7 Dual Energy

Dual Energy is an application for review and analysis of CT dual-energy scans.

NOTICE

Before loading scans into the Dual Energy application, ensure a suitable dual-energy scan protocol (Exam Card) was used. Refer to the documentation that came with your scanner for more information.

Dual Energy consists of 3 stages:

1. **Registration.** Use this stage to align the two scans that were performed at two energy levels (for example: 80kV and 140 kV).
2. **Analysis.** Use this stage to conduct an analysis of the different energy series. Three analysis methods can be performed: binary separation; vectors separation (non-binary range); probability classification.
3. **Segmentation.** In this stage you will use the spectral tissues obtained from the Analysis stage and manually segment the region of interest. The results of the segmentation may be reviewed against the original series (with and without registration results) as well as with the combined series.

WARNING

When loading images into the application, all images which contain 16 bit data are converted into 12 bit images. (Therefore, when the rescale intercept equals -1000, Hounsfield Unit values above 3095 are displayed as 3095, and when the rescale intercept equals -1024, Hounsfield Unit values above 3071 are displayed as 3071.)

NOTICE

Depending on your Portal configuration, this application may not be available.

Indications for Use

The CT Dual Energy Viewer is designed to assist in review and analysis of Dual-Energy CT Scans and assist in characterization and dual-energy analysis of different tissue materials based on their energy value.

Registration Stage

The Registration stage provides tools for rigid registration of two scans of the same patient acquired at different energies.

Registration Workflow

1. Select the Base and Aligned series and start Registration.
2. Position the Aligned series to directly overlay the Base series.
3. Accept the registration. The Spectral combined series is created.
4. Before moving to the next stage, make sure that the active series is the spectral combined series with which you want to perform energy separation.
5. Use the Weighted Energy slider to select the weighted energy to create different, multiple series with different KV values using the same base and aligned series.
6. When verified, move to stage 2, Analysis. See section “Analysis Stage” on page 254.

Registration Tools

Use these tools to accurately align the Aligned series over the Base series.

Show Crosshair (default)

Shows the crosshairs on reference images.

Rotation Center

Show the center point around which the volume can be rotated.

Center Cursor

This function moves the middle of the image to the rotation center.

Select the Base and Aligned Series

Each series is displayed with it’s kV value to help with selection. The Base series does not move. The Aligned series appears as a translucent layer for you to move over the Base series. If desired, you can switch the series.

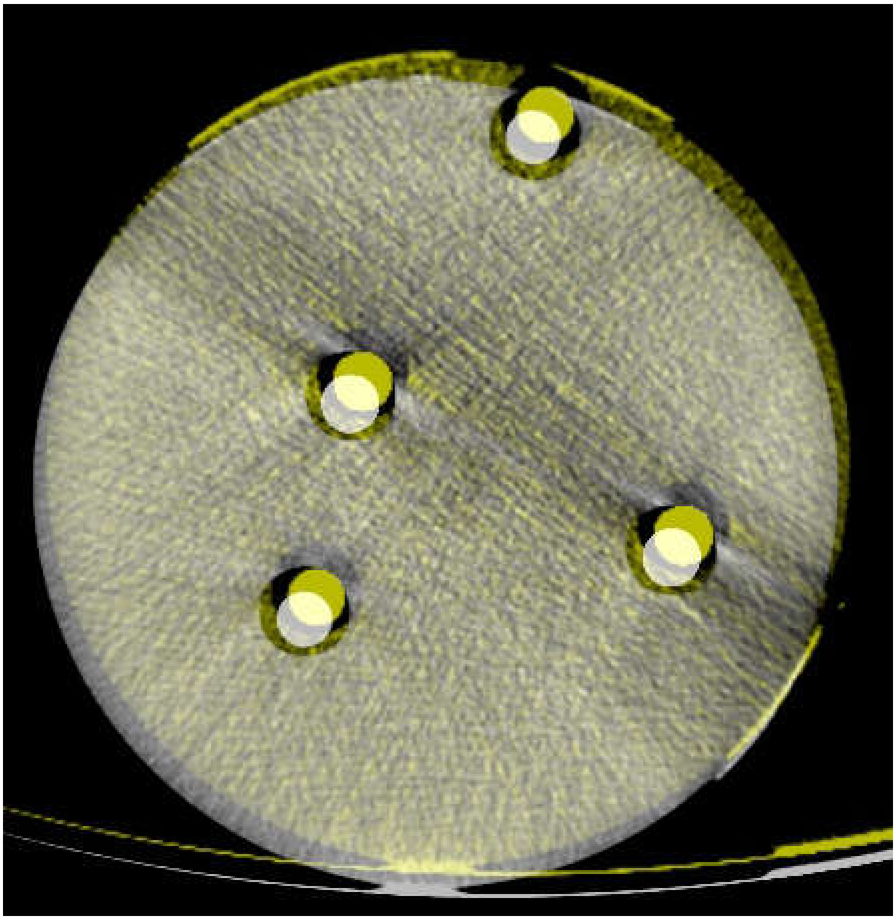
Swap Series

Click this button to switch the two series between Base and Aligned.

Apply Registration

Click this button after selecting Base and Aligned series. This will place the aligned data on top of the base data with a yellow, semi-transparent overlay.

In addition, when the Apply Registration button is selected, the Translate and Rotate buttons, as well as the “create registered series” checkbox are activated.



Windowing

This tool controls display of the overlay data (of the Aligned volume).

Subtract Series

This tool helps you perform the registration of the two series images. Checking this tool changes the display to a subtraction image of the base and aligned series. The best registration is achieved when the subtraction image is completely black.

Translate

Use the Translate button to pan the aligned data according to the base data. Using the mouse scroll wheel for windowing in rotate or translate modes, the windowing is overlaid. You may also use the Ctrl+Shift+scroll wheel shortcut.

Rotate

Use the Rotate button to move the aligned data according to the base data.

Create Series/Create Weighted Series

✓ Click on the check mark to create a new Spectral Combined series using the current setting in the slider.

Weighted Energy

The Weighted Energy slider controls how the High energy series and Low energy series are combined. Moving the slider to the right results in a combined series with more high-energy data. Moving the slider to the left results in a combined series with more low-energy data.

Apply Colormap

Use the Colormap function as a visual aid during image alignment of the Base and Aligned series. The Colormap function lets you choose a predefined colormap overlay for the Base series.

Click the **Apply Colormap** checkbox to activate the function. The Edit Colormap dialog opens.

Select the desired colormap from the Colormap Preset. The buttons in this dialog provide these functions (from left to right):

💾	Save the edited colormap preset.
✗	Delete the current colormap preset.
✎	Edit the colormap preset using the preset editor tool. (The editing procedure is the same as in the CT Viewer application.)
Abc	Rename the current colormap.

See **Report**, **Film**, **CT Common Processes** and **CT Common Tools** for information on using common options, tools, functions, and processes.

Combined Volume

WARNING

The Spectral Viewer volume image is created by combining high- and low-energy data. Combined images should not be used as the SOLE basis for clinical diagnosis.

The combined spectral volume is created as a temporary series. It is not saved to the database by default. To save it:

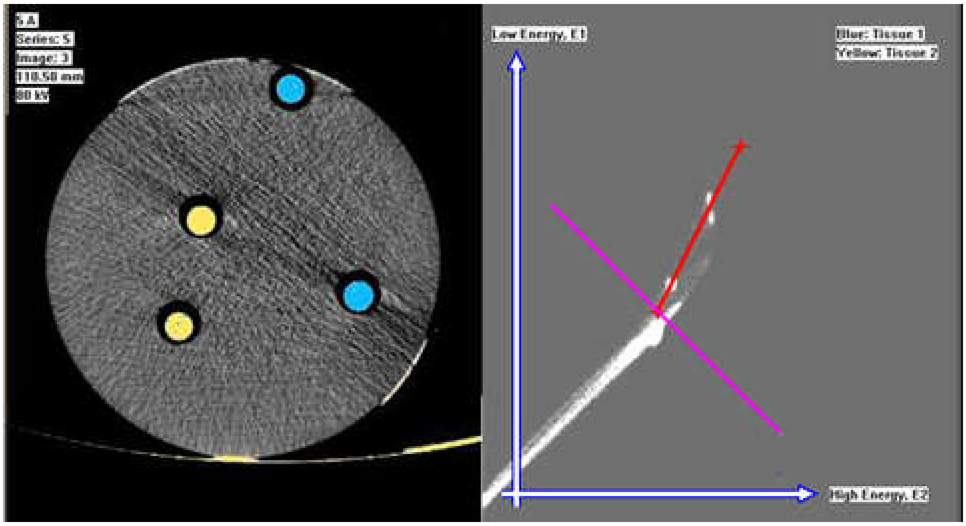
- Right click on it in the series list.
- Select **Save.**

Analysis Stage

The Analysis stage is used to perform a separation between different tissue materials, based on their energy values.

Each tissue pixel in the scanned volume has two CT values, one for high energy and one for low energy.

When you open the Analysis stage, each pixel in the CT image is characterized by the ratio of low and high energy values, and displayed on an Energy Map, shown in the viewport at right below.



An Energy Map displays, plotting values on a 2-dimensional diagram, where the vertical axis (E1) is its low-energy value and the horizontal axis (E2) is its high-energy value. (The corresponding CT image, in the left viewport above, is also displayed. The CT image will be used for review and analysis in the third stage, Segmentation.)

Analysis Tools

This section provides instruction for using tools and processes specific to the application or viewer.

Smooth

A filtering operator that is applied to the images before they undergo a separation procedure. The Smooth level may be adjusted from 1 (low smoothing) to 300 (high smoothing).

Binary

When active, this function changes the presentation:

- quantitative assessment = hue of pixels of the tissue;
- non-quantitative assessment = solid-color; and
- (also effects the Tissue 1 and Tissue 2 visualization).

Show Tissue 1 Map, Show Tissue 2 Map

These functions each add a new viewport to the display, and calculate new spectral tissue 1 or tissue 2 series, respectively, according to the chosen separation mode. (An example display is shown on the next page.)

- **Show Tissue 1** enhances tissue 1 pixels and suppresses Tissue 2 pixels.
- **Show Tissue 2** enhances tissue 2 pixels and suppresses Tissue 1pixels.
- Pixels below the defined Threshold are clipped to 0.

To save the new calculated series, right-click on the image for the save menu. (You can import the saved series from D/pms/data/DualEnergySeries.)

Separation Modes

You can choose from three methods of Analysis:

- Separation by Graph line (binary separation).
- Separation by Vectors (non-binary range).
- Separation by Probabilistic classification.

Threshold

Setting this (to any value other than –1024) allows you to define the lower limit for the CT values that should be separated and displayed on the Tissue Maps.

Save state - Use this to save:

- the graph;
- the graph position;
- the parameters of each method (smooth, binary, and threshold); and
- the meeting point (for Vectors and Probability modes only).

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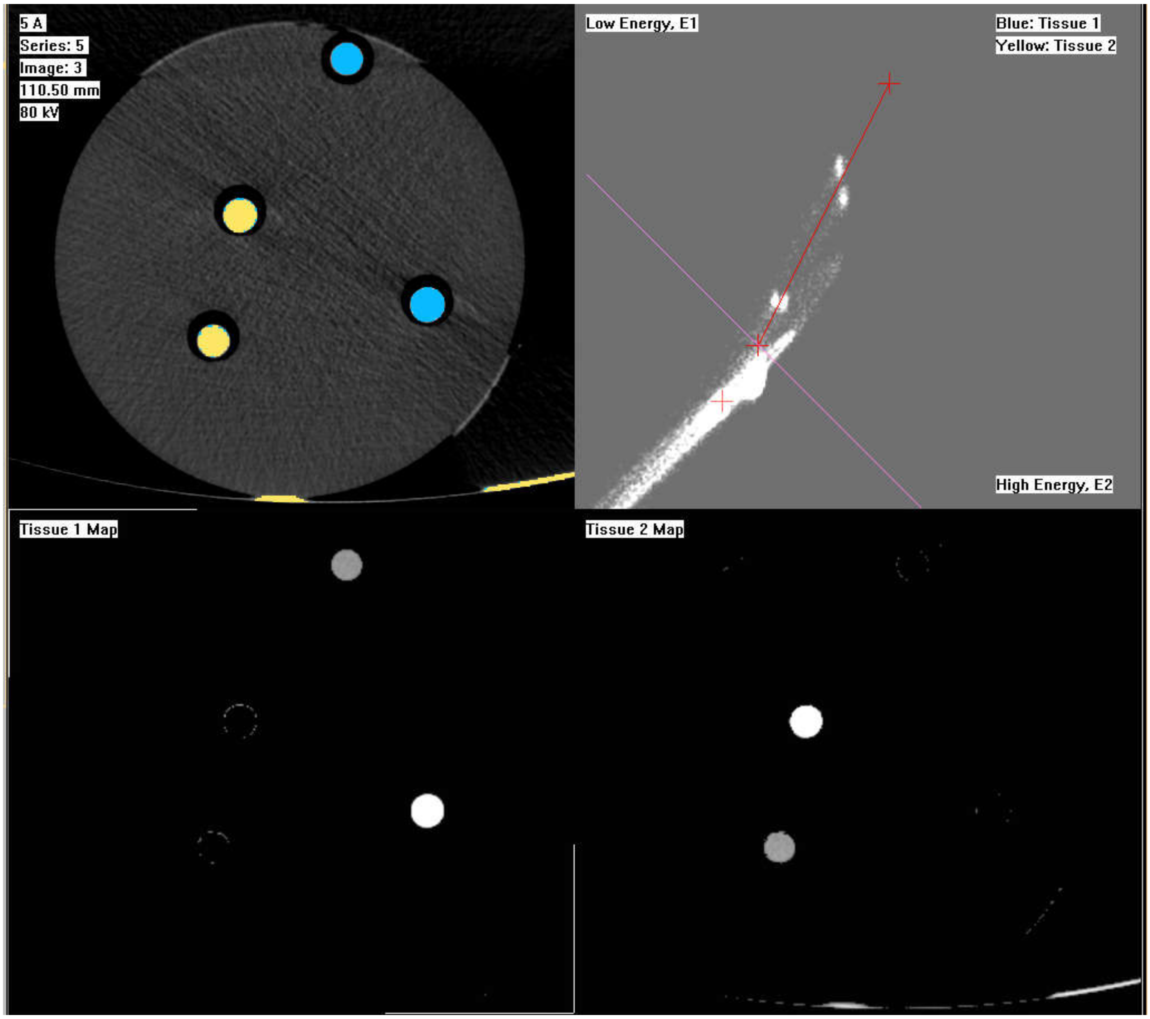
Load State

Use this to load a saved state (as described above) from each separation method.

Prepare Tissues

Calculates the tissues for the segmentation scene (2 or 3 tissues).



Right-click Context Menu

Right click in the CT image viewport to access additional options.

Define ROI

Use this function to drawing a circular ROI on the CT image. As a result, only the pixels within the ROI will be displayed on the energy map.

- You may define several ROIs.
- To move the ROI, left click in the middle of the ROI and drag with the mouse.
- To change the ROI shape, grab the ROI in either of the 4 (invisible) areas (12, 3, 6, and 9 o'clock) and drag to a new shape.

More options are available from a right click menu inside the ROI:

- delete;
- copy to Tissue maps;
- set color;
- rename; and
- text.

Select Image (Ctrl+G)

Use this function to select a specific image. A Go To box opens where you can enter an image number.

Next series (Ctrl+N)

Use this function to move between different loaded series (low energy, high energy, weighted).

Local Focus

Use this function to optimize automatic window parameters for better visualization of features at the location you point to with the mouse.

Toggle Colors (Ctrl+C)

Use this function to alternate between displaying an overlay tissue color, or no color on the CT image.

See **Report**, **Film**, **CT Common Processes** and **CT Common Tools** for information on using common options, tools, functions, and processes.

Separate by Graph Line

There are three ways to separate tissue materials using the graph line:

- Separate into two materials.
- Separate into three materials.
- Characterize several materials by defining a set (or sets) of reference lines.

Graph Separation into Two Materials

When you choose Graph separation, a red separation line is displayed on the energy map, with X-marks at each end. Attached to the lower point of the red line is a purple line which represents the Threshold value.

- All pixels on the energy map below the Threshold line are not included in the Spectral Analysis.
- All pixels above the threshold line and above the red line are classified as one substance (colored in light blue in the CT image)
- All pixels above the threshold line and below the red line are classified as another substance, (colored in yellow in the CT image).

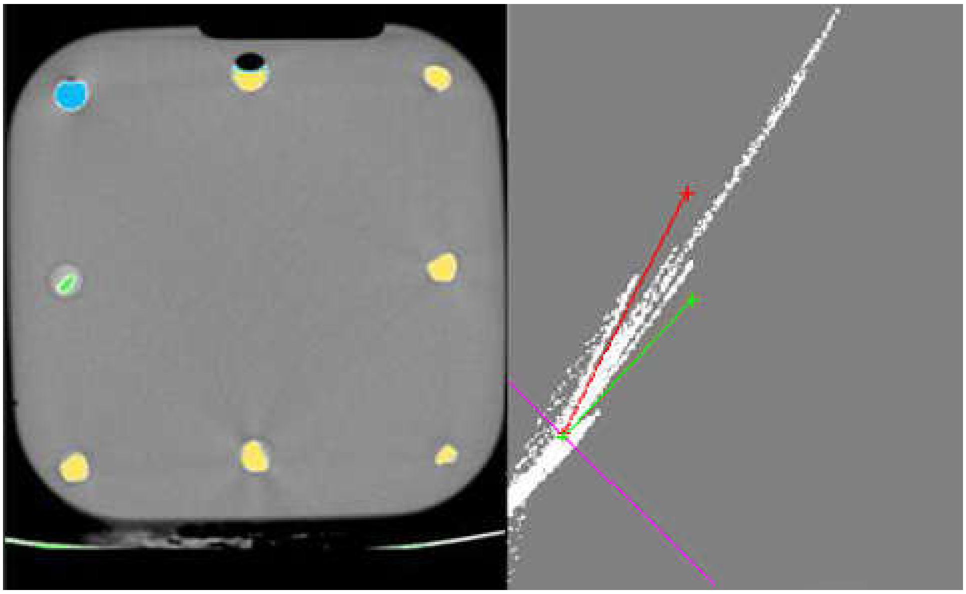
To move the separation and threshold lines, the red line can be edited by moving the X-mark at either end in any direction. The lower X-mark also moves the Threshold line. (You can also change the position of the Threshold line by changing the Threshold parameter in the tool-box.)

Graph Separation into Three Materials

By adding a second separation line you can define a third material.

- Right-mouse click in the map and select “Add Second Graph.” A green line is added to the graph viewport below the red line.
- You can change the location of the second line by dragging the line by its edge. (You can remove the second line by selecting “Remove Second Graph” from the right-mouse menu in the Energy Map.)

With two separation lines on the Energy Map, all pixels above the threshold line and below the second separation line are classified as a third substance (colored in green in the CT image).



User-defined Characterization for Several Materials

In this method you can create, name and save a set of your own reference lines. You can designate any set as the default set.

The Edit-Create Function

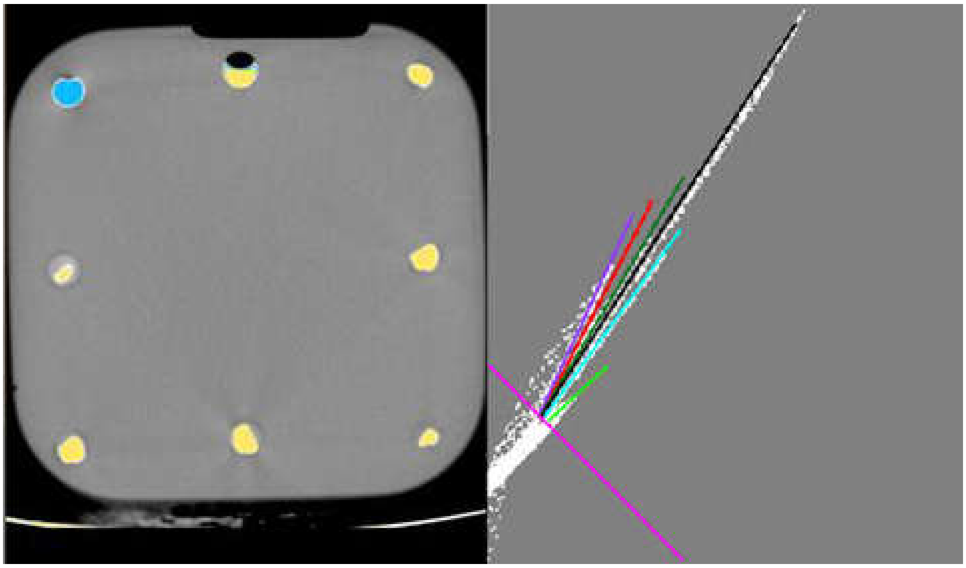
Right-click on the desired line in the Energy Map. A context menu opens. From the menu select the desired function: add a new line (above or below the line you clicked), rename the line, change the color, or delete it.

The Save-Load Function

To access this function, right-click on an open area in the Energy Map. A different context menu opens, with these selections:

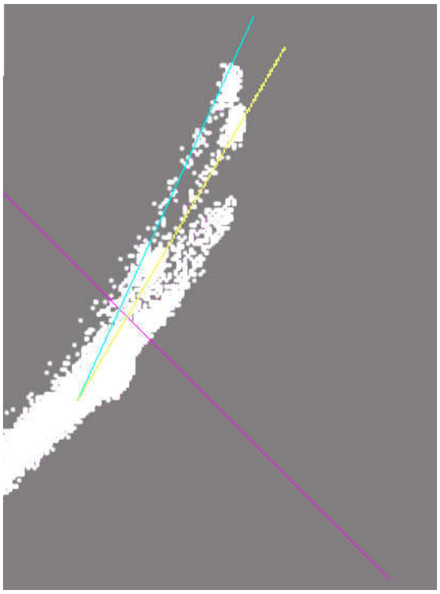
- **Load reference lines.** Load a set of saved reference lines.

- **Save reference lines.** Save a new set of lines.
- **Load default lines.** If you saved lines as “default” this option displays the default set of lines.

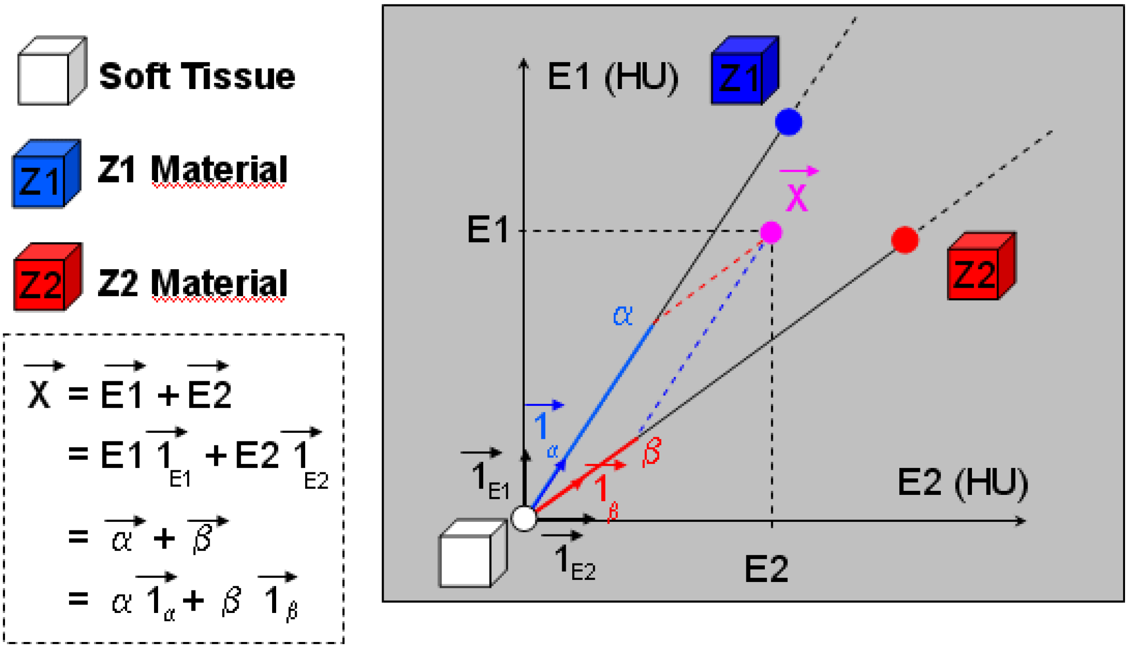


Separate Materials by Vectors

This method of separating materials assumes that the CT value of each voxel may be analyzed as a composition of two materials. When you select this method, two vector lines, blue and yellow, are displayed on the Energy Map. You should position these two vector lines on the corresponding material axis which represents the “pure” behavior of the two chosen materials.



The CT value of each voxel is seen as a vector summation of two vectors along those basic directions, as shown in the “Material Specific Base Projection Method” diagram below, which shows parallel projections in (E1,E2) plane.



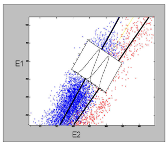
$$\begin{aligned}\vec{X} &= \vec{E1} + \vec{E2}\\ &= E1\,\vec{1}_{E1} + E2\,\vec{1}_{E2}\\ &= \vec{\alpha} + \vec{\beta}\\ &= \alpha\,\vec{1}_{\alpha} + \beta\,\vec{1}_{\beta}\end{aligned}$$

The coordinates **α**, **β** of the two vectors along the basic directions represent the concentration of each material in the corresponding voxel. To view material-specific images that correspond to the coordinates **α** and **β**, click **Show Tissue 1 Map** and **Show Tissue 2 Map**, respectively.

Changing Vector Parameters

- **Meeting point.** The blue and yellow vector lines are tied together and define the meeting point of the Energy Map. You can change meeting point location by selecting one of the following parameters:
  - **Water.** The vector lines are tied in water reading (0,0).
  - **Air.** The vector lines are tied in air reading (-1000,-1000).
  - **User Defined.** You can change the meeting point to any desired coordinate value.
- **Threshold** in the Vector method works the same as it does in the Graph method. But, unlike in the Graph method, the purple line is not tied to the meeting point.

Probabilistic Separation



The Probabilistic Separation method uses a statistical model to separate between two materials. An advantage to the Probabilistic method is that it gives not only a binary separation, but also quantitative assessment of its statistical signification. When using this model, the separation is adaptive to the local structure of the volume, which enables advanced non-linear classifications. The output of this method is an estimate of the probability that each voxel is either material 1or material 2. When you select this method, two vector lines, blue and yellow, are displayed on the Energy Map (the same as in the Vectors method). Each line represents the “pure” behavior of the two materials. You can change the location of the two lines. Note the illustration of the Probability estimate method, showing the fitting of mixture Gaussian model to the measurements.

	Probabilistic Parameters
Meeting point	The Probabilistic meeting point operates the same as it does in the Vector separation method.
Noise level	This HU value defines the mean noise standard deviation of the study (according to the average between the standard deviation of the low and the high energy images). Sigma may be adjusted from 0.1-80
Threshold	Threshold in the Probabilistic method works the same as it does in the Graph and Vector methods. Unlike in the Graph method, the purple line is not tied to the meeting point.

Segmentation Stage

The Segmentation scene allows the viewing and analysis of the spectral tissues which were created in stage two. The tissues are available from within the tissue management tab. Also in the tissue management tab are tools for manual editing of the tissues.

Function Tabs in Segmentation

The Segmentation stage is based on the CT Viewer - Volume mode application.

Tissue Management Functions

Tissue management tab displays the list of tissues of the active series. Use it to control display of tissues. Spectral tissues which were created in the second stage appear as Tissue 1, Tissue 2, etc. in the tissue list. Couch “tissue” is automatically created and the couch is removed from the image.

Functions Useful in Analysis Segmentation

Change color of active tissue.

Change the volume rendering protocol of active tissue.

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Remove residuals (as in CT Viewer). Useful to clean the tissues and remove unwanted remnants.

Perform clipping of the active tissue.

Expand / erode the active tissue.

Reset the active tissue to the same settings it had when it was created in stage 2.

Saving the tissues is done from the Save results button.

See **Report**, **Film**, **CT Common Processes** and **CT Common Tools** for information on using common options, tools, functions, and processes.
