Color Look Up Table

When you display a series in the 2D Viewer, a CLUT to the pixel data. A CLUT is short for Color Look Up Table. The default CLUT is Black & White (also referred to as No CLUT), which will match black to low intensity pixels, white to high intensity pixels and different levels of grays for the pixel intensities in between. A CLUT table is coded on 8-bit values from 0 to 255. It is applied on the 8-bit image, after the WL/WW are applied. You can also display a color bar on the right of the image to show the colors assigned to each pixel intensity (Fig. 6.54). You can show or hide this bar selecting or deselecting 2D Viewer >Color Look Up Table Bar.

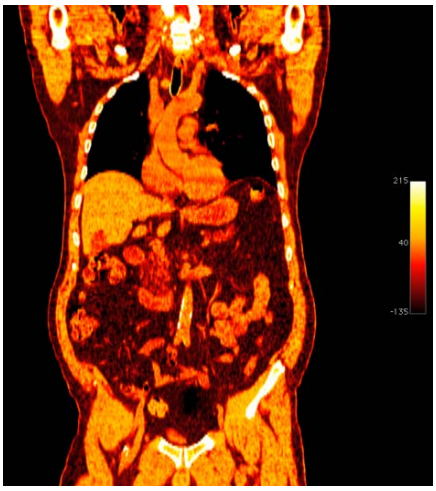


Figure 6.54. The CLUT Bar on the right displays pixel intensities for the Muscles and Bones CLUT.

You can choose from a variety of preset CLUTs (Figure 6.55) by clicking on the CLUT dropdown list in the WL/WW & CLUT tool in the toolbar. Alternatively, you can access the CLUT list by 2D Viewer > Color Look Up Table. Because CLUTs simply assign a new color value to the pixel intensity there is rule for which CLUT to use other than user preference. However, PET series are displayed by default with the B/WW Inverse CLUT or when fused with the PET CLUT. You can change these settings in the PET Preferences (See Chapter 2).

Figure 6.55. The options for preset CLUTS from the WW/WL &CLUT dropdown list in the toolbar.

The following CLUTs are available:

CLUT Name	*0* *255*
No CLUT	
BW Inverse	
BlackBody	
Endoscopy	
Flow	
GEColor	
GrayRainbow	
HotGreen	
HotIron	
HotMetal	
Hue1	
Hue2	
Ired	
Jet	
NIH	
PET	
Rainbow	
Rainbow2	
Rainbow3	
Ratio	
Spectrum	
Stern	
UCLA	
VR Bones	
VR Muscles-Bones	
VR Red Vessels	

Figure 6.56

Navigator

Clicking on the Navigator button (assuming you have added it to your toolbar) displays the Navigator Panel, under the 2D Viewer window. The Navigator panel shows all the images in a series as thumbnails in a single row. If the current 2D Viewer window contains a 4D series, the 4th dimension series will each be displayed in a separate row (Figure 6.57). This panel allows you to quickly review the entire series. You can apply the same shortcut keys and functions to each thumbnail image, for pan, zoom, window levels, and the like.

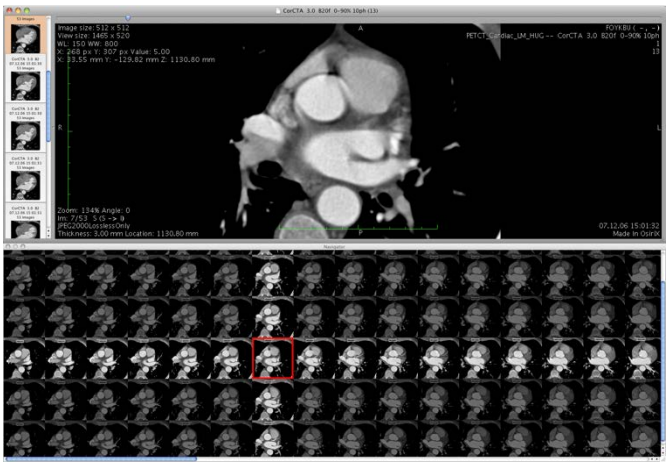


Figure 6.57. The Navigator Panel displayed for a 4D dataset.

Image Subtraction

Digital angiography and some other imaging modes benefit from subtracting a mask image that removes those parts of the image that do not change over time (DSA or Digital Subtraction Angiography). In digital subtraction angiography, for example, the mask is an image taken prior to the injection of a contrast agent administered via a catheter. If the mask is chosen to reflect a loss of contrast material, the subtracted images may appear white, whereas if the mask was chosen to reflected an increase in contrast agent, then the subtracted images will appear dark. Unchanged areas in the images will remain gray.

The dynamic subtraction tool is available from the Format > Custom Toolbar in the Horos menu (Figure 6.58) or from the Horos 2D Viewer menu. This technique takes the numeric value of pixels from one image (the mask) and subtracts them from the remaining images.

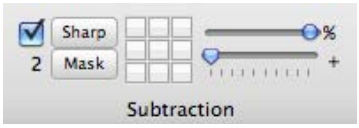


Figure 6.58. The Subtraction tool options.

You can use the subtraction tool to adjust the parameters of the subtraction function. Once you are at the image slice you wish to use as the mask image, go to 2D viewer in the Horos menu and select Subtraction > New Mask from the dropdown list (Figure 6.59). If the Subtraction tool is in your toolbar click on the mask button. This image will then be dynamically subtracted from the remaining images in the series. Pressing the spacebar will display the images in a looped movie with the mask subtracted. To turn on and off the subtraction feature simply click on the on/off checkbox. You can also adjust the percent of subtraction using the small slider at the top of the Subtraction tool. The lower slider bar changes the number of frames to add to the mask. The 3 x 3 boxes shift pixels north, east, south ,or west. These pixel shift options are also available from the 2D Viewer dropdown list (Figure 6.59). An example of a digital subtraction angiogram is shown in Figure 6.60.

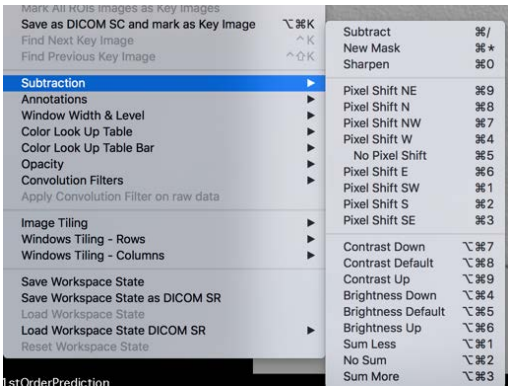


Figure 6.59. The Subtraction options from the 2D Viewer menu list.

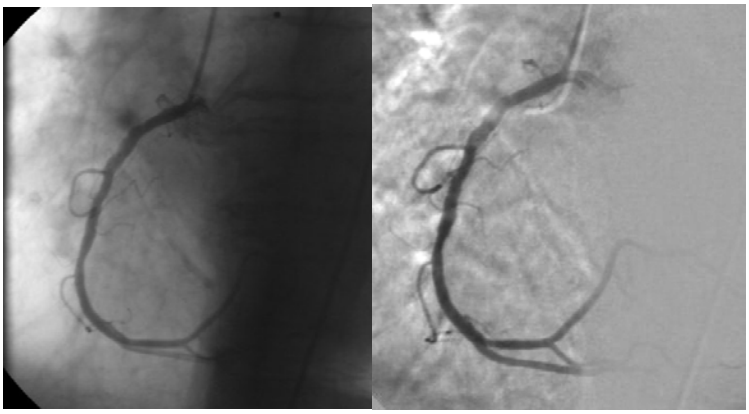
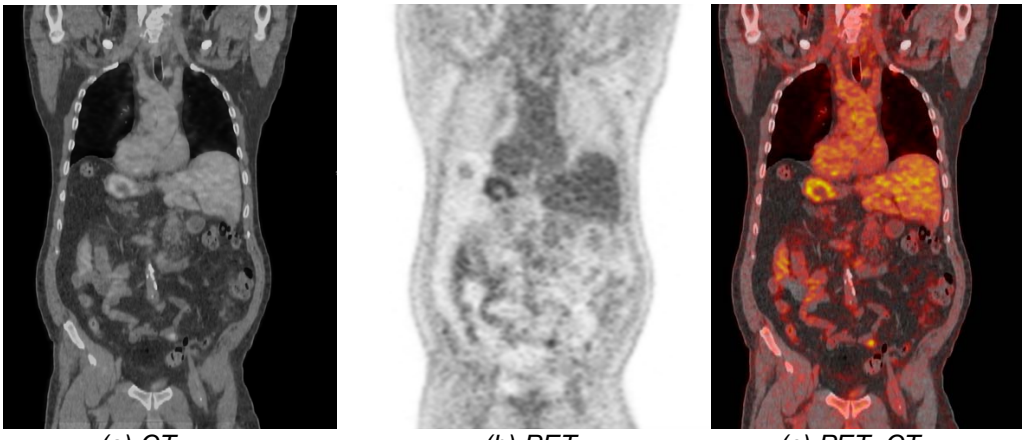


Figure 6.60 An image before (left) and after (right) subtraction.

Image Fusion

Positron emission tomography (PET) generates images of metabolic processes that are clinically useful in detecting cancer and other pathological processes. However, PET images are relatively noisy making small tumors difficult to detect. By fusing a metabolic PET series with a higher resolution CT series, you can precisely register regions of high metabolic activity (Figure 6.61).


(a) CT *(b) PET* *(c) PET–CT*
Figure 6.61 Fusion of the PET on the CT

You can fuse any series with another so long as both share the same dimensions. For example, you can fuse two 2D series or two 3D series, but not a 2D series with a 3D series. Likewise, a CR cannot be fused on a CT.

Open two series from the same patient, one a CT and the other a PET. Click and hold down the mouse on the title of one of the series (PET in this example) until a small icon with the series tile appears. Drag and drop this icon onto the other series (Figure 6.62). A popup window appears (Fig.6.63) giving you the choice to resample, reorient, or register the two image series.

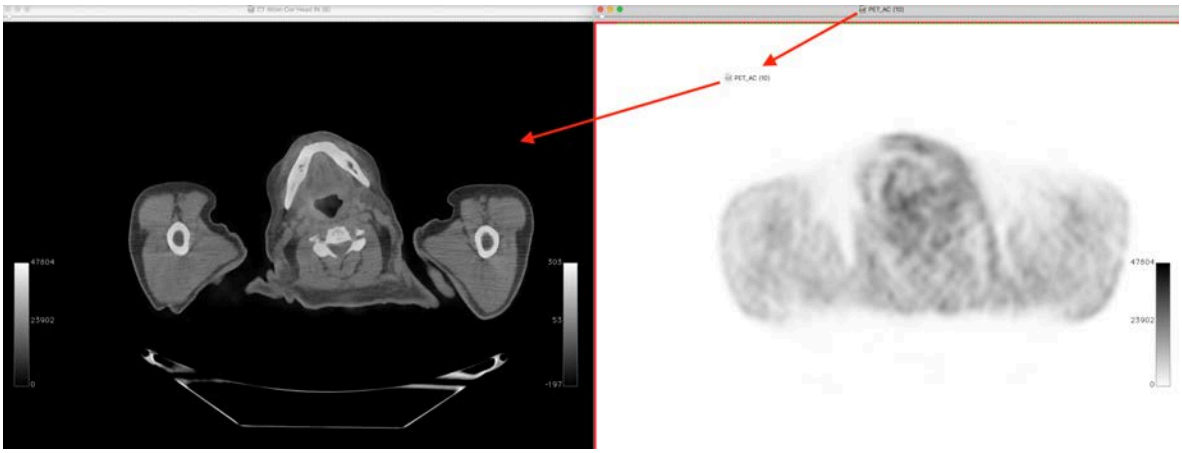


Figure 6.62. Drag and drop the icon from one window to another.

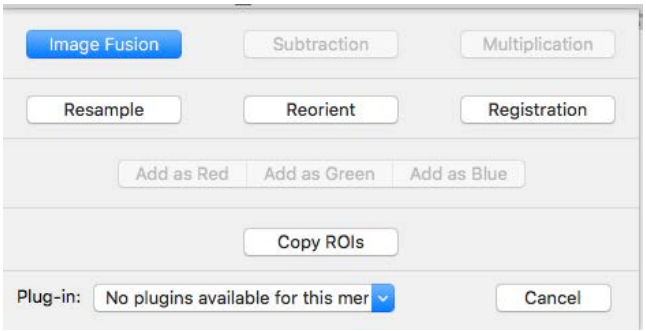


Figure 6.63. The image fusion popup window.

Horos will automatically fuse the PET-CT or SPECT-CT studies when both are open as long as both series are part of the same study. Automatic fusing can be turned on or off in the PET Preferences or using the Fuse/De–Fuse PET/SPECT – CT option from the 2D Viewer menu (⇧ ⌘ F shortcut).

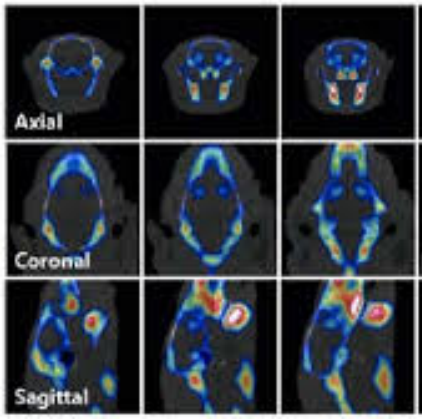


Figure 6.64. A PET–CT study in three planes.

3D Position

Occasionally, the fused images are misaligned. You can manually correct the alignment using the 3D Position tool found in the 2D Viewer menu (Figure 6.65). The 3D Position tool allows you to nudge the two image stacks up, down, left and right by clicking on the arrows or by clicking and holding the thumbnail icon in the middle. These adjustments can be made in the axial, coronal and sagittal planes by selecting the plane from the list on the left.

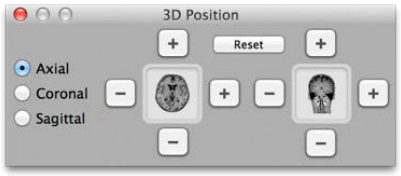


Figure 6.65. The 3D Position Panel

Series Registration

You use the 3D Position Panel (Figure 6.65) to register two 3D datasets along the orthogonal axis. However, sometimes you may need to scale and rotate images to properly register two 3D datasets (i.e., when registering a coronal MR series with an axial CT series).

Horos allows you to use a point-based registration algorithm, based on Horn registration algorithm [6]. You can do this by selecting the Point ROI tool from the Mouse button function too in the toolbar. Then click on matched pairs of points in each of the series. Be careful to ensure that the label of the point in one series matches the same point in the other image series. Each pair of points will be assigned sequential numbers as they are added.

Three pairs of points are needed to realign one image set over another. This technique uses a rigid registration method; it that applies scaling, rotation and translation transforms, but not warping or local image deformations to match the selected points. The point-based registration uses a transformation matrix computed via the Horn registration algorithm [6].

To complete the point-based registration, drag and drop one series over the other (as described above, grab the small icon located on top of its window and drop it onto the target series window). When the image fusion dialog box appears (Figure 6.66), press the Point-Based Registration button to realign the series using the 3D point ROIs you selected.

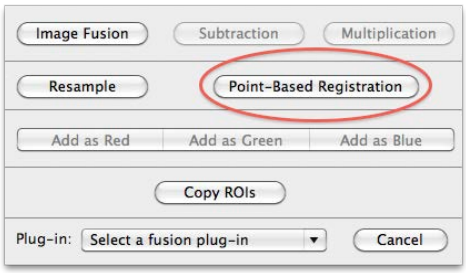


Figure 6.66 The Point-Based Registration function.

Image Stitching

Studies often come with different image series covering different parts of the body (i.e. a thoracic series and an abdominal series. In Horos, you can use the image fusion tool to stitch multiple series into a single larger image (Figure 6.67). Image stitching is particularly useful for viewing merged series in coronal or sagittal views.

To merge a thoracic MR with an abdominal MR drag and drop the thoracic MR series onto the abdominal series as described above for image fusion. Then select Flatten Fused Images from the 2D Viewer Menu. The raw data for the thoracic MR and the abdominal MR are now merged and can be processed as any other 3D dataset. For example, you can apply MPR or save it as a new 3D series in the database. Planar CT images can also be merged.

You may need to crop the original images using the shutter too if the image intensities of the two series are very different. This avoids edges caused by intensity differences.

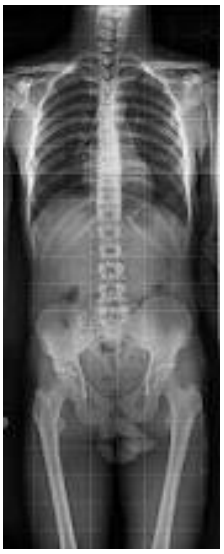


Figure 6.67. Image Stitching.

Annotations

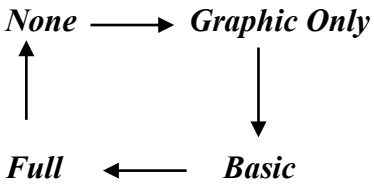
The 2D Viewer displays several annotations on the image, including:

- *Textual labels (WL/WW, zoom, patient name...)*
- *ROIs*
- *CLUT bar*
- *Cross Reference Lines*
- *Scale bars*

You can hide some or all of the annotations by selecting Annotations from the 2D Viewer menu. The options are:

- ***None*** — only the image is displayed
- ***Graphics Only*** — no textual label is displayed
- ***Basic*** — all textual labels are displayed, except the patient name.
- ***Full*** — all textual labels are displayed
- ***Plugin Only*** — some plugins can display information on the image.

You can also activate these annotation options using the tab key on the keyboard. Pressing the tab key sequentially changes the option in a cyclical manner. For example, if the current state is None, pressing the tab key will switch the state to Graphics Only. Pressing tab again switches the state from Graphics only to Basic, pressing tab a third time switches the state from Basic to Full annotation, and pressing tab a fourth time cycles the annotation state back to None. The tab key does not activate the Plugin Only state.



The Annotations > Display Cross Reference Lines item in the 2D Viewer list also allows you to display or to hide the cross-reference lines. Selecting Color Look Up Table Bar from the 2D Viewer list toggles on or off the CLUT bars.

You can modify textual annotations to display any DICOM or database fields. For example, you can display mAs and KV for a CT study or the MR sequence for a MR study. You can also modify font size and typeface for textual annotations using Format > Font.

Shutter Tool

You can reduce the size of the displayed area (without deleting any original data) using the shutter tool (Figure 6.68). The shutter tool is available from the custom tools using Format > Custom tools in the 2D Viewer menu. To use the shutter tool, first choose the Rectangle ROI

tool from the mouse button items and draw a rectangle enclosing the area you want to keep. Clicking on the shutter tool icon makes everything outside the rectangle black.

Figure 6.68. The shutter tool icon from the custom tools.

Convolution Filters

Images can be enhanced by image processing using pre-configured filters to smooth, blur, sharpen, etc. These filters operate in the same way as filters in Photoshop or Gimp. Each filter uses a 3 x 3 or 5 x 5 matrix of pixels. The filter takes the original value of each pixel in the matrix and multiplies it by the corresponding value in the kernel (an array of numeric values). For example, suppose you have an image with the intensity values (from 0 -255 in gray scale) shown on the left in Figure 6.69. The central pixel has an initial value of 94. The filter will multiply the initial pixel value of 94 and its 8 surrounding neighbors by the values in the 3 x 3 kernel (shown in the center of Figure 6.69. The filter will begin in the upper left corner with pixel 140, work across the top row, then jump back to the left side of the middle row and continue until it reaches pixel 81 in the lower right. Thus, the central pixel with an initial value of 94 will become a pixel with a filtered value of 9 because (140 x 0) + (151 x $^{-}$1) + (156 x 0) + (104 x $^{-}$1) + (94 x 5) + (103 x $^{-}$1) + (119 x 0) + (103 x $^{-}$1) + (81 x 0) = 9. The filter actually works on a copy of the image so the original data is preserved. The kernel of the filter, is an array of numeric values, which in this case is the sharpen kernel.

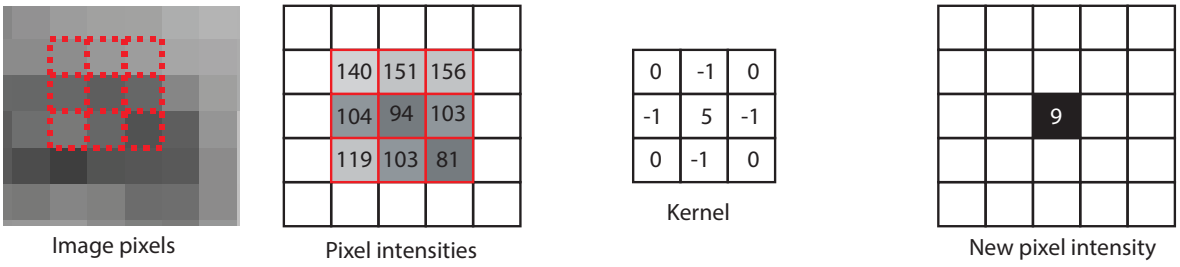


Figure 6.69. Convolution filers using the sharpen kernel.

In general terms, let A(m,n) be the pixels matrix of an image of size m × n: