformed.

- When finished close Register.
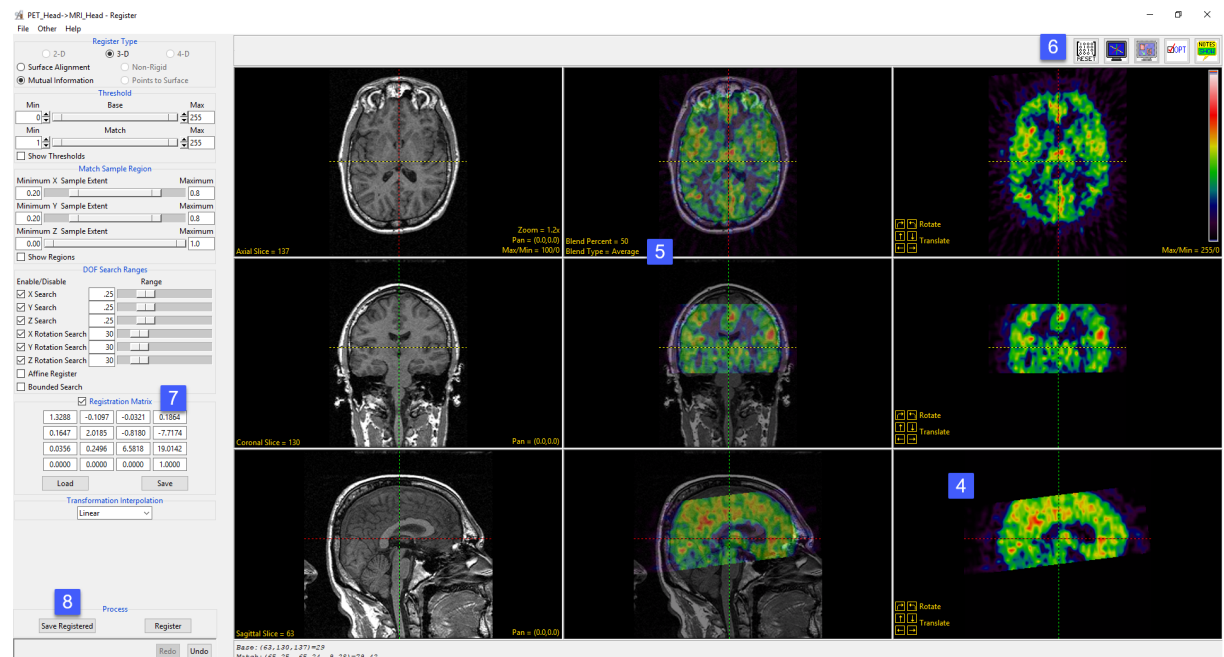
# Troubleshooting Registration Problems

Sometime image registration will fail, fortunately the Register module provides several tools to help optimize conditions to achieve registration. Common problems include:

- · • Not enough overlapping information between input data sets
- · • Background or artifact noise
- · • Adjusting the sample region to include/exclude regions in the match data

## Not enough overlapping information between input data sets

- Download data sets Register_MRI_Base.avw and Register_MRI_Match.avw from analyzedirect.com/data to follow along.

- Use Input/Output to load the two data sets into Analyze. Select the Register_MRI_Base data set and while holding down the Ctrl key, select the Register_MRI_Match data set and then open Register.

- Select File > Input/Output Ports to view the input and output ports at the bottom of the Register window. Confirm that the Register_MRI_Base data set is assigned as the 'Base Volume' and Register_MRI_Match data set is assigned as the 'Match Volume'. If the data is loaded incorrectly use the Swap Inputs option to correct.

- Use the Blend Type [1] to set a Red-Green blend for the fused image. The blend will help with visual assessment of the registration result as both the base and match data sets are grayscale.
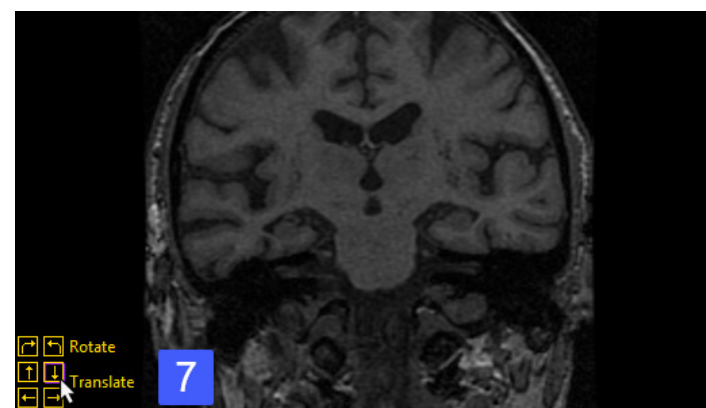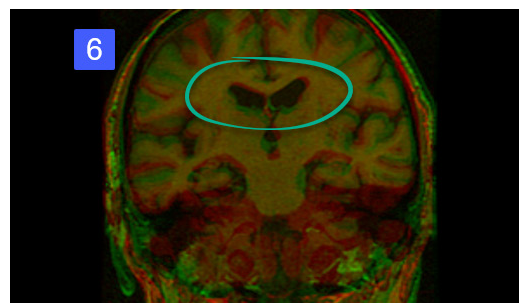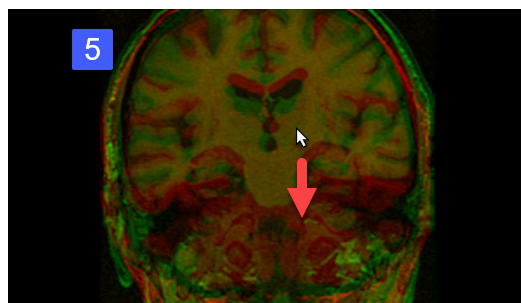
- Press the Register button [2].
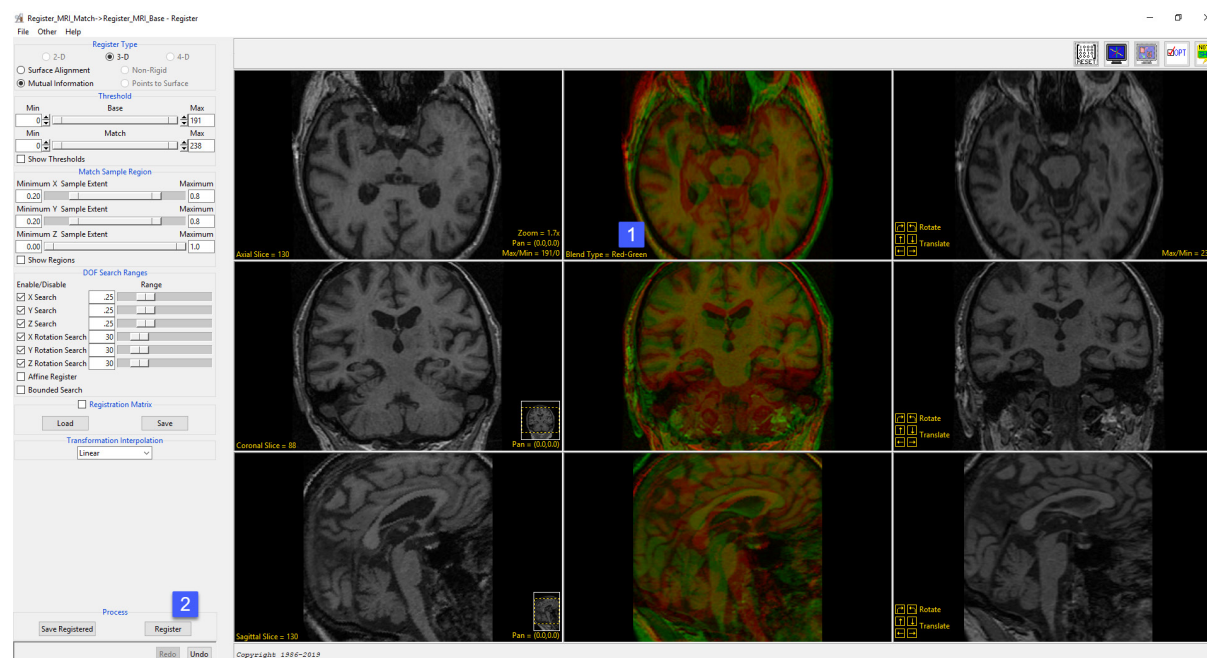
# Not enough overlapping information between input data sets

- Examine the Fused image data in the center column [3]. It is clear to see that the registration process failed. These image inputs do not have enough overlapping mutual information to facilitate a successful registration, however, the resolution to this issue is quite simple, the match data set needs to be manually adjusted so it has a new starting point closer to the base image.

- Since the registration is not acceptable click the Reset Matrix button [4].
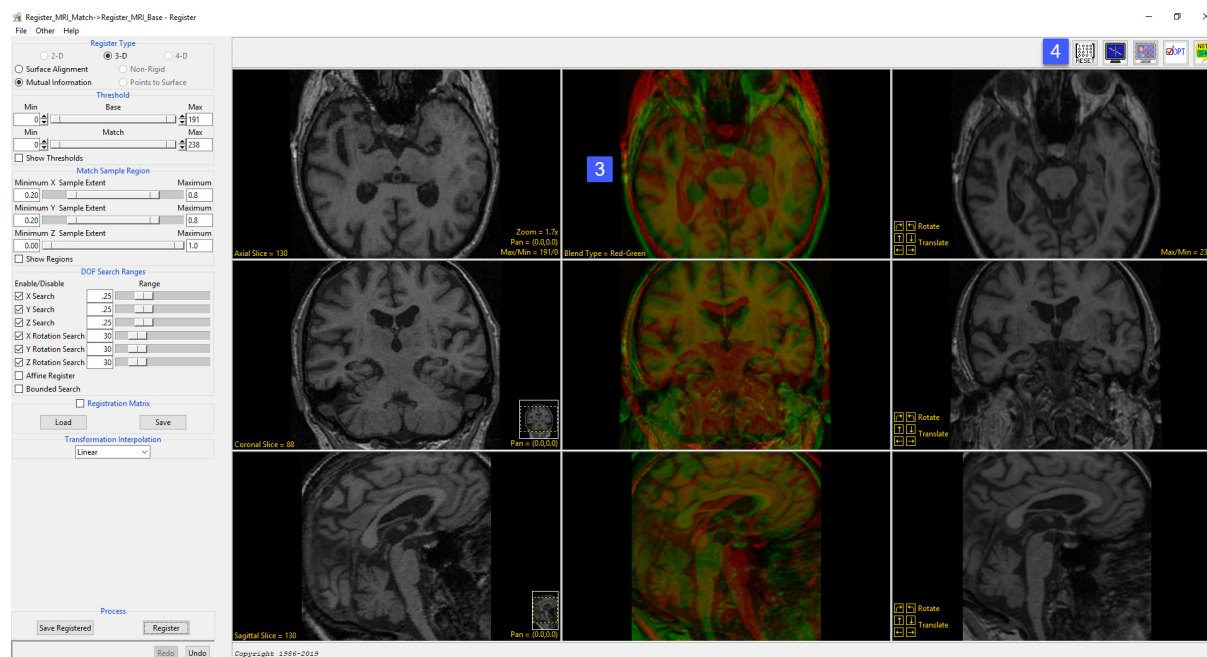


- Left click on the coronal fused or match image and drag the data down slightly [5]. Release the mouse when the ventricles are aligned closer [6].

- Alternatively, use the down translation arrow [7] to move the coronal match image down 5 voxels.

# Not enough overlapping information between input data sets (continued)

- Press the Register button.

- This time the image data will register correctly. Notice that the fused image will appear yellow [8] when aligned correctly. Use the Save Register [9] to save the transformed image data to the workspace.

- Note that when troubleshooting data you are experiencing problems with may need to make larger adjustments that could also include rotations and manipulations in all three orientations.

- Close Register.
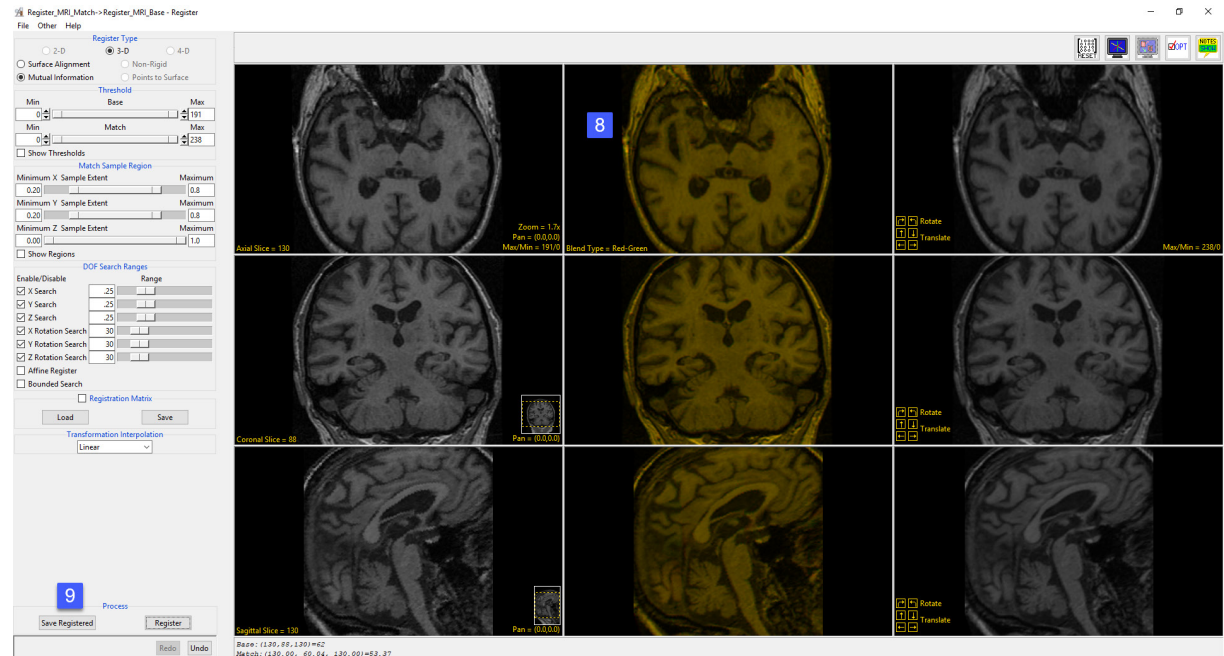
# Background or artifact noise

Noise in the background of the image or from artifact in the image can prevent successful registration of image data.

In this example, registration of a post-operative CT to a pre-operative MRI fails due to the artifact from the electrodes in the CT data set [1].

However, simply setting a threshold range to exclude the voxels in the match data set that represent the electrodes, by decreasing the maximum threshold value [2], and the streak artifact from the electrodes, by increasing the minimum threshold value [3], allows for a successful registration [4].
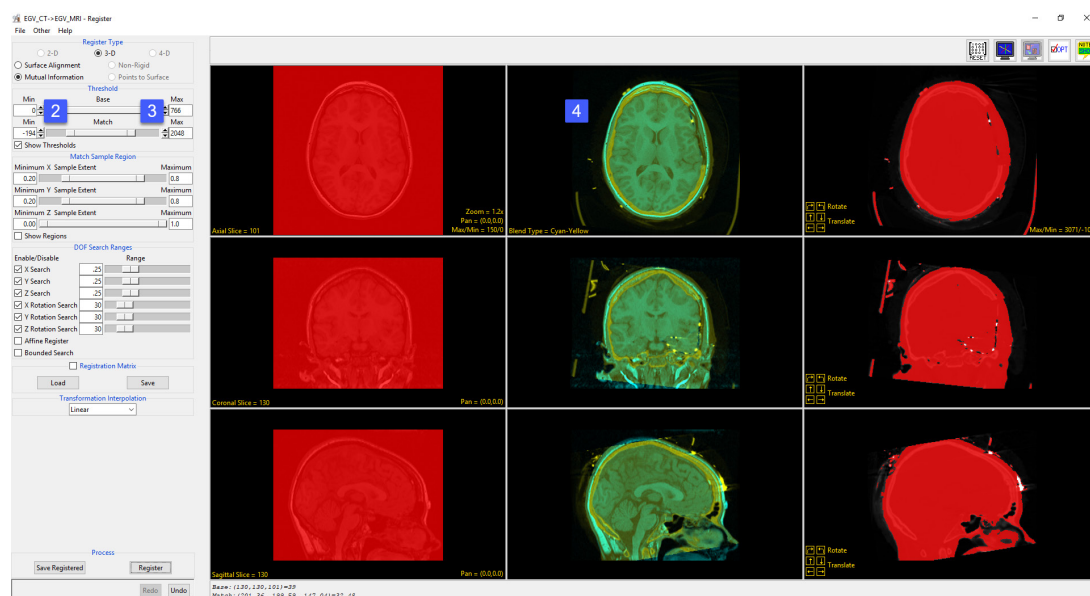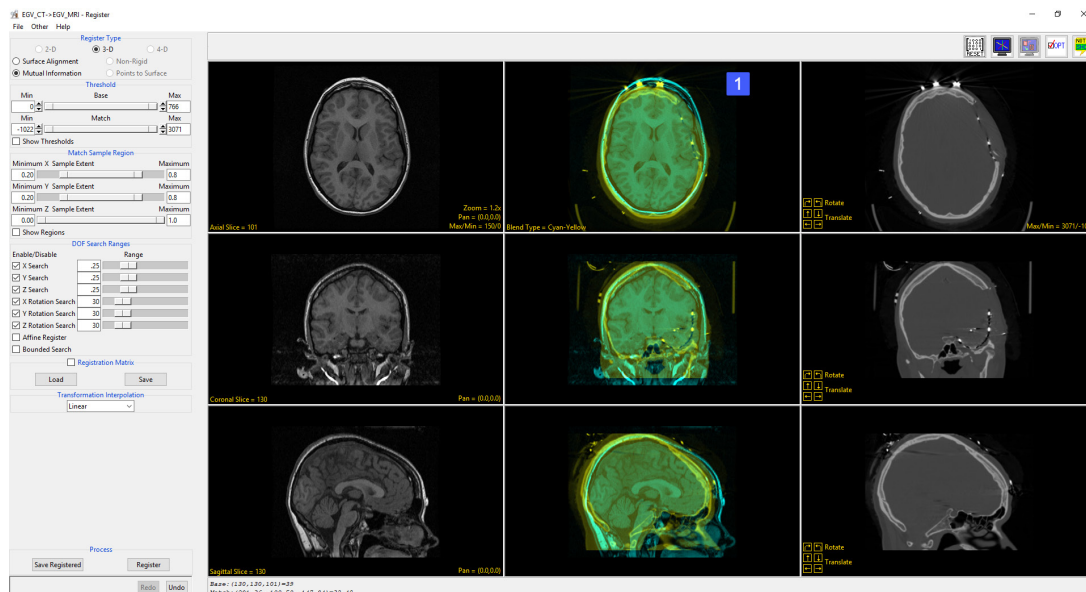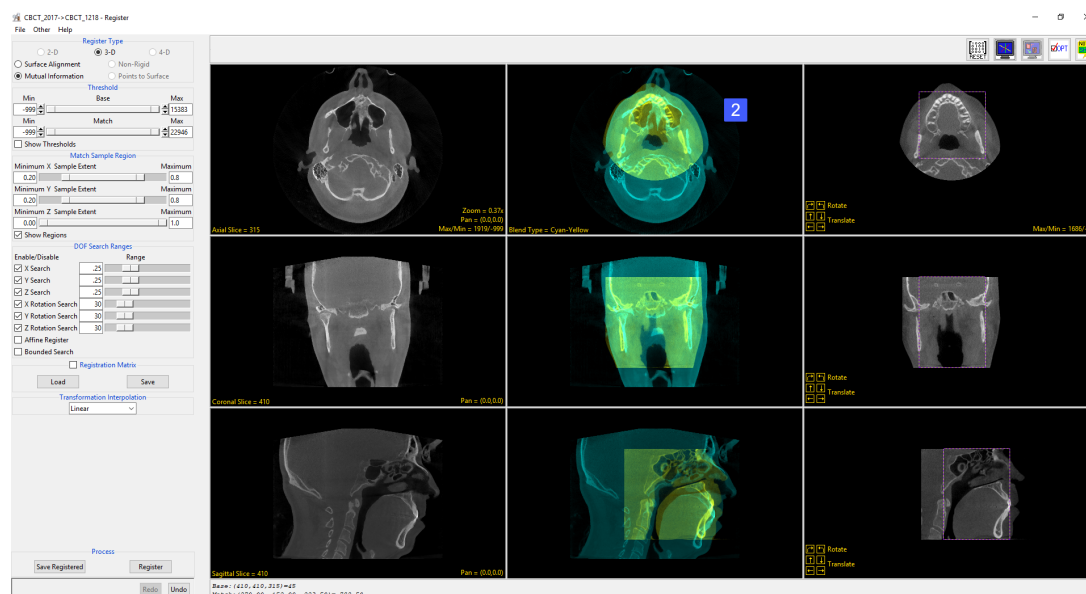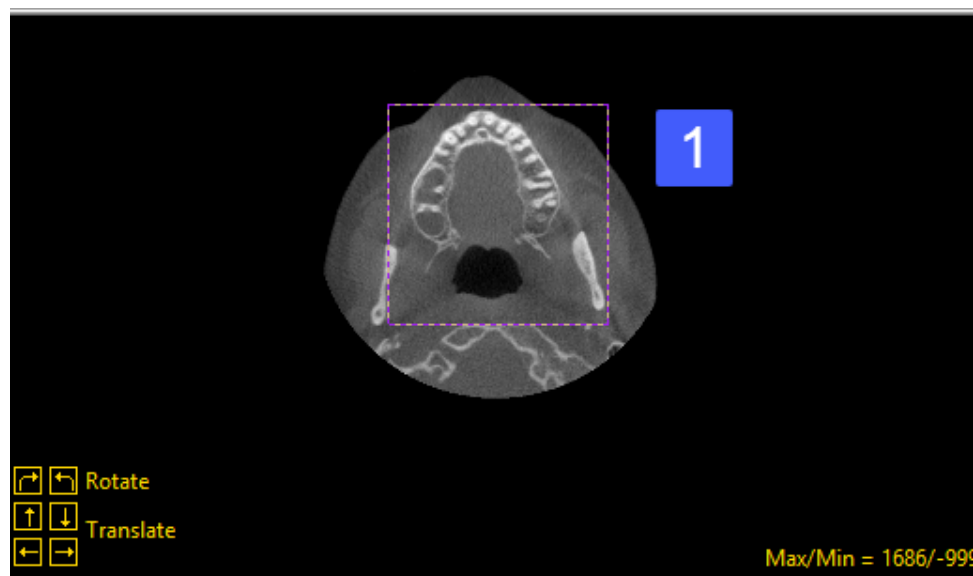
# Adjusting the sample region to include or exclude regions in the match data

Registration can fail if not enough of the match data is considered for the registration. Registration can also fail if the match region considered for registration contains a region of large morphological change from the base data set, such as an implant in a post-implant data set. The match sample region allows users to adjust to match region considered for the registration, increasing or decreasing the match region as necessary.



The match sample region provides X, Y and Z sample extent sliders that define a specific spatial region used for registration. A dotted boundary line will appear on the right match image column [1] when the option is enabled.

In this example registration between a pre-procedure and post-procedure Cone Beam CT (CBCT) scans fails as the CBCT scans were acquired from different scanners with different parameters [2].

# Adjusting the sample region to include or exclude regions in the match data (continued)

Adjustment of the match sample region to increase the X sample range [3] remedied the problem and allowed for successful registration of the image data [4].