The Compute volume tool uses the areas of all the selected ROIs of the same name along with the slice thickness of the series to estimate a volume. The Compute Volume option only works with polygon, brush, and pencil ROIs. Importantly, this tool only uses ROIs of the same name.

The ROI Volume popup window (Figure 6.88) displays the 3D volume along with several options. You can choose to display the 3D Volume as a wireframe, change its color, toggle texture on and off, and modify the volume's opacity. In addition, you can choose from three reconstruction filters, power crust (default), Delaunay, and iso contour. You will see the statistics associated with the 3D Volume on the right side of the ROI Volume window. These include the volume in cm^3. Finally, you can choose to save the 3D volume image as a DICOM file.

You can create ROIs for every slice in the series where a structure of interest appears (i.e. a tumor), or you can let Horos do some of the ROI creation for you. Suppose you creates an ROI for every third slice in the series. You can choose the ROI Volume > Generate Missing ROIs option from the ROI menu and Horos will automatically generate ROIs for the skipped slices. Horos uses a morphing algorithm based on the ROIs on either slide to fill in the missing ROIs. You should check them to see how accurate they are. If you need to modify one of the automatically generated ROIs you can do so using the repulsor ROI tool. The automatically generated ROIs contain the comment "morphing generated". You can delete only the automatically generated ROIs using the ROI Volume > Delete Generated ROIs option in the ROI menu.

 Angle of Cobb

The Angle tool in the ROI dropdown list is useful for measuring simple angles between two lines. However, it may not be appropriate for measuring the angle of Cobb. The Cobb method is frequently used to measure the degree of scoliosis or other vertebral column abnormalities. The angle of Cobb is the angle formed between a line drawn parallel to the superior surface of a <u>vertebra</u> above a spine deformity and a second line drawn parallel to the inferior surface of a vertebra below the deformity (Figure 6.89).
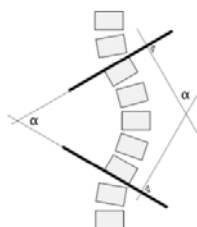

Figure 6.89. The angle of Cobb (represented by α).

To compute the Cobb angle, Select the Line ROI tool and draw two lines on the image. Horos displays the length of each line in cm or pixels, but not an angle. You can have Horos compute and display the Cobb angle by using the Cobb Angle tool in the Custom toolbar. Click on the

Cobb tool and then select one line. This line will be highlight it in yellow and angle of Cobb is displayed in the other line's info box (Figure 6.90). If more than two lines are drawn on the image, each line will display the Cobb angle relative to the selected line. When Cobb angle is activated it stays active until it is de-activated by clicking the Cobb tool in the toolbar a second time.
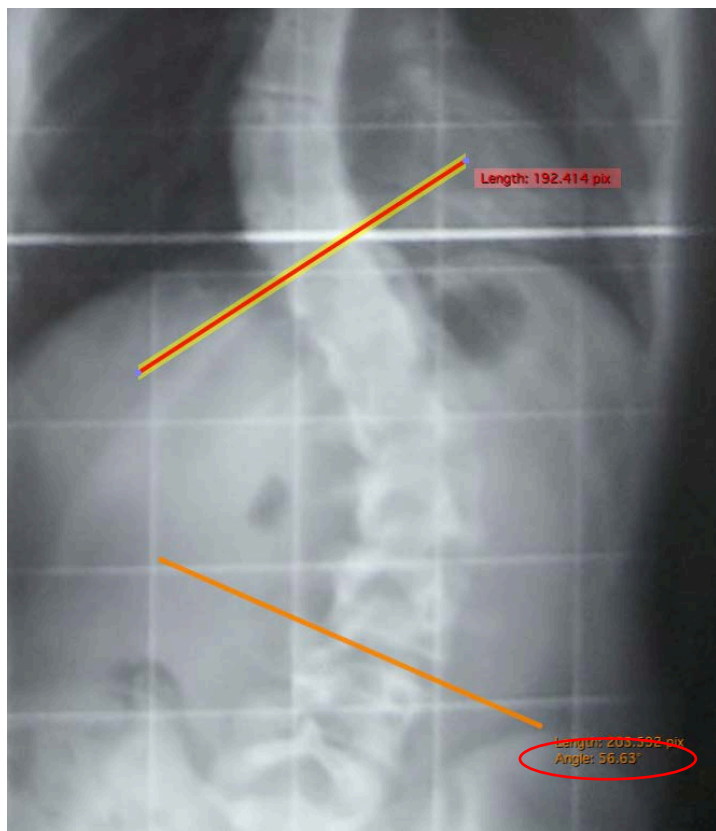

Figure 6.90. Cobb's Angle as displayed in Horos (circled).

Region Growing

Region growing algorithms begin from a seed region (typically one or more pixels) located inside the object to be segmented. The seed pixel's neighbors are then evaluated to determine if they should be considered part of the object. If they are considered part of the object, they are added to the region and the region grows. This process continues as long as there are new pixels to be added to the region. Because the process is iterative, the region grows according to a set of parameters set by the user. In medical imaging, image segmentation is often used to generate 3D reconstructions.

The Region Growing tool in Horos supports 2D and 3D black and white images (RGB images are not supported) and is based on the ITK toolkit.

You begin by clicking on the optional Growing tool from the 2D Viewer toolbar (Figure 6.91). This tool is found in Format > Custom Tools in the 2D Viewer menu. Alternatively, you can choose ROI > Grow Region (2D/3D Segmentation) from the 2d Viewer menu. This brings up the Segmentation Parameters popup window (Figure 6.92). Click on a point on the image that you wish to use as a seed point. A 2D preview is computed and displayed (based on the default parameters) with the segmented region in green (Figure 6.93).
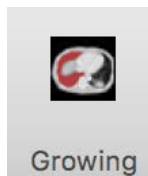

Figure 6.91. The Region Growing tool from the list of custom tools.
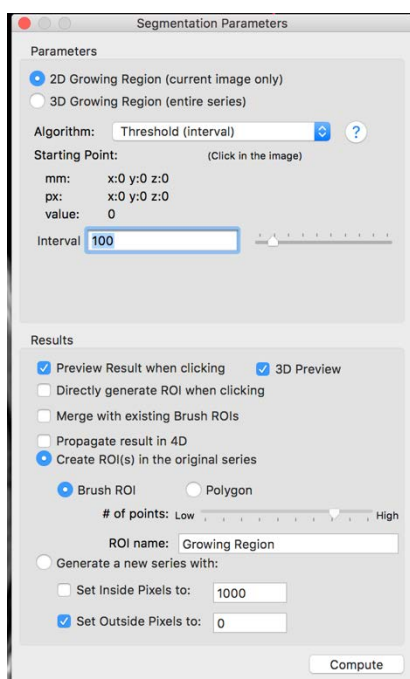

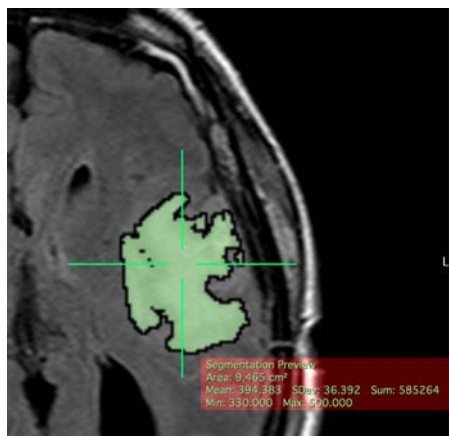Figure 6.92. The Segmentation Parameters popup window.

Figure 6.93. The segmentation preview of a brain tumor seeded by a single point (at the cross hairs).

You can adjust the green segmentation area on the 2D image using the interval slider in the segmentation parameters window. You can generate the final segmentation by clicking the Compute button at the bottom of the segmentation parameters popup window. Note that the preview segmentation is a 2D image only. The final segmentation is 3D and can look quite different if there are many connections among neighboring pixels in other images in the series. Remember that a 3D Region Growing that involves a large series of images may take some time to compute. The final region can be displayed as a brush ROI or a polygon ROI and can be edited in each slice using the ROI tools.

You can also create a mask series using the Generate a new series option at the bottom of the parameters window (figure 6.94). By also changing the pixel values in the Set Outside Pixel Values (or Set Inside Piexl Values if that box is checked), you can change the pixel intensity of the ROI.
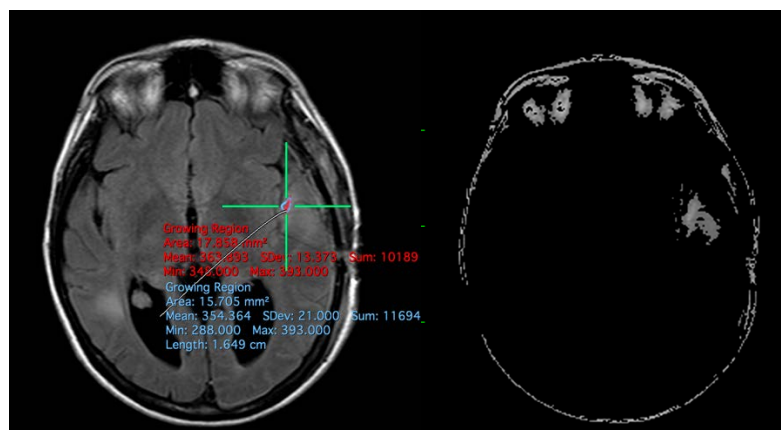

Figure 6.94. The image on the right is the mask generated from the 3D growing region on the left.

Horos implements four Region Growing algorithms. The two threshold algorithms consider only the value of the pixel itself. If the pixel's value is within the interval it is included in the region, otherwise it is omitted. In contrast, neighborhood algorithms consider a defined neighborhood surrounding the pixel and require each neighbor pixel intensity to within the interval for inclusion in the region. Neighborhood algorithms makes it less likely that small structures will be included in the region.

> *Threshold (interval)* – Uses the seed point intensity to generate a connected set of pixels whose intensities are within the defined interval.

> *Threshold (lower/upper bounds)* - Extracts a connected set of pixels whose intensities are within the defined upper and lower threshold values.

> *Neighborhood* - Only accepts a pixel if all its neighbors have intensities that fit in the interval. Neighborhood size is defined by the integer radius provided by the user.

> *Confidence* - Extracts a connected set of pixels whose pixel intensities are consistent with the pixel statistics of the seed point. The algorithm first calculates the mean and

standard deviation of intensity values for the seed point(s). It then uses a multiplier (set by the user) to generate a range and groups those pixels connected to the seed point that also fall with this range. The range is the mean plus or minus the multiplier times the standard deviation. The algorithm next re-calculates the mean and standard deviation for this new set of connected pixels and the iterative process repeats until no additional pixels can be added to the region, or the maximum number of iterations is reached.

Note that a multiplier of 2.5 would define a range wide enough to include 99% of the samples in the segment if the segment were Gaussian.

You can calculate the volume of a structure using the Region Growing tool. For example, you can use the region growing tool on a brain tumor by using a 3D ROI and then use ROI Volume > Compute Volume from the ROI menu.

Set Pixels Values

Pixel intensity can be changed using the Set Pixel Values popup window from the ROI menu in the 2D viewer (Figure 6.95). You can choose to modify pixel intensities for all pixels in the series, all pixels in ROIs with the same name, or all pixels in all ROIs. Furthermore, you can choose to modify pixels inside the ROIs or only the pixels outside the ROIs. Finally, you can set an upper and lower threshold to modify only those pixels within the threshold range. The original pixels are saved and can be reloaded simply by choosing the Revert Series
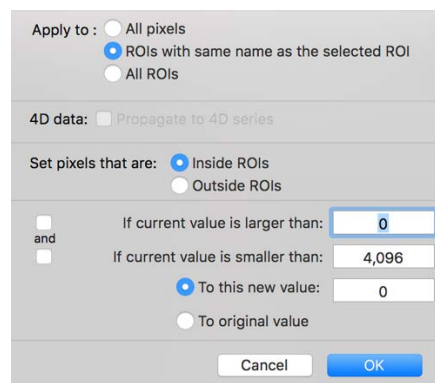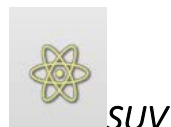

Figure 6.95. Set Pixels Values popup window.

You can reload the original pixels at any time by selecting Revert Series in 2D Viewer menu or by using its keyboard shortcut (⇧ ⌘ R).

 SUV

The SUV function is frequently used with PET series where a radioactive tracer, such as 2-deoxy-2-[^{18}F]fluoro-D-glucose (FDG), is used to mark the position of cancers. There are several ways to measure the rate of accumulation (or the total amount) of radioactive tracer in a tumor.

Usually, it is the relative uptake of tracer that is measured because it somewhat compensates form variation in the amount of tracer injected and the patient's body size.

The basic equation is:

$$SUV = \frac{tissue\ radioactivity\ concentration}{decay - corrected\ injected\ activity/body\ weight}$$

Note that Horos does not support SUVs adjusted for body surface area (SUV_{bsa}) or adjusted for lean body mass (SUV_{bm})

SUV is calculated as:

$$SUV_{bw} = \frac{Pix \cdot P_w}{C}$$

Where Pix is the pixel intensities from the ROI in the PET scan, P_w is the patient's body weight (g), and C is the corrected activity. Corrected activity (C) is calculated as:

$$C = T \cdot 2^{-\frac{t_S - t_M}{t_{1/2}}}$$

Where T is tracer activity, t_S is the scan time, t_M is the measured time for the activity dose, and $t_{1/2}$ is the half-life of the tracer.
SUV values are calculated from DICOM metadata fields for:

- weight = patient weight = Study Patient Weight (0x0010, 0x1010)
- height = patient height = Study Patient Size (0x0010, 0x1020)
- sex = patient sex = Study Patient Sex (0x0010, 0x0040)
- tracer_activity = Total Dose (0x0018, 0x1074)
- measured_time = Radio Pharmaceutical Start Time (0x0018, 0x1072)
- half_life = Radio Nuclide Half Life (0x0018, 0x1075)
- scan_time = Image Acquisition date and time, as defined in PET Preferences window (see 2.2.3.6)
- decay_factor=DecayFactor(0x0054,0x1321), used on Siemens PET studies to correct the final pixel value (according to beds acquisition time)

At the time of writing these values are valid for Siemens and GE PET studies. Phillips PET studies store a proprietary field (0x7053, 0x1000) which allows you to multiply pixel values by this field to obtain SUV values.

In Horos, you can convert between original and SUV values by clicking on the SUV icon from the toolbar (found in the Custom Toolbar options). This opens the SUV parameters window (Figure 6.96).
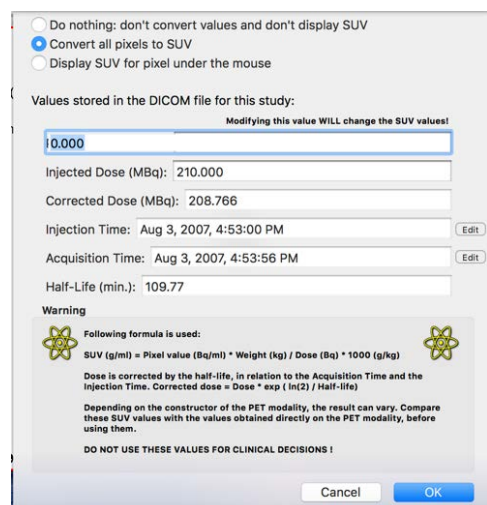
Figure 6.96. The SUV parameters popup window.

From the SUV parameters popup window you can choose to convert all pixel values to SUV, or convert only those pixels under the mouse to SUV (the SUV values displayed on the image change dynamically as you move the mouse).

The middle fields in the SUV parameters window allow you to check the values stored for:

> • *Patient's weight (in [kg])*
> • *Injected dose (in [MBq])*
> • *Corrected dose (in [MBq])*
> • *Injection time*
> • *Acquisition time*
> • *Half-life (in minutes)*

You can edit the following three values:

> • *Patient's weight (in [kg])*
> • *Injected dose (in [MBq])*
> • *Injection time*

You can automatically convert pixel values to SUV when loading a PET or a NM series by editing the PET Preferences (Figure 6.97) from the Horos Preferences.
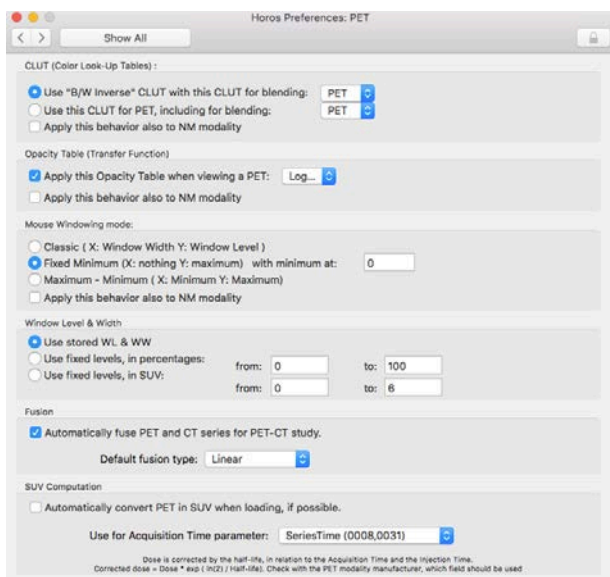
Figure 6.97. The PET Preferences window showing the automatic SUV conversion at the bottom.

Reconstruction Tools

There are eight possible reconstruction tools available for image stack loaded in the 2D Viewer (figure 6.98).
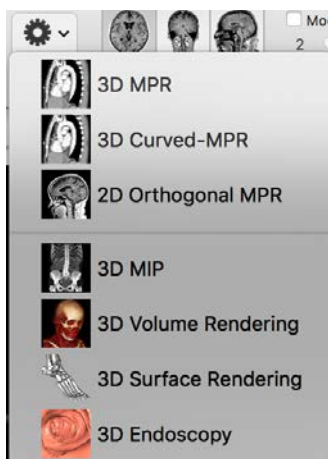

Figure 6.98. The 2D/3D reconstruction tools dropdown list from the 2D Viewer menu.

3DMPR

The 3D Multi-Planar Reconstruction is a technique used in 2D CT and MRI imaging to generate sagittal, coronal, and oblique views from axial sections (Figure 6.99). Multi-Planar images can be "thickened" into slabs and displayed as maximum intensity projections (MIP), minimum intensity projections (minIP), mean, and volume rendering projections (see Chapter 7).
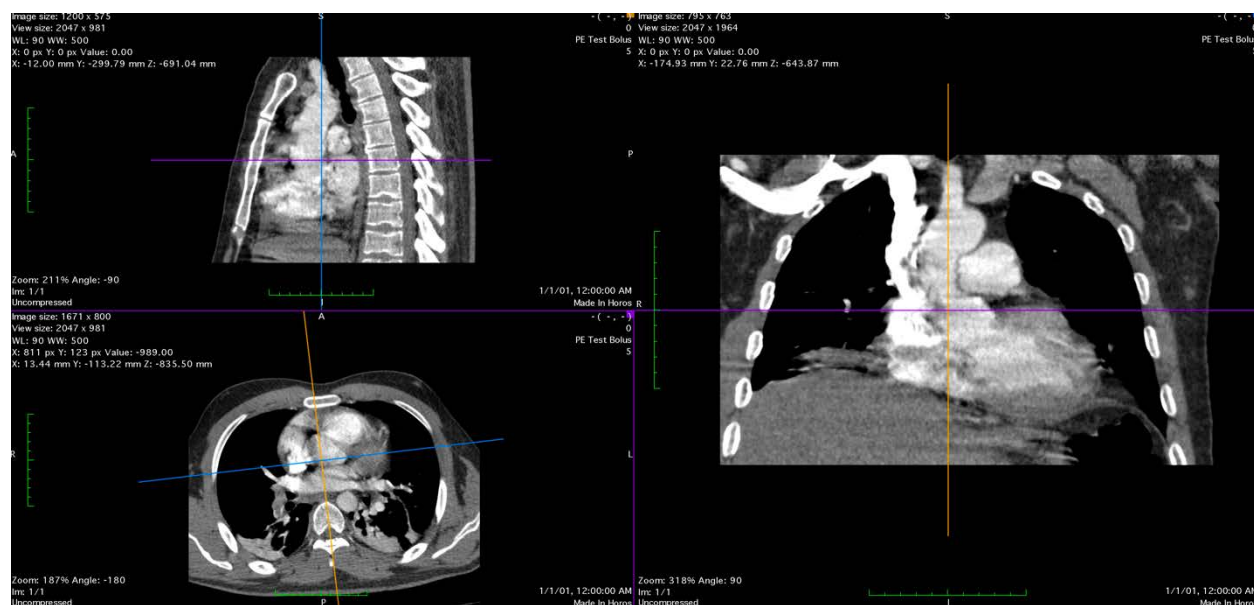
Figure 6.99. The 3D MPR windows.

2DCurved-MPR

The Curved MPR aligns the long axis of the image plane with a specific anatomic structure, such as a blood vessel or vertebral column, rather than with an arbitrary imaging plane (Figure 6.100).
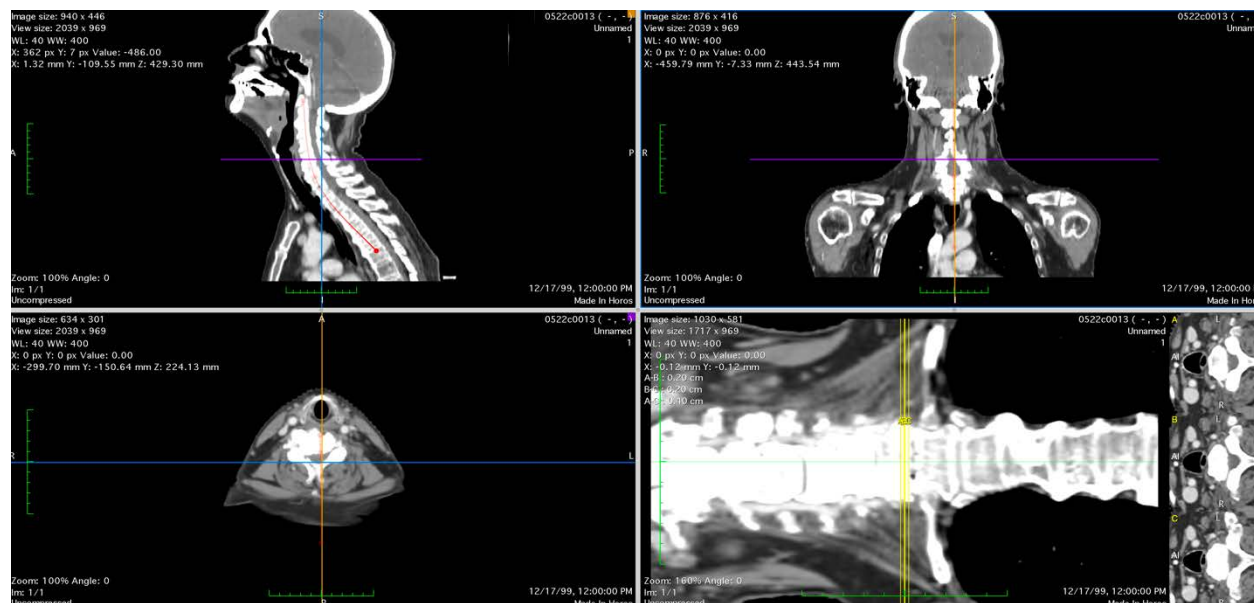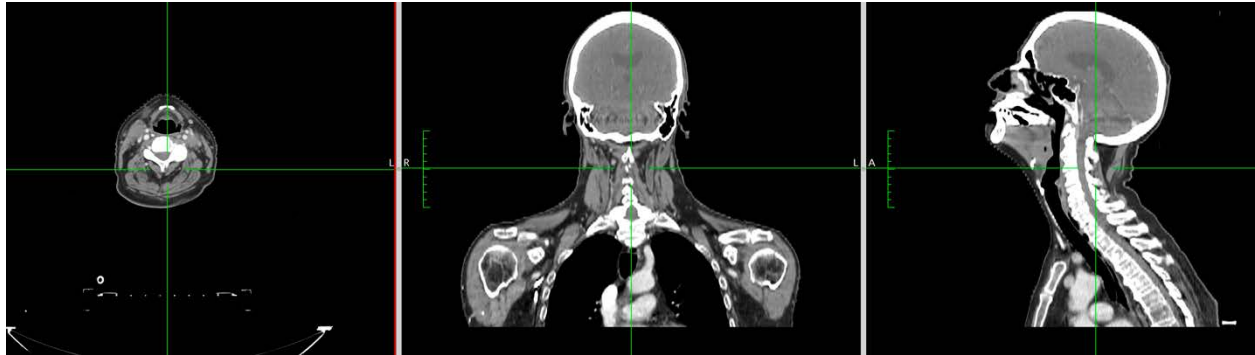

Figure 6.100. The 2D Curved MPR aligned along the vertebral column (red lines in upper left image).

2D Orthogonal MPR

You can reformat the image volume according to 3 orthogonal planes (Axial, Coronal and Sagittal) using the 2D Orthogonal MPR tool (Figure 6.101).

6.101. A 2D Orthogonal MPR.

3D MIP

This reconstruction creates a 3D Volume Rendering using maximum intensity projection (MIP, Figure 6.012).
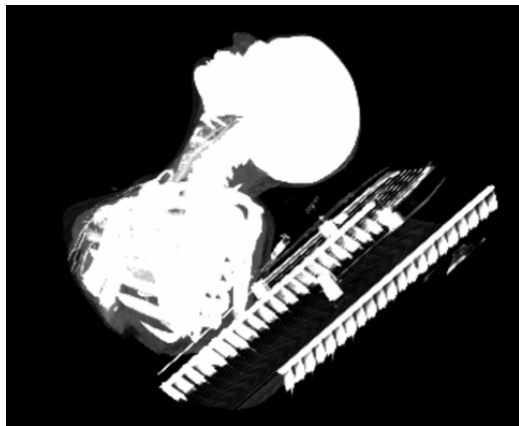

Figure 6.102. A 3D MIP of the same series used in Figure 6.101.

3D Volume Rendering

This tool renders the data using the 3D Volume Rendering (Figure 6.103) technique described in detail in Chapter 7.