Spectral Applications

English

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Instructions for Use

IntelliSpace Portal

PHILIPS

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1 About the Spectral Applications IFU

This guide includes information about using the Spectral applications. For Intended Use, Safety and Security, and other important information, please refer to the "Instructions for Use" included with your IntelliSpace Portal system before using the Spectral applications.

NOTICE

When loading data into an application, ensure the orientation shown on the images is consistent with the images' appearance. This precaution is required for data that contains wrong orientation information because the data will be incorrectly presented within the application.

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

Load Multiple Studies in Application

To load multiple studies in the application:

1. Use the **Ctrl** key when selecting studies from the Directory list.
2. Select the application from the Applications menu.
3. Confirm the studies are from the same patient.

NOTICE

Some application icons may be grayed out if the application is not suitable for the study or studies you have selected. Example: Loading multiple studies to an application that only supports loading one study. In addition, your Portal configuration may not support every analysis application.

Spectral Analysis Applications

Analysis applications allow you to access powerful Portal software for analyzing patient studies.

After selecting the desired study and/or series from the Directory, you may launch the appropriate Analysis application (only one at a time) and begin image processing and analysis functions.

Click the Analysis down-arrow to display a selection of application icons.

Click the icon of the desired application to load your selected study into the application.

Spectral Review Applications

After you have selected the desired study and/or series from the Patient and Series lists, you may launch Review, which allows you to view and examine patient studies quickly and easily.

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CT Viewer is the default viewer. Click the down-arrow to access a different viewer.

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2 Indications for Use

The Philips Spectral CT Applications support viewing and analysis of images at energies selected from the available spectrum in order to provide information about the chemical composition of the body materials and/or contrast agents. The Spectral CT Applications provide for the quantification and graphical display of attenuation, material density, and effective atomic number. This information may be used by a trained healthcare professional as a diagnostic tool for the visualization and analysis of anatomical and pathological structures.

The Spectral enhanced Advanced Vessel Analysis (sAVA) application is intended to assist clinicians in viewing and evaluating CT images, for the inspection of contrast-enhanced vessels.

The Spectral enhanced Comprehensive Cardiac Analysis (sCCA) application is intended to assist clinicians in viewing and evaluating cardiovascular CT images.

The Spectral enhanced Tumor Tracking (sTT) application is intended to assist clinicians in viewing and evaluating CT images, for the inspection of tumors.

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3 Understanding Spectral Results

Philips Spectral CT delivers multiple layers of retrospective data in a single, low dose scan, empowering you to improve clinical confidence that may impact your quality outcomes. The spectral detector can simultaneously distinguish between X-ray photons of high and low energies. This spectral analysis allows the discrimination of materials consisting of specific atomic numbers, such as iodine or calcium. Various elements are assigned individual colors, allowing them to be visually distinguished on CT scans.

Spectral Result Images

Spectral result images are CT images reconstructed using advanced spectral algorithms applied to photo-scatter images generated from the dual-layer spectral CT system. This photo-scatter information is stored in a series of spectral base images (SBI). Spectral result images can be displayed in the same way as conventional CT images (such as axial, MPR, MIP).

NOTICE

- It is always recommended to compare the spectral results with conventional images.
- In cases where the conventional images have very high pixel values, such as in strongly attenuating metal, the CT number of spectral results of these pixels cannot be used for quantitative analysis.
- Philips recommends the reconstruction of spectral results to be with an FOV larger than 220 mm to avoid sub-optimal image quality.
- The scanner limits the reconstruction of spectral results to a matrix size of 512x512.
- Spectral results can be created when utilizing voltage values of 100, 120 or 140kVp.

WARNING

It is always recommended to compare the spectral results with conventional images prior to finalizing diagnosis.

NOTICE

Spectral images should be exported from the spectral applications with a relevant label stating the spectral image type, as well as a series description stating the relevant spectral image type. Ensure exported images contain the relevant annotations exported with them.

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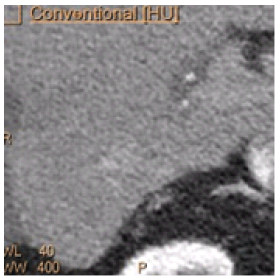
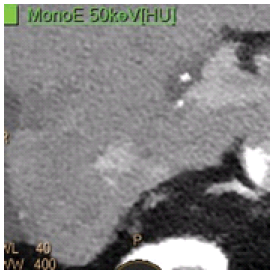
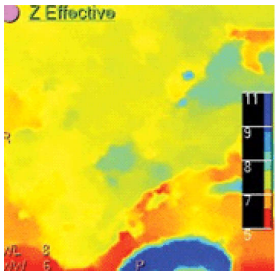
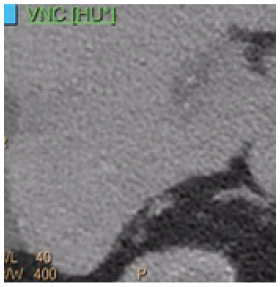
Spectral Result Categories

Conventional	MonoEnergetic	Non-HU-based	Modified HU-based
			
Conventional CT images	MonoEnergetic (MonoE) images at various keV energies (voxel value units are HU)	Material density results (voxel value units are mg/ml or mg/ml*) and Z Effective result (not expressed in units)	Results in which certain materials were removed (the voxel value units are HU or HU*)

An asterisk (*) next to the unit measure means that due to suppression of a certain material within this result, the measurements (such as HU) in some areas were significantly modified.

Each spectral category has a different on-screen indicator to aid in correct identification of the displayed spectral result. These appear in the upper left of the result.

Spectral Base Images (SBI)

What is a Spectral Base Image (SBI)

The SBI series contains the spectral information used to reconstruct any spectral result within spectral applications. The size of the series is up to three times the size of the matching conventional DICOM images series. The SBI series allows you to see any spectral result, on demand, without the need to reconstruct this as a separate series on the scanner.

Accessing Spectral Results From SBI

To access the spectral result of your choice, select the SBI series in the directory and load it into the Spectral CT Viewer on the scanner. When you reconstruct a conventional result you can also request that the corresponding SBI series be saved.

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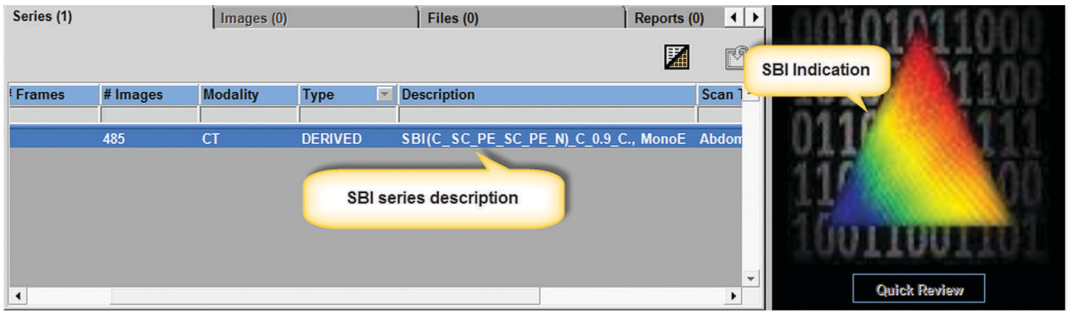

On Patient Directory, the SBI series can be identified by its series description prefix: **SBI** and a special spectral indication within the Quick Review window.

MonoE – Mono-Energetic [HU] Spectral Results

MonoE is a virtual mono-energy image that can range between 40-200 keV. The voxels in these images represent Hounsfield values. The series appears as “MonoE X” in the software user interface (for example, as “MonoE 75” where “75” is the keV value).

NOTICE

• When performing HU measurements on MonoE images, pay close attention to the keV value since it has a significant effect on the HU value. The extent of this effect depends on the material being measured.

• Darkening or brightening of artifacts can appear on low and high mono energy images. These artifacts are expressed more strongly as the keV value approaches one of the edges of the keV range (40 or 200), see water phantom below (Image 2). In the mid range keV (typically between 60-120), these artifacts are less expressed. These artifacts can also be present in other spectral result types.

• At low kev MonoE, HU variability can be seen for the same tissue, between the isocenter and the periphery of the scanner. For monoenergetic images at less than 60 keV, Water HU variation may be wider than +/-8 HU.

How MonoE Helps In Clinical Work

MonoE images have the potential to reduce image artifacts, such as beam hardening while using the high-range keV, typically above 80. MonoE also provides enhanced visualization of iodine and iodine-enhanced tissues (see Image 1) using the low-range keV, typically lower than 60.

MonoE xx keV Definition (Equivalent to Conventional CT)

This result, where xx is the keV value, has almost the same HU value as a conventional image generated from 120 kVp voltage (regardless of the actual tube voltage used during the scan). This type of result has the potential to improve image quality while preserving HU values.

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Differences Between kVp and keV

kVp (or KV) is the maximum voltage applied across an X-ray tube. keV is the energy an electron acquires by moving through a potential difference of 1 kV. A conventional CT image is created from a polyenergetic X-ray tube with a certain maximum voltage (for example, 100 kVp, 120 kVp) so it is reconstructed from multiple energies. The mono-energetic (MonoE) series represents a single energy (for example, 70 keV), allowing a reduction in potential negative effects of the polyenergetic beam, such as beam-hardening artifacts.

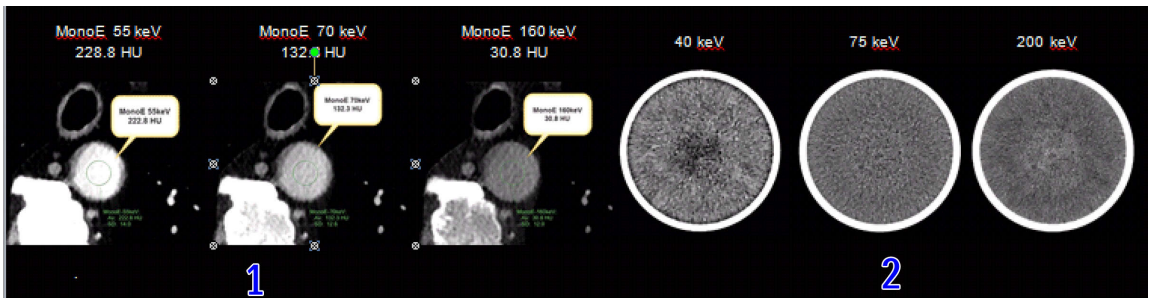

Image 1: Change in average HU value within iodine when measured using three different MonoE energies.

Image 2: To magnify the visibility of the artifact, a narrow window was used (WW- 30 HU, WC- 0 HU).

Non-HU-Based Spectral Results

Iodine no Water [mg/ml*]

This is an image in which the voxel values represent the iodine concentration of the displayed tissue in mg/ml. Non-enhanced soft tissues are set to approximately 0 mg/ml.

NOTICE

- ROI measurements are valid only on areas that contain iodine, without calcification. Iodine no Water [mg/ml*] visually enhances all iodine-like materials and so this image will also visually enhance materials such as calcium.
- The accuracy of Iodine quantification may be reduced when measuring Iodine concentrations which are less than 5 mg/ml.

How Iodine No Water [mg/ml*] Images Assist in Clinical Work

Iodine no Water [mg/ml*] images have the potential to allow for improved visualization of iodine-enhanced tissues. This result can also be used for iodine quantification, but only in areas where iodine is present.

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Z Effective

This is an image in which the voxel values represent the effective atomic number of the displayed tissue. Images can be displayed in color or gray scales. While imaging the body, the dynamic range is between 5 and 30. Water and non-enhanced soft tissues have Z Effective value of approximately 7.4. Fatty tissues have lower Z Effective while bone and contrast-enhanced tissues have higher values. Metal implants tend to have Z Effective higher than 30.

Z Effective images have the potential to differentiate tissues based on atomic number values (e.g., stone characterization).

NOTICE

The Z Effective average value depends on the material composition within that area. Different tissues (such as bones) or compounds (such as intra-vascular contrast) might have a close Z Effective value depending on the concentration of those tissues/compound.

WARNING

Effective-Z images should not be used as a *sole* basis for clinical diagnosis.

Iodine Density [mg/ml]

This is an image in which the voxels values represent the iodine concentration of the displayed tissue in mg/ml. Voxels without iodine are equalized to 0 mg/ml (visualized as black).

Iodine Density [mg/ml] images have the potential to quantify iodine enhancement and improve visualization of iodine within contrast-enhanced tissue. It is recommended to visualize iodine density as a color overlay to a conventional or MonoE image.

NOTICE

ROI measurements are only valid on areas that contain iodine. Due to various effects such as noise, the image may also contain calcium remainders.

The accuracy of Iodine quantification may be reduced when measuring Iodine concentrations which are less than 5 mg/ml.

WARNING

Please note that the appearance of non-HU images on third party viewers can be similar to standard HU imaging. Please verify that the proper information is saved with non-HU images when exporting images.

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How Iodine Density [mg/ml] Helps in Clinical Work

Iodine Density [mg/ml] images have the potential to quantify iodine enhancement and improve visualization of iodine within contrast-enhanced tissue. It is recommended to visualize iodine density as a color overlay to a conventional or MonoE image.

Electron Density [%EDW]

This is a spectral CT image generated from spectral acquisition. A dedicated algorithm uses spectral data to estimate the electron density (ED) of each voxel. The ED values presented in the image are relative to the electron density of water ($3.34x10^{29}$ electrons x m^{-3}) in units of percent, for example, the expected value for water in these units is 100 [%EDW].

How Electron Density [%EDW] Helps my Clinical Work

This image can potentially provide more accurate tissue characterization, since it is a direct result in which no conversion between HU to ED is required.

Modified HU-Based Spectral Results

VNC [HU*]

This is an image in which all soft tissues except iodinated tissues remain similar to MonoE 70 keV (HU values are reduced for skeleton bones and calcified structures). Iodinated voxels are replaced by virtual HU values as similar as possible to their HU without contrast enhancement.

NOTICE

- VNC images are recommended to be used on body scans only.
- Soft tissue HU inaccuracy may be present, due to sub-optimal iodine quantification and detection.
- The quality of iodine removal may be reduced at iodine concentrations typically larger than 20 mg/ml.
- Under selected Cardiac gated scans, HU values of calcified structures are preserved in their MonoE 70 values. Note that the classification methods target calcified structures rather than skeleton bones.

How VNC [HU*] Helps in Clinical Work

VNC images have the potential of replacing a true non-contrast series.

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Iodine Removed [HU]

In this result, all the voxels that do not contain iodine remain identical to MonoE 70 keV. Voxels that contain iodine are equalized to HU= -1024 (visualized as black).

NOTICE

• ROI measurements are intended to be taken only on areas that do not contain iodine. Due to various effects such as noise, the image may also contain iodine remainders.

• Under selected Cardiac gated scans, classification methods used to generate this result target calcified structures (rather than skeleton bones).

How Iodine Remove [HU] Helps in Clinical Work

The image is generated to focus on the non-enhanced structures while removing the enhanced structures. Depending on various factors, some of the enhanced structures can still appear in the image.

Contrast-Enhanced Structures [HU]

In this result, all the soft tissue voxels remain identical to MonoE 70 keV. Bone and calcified structure voxels are equalized to HU= -1024 (visualized as black).

Contrast-Enhanced Structures [HU] images have the potential to provide bone-free images which can help in visualizing vascular structures without bone or calcifications.

NOTICE

• Due to various effects such as noise, the image may also contain calcium remainders. ROI measurements are intended to be taken only on areas that contain iodine.

• Under selected Cardiac gated scans, classification methods used to generate this result target calcified structures (rather than skeleton bones).

How Contrast-Enhanced Structures [HU] Help in Clinical Work

Contrast-Enhanced Structures [HU] images have the potential to better visualize lumen vessels. The image is generated to focus on the iodine-enhanced structures while removing bones and calcified structures. Depending on various factors, some of the bones and calcified structures can still appear in the image.

NOTICE

Under selected Cardiac gated scans, classification methods used to generate this result target calcified structures (rather than skeleton bones).

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Uric Acid [HU]

In this result, all voxels that contain uric acid remain identical to MonoE 70 keV. Voxels that do not contain uric acid are equalized to HU= -1024 (visualized as black).

NOTICE

- ROI measurements are intended to be taken only on areas that contain uric acid. Due to various effects such as noise, the image may also contain calcium remainders.
- At typical clinical abdomen scan dose, uric acid stones smaller than 3 mm may not be detected.

How Uric Acid [HU] Helps in Clinical Work

Uric Acid [HU] images have potential use in gout disease diagnosis and stone characterization. It is recommended to visualize the Uric Acid [HU] as a color overlay on top of a conventional image or a MonoE image.

Uric Acid Removed [HU]

In this result, all the voxels that do not contain uric acid remain identical to MonoE 750keV. Voxels that contain uric acid are equalized to HU= -1024 (visualized as black). The two image types, Uric Acid Removed [HU] and Uric Acid [HU], complement each other.

NOTICE

- ROI measurements are intended to be taken only on areas that do not contain uric acid. Due to various effects such as noise, the image may also contain calcium remainders.
- At typical clinical abdomen scan dose, uric acid stones smaller than 3 mm may not be detected.

How Uric Acid Removed [HU] Images Helps in Clinical Work

Uric Acid Removed [HU] images have potential use in gout disease diagnosis and stone characterization (for example, uric acid stones). It is recommended to visualize the Uric Acid Removed [HU] as a color overlay on top of a conventional image or a MonoE image.

Calcium Suppression X Index [HU*]

This is a HU-based spectral CT image generated from spectral acquisition. A dedicated algorithm uses spectral data to identify and suppress calcium that normally overlays the underlying tissue. In this image, voxels containing calcium are replaced by virtual HU values as similar as possible to their HU without calcium contribution to the attenuation. The user has the

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ability to select preferred suppression index of the calcium- ‘X’, in a range of 25-100. A low index value selection targets tissues with a low calcium composition weight; a high index value selection targets tissues with a high calcium composition weight.

NOTICE

• This image is meant to be used for analysis of bones only, soft tissue HU values may be shifted.

• Darkening or brightening of artifacts can appear on low Calcium Suppression Index images (for index value below 50). These artifacts are expressed more strongly as the Calcium Suppression Index decreases.

How can Calcium Suppression x Index [HU*] Helps in Clinical Work?

The image has a potential to visualize bone marrow pathology in osseous regions.

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4 Common Spectral Processes

Spectral Plots

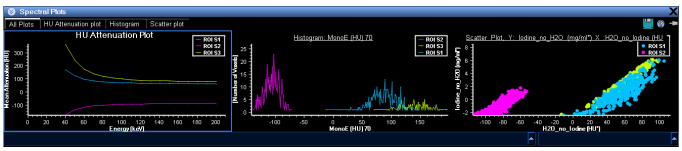
Draw ROI for Plot

To draw a Spectral plot ROI:

1. Draw a common toolbox ROI (circle).
2. Right-click the ROI and select from the context menu to change it to a spectral plots ROI.

Show Plots Panel

Click this to open the Spectral Plots dialog.



Use the tabs at the top of the dialog to view All Plots (as shown), the HU Attenuation Plot only, the Histogram only, or the Scatter plot only.

You can change the image type (and value if applicable) used in the plots (the default plots are created with Iodine vs. water). Click the header above the Histogram to view the options, then select a new value if desired (the histogram can be drawn for any spectral parameter). You can also change the X and Y Axis on the Scatter Plot using the same method. All information updates in real time.

Save Plots

Save the currently active (selected) plot.

Attenuation Curve

The attenuation curve is a plot of Hounsfield Unit (HU) values (of a region of interest) over the complete energy range (40 keV to 200 keV). This curve shows the attenuation of the region of interest at each energy, and the overall shape for the energy range. Each region is plotted with a different color that matches the color of the ROI.

Scatter Plot

A scatter plot is a type of graph that displays two variables for a region of interest. An ROI can be plotted as a set of pixel values from two different spectral results. This generates a plot that shows a scatter of points, each point has a value from two axes: iodine level and water level (based on water/Iodine material density pair).

NOTICE

In particular cases, some pixels in the material density scatter plot may have negative values. Such negative concentration values should be interpreted as a concentration of zero. Negative values might be created due to the impact of noise on measurement.

Histogram

The histogram is a distribution of voxels (over a region of interest) over the complete energy range (40 keV to 200 keV).

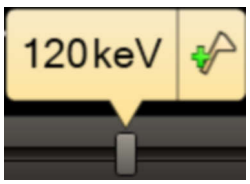
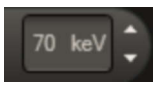
The histogram (created by an ROI) displays the range of HU values on the X axis, and the frequency on the Y axis. It is possible to plot any type of Spectral result as the X axis. See section “Spectral Plots” on page 21 for more information.

keV slider

Use the keV slider to adjust the keV value of a MonoE image.

To open this function, click the half circle that appears in the image. The slider displays.

The slider includes the following functions:

Icon/Function	Description
	Click the pin to keep the slider open in the window. Click the pin a second time to allow the slider to close.
Horizontal Slider	Use the slide function to view the image at various energy values.
	Click the flag with the green symbol to bookmark an energy value on the keV slider. This opens the dialog box to label the energy level. Type the desired name in the Label energy field and click OK.
	Click the flag with the red symbol to delete an energy value bookmark.
	Click the up and down arrows to change the keV value by an increment of one. You can also click on the displayed value and type in a number.

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Icon/Function	Description
	Click the arrow to play a cine of the different energies. During play of the cine, the function changes to Pause.
	Click to change the frame rate of the cine (frames per second).

NOTICE

If the viewport is larger than 500 pixels, all functions display.

If the viewport is between 300 and 500 pixels, the cine functions will not display.

If the viewport is under 300 pixels, the cine functions and the horizontal slider will not display.

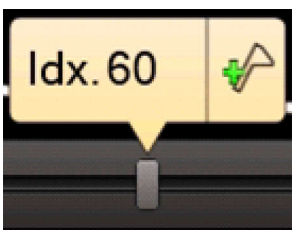
The kVp equivalent energy is displayed as a green flag (by default) on the slider.

Calcium Suppression Slider

Use the Calcium Suppression slider to adjust the index value of a Calcium Suppression image.

To open this function, click the half circle that appears in the image. The slider displays.

The slider includes the following functions:

Icon/Function	Description
	Click the pin to keep the slider open in the window. Click the pin a second time to allow the slider to close.
Horizontal Slider	Use the slide function to view the image at various index values.
	1. Click the flag with the green symbol to bookmark an index value on the index slider. This opens the dialog box to label the index level. 2. Type the desired name in the Label index field and click **OK**.

Icon/Function	Description
	Click the flag with the red symbol to delete an index value bookmark.
	Click the up and down arrows to change the index value by an increment of one. You can also click on the displayed value and type in a number.

NOTICE

The Calcium Suppression 76 index value is displayed as a green flag (by default) on the slider.

Generate Series

Click **Save selected view as new series** to open the Batch Preview dialog box. You can then choose to Save, Film, Film\Save, and Report. See Batch Functions (located in the Common Processes section) for details about saving a batch of images.

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

Adaptive Windowing per keV

Philips IQon Spectral CT enables the generation of MonoEnergy images at various keV energies.

The review of MonoEnergy images within the Spectral CT Viewer requires manual window level/center settings, (set by user), as some tissue types, as well as the presence of contrast media, can affect the displayed HU values when the keV values of such images change.

This IntelliSpace Portal option enables automatic window setting adaptation when the energy of MonoEnergy images is altered, either via type in or keV slider, while in Spectral CT Viewer.

When the option is activated, the Adaptive Window settings are calculated and suggested using the initial image window settings, as long as there is no manual change of the window settings. Manual changes of window settings are used as the updated reference.

WARNING

The option is based on algorithm suggestions of window settings per keV values, and therefore sub-optimal visualization may occur in the following cases:

- **Low contrast structures**
- **Iodine-calcification contrast in vessels**
- **Highly enhanced structures (for example: kidney cortex)**

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Recommendations

- Review conventional images prior to finalizing diagnosis. Spectral images should not be used as the sole source for clinical diagnosis.
- The Adaptive Windowing per keV option serves as a starting point and additional manual window settings tuning may be required.

NOTICE

The Adaptive Windowing per keV option is NOT available when ready-made results from the scanner are loaded to the application. Only SBI series are supported by this option.

Using Adaptive Windowing per keV

To enable this function, click the button on the slider or click **Enable keV Windowing** on the right click context menu.

NOTICE

By default, the Adaptive Windowing per keV option is not activated

The Adaptive Windowing per keV includes the following functions:

Icon/Function	Description
	Click this icon to set the Adaptive Windowing button per keV mode ON or OFF. This option is available in the large slider, if the viewport is larger than 500 pixels.
	Use the right-click menu option to set Adaptive Windowing per keV mode ON or OFF. **Note**: This option is available in all viewport sizes, including Spectral Magic Glass.

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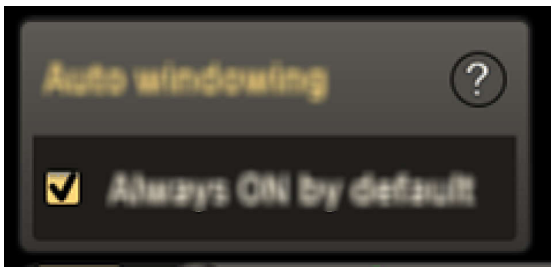
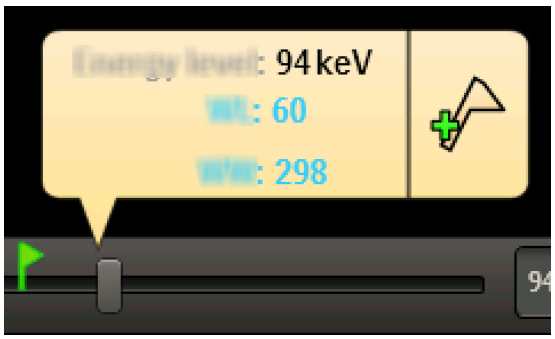
Icon/Function	Description
	Enable the **Always ON by default** option to enable Adaptive Windowing per keV mode by default upon application launch.
	The balloon notification specifies the energy level and changes in windowing when the Adaptive Windowing per keV mode is ON. Click the flag with the green symbol to bookmark an energy value on the keV slider. This opens the dialog box to label the energy level. Type the desired name in the Label.

Spectral Sub Segmentation

- Spectral Sub Segmentation allows the manual division of a tissue into up to 4 sub-tissues, using Spectral data.
- The mode is enabled per license, for SBI or conventional series and external/internal segmentation.
- The available tissues for sub-segmentation are those tissues with the same 'ACQUISITION_TIME' DICOM tag value as the loaded SBI/conventional series.
- Spectral Sub Segmentation includes three stages:
  - Tissue List
  - Set Tissue Parameters
  - Results

Stage 1 - Tissue List

In order to begin Spectral Sub-segmentation, the tissue segmentation of the loaded SBI/ conventional series must be approved in the Tissue List.

If an SBI series was loaded, spectral results can be modified in this stage. It is not possible to modify segmentation in the Spectral CT Viewer application.

1. Select a tissue in the Tissue List.
2. Review the segmentation on all slices.

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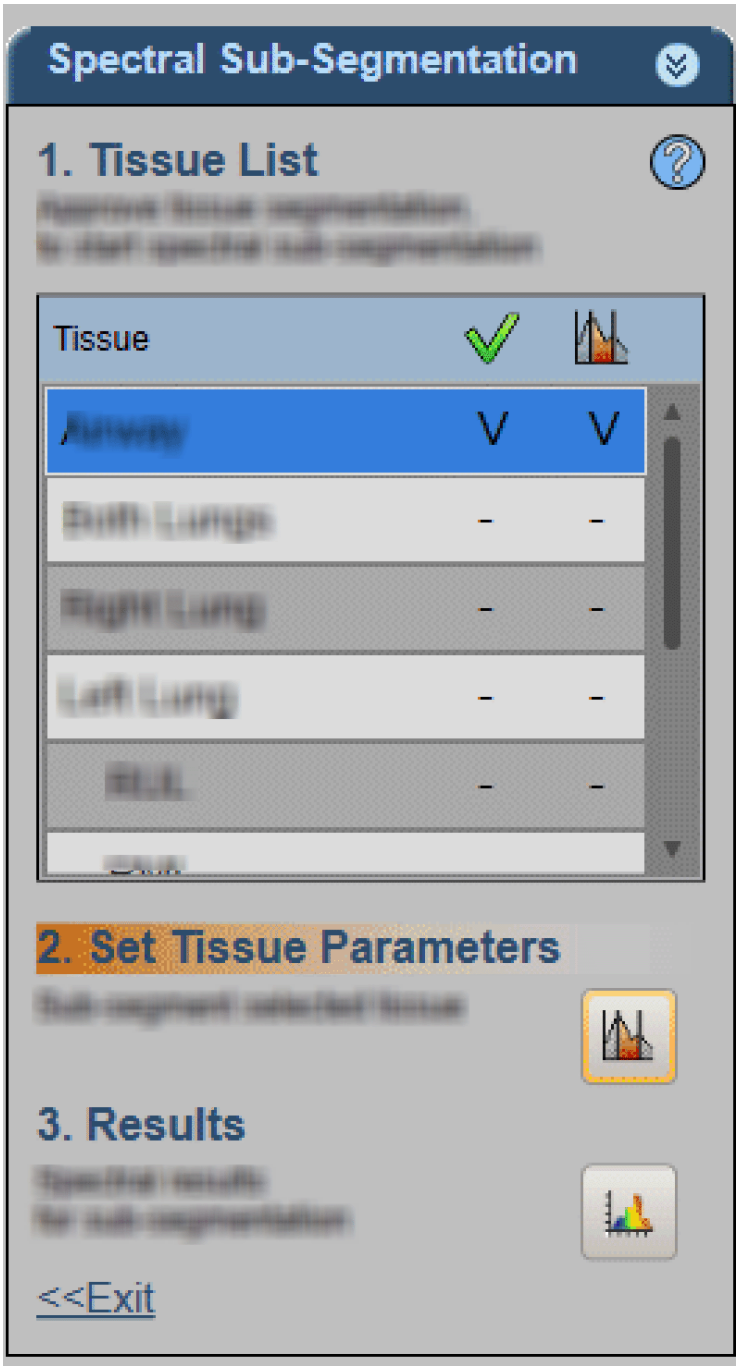
3. Approve the segmentation using the right click menu or via the floating dialog on the main viewport.

Once approved, the second stage is activated by default for the currently selected spectral result.



Stage 2 - Set Tissue Parameters

The Set Tissue Parameter stage includes five viewports. The viewports are described below.

Viewport	Description
1. **Conventional Axial**	• **Viewport** - Axial • **Orientation** - Can be changed. • The selected segmentation is available as an overlay on the images. • **Change Spectral Result** - This is an anatomical reference viewport. There is no option to change the Spectral result.
2. **Conventional Coronal**	• **Viewport** - Coronal • **Orientation** - Can be changed. • The selected segmentation is available as an overlay on the images. • **Change Spectral Result** - This is an anatomical reference viewport. There is no option to change the Spectral result.
3. **Spectral Axial**	• **Viewport** - Axial • **Orientation** - Can be changed • The selected segmentation is **not** available as an overlay on the images – this is a Spectral reference viewport • **Change Spectral Result** - Spectral results can be modified in this stage (applicable for SBI series only).
4. **Spectral Volume**	• **Viewport** - Volume, showing only the selected segmenation. • **Orientation** - Can be changed • A legend appears on the viewports with the selected Spectral result and the ranges of the selected segmentation.
5. **Parameters Selection Panel**	The parameter selection panel allows the user to set sub-segmentation parameters.
a. **Select Spectral Result**	• Use the Spectral results drop down menu to select the Spectral result for the basis of the sub segmentation (applicable for SBI series only). • The Spectral images are updated on the images. • It is possible to change the Spectral result from the images in the spectral viewports (applicable for SBI series only).

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Viewport	Description
b. **Favorites**	• Use the Favorites drop down menu to select a favorite protocol. • The favorite protocol stores the selected Spectral Result, the number of sub tissues, the values of the thresholds, the scaling factor and the number of bins. To create a favorite: 1. Select a Spectral result (applicable for SBI series only). 2. Define number of sub tissues. 3. Scale data if required. 4. Select **Add to favorites** button (below the histogram).
c. **Scaling**	Use the Scaling option to scale all pixel values of the tissue based on the following formula: *New Voxel Value = Old Voxel Value/Reference Value x100%* To scale the pixel values: 1. Select the required Spectral results (applicable for SBI series only). 2. Check the Scaling option. 3. Type in a reference value for the Scaling. It is possible to type in any value within the possible range based on the selected Spectral result: • For HU based Spectral results, type any value between (-)1024.0 - 3095.0 HU (excluded 0). • For Iodine based Spectral results, type iany value between 0.01 - 50.00 mg/ml. • For Z-Effective based Spectral result, type any value between 0.01 - 53.00. • For Electron Density based Spectral result, type any value between 1 - 410.0 %EDW.

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Viewport	Description
d. **Select Number of Sub Tissues**	• Use the **Number of Sub Tissues** buttons to select the number of sub tissues to segment to the original tissue. • It is possible to divide a tissue into up to four sub tissues. • Every sub tissue option adds a threshold to the histogram (for n sub tissue, there are n-1 thresholds in the histogram).
e. **Select Number of Bins**	Use the **Select Number of Bins** option to define the required number of bins in the histogram. It is possible to divide the histogram bins within a range of 5-80. To modify the bin's value in the histogram: 1. Select the required Spectral results (applicable for SBI series only). 2. Select the number of sub tissues. 3. Check the **Select number of bins** option. 4. Type in a required value withinin 5-80 to update the histogram. The optimal calculated number of bins appears in the type in box when the option is unchecked or is first checked. When you uncheck the option, the histogram is divided according to the optimal default number of bins.

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Viewport	Description
f. **Histogram**	• Use the histogram as an illustration of the distribution of the voxel values within the selected tissue according to the selected Spectral result. • The histogram represents the selected range of each sub tissue with a unique color, which is also presented on the images. • The ranges of each sub tissue in the histogram are limited with thresholds added in default locations. • To modify the thresholds of the sub tissues ranges, manually change the location of the threshold or type in a value within the range of the histogram. • To manually modify the thresholds of the sub tissues ranges: – Select a Spectral result (applicable for SBI series only). – Select number of sub tissues – Use the 'hand' to change the threshold's location – Click on a threshold's value and modify it
g. **Reset**	Use the reset option to go back to the default parameters.

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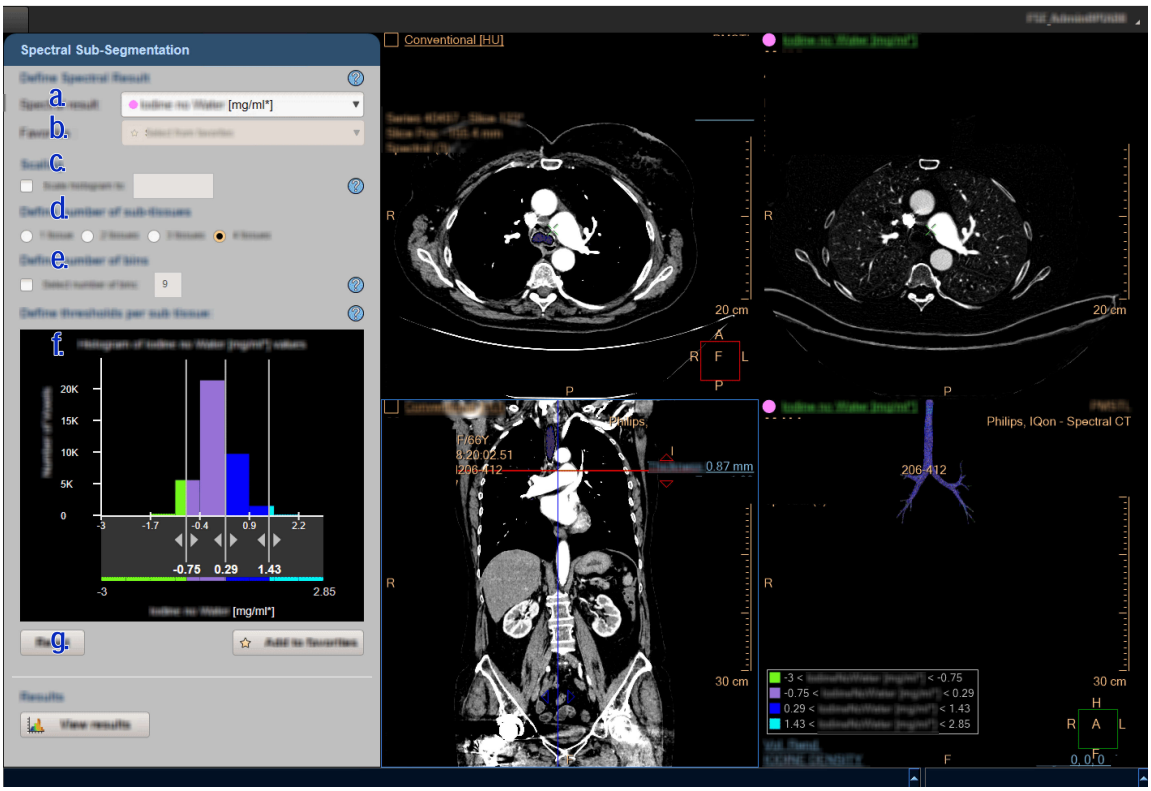

Stage 3 - Results

The Results stage includes five viewports. The viewports are described below.

Viewport	Description
1. **Conventional Axial**	• **Viewport** - Axial • **Orientation** - Can be changed. • The selected segmentation is available as an overlay on the images. • **Change Spectral Result** - This is an anatomical reference viewport. There is no option to change the Spectral result.
2. **Conventional Coronal**	• **Viewport** - Coronal • **Orientation** - Can be changed. • The selected segmentation is available as an overlay on the images. • **Change Spectral Result** - This is an anatomical reference viewport. There is no option to change the Spectral result.

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Viewport	Description
3. **Spectral Volume**	• **Viewport** - Volume, showing only the selected segmentation. • There is no option to change the Spectral result. To modify a Spectral result, return to the **Set Tissue Parameters'** stage (2nd stage - see section "Stage 2 - Set Tissue Parameters" on page 27). • A legend appears on the viewports with the selected Spectral result and the ranges of the selected segmentation.

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Viewport	Description
4. **Resulting Table**	• The Resulting Table represents user measurements of the created sub tissues. • Each sub tissue is represented with a unique color. • The resulting table represents the range of each one of the sub tissues. • Mathematics and statistical measurements of each sub tissue are displayed: – Volume (cm^3) – % Volume (out of the full/original segmentation) – Average according to the selected Spectral result – Standard Deviation (SD) according to the selected Spectral result – Average according to Conventional result – Standard Deviation (SD) according to Conventional result – Kurtosis – Skewness • The last row in the table represents data relating to the full segmentation before dividing it. • It is possible to show/hide each one of the sub tissues. • It is possible to show/hide the units in the table. • It is possible to export the table as an image or as a CSV file.
5. **Histogram**	• The histogram represents: – An illustration of the distribution of the pixel values within the selected tissue according to the selected Spectral result. – The selected range of each sub tissue with a unique color, which is also presented on the images. • The range of each sub tissue in the histogram is limited with thresholds as defined in 'Set Tissue Parameter' stage (2nd stage). • In order to modify the thresholds of the sub tissues ranges you need to go back to 'Set Tissue Parameter' stage (2nd stage).

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Viewport	Description
	• It is possible to show/hide the thresholds on the histogram using the right click menu. • When hiding the thresholds on the histogram, the distribution into sub tissues is kept on the histogram, including the relevant colors of the sub tissues. • It is possible to show/hide the legend on the histogram using the right click menu.

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5 Spectral CT Viewer

The Spectral CT Viewer is a software application that allows comprehensive review and analysis of the acquired spectral data. The viewer requires the SBI DICOM data series to enable all the spectral Review and Analysis features (SBI is a DICOM image with proprietary parts). Without the SBI, the Spectral CT Viewer allows limited review and analysis of loaded conventional DICOM data.

NOTICE

It is recommended that you review conventional images prior to finalizing diagnosis.

Loading Data into Spectral CT Viewer

1. From the Directory, select the desired study. The Series list displays.
2. Select the series you want to load. Load the SBI to use the full spectral capabilities of the Spectral CT Viewer.
3. From the Review menu, select **Spectral CT Viewer**.

Spectral images are annotated with a 'burn-in' mark to signify their origin. This mark appears in the upper left of the image. See section “Understanding Spectral Results” on page 11 for more information on the types of spectral results indicated by these marks.

WARNING

The interpreting physician must be made aware of the appearance of non-HU images (and related measurements) in the reading environment. Confirm the image type and applicable values in the labels of all images used for diagnosis.

WARNING

It is always recommended to compare the spectral results with conventional images prior to finalizing diagnosis.

Some DICOM viewers may be incompatible with non-HU images. This can result in erroneous measurements.

One or more of the following image types may appear in this application: curved MPR, straightened MPR, volume images, and thick slab images. Measurements you make on such processed images can sometimes be misleading. When saving such images, make sure they are properly labeled.

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WARNING

When you select one of the options which include resolution reduction, the image resolution and quality will be reduced during interaction. When loading images into IntelliSpace Portal applications, all images which contain 16-bit data are converted into 12-bit images. This means that for rescale intercept equal to -1000, HU values above 3095 are displayed as 3095. For rescale intercept equal to -1024, HU values above 3071 are displayed as 3071.

DICOM tags exist to ensure that the image type and keV can be recognized in all viewports. Enable the appropriate image title options under the Image Titles menu of your system Preferences.

CAUTION

When loading data into an application, ensure the orientation shown on the images is consistent with the image appearance. Data that contains wrong orientation information will be incorrectly presented within the application.

When loading data into an application, ensure the orientation shown on the images is consistent with the image appearance. This precaution is required for data that contains wrong orientation information because the data will be incorrectly presented within the application.

Common Tools, and Common Processes

A number of tools and process functions are common throughout the Review and Analysis applications. For additional information, please refer to CT Common Tools and CT Common Processes sections in the IntelliSpace Portal CT Review IFU.

Indications for Use

The Spectral CT Viewer is a software application allowing visualization and analysis of spectral images derived from spectral data acquired with the IQon Spectral CT Scanner.

Function Tabs

Click the arrow in the tab window. The list of available functions displays.

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Tab Name	Description
Series	The series tree displays a list of the studies and series that are loaded into the viewer, and also any other elements (such as batches) that have been created. The series tree elements display in a format similar to the way directories, folders, and files are shown in the operating system. Each element of the series tree has a small icon to identify the type of element listed.

Tab Name	Description
Bookmarks	Existing bookmarks for the current application (or viewer) display. Click on the bookmark of your choice. The system returns the patient study to the condition it was in when you saved the bookmark.

Tab Name	Description
Clip & 3D Segmentation	Bone removal (3D) is a threshold-based tool that affects connectivity between objects. Clicking on a point removes all areas connected to the object that have an HU value greater than the threshold.
	If bone removal does not remove smaller, unattached volumes completely, the Remove residuals tool may be helpful. Residual bone volumes are typically 20 to 30 cc.
	Use Clip functions to isolate tissues for better viewing of volumes of interest. The Clipping Plane is a single, movable, infinite plane that cuts through the true volume, removing the volume on one side of the plane and leaving a volumetric view on the other side of the plane. Target Volume is used for segmenting large, complex volumes. Bounding cube is used for analyzing small objects. Using either of these functions enables the Lock/Unlock, Hide/Show, and Reset options.
	Use the Smart Segmentation Tools (3D) to improve the 3-dimensional segmentation of various organs and anatomies.
	Use the Inject and Erase tools to create (and edit) a tissue of the volume of interest. Add contrast using Inject; remove contrast using Erase. You can set the sphere of the Eraser (3D).

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Tab Name	Description
	Expand (3D) and Erode (3D) are included in the Tissue Management tab description.
	The Fill Holes option functions similarly to the Fill function, adding to the injected soft tissue, filling in holes within the volume.
	You can choose to show the blue Overlay, or Only Tissue, as you manipulate the reference images.
	Three Region of Interest (ROI) sculpting tools are available: Freehand, Rectangle, and Circle, in two variations, Exclude (3D) and Include (3D). The Exclude (3D) function removes everything enclosed within the ROI. The Include (3D) function removes everything outside of the ROI.
	Click Accept after you have completed your tissue definition. The tissue is stored in Tissue Management.
	Click Reset to undo all of your tissue definition changes and return the image to its original state.
	Click Undo/Redo to reverse your most recent action.

WARNING

Verify bone removal does not affect vessel completeness. Bone removal is intended for use with the body, not the head.

When placing the seed on the volume image, verify its location on the reference images.

The Eraser function removes from the volume, not only the slice you use it on. Verify the results by scrolling the reference images.

The size and shape of anatomies can change when making adjustments. To prevent wrong interpretation, follow the recommended modification procedure.

Tab Name	Description
Batch	Determine the composition of the batch by performing the image preparation functions, and then specifying the desired images of the batch (Start/End, All, Preset, etc.)
	After defining the batch, you can change the Parameters (thickness of the slabs, the X increment, and/or the total number of images). Additionally, you can Add other images (the parameter information frame, reference image, and/or a mini image of a reference viewport).

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Tab Name	Description
	The Tile view displays the batch images in a static, tile-sized format.
	Prior to saving, click Preview to view your batch.
	Click Clear batch to undo all of your batch changes and return the series to its original state.

Tab Name	Description
Tissue Management	Tissue Management lists the tissue definitions created for the current study. The list includes tissues defined in the current work session as well as those defined during previous work sessions, and from other applications (if they are loaded with the study). You can choose to show or hide select tissues. You can select a color for the tissue and/or select a different rendering preset than what is currently chosen. Edit the selected tissue using the Fill, Expand (3D), and Erode (3D) functions to add to the injected tissue, increase the edges of the tissue, and decrease the edges of the tissue. Click Reset to undo all of your changes and return the image to its original state.

Tab Name	Description
Analysis	Use the Spectral Plots tools to show or hide the Spectral Plots banner. See section “Spectral Plots” on page 21 for information. To use the Overlay function, first select a fusion layout from the Viewing Presets. Then choose the desired overlay result, adjust the colormap and opacity of the overlay.

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Tab Name	Description
Fusion	The Fusion function tab contains the following tools for working with fused series: Click the left and right arrows to change the color map of the series, and to change the color map of the overlay image data on the fused series. Use the blending slider to control the proportion of the two image types in the display. The overlay image can be offset and/or rotated relative to the CT image using two methods: 1) interactively, using the Pan and Rotate buttons and 2) using the Type-in Registration Parameters function. Click Reset to undo all of your changes and return the image to its original state. Click Undo/Redo to reverse your most recent registration action.

Tab Name	Description
Spectral Sub Segmentation For details, see section “Spectral Sub Segmentation” on page 26.	Spectral Sub Segmentation allows the manual division of a tissue into up to 4 sub-tissues, using Spectral data. The mode is enabled per license, for SBI series and external/internal segmentation. The available tissues for sub-segmentation are those tissues with the same ‘ACQUISITION_TIME’ DICOM tag value as the loaded SBI.

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Presets Layout

Icon	Function	Description
	Viewing Presets	Click the arrow to open the Viewing Presets dialog box. Click on a clinical indication group thumbnail image to see the preset layouts currently available within that group. • A preset layout includes a combination of: – Spectral data screen layout – General and Spectral tools – Fusion setting (overlay, opacity, color map) • Preset layouts may be repeated within different groups. • You have the ability to save your current workspace as a Preset, or delete a Preset layout from a group. Within factory defined presets, only the Spectral image types and fusion setting can be changed. • Select a Slab Preset layout from the General group to open additional slab layout options. • Selecting a Conventional 2D layout adjusts the viewing options of the workspace. • Presets that include more than one data type are linked for geometrical parameters (scroll, zoom, pan, and thickness). • The Preset name indicator updates in real time as you switch groups.

Suggested Presets

Suggested presets will be adequate for a clinical indication and will be presented according to a smart algorithm. The algorithm uses matching calculation activated on DICOM tags of the series such as SERIES DESCRIPTION, PROTOCOL NAME, etc. and uses “solid” DICOM fields such as CONTRAST, WINDOW, etc.

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The algorithm combines the inputs into a single output, taking into consideration multiple DICOM tags in order to greatly increase success rate.

To create suggested presets you can:

1. Create a new preset.
   - Organize the screen layout.
   - Select the data types, orientation and other parameters for each viewport.
   - In the **Preset** menu select **Save current layout**.
   - Type a name for the preset and select a category.
   - Make sure the **Show this preset in “My Suggestions" (when relevant)** option is checked.
   - Click **Save**.
2. Mark existing preset as suggested:
   - In Preset menu select right click option on existing preset.
   - Select **Add to "My Suggestions"**.

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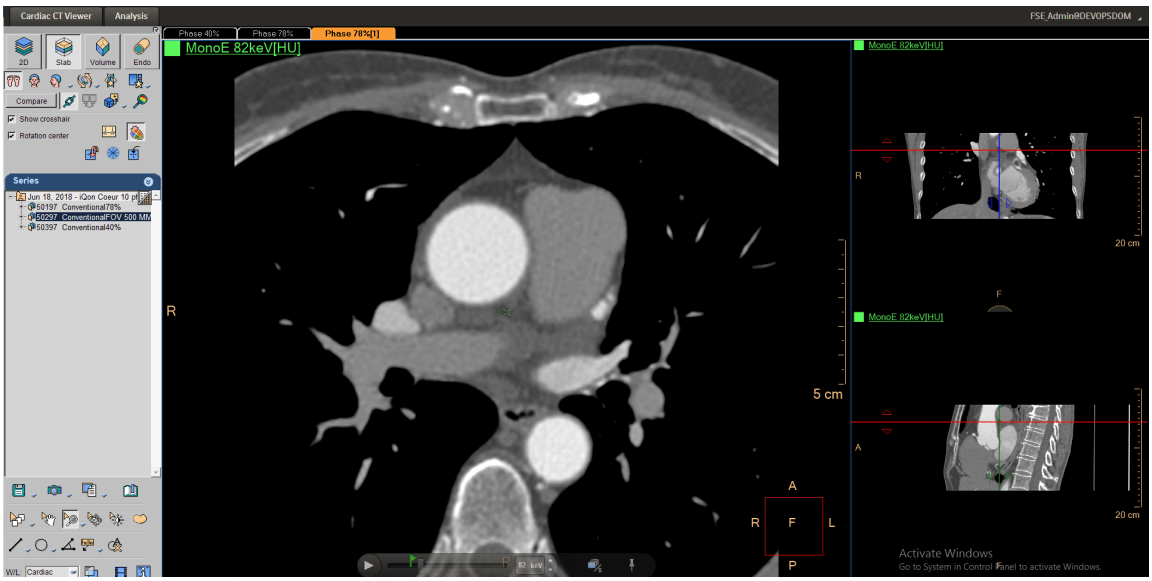
6 Spectral CT Cardiac Viewer

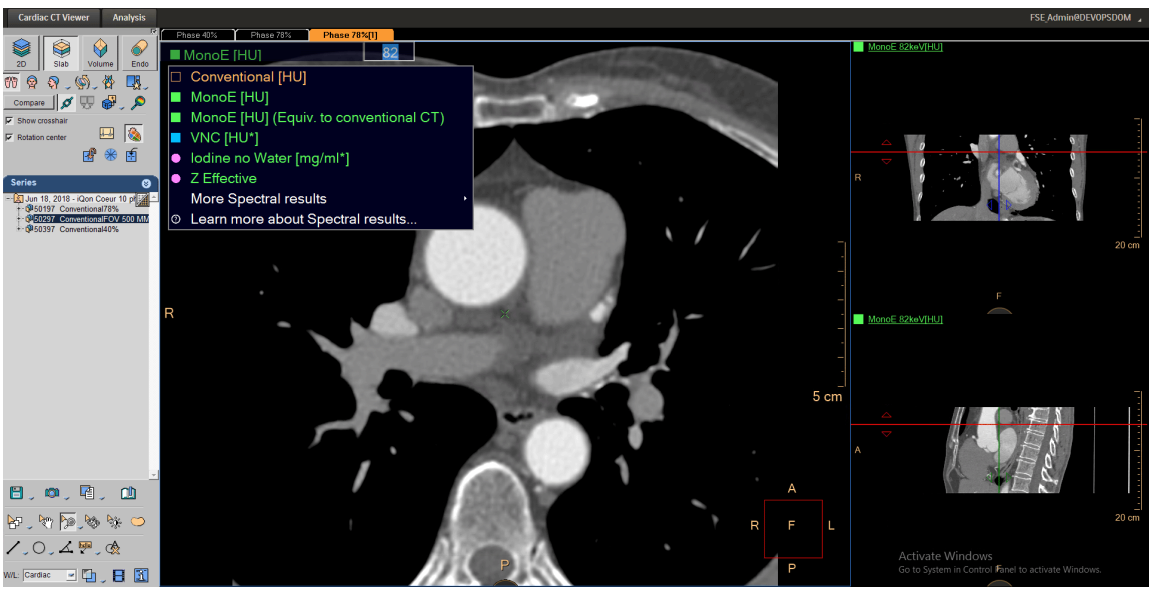
Indications for Use

The CT Cardiac Viewer is indicated for viewing, processing and analysis of cardiac CT datasets.

Enabling Spectral Image Viewing

The CT Cardiac Viewer application includes spectral capabilities that are enabled via the datatype selector (or dropdown menu).





These spectral capabilities introduce a system based on two layers of detectors, allowing simultaneous high and low energy discrimination.

The acquired dual energy data can be combined to reconstruct standard CT images. This “spectral” data can be used to produce new types of CT images, allowing users to extract additional tissue information, leverage image quality and increase the visualization of unenhanced and contrast media enhanced tissue.

Recent research results have shown additional clinical value such as the quantification of contrast-enhanced tissues. [1]

[1]Pelgrim, G.J., van Hamersvelt, R.W., Willemink, M.J. et al. Accuracy of iodine quantification using dual energy CT in latest generation dual source and dual layer CT. Eur Radiol 27, 3904–3912 (2017). https://doi.org/10.1007/s00330-017-4752-9

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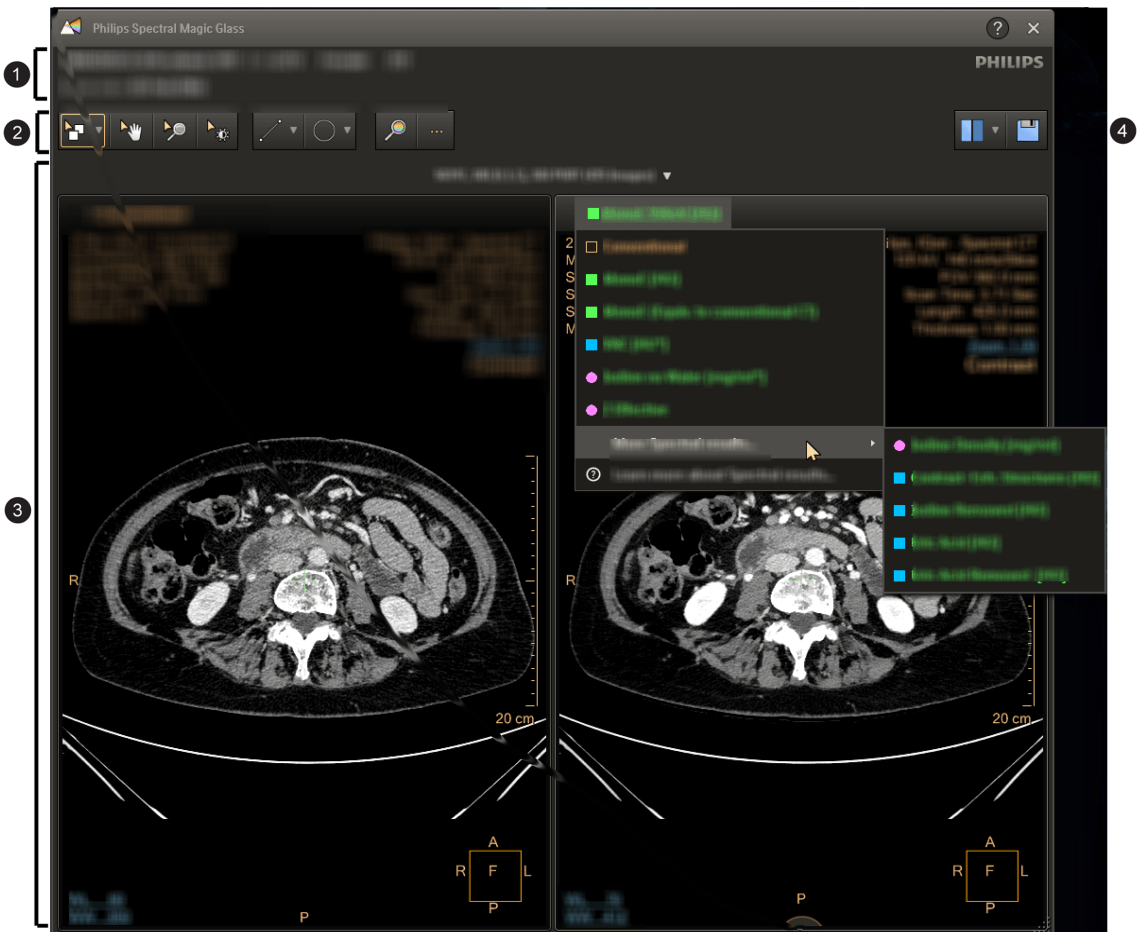
7 Spectral Magic Glass on PACS

The Spectral Magic Glass on PACS introduces a set of tools to enhance the viewing of spectral CT images directly within the PACS viewer, in order to assist personnel in visualization and analysis of anatomical and pathological structures. It is intended to be used for review and spectral analysis of any Philips spectral CT dataset.

Indications for Use

The CT Spectral Magic Glass on PACS (sMGoP) provides a set of tools to review and analyze Philips spectral CT datasets directly within the PACS viewer.

Application Window



1. Patient, Study, and Series Information
2. Toolbar
3. Images

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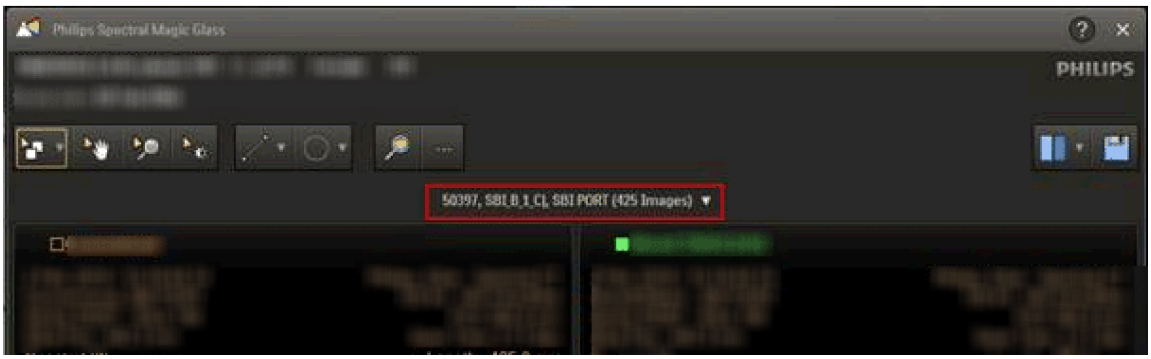
4. Layout, Save

SBI Selector

The SBI Selector is accessed from the dropdown menu that appears above the sMGoP viewports.



- The SBI Selector enables selecting an SBI series from which images will be displayed in the sMGoP viewports.
- When selecting an SBI series from the SBI Selector, the sMGoP viewports display images from the selected SBI series in all of the viewports (Note: The displayed series in PACS viewer will not change).
- The SBI Selector shows all the SBI series that are available for the same study as the images in the PACS viewer from which the sMGoP was activated. -
- The SBI series displayed in the SBI Selector may belong to the same acquisition as the images displayed in the PACS viewer, or to other acquisitions in the same study. Therefore, the SBI series are divided to two groups (when applicable): **Same acquisition as the series from which sMGoP was opened** and **Other acquisitions**.
- Each SBI series in the SBI selector has the following information displayed next to it: representative conventional thumbnail, series number, series description, number of images, slice thickness and increment, reconstruction filter and contrast indication (when applicable).

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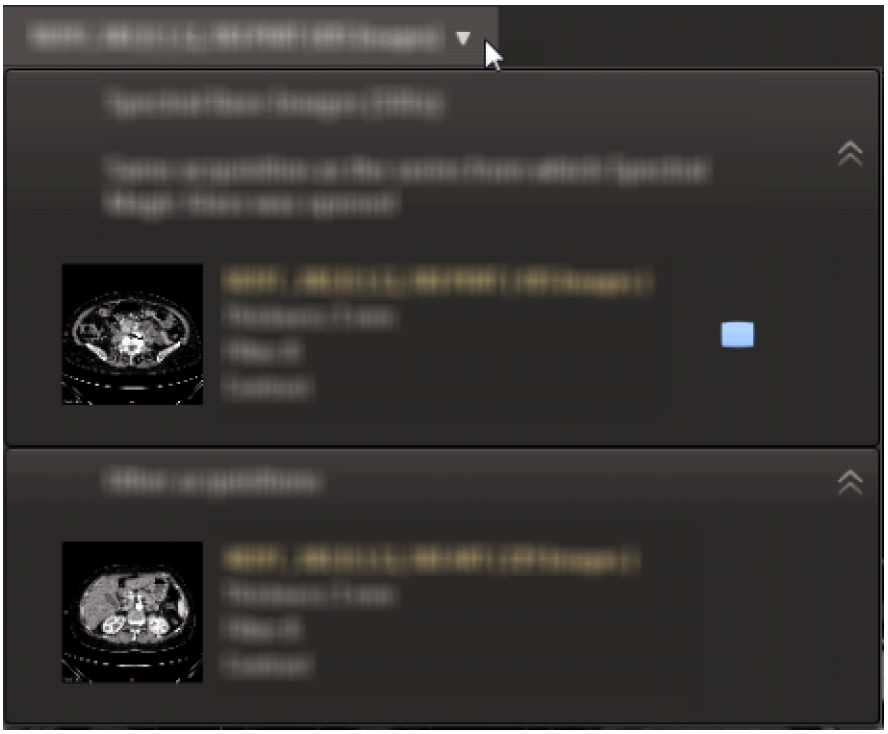
The currently selected SBI, which is used in the sMGoP viewports, displays the following indication in the SBI Selector  .



Supported PACS Versions

The following PACS versions are compatible with Spectral Magic Glass.

	PACS Type	PACS Version	ISP Version
1.	Sectra	All	ISPv6.5.3 , V9 and above
2.	iSite	4.4.x	
3.	Carestream	Vue PACS- version 12.1.5.0.440	
4.	AGFA	IMPAX EE, Rel 15.SU2	
5.	Telmis	TM-Reception- High End 4.70.32194	
6.	PSP	EV Insite.R	
7.	INFINITT	• V5.0 • V3.1 • Model G V11.3	
8.	GE	Centricity	

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	PACS Type	PACS Version	ISP Version
9.	FUJI SYNAPSE	Version 4.4.100	
10.	MDC	2.4	ISP V10 and above
11.	Neusoft	PACS-RIS 5.5	ISPv6.5.3 , V9 and above
12.	Illumeo	V3	TBD

NOTICE

PACS vendors must have the correct licensing level for external integration.

Activation from PACS Viewer

The Magic Glass on PACS is activated from the viewports within your PACS Viewer. It is configured as a plugin to the PACS. The activation method will vary depending on your specific PACS Viewer.

The Magic Glass on PACS can be activated via several different methods, depending in your PACS:

- Right-click on a view in the PACS and select the **Spectral Magic Glass** option.
- If the PACS Viewer allows you to configure a shortcut to activate a plugin, point to a view in the PACS and press the hot-key as defined by your configuration.
- Launch from an SBI series.

When activating the Spectral Magic Glass on PACS:

- The plugin identifies the study and the series within the view on the PACS
- The plugin identifies the active axial slice shown within the PACS Viewer
- The plugin retrieves the matching spectral information
- The Spectral Magic Glass shows a conventional series and axial slice matching the series shown within the PACS viewer, comparing it to one of the Spectral results.

WARNING

It is always recommended to compare the spectral results with conventional images prior to finalizing diagnosis.

Conditions for Activation

The Spectral Magic Glass on PACS can only be activated for series in which:

- The viewed series is a CT series scanned with the Philips IQon Spectral CT system.

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- The viewed series (usually conventional) has a matching SBI series available within a local directory of IntelliSpace Portal. A matching SBI series is an SBI series which shares the same acquisition as the series viewed on the PACs. In addition:
  - The SBI series must not be flipped in orientation compared to the viewed series
  - The SBI series must match (at least partially) the viewed series in the patient's X axis

If all conditions are met, the Spectral Magic Glass can be activated. If one or more of the above conditions is not met, the Spectral Magic Glass cannot be activated for the currently displayed series within the PACS viewer.

WARNING

Some DICOM viewers may be incompatible with non-HU images. This can result in erroneous measurements.

PACS Without Series Level Integration

If the PACS system integration provides study level integration without series level integration, the Spectral Magic Glass is presented with the SBI selector open, allowing the selection of the desired SBI that will be displayed in the viewers.

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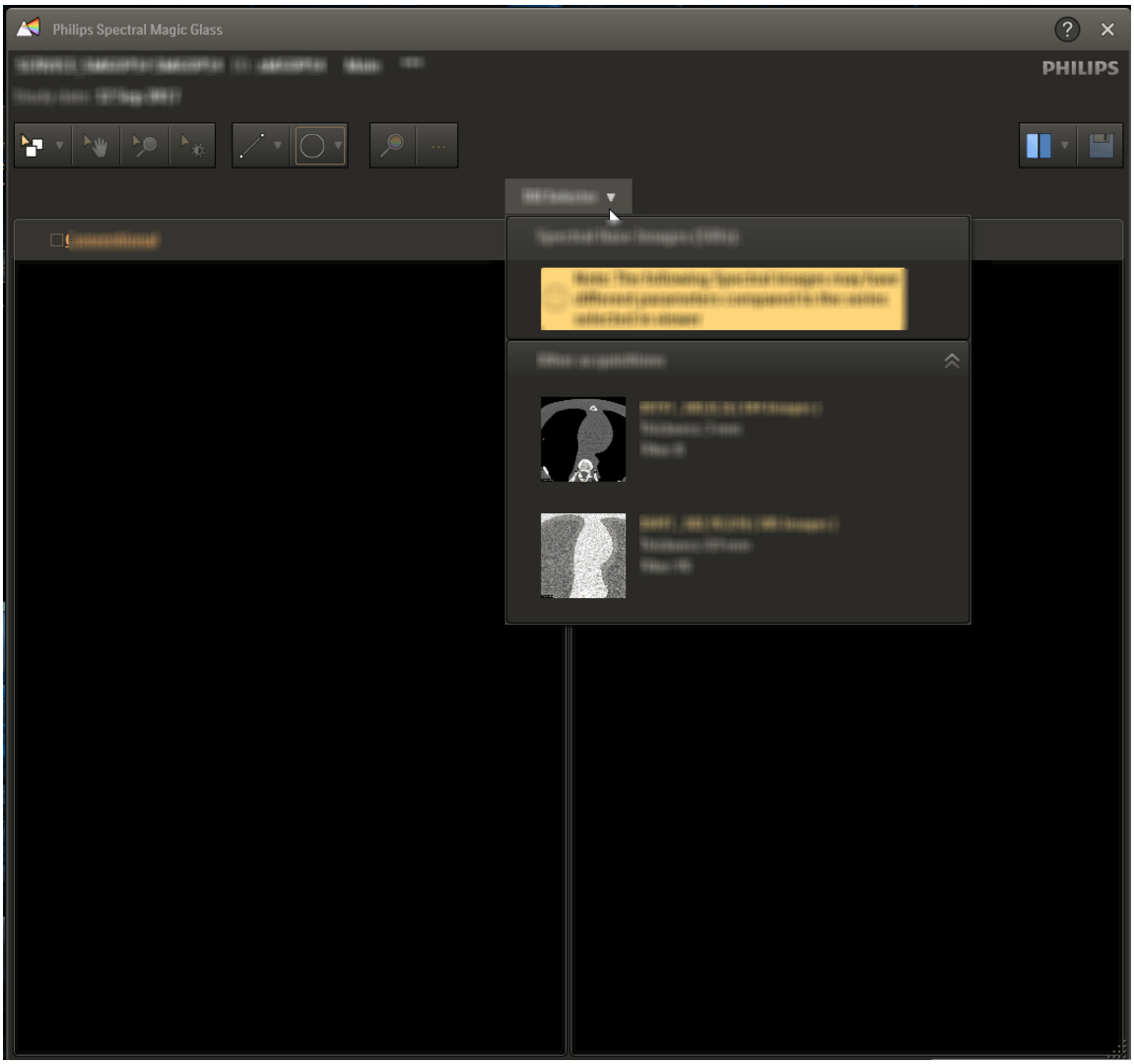

Series Mismatch

If no SBI series is available matching the images series shown within the PACS viewer:

1. Open a different series from the study that has a matching SBI series and activate the Spectral Magic Glass.
2. Reconstruct an SBI series on the IQon Spectral CT scanner with the required parameters (refer to the document IQon Spectral CT Instructions for Use for more information).

   If other SBI series are available in the same study that do not match the image series shown within the PACS viewer, the Spectral Magic Glass is presented with the SBI selector, allowing the selection of another SBI from the same study to be displayed in the viewers.

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Possible Mismatches

The following are potential mismatches that may occur between the Spectral Magic Glass and the PACS viewer.

Thickness Mismatch

The Spectral Magic Glass on PACS opens with the original slice thickness as embedded in the DICOM information of the matching SBI series.

The thickness of the series displayed in the Spectral Magic Glass may differ from the thickness of the images displayed in the PACS viewer.

A thickness mismatch can occur in some PACS viewers, in specific modes, when changing the slice thickness within the PACS Viewer and then activating the Spectral Magic Glass on PACS, the Spectral Magic Glass on PACS shows the original slice thickness. This scenario can occur if the series viewed within the PACS viewer allows activating the Spectral Magic Glass from an MPR view or volume (3D).

WARNING

Upon activating the Spectral Magic Glass on PACS, note the thickness annotation shown on the images as in certain cases it may differ from the series Spectral Magic Glass was activated from.

Orientation Mismatch

The Spectral Magic Glass on PACS opens with Axial image orientation as embedded in the DICOM information.

In some PACS viewers, in specific modes, flipping the orientation within the PACS Viewer (e.g. change from right on left to left on left display), activates the Spectral Magic Glass on PACS, the Spectral Magic Glass on PACS shows the original orientation (e.g. right on left). When activating the Spectral Magic Glass on PACS from an MPR image, the Spectral Magic Glass on PACS shows Axial orientation.

WARNING

Upon activating the Spectral Magic Glass on PACS note the orientation annotations shown on the images as in certain cases it may differ from the series Spectral Magic Glass was activated from.

Study or Series Mismatch

Always double check that the patient, study and series information of the loaded images within the Spectral Magic Glass on PACS match your expectations.

The patient, study and series details are also viewable as image annotations.

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WARNING

Verify the patient, study and series details to the upper left of the toolbar.

Displayed Slice Mismatch

In some cases, the plugin cannot detect the exact slice location shown within the PACS view. In these cases the loaded series will display the middle slice within the series.

WARNING

Verify that the axial slice displayed within the Spectral Magic Glass is the one you intended to examine.

Other Mismatches

The Spectral Magic Glass on PACS opens with the original images belonging to the SBI series that was identified as the closest one that matches the series in the PACS viewer. Therefore, the images displayed in the Spectral Magic Glass on PACS may differ from the series in the PACS viewer in some of its parameters (e.g. anatomical area, slice thickness & increment, image order, FOV, reconstruction filter etc.). In addition, any post-processing performed within the PACS viewer (e.g. enhancement, processing filters, changing to MIP, etc.) will not be shown within the Spectral Magic Glass on PACS.

WARNING

It is always recommended to compare the spectral results with conventional images prior to finalizing diagnosis.

WARNING

When you load Spectral Magic Glass on PACS note that you are viewing the original images, without any post processing performed on the PACS.

Viewport

The top of the Magic Glass on PACS window displays information such as patient name, ID, gender, and age, and series or study details. The window can be resized to fit your needs. Click and drag within the MGoP field of view to scroll between image layers.

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MonoE Images

Each monoenergetic viewport includes controls to change the viewed energy level. When you click the control parameter, a selection box opens. There are three ways to change parameters within selection boxes:

- Click and highlight the current parameter in the selection box and type a new one over it.
- Click the parameter selection box arrow buttons up or down to change the parameter.
- Use the slider bar in the selection box slider to scroll continuously through energies (40 keV to 200 keV).

Tools and Settings

Tool	Name	Description
	Fast Scroll	Used for rapid viewing of images on the monitor by dragging the mouse cursor in the viewport.
	Continuous Scroll	Continually scroll through the images without skipping any images.
	Pan	Move (drag) an image within a viewport or frame. It allows you to center the feature of interest in the viewport by dragging the image in the window.
	Zoom	Used to magnify or reduce the size of the image in the display.
	Change Window Level	Drag the mouse in the active viewport up and down, and left and right, to change window level.
	Line	Lines are used to measure distances on images in millimeters.
	Double Line	Double line allows you to place two lines on the image for measuring vessel or organ diameters.
	Circle ROI	Used to create a circular graphic around a region of interest. Drag the mouse to enclose the desired region. Release the mouse button to end the drawing.
	Ellipse ROI	Used to draw an area oval in shape around the region of interest. To start the ellipse, click the mouse at the center point of the region and drag to the desired size. Release the mouse button to end the drawing.

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Tool	Name	Description
	Spline Contour	Used to create a region of any user-defined shape. A Spline ROI has rounded “corners.” While drawing the Spline ROI, wherever you click is where a vertex is set. Doubleclick on the last point to end the drawing.
	Local Magic Glass	Opens a rectangular ROI window in the viewport. Point to the ROI window to show control points. Click and drag these points to resize the ROI window. Upon activation, two satellite views open. These show the same anatomic regions as the rectangular ROI, except with different spectral image types. Use the mouse wheel or the Scroll tool within the satellite views to scroll through images. Right-click within a satellite view to access line measurement, ROI measurement, and save options, or to add another satellite view.
	Reset All	If changes have been made to the image, this function resets the current scene to its original state when it was loaded into the application.
	More tools menu	Dropdown menu of additional tools.
	Show relate cursor	Shows or hides the relate cursor. Click on any pixel in any viewport. The location of that pixel is automatically marked on the other viewports.
	Angle	Draws two lines, joined at a vertex, which may be placed along two image features to measure the angle between them.
	Draw Text+Arrow	Used to point to features of interest on the image and, if you desire, type in corresponding text.
	Show/Hide Image Titles	Toggles image title display on and off. The spectral label, patient name, and patient details are not hidden with this option.
	Remove All Graphics	Removes all added graphics from the image.
	Layout 1 x 1	Sets the layout to a single image.
	Layout 1 x 2	Sets the layout to two images side by side.
Set current display as default		Sets the layout of the floating window and the spectral result types shown within each viewport. This setting also determines whether the Local Magic Glass tool is on or off, as well as the spectral result types shown within the tool.

Tool	Name	Description
Restore Factory Preset		Restores the default layout for future uses of the application (default is image on PACS side by side with monoE70).
Left and Right **<Alt>** keys (on keyboard)		Used to change spectral results by selecting the right **<Alt>** key to go forward (in dropdown menu) and the left **<Alt>** key to go in the opposite direction.
Up and /Down arrows (on keyboard)		Used to change energy level and Idx values (by selecting the Up or Down arrows on the keyboard).
Space Bar (on keyboard)		Used to reset to Conventional spectral results.
	Save All Displayed Images	Saves a series of images, one for each viewport within the Spectral Magic Glass window.
	Copy Screen Snapshot to Clipboard	Available from Context menu (and **Ctl+C** shortcut). Copies the screen display of the sMGoP to the clipboard (including the local Magic Glass when it is open) and can then be pasted.
	Save This Spectral Result As a Series of Images	Available from Context menu. Saves the selected spectral result (the one that the context menu was opened for) as a new series in a destination according to the user's selection (via Save window).

Spectral Series

For detailed information on spectral results and spectral reconstructions, see section "Understanding Spectral Results" on page 11.

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8 CT Spectral Light Magic Glass

The CT Spectal Light Magic Glass (LMG) option enables the user to review spectral data in a range of CT applications that are not Spectral enhanced.

The purpose of the Light Magic Glass option is to allow retrospective use of spectral data that was saved as an SBI.

The Light Magic Glass option allows fast review of spectral data and identification of most relevant results to be launched into the conventional CT application for routine work.

The option is available from the following applications:

- Brain Perfusion
- Functional CT (FCT)
- Liver
- PAA
- TAVI
- Trauma Viewer (Acute Multifunctional Review)
- Virtual Colonoscopy

Spectral Magic Glass can be launched only for images that meet the following conditions:

- CT images
- Images were created on the Philips Spectral Detection CT IQon

Indications for Use

The CT Spectral Light Magic Glass (LMG) option enables the user to review spectral data in a range of CT applications that are not spectral-enhanced.

Launching CT Spectral Light Magic Glass

Launch theCT Spectral Light Magic Glass option using either the  Spectral Magic Glass icon in the upper tool box, the **F5** key or the **Spectral Magic Glass** option in the context menu.

Once launched, the sMGoP (Spectral Magic Glass on PACS) application is launched from ISP.

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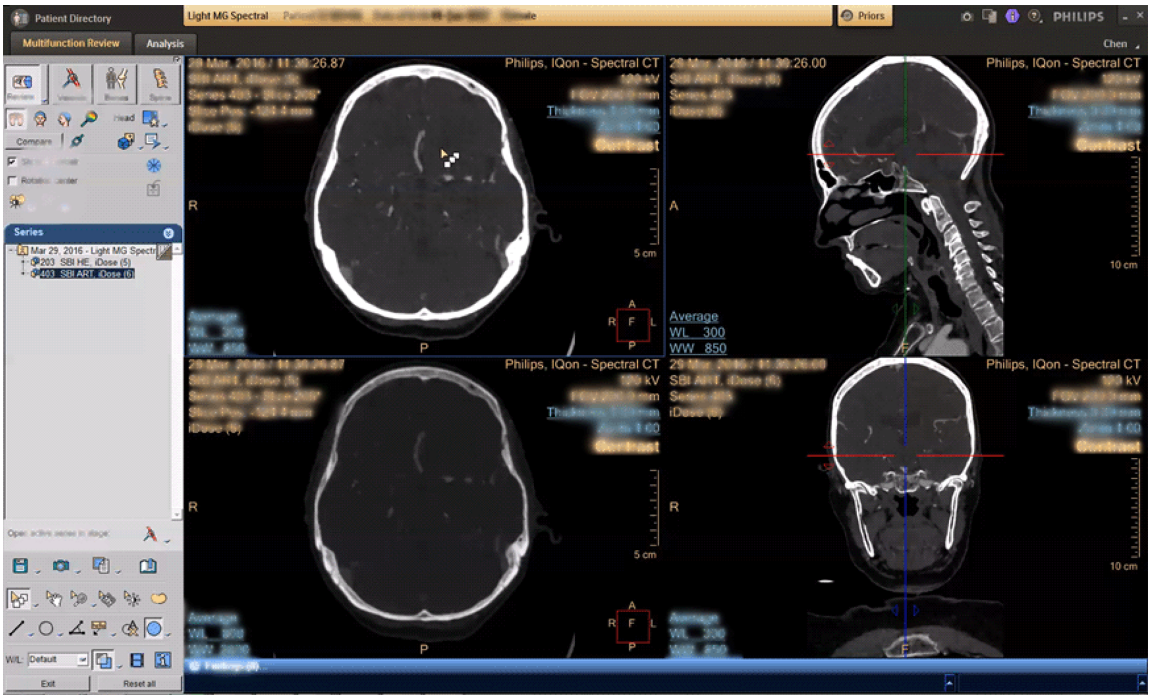

For information on working in this application, please refer to section “Spectral Magic Glass on PACS” on page 47.

Functionality

- The LMG dialog is movable and resizable.
- The LMG dialog closes once the sMGoP application is closed.
- It is possible to keep working with the sMGoP application while the LMG dialog is open.
- It is not possible to open more than one LMG in parallel (a message is displayed when attempting to do so).
- If LMG is launched when an axial viewport is active, LMG will show, by default, the same slice as displayed in the Axial viewport .
- If LMG is launched LMG when a non-axial viewport is active, LMG will display, by default, the middle slice of the series.

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9 Spectral Advanced Vessel Analysis

The optional Advanced Vessel Analysis (AVA) application offers a set of tools for general vascular analysis and stent planning from body and skull (head and neck) studies. Automatic and semi-automatic bone removal functions (one for body and one for skull) are available, as well as manual methods of bone removal.

NOTICE

Before continuing, refer to the “Instructions for Use” that came with your scanner.

Automatic vessel centerline extraction is performed after bone removal. Lumen (inner) and vessel (outer) contours are generated after body bone removal (for skull, lumen contours only). Vessel contours include hard plaque (mostly calcium) and thrombus (partially). Automatic vessel labeling of major vessels is performed, if detected. Other unlabeled vessels (in body studies) are available for the user to review and label.

WARNING

It is always recommended to compare the spectral results with conventional images prior to finalizing diagnosis.

WARNING

When loading images into Advanced Vessel Analysis, all images which contain 16 bit data are converted into 12 bit images. This means that for rescale intercept equal to -1000, HU values above 3095 are displayed as 3095. For rescale intercept equal to -1024, HU values above 3071 are displayed as 3071.

Various review modes may be used, such as Volume Rendering, Maximum Intensity Projection, Volume Intensity Projection, Axial/Coronal/Sagittal orientation, and curved MPR view with cross-sections.

Images show aneurysms, the presence of mural calcification and lining mural thrombus, and branch vessels.

Image viewing features in AVA can provide valuable information when analyzing vessels.

Measurements are provided for vessel assessment, including maximum and minimum cross section diameters, lumen areas, and vessel lengths

Also available is the Stent Planning stage that allows you to assess suitability of stent graft placement. Available measurements include length and tortuosity of vessel segments and the angles of vessels.

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AVA Application Stages

1. **Bone Removal** is the first workflow stage. Use the Bone Removal stage to make sure that automatic bone removal and vessel centerline extraction has been correctly performed. The Bone Removal stage provides tools and functions that help you to examine the results and make corrections as needed.
2. **Vessel Extraction** allows you to view the extracted vessels in high detail. In this stage you can extract new vessel centerlines, extend centerlines beyond where they were automatic extracted, correct centerline placements, and correct vessel contours.
3. **Measurements** allows you to view and save quantitative measurements about vessels, such as cross-sectional areas, diameters, vessel lengths, stenosis estimation and thrombosis estimation.
4. **Stent Planning** allows you to access quantitative information and stent design parameters for configuring stents and other interventional devices.

NOTICE

Clicking on the left or right arrows of the workflow menu will return you to the previous work stage or advance you to the next work stage. Clicking on the down-arrow allows you to select from the list of workflow steps. (A grayed out right arrow or work stage name means that you have not finished the current work stage.)

NOTICE

While following the workflow, you can go back to a previous stage without losing any work performed in the current stage. However, returning to a previous stage and making changes (for example, returning to Vessel Extraction from the Measurements stage and making changes to vessel contours) affects your previous work.

Load Multiple Studies in Application

To load multiple studies in the application:

1. Use the **Ctrl** key when selecting studies from the Directory list.
2. Select the application from the Applications menu.
3. Confirm the studies are from the same patient.

NOTICE

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

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Indications for Use

The CT Spectral Advanced Vessel Analysis (sAVA) application is intended to assist clinicians in viewing and evaluating CT Angiography (CTA) cases, as contrast enhanced and whole body CTA scans, acquired on the IQon CT scanner for the inspection of contrast-enhanced vessels.

About Body Studies and Skull Studies

When processing the two types of studies, the AVA application uses two distinct software algorithms to remove bone, extract and name vessel centerlines, and contour vessels.

There are some differences in the operation procedures of the two algorithms. These differences will be explained as they occur.

Also, there are some differences between the results of the two algorithms:

- The skull version produces only lumen (inner) contours, while the bone version creates both lumen and vessel (outer) contours.
- In Body studies, a bone that may have been missed by the automatic bone removal process can be removed with a single click. In Skull studies, bone removal is virtually complete, and bone editing is not available.

Warnings for All AVA Studies

NOTICE

Always use the original CT images to correlate existing pathology and/or anatomical study.

NOTICE

Advanced Vessel Analysis should not be used as the SOLE incontrovertible basis for clinical diagnosis.

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WARNING

Verify that Bone Removal does not effect vessel completeness.

Verify the accuracy of the centerline curves on the screen and correct them manually when required.

Verify the accuracy of the cross-sectional lines on the screen and correct them manually when required.

The volume image displays the anatomy according to the defined protocol. Do not use the volume image as the sole basis for a diagnosis.

When thick-slice Brain images are viewed in the slab mode some partial volume artifacts might occur.

Cross sectional images might rotate around the centerline. Please note orientation annotations on images.

In cases where the orientation annotations are not displayed on the image - you must not assume any specific orientation. For correct orientation information - use only the images which display such information.

One or more of the following image types may appear in this application: curved MPR, straightened MPR, volume images, and thick slab images. Measurements you make on such processed images can sometimes be misleading. When saving such images, make sure they are labeled properly. (AVA automatically provides a default description for most images when you save them. You can edit the name if more description is desired.)

Objects in thick curved MPR images may appear distorted. Use caution when making measurements on MPR images.

When using the Inject Dye (3D) tool verify the correctness of volume segmentation. If necessary, correct the dye tracing using correction tools supplied by this application.

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Warnings for AVA Studies Employing Skull Removal

WARNING

A thin layer of residual bone in the siphon can mimic calcium plating along a vessel. Use Curved MPR as cross reference to verify correct segmentation.

Automatic segmentation may force a connection even through a completely occluded vessel. Use Curved MPR as cross reference to verify correct segmentation and accurate vessel delineation.

Results do not include soft plaques or calcium deposits within the contour boundaries. Use Curved MPR and Cross Sectional Cuts as cross reference to verify correct segmentation.

Strong dental or metal artifacts may impair the accuracy of the segmentation. This may compromise vessel quality near affected regions. Use Curved MPR and Cross Sectional Cuts as cross reference to verify correct segmentation.

Neck-only scans should include enough brain tissue for good segmentation. Verify that the Carotid entry into the Circle of Willis is included in the scanned volume.

Proper contrast timing is required for good results. Poor contrast timing can cause veins to have higher HU than arteries. Contrast in the jugular vein, for example, can cause it to be extracted, instead of the artery.

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Bone Removal

Bone Removal Methods for AVA	
Bone Removal during Launch (an available software option) 8 gByte memory required (The “one-click” option)	On systems with this Processing option, you can select the desired study from the Directory and activate the Bone or Skull Removal function during launch. The removal process works in the background, while you work on other tasks, and you can observe the process and results in the Queue Manager. The results are saved in the directory. When the series is loaded with the result series, the study will open with the bones removed.
Bone Removal after Launch (included in the AVA software)	You can perform Bone Removal after opening the study into the AVA application. This will take several minutes to complete. Some functions available in Processing are not performed by this method, where noted.
Manual bone removal	Manual bone removal functions are also available with the Clip functions.

NOTICE

Bone Removal during Launch Processing is a purchasable option. Bone Removal during Launch is not applicable to scans acquired using the CTA exam protocol.

The Bone Removal during Launch and Bone Removal after Launch functions perform a full bone/skull removal procedure on the conventional data.

One-click Processing

Systems with the “one-click” Processing option should use the following procedure before launching the study into the AVA application. (On 8 gByte systems, running this "one click" Processing might cause system slowness.)

1. Start in the Patient Directory.
2. Find and click on the desired study.
3. Under the Series tab of the study, right click the mouse to display the context menu.
4. Click **Run Processing**.
5. There will be 2 AVA options: AVA - Skull Removal and AVA - Bone Removal.
6. Select the relevant AVA option, depending on whether you are working with a body scan or a head and neck scan.

Processing begins. When done, the study opens with the bones removed and the vessels extracted and contoured.

Remove Bone on Launch

If you load a study into AVA without using an automatic Processing function, the application examines the study’s DICOM data to identify the Scan Procedure.

If the Type of Scan Procedure Is Clearly Identified

If the scan procedure is clearly identified, either as a body study, or a head and neck study, AVA opens in the appropriate first stage, Bone Removal or Skull Removal.

If the Type of Scan Procedure Is Ambiguous

If AVA cannot identify the scan procedure type as body or head and neck, you will have to identify it for AVA. When the study’s identification is ambiguous, AVA will open with the Series tab.

Point to or click the tab drop-down arrow. From the list of Function tabs, select the appropriate Removal tab.

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Remove Bone After Launch

This describes the “Remove All Bones” and “Remove Skull” procedure after a study is launched in AVA.

NOTICE

When to use this procedure:

- if your system does not have an optional Processing function;
- if you choose not to use the Processing option; or
- if the Processing option failed to perform Bone Removal.

At the top of the Bone Removal tab or Skull Removal tab are the functions to **Remove All Bones** or **Remove Skull**.

1. Click the appropriate button. The automatic Bone Removal or Skull Removal function is initiated.
2. The function will take several minutes to complete. A progress message is displayed in the lower right corner.
3. Once the results are done, you can proceed through the AVA application.

Bone Removal Work Stage

The Bone Removal work stage provides tools and viewing functions that help you to assess and correct, if needed, the results of automatic Bone Removal processes.

NOTICE

If you have not performed automatic Bone Removal Processing, do so now. See section “Bone Removal” on page 65.

Most of these instructions apply also to Skull studies. For additional information relating specifically to Skull studies, see section “Bone Removal Stage with Skull Studies” on page 74.

Below is the “one by two” layout after Bone Removal processing. The “Vessel View” image is at left, the “Bone View” image is at right.

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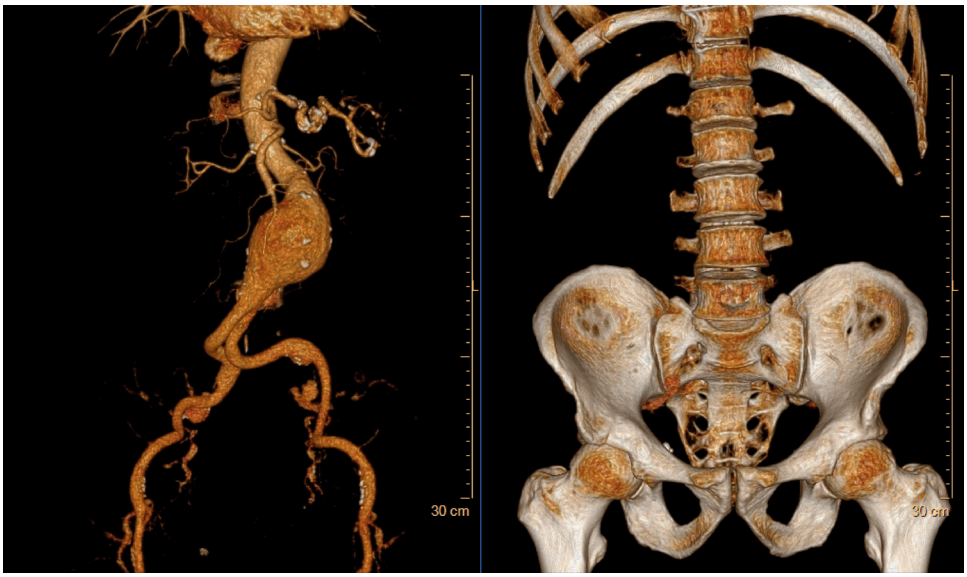

WARNING

Verify bone removal does not affect vessel completeness. If necessary, manually correct the vessel definitions using the correction tools provided in this stage.

Image Types

In any viewport, you can choose to view Conventional or MonoE images. Pause the pointer on the name of the data type to see the options; and click to make your selection. In addition, you can adjust the MonoE keV level using the accompanying arrows. These actions adjust the associated viewports accordingly.

Remove All Bones

This button initiates the Manual Bone Removal function (see section “Remove Bone After Launch” on page 67). When bone removal has been done, clicking on this button returns the display to the original volume view.

Add Vessel

This tool is available on the 3D Bone View and is the recommended tool for moving small to medium sized vessels that are hugging bone, from the Bone View into the Vessel View.

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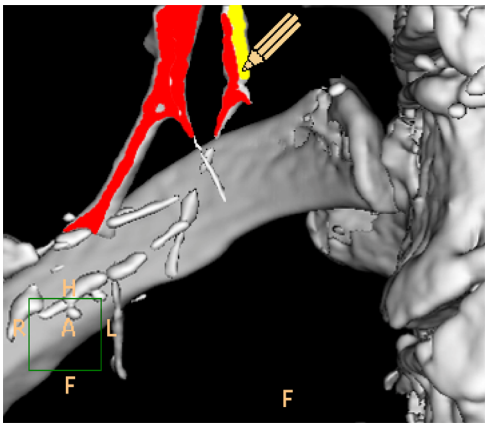


1. Click the **Add Vessel** button to activate the function. The Bone View image is rendered in grayscale (monochrome). The mouse pointer is a pencil.
2. Point to a vessel you want to “add” (“move”) from the Bone View to the Vessel View. The area of the vessel within a range of HU values is highlighted in yellow.
3. If the area is acceptable, click on it. It is now highlighted red.
4. Point to additional vessel volumes to highlight them in yellow. Click the mouse to accumulate them.
5. When the entire vessel is defined click Accept Vessel. The accumulated vessel volume is moved from the Bone View to the Vessel View.

For vessels that are very closely hugging the bone, altering the Threshold of the image, using the middle mouse button, may provide some separation between the bone and vessel, and thus make the Add Vessel tool more effective.

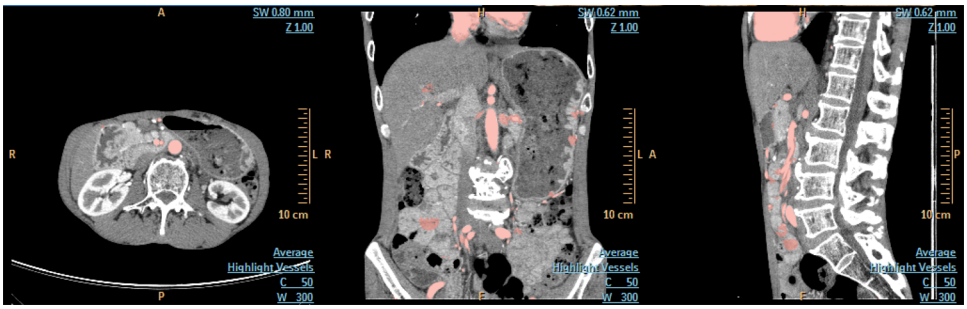
NOTICE

For small vessels, you should zoom in on the vessel before applying the Add Vessel function. This can reduce the number of clicks needed on the vessel to select it.

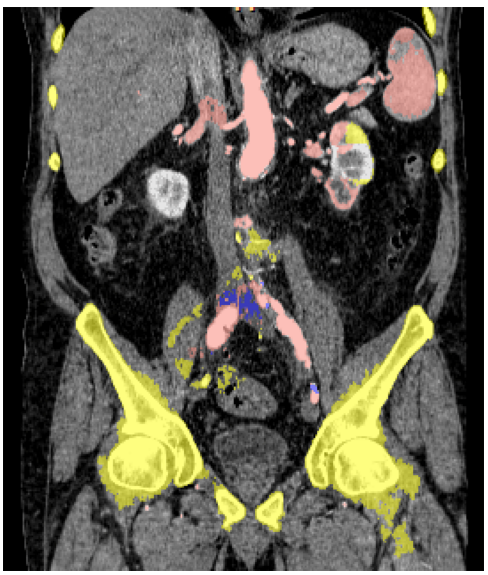
If the vessels are not hugging the bone or if the vessels are large, you should use the Smart Sculpting tool, optionally with a bounding box, for quickly moving vessel from the Bone View to the Vessel View.

Highlight Vessels

You can view colored vessel and bone overlays in the reference images. (This feature is not available in the One by Two layout.)



By default, the vessels are shown with pink overlays (shown above). Click on the Highlight Vessels viewport control to access all highlight options. The Highlight Vessels & Bones option, with vessels having a pink overlay, and bones with a yellow overlay is shown below.



Remove Bone

You can remove bone fragments that remain in the Vessel View. These fragments were mistakenly classified as vessels. The bone you remove from the Vessel View is moved into the Bone View.

1. Click the **Remove Bone** button.
2. Point into the Vessel View image. The pointer becomes a pencil.
3. Click on a bone fragment in the Vessel View image. Monitor the Bone View image and observe the fragment move into it.

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3D Sculpting (Freehand Exclude)

You can use this function to remove tissue(s) in the Bone View. This function works on the volume and the reference images. It works regardless of whether the tissue is vessel or bone, and regardless of the HU of the tissue. Sculpting cuts through the entire volume.

Show Calcium on Vessels

This function allows visualization of calcium in the vessels. It is helpful when vessels are completed or partially occluded due to calcified plaque. The function toggles high density residuals from the Vessel View to the Bone View. Stent grafts are included in the “calcium tissue.”

MEASURING VOLUME OF CALCIUM

In the 1+3 and 2x2 layouts, with the volume rendered viewport selected, if you click on the Calculate button, the Vessel View image frame shows the volume of all remaining tissue and calcium in green text. If you uncheck Show Calcium on Vessels, the calculated volume will be reduced by amount of calcium in the vessels and aneurysm. The difference between the two values is the volume of the calcium.

Show Vessels / Show Bones

This viewport control function is in the lower right corner of Volume viewport in the 1+3 and 2x2 layouts. Use this function to switch the image between the Vessel View and the Bone View.

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Smart Sculpting

Smart Sculpting is useful with the following types of editing tasks:

- Moving floating bone fragments from the Vessel View to the Bone View.
- Moving “floating” vessel sections (small vessel sections that are not close to bone) from the Bone View to the Vessel View.
- Moving sections of large vessel from the Bone View to the Vessel View.

  It can be difficult sometimes to avoid including unwanted tissue in a sculpted region. You can use a bounding box in conjunction with the Smart Sculpting function to constrain the sculpting within the bounding box region.
- Move a number of closely spaced calcifications from the Bone mask to the calcification mask.

  Note: All tissue within the sculpted region that is not calcification will be moved to the contrast mask.

The Smart Sculpting function works in the volume image, either the Bone or Vessel View. You can move bone from the Vessel View to the Bone View, and move vessel from the Bone View to the Vessel View.

When used in the Bone View, Smart Sculpting will remove all the tissue in the cut region and put it in the contrast view.

Smart Sculpting does not cut through the entire volume but stops after the higher-intensity parts. When a MIP image is displayed there will not be a black “hole” in it.

When used in the Vessel View, the Smart Sculpting will perform the following:

- it will move to the Bone View all tissue within the cut region that was incorrectly determined to be vessel; and
- it will move to the Bone View any high intensity pixels of the remaining tissue in the cut region.

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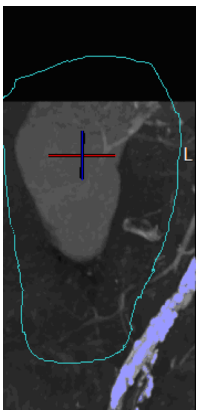
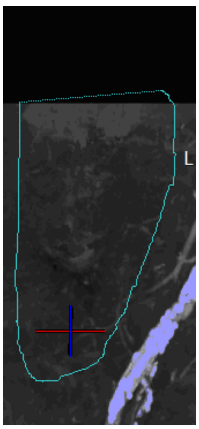
Repeating the Smart Sculpting Function

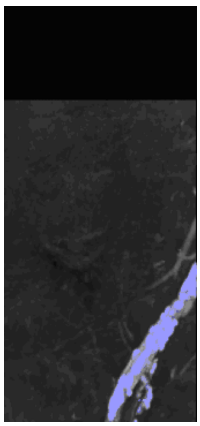
Using Smart Sculpting on a region more than once can progressively move lower and lower non-vessel contrast to the Bone View. As an example, the following pictures illustrate two successive Smart Sculpting operations:



Smart Sculpting applied to kidney area.



Result of first Smart Sculpting. A second kidney removal sculpting is applied.



More kidney is removed by the second sculpting.

Whole Volume

This viewport control function (also referred to as the “Quick Focus” function) is in the upper right corner of Volume viewport in the 1+3 and 2x2 layouts. Click on the desired anatomical region, and the region is zoomed to fit the viewport and is centered in the field of view.

NOTICE

Remove Bone is recommended for quickly moving "chunks" of bone from the contrast view to the Bone View.

If the bone region is diffuse with some gaps in the bone (i.e., not one contiguous piece), the 'Smart Sculpting' function is recommended for moving bone to the Vessel View.

Remove Bone will not "jump" across any gaps in the bone.

Remove Bones/Remove Skull on Selected Energy

You can use this function to re-run bone or skull removal on the current series. For example, you can change the MonoE energy level to 65 keV, and then use this function. The newly processed images replace the old/current ones.

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Bone Removal Stage Options and Tools

Use the options and tools (in the upper tool box) during each stage, except where noted, to modify the view and perform analysis.

Viewing Options, Common Tools, and Common Processes

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

Bone Removal Stage with Skull Studies

When you are working with Skull studies, some operations of the Bone Removal stage are different than when you are working with Body studies (see section “Bone Removal Work Stage” on page 67). This section describes those differences and the procedures to use them.

NOTICE

Series Tab - If, when you launch a skull study into AVA, the study cannot be identified as a skull study, AVA will open it with the Series tab active. To proceed, point to or click the tab drop-down arrow and select the Skull Removal tab.

Common Viewing Tools, Common Tools, and Common Processes

A number of tools and process functions are common throughout the Review and Analysis applications.

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

Skull Removal

The Skull Removal tab opens. Click the **Skull Removal** button to begin the process. When completed, the Skull Removal window appears. The major skull vessel centerlines have been extracted, named, and displayed.

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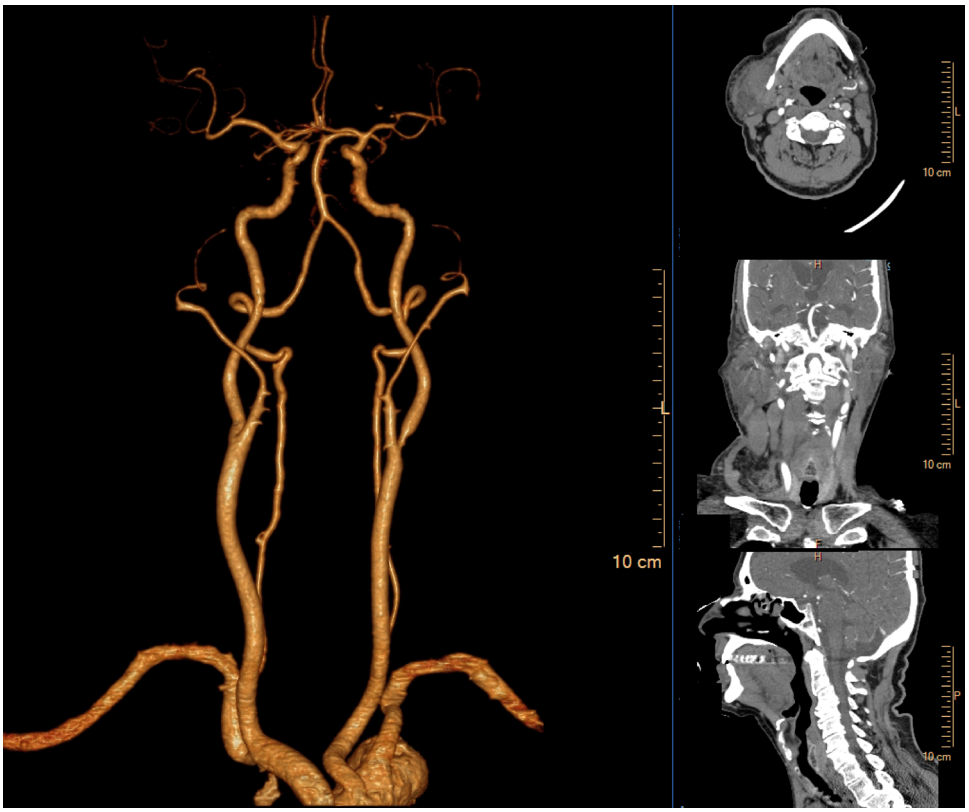

Show Names in Vessel List

The vessels have also been named, but the names may not be shown in the Vessel List. To show the names in the Vessel list:

- Click **Place Seed**.
- Click on any major vessel in the volume image.

In the Vessel naming list that appears, click **Cancel**. The Skull removal tab now lists all named vessels.

Assess Vessels in Skull Removal Stage

In the Skull Removal stage, bone removal is virtually complete, and bone editing is not available.

WARNING

Verify bone removal does not affect vessel completeness. If necessary, manually correct the segmentation using the correction tools provided in this stage.

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The main function of this stage is to allow you to examine the extracted vessels, and correct them by re-running a second Skull Removal.

Correcting vessel extraction is done as follows:

1. Examine vessels in the volume viewport. Look for incomplete or “broken” vessels.
2. If you find any problem vessel(s), click the **Place Seed** button.

3. Click on a problem vessel.
4. From the Vessel naming list, select the vessel name:
   - Right External Caro
   - Left External Carotid
   - Right Internal Caro
   - Left Internal Carotid
   - Right Vertebral
   - Left Vertebral
5. If more problem vessels exist, place seeds on them also, and name them.
6. To undo the last seed mark, click **Undo Place Seed**.
7. When finished marking problem vessels, click **Run Skull Removal**. Skull Removal processing is run, but only the vessels you marked are re-extracted; the other vessels are not re-processed.

Alternate Vessel Segmentation During Skull Bone Removal

You can perform semi-automatic segmentation on marked vessels only. This is done by placing seeds on one or more specific vessels, rather than allowing the Skull (bone) Removal function (see section “Bone Removal Work Stage” on page 67) to segment all 6 standard vessels.

1. Place 2 or more seeds on the desired vessel(s). The seeds are used as a guide to assist the semi-automatic segmentation process.
2. Click the **Remove Skull** button. A message appears, asking whether you want the Skull removal function to operate in either of 2 modes:
   - **Partial.** Segment only the seeded vessels and Brain tissue (including vessels)
   - **Full.** Use the full automatic algorithm for all 6 vessels
3. After clicking Remove Skull once, additional vessels can be extracted by placing seeds again, then clicking the **Accept** button.

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Vessel Extraction Work Stage

During the automatic Bone Removal process, other automatic functions were also performed: the vessel centerlines were extracted, the major vessels were named, and the vessel contours (both lumen and vessel for Body studies) were generated.

NOTICE

When a procedure is different for a Skull study, it is explained.

In this stage you should verify that:

- the centerlines are complete, properly located and positioned in the vessel centers;
- the vessels are correctly named; and
- the contours are correctly located.

You should correct any problems that exist in centerlines, such as the line not extending the full length of the vessel, being “broken” into parts, and not being extracted.

WARNING

Verify the accuracy of the vessels and their labels. If needed, use the manual tools provided in this stage of the AVA application to correct vessel extractions and labels.

When the Vessel Extraction Stage is launched, the labeled vessels appear in the list in the Vessel Extraction tab. Only one centerline and vessel name appears at a time on the volume image when you select it. Select vessel by clicking on the centerline in the volume image or by clicking its name in the Vessel Extraction tab.

Image Types

In the main viewport, you can choose to view from among all spectral results. Pause the pointer on the name of the data type to see the options; and click to make your selection. In addition, you can adjust the MonoE keV level using the accompanying arrows. These actions adjust the associated viewports accordingly. Additionally, the default workspace layout for Vessel Extraction includes a side-by-side display of the same anatomic region of two different spectral datatypes (default types are Conventional and MonoE). These viewports are geometrically linked.

Vessel Contour Functions

The Vessel Contours function allows you to examine the contours of the vessels as they were defined by automatic processing, and correct them as necessary.

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WARNING

Verify the correctness of the cross-sectional contours on the screen and correct them manually when required.

Contour Types

The Contours Type function allows you to display contours in the axial viewport and edit (correct) them. The default state (in the Body study) is the Lumen contour visible, the Vessel contour hidden, and Edit contours active.

Show Lumen Contours

When this button appears depressed, the Lumen contour is displayed. Click the button to hide it.

Show Vessel Contours

When this button appears depressed, the Vessel contour is displayed. Click the button to hide it.

Edit/Add Contours

The Edit/Add Contours function allows you to correct contours if automatic contouring was not precise enough. The Edit function is active by default. From the drop-down you can select to “draw contours” with buttons called Add lumen Contour and Add Vessel Contour.

Correct Contours

In the image below, both contour types are displayed. The Lumen contour is colored orange and the Vessel contour is blue. Statistical data is shown along with the vessel name and the image’s position along the vessel centerline.

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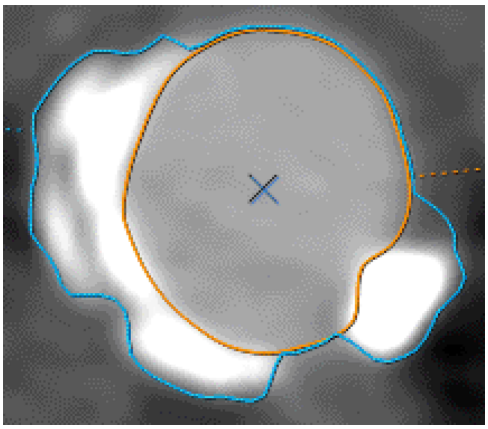
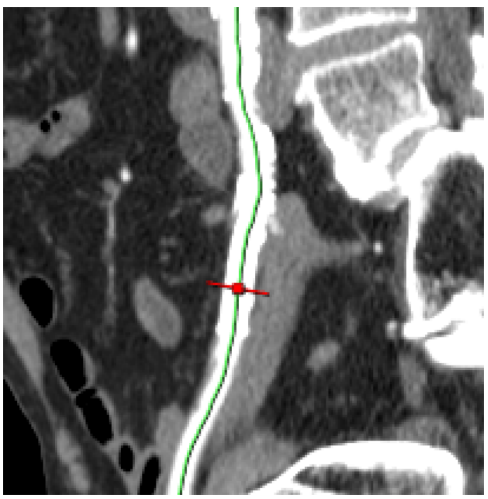


To view additional contours along the vessel:

- scroll the image in the viewport (above); or
- drag the reference marker (shown at left) along the centerline in a cMPR viewport.



Edit a Contour

1. Select the contour by activating the appropriate button.

2. Activate the **Edit** button. The selected contour will display with “control points.” As you approach the contour with the mouse, the contour color will change to yellow, indicating the editing function is active.
3. Drag the points as needed to correct the contour.

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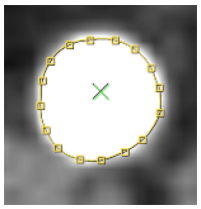


4. When finished correcting one contour, scroll the viewport or drag the reference line in the cMPR image to view all contours, correcting as necessary.
5. When finished with one contour type, hide it and activate the other.
6. Repeat the editing procedure as needed.

Draw a Contour

If the existing contour is too distorted to change efficiently, you can delete it and draw a new one.

1. Right click on the contour. The Delete command appears in a context menu.
2. Click **Delete.**
3. Click the **Edit Contour** down arrow to access the Add contours buttons. The contour type you deleted is active; the contour type you did not delete is grayed out.
4. Using the mouse to draw, click repeatedly in the viewport, following the anatomy, to draw a new contour.
5. Double click to end drawing.
6. If needed, use the Edit Contours function to refine the contour.

Vessel Extraction

At the top of the Vessel Extraction tab is the List of vessels. Right mouse click on a vessel in the vessel list to access the following functions:

- **Delete vessel.** Select this function to delete the vessel you clicked on
- **Rename vessel.** his selection opens the “Vessel Labeling Dialog,” described later in this chapter.
- **Edit Vessel.** This selection opens the “Configure Vessel List.”

NOTICE

Segmentation completed on one Spectral data type is propagated (by default) to all other available spectral data types from the same SBI.

Placing Seeds and Adding New Centerlines

Tools in the Vessel Extraction tab allow you to extract new centerlines and add them to the vessel list. There are four ways to extract new vessels: Auto Track, Create Aorta & Iliacs, Auto Track Tree, and Manual. Their buttons are grayed out until you begin placing seeds.

NOTICE

After using seed placement and creating new centerlines, ensure that the start and end points of each centerline are accurate. If necessary, extend the centerline as appropriate.

Auto Track (two clicks)

This function automatically extracts a new vessel centerline with two clicks.

1. Click **Place Seed**.

2. Using axial or volume images, click on two location of the vessel that you wish to define. The Auto Track Sequence button becomes active.
3. Click **Auto Track Sequence**. The system calculates and displays a new centerline and displays the Vessel Name Selection list.

4. Name the vessel by clicking on its name in the list or typing in a new name.
5. Click OK. Edit the centerline if necessary.

NOTICE

If the system is unable to define a vessel, a centerline does not appear and the message “Vessel not found” is shown.

Switching Between Body and Head Vessel Lists

Sometimes the wrong vessels list is displayed when clicking on an unnamed vessel. If this is the case, switch to the desired list by clicking in the vessel list on the “Switch to Body (or Head) vessels list.”

Create Aorta & Iliacs (three clicks)

This is a manual vessel extraction procedure for Abdominal and Runoff studies. Use it only if you have not used the optional Processing function.

NOTICE

This function only works with the Aorta & Iliacs vessels. Do not use this function for Internal and External Carotids because the automatic vessel labeling function may mis-label the vessels.

- Place 3 seeds to mark the Aorta and both Iliac vessels.
- Click the **Create Aorta and Iliacs button** (from the drop-down) to extract the vessels. The vessels will be labeled automatically as Aorta & Right Iliac and Aorta & Left Iliac.

NOTICE

If you modify the bifurcation point in the 'Edit centerline' mode, this button becomes enabled. A message will appear in the status line, instructing you to click the button to readjust the position of the bifurcation point.

Auto Track Tree (three clicks)

This function automatically extracts a new vessel tree centerline with three clicks. Use the Track Tree function to create a multiple vessel tree, such as the Mesenteric branches.

The Track Tree function does not mark a bifurcation point. Because of this, vessels made with the Track Tree function cannot be used for stent planning of AAA stent grafts.

1. Click **Place Seed**.

2. Using axial or volume images, click on three locations of a new vessel tree that you wish to define. The Auto Track tree button becomes available from the drop-down.
3. Click **Auto Track Tree**. The system calculates and displays a new centerline and displays the Vessel Name Selection list.
4. Name the vessel by clicking on its name in the list or typing in a new name.
5. Click **OK**.
6. Edit the centerline if necessary.

Manual Centerline (four or more clicks)

This function allows you to define a new vessel centerline by marking points along the path.

1. Click **Place Seed**.

2. Using axial or volume images, click on 4 or more locations on the centerline of a new vessel that you wish to define. Start and finish at the farthest ends of the vessel. Add enough points to follow the vessel’s curvature. The Manual Vessel Path button becomes active after 4 clicks.
3. Click **Manual Vessel Path**.

The system calculates and displays a new centerline and displays the Vessel Name Selection list.

4. Name the vessel by clicking on its name in the list or typing in a new name.
5. Click **OK**.

Edit and Extend Vessel Centerlines

These two tools in the Vessel Extraction tab allow you to edit centerlines (correct them) and to extend them if they do not completely define the vessel.

The automatically defined centerline will, in most cases, pass though the center of the lumen. If not, use the "Edit centerline" tool to make corrections. In the Edit Centerline mode, control points appear along the centerline path on both the Curved planar reformed and the volumetric views. You can change the position of each point by dragging it to the correct position.

1. Select a vessel from the list in the Vessel Extraction tab. The centerline appears red in the volume image and green in the cMPR images.
2. Click the **Edit centerline** tool.

Control points appear along the centerlines A cross-section cut also displays the centerline location at the selected control point. You can edit any point by dragging it to the correct location, including the cross-sectional cut.

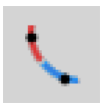
3. To add a control point, double-click the desired location on the centerline.
4. To remove a segment from the centerline, drag a control point to overlap another control point farther along the centerline.

Extend Centerline

This function allows you to add vertices beyond the distal and proximal ends of the extracted vessel centerline. You can select which end will be continued from the drop-down.

1. Select the vessel to be continued.
2. Decide which end you want to continue, distal or proximal, and click the appropriate button. The cMPR, volume, and axial images update.
3. Locate the continuing vessel using the volume and/or axial images. To rotate the volume image while remaining in Continue Centerline mode, hold <Ctrl+Shift> and drag or scroll the axial image.
4. Using the mouse crosshair pointer, click on the continuation of the artery that does not have a centerline mark to continue the vessel. The red centerline extends and the Curved planar reformed image updates to display the extended vessel.
5. Click the end point on the axial image (pink colored tissue) to continue the vessel.

Connect - Body Studies Only



The Connect function allows you to create a new vessel centerline. For example, in Figure 1 below, a new centerline was created by clicking at the two locations.

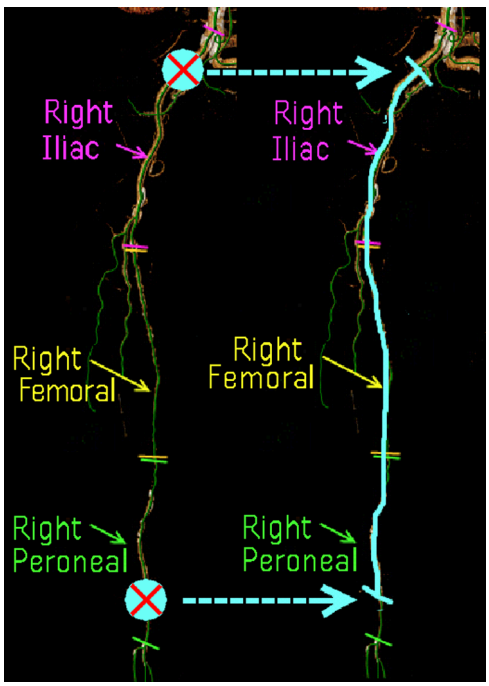


Figure 1. The locations are marked with the following icon:

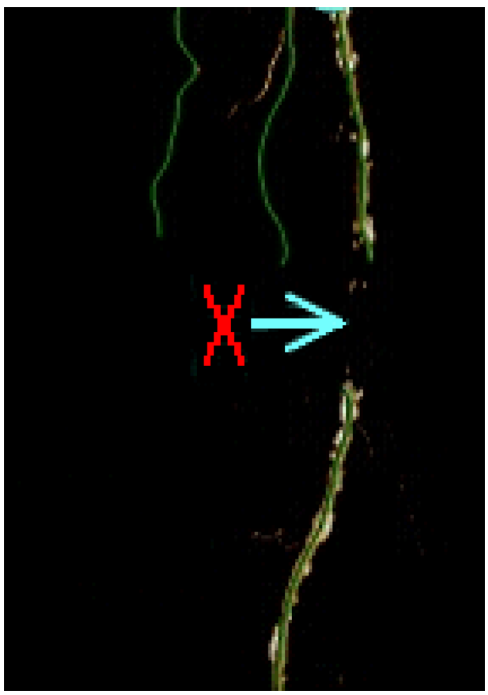


Figure 2. The Connect function cannot bridge gaps between centerlines. Centerlines must be corrected in the Bone Removal stage.

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NOTICE

The vessels must be continuing vessels (e.g. Iliac and Femoral).

The two vessels must have an extracted path between them.

The existing vessels are not replaced.

You should place the marks on the ends of the path you want to create, at the beginning of the first vessel and at the end of the last vessel.

You can also Split an existing vessel. Click on 2 locations on the same centerline to create a shorter centerline.

When you are finished creating a new vessel centerline, the Vessel labeling dialog opens for you to provide a label for the new vessel.

Vessel Extraction Stage Options and Tools

Common Viewing Tools, Common Tools, and Common Processes

A number of tools and process functions are common throughout the Review and Analysis applications.

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

Measurements Work Stage

The Measurements stage of AVA allows you to perform general measurements to gather data about vessels, such as cross-sectional area and diameter, vessel length, stenosis estimation, and thrombus estimation.

NOTICE

Semi-3D editing may be performed using the sMPR image when the **Edit Contours** button is active. The sMPR image can be zoomed and panned similar to the other viewports.

Viewing Tools and Functions

Most viewing tools carry over from the previous stages. In addition to the Select Vessel function, you can access other common functions as needed.

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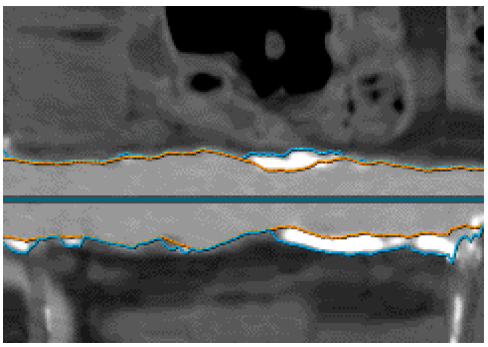
Edit Contours on sMPR Image

Semi-3D editing may be performed using the sMPR image when the **Edit Contours** button is active. The sMPR image can be zoomed and panned similar to the other viewports. The sMPR image does not display any control points (to avoid hiding the vessel borders).



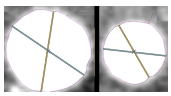
To edit, hover over the contour (it become yellow). The cursor will change to indicate which contour is activated (lumen is orange cursor for the lumen contour or blue for the vessel contour).

NOTICE

Segmentation completed on one Spectral data type is propagated (by default) to all other available spectral data types from the same SBI.

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

Contour Images (Cross-section Mode)



These images are showing Lumen only, at the currently active diameter, in the Cross-section mode, at the Reference and Lumen locations. Minimum and Maximum Diameter lines are shown. They are color coded: the maximum diameter is a blue line; and the minimum diameter is a yellow line.

They can be removed via a right mouse menu click.

The vessel name, the cross-sectional area, the average HU, and the standard deviation measurements are shown, along with the position along the centerline.

Measurements

A full-screen version of the measurements table is obtained by double clicking in the normal table viewport (double click again to return the table to original size). The full screen table shows all the possible content, including lumen, vessel and wall measurement data and calculations. If wall thickness is less than 0.55 mm, wall measurements are not displayed in the table (asterisks are displayed instead).

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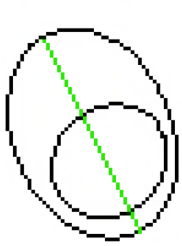
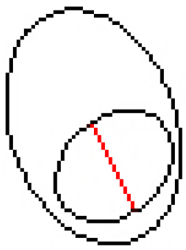
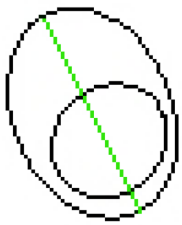
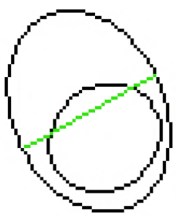
NOTICE

Table measurements can also be based spectral data. This causes the table values to change accordingly (for example, mg/ml instead of HU).

Calculation of Measurements			
Difference	–	(reference-lesion) / reference*100%	%
Position	–	position along the center line in mm (beginning of centerline = 0 mm)	mm
Position difference	–	(position of lesion - position of reference)	mm
Maximum Lumen Diameter		the longest diameter through the center of the lumen	mm
Minimum Lumen Diameter		the shortest diameter through the center of the lumen	mm
Maximum Vessel Diameter		the longest diameter through the center of the vessel	mm
Minimum Vessel Diameter		the shortest diameter through the center of the vessel	mm

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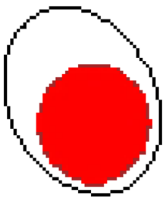
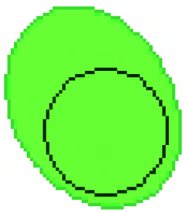
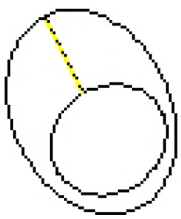
Calculation of Measurements			
Lumen area		the area enclosed by the lumen contour	mm2
Vessel area		the area enclosed by the vessel contour	mm2
Lesion area / Reference area	–	(vessel area at lesion) / (vessel area at reference)	–
Wall area		vessel area - lumen area	mm2
Wall burden	–	100 x (wall area / vessel area)	%
Maximum wall thickness		the maximum distance between the lumen contour and vessel contour	mm2
Minimum wall thickness		the minimum distance between the lumen contour and vessel contour	mm2
HU (mean/SD)	–	the average and standard deviation of the HU within the area of the vessel\lumen\wall	–
Eccentricity	–	calculated from the vessel's cross-section based on: Maximum Diameter-Minimum Diameter/Maximum Diameter. Measurement is available both in relative and cross section mode.	–

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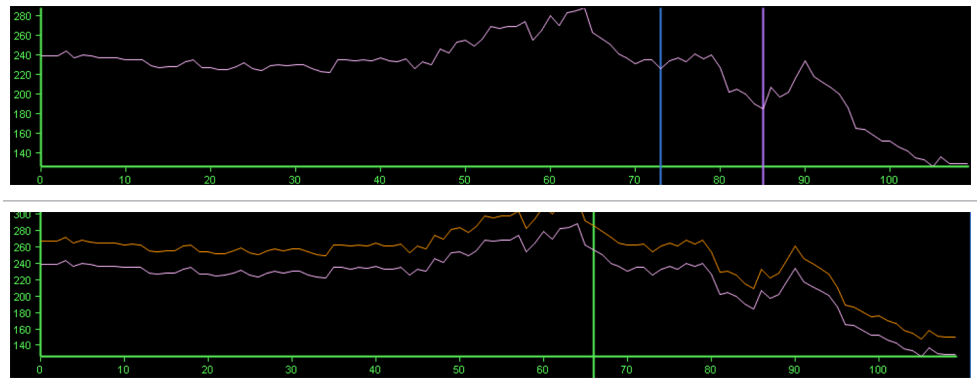
Calculation of Measurements			
Effective diameter	–	Calculated by: d_ef=2*sqrt(Area/pi). Measurement is available both in relative and cross section mode.	–
Tortuosity	–	Calculated from 2 cross-sectional locations between the reference and lesion locations. Based on the distance between the reference and lesion along the centerline; and the distance between the reference and lesion locations (the centerline location) along a straight line. Measurement is available only in the relative mode.	–

Contour Graphs

The two contour graphs shown below both display cross-sectional area along the vessel centerline.



You can also display Maximum Diameter from the right mouse context menu.

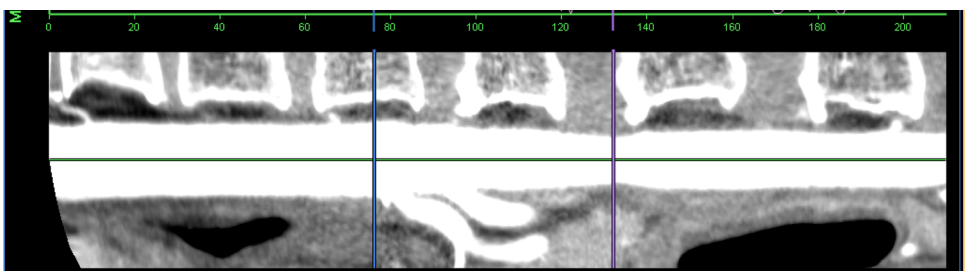
In the upper graph, which displays in the Relative mode, only the Lumen contour is represented.

In the lower graph, which displays the Cross-section mode, both Lumen and Vessel contours are represented.

Dragging the vertical reference lines updates all viewports and the measurements.

Strip Image

The strip image is joined to the graph display, and displays the straightened MPR view of the vessel.



You can rotate the image around the centerline. Dragging the vertical reference lines along the centerline updates all viewports and updates the measurement calculations.

Color Map Image

Use this function to help visually distinguish between contrast and soft plaque.

Pathology	Range (HU)	Color
Lipid plaque	-40 to 60	Blue
Intermediate plaque	60 to 115	Green
Blood (contrast)	115 to 350	Red
Calcified plaque	350 to 735	White

Stent Planning Work Stage

When you open the Stent Planning stage it opens to one of three possible layouts, depending on the layout last used with this application.

NOTICE

The Stent Planning stage supports only conventional data.

Stent Planning Measurement Functions

You can choose the stent graft protocol you want to work with from a drop-down list in this tab. Alternately, you can make your own protocols using the Stent Protocol Editor (described later in this chapter).

There are five factory protocols that you can choose from. There are two types of stent grafts, a regular type (Aorta) and a type for cases with bifurcation (i.e. Aorta and Iliacs).

In the Measurements tab:

- The graphic image on the right side is a schematic diagram of the AAA stent. In the example, diameter D1 is active (highlighted in the list and colored red in the graphic).The active diameter is also the diameter that is depicted/identified/measured in all viewports.
- The AAA stent is currently selected.
- The list on the left contains the measurements used for planning the AAA stent.

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- The entry for the D4 diameter contains a red B character, identifying it as the diameter at the bifurcation location.

Add Measurement

Other measurements may be required for the stent you are planning to use. You can add your own measurement entry to the current stent. Click the **Add Measurement** button. The Add Measurement dialog opens.

1. Click in the Name box to type in the measurement name.
2. Click in the Type box to select the measurement type from the drop down list. (Diameter, Length, Tortuosity, Angle).
3. Click in the **Description** box to type a description of the measurement.
4. Click **OK**.

The added measurement appears in the measurement list and by default is located in the middle position of the centerline. (It does not appear in the graphic image in the Measurements tab.)

Delete Measurement

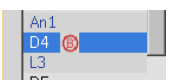
Use this procedure to remove an unwanted measurement that was previously added.

- In the Measurements Function tab, right mouse click on the measurement you want to delete. A menu appears, as shown at left.
- Click the Delete Measurement selection. A message displays describing the result. (A typical message is “Following measurements will also be deleted X1, Y3”.)

NOTICE

Only the selected and added new measurements may be deleted (removed from the list and image display). The default measurements, defined by the protocol, cannot be removed. You can not delete default measurements that were defined in the Stent protocol editor.

Bifurcation Point



The D4 location (the bifurcation diameter location defined in the Stent Editor) is fixed on the stent measurement page. It cannot be changed in the Measurements stage, because other calculations were made based on its original location. To change it, you must return to the Vessel Extraction stage.

If you try to change the point, the following message displays: “Editing the bifurcation point is not possible in this Stage. Move to Vessel Extraction Stage to edit it.”

Cross-sections for Stent Planning

By a common convention, five cross-sections are defined for stent planning measurements:

- proximal part of proximal neck (D1);
- distal part of proximal neck (D2);
- aneurism (D3);
- proximal part of distal neck (D4); and
- distal part of distal neck (D5).

Once you locate the five cross-sections, AVA calculates their areas and diameters, as well as the distances between them, and makes pertinent angular measurements.

You may edit the cross-sections contours using the manual editing tools.

CAUTION

Verify the correctness of the placement of the cross sectionals for the measurements. Verify the measurements themselves (area, diameter, length and angle) as well as the correctness of the centerline and cross sectional contours. Make corrections manually with the tools provided by the AVA application, as needed.

Locate and Define Cross-sections

To aid in making and recording measurements, a dynamic image is displayed, showing a schematic diagram of a stent (the Aorta schematic is shown at left; a different schematic is displayed for Aorta & Iliacs). The measurements are listed in the order they are expected to be carried out. The current measurement is highlighted in red on the schematic diagram.

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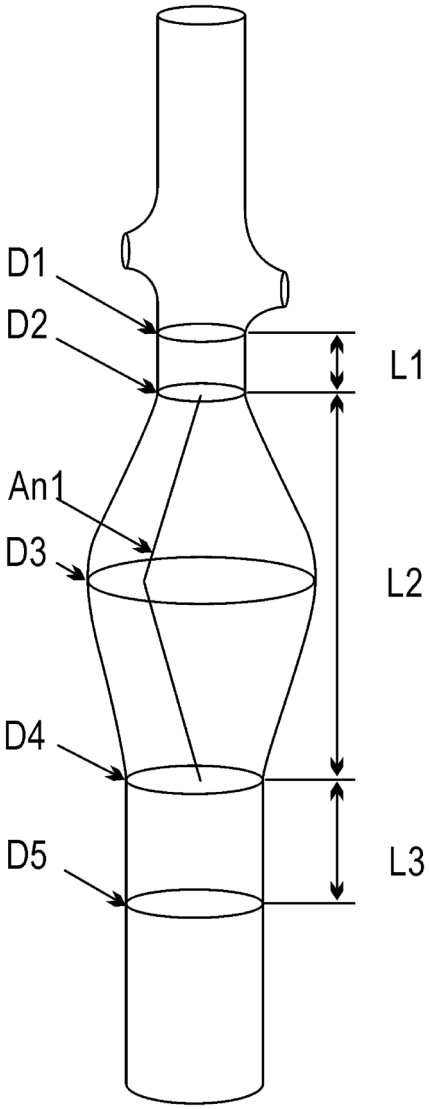
1. Click the D1 box (diameter of proximal neck).
2. The D1 line appears highlighted red in the CPR images. The contour for D1 appears in the cross section image. Move the pointer up to the line and the pointer turns into a pencil.
3. With the pencil pointer, move the D1 line to the location of the proximal neck on the strip image. (Alternately, scroll the images in the upper-left quadrant to move the D1 line.)
4. Continue as above with D2, D3, D4, and D5. You can Add Measurements if needed, as described earlier.
5. When done, you can proceed to the Report function.

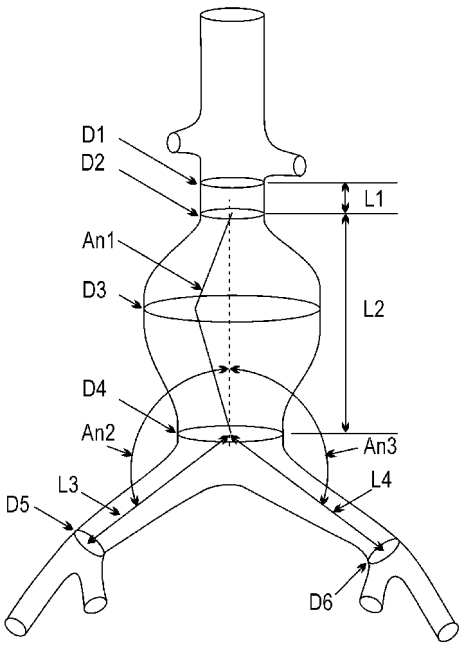


Schematic of Stent Measurements

Aorta & Iliacs Stent Planning Measurements

AAA Stent Planning Regions		AAA Stent Graft	
D1	Proximal part of proximal neck (below renal arteries)	D1	Diameter of proximal neck (mm)
D2	Distal part of proximal neck	L1	Length of proximal neck (mm)
D3	Aneurism	D2	Diameter of distal end of proximal neck (mm)

AAA Stent Planning Regions		AAA Stent Graft	
D4	Right common iliac attachment site	A2	Area of distal end of proximal neck (mm2)
D5	Left common iliac attachment site	D3	Diameter of aneurism (mm)
		L2	Length of stent (mm)
		An1	Angulation of aortic neck (degrees)
		D4	Diameter of distal right iliac artery (mm)
		D5	Diameter of distal left iliac artery (mm)
		L3, L4	Length from aortic bifurcation to the internal right/left artery attachment sites (mm)
		An2,An3	Angulation of right/left iliac arteries (degrees)

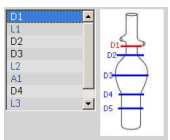


Schematic of Stent Measurements with bifurcation of Aorta & Iliacs

Stent Planning Stage Tools and Options

Most viewing tools carry over from the previous stages. Tools specific to this stage are presented below.

Show All Measurements



When this box is checked, the vessel diameter lines are visible in all viewports that have vessel centerlines. Items D1 through D5 are the diameter lines for the chosen stent protocol. The active diameter is the last diameter you worked with. An active diameter is colored red in the viewports that show vessel centerlines.

Summary Table

The table is off by default. Click to show or hide all the measurements of the protocol. The Summary table shows the position, diameter, area, length, and angle measurements calculated by AVA. The Names and Descriptions in this table originate from stent parameter descriptions. See section “Stent Planning Protocol Editor” on page 96.

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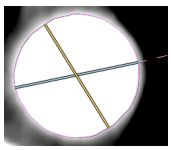
Contours Type

Three functions are available. With the button on the left you can show or hide lumen contours. With the button on the right, you can activate the Edit contours mode to correct the lumen contouring. From the drop-down, you can Add Lumen contours.

Only lumen contours are displayed and measured in this stage.

Cross-section Image



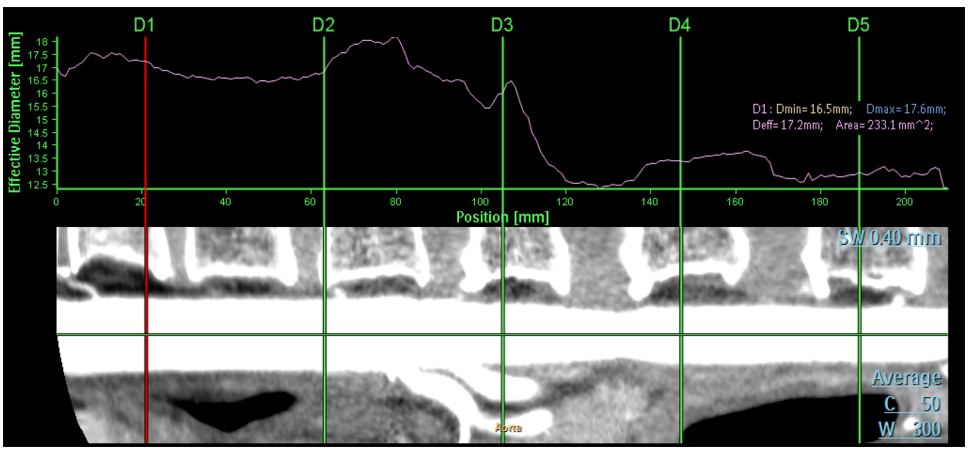
The cross-section image shows the axial view at the currently active diameter. Displayed are the vessel name, the lumen contour, the maximum diameter (blue line) and the minimum diameter (yellow line). Also shown are the cross-sectional area, average HU, and standard deviation, along with the position along the centerline.

WARNING

Verify the accuracy of the contour. Use the Edit Contour function to make corrections, if necessary.

Strip Image and Graph Display

The strip image (straightened MPR) and the graph display are joined in one viewport. The vessel diameter lines are shown. on the viewport. The active diameter is red.



Dragging the diameter lines updates all viewports and updates the measurement calculations.

You can display four different sets of vessel data on the graph from the right mouse context menu.

For the vessel diameter marked by the red line, the same four data values are shown at the right of the graph.

Viewing Options, Common Tools, and Common Processes

A number of tools and process functions are common throughout the Review and Analysis applications.

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

Stent Planning Protocol Editor

The Protocol Editor allows you to create new stent protocols. All factory protocols are available in the editor.

Before You Start

You will need:

- a graphic image of the stent protocol you are creating (in electronic graphic file form); and
- the manufacturer's stent data sheet. This is needed for specification measurements, other data. It is also the source for the user questions that will be part of the protocol you are creating.

NOTICE

If a new stent protocol is created on a client under a specific user name and password only that user has access to the new stent protocol. If there are multiple users they should create the same stent under their own user names.

Open Stent Planning Protocol Editor

1. From the Directory window, click Preference.
2. Select AVA from the directory on the left.
3. Click the **Launch Stent Protocol Editor** button to open the Stent Protocol Editor.

The protocol editor consists of four work stages; Protocol, Image, Measurement and Questions. Each of these stages is accessed from the drop-down menu. Click the forward arrow in the function menu to move to the next stage.

List New Protocol

After you import and save a new Stent Protocol, the protocol name will not immediately appear in the stent list. In order for the new protocol to appear in the list, you must right mouse click in any image viewport and select **Reload Stent Protocols**.

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Show Diameters

The **Show Diameters** checkbox allows you to turn on/off the diameter lines on the cross-sectional images. (This function is grayed-out when contours are disabled.)

Create New Stent

1. Click **New**.
2. Fill in the Protocol Name. The name of the protocol can be changed.
3. Fill in a brief Description of the protocol.
4. Click the check box next to the statement “This is a Stent for the Aorta and Iliacs” if the stent is to be used for Aorta and Iliac. This indicates that a bifurcation is needed.

Import and Export

Use these functions to import or export protocols from and to external sources.

Protocol List

Lists existing factory protocols and the new protocols that you create.

- AAA Stent
- Access Assessment TAVI (available visible when selecting the automatic extracted aortic-iliac vessels)
- AneuRx Stent Graft
- Excluder
- Powerlink
- Stent General

Click on an existing protocol and all of its data fills the Protocol Editor data fields.

NOTICE

You can modify any of the existing parameters using the same general procedures that are described for creating a new protocol.

Delete or Rename Stent Protocols

To delete or rename stent protocols from the list:

1. Select the desired name.
2. Right click in the menu.
3. Select the desired action.

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Share Stent Protocol with All Users

If you are a Clinical Administrator and are creating a new stent protocol, the Share with all users function is available. (It is grayed out for non-administrative users.) When a Clinical Administrator shares a stent protocol, it becomes available to all existing and new users of the originating IntelliSpace Portal system. (Non-administrative users cannot delete, rename, overwrite, or modify shared presets).

Stent Protocol Image

1. Click the name of the image file you are creating.
2. From the menu on the left, click the name of the image file that corresponds to the protocol you are creating. If the image you want has not been loaded, it does not appear in the list of available images.
3. To move to the Measurements Stage, click the right arrow in the function menu.

Stent Protocol Measurement

Place the diameter and bifurcation lines on the image. Specify the length and tortuosity measurements.

Place Diameter Line

1. Click the **Diameter** button.
2. Place the mouse on the image.
3. A line automatically draws on the image. The diameter is automatically named (D1).
4. You can enter a description in the Description field of the Parameters view. The active measurement line is red; inactive lines are blue.
5. You can position the diameter line anywhere on the image by dragging it. Use either end of the diameter line to adjust its length or rotation.
6. To create another diameter line, left mouse click on the Diameter and drag into the image.

Place Bifurcation Line

1. Click the **Bifurcation** button.
2. Drag the mouse into the image. A line is automatically drawn on the image. The diameter is automatically named (D Bi).
3. You can enter a description in the Description field of the Parameters window. If using an Aorta and Iliac Stent, you must place a bifurcation diameter on the image. Only one bifurcation can be placed - after placing the line the button becomes be grayed out.

Specify Length

Click the Length button to specify a length measurement. You are prompted to "Click on 2 diameter lines" to indicate the start and end points of the measurement.

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Specify Tortuosity

Click the Tortuosity button to specify a tortuosity measurement. You are prompted to "Click on 2 diameter lines".

Stent Protocol Worksheet

Specify the angle; complete the measurement summary; change the list order; show or hide parameters in the strip image; and preview the active protocol.

Specify Angle

Click the Angle button. You are prompted to "Click on 3 diameter lines."

Measurements Summary

All existing measurements parameters are listed here. Drag the bar on the right to scroll up and down to view the complete list. When you click on a list item it turns red on the image so you can identify it.

NOTICE

Multiple lines turn red when you click on the Angle, Tortuosity, or Length parameter.

Changing the List Order

By using the Up or Down buttons you can change the order of the Measurements Summary List. Arrange the list in the same order you want the measurements to be presented in the AVA application.

Measured Values

To have all the listed parameters display in the in the AVA Stent Planning strip image in the lower viewport click all four check boxes.

AVA Preview

The AVA Preview window shows the graphic image of the stent protocol that is currently active.

Stent Protocol Questions

When finished with the Measurements work stage of the Protocol Editor, access the Question work stage.

Stent manufacturers usually present a series of questions to be answered when ordering a stent. Enter these questions into this window.

These questions and answers are included in the report that can be generated from the AVA Stent Planning function.

Question Button

Click the Question button to start a new question. The questions are automatically numbered and added to the list in the Questions Summary.

Click any question in the summary list to review it.

Question Panel

The new question number appears in the field at the top of the Question panel. Type in the manufacturer's question in the text box below the question number.

Answer Panel

Type in the manufacturer's permissible answers in the Answer boxes that are listed. If you do not enter an answer, the question section has a blank text field, where you can insert free text.

For AVA Users

- **Single Answer.** Select this to limit the your response to one choice only.
- **Multiple Answer.** Permits several answers to a question, as allowed by the manufacturer.
- **Allow Other.** Permits a different form of answer.

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10 Spectral Comprehensive Cardiac Analysis (SCCA)

For additional information on Spectral CCA, please refer to the Comprehensive Cardiac Analysis (CCA) section of the IntelliSpace Portal CT Analysis IFU.

Please note that Spectral information is included where relevant in this IFU.

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11 Spectral Multimodality Tumor Tracking (SMMTT)

For additional information on Spectral Multimodality Tumor Tracking, please refer to the Multimodality Tumor Tracking section of the IntelliSpace Portal Multimodaliy Applications IFU.

Please note that Spectral information is included where relevant in this IFU.

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12 CT Multiphase Analysis

The CT Multiphase Analysis application generates color maps by applying various mathematical operations between registered acquired conventional and spectral CT phases for visualization of enhancement differences between acquired phases.

When a map is calculated from more than a single series, the application performs automatic registration between the series and allows the user to review the registration results.

In order to obtain quantitative values, it is necessary to normalize the values with respect to the aorta. The assumption is that the Aorta with contrast material has the highest HU values and hence displays the maximum values of the summary maps (~100%).

The CT Multiphase Analysis application includes three stages:

- Summary Map Selection
- Registration and Normalization
- Results

The CT Multiphase Analysis application is enabled per license for SBI series, MonoE series and conventional data.

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Indications for Use

The CT Multiphase Analysis application creates tissue enhancement maps from multi-phase conventional or spectral contrast-enhanced CT data.

The application supports the following maps:

- **Arterial Enhancement Fraction (AEF)** - the ratio between the absolute enhancement of the tissue in the arterial phase and the portal venous phase.
- **Extracellular Volume (ECV)** - the absolute enhancement of the tissue in the equilibrium/late phase.

The AEF map is intended for the assessment of liver lesions for oncology patients.

The ECV map is intended for the assessment of myocardial fibrosis and the assessment of liver fibrosis.

NOTICE

Based on the dual-enegery Gammex® phantom, the AEF and ECV values on the calculated maps are within a tolerance of 2%.

CAUTION

Please verify input images and confirm artifacts are not presented.

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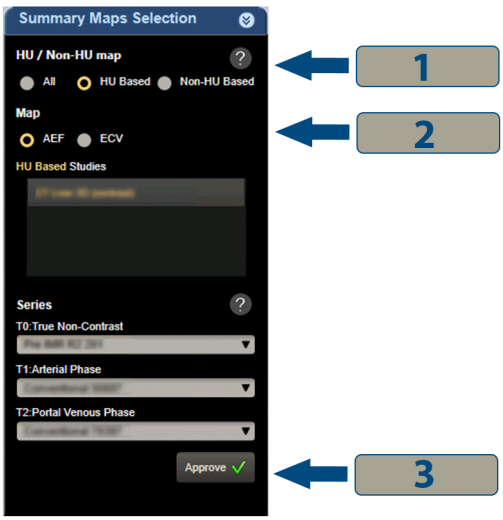
CAUTION

The CT Multiphase Analysis map should not be used as the sole basis for diagnosis.

Summary Map Selection



The steps below should be performed in order to continue to the Registration and Normalization stage. Use the table below for additional information on the options.

1. Select one of the HU/Non-HU map options (**HU Based**, **Non-HU Based**, or **All** (#1).
2. Choose a map (**AEF** or **ECV**) (#2).
3. Verify that the displayed series in the **Series** area are the results of the relevant phases and click **Approve** (#3).

   Approve is enabled only if a map is selected.

HU Based/Non-HU Based Map Selection	All	When selected, the SBI series includes the following data-types only: **Conventional**, **MonoE**, **Iodine density** and **Iodine no water**.
	HU Based	This map is generated using HU based series. For HU based maps, one of the series must be the result of a non-contrast scan. When selected, the SBI series includes the following data-types only: **Conventional** and **MonoE**.
	Non-HU Based	In Non-HU based maps, there is no need for a non-contrast scan result. When selected, the SBI series includes the following data-types only: **Iodine density** and **Iodine no water**.

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Map Type Selection	AEF	Arterial Enhancement Fraction (AEF)- The ratio between the absolute enhancement of the organ in the arterial phase and the absolute enhancement of the organ in the portal venous phase.
	ECV	Extracellular Volume (ECV)- The absolute enhancement of the organ in the equilibrium phase.
	These buttons are not enabled if **All** was selected above. In order for a map to be activated, the displayed study must comply with the Conditions for Map Creation. Conditions for Map Creation are described in the section below.	

NOTICE

Please select the same monoE energy level across all selected phases for map creation, to ensure maps are created properly.

For cardiac scans, please select the same cardiac phase across all selected phases for map creation, to ensure maps are created properly.

Conditions for Map Creation

Conditions for AEF Map Creation

An AEF map can be generated only if the displayed study complies with the following conditions:

- For HU based maps, the study must include at least three series (SBI, conventional or combination).
- For Non-HU based maps, the study must include at least two SBI series.

Conditions for ECV Map Creation

An ECV map can be generated only if the displayed study complies with the following conditions:

- For HU based maps, the study must include at least two series (SBI, conventional or combination).
- For Non-HU based maps, the study must include at least one SBI series.

Registration and Normalization

When choosing a map that was generated using more than one series, when navigating from Stage 1 to Stage 2, registration is performed (FEIR Elastic Liver registration), when all series are registered according to a reference series.

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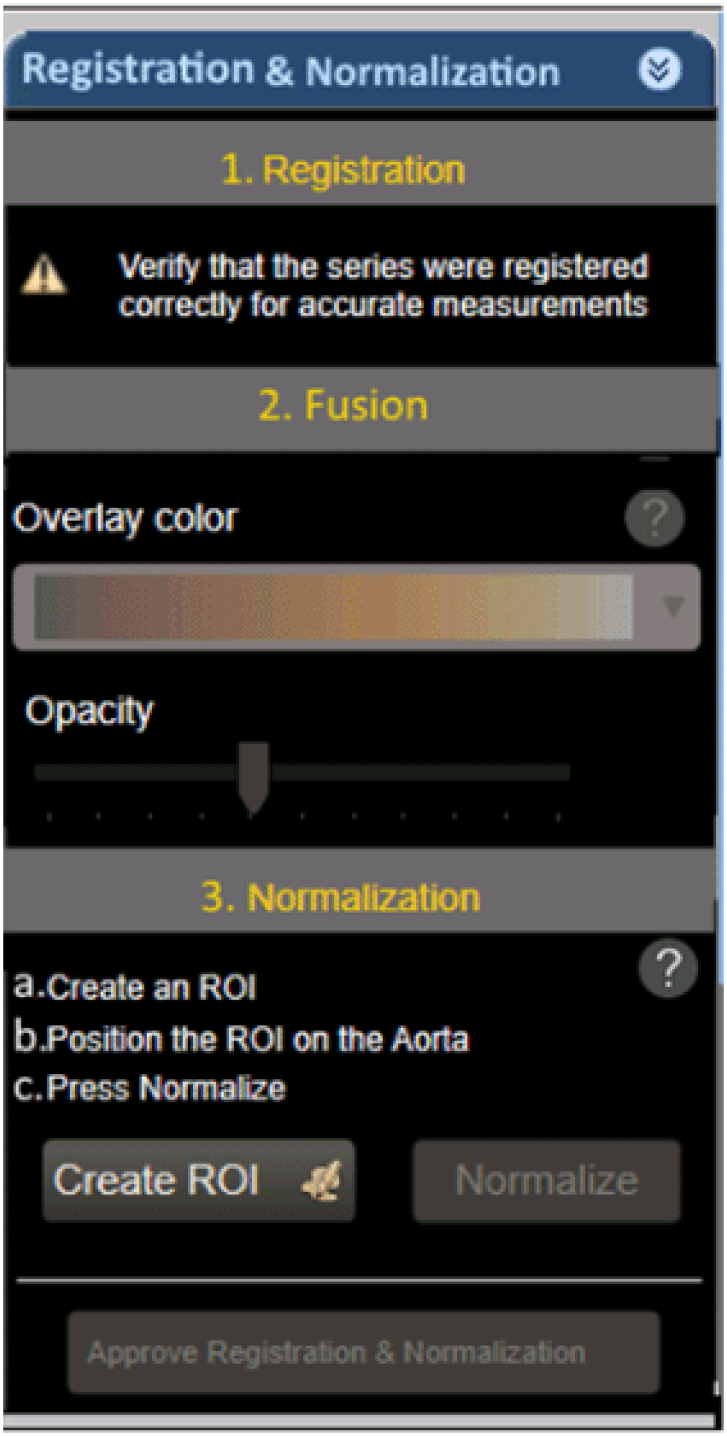
1. Verify the quality of the registration using the common tools (Scroll, Pan, Zoom etc.)
   It is not possible to perform measurements in a fusion viewport .
2. For normalization:
   – Select **Create ROI**.



   – Place the **Normalization ROI** on the aorta.

– Select **Normalize**.

3. Select **Approve Registration & Normalization** .

   The **Approve Registration & Normalization** button is only enabled after performing normalization according to the steps described above.

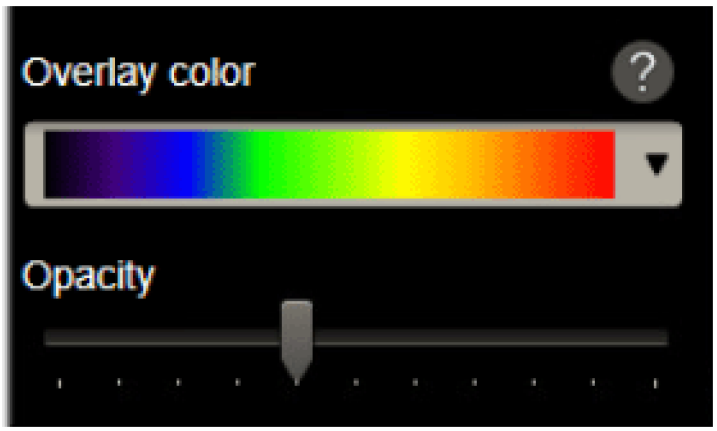
Workspace	Notes
Includes more than 1 series	• When **Create ROI** is selected, the workspace changes and the reference series is displayed (non-registered series). To return to previous workspace, follow the instructions for normalization. • The workspace includes at least one fusion viewport • In a fusion viewport, the underlay is the reference series (displayed in the non-fusion viewport) • In a fusion viewport, the overlay is a registered series (according to the reference series. This series is a deformed)

Results

In the Results Stage, the map is displayed along with the original series that the map was generated from.

For optimal results, change the displayed color map as described below.

1. Select the color map bar and choose a different color map.



2. Change the range of the displayed map by changing the WL (window level) and WW (window width) of the map.

Hematocrit

When choosing ECV map, modify the Hematocrit value by typing a new value.

Exporting Maps

Exporting a Map as an RGB Image

When pressing on the **Save results as** tool, located in the tool bar in the left panel, the displayed image is saved as an RGB image. It is not possible to perform measurements on the saved RGB image.

Exporting a Map as a DICOM Monochrome2 Series

When pressing the right mouse button and selecting **Save map as gray scale series**, the displayed map is saved as a DICOM series with quantitative percentage values.

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