Analyze 10.0

Apps & Add-Ons

Exercise 49 : SISCOM

Epilepsy Seizure Focus Localization with SISCOM (Subtraction Ictal SPECT CO-registered to MRI) automates the technique for advanced imaging of epilepsy patients that was developed with Analyze at the Mayo Foundation. This method uses a combination of SPECT and MRI imaging for improved diagnosis of areas of regional activation in the brain during a seizure. The SISCOM technique requires acquisition of ictal (during the seizure) and interictal (resting, or between seizures) SPECT images and an MRI volume spanning the entire brain. This exercise will demonstrate how to use the SISCOM module within Analyze.

1. Load the data sets **SISCOM_Ictal_SPECT.avw**, **SISCOM_Interictal_SPECT.avw**, and **SISCOM_MRI.avw** from the **$:\BIR\images\TutorialData** directory.

2. Select the data sets in the following order (hold down the <CTRL> key to select multiple data sets, or click using the middle mouse button):
   - **SISCOM_Ictal_SPECT.avw**
   - **SISCOM_Interictal_SPECT.avw**
   - **SISCOM_MRI.avw**

   Note the selection order: Ictal, Interictal, MRI. If the data is not loaded in this order the SISCOM procedure will fail to run correctly.

3. Open the **SISCOM** module (**Apps > SISCOM**).

4. Open the **Register SPECT** option (**Process > Register SPECT**) to compute an activation map.

   i. Set the Interictal SPECT minimum Cerebral Activity Threshold level to 75 [**A**]. Note the change in the binary image.

   ii. Ensure that the Interictal Transformation Type is set to Linear [**B**].

   iii. Use the Activation Level slider bar to set the standard deviation to 2.0 [**C**].

   iv. Next, select the Register and Map button. The Register SPECT tool will automatically register, normalize, subtract, select the statistically significant voxels of activation, and output the activation map based on the parameters specified above. Note that the tool will update, displaying the Activation Map [**D**].

5. Select **Next** to continue onto the next step of the SISCOM procedure, MRI brain extraction.

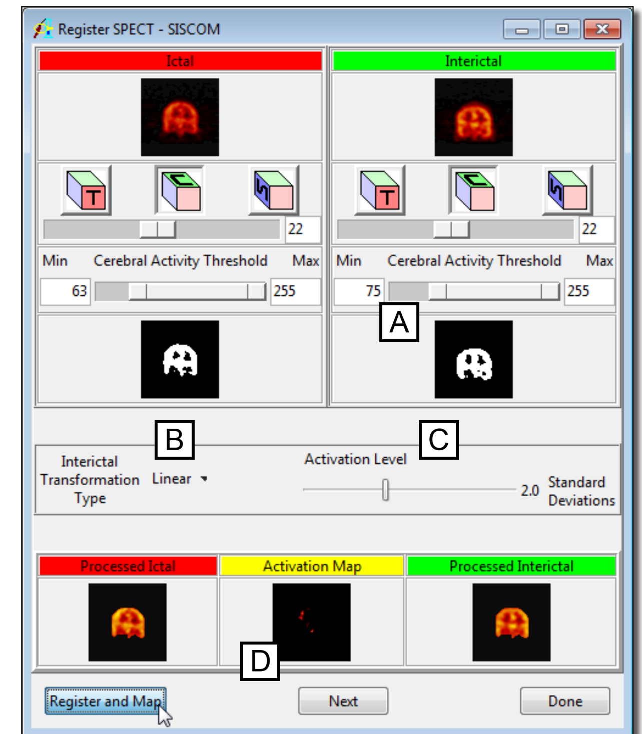


Figure 1

6. The Extract MRI Brain tool allows for segmentation of the brain for SPECT-MRI registration.

7. Right-click in the MRI data display window and select the Intensities option. In the Intensity (MRI) window returned, change the **Maximum** to **101** then click Done to close the Intensity Tool.

8. Use the slider bar to adjust the minimum and maximum threshold values to obtain the best definition of the cortical boundary as possible. In this case, the threshold values do not need to be adjusted.

9. Select **Extract Brain** to segment the brain. After segmentation is complete, the extracted brain is automatically displayed in the **Extract MRI Brain** tool. The segmentation can be reviewed using the Slice slider bar (figure 2).

10. Select **Next** to continue to the next step, registration of the SPECT data sets to the MRI data sets.

11. The **Fuse SPECT & MRI** tool will automatically open and immediately run the Match Surfaces process, registering the SPECT data sets to the MRI data set and displaying the Activation Map overlaid on the MRI data set. The activation map and MRI can be reviewed using the orthogonal orientation buttons and the slice slider bar (figure 3).

12. Select Fuse Volumes. The activation map and MRI will be fused and automatically be saved to the Analyze workspace. Select **Done** to close the Fuse SPECT & MRI tool. Also close the Extract MRI Brain and Register SPECT tools.

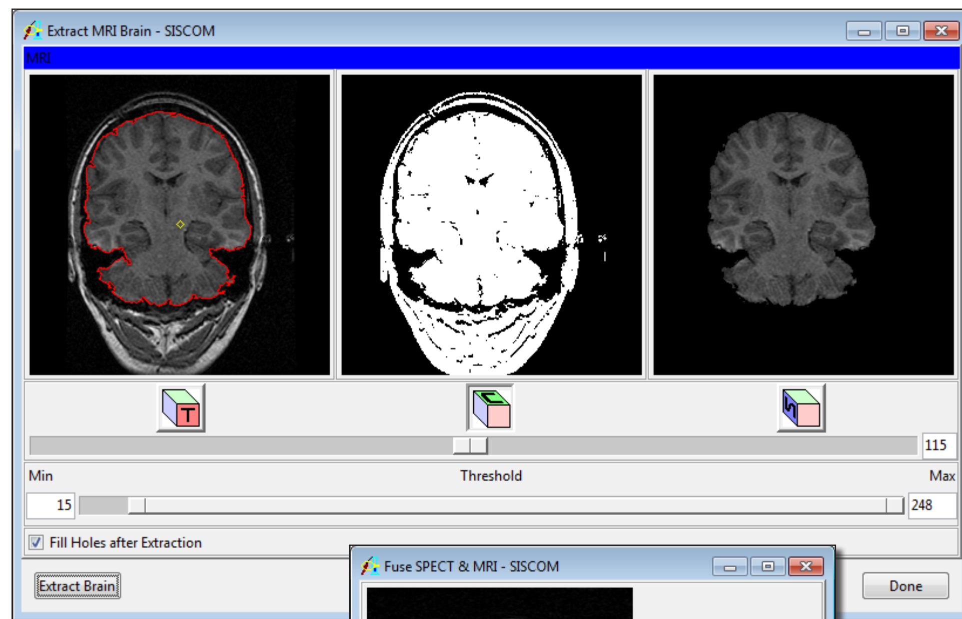


Figure 2

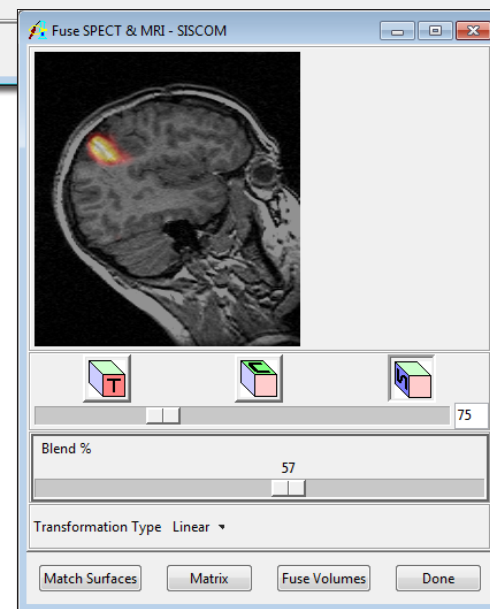


Figure 3

13. Select the **Compare Tool** option (**Process > Compare Tool**). The Compare Tool provides an interface for users to display and visually inspect the accuracy of the registration and fusion of the volumes created in the SISCOM process. Use the drop down menu options under each image [**A**] to select the volumes to compare (figure 4). Select Done when review is complete.

14. Select the **Create Object Map** option from the **File** menu to generate an object map based on the areas of activation.

15. Select **Output Object Map**. The object map will be automatically saved to the location specified using the **File** option. The Render tool (figure 5) will automatically open, allowing for interactive review of the object map.

16. Close all windows related to the SISCOM module before proceeding to the next exercise.

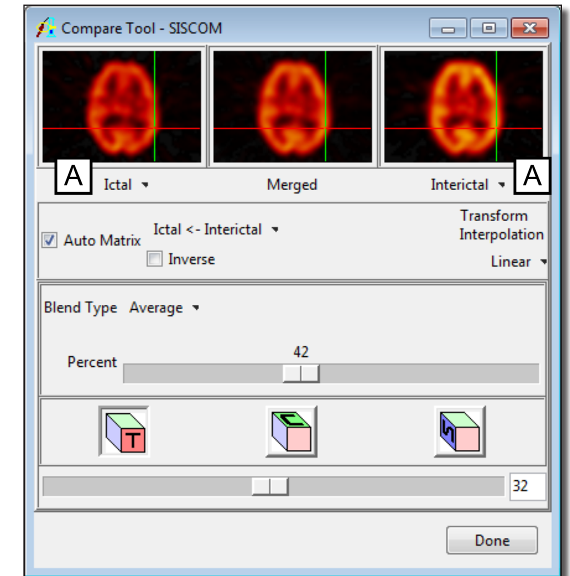


Figure 4

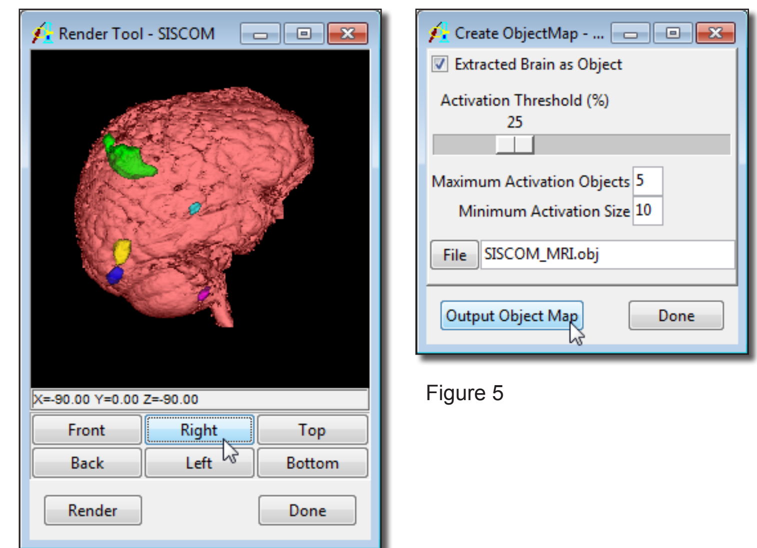
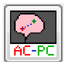


Figure 5

Exercise 50 : Mayo 3D Brain Atlas

The Analyze Mayo 3D Brain Atlas add-on provides a unique 3D implementation of the Talairach anatomical atlas of the human brain. The Mayo 3D Brain Atlas add-on allows for 3D navigation of the atlas and interactive query and reporting of atlas-based coordinates in many common volumetric and neuroanatomical and neurofunctional frames of reference, including TT, MNI, SPM, FSL and ICBM coordinates. In addition, atlas-derived neuroanatomical regions can be output from the module and then utilized directly in many other Analyze modules. This exercise will demonstrate how to use the Mayo 3D Brain Atlas add-on.

1. Load the **MRI_3D_Head.avw** data set from the **$:\BIR\images\TutorialData** directory.
2. Select the **MRI_3D_Head.avw** data set then open the **Mayo 3-D Brain Atlas** module (**Apps > Mayo 3D Brain Atlas**).
3. The PowerBar buttons in the main **Mayo 3D Brain Atlas** window are set up in the sequence of operations performed. The first step to using the atlas is AC-PC based alignment of the loaded image data to the Talairach-Tournoux coordinate and proportional grid system.



4. Open the **Align AC-PC** window (**Tools > Align AC-PC**).
5. Use your cursor to move the **AC** and **PC** points to the appropriate location on the sagittal image. Enlarging the image may help to identify the AC and PC; right-click on the display and select **Size > Double**. Note that the left and right arrows and rotation buttons can be used to adjust the data set to correct for symmetry.
6. Select the AC point and move it to the appropriate location. The magnify window will automatically display helping you to determine the precise location of the AC (figure 1).

7. Select the PC point and move it to the appropriate location.
8. Select **Align AC-PC**. The image volume will realign to the AC-PC.
9. Select **Next** to open the **Extract Brain Tool**. A seed point and threshold range are automatically set by the **Extract Brain Tool**. These can be adjusted if necessary.
10. Check the **Fill Holes after Extraction** option and then select **Extract Brain**.
11. The extracted brain can be reviewed using the **Slice** slider bar (figure 2).

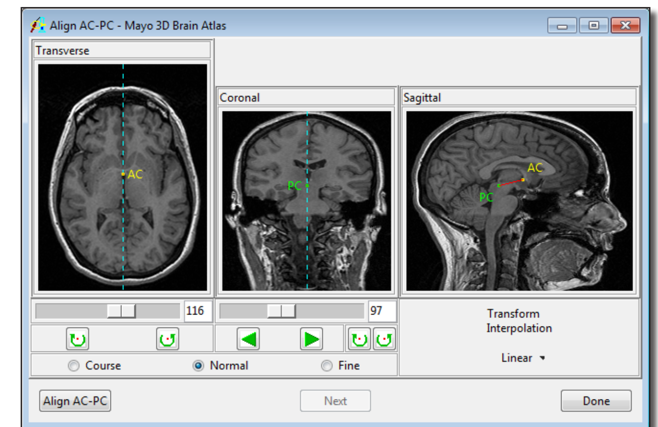


Figure 1

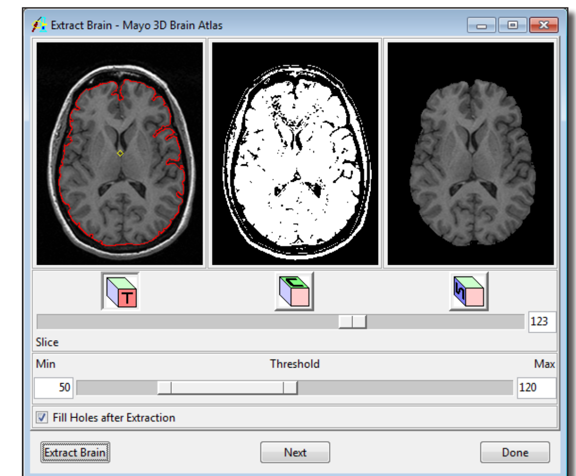


Figure 2

12. Select **Next** to open the **Adjust Registration** tool (figure 3). If needed the atlas can be adjusted. Right-click in any of the orthogonal display panes and select **Restrict > None**. Note the right-click menu also provides options to display the loaded or extracted volume and increase the display size.

13. The grid can now be manipulated. Move the grid lines in any of the orthogonal displays to adjust the atlas. When you are finished making adjustments, right-click in any of the orthogonal displays and set **Restrict** back to "All."

14. Move the yellow square marker in any of the orthogonal displays to move through the loaded volume. Note that when the marker is moved the name of the atlas region and the coordinates of the current marker point will appear in the lower left-hand corner of the window.

15. To query specific structures by coordinates, navigate back to the main module window and select the **Query Atlas** button from the PowerBar.

16. The **Adjust Registration** window and the **Query Atlas** window work together. The **Query Atlas** window will return the atlas structure and coordinates for the current location set in the **Adjust Registration** window.

17. In the Adjust Registration window, move the Yellow marker to a location you wish to query.

18. In the Query Atlas window click the **Query** button, the structure and location of the Yellow marker will be returned.

19. Check the Query Range option and set the Range to 5. Click the Query button again. All structures with in a 5 voxel range will be reported in the query window (figure 4). Please note: The information returned can be saved as a text file by right-clicking in the Query window and selecting the **Save As** option.

20. Close the **Query Atlas and Adjust Registration** windows.

21. To save the atlas as an object map open the **Generate Output** window by clicking on the **Output** button in the PowerBar.

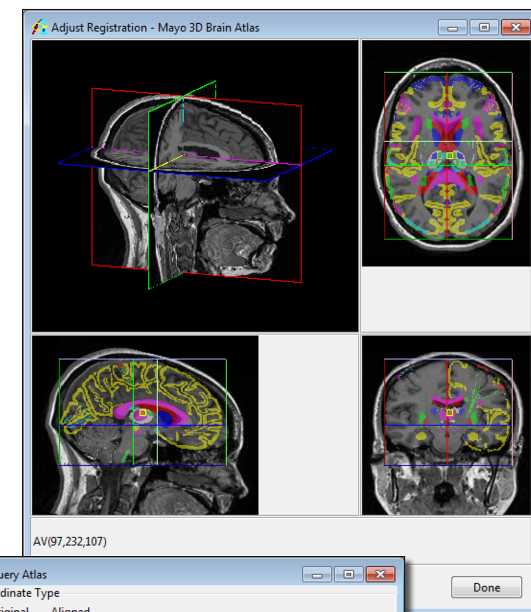


Figure 3

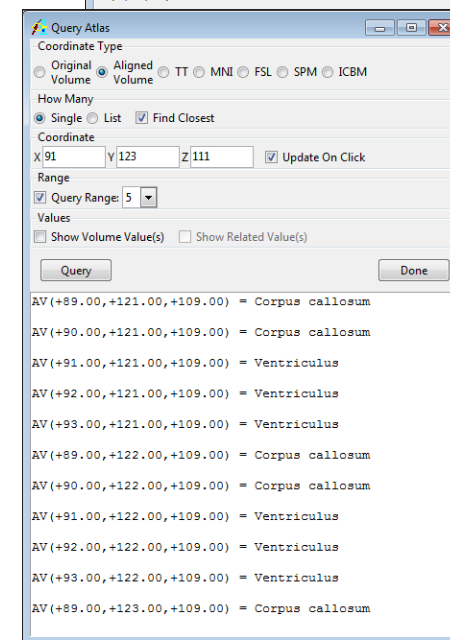


Figure 4

22. In the **Generate Output** window returned (figure 5), make sure the following options are set:

    i. Set **Output What** to **Specified Atlas**
    ii. Set **Space** to **Original Volume**
    iii. Set **Which Atlas** to **Transverse**
    iv. Set **Output As** to **Object Map**

23. Next change **Object(s)** to **Specified** and then click on the List button. The **Object List** window returned allows you to select only the objects you wish to output to the object map, click **Done** to close the window and then set **Object(s)** back to **All**.

24. Select **Generate Output**. The object map will be saved as '**AtlasOutput_MRI_3D_Head.obj**' in the specified directory.

25. Select **Done** in the **Generate Output** window and close the **Mayo 3D Brain Atlas**.

26. To review the Atlas object map created, select the **MRI_3D_Head** data set from the Analyze workplace and then open the Multiplanar sections module. Select **File > Load Object Map** and load the object map saved in step 23. Select the Traffic Signal icon to begin the sequence display of the data.

27. Close all windows before proceeding to the next exercise.

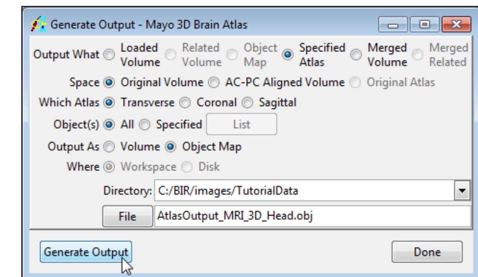


Figure 5

Exercise 51 : T2 Projection

The MRI T2 Optimization Add-On provides the ability to enhance the relative contrast between different tissue types in T2 weighted MR images post-acquistion. The add-on uses a piecewise non-linear intensity transformation based on priori knowledge. The prior knowledge is derived from training multiple post-processed data sets acquired at different relaxation (TR) and echo (TE) times. The transformation does not make any assumption on the pulse sequence parameters associated with the image to be projected. This exercise will demonstrate how to use the add-on to enhance a T2 MRI data set.

1. Load the **MRI_T2.avw** data set from the **$:\BIR\images\TutorialData** directory.
2. Open the **T2 Projection** add-on (**Apps > T2 Projection**)
3. The input, or pre-enhanced, T2 data is displayed on the left side of the window, the post enhanced data is displayed on the right side

4. Click **Show Forward**, until Slice 15 is displayed.
5. The **Relaxation Time** (**TR**) can be adjusted by selecting a value from the **TR (msec)** drop-down menu. Select **1800**. Note that the post-enhanced display updates when a new value is selected.
6. Similarly, the **Echo Time** (TE) can be adjusted by selecting a value from the **TE (msec)** drop-down menu. Select **110**.
7. To save post-enhanced T2 select the **Create Projection** button. The projection will be saved to the Analyze workspace. Note the enhanced images are named according to the TR and TE values used. For example MRI_T2_1800-110.
8. Close all windows associated with the T2 Projection module before proceeding to the next exercise.

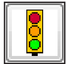
Figure 1

Exercise 52 : Volume Metrics

The Volume Metrics Add-On provides tools to assess the quality of multiple associated volumes, allowing the creation of a set of statistics based on the type of metric chosen. The add-on can be used to assess the similarity of two co-registered three dimensional volumes using 15 parametric or 12 non-parametric similarity indices. The add-on can also be used to assess the concordance of different segmentation results with ground truth data using 47 popular binary similarity metrics. This exercise will demonstrate how to compute similarity metric values for two related data sets.

Calculating and Logging Metrics

1. Load the **MRI_3D_Head.avw** and the **MRI_3D_Brain.avw** data sets from the **$:\BIR\images\TutorialData** directory.
2. With both volumes selected, open the **Volume Metrics** module (**Apps > Volume Metrics**).



3. To calculate all of the statistics for a specific metric option, select the Metric Type [**A**], then click the **Calculate Metrics** button [**B**]. The metrics are calculated and displayed next to each Similarity Value [**C**].
4. To log the metrics in a log file, click on the **Log Metrics** button.
5. The **Volume Metrics Log** (figure 2) contains all of the metrics that are checked in the main window. To save the metrics log file to disk, right click in the log window and select **Save Log**.
6. Click **Done** to close the log screen.
7. Close all of the windows associated with Volume Metrics before proceeding to the next exercise.

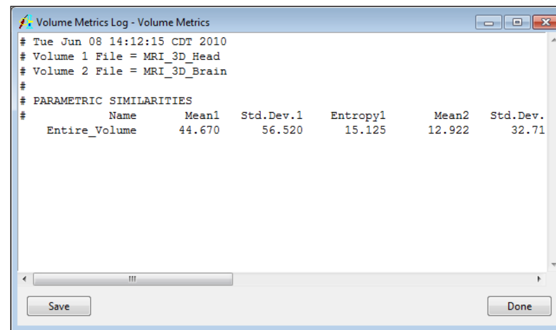


Figure 2

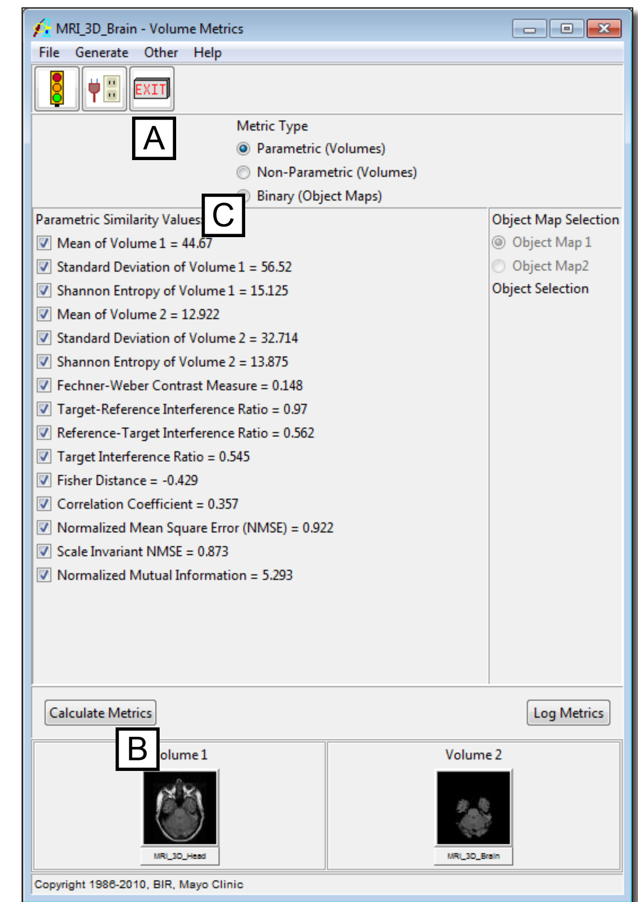


Figure 1

note | Volume 1 is the input volume, while Volume 2 is the comparison volume.