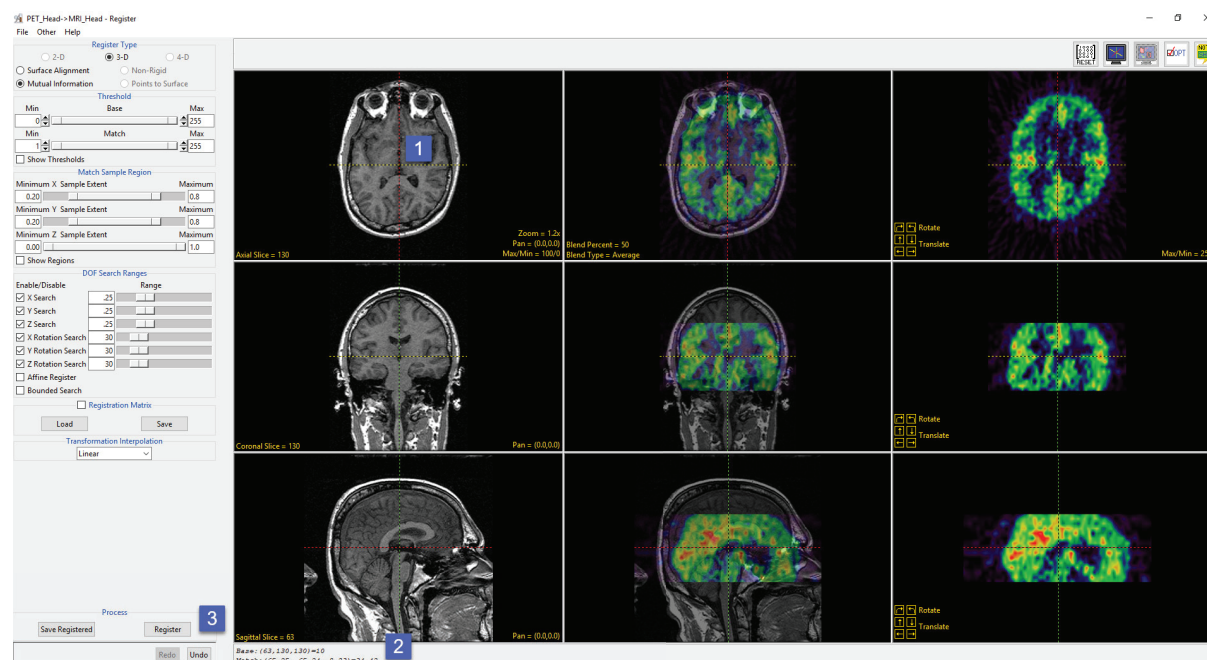




# 3D Registration - Mutual Information

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](http://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.

