

Process

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Introduction

The Process module provides access to image enhancement tools that allow data to be refined, such that image features can be seen easier or detection of regions is improved during segmentation.

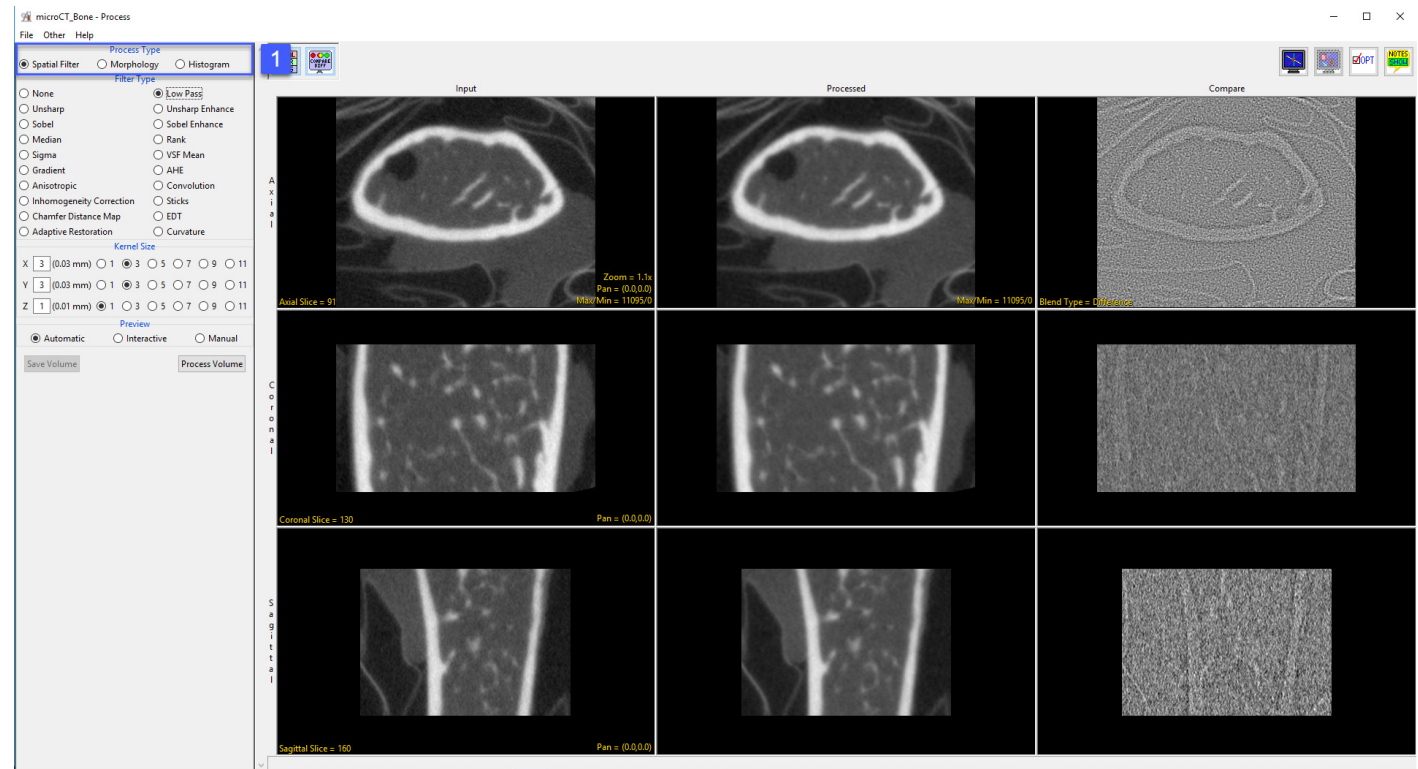
There are three main process functions [1] available:

Spatial Filters - for the filtering of image data to reduce image noise or increase contrast between structures of interest.

Morphology - mathematical segmentation operations for the pre-processing of image data for segmentation.

Histogram - for the modification of the image histogram to enhance image quality or enhance features.

All of these functions are used to prepare data for further segmentation and analysis.



Spatial Filters

There are 19 different spatial filters that can be applied to a data set. These are described in the table below. A filter can be applied to the entire volume or to selected objects if an object map is loaded.

Filter Type	Description	Method
Low Pass	dampens noise, smoothes volume	replaces the value of each voxel with the average value of the neighborhood*
Unsharp	eliminates homogeneous regions, highlights edges and noise	subtracts a low pass filtered volume from the original volume
Unsharp Enhance	combines unsharp with original volume	adds an unsharp filtered volume to the original volume
Sobel	highlights edges	performs a classic edge detection filter
Sobel Enhance	combines Sobel with original volume	adds a Sobel filtered volume to the original volume
Median	dampens noise, smoothes volume	replaces the value of each voxel with the average value of the neighborhood*
Rank	generic rank filter	orders all the values of voxels in the neighborhood* and returns the value corresponding to the rank in the ordered list†
Sigma	smoothes noise while preserving edges and thin lines	replaces the value x of each voxel with the average value of voxels in the neighborhood* having values of $x \pm 2\sigma$ ‡
VSF Mean	smoothes noise while preserving edges and thin lines	replaces the value x of each voxel with the average value of voxels in the neighborhood§ having values of $x \pm \sigma$
Gradient	highlights edges	replaces the value of each voxel with the maximum absolute difference between its value and that of its orthogonal neighbors



Filter Type	Description	Method
AHE	enhances contrast for viewing (not for measurement)	adjusts voxel values based on histogram of a localized region¶
Anisotropic	reduces noise while preserving edges	performs 2D affine, unbiased or biased anisotropic diffusion for the number of iterations and time per iteration specified
Convolution	smoothes noise, resulting in a blurry image	performs spatial convolution of volume with user-supplied point spread function
Inhomogeneity Correction	corrects low-frequency grayscale gradients	replaces voxel intensity with $I_i * \text{global mean} / \text{local mean}$, where I_i is the input voxel intensity
Sticks	suppresses noise while enhancing thin edges	applies directional masks and determines output based on Type parameter
Chamfer Distance Map	creates a map that may be used for shape recognition	calculates Chamfer distance of each voxel to nearest nonzero voxel
Euclidean Distance Transform	creates a map that may be used for shape recognition	calculates Euclidean distance of each voxel to nearest nonzero voxel
Adaptive Restoration	reduces noise using an adaptive method	degrades image by constant-power additive noise, then applies a low pass filter
Curvature	creates a map of instantaneous local surface curvature	sums binary voxel values in the 26-connected neighborhood of each voxel to give a curvature value from 0-26

*The neighborhood around each voxel is defined by the kernel dimensions selected in the Kernel Size options.

†The kernel size determines the number of voxels whose values are ranked, e.g. a 3 X 3 X 3 kernel has 27 voxels, a 5 X 5 X 5 kernel has 125 voxels and a 7 X 7 X 7 kernel has 343 voxels. The larger the kernel size, the more computationally intensive this filter becomes. It is recommended to use a smaller kernel size such as 3 X 3 X 3. In a 3 X 3 X 3 kernel, a rank of 1 would return the minimum value, a rank of 14 would return the median value and a rank of 27 would return the maximum value.

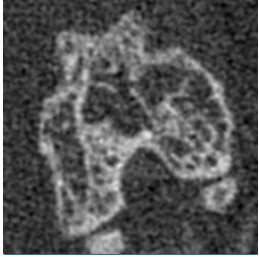
‡If fewer than 9% of the voxels in the kernel fall within the $x \pm 2\sigma$ range, the voxel in question will not be changed. Sigma (σ) is defined using the text box or slider bar.

§The circular neighborhood around each voxel is specified by the Ring parameter.

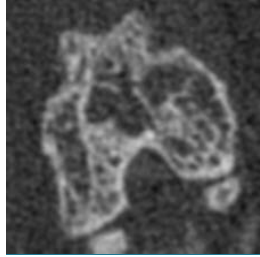
¶Clip Fraction — Specifies the limit of contribution of any given grayscale value, reducing the enhancement of noise in the resulting image or volume. This method is particularly effective for images which have subtle detail in both very bright and very dim regions of the image. It may also be used to expand the dynamic range of grayscale in a region which has subtle but significant changes.

||A value of 0.25 is recommended for general use and will be used as the default if the supplied value is zero or negative. However, a value of 0.10 or less is required to guarantee stable behavior. The lower value will require more iterations but should be used if absolutely correct results are essential. This option is only available when Type is set to Affine.

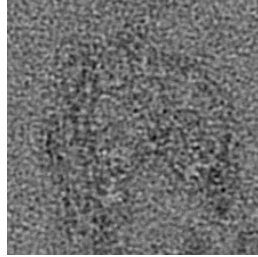
No Filter



Low Pass



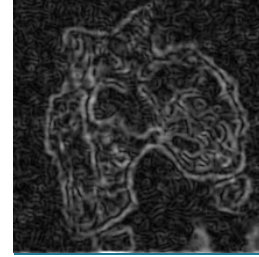
Unsharp



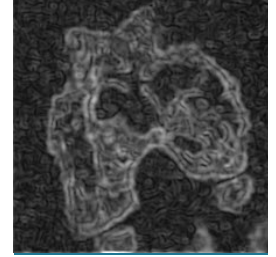
Unsharp Enhance



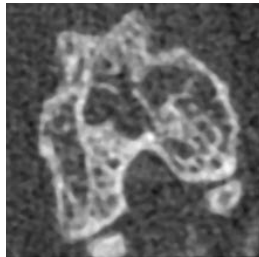
Sobel



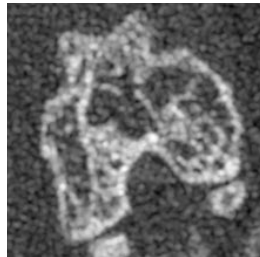
Sobel Enhance



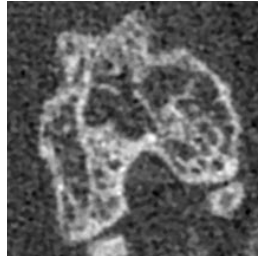
Median



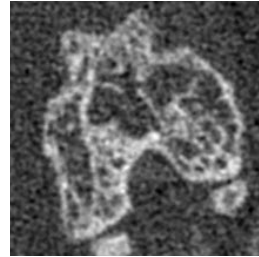
Rank



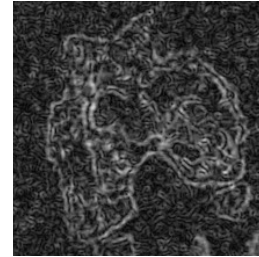
Sigma



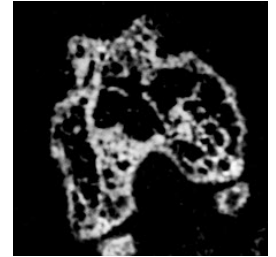
VSF Mean



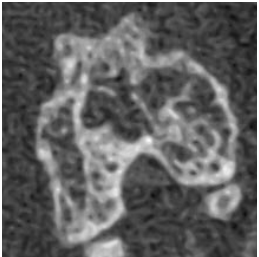
Gradient



AHE



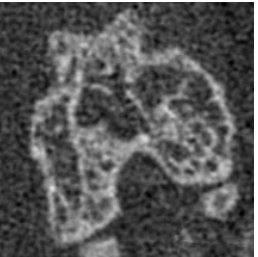
Anisotropic



Convolution



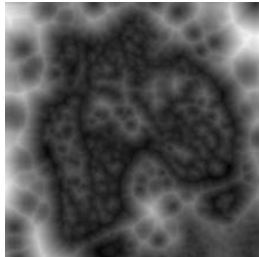
Inhomogeneity Correction



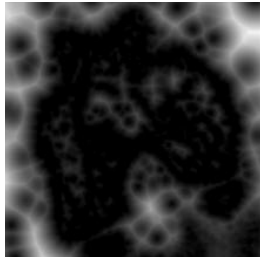
Sticks



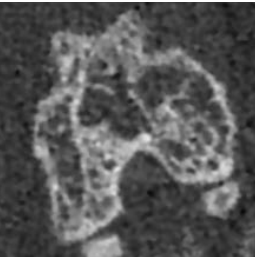
Chamfer Distance Map



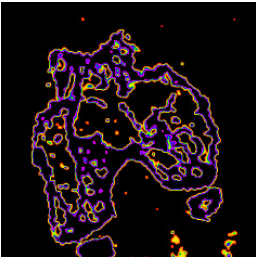
Euclidean Distance Map



Adaptive Restoration



Curvature



Applying a Filter to a Data Set

Download the microCT_Bone.avw data set to follow along, from <https://analyzedirect.com/data>.

This exercise will show how to apply a median filter to a microCT bone data set.

Use the Input/Output module to load the microCT_Bone.avw data set into the software.

Select the data set [1] and open Process [2].



Applying a Filter to a Data Set (continued)

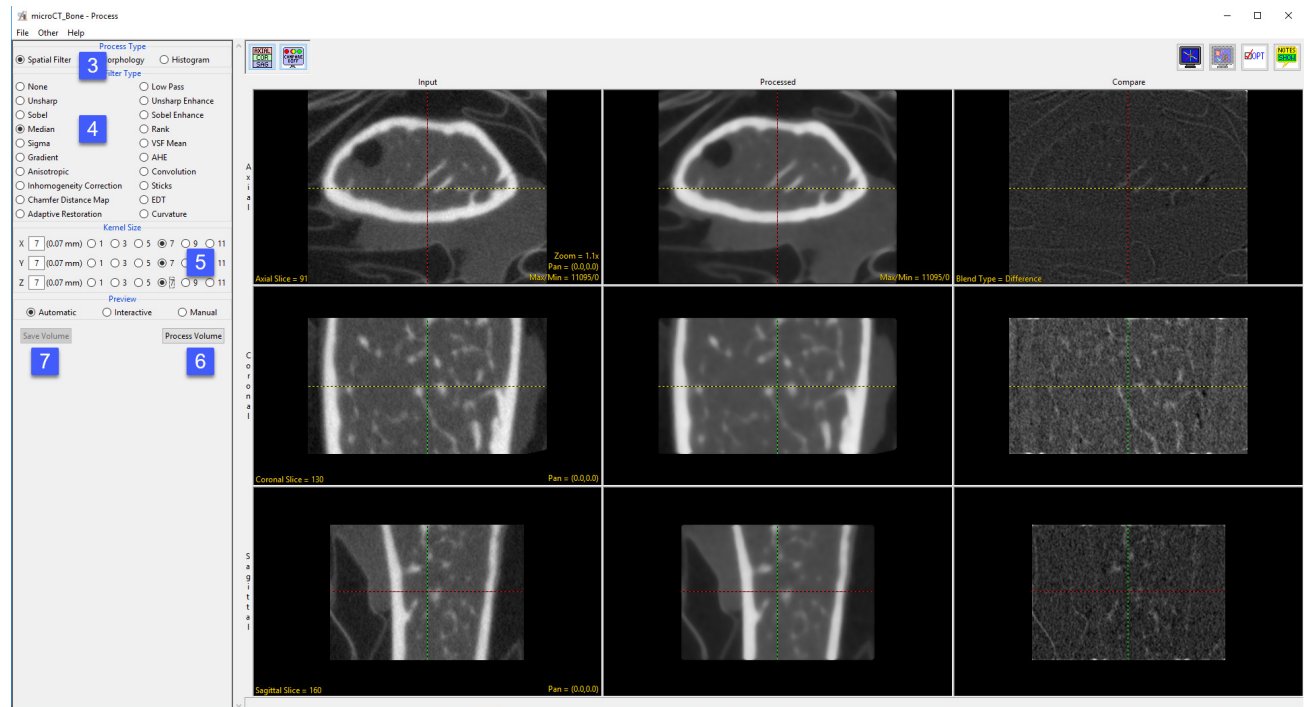
Choose Spatial Filter as the Process Type [3].

Choose a Filter Type [4]. Low Pass and Median filters are commonly used to smooth noisy data.

Set the Kernel Size in the X, Y and Z dimensions [5]. A kernel size of 7 X 7 X 7 is often used for microCT data acquired using a PerkinElmer scanner.

Click Process Volume [6].

Once the processing is complete, the Save Volume button will become available. Click Save Volume [7].

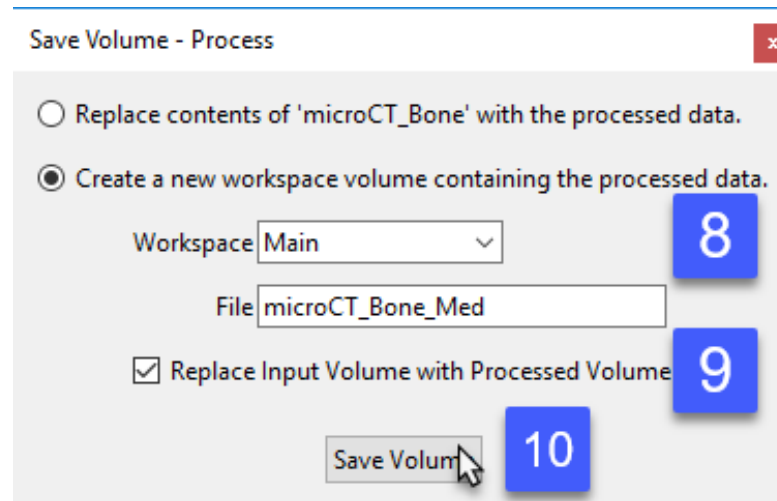


Applying a Filter to a Data Set (continued)

In the Save Volume window, choose to replace the input data set with the processed data set, or to create a new data set [8].

The new data set can be saved in any workspace in the current project and renamed in the File checkbox. Check the Replace Input Volume with Processed Volume box if you want to further process the processed volume [9].

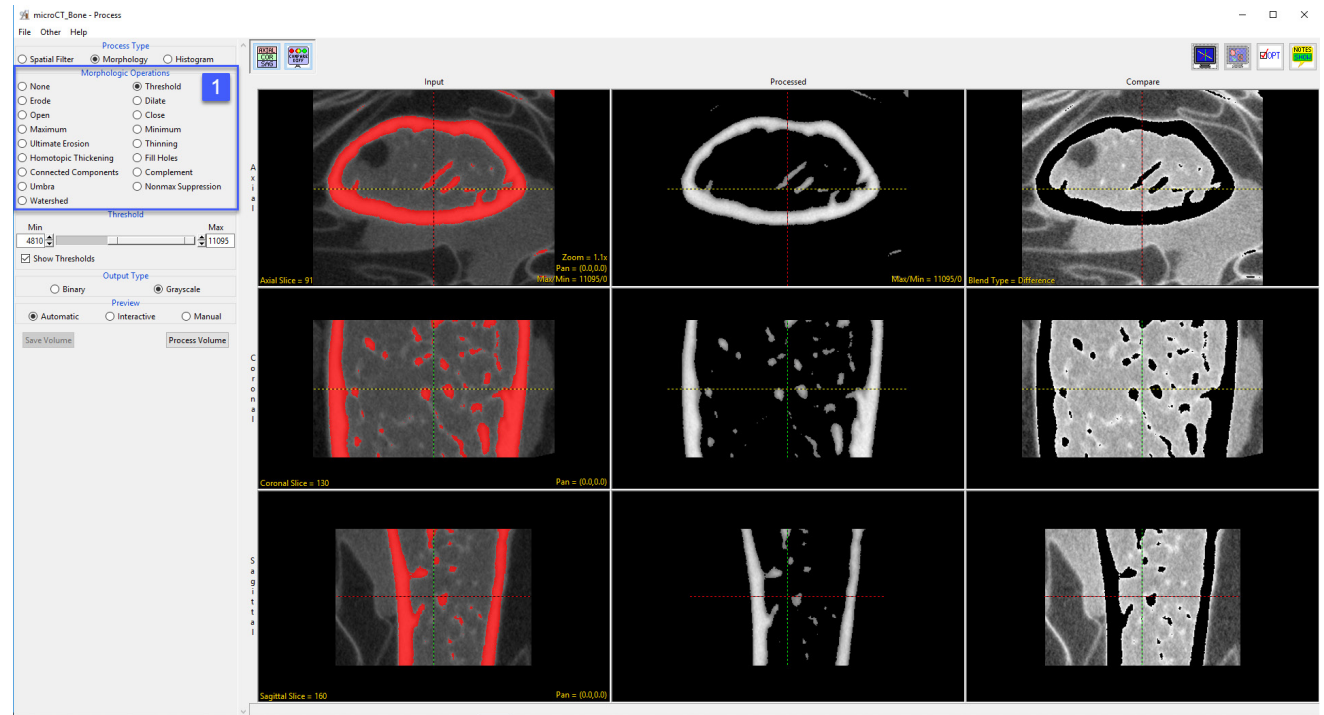
Click Save Volume [10].



Morphology

A number of morphologic operations are available [1], and these are described in the table on the next page.

These operations can be performed on the entire volume or on selected objects if an object map is loaded.



Available Morphological Operations

Morphologic Operation	Description	Method
Threshold	isolates structures defined by a difference in intensity	sets voxels between and equal to the specified maximum and minimum to 1 and all other voxels to 0
Erode	peels a layer from the outer edge of large objects and deletes small objects	retains voxels in inner areas of the object, as determined by the structuring element dimensions and shape
Dilate	expands small objects in a binary volume	adds voxels to outer areas of the object, as determined by the structuring element dimensions and shape
Open	removes small objects and breaks isthmuses	erosion followed by dilation
Close	fills thin gulfs and small holes	dilation followed by erosion
Maximum	emphasizes high-intensity regions	grayscale equivalent of binary dilation
Minimum	emphasizes low-intensity regions	grayscale equivalent of binary erosion
Ultimate Erosion	shows the last voxels remaining of disconnected components	performs successive erosions on the object until the last erosion before the components would disappear
Thinning	thins an object in binary or grayscale	thins the object based on the number of iterations specified, using template matching
Homotopic Thickening	thickens an object in binary or grayscale	thickens the object based on the number of iterations specified
Fill Holes	fills holes in a volume	fills holes in 2D or 3D, based on the connectivity value chosen
Connected Components	finds connected regions in a volume	performs a 2D or 3D connected component analysis
Complement	generates inverse of an image	generates the binary or grayscale complement of the image
Umbra	darkens the image	decreases the intensity value of all voxels by the specified intensity cutoff value
Nonmax Suppression	shows voxels of highest intensity	sets voxels which are not at a local maximum to zero
Watershed	performs classic watershed operation	thresholds a binary volume, performs repeated erosions, sets voxels to erosion level and connects components

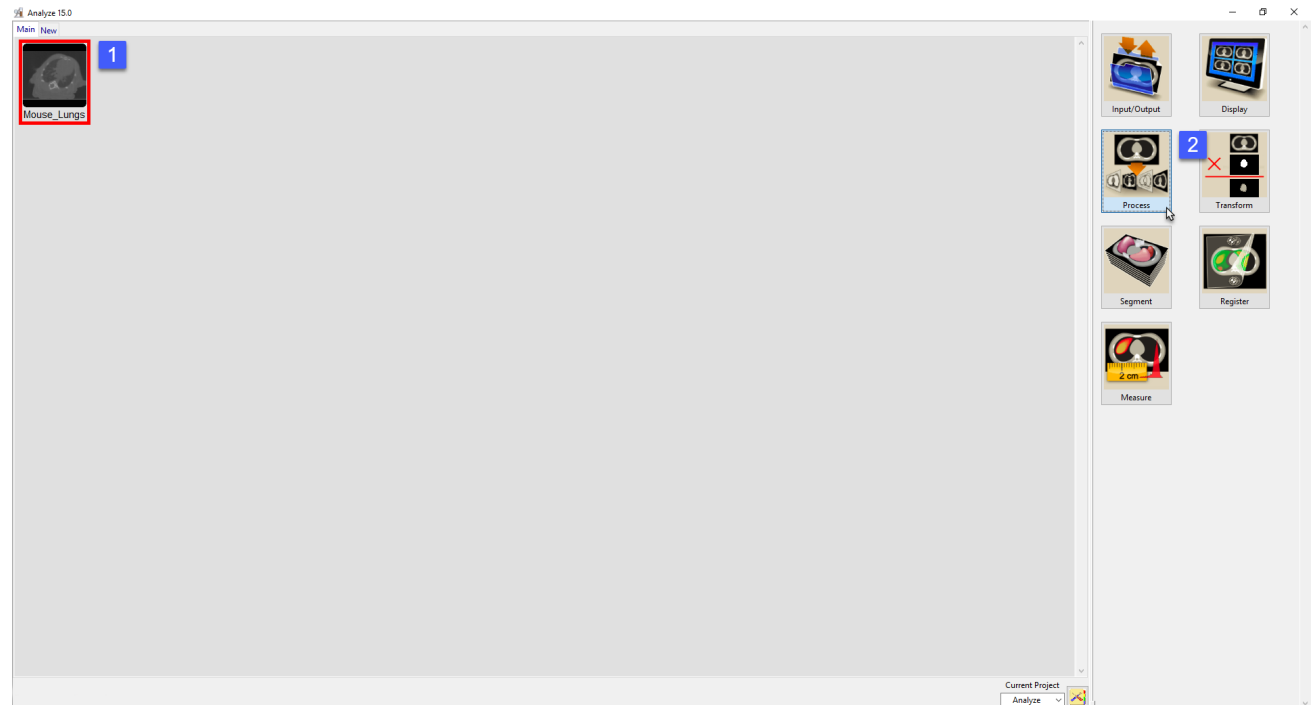
Applying Morphological Operators to Data

Download the Mouse_Lungs.avw data set to follow along, from <https://analyzedirect.com/data>.

This exercise will show how to apply a series of morphological operations to a data set to isolate an object of Interest while removing as much unwanted tissue as possible. This will prepare the data for further analysis. In this example we will isolate the lungs from a preclinical micro-CT data set by using various morphological operations including thresholding, eroding, and opens.

Use the Input/Output module to load the Mouse_Lungs.avw data set into the software.

Select the data set [1] and open Process [2].



Applying Morphological Operators to Data (continued)

The first step in this process is to eliminate the background noise.

Choose Morphology as the Process Type [3].

Choose the Threshold option as the Morphological Operation [4].

Set the Minimum Threshold level to 1105 [5]. Note that this will eliminate the background single.

Set the Output Type to Grayscale [6].

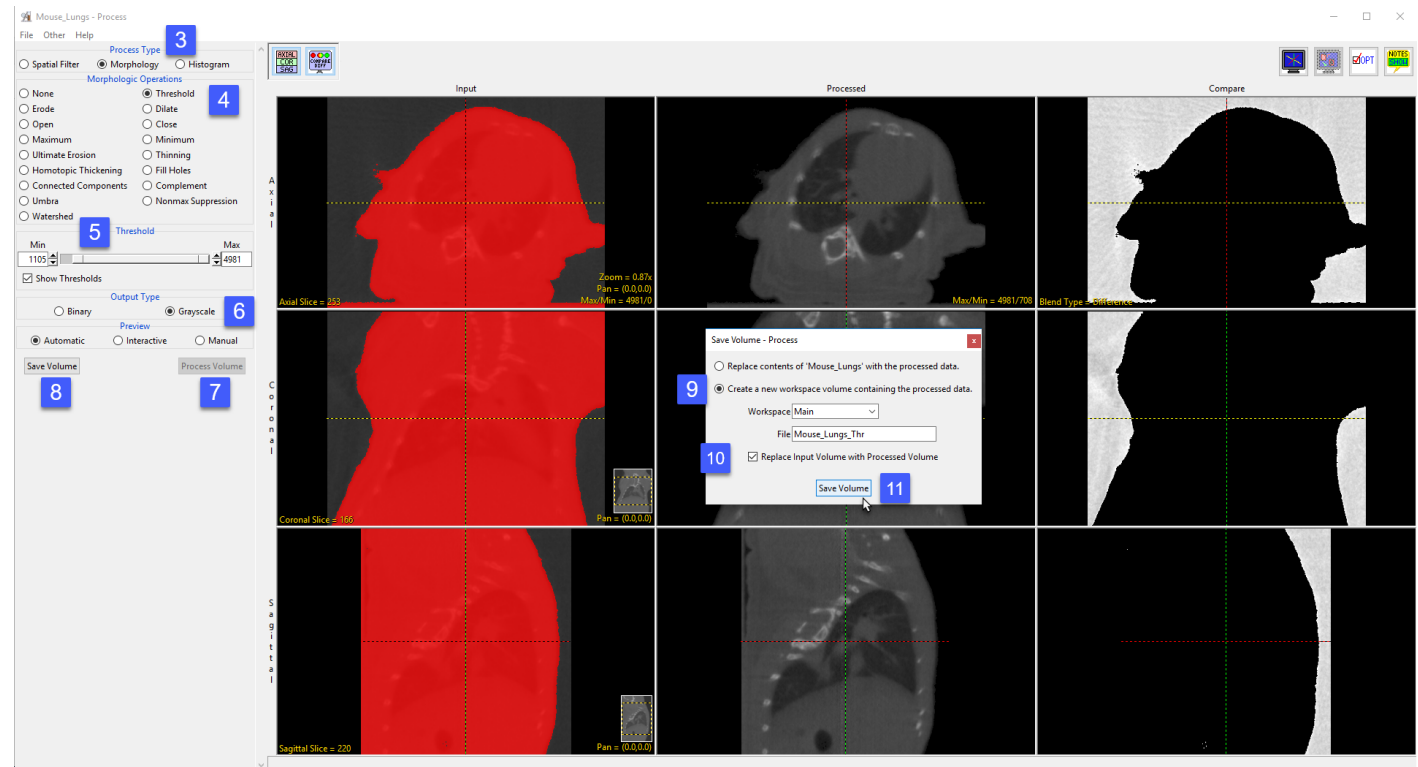
Next, click Process Volume [7].

When processing is complete click Save Volume [8].

In the Save Volume window ensure the 'Create a new workspace volume containing the processed data.' option is selected [9].

Also, ensure the 'Replace Input Volume with Processed Volume' option is checked [10].

Click Save Volume [11]. The processed data will be saved as a new volume in the workspace and will also be set as the Input Volume for Process.

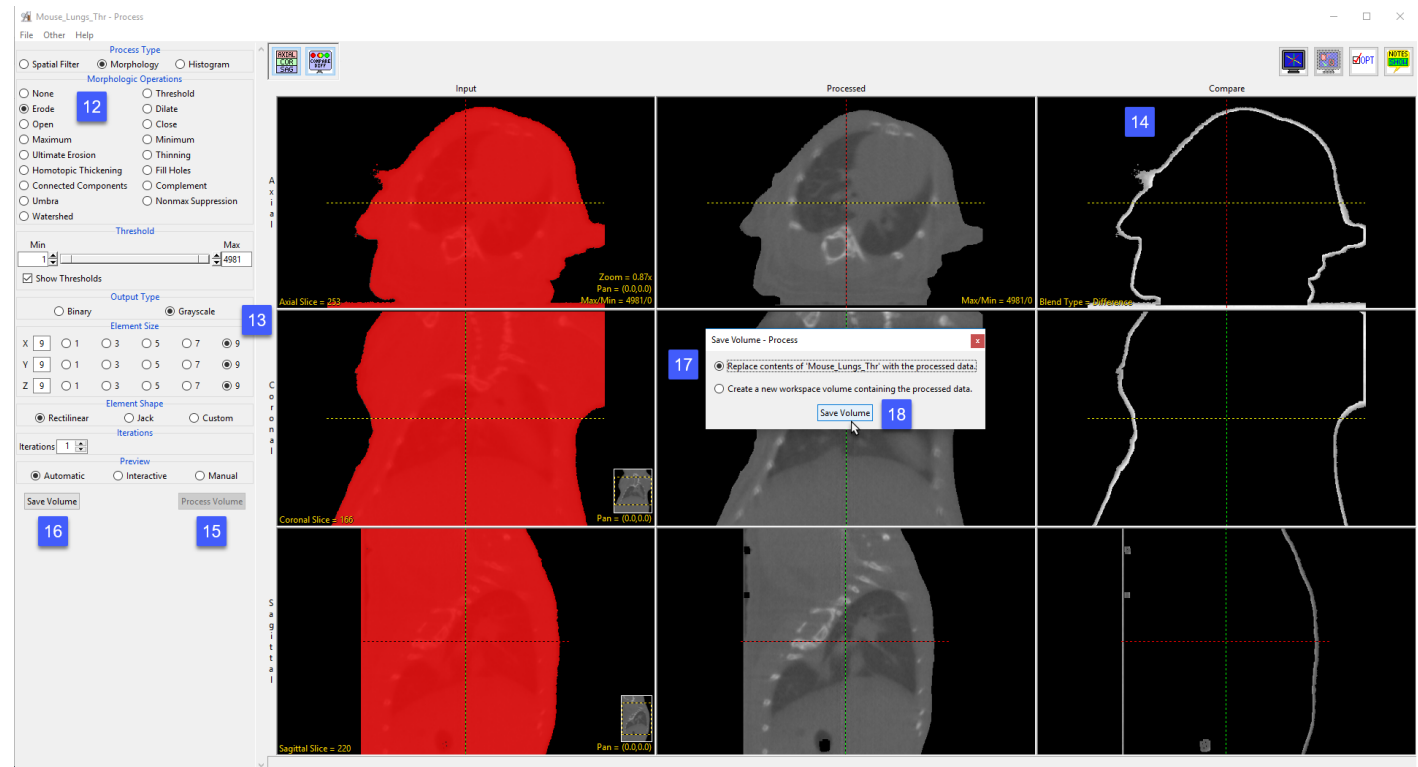


Applying Morphological Operators to Data (continued)

The next step is to remove a layer of voxels from the outer surface of the body. This step is completed in order to prevent these voxels from being included when we use thresholding in the next step to isolate the lungs.

Select the Erode option from the Morphological Operations menu [12].

Set the Element Size to 9 by 9 [13]. The voxels that will be eroded from the data can be seen in the Compare column [14].



Next, click Process Volume [15] and when processing is complete click Save Volume [16].

This time in the Save Volume window check the 'Replace contents of 'Mouse_Lung_Thr' with processed data.' option [17]. This will overwrite the volume and prevent an additional volume being written to the workspace.

Click Save Volume [18]. The processed data will be saved over the input volume and also be set as the Input volume.

Applying Morphological Operators to Data (continued)

Now we will use Thresholding to isolate the lung parenchyma.

Choose the Threshold option from the Morphological Operation menu [19].

Set the Minimum Threshold level to 1 and the Maximum Threshold level to 1639 [20].

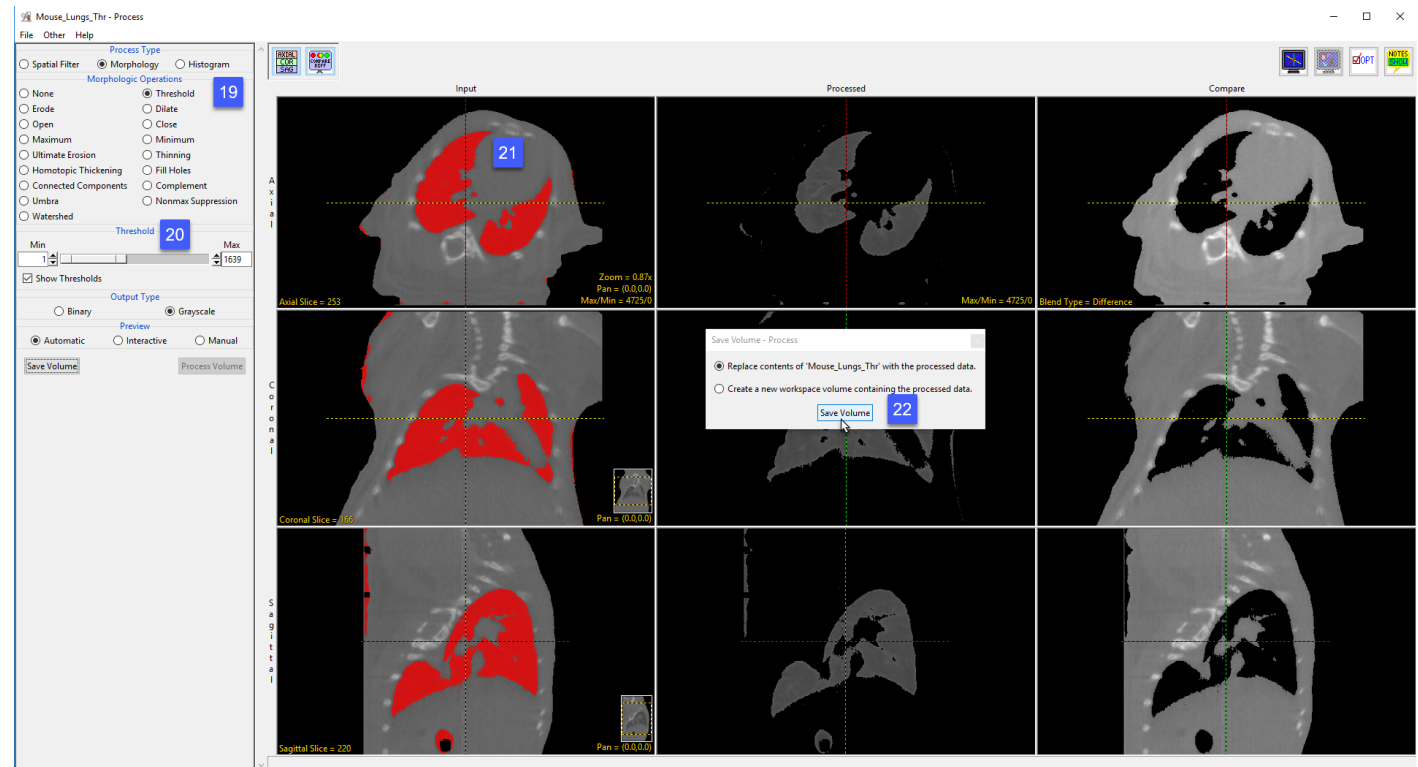
Note that this threshold range will isolate the lungs [21].

Next, click Process Volume and when processing is complete click Save Volume.

In the Save Volume window

leave the option set to 'Replace contents of 'Mouse_Lung_Thr' with processed data.'

Click Save Volume [22]. The processed data will be saved over the input volume and be set as the Input.



Applying Morphological Operators to Data (continued)

The final step to process this data set is to conduct a morphological Open operation on the image data. An Open operation is an erode followed by a dilation. The erode will take away layers, removing areas of noise. The dilate operation will then add back layers of voxels removed from the lung.

Set the Morphological Operation to Open [23].

Set the Element Size to 7 by 7 by 7 [24].

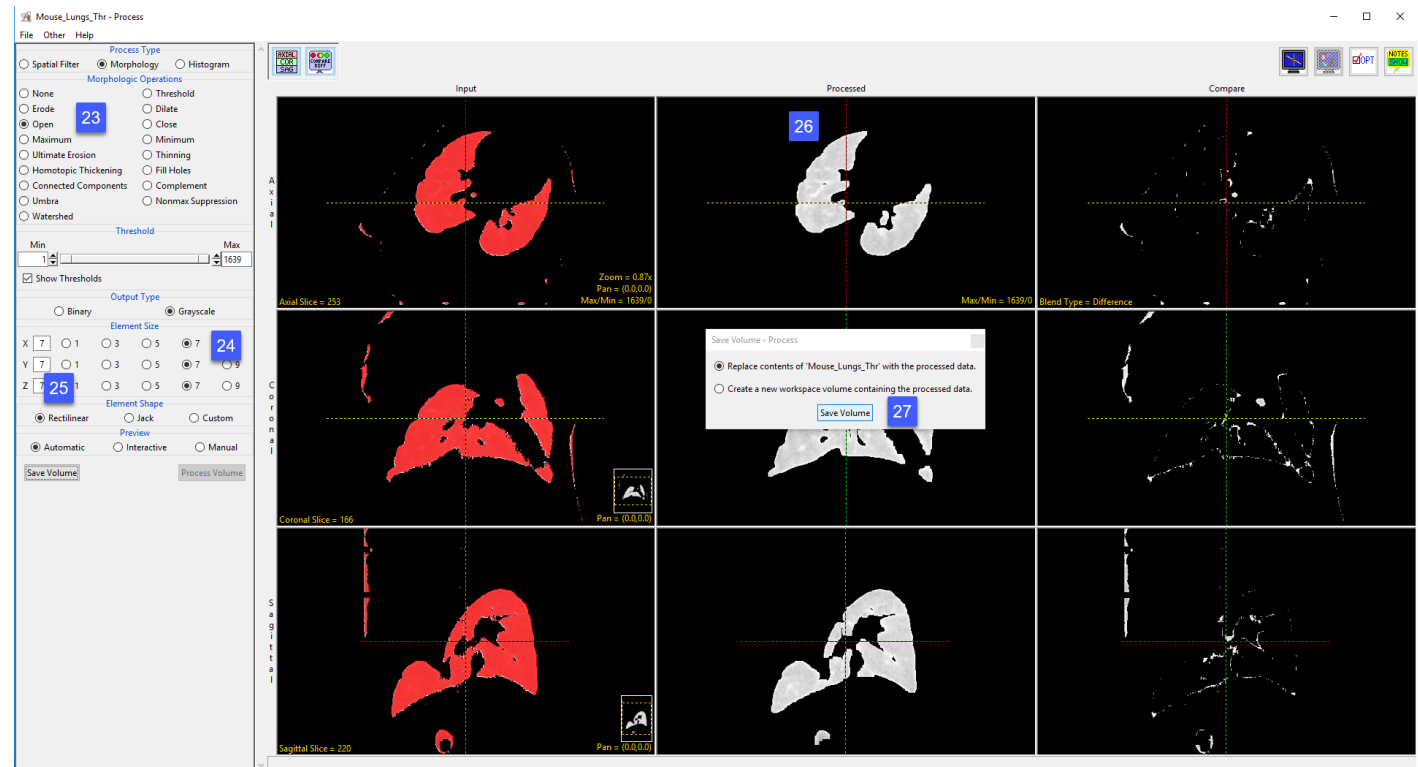
Ensure the Element Shape is set to Rectilinear [25]. Note the preview of the final isolated lung data set [26].

Next, click Process Volume and when processing is complete click Save Volume.

In the Save Volume window leave the option set to 'Replace contents of 'Mouse_Lung_Thr' with processed data.'

Click Save Volume [27]. The processed data will be saved over the input volume and be set as the Input.

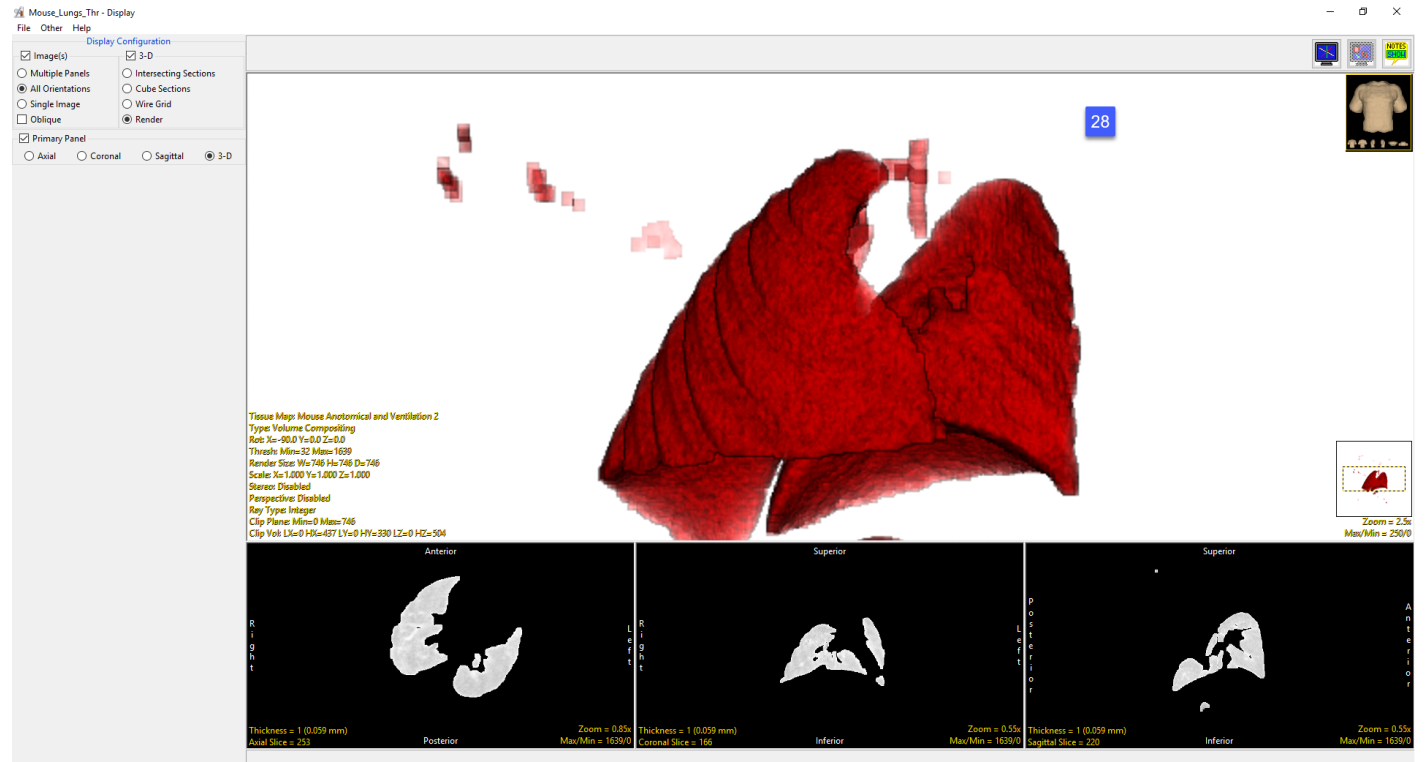
Close the Process module.



Applying Morphological Operators to Data (continued)

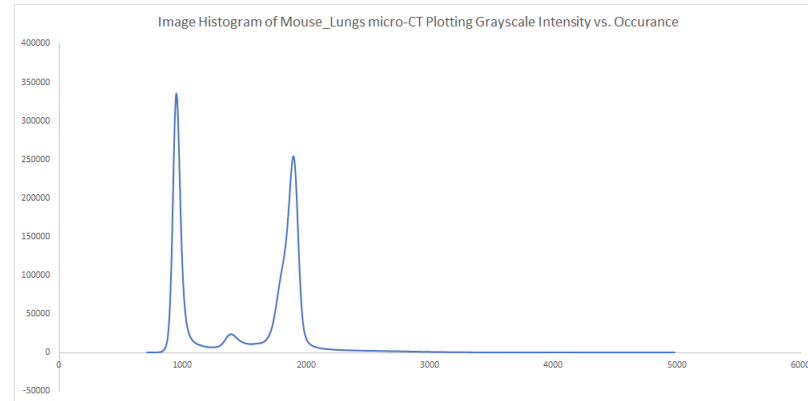
Select the processed image data 'Mouse_Lung_Thr' from the workspace and view it using the Display module [28].

In four easy steps we have isolated the lungs with a minimal amount of surrounding noise. This data is ready for visualization, volume measurement, or further segmentation.



Histogram

The histogram of an image is a function that relates the number of pixels in the image to the range of brightness values of those pixels. This can be expressed in a 2-D graph, plotting brightness vs. number of pixels.



The Histogram Process Type [1] allows users to perform the manipulations to alter the shape of the gray level histogram of an image to reduce noise, enhance contrast, or detect edges.

The Histogram Operations [2] available are:

- Flatten (also known as equalization)
- Preserve
- Normalize
- Match

Histogram Operations

The available histogram operations are Flatten, Preserve, Normalize and Match. These operations can be performed on the entire volume or on selected objects if an object map is loaded.

Histogram Operation	Description	Method
Flatten	maximizes contrast	evenly distributes voxels across the specified intensity output range
Preserve	brightens image while preserving contrast	maps the input intensity range onto a narrower output range in a statistically optimal manner
Normalize	allows comparison of data sets	forces the mean or mode of the histogram to specified values
Match	allows comparison of data sets	matches the intensity distribution to a loaded histogram file or the histogram of another volume

Histogram Flatten

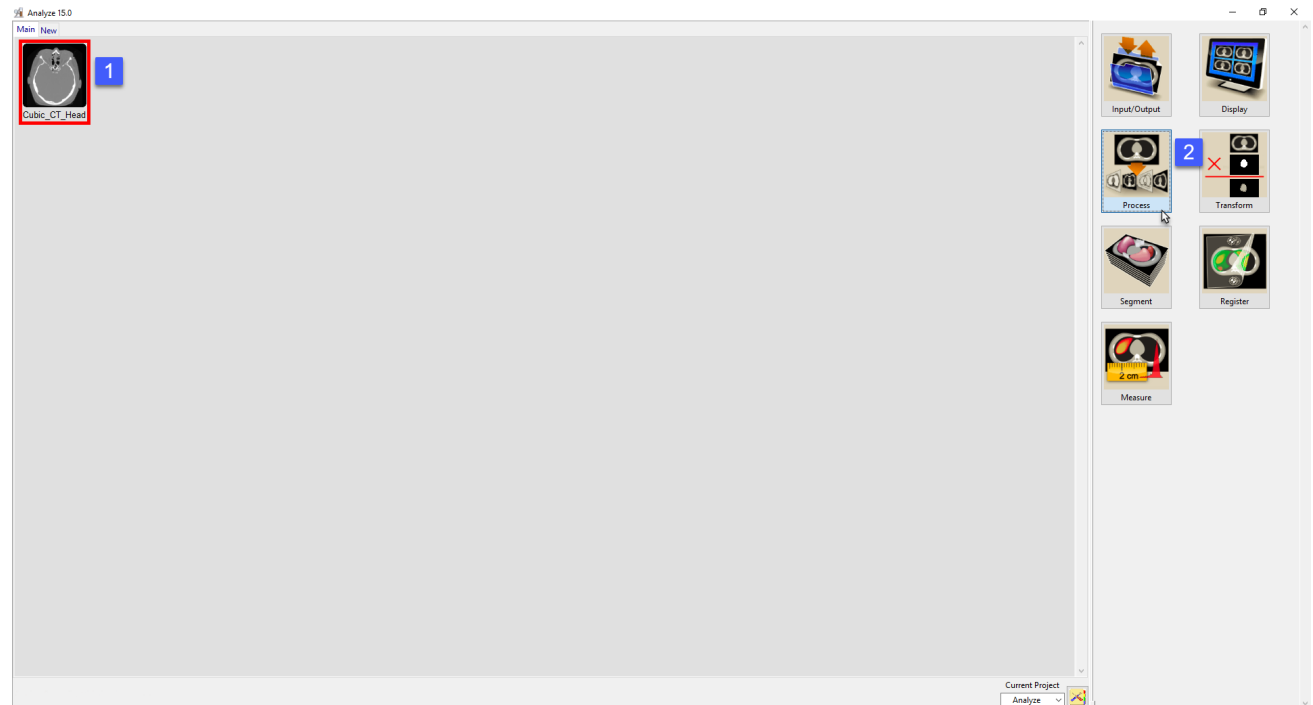
The histogram flattening function allows users to attempt to produce an even distribution of voxels across the gray scale range specified by the Output Range minimum and maximum. A volume which has roughly equal numbers of voxels at every gray scale value will tend to exhibit maximal contrast across the entire gray scale range. Original grayscale values may be brightened, darkened, and or binned together to affect the flattening procedure.

In this exercise we will apply the histogram flattening function to Cubic_CT_Head data set and observe the effects.

Download the Cubic_CT_Head.avw data set to follow along from <http://analyzedirect.com/data>

Load the Cubic_CT_Head.avw into Analyze using the Input/Output module.

Select the Cubic_CT_Head data set from the workspace [1] and open Process [2].



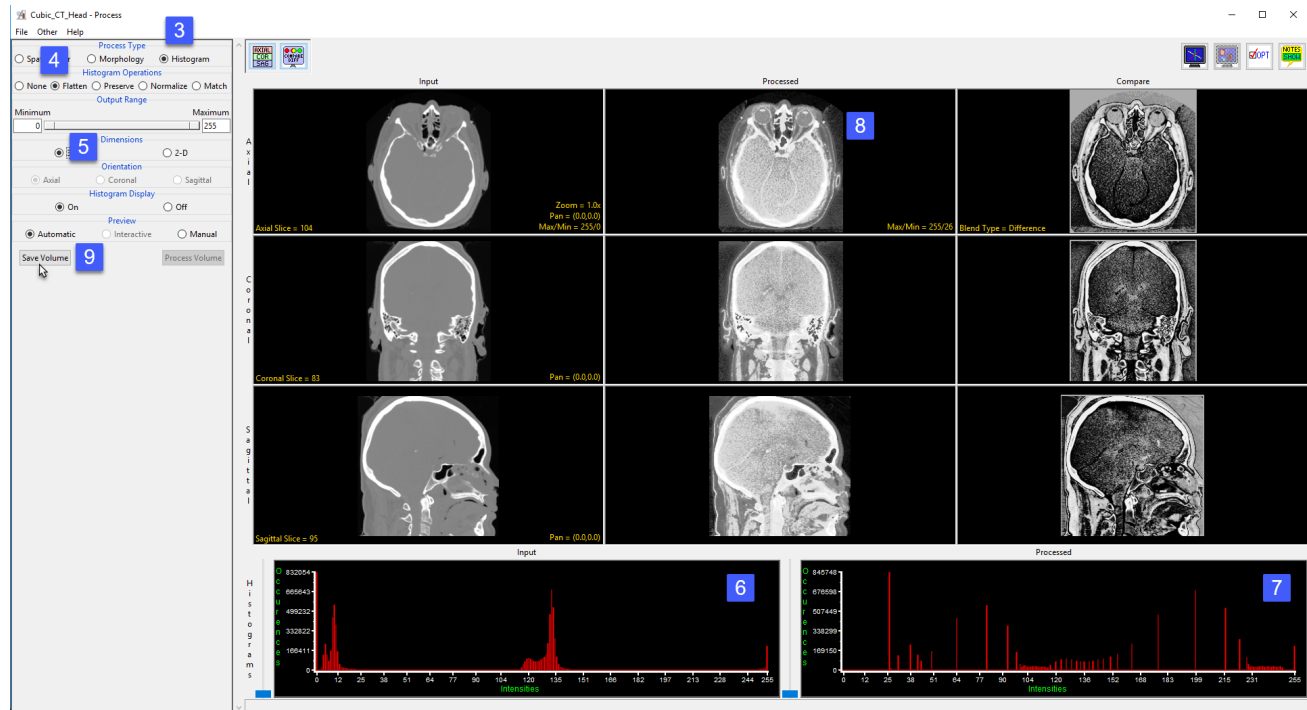
Histogram Flatten (continued)

Select the Process Type Histogram [3].

Set the Histogram Operation to Flatten [4].

Leave the Output Range Minimum set to 0 and Maximum set to 255 [5].

Note the input histogram [6] and the flattened output histogram [7]. The histogram flattening function has evenly distributed the range of voxels from the input volume across the grayscale range of the output volume.



Review the enhanced processed data set [8]. Additional structure in the brain can be seen in the processed image that is not visible with the current Max/Min levels set for the input volume.

Click Save Volume [9] to save the processed image data to the workspace.

Histogram Preserve

The histogram preserve function provides a utility for feature enhancement with in the input data set. The function works by mapping a broad grayscale range into a narrow range in a statistically optimal manner. For example, this function may be used to map 16384 gray level bins of a 16-bit image into 256 bins of an 8-bit image. The ideal distribution would place 1/256 of the total pixels in each of the 256 bins.

In the exercise we will demonstrate how to use the histogram preserve function to map the histogram of a 16-bit CT cardiac data set to an 8-bit data set and review the resulting



Download the CT_Heart.avw data set to follow along from <http://analyzedirect.com/data>

Load the CT_Heart.avw into Analyze using the Input/Output module.

Select the CT_Heart.avw data set from the workspace [1] and open Process [2].

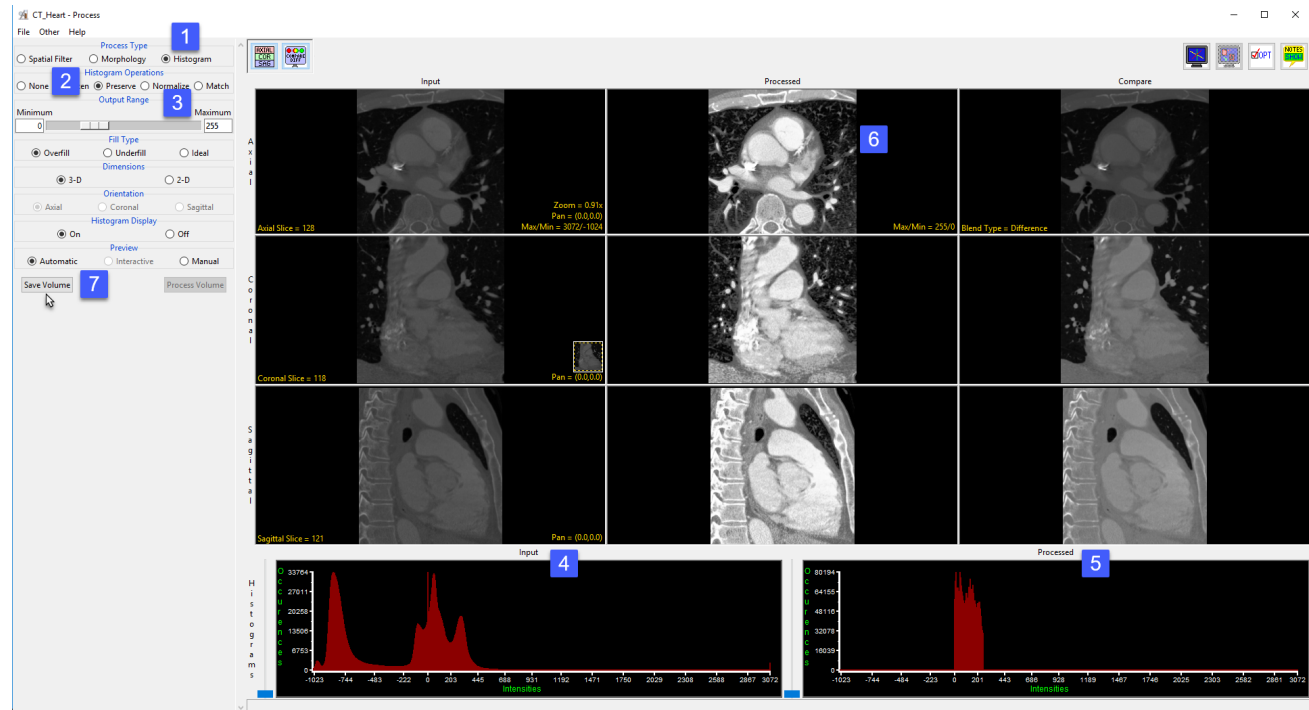
Histogram Preserve (continued)

Select the Process Type Histogram [1].

Set the Histogram Operation to Preserve [2].

Set the Output Range Minimum to 0 and the Maximum to 255 [3].

Note the input histogram [4] and the processed output histogram [5]. The histogram preserve function has mapped the entire range of the signed 16-bit input data set (-1024 to 3072) to the range of an unsigned 8-bit data set (0-255).



Review the enhanced processed data set [6].

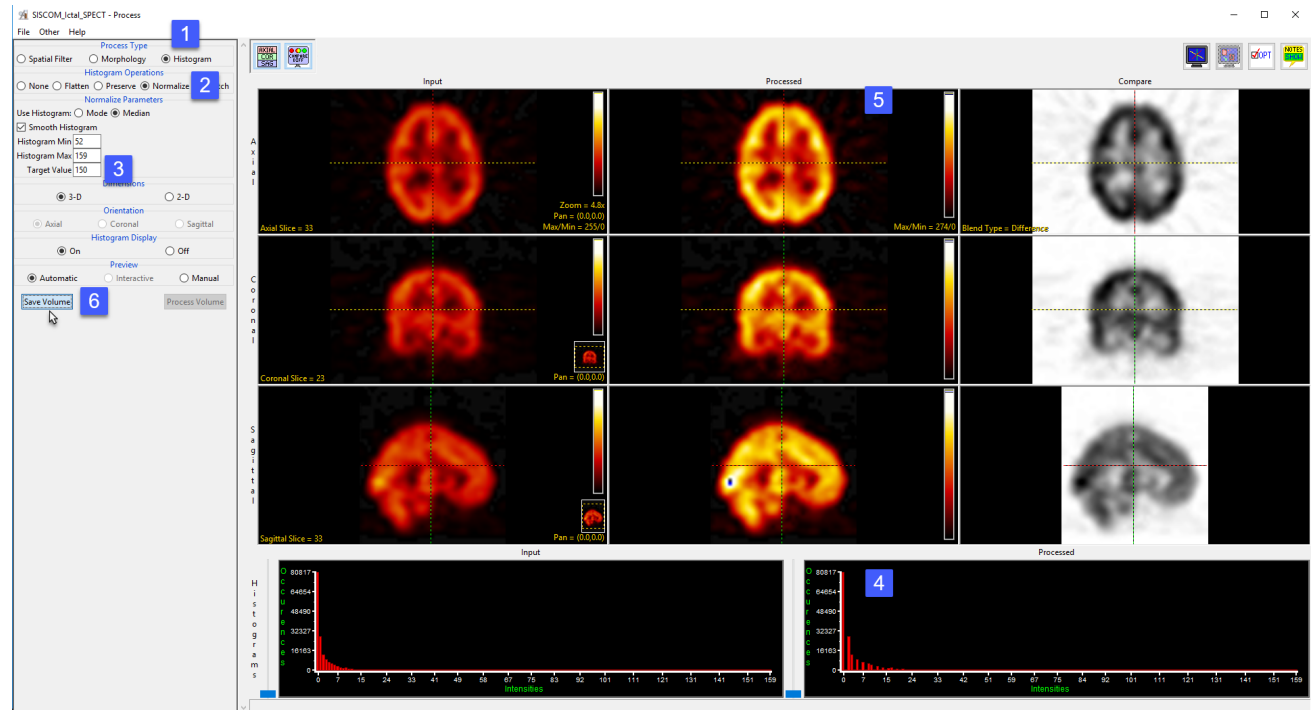
Click Save Volume [7] to save the processed image data to the workspace.

Histogram Normalization

Histogram Normalization forces the Gaussian parameters of the image histogram (mean or mode) to specified values.

This exercise will show how to normalize the histogram of two functional data sets to the same median value so that they can be compared to each other.

Download the two data sets SISCOM_Ictal_SPECT.avw and SISCOM_Interictal_SPECT.avw from <http://analyzedirect.com/data> and load both datasets into the Analyze workspace using Input/Output.



Select the SISCOM_Ictal_SPECT.avw data set from the workspace and open Process.

Set the process type to Histogram [1] and choose Normalize [2] as the histogram operation.

Set the parameters to use the histogram median and a target value of 150 [3]. Note the update to the processed histogram [4] and processed data set [5]. Setting the target value of each data set to the same value will allow comparison between the two.

Click Save Volume [6].

Histogram Normalization (continued)

In the Save Volume window, choose to replace the input volume with the process volume [17] or create a new workspace volume [7].

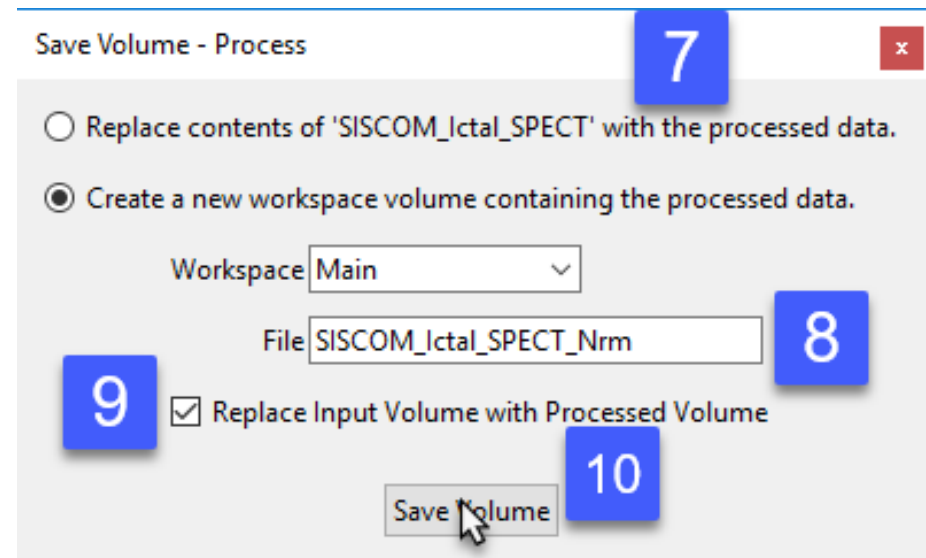
Name the file, if creating a new workspace volume [8].

If you want to process the volume further, choose to replace the input volume with the process volume [9].

Click Save Volume to apply the changes [10].

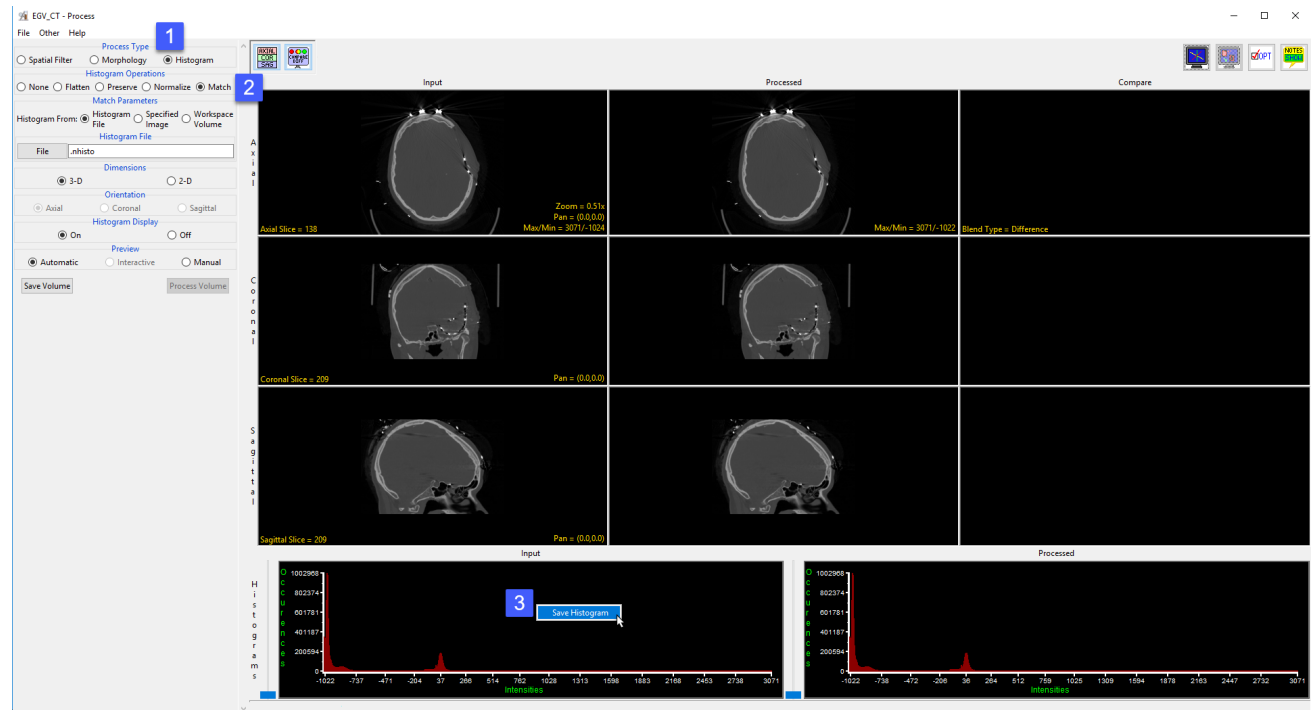
Repeat these steps for the second data set, SISCOM_Interictal_SPECT.avw.

The two new volumes you have created have been normalized to the same value, so equivalent numbers in the images now indicate levels of metabolic activity. The data sets can be subtracted to create a difference map or otherwise quantitatively compared.



Histogram Match

Histogram matching matches the intensity distribution of a volume to a histogram. The function forces the histogram of the input volume to match the grayscale distribution of the specified histogram file from another data set. Volumes of the same subject should have the same general distribution of gray levels, even though the parameters of a particular volume (exposure, brightness, contrast) may vary widely. Histogram matching may be used to normalize the absolute grayscale values of a set of volumes to a selected optimal example.



The goal of this exercise is to match the histograms of two data sets acquired for the same subject. Download the EGV_CT.avw and EGV_MRI.avw datasets from <http://analyzedirect.com/data> to follow along.

Load the two data sets into Analyze using the Input/Output module. Select the EGV_CT data set and open Process.

Set the Process Type to Histogram [1] and select the Match Histogram Operations option [2].

Right-click on the Input histogram and choose Save Histogram [3]. Save the histogram file to the Desktop. Close the Process module.

Histogram Match (continued)

Select the EGV_MRI data set and open Process.

Set the Process Type to Histogram and select the Match Histogram Operations option.

Click the File button under Histogram File [4] and then navigate to and select the .nhisto file saved for the EGV_CT data set and then click open.

The histogram will be applied to the data set. Note the change in the processed histogram [5] and the processed MRI data [6].

Click Save Volume to save the processed data to the workspace.

