2 Multimodality Advanced Vessel Analysis

Philips Medical Systems' Multimodality Advanced Vessels Analysis (MM AVA) application is intended for visualization, assessment, and quantification of vessels in CTA and MRA data with a unified workflow for both modalities.

For CTA data, it provides both automatic and manual bone removal and vessels segmentation including extraction of vessel centerlines, lumen contours and vessel contours.

For both modalities, it provides tools for extracting and editing centerlines.

NOTICE

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

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.

WARNING

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

For CT Angio (CTA), the reconstruction orientation **Left on Left** is not supported. Only the standard reconstruction orientation **Left on Right** is supported.

MM AVA Workflow Stages

1. **Vessel Extraction**

   This stage allows you to view the automatically extracted vessels in high detail. In addition, you can extract new vessel centerlines, extend centerlines beyond where they were automatic extracted, and correct centerline placements.

   Automatic vessel labeling of major vessels is performed, if detected (CT studies only).

   In this stage, you can also edit and clean the volumetric image of the vessels.

2. **Inspect and Measure**

   This stage allows you to quickly inspect the data using cross sectional and longitudinal or curved views. During the inspection, you can create and save quantitative measurements about vessels, such as cross-sectional areas, diameters, finding lengths and stenosis estimation. You can then review comprehensive information about each measurement in an optimal display layout.

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 Inspect and Measure stage and making changes to the centerline) affects your previous work.

For information on spectral capabilities, see section “Spectral Capabilities in AVA” on page 70.

Key Features

- Provides automatic bone removal for CTA data
- Provides automatic vessel centerline extraction and labeling for the main vessels (CTA data)
- Provides a set of centerline creation and editing tools (manual and semi-automatic)
- Provides dedicated views for vessel review: Curved MPRS, Straighten MPR, Cross-sectional and Longitudinal MPR
- Provides 3D Volume rendering capabilities for CTA and MRA, including different volumetric presentation options such as Volume rendering, MIP (Maximum Intensity Projection) etc.
- Allows measurements along a vessel centerline, based on a user selected location/s, such as Max Diameter, Min Diameter and Area
- Allows the calculation of measurements such as: Length, Angle, Tortuosity, Stenosis, Aneurysm etc. based on user selected locations and their intra-correlations
- Allows navigation and local inspection of images, (even without predefined centerline) including capturing measurements such as diameters (Quick Inspection)
- Allows Batch (series of images processed by user) generation for any of the selected user views

Indications for Use

The Multimodality Advanced Vessels Analysis (MM AVA) application is intended to assist the user in viewing, processing and quantifying vascular conventional or spectral CTA and MRA datasets of patients with suspected or diagnosed vascular diseases, for the analysis of vessel anatomy.

Intended Users

Advanced Visualization Workspace Multimodality Advanced Vessel Analysis application is intended to be used by adequately trained and qualified medical professionals, including but not limited to physicians and medical technicians. The main clinicians or medical and para-medical professionals who use the Philips Advanced Visualization Workspace Multimodality Advanced Vessel Analysis application are listed below:

- Radiologists in the radiology department/clinic

- 3D technologists in the radiology department

Other clinicians/roles using the Philips Advanced Visualization Workspace are listed below:

- Cardiologists and Cardiology technologists
- Referring Physicians

Intended Patient Population

The MM AVA application is indicated for all patients that had a CTA or MRA as part of their imaging exam.

Benefits

When used as specified in the Intended Use, under the circumstances and conditions as specified in the Indications for Use, the application assists the user with interpreting the clinical image data on par with the state of the art thus realizing a positive impact on diagnosis or patient management.

More specifically, the Advanced Vessel Analysis application assist the user with viewing and interpreting of a CTA or MRA vascular dataset to confirm or rule out the presence of any vascular pathology. The expected patient benefits are:

With the resulting radiological conclusion the referring physician can advice the patient with options to prevent reoccurrence or worsening of the presenting symptoms and optionally (if diagnosed) control the evolution of the vascular disease by taking action in controlling risk factors with heart-healthy lifestyle changes and/or medicine or further investigations.

Contraindications

None.

Limitations for Use

Warnings for All AVA Studies

NOTICE

Always use the original 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.

NOTICE

Increasing the slice thickness in slab mode also increases the possibility of partial-volume averaging artifacts.

NOTICE

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.)

WARNING

Contours are determined using FWHM analysis. Therefore, the derived diameter measurements might be overestimated for vessels that have a diameter smaller than 3 times the voxel size.

Verify the accuracy of the centerline curves 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.

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.

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

⚠ **WARNING**

When you use the Magic Glass tool, the annotations and measurements do not represent the Magic Glass ROI but the underlay image.

Warnings for AVA Studies using Bone Removal

⚠ **WARNING**

Verify that Bone Removal does not affect vessel completeness.

Warnings for AVA Studies using Skull Removal

NOTICE

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.

NOTICE

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.

NOTICE

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.

NOTICE

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.

WARNING

Vessels that are very close to bony structures might be missed by the automatic segmentation. Use the MPR images 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.

Summary of Performance Testing

Non-clinical performance testing has been performed on the Multimodality Advanced Vessels Analysis (MM AVA) application and demonstrates compliance with the following International and FDA-recognized consensus standards:

- **ISO 14971 Medical devices** – Application of risk management to medical devices
- **IEC 62304 Medical device software** – Software life cycle processes
- **NEMA PS 3.1-3.21** – Digital Imaging and Communications in Medicine (DICOM) Standard
- **IEC 62366-1 Medical devices** – Part 1: Application of usability engineering to medical devices

Philips Medical Systems Multimodality Advanced Vessels Analysis (MM AVA) application was tested in accordance with Philips verification and validation processes. Verification and Validation tests have been performed to address intended use, the technological characteristics, requirement specifications and the risk management results.

The test results in this 510(k) premarket notification demonstrate that Multimodality Advanced Vessels Analysis (MM AVA) application:

- Complies with the aforementioned international and FDA-recognized consensus standards and FDA guidance documents, and
- Meets the acceptance criteria and is adequate for its intended use and specifications.

Run Processing (Option for CT Studies Only)

When CTA data is a launched to AVA, a bone removal algorithm separates the vessels and the bones, segmenting the main vessels (arteries), finding their centerline and labeling them as much as possible.

Processing is performed in the background, while you work on other tasks (progress indication appears in the bottom left corner). Viewing operations can be performing while processing is in progress. The results are saved in the Directory. When the series is loaded with the result series, the study will open with the bones removed.

NOTICE

The bone removal algorithm for Body CTA cases may not complete successfully in scenarios where arms are not positioned upwards or when the scan width does not cover the whole range of the body width.

The algorithm considers the aortic arch as the upper location for the "Body" algorithm [i.e., upper end of the body in Z axis (instead of the neck)] . An exam with an acquired range covering less than 30 cm from the aortic arch, may not be processed by the algorithm.

NOTICE

Depending on your system configuration, using the Run Processing option might cause system slowness.

Viewing Options

The upper toolbar includes the following tools (general for all stages):

- Show/Hide Bones
- Show/Hide glass rendered bones
- Show/Hide transparent bones
- Show/Hide cube edges
- Calculate volume
- Show main vessels only (only for head and neck, to show cleaner vessel tree as in earlier ISP versions)
- Show/Hide calcifications
- Show/Hide lumen contours
- Show/Hide vessels contours
- Show/Hide diameters
- Show/Hide dense organs (body only)
- Layout selection: The user can select one of 4 layouts, and may show full MPR option
- Viewport Orientation
- General mouse interactions (scroll/zoom/pan/rotate/windowing)
- Standard annotations tools
- Show annotation level options
- Invert
- Cine
- Information
- Reset all

Hide Calcium on Vessels

This function allows visualization of the true lumen of the vessel. It is helpful when vessels are completely or partially occluded due to calcified plaque. The function toggles visualization of high density residuals.

The visualization of calcifications are colored purple in the reference images. The function is available in the upper toolbox and is by default unchecked.

Show Main Vessels Only

Selecting this option enables the display of main vessels only.

NOTICE

This option is enabled only for Skull cases.

The function is available in the upper toolbox and is by default unchecked.

Once this option is enabled, all of the editing tools under **Edit Vessel Segmentation** are disabled.

NOTICE

In this mode, Bone Removal editing is limited and fewer tools are available than when the default option is used.

Hide Dense Organs on Vessels

Sometimes hide dense tissues like the heart can block the view on the aorta. In the upper toolbox, a checkbox is provided to remove these dense organs from the vessel view. The checkbox is by default unchecked. This feature is only available on body bases.

WARNING

Verify segmentation correctness on the vessels view. Edit if required or uncheck the feature if needed.

The visualization of dense organs is colored dark pink in the overlay of the reference images.

Volume Tools

Volume tools allow editing the volume image.

NOTICE

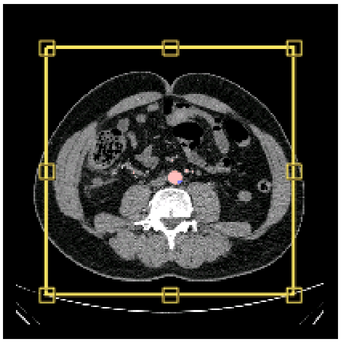
When using the editing/extracting/extending centerline tools, the volume image updates automatically to include the newly added vessel portion or to remove a portion where centerline was removed. Therefore, it is recommended to first edit the centerlines and then, for the remaining editing, use the volume tools.

- **Remove bone** (#1): Click on isolated non-vessel structures (e.g. bones, veins) to remove from the volume images.
- **Remove residuals** (#2): Remove isolated small residuals from volume image
- **Smart exclude region- freehand** (#3): Smart sculpting does not cut through the entire volume and will not remove segmented vessels where centerline exists. Exclude region-freehand (3D) Use in case “Smart sculpting “is not working. Cuts through the whole volume.
- **Exclude region- freehand (3D)** (#3): Use if “Smart sculpting “is not working. Cuts through the whole volume.
- **Bounding box/cube** (#4): Isolate a region of interest on the volume image by using a 3D box. Use the MPR images to adjust the box location and size. Use middle mouse roll to increase the cube size.

Volume Review and Inspection Tools

These tools allow users to inspect the full volume and use the cutting tools (Instead of opening CT Viewer in addition to AVA).

The following volume viewing tools are available:

Icon	Tool	Use
🔒	Target Volume (and lock)	**How to Use** 1. In the task guidance panel, click **Bounding Box**. 2. Position the box over the area that you want to investigate. ⇨ The selected area is isolated for inspection and editing. The rest of the volume is hidden. This may improve system performance while you make corrections. 3. To change the size of the box using the Vessel view, drag the yellow dot on one of the box planes.  **Fig. 1:** Bounding Box in the Vessel View 4. To change the size of the box using a Reference view, move the pointer over the box and drag the yellow handles.  **Fig. 2:** Bounding Box in a Reference View 5. To temporarily hide the box, click **Hide/Show Box** in the task guidance panel. ⇨ Click **Hide/Show Box** again to show the box.

Icon	Tool	Use
	Target Cube	**When to Use** Used to focus on a segment of a centerline. **How to Use** 1. In the task guidance panel, click **Target Cube**. 2. The cube can be located on a centerline and will move following the cursor. Use the mouse wheel to increase/decrease.
	Cutting Plane	**When to Use** The clipping plane allows you view behind structures to see if there are any remaining vessels. This is especially useful for finding vessels in the skull base in skull studies. **How to Use** 1. In the task guidance panel, click **Clipping Plane**. 2. To change the position of the clipping plane, do one of the following: • Press the left and right mouse buttons and drag to rotate the volume. • Press the left mouse button and drag to move the clipping plane in the volume view. • Drag the clipping plane in an MPR image.

Support for Multiple Volumes and Subvolumes

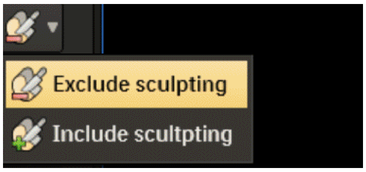
The application can analyze multiple volumes in a single session. If your selection contains multiple series or series with multiple volumes (for example an MR series with multiple dynamics), you can navigate between the volumes and create measurements on each individual volume. The findings list will only show the measurements of the selected volume or subvolume. However, all findings will be sent to the report application. Note that measurements are not applied to all volumes or subvolumes.

Volume Operations When Bones Are Not Removed

WARNING

Verify the segmentation after any editing is applied. If required continue editing or press Undo. If desired, all editing actions can be undone immediately by pressing Reset all

The following tools are available:

	Tool	
	Sculpting tool	**When to Use** Used to remove tissue or bone from the volume view. This tool can be used on both the vessels view as well as on the bone view.
	Remove Above Threshold	**When to Use** Used to manually move remaining bone fragments from the vessel view to the bone view with a single click. This tool is recommended for quickly moving "chunks" of bone from the vessel view to the bone view. However, the tool will not span gaps in the bone. If the bone region is diffuse and not contiguous, the smart sculpting tool is recommended for removing bone from the vessel view. **How to Use** When selected, an option to set the threshold opens. 
	Remove Residuals	**When to Use** Used to remove small high density residues. This tool is only available when viewing a body study. **How to Use** Depending on the size of the residues, you can select small, medium, or large residuals.

Viewports

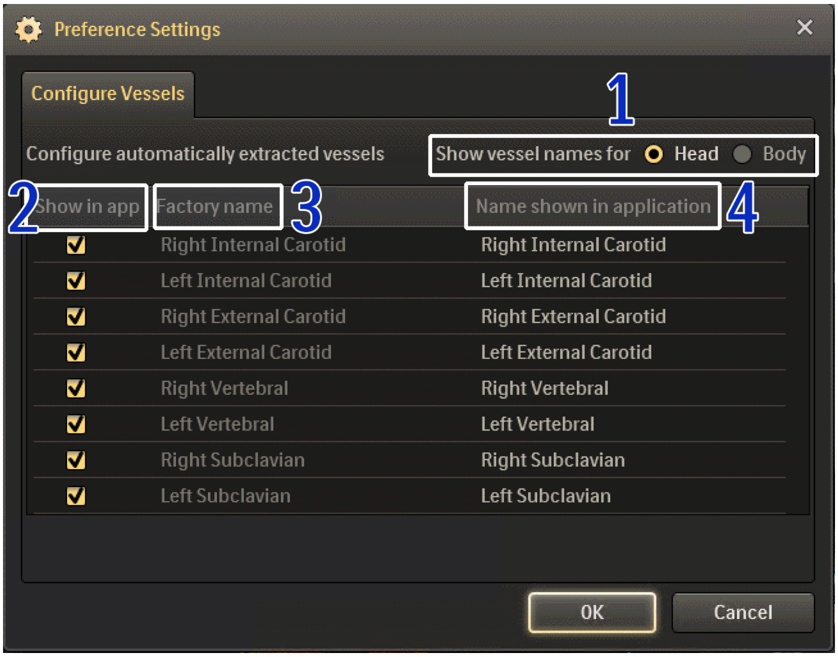
The following types of viewports are available in the application:

- **Volume viewport**: Volumetric image. Users can select between Volume rendering and other options such as MIPs
- **cMPR (curved MPR) of the selected vessel**: A reformatted image that follows the selected centerline along the vessel. The curved view is intended to show the entire vessel along the centerline. Users can perform the following operations:
  - Review by rotating around the centerline
  - Refine centerline by moving the seeds on the cMPR
  - In Cut and Extend, users can mark the location to cut on the cMPR
- **Cross sectional**: A reformatted image allows scrolling along the slices that are perpendicular to the selected centerline (in correlation to the cursor location on the volume). Users can scroll along the centerline on the cross sectional; the tracker on the volume image and on the cMPR image reflects the location of the cross sectional image.
- **Axial/Coronal/Sagittal** viewports: Standard original orientations of the acquired data (no reformat).
- **sMPR**: Straighten MPR shows the centerline as a straight line; this allows easy inspection of the contour changes along the centerline.
- **Longitudinal MPR**: Used when no centerline exists. Based on the location of the cursor, this shows a view of the longitudinal vessel around the location of the cursor.

Configure Vessels Preference Settings

The Configure Vessels Preference settings feature allows users to define how automatically extracted vessels appear in the Vessel list.

Click on the ⚙ Preference Settings icon on the toolbar.



Configure automatically extracted vessels

Show vessel names for ● Head ○ Body

Show in app	Factory name	Name shown in application
☑	Right Internal Carotid	Right Internal Carotid
☑	Left Internal Carotid	Left Internal Carotid
☑	Right External Carotid	Right External Carotid
☑	Left External Carotid	Left External Carotid
☑	Right Vertebral	Right Vertebral
☑	Left Vertebral	Left Vertebral
☑	Right Subclavian	Right Subclavian
☑	Left Subclavian	Left Subclavian

1	**Show vessel names for Head/ Body**	Select either **Head** or **Body** to configure vessel display.
2	**Show in app**	Place a check mark in this column to display the vessel in the Vessel list. If there is no check mark, the vessel will not appear.
3	**Factory name**	By default, the **Factory name** and **Name shown in application** are identical.
4	**Name shown in application**	To change the name shown in the application (Factory name), click on a name and type a new name. Once **OK** is selected, the name changes in the Vessel list.

To change the vessel display order, select a row in the table and drag to the desired location.

Launching MR Data

- MRA and 4D data can be launched on 4D data. Use the **<Alt>+→** keys to navigate between time-points.
- Default rendering mode for MR is MIP; it is possible to change to volume rendering and use on the MRA presets.
- There is no automatic centerline extraction on MR data; users can define centerlines, and then use them in similar way to the CT data.
- Users can create center lines in the Vessel Extraction stage on MR data (same operations available as in CT with a different algorithm).

Vessel Extraction Stage

The Vessel Extraction stage provides the following functionalities:

- Review and clean the vessel volume
- Review centerlines, using volume,cMPR, crossectional and MPRs images as needed
- Correct (edit) centerlines that require editing
- Create centerlines for vessels that were not detected during automatic processing
- When necessary, the full bone removal option is available within the Vessel Extraction stage.

484 of 688 images have been loaded...

Vessel extraction is slightly different for CT studies and MR studies. The system automatically recognizes the type of data set that you are viewing, and provides tools as appropriate.

Left Control Area

There are three expandable trays in the Vessel Extraction stage:

- Verify vessel extraction
- Verify bone removal
- Tissue Management
- Key image

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.

Please refer to the following sections of the Advanced Visualization Workspace Spectral Applications IFU for information on spectral results and processes:

- Understanding Spectral Results
- Common Spectral Processes

CT Studies

During the automatic bone removal process for a CT study, the following automatic functions are also performed:

- Vessel centerlines are extracted.
- Major vessels are named.

The vessel list is displayed at the top of the task guidance panel when you start the Vessel Extraction step. The vessel list contains an entry for each segmented vessel.

In the volume image, only one centerline and vessel name appears at a time (when selected).

For CT studies, you should verify the results of the automatic vessel segmentation:

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

MR Studies

Automatic vessel segmentation is not applied when you open an MR study. Therefore the vessel list is empty the first time that you open an MR study. You should create centerlines using the following procedures.

Two volume rendering presets are available when an MR data set is launched. One preset is optimized for images with contrast and the other for images without contrast.

The application adjusts the preset’s opacity and color level windowing WW/WL dynamically for each volume.

Vessel Extraction mode displays a list of labeled centerlines.

⚠ **WARNING**

Verify the accuracy of the centerlines and their labels. If needed, use the manual tools provided in the Vessel Extraction stage.

Vessel List

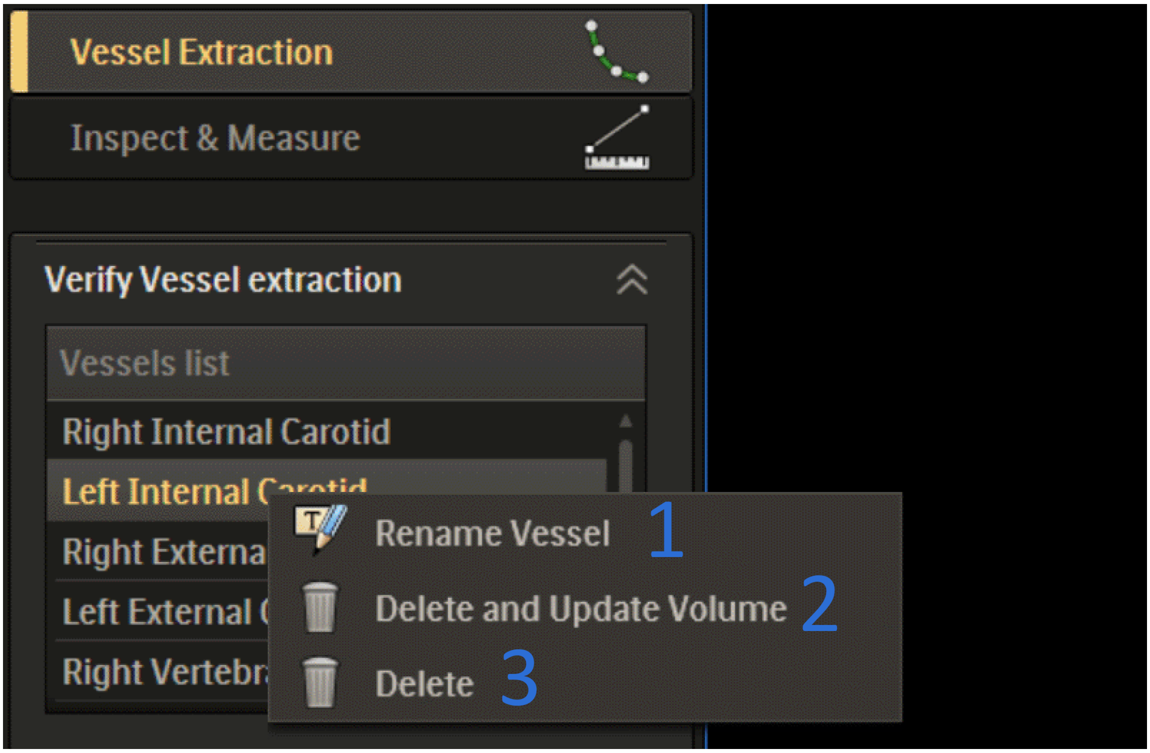
The vessel list shows all the extracted and labeled vessels.

To select a vessel from the list, hover on the volume image and click on a centerline or select directly from the list.

All of the viewports in the layouts reflect the selected centerline.

The following operations can be performed on a vessel via the context menu:

- **Rename Vessel** (#1)
- **Delete and Update Volume**: When the centerline is deleted, the vessel volume image is updated accordingly. (#2)
- **Delete**: Deletes the centerline but does not update the volume. (#3)



NOTICE

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

Aorta and L/R Iliac Creation

In body cases, if the Aorta and two iliac vessels were created successfully, additional vessels appear in the list:

- **Aorta & Left Iliac**
- **Aorta & Right Iliac**
- **Aorta & R/L Iliac**: When aorta and R/L iliac are recognized by the application this entry appears in the list. When selected, a special layout appears, showing the volume and both the aorta and right iliac and aorta and left iliac. This layout is the only layout where the bifurcation point is displayed. The bifurcation point is fixed and is determined by the centerlines of the left and right aorta-iliac vessels.

  The birfurcation point is relevant for Pre-procedural Vascular Planning (see section “Pre-procedural Vascular Planning (Multiple Rings-based Measurement)” on page 48). In this mode, two **Refine** tools are available:

  – **Refine bifurcation point**: Allows editing/moving the bifurcation point.

- **Refine centerline**: When refining the centerlines, the results are reflected on the separated centerlines (Aorta & Left iliac and Aorta and Right iliac).

NOTICE

The application may fail to create the combined vessel due to incomplete results of its components.

In the section below, **combined vessel** refers to the **Aorta & Left Iliac** and **Aorta & Right Iliac**; **Vessel tree** refers to the **Aorta & R/L Iliacs**.

- If editing a common segment on one combined vessel (aorta), the same editing results are reflected in the other combined vessel that includes the same segment. As a result, this operation may take a bit longer.
- When editing a combined vessel or on the vessel tree, the relevant segment (iliac or aorta) is reflected in the editing results (i.e if the Aorta was edited on the vessel tree, the "Aorta" segment reflects the same editing results).

  When editing a separate vessel that is a segment of the combined vessel, the editing results are reflected in the combined vessel, unless there is no possibility to connect the segments (as they do not meet). In such cases, it remains separated.
- When one of the combined vessels is selected, it appears as if one long centerline is selected (cMPR shows the whole center line end to end).
- When the vessel tree is selected, there are two centerlines that are selected; there are two cMPRs on the layout, each of them shows another centerline. The trackers shown on each of the center lines appear in different colors (yellow and purple).

Vessel Extraction Layouts

The following layouts are available for the user selection in the Vessel Extraction stage:

- Volume + 2 cMPRs + CS + axial
- Volume + 2cMPRs + CS (as in legacy AVA)
- Volume + 2 cMPRs +CS + Axial (similar to CCA layout)
- Volume + cMPR+CS + Axial+coronal+sagittal
- Volume + 2CMPR+CS + Axial+coronal+sagittal

Vessel Creation and Editing Tools

Users can create new centerlines with one of the tools described below:

Icon	Tool	Use
	Create new centerline - Automatic	**When to Use** This tool is used to create a new centerline when no centerline is shown or where the existing centerline is unsatisfactory. **How to Use** 1. Allocate a seed at each end of the expected centerline. 2. Use volume images and MPRs to find accurate locations for the seeds. 3. Click the **Accept** button ✓. The application automatically calculates the route between the two seeds. In case of failure, try again with more than two seeds
	Create automatic Aorta and Iliacs	**When to Use** This tool is used if automatic segregation did was not sufficient and re-tracking of the aorta and both iliacs is needed. **How to Use** 1. In the volume or MPR view, click to place a seed in each of the four vessels (end of aorta, bifurcation point and both iliacs). 2. When the tree is correctly defined, click **Accept**.
	Create new centerline - Manual	**When to Use** This tool can be used to create a new centerline when no centerline is shown and there is no contrast in the vessel. **How to Use** 1. Allocate seeds along the route of the expected centerline. 2. Click the **Accept** button ✓. The application connects between the seeds using the spline function, without impacting image processing.

Icon	Tool	Use
	Extend distally/proximally (automatic)	**When to Use** This tool can be used to extend an existing centerline from one of its edges, using an automatic algorithm. **How to Use** 1. Allocate a seed in the location of the expected extension end point. The seed can be located (and modified) on the volume and MPRs images. 2. Click the **Accept** button ✓. The application automatically calculates the route between the end of the centerline and the new seed. In case of failure, try again with more than two seeds. Note: To extend to a location, right-click on the centerline.
	Extend distally/proximally (manual)	**When to Use** This tool can be used to extend an existing centerline from one of its edges, when there is no contrast in the extended segments (or automatic tool fails). **How to Use** 1. Allocate seeds along the route of the expected extension. 2. Click the **Accept** button ✓. The application connects between the added seeds using a spline function, without impacting image processing.
	Cut and extend	**When to Use** This tool is useful when an end of a centerline goes off the vessel. The tool combines two operations, cut and extend to another direction. Use this tool when the portion to cut is smaller than the portion to keep; or use **Cut** first and only then the extend. **How to Use** 1. Locate the first seed on the centerline (recommended on the cMPR viewport) a bit before the location is off the vessel. 2. Use the volume and MPR images to find the correct extension of the vessel and allocate the second seed there. 3. Click the **Accept** button ✓ . The application cuts the centerline in the location of the first seed and extends it to the new location. To “Cut” (without extend), position the cursor at the location to be cut and use the context menu (right click) to cut above or below.

Icon	Tool	Use
	Extend to relate point	**When to Use** Used to find a location to extend to on MPRs, and then to extend. **How to Use** 1. Use the MPR images to find a location to extend the currently selected centerline. 2. Click **Extend to relate**. The application extends the selected centerline to the clicked location. Any click repositions the centerline (as in relate mode).
	Cut Distal/Proximal	**When to Use** This tool is useful to cut the incorrect portion of a vessel. **How to Use** Click on the centerline to locate the tracker in the location of the cut Position the cursor on the curved MPR or volume image, right click and select **Cut proximally/ distally**.

NOTICE

If a failure occurs when using the automatic tools for vessel extraction and editing, a notification appears on the bottom of the screen. If this occurs, either try again or use manual tools.

Bone Removal Tools

The main vessels are extracted and segmented during Bone Removal. Results are displayed once the process is completed. The first time that a study is launched in the application, the results show the vessel view, the bone view, and MPR images.

A full range of bone removal tools are available in the Vessel Extraction stage. The tools can be used to clean the vessel volume when needed and are located in the **Verify Bone Removal** tab on the left panel.

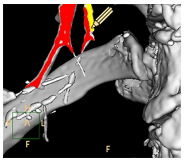
⚠ **WARNING**

You should verify that bone removal does not affect vessel completeness. If necessary, manually correct the vessel definitions using the correction tools provided.

The following tools are available to clean the vessel volume image in the Vessel Extraction stage (or Bone Removal) mode.

Icon	Tool	Use
	Remove Bone	**When to Use** This tool can be used to remove “non-vessel” components from vessel volume to the “bone” volume. **How to Use** Pick the tool and click on parts of bones or other tissues (i.e. veins) on the vessel volume. 1. In the task guidance panel, click **Remove Bone**. ⇨ Activating this tool starts the bone removal mode. 2. Click a bone fragment in the vessel view. ⇨ The bone fragment is removed from the vessel view and added to the bone view. 3. Continue removing bone fragments from the vessel view, as desired. 4. When you have completed bone removal, click **Remove Bone** again to switch off bone removal mode.
	Remove Residuals	**When to Use** This tool is only available for body studies. It can be used for removing high density residues from vessel volume. **How to Use** 1. In the task guidance panel, select a size option: small, medium, or large. 2. Click **Remove Residuals**.

Icon	Tool	Use
	Smart and Aggressive Sculpting	**When to Use** The smart sculpting tool can be used on both the vessel view and the bone view in the volume image. Smart sculpting recalculates the centerline. It 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 from the bone view to the vessel view. • Moving sections of large vessel from the bone view to the vessel view. Sometimes it can be difficult to avoid including unwanted tissue in a sculpted region. In this case, use a bounding box in conjunction with the smart sculpting tool to constrain the sculpting within the bounding box region. **How to Use** 1. In the task guidance panel, click **Smart Sculpting**. 2. In the vessel view or the bone view, draw a region around the area that you want to sculpt. ⇨ When used in the vessel view, smart sculpting moves all tissue that was incorrectly determined to be vessel in the sculpting region, and any high intensity pixels of the remaining tissue in the sculpting region, to the bone view. ⇨ When used in the bone view, smart sculpting moves all the tissue in the sculpting region to the vessel view. ⇨ Smart sculpting does not cut through the entire volume but stops after the higher intensity parts. This avoids leaving a "hole" in a MIP image, for example.
	Add vessel by seeds	**When to Use** Used when a piece of vessel was mistakenly removed from the vessels and added to the bones and you need to recover the vessel. **How to Use** 1. In the task guidance panel, click **Add Vessel**. 2. For head, click on a vessel remaining on the bone volume. It will be added to the vessels. 3. For body, locate two seeds on the two ends of the vessel in the bones, or on the gap on the vessels. The application will complete and it will be added to the vessels.

Icon	Tool	Use
	Add vessel by segmenting the missing vessel on the bone image.	**When to Use** The manual vessel tool is used on the bone view of the volume image. For skull studies, this tool can also be used on the MPR images. This tool removes vessel tissue that was mistakenly identified as bone. For small vessels, zoom in on the vessel before using the manual vessel tool. This can reduce the number of clicks needed to select a vessel. **How to Use** 1. In the task guidance panel, click **Add Vessel**. ⇨ When viewing a body case, the bone view image is rendered in grayscale (monochrome). 2. Move the pointer over a vessel that you want to move 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. ⇨ The manual vessel tool functions slightly differently, depending on whether you are analyzing a skull study or a body study. ⇨ For a skull study, the manual vessel function immediately removes the vessel when you click in the bone view or MPR image, and adds it to the vessel view. Repeat this process to remove more vessels. ⇨ For a body study, when hovering over the volume image, the yellow overlay indicates what will be included when marked, for remove from the bone view. Upon clicking, this area is marked in red. You can now mark more vessel parts. When the interesting vessels have been marked, click **Accept** in the task guidance panel. The accumulated marked vessels are moved from the bone view to the vessel view. 

The Remove Bone, Remove Residuals and Smart Sculpting Tools are also available in a floating toolbar in the View image viewport.

Inject/Erase Tools

The Inject/Erase tools are available either:

- Under the **Clip & 3D Segmentation** tab
- In the MPR image view ports within the Floating Dialog tool bar

Colors additional unsegmented areas and adds them to the active tissue. The rate and type (viscosity) of the injection can be controlled by the relevant boxes.

WARNING

When using the Dye Injection tool verify the correctness of volume segmentation. If necessary, correct the dye tracing using correction tools supplied by this application.

Expand and Erode

The Expand function allows you to increase the edges of the tissue. Each click expands the edge by a one-voxel increment.

The Erode function allows you to decrease the edges of the tissue. Each click reduces the edge by a one-voxel increment.

Eraser (3D)

Removes volume from the active tissue.

Tissue Management

The Tissue Management tab lists all current and all saved tissues of the study.

Verify Bone Removal Mode

The Bone Removal mode provides a dedicated layout and set of tools for cleaning and editing the volume image. The same tools that are available to clean up the vessel volume are provided, with additional tools such as inject dye.

NOTICE

The **Bone Removal** mode is not applicable for MR studies.

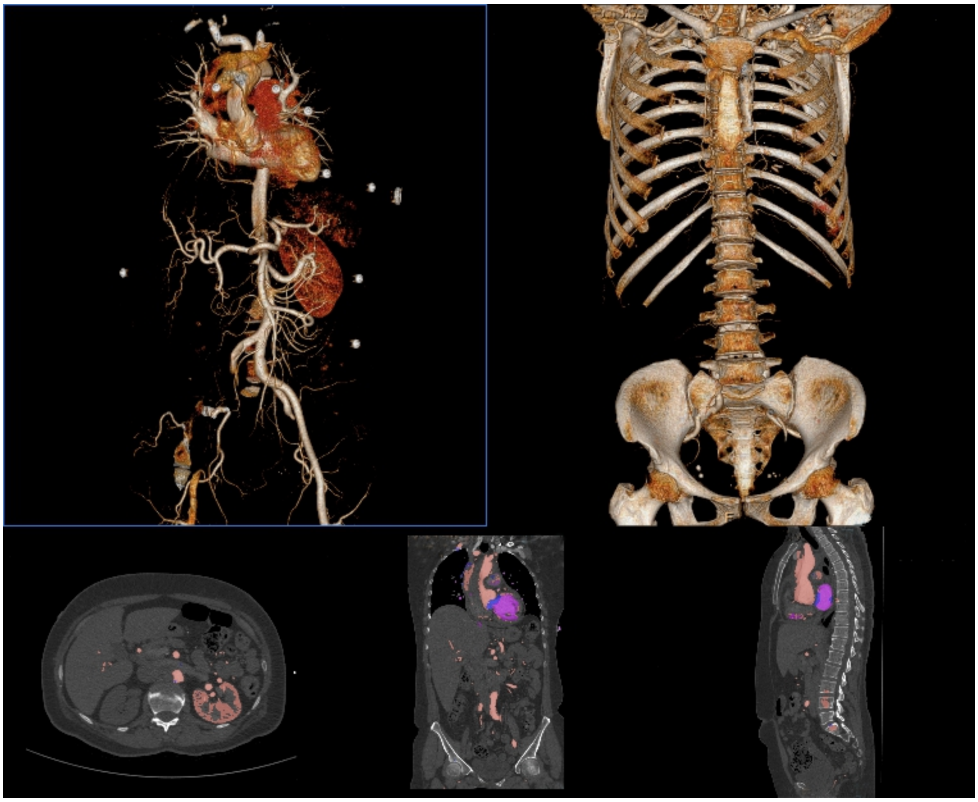


Fig. 3: Bone Removal step results

The main purpose of the **Bone Removal** panel is to perform corrections on the vessel volumetric image, such as remove bones or other compartments from the vessel volume, or copy vessels from bones volume to vessel volume, if desired.

WARNING

You should verify that bone removal does not affect vessel completeness. If necessary, manually correct the vessel definitions using the correction tools provided.

WARNING

Verify the accuracy of the automatic segmentation. If necessary, manually correct the segmentation using the Segmentation correction tools provided in this stage.

WARNING

Verify the correctness of the segmentation of the body. Edit if required.

WARNING

Verify the correctness of the segmentation of the head and neck. Edit if required.

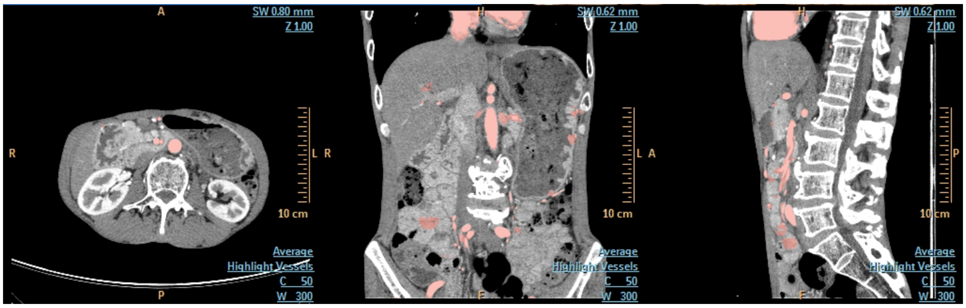
Bone Removal Reviewing Options

Highlight Vessels and Bone

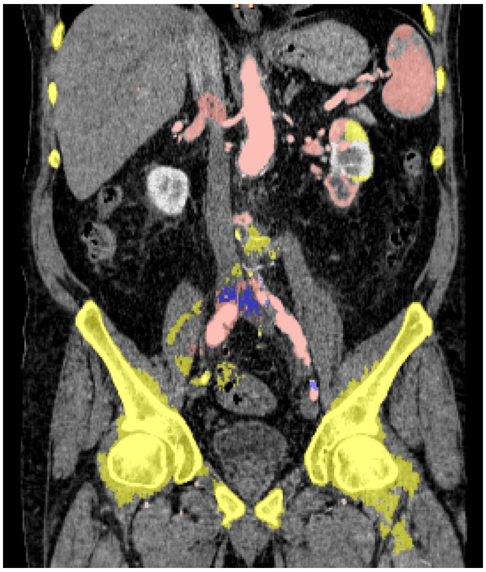
You can view colored vessel and bone overlays in the reference images. (This feature is not available in the One by Two layout.)

For body cases, the colored overlays give an indication if a tissue is segmented as bone or as vessel.

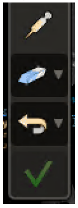
For skull cases, the colored overlays give an indication of the vessels that are extracted and labeled. Labeling can only be verified in the vessel extraction step. In case a carotid or vertebra is not identified, this can be identified as it is not colored.



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.



Inject/Erase Tools

The Inject/Erase tools are available in the MPR image view ports within the Floating Dialog tool bar. 

Colors additional unsegmented areas and adds them to the active tissue. The rate and type (viscosity) of the injection can be controlled by the relevant boxes.

WARNING

When using the Dye Injection tool verify the correctness of volume segmentation. If necessary, correct the dye tracing using correction tools supplied by this application.

Eraser (3D)

Removes volume from the active tissue.

Inspect & Measure Stage

The Inspect & Measure stage allows you to inspect vessels and create measurements to assist with analyzing vascular problems. The collected results of a measurement are called findings. These findings are collected in a list.

Measurements are collected along a vessel, either with or without a centerline and contours. Once collected in the findings list, measurements can be exported. Captured measurements are be saved as part of saved results.

When entering the Inspect and Measure stage, the last selected centerline in the Vessel Extraction stage is active and a diameter is located on the last location of the cursor. You can navigate along this location with the diameter or select another tool or centerline.

In this stage the user can either use the centerline and contours for creating measurements and findings, or use the **Quick Inspection** mode to create measurements without a centerline.

Please refer to the following sections of the Advanced Visualization Workspace Spectral Applications IFU for information on spectral results and processes:

- Understanding Spectral Results
- Common Spectral Processes

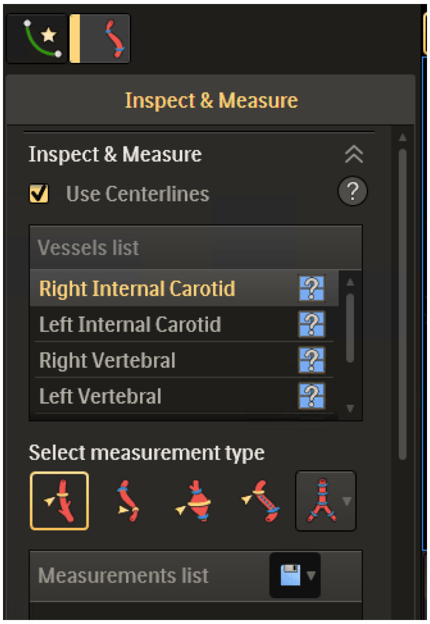
⚠ **WARNING**

Verify the automatic extraction of the lumen and vessel contours. If necessary, correct the contours using the tools provided in this application.

⚠ **WARNING**

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

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



Layout Selection

In the Inspect and Measure Along Centerline mode the display is divided into two sections:

- the left side is based on the selected layout
- the right side is derived from the selected measurement tool

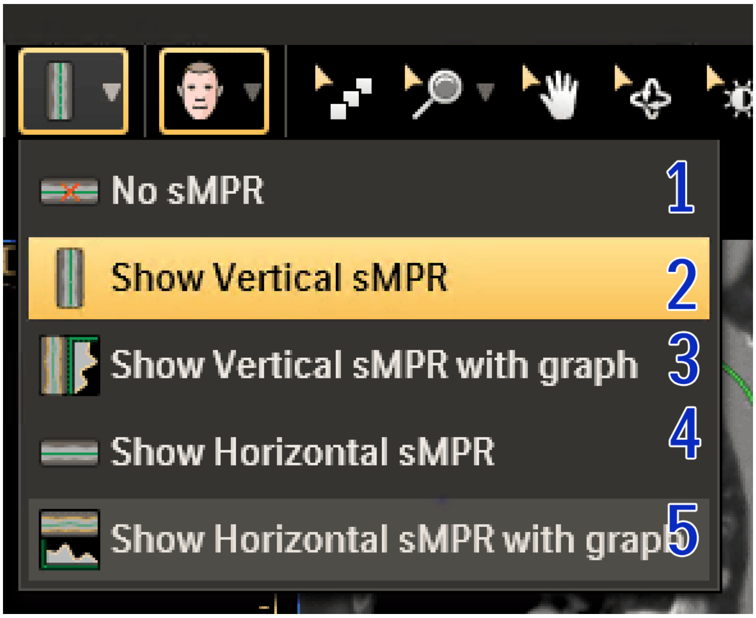
The sMPR can always be added to the layout either in vertical of horizontal mode. The result table is always located on the left side, and it can be shown collapsed or expanded.

The following layouts are available:

- Volume
- MPRs
- Coronal
- Volume + MPRs

On the right side of the viewing area the user can see the cMPR of the selected vessel and the Cross sectional viewports of the relevant rings

Showing sMPR Options



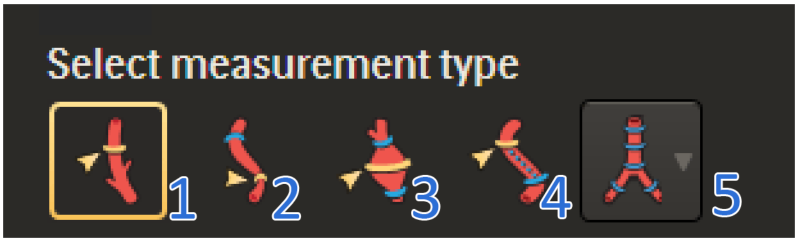
The sMPR viewport mode can be selected from the upper toolbar and has the following options:

- No sMPR (#1)
- Show Vertical sMPR (default for landscape monitors) (#2)
- Show Vertical sMPR with graph (#3)
- Show Horizontal sMPR (default for portrait monitors) (#4)
- Show Horizontal sMPR with graph (#5)

Measure Along Centerline

This mode allows the creation of measurements based on the extracted centerline and contours. The following type of measurements are available in this mode:

- Diameter (Location): single ring (#1)
- Stenosis (Lesion and Reference): two rings (#2)
- Aneurysm (Max D): three rings (#3)
- Length between two diameters: two rings (#4)
- Stent: Multi-ring template (#5): This is enabled only if the option is purchased.



Each of the tools is optimized according its characteristics, and a set of relevant measurements is calculated according the selected tool.

For each of the selected tools, all relevant rings are positioned on the centerline on the first click.

Once positioned, users can modify their location along the selected centerline on any of the viewports. The user decides when to add a measurement to the list. A measurement from the list can be selected and reviewed at any time.

Measurement Workflow

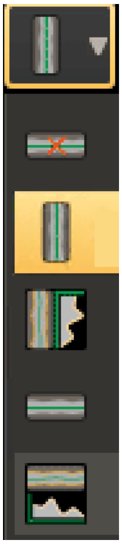
1. Select the centerline with the pathology to be measured.
2. Select a tool based on the pathology.
3. Click on the centerline, on the location of the finding (stenosis location, max aneurysm, location etc.).

   After clicking, rings are located on the centerline. The main ring is located on the clicked location, while additional rings, when relevant, are automatically located nearby, based on the application's estimation.

   The correlating CS images are displayed and the trackers of the rings appear on the volume and cMPR.
4. To relocate the rings, either scroll in the CS images or drag the tracker on the cMPR or volume image.
5. Once the rings are in the correct location, click  **Add measurement**. This adds the measurement to the table.
6. At any stage, it is possible to select a measurement from the list, activating the measurement and allowing editing if needed.
7. Any attempt to change the centerline, without adding the measurement to the table, triggers a notification that allows continuing or returning to select **Add measurement**.

Along Centerline Mode Graph

While using Along Centerline mode, you can display a graph providing quantitative information about the selected vessel.



To display a graph, from the toolbar, click on an sMPR viewing icon and choose either **Show Vertical sMPR with Graph** or **Show Horizontal sMPR with Graph**.

By default, the graph displays the minimum lumen diameter. To select an alternative graph option, right-click on the graph to select:

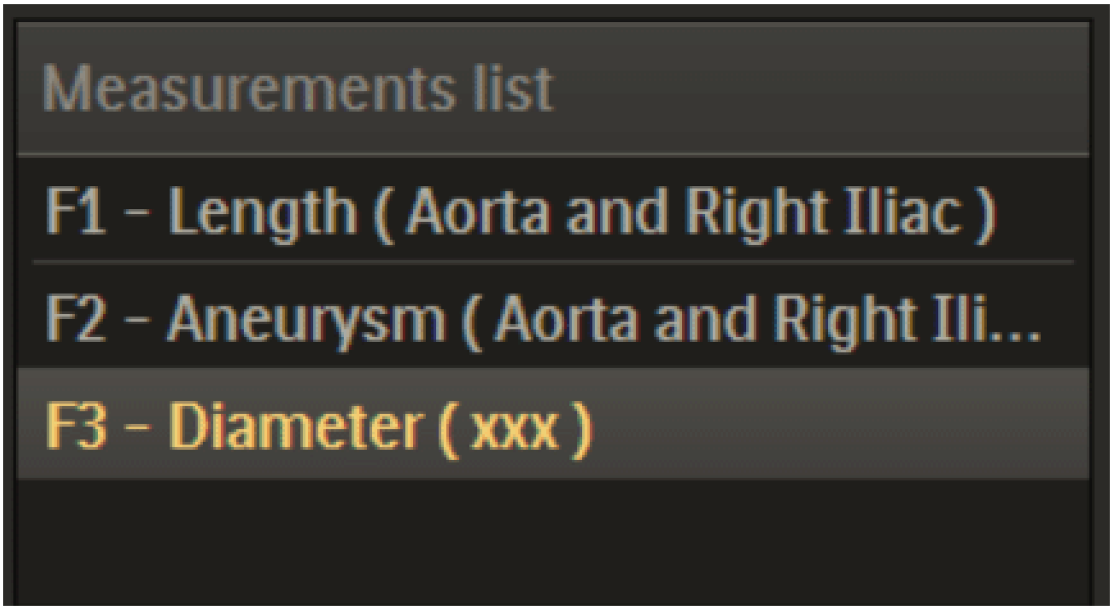
- Lumen Area
- Effective Lumen Diameter
- Minimum Lumen Diameter
- Min and Max Lumen Diameter

All ring locations in the sMPR image are indicated in the graph and the value of the active ring location is displayed next to the corresponding line. This measurement is updated if you move the ring, or if you modify the contours at that location.

Saving Measurements and Measurement List

Measurement List

The measurement list is located on the left panel.



Measurements list

F1 - Length (Aorta and Right Iliac)

F2 - Aneurysm (Aorta and Right Ili...

F3 - Diameter (xxx)

Each measurement name is constructed from a name (F1) , its type (Length, Aneurysm..) and the vessel name (when known).

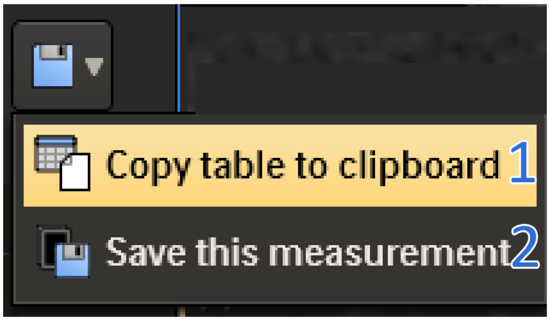
By selecting an item in this list, the application changes the layout on the right side to show the selected measurements, with the ring locations displayed in the Cross sectional viewports.

The following operations are available on a selected measurement via the context menu:

- Rename (only the name of the measurement)
- Delete

Capture Measurement

The following options are available from the top of the measurement table:



- **Copy table to clipboard** (#1): This allows copying and pasting the table to Excel or Notepad.
- **Save this measurement** (#2): Generates a series with all the relevant images for the measurement that is shown in the table. The series includes a screen capture of each of the shown viewports, and the screen capture of the whole display

Measurement Table

The measurement table is located in a collapsible viewport on the left side of the display. The table has three modes:

- Collapsed
- Show summary
- Show full results

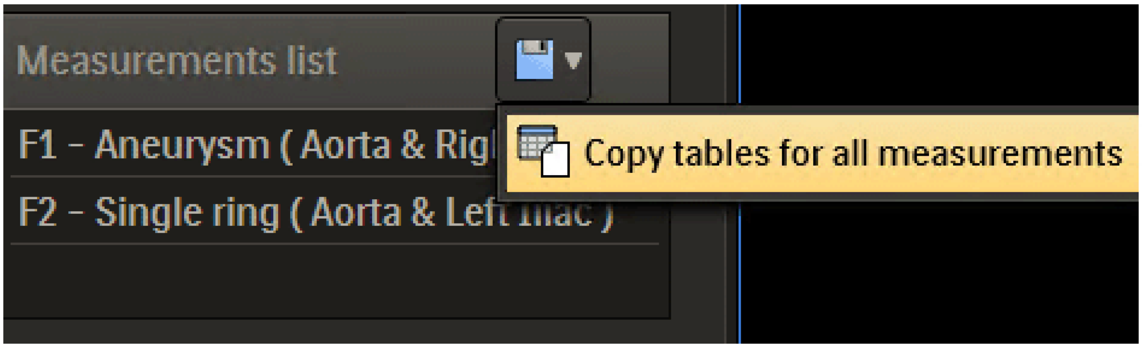
When relevant, the user can select whether to display the Lumen and Vessel results or just Lumen results.

Context Menu on a Measurements

- **Rename**: Used to change the measurement name.
- **Copy table**: Used to copy the table content for the selected measurement to the clipboard.
- **Save this measurement**: Used to save from the top of the table.
- **Delete**: Used to delete a measurement.

Copy all Measurements to Clipboard

From the table title, click **Copy tables for all measurements** to copy all measurements.



Paste into Microsoft Word, Notepad or Excel.

Focus Mode

The **Focus on measurement** icon enables Focus mode. When enabled, the selected measurement is centered and zoomed.

To use this mode, select a measurement ring and enable **Focus on measurement** via the icon or keyboard shortcut (<Ctrl > + F).

If two or more measurements appear in the Measurements list, it is possible to alternate viewing in focused mode between the measurements.

Quick Inspection

Quick inspection is used for measuring vessels that do not have a pre-defined centerline.

The tools are based on the vessel explorer algorithm, which allows navigation along a vessel in an interactive mode.

When in Quick Inspection, the following tools are available:

- Diameter
- Stenosis

The main difference between Quick Inspection mode versus “Along Center line” mode is that there are no cMPR and sMPR images. Instead the application shows a “Longitudinal MPR” which is based on the location of the ring.

The workflows are similar, such that users can choose a tool, click on the location of the finding and add the finding to the list.

You can move the inspection ring by dragging it in the overview image or in the longitudinal view, or by scrolling in the cross section view. All views are automatically updated when you move the inspection ring.

While inspecting the vessel in the longitudinal view, you can change the plane of the cross section view by adjusting the red rotation handles. Pause the pointer over a handle. When it turns yellow, drag it to a new position.

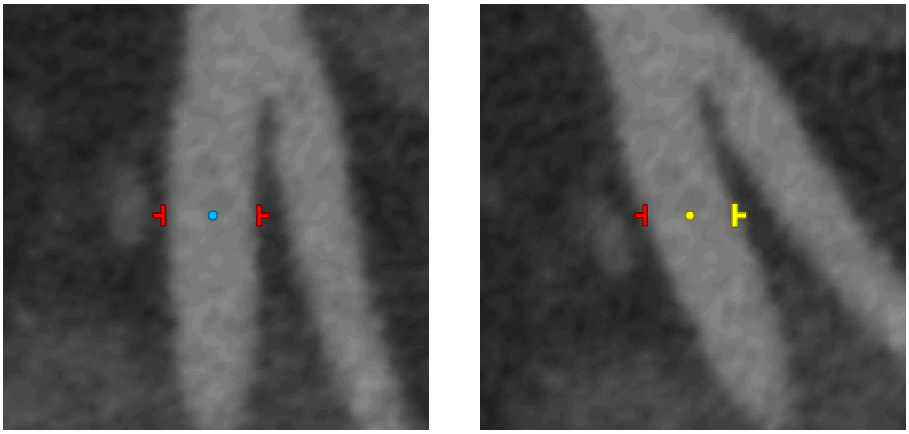


Fig. 4: Changing the Plane of the Cross Section

While inspecting the contour in the cross section view, you can correct the contour, if needed, by adjusting a control point in the contour. Pause the pointer over the contour. When a control point is displayed in yellow, drag it to a new position.

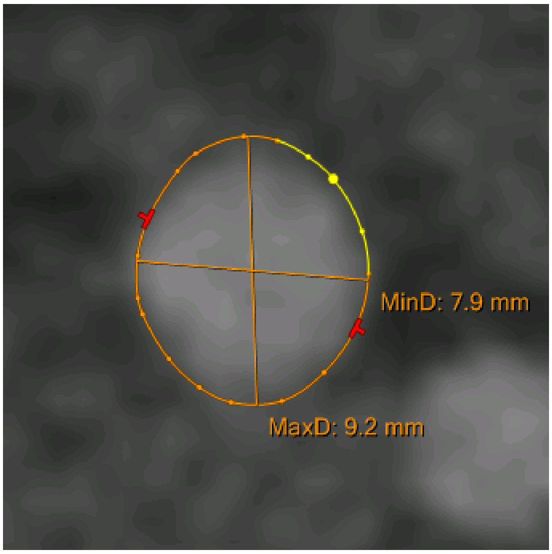


Fig. 5: Adjusting a Contour Control Point

To view beyond the vessel at the location of the inspection ring (without moving it), press CTRL and drag.

You can also move the inspection ring by clicking on another point on the vessel.

Pre-procedural Vascular Planning (Multiple Rings-based Measurement)

NOTICE

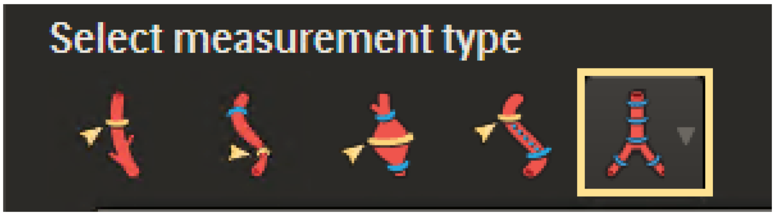
This feature requires the Stent Planning license.

NOTICE

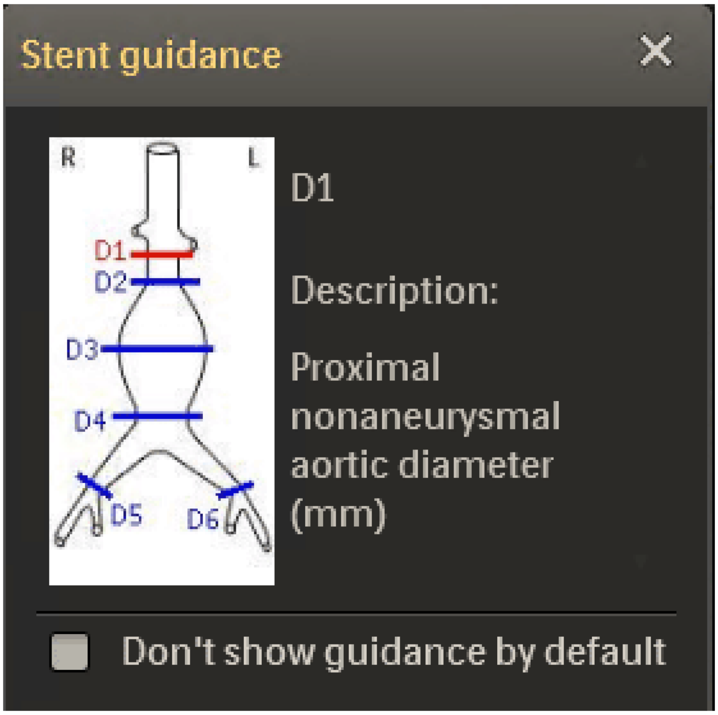
Pre-procedural Vascular Planning is only available for CT studies.

Pre-procedural Vascular Planning displays multiple measurements in different locations together with potential inter-relationships between the measurement location. These pre-procedural vascular findings are based on a predefined template that defines rings and measurement between the rings.

To start the **Pre-procedural Vascular Planning** mode, select a vessel and then select the Stent option (highlighted in yellow)..



A schematic diagram of the selected protocol and a list of associated measurements is displayed.



D1

Description:

Proximal nonaneurysmal aortic diameter (mm)

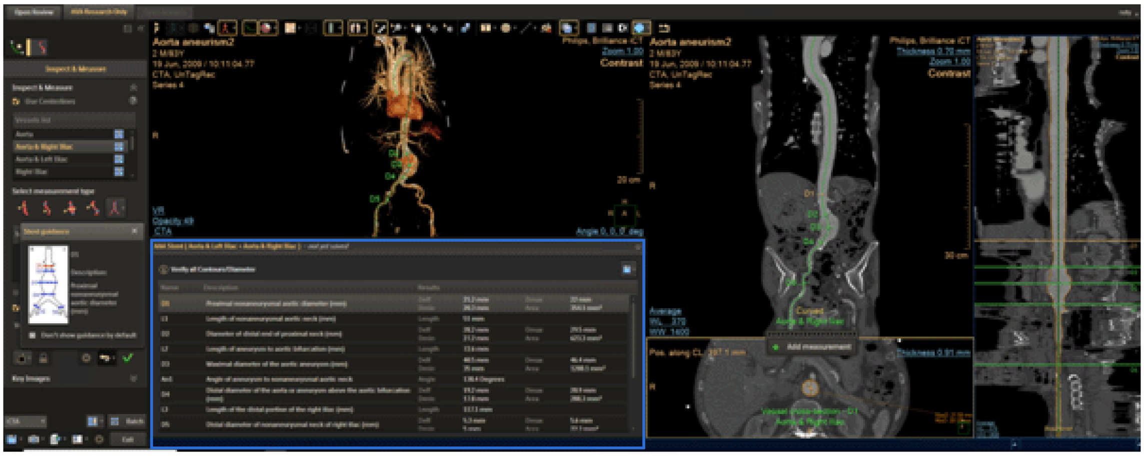
☐ Don't show guidance by default

The displayed measurements are specific for each stent protocol. To see a description of the measurement, pause the pointer over a measurement in the list.

If the stent protocol includes a bifurcation point, it is indicated with **B** in the list. This bifurcation point is fixed and determined by the centerlines of the left and right aorta-iliac vessels. To change the position of this point, return to the **Vessel Extraction** stage and manually edit the position of the point using **Refine**.

Choose a protocol from the drop-down list. The application provides several factory protocols. The protocols that are available in the list depend on the type of vessel selected. For example, to see a protocol list including the bifurcation point, select one of the aorta-iliac vessels. Alternately, you can make your own protocols using the Stent Protocol Editor (see Stent Planning Protocol Editor on page 51).

The application locates the rings defined in the selected template on the selected centerline and displays the expected measurements in the table.

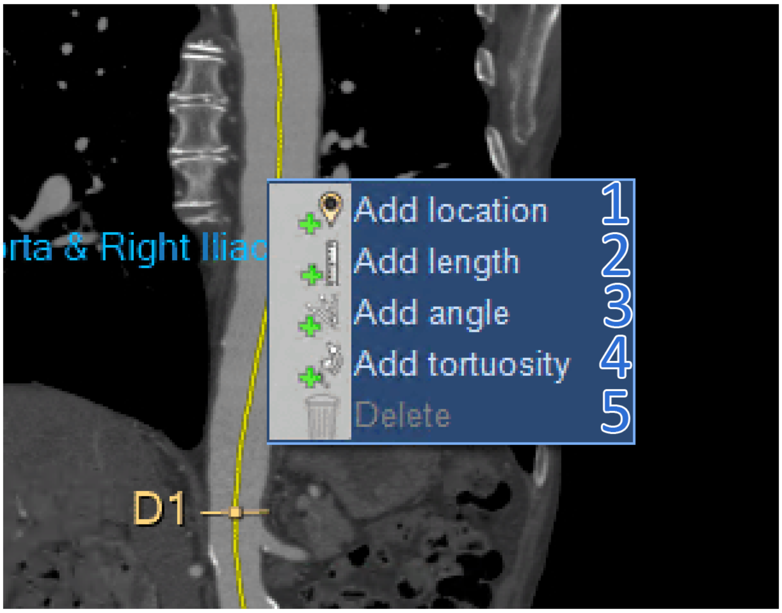


The following operations are available in the measurements table:

- **Selecting an entry in the table**.

  This highlights the relevant rings in the table and on the images. For example when a length measurement is selected, the two rings that are used to calculate the length will appear with colors on all images, and the corresponding CS images are displayed.
- **Dragging and relocating a ring location along the centerline.**
- **Adding/Editing a measurement**:
  - Right click on the centerline.

    This opens four measurement options that can be added to the current template. Options include Add location (#1), Add Length (#2), Add angle (#3), Add tortuosity (#4) and Delete (#5).

  - Select an option.

- In the window that appears, input in a measurement name. Once saved, additional rings are added on the centerline, which allows adding measurements to the template.
- Use **Add measurement** to add the multi-ring measurement to the measurement list. Once added, it is saved as part of the results and allows all operations, including **Save images to study** and **Copy to clip board** .

Deleting (#5 above) a ring or an entry from the measurement is possible when there is an active pre-procedural vascular finding.

Pre-procedural vascular findings can include an unlimited number of rings with the following measurements:

- **Diameter**: Deff, Max D, MinD, Area
- **Length**: Distance between two rings along the centerline
- **Angle**: The angle which is created between 3 rings
- **Tourtosity**: The tortuosity calculated between 2 ring

Bifurcation Point

- The pre-procedural vascular findings template can include one ring, defined as the "Bifurcation ring".
- The bifurcation ring must be located exactly on the bifurcation point on the Aorta and Iliac vessel.
- Changing the location of the "Bifurcation ring is only allowed in the Vessel Extraction stage.

Stent Planning Protocol Editor

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

NOTICE

You can launch Protocol Editor from this application and from Preferences, where it is in the “Viewing Applications” page.

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

You can use an existing stent protocol to create and configure a new protocol.

Starting the Protocol Editor

1. Click **Open Editor** in the task guidance panel.

⇨ The Protocol Editor dialog box is displayed. You use this dialog box to configure existing stent protocols and add new protocols.

When you are creating or editing a stent protocol, you work through the following stages in the Protocol Editor:

- Protocol
- Image
- Measurements
- Questions

The current stage is indicated in the upper-left corner of the Protocol Editor.

- To step through the stages, click the left or right arrow next to the stage name.
- To jump directly to a stage, click the down arrow next to the stage name and select a stage.

Protocol Stage

Protocol List

The protocol list displays all available protocols. The list contains factory protocols as well as protocols that you have created. If you import a protocol, it is also displayed in the list. You can view the parameters of the factory protocols, but you cannot modify them.

Creating a New Stent Protocol

1. Click **New** in the **Protocol** stage of the Protocol Editor.
2. Enter the **Protocol Name**. The name of the protocol can be changed.
3. Enter a brief **Description** of the protocol.
4. If the stent protocol is to be used for Aorta and Iliac vessels, select **This is a Stent for the Aorta and Iliacs**. This indicates that a bifurcation point is needed.

⇨ The AVA Preview panel displays a preview of the new protocol.

NOTICE

You can also create a new protocol using an existing protocol as a template: Select a protocol in the protocol list, enter a new name in the **Protocol Name** field, and then click **Save**. Modify the new protocol as desired using the procedures given below.

Importing and Exporting Protocols

You can import an existing protocol for use with the application, or to use as template for a new protocol. Additionally, after creating a protocol, you can export it to another location for use elsewhere.

1. To import a protocol, click **Import**, and do the following:
   - Navigate to the location of the protocol in the **Import Files** dialog box.
   - Select the protocol and click **OK**.
2. To export a protocol, click **Export** and do the following.
   - Navigate to the location to which you want to export the protocol in the Export Files dialog box.
   - Click **OK**.

Click on an existing protocol to view its parameters in the Protocol Editor.

Renaming a Protocol

1. Right-click the protocol in the protocol list.
2. Click **Rename**.
3. Enter a new name in the dialog box and click **OK**.

Deleting a Protocol

1. Right-click the protocol in the protocol list.
2. Click **Delete**.

Image Stage

1. From the list on the left, click the name of the image file that corresponds to the protocol you are creating.
2. If the name of the image that you want to use is not available, do the following to import it:
   - Click **Import** of the Image stage of the Protocol Editor.
   - In the **Import Files** dialog box, navigate to the location of the file that you want to import.
   - Select the file (JPG format) and click **OK**.

Measurements Stage

In the **Measurements** stage, you can add measurements for the selected protocol.

Length, tortuosity, and angle measurements are based on diameter measurements. You can only add these measurements after adding a sufficient number of diameter measurements. A guidance message is displayed when you select one of these measurements, indicating the number of diameter measurements that you need to select.

Image Panel

The **Image** panel displays the name and location of each diameter measurement that has been configured. Diameter measurements that are relevant to the selected measurement in the **Measurements Summary** list are highlighted.

Measurements Summary List

All configured measurements are displayed in the **Measurements Summary** list. Measurements are added to this list as you create them using the following procedures. When you click on a measurement in the list, the diameters that are associated with that measurements are highlighted in the **Image** panel.

1. To delete a measurement, select it in the **Measurements Summary** list and click **Delete** in the **Parameters** panel.
2. To change the order of the measurements in the **Measurements Summary** list, select the measurement in the list, and then click **Up** or **Down**.

⇨ You can arrange the list in the same order that you want the measurements to be displayed in the application.

Parameters Panel

The **Parameters** panel provides configuration options for each measurement that you create. The options that are available depend on the type of measurement selected. After creating a measurement, you use the **Parameters** panel to configure the measurement according to your needs.

To Add a Diameter Measurement

1. Click the **Diameter** button and keep the left mouse button pressed while moving to the stent image.

⇨ The pointer changes from arrow to an index finger to indicate where to allocate the diameter measurement on the image.

⇨ A line is automatically displayed on the image after releasing the mouse. The diameter is automatically named (D1).

2. If desired, rename the diameter and add a description in the **Parameters** panel. The active measurement line is red; inactive lines are blue.
3. 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.
4. In the **Parameters** panel, select the **Measured Values** that you want to display in the stent planning image.
5. To show control points, select **Control Points** in the Parameters panel.

To Add a Bifurcation Measurement

1. Click the **Bifurcation** button and keep the left mouse button pressed while moving to the stent image.
2. If desired, rename the bifurcation and add a description in the **Parameters** section of the stage. 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.

⇨ The pointer changes from arrow to an index finger to indicate where to allocate the bifurcation measurement on the image.

To Add a Length Measurement

To specify a length measurement, you select two diameters in the stent protocol image to indicate the start point and the end point of the measurement.

1. Click the **Length** button.
2. Click a diameter on the stent protocol image to indicate the start position of the length.
3. Click another diameter on the stent protocol image to indicate the end position of the length.

⇨ The measurement is added to the measurement list with the prefix **L** and a sequential number. You can rename the measurement in the **Parameters** panel, if desired.

4. Enter a description in the **Parameters** panel.

⇨ The description is displayed in a tooltip when you pause the pointer over the measurement in the **Measurement** task.

To Add a Tortuosity Measurement

To specify a tortuosity measurement, you select two diameters in the stent protocol image. The measurement indicates the tortuosity between the selected diameters.

1. Click the **Tortuosity** button.
2. Click a diameter on the stent protocol image.
3. Click another diameter on the stent protocol image to create the tortuosity measurement.

⇨ The measurement is added to the measurement list with the prefix **T** and a sequential number. You can rename the measurement in the **Parameters** panel, if desired.

4. Enter a description in the **Parameters** panel.

⇨ The description is displayed in a tooltip when you pause the pointer over the measurement in the **Measurement** task.

To Add an Angle Measurement

To specify an angle measurement, you select three diameters in the stent protocol image. The measurement indicates the angle between the diameters.

1. Click the **Angle** button.
2. Click a diameter on the stent protocol image to indicate the upper leg of the angle.

3. Click a diameter on the stent protocol image to indicate the apex of the angle.
4. Click a diameter on the stent protocol image to indicate the lower leg of the angle and to create the angle measurement.

⇨ The measurement is added to the measurement list with the prefix **A** and a sequential number. You can rename the measurement in the **Parameters** panel, if desired.

5. Enter a description in the **Parameters** panel.

⇨ The description is displayed in a tooltip when you pause the pointer over the measurement in the **Measurement** task.

Questions Stage

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.

Saving a Protocol

1. After configuring a stent protocol, click **Save** in the Protocol Editor to save your changes.
2. To return to the **Measurements** task of the **Stent Planning** step, click **Exit** in the Protocol Editor.

Sharing Protocols

If you are a Clinical Administrator and are creating a new stent protocol, the **Share with all users** check box is available in all stages of the Protocol Editor. (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 Advanced Visualization Workspace system. (Non-administrative users cannot delete, rename, overwrite, or modify shared presets).

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.

Refreshing the Protocol List

After you import and save a new stent protocol, the protocol name does not immediately appear in the stent list. To display the new protocol in the list, click **Refresh Stent List** in the task guidance panel.

Saving and Capturing Measurements

To save or capture measurements, select one of the following options:

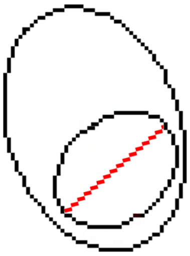
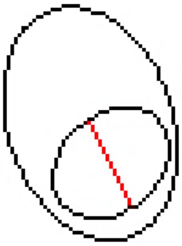
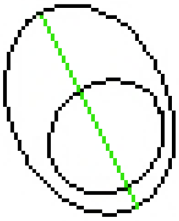
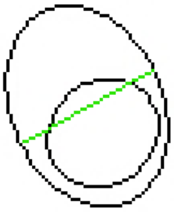
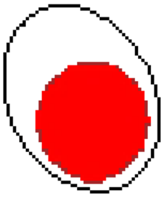
- **Copy table to clip board**: Allows pasting into Excel or Notepad.
- **Save this measurement**: Generates a series with all the relevant images for the measurement that is shown in the table. The series includes a screen capture of each of the shown viewport, and the screen capture of the whole display.

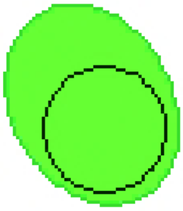
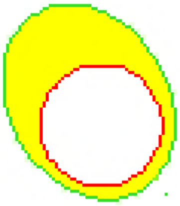
Calculation of Measurements/Measurement Definitions

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			
Stenosis	–	(reference-lesion) / reference*100%	%
Stenosis (MinD)	–	((Minimum lumen diameter at the reference - Minimum lumen diameter at the lesion) / Minimum lumen diameter at the reference) * 100%	mm
Stenosis (Area)	–	((Minimum lumen area at the reference - Minimum lumen area at the lesion) / Minimum lumen area at the reference) * 100	mm^2

Calculation of Measurements			
Position	–	Position along the center line in mm (beginning of centerline = 0 mm)	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
Lumen area		The area enclosed by the lumen contour	mm^2

Calculation of Measurements			
Vessel area		The area enclosed by the vessel contour	mm^2
Wall Area		vessel area - lumen area	mm^2
Area stenosis	–	(vessel area at lesion) / (vessel area at reference)	–
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.	–
Effective diameter	–	Calculated by: d_ef=2*sqrt(Area/pi).	–
Length	–	Length along the centerline between 2 rings (valid only when the measurement is done along centerline)	mm
% Change between two rings (D1 & D2)	–	(1 - Measurements of D1/Measurement in D2) x 100 %	mm
Absolute change	–	= Measurements of D1/- Measurement in D2	mm
Wall area	–	The area of the wall in a ring location (delta between the vessel area and lumen area)	mm^2

Diameter

This is the most general tool. It includes a single ring, which typically will be used to measure a diameter on a location of a lesion. Once user picked a diameter he can click on any of the viewports – the application will allocate a ring on the selected centerline.

NOTICE

Note: If the user clicks on another centerline , Which is not the one that was selected when he picked the tool, the other centerline will be first selected and then the ring will be located on it.

The location of the ring is shown on the volume (as a ring) , cMPR (dash) and sMPR (dash) while the CS view shows the Crossectional slice of the vessel in the location of the ring. User can modify the location of the ring by:

- Scrolling in the CS viewport
- Drag the tracker on the volume, cMPR or sMPR to another location along the centerline

The following values can be captured for a diameter measurements (for Lumen and vessel) :

- Min Diameter
- Max Diameter
- Area
- Eccentricity
- Effective Diameter
- Position

Stenosis Measurement

The stenosis measurement includes two rings, lesion and reference. The location which user clicked on, is marked as the “Lesion” and the “Reference” ring is automatically allocated few mm above the lesion. The user can move each of the rings to a better location according his understanding.

The following values can be captured for a stenosis measurements (for Lumen and vessel) :

- Min Diameter : Lesion & reference and %of change
- Max Diameter: Lesion & reference and %of change
- Area: Lesion & reference and %of change
- Eccentricity: Lesion & reference and %of change
- Effective Diameter: Lesion & reference and %of change
- Position: Lesion & reference
- Length between lesion to reference

Aneurism

The aneurism measurement includes three rings: Start , End and MaxD . The user is expected to click on the below the aneurism, the end ring is positioned 1 cm above (by default) and the MaxD is calculated as the maximum diameter between the start and the end. On every change of the start and end the MaxD is re-calculated, unless user changed directly the MaxD location

The following results can be captured for Aneurysm (Lumen & Vessel):

- Min Diameter of Start, MaxD and End rings (Only in full modes)
- Max Diameter of Start, MaxD and End rings (Both modes)
- Area of Start, MaxD and End rings (Both modes) (Only in full modes)
- Eccentricity of Start, MaxD and End rings (Only in full modes)
- Effective Diameter of Start, MaxD and End rings (Only in full modes)

- Position of Start, MaxD and End rings (Only in full modes)

In addition, the following measurements shall be included in the Aneurysm result view in both modes:

- Lumen Volume
- Aneurysm Wall Volume
- Aneurysm Total Volume
- Aneurysm Length (Start to End)

Length

The length measurement include two rings which just represent two locations along the centerline, and is used to calculate the length along the centerline between the rings

The following results shall be calculated for Stenosis (Lumen and Vessel) and displayed in a tabular format

- Length of the centerline from Start to End (Both)
- Shortest Distance straight line from start to end (Both)
- Tortuosity (Both)
- Min Diameter of the start and the end (Only in full modes)
- Max Diameter of the start and the end (Only in full modes)
- Area of the start and the end (Only in full modes)
- Eccentricity of the start and the end (Only in full modes)
- Effective Diameter of the start and the end (Only in full modes)
- Position of the start and the end (Only in full modes)

Batch Creation

Batches can be defined and saved on any view port and can be saved as Presets.

NOTICE

Instructions for using the Batch functions are provided in the Batch Functions section in the CT Review Instructions for Use.

Multi-batch

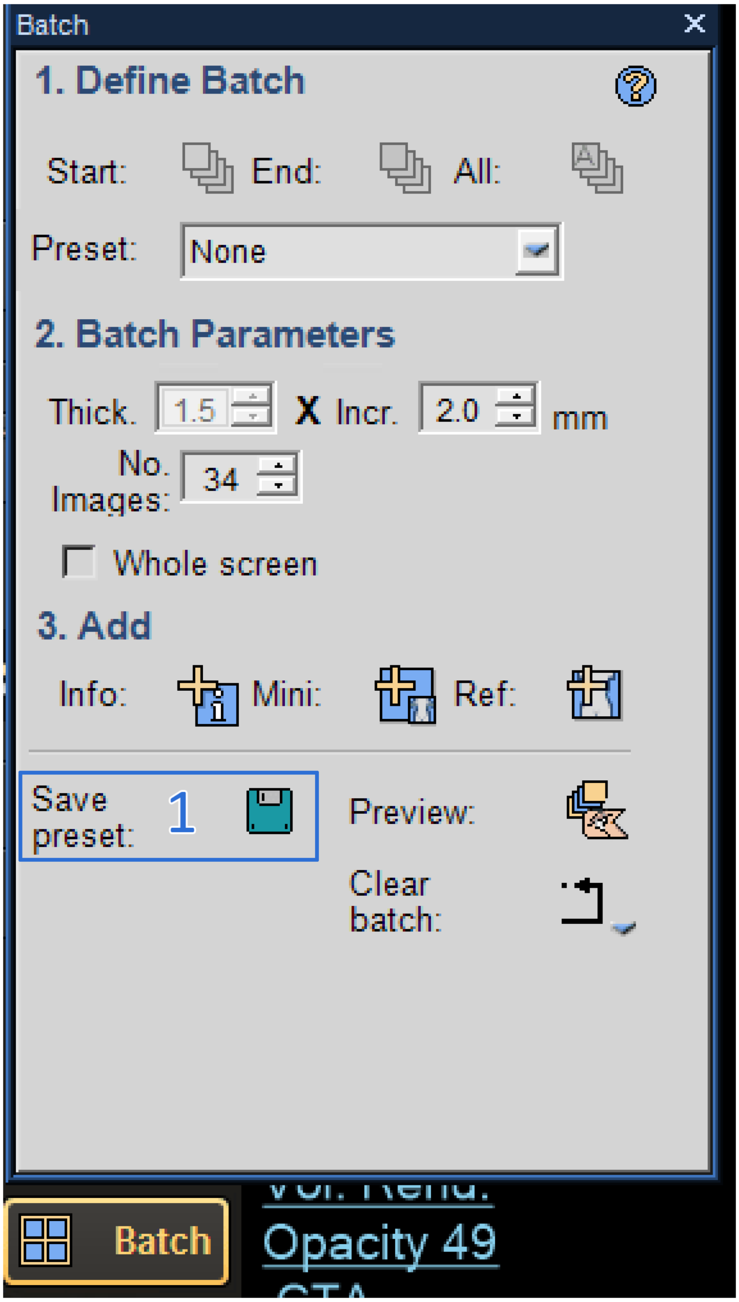
The Multi-batch option allows saving a group of batches based on pre-configured batch presets.

Multiple batches can be created easily using Multi-batch creation. This feature is primarily intended for use with 3D technologies. Batches are created in parallel with the user's workflow, allowing users to continue working (or even exit without waiting for the process to end).

Configuring and Activating Multi-batch

The Multi-Batch option under AVA Preferences (Preferences > Application Preferences) must be enabled to use the multi-batch functionality.

1. Prior to batch creation, inspect the study and complete all required editing.
2. Select **Batch** to open the Batch tool.
3. Use the batch creation tools to create the required batch.
4. Select **Save preset:** (#1).



Thick. 1.5 X Incr. 2.0 mm

No. Images: 34

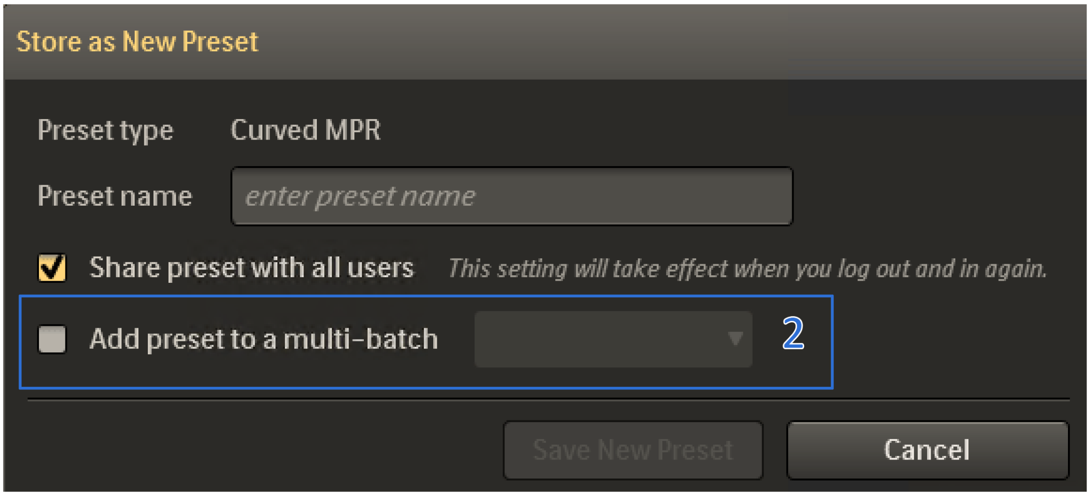
☐ Whole screen

Preset: None

5. In the **Store as New Preset** window, enter a Preset name.

300012062511_A/881 * 2023-06-30

Philips



Store as New Preset

Preset type Curved MPR

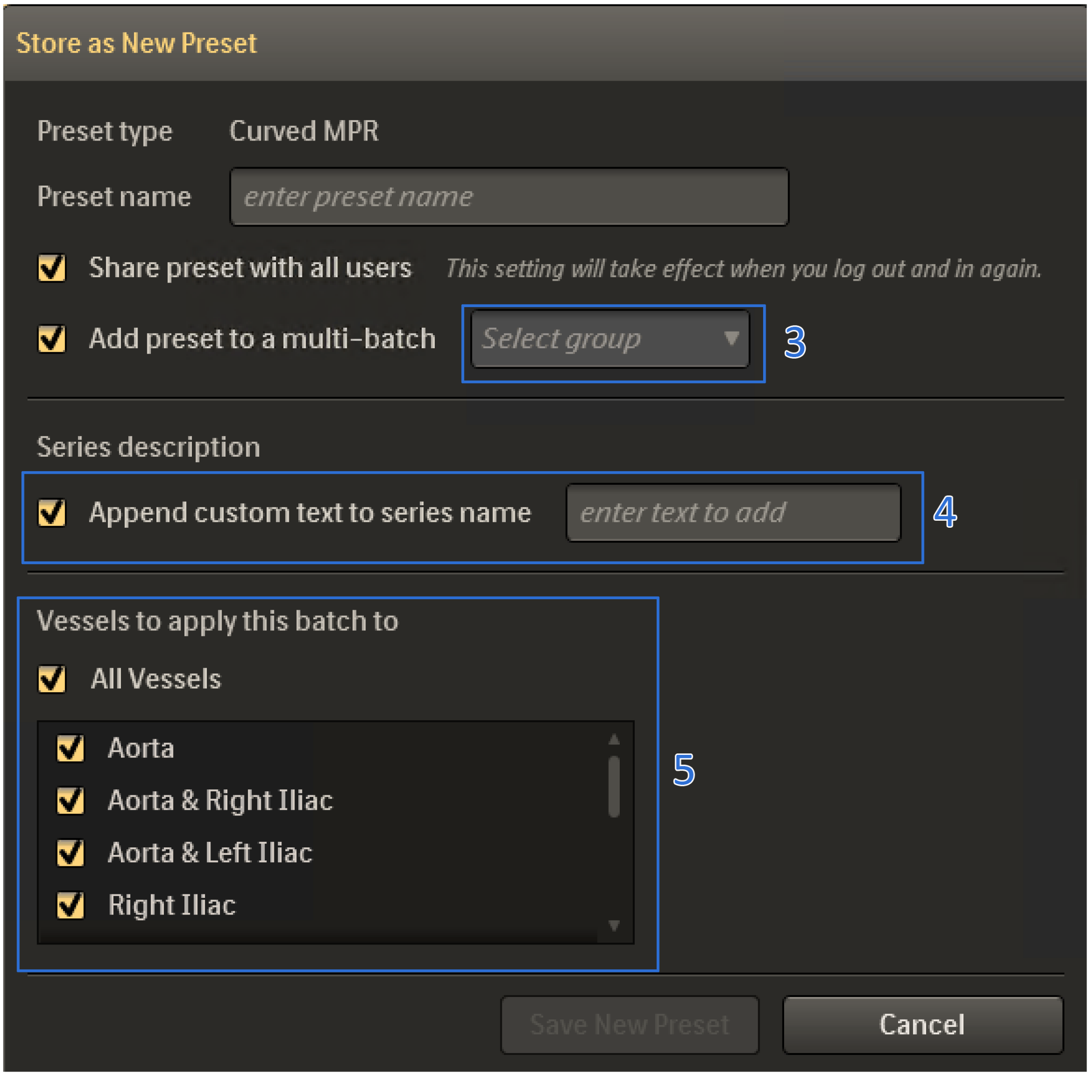
Preset name *enter preset name*

☑ Share preset with all users *This setting will take effect when you log out and in again.*

☐ Add preset to a multi-batch

6. Enable **Add preset to a multi-batch** (#2).

   The window expands with additional parameters for batches that are derived from centerlines.



Store as New Preset

Preset type Curved MPR

Preset name *enter preset name*

☑ Share preset with all users *This setting will take effect when you log out and in again.*

☑ Add preset to a multi-batch *Select group*

Series description

☑ Append custom text to series name *enter text to add*

Vessels to apply this batch to

☑ All Vessels

☑ Aorta
☑ Aorta & Right Iliac
☑ Aorta & Left Iliac
☑ Right Iliac

For volume or MPRs presets, the lower part of the dialog is not included.

7. Add the preset to an existing multi-batch group or create a new group (#3), Append custom text to a series name (#4) and define which vessels this preset will be applied (#5) once the multi-batch will be triggered.
8. Select **Save New Preset**.

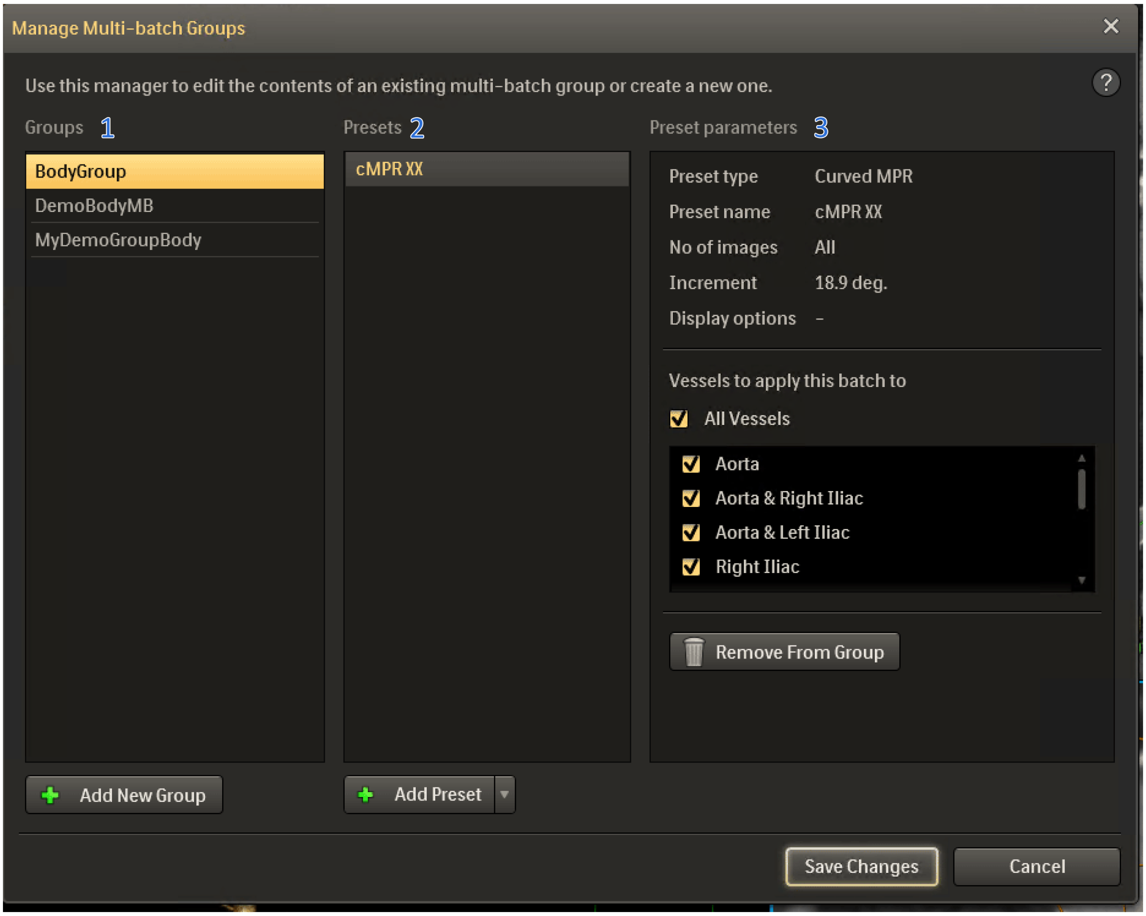
   A group is created with this preset. Repeat this process to add more batch presets to the group.

Mutli-batch Manager

The Manage Muli-batch Groups window includes three sections:

- **Groups** (#1): Displays list of groups and includes the options to create and edit groups. Right click on a group to rename, delete or duplicate.
- **Presets** (#2): Displays a list of Presets included in the selected group. To remove a preset from the selected group, right click on the preset and select **Remove from group**.

- **Preset parameters** (#3): Displays parameters and a list of vessels that will be created for the selected preset. It is possible to modify the list of centerlines generated per preset.



Manage Multi-batch Groups

Use this manager to edit the contents of an existing multi-batch group or create a new one.

Groups 1

- BodyGroup
- DemoBodyMB
- MyDemoGroupBody

Presets 2

- cMPR XX

Preset parameters 3

Preset type	Curved MPR
Preset name	cMPR XX
No of images	All
Increment	18.9 deg.
Display options	–

Vessels to apply this batch to

☑ All Vessels

☑ Aorta
☑ Aorta & Right Iliac
☑ Aorta & Left Iliac
☑ Right Iliac

To create a multi-batch group using existing presets, use the Manage Multi-batch Groups window as follows:

1. Select **Add New Group** under **Groups** to create a new group.
2. Select **Add Preset** under **Presets** to choose one of the available presets and add to the group. Repeat for all needed presets. Edit the vessels to be included in a preset if need..
3. Select **Save Changes**.

NOTICE

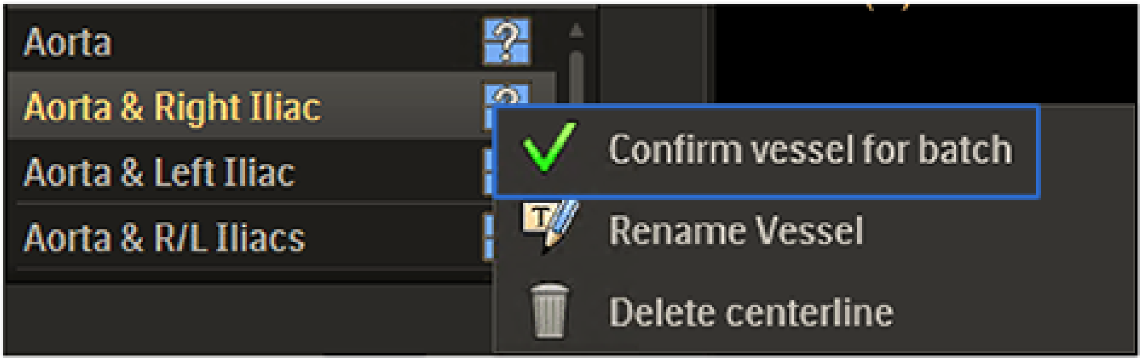
When editing a curved MPR of cross section preset for one of the groups, this preset is changed within any other group that ti is part of.

Review and Approve

As part of the editing, users must **Confirm vessel for batch** for each centerline that was completed to review/edit.

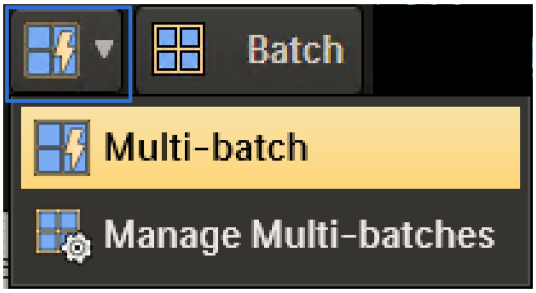
Review the centerlines and perform the required editing.

Once a centerline is correct, right click on the question mark icon and **Confirm vessel for batch**. A confirmed vessel is marked with a check mark.



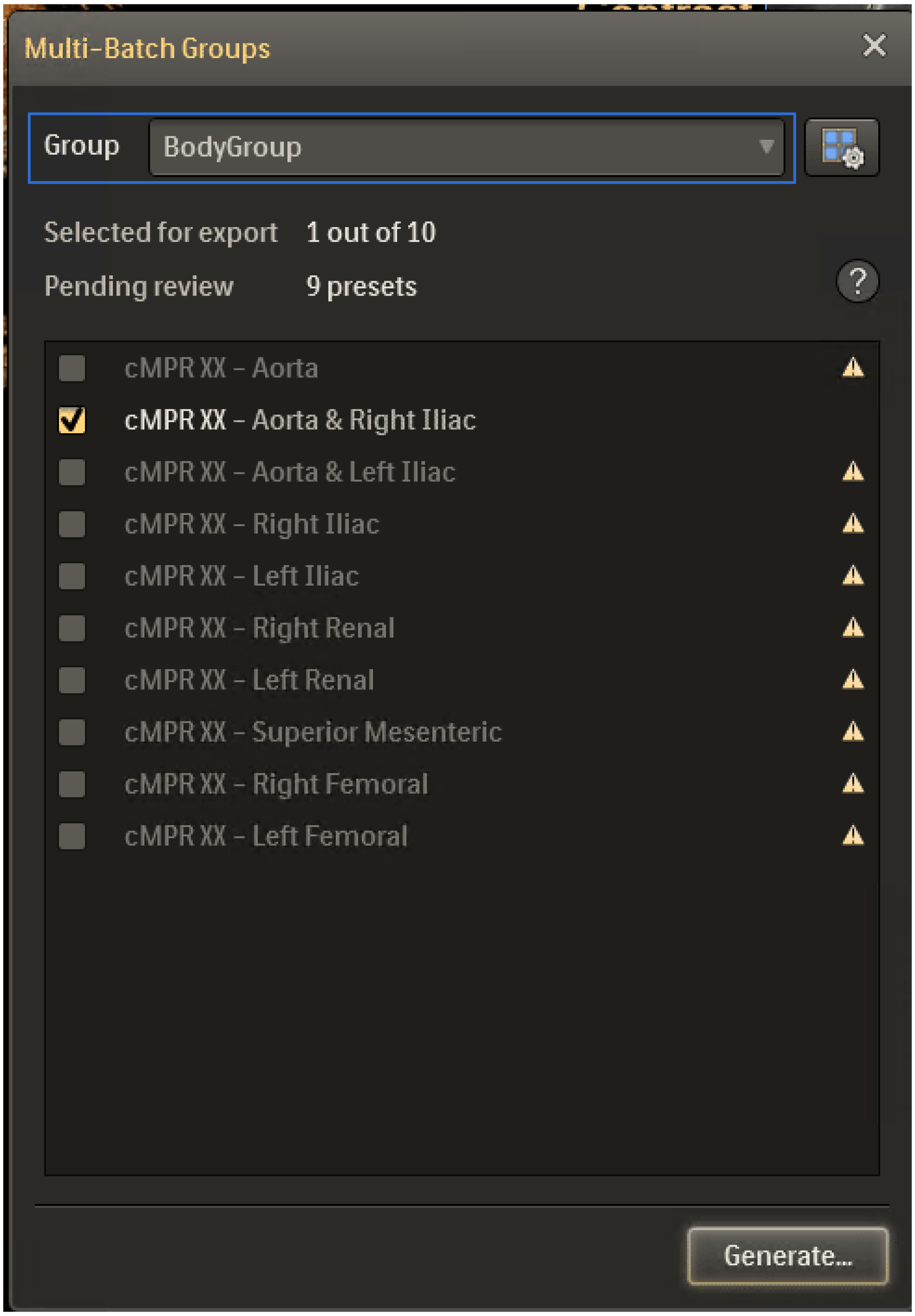
Working With Multi-batch

Select the Muli-batch icon to open the following dialog.



- **Multi-batch** triggers the batch generation once reviewed and approved.
- **Manage Multi batches** opens a manager dialog that allows group management (adding , deleting and editing). This dialog can also be accessed from form the creation Generate Multi Batch:

After Multi-batch is selected, the following dialog opens.



Multi-Batch Groups

Group: BodyGroup

Selected for export: 1 out of 10

Pending review: 9 presets

☐ cMPR XX – Aorta ⚠
☑ cMPR XX – Aorta & Right Iliac
☐ cMPR XX – Aorta & Left Iliac ⚠
☐ cMPR XX – Right Iliac ⚠
☐ cMPR XX – Left Iliac ⚠
☐ cMPR XX – Right Renal ⚠
☐ cMPR XX – Left Renal ⚠
☐ cMPR XX – Superior Mesenteric ⚠
☐ cMPR XX – Right Femoral ⚠
☐ cMPR XX – Left Femoral ⚠

This dialog allows group selection from the upper combo and displays the batches that will be generated by this group. Batches that are related to unapproved centerlines appear as disabled and are not included in the generated results.

1. Select one of the available batch group from the upper combo.
2. Review batches configured to be part of the export and uncheck batches that should be excluded.

   Hover over a batch to view a tooltip displaying batch parameters.

3. Click **Generate** to export.
4. Select a target location (internal or any external drive including PACs) for saving the results.

   All requested batches are activated in the background. Exiting the application and launching another study will not affect batch creation.

NOTICE

A batch of curved MPR or cross-sectional images of a specific vessel will be available for export only if the vessel was reviewed and approved for the saving. To enable a batch to be saved, select the relevant vessel in the application, review and edit if needed. Right click the vessel and select **Confirm vessel for batch**.

Measurement Accuracy

Please refer to the generic Measurement Accuracy section in the Advanced Visualization Workspace System Instructions for Use (Before You Begin > Measurement Accuracy).

Appendix

CT Subtraction Method

The CT Subtraction method in AVA allows subtracting a non contrast series from a contrast series (with registration).

In some situations, this method may be used to remove bones and keep only the vessels instead of using the smart Bone Removal algorithm.

NOTICE

Using subtraction results in AVA is not considered "Bone Removal" .

Users are responsible for verifying that the subtraction results include all of the required information for analysis.

For cases where a CTA study includes series of Non contrast and contrast phases, it is possible to subtract the NC (Non Contrast) phase from the Contrast phase and launch the result series to AVA . This can be done as follows:

1. Select a study from the Patient Directory.
2. In the series list select the Non contrast and the contrast series.
3. Right click and select **Run Processing** > **CT Subtraction**.

Processing is applied in the background. When completed, a new series is generated and displayed in the same study.

Subtraction between the two series is calculated after the series are registered automatically (using the elastic registration method).

NOTICE

There is no feature that allows reviewing or modifying registration; the process is automatic.

NOTICE

The quality of the subtraction results depends on the quality of the input series and their similarities. In this scenario, the application does not determine whether the selected series are appropriate for subtraction.

Launching Subtraction Results to AVA

When a subtraction result series is launched to AVA, the application does not apply the bone removal and vessel extraction algorithm. The series is launched in the Vessel Extraction stage without extracting centerlines.

Use the vessel creation and editing tools to create centerlines and measure along the centerline, or use the **Quick Inspection** mode in the **Inspect & Measure** stage to calculate measurements without centerlines. For additional information, refer to Quick Inspection on page 47.

Quick Vessel Analysis

Quick Vessel Analysis (QVA) is an application based on AVA .

This application consists of a **Quick Inspection** mode, which is also available in AVA.

The application is launched in the **Inspect & Measure** stage and allows dropping rings anywhere on the vessel, exploring and measuring. The QVA application does not perform any processing, such as bone removal and vessel extraction. For additional information, refer to Quick Inspection on page 47.

Keyboard Shortcuts

Shortcut	Action
<Shift>+C	Show/Hide centerline
<Shift>+D	Show/Hide diameters (On CS image)

Shortcut	Action
<Shift>+L	Show/Hide Lumen contours
<Shift>+V	Show/Hide vessel contours
<Shift>+T	Show/Hide Transparent bone volume
<Shift>+G	Show/Hide glass view
<Ctrl> + F	Focus on Measurement

Spectral Capabilities in AVA

⚠

WARNING

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

NOTICE

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

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.

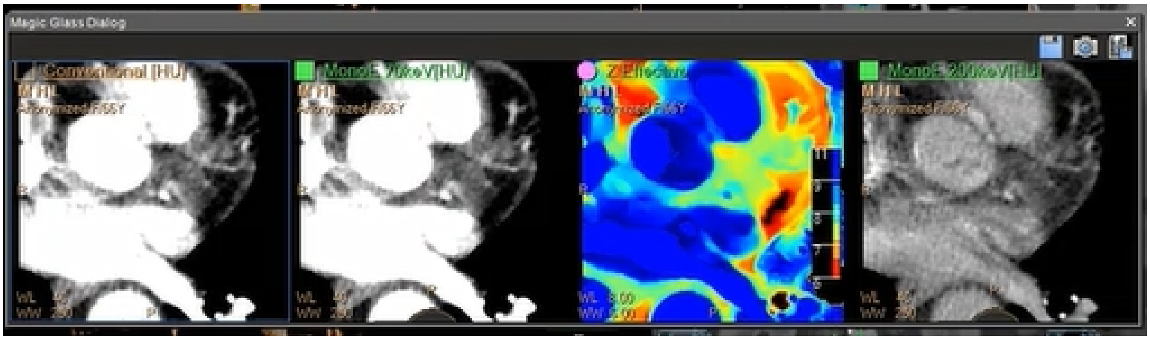
By default, data opens with MonoE 200 next to conventional image

When spectral data is opened, the viewport controller is available, allowing the display/color coded:

- Conventional [HU]
- MonoE [HU]
- MonoE [HU] (Equivalent to conventional CT)
- VNC [HU]
- Iodines no Water mg/ml
- Z Effective
- More Spectral results... (Iodine Density, Contrast-Enh. Structures, Iodine Removed, Uric Acid, Uric Acid Removed)

Spectral Magic Glass

When standing on a cross-sectional or axial image, the Spectral Magic Glass icon 🔍 is enabled on the upper toolbar. This opens the Magic Glass tool and opens a new window. You can control the size and can scroll.



MonoE Slider

When MonoE is selected from the dropdown, the kev slider appears. This enables changing energy. The image is automatically updated.

Reapply Bone Removal

To perform Bone Removal on MonoE data. select MonoE data and select the **Reapply Bone Removal** icon on the upper toolbar..

The Re-apply bone removal tool may be used 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 current images. The new bone removal is propagated to all other series.