4 CT Acute Multifunctional Review

The CT Acute Multifunctional Review allows quick triage and the detection of life threatening conditions, as well as fast communication to the relevant parties in the hospital.

Operation of the CT Acute Multifunctional Review is very similar to the CT Viewer. This application supports volumetric and 2D CT images.

Loading the Application

When loading a study with multiple series into CT Acute Multifunctional Review, the series are loaded in the same order as listed.

You can scroll though the loaded axial images of the active series, even while the entire volume is being loaded.

When the entire volume is loaded, the reference/VR images also appear.

When you select a series not yet loaded from the series list, the images of the selected series start loading immediately, even if the series is not the next one in the list.

Workflow

The CT Acute Multifunctional Review consists of four stages:

Review

Vessels

Bone

Spine

WARNING

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.

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Switching Between Stages

- To switch between the stages, click on the stage buttons in the upper toolbox.
- When opening a stage for the first time after loading the application, the currently selected series will be loaded into the selected scene.
- When opening a stage in a later session, the status of the stage appears as it existed when the stage was last visited.
- To send a series to a specific stage, whether a series is already open or not in that stage, select the desired stage from the **Open active series in stage:** drop-down menu. The active series opens in the selected stage, instead of the series that may already be open.

Dual Monitor Support

If using a dual monitor configuration, the Review stage will always stay open on the left monitor and the other stages (Vessels, Bones, Spine, 2D) will be open on the right monitor.

Indications for Use

The CT Acute Multi-Functional Review (AMFR) application provides dedicated tools for findings detection, visualization and assessment of vessels, bones, discs and spine anatomies, all within a single application.

Review Stage

The Review stage allows quick review of series with different windowing, thickness and rendering modes, as may be suitable for specific body parts.

Review Modes

The Review Modes feature allows reviewing the same series with different settings in parallel. This feature can be accessed from a drop-down menu in the upper toolbox.

The review modes are available in six groups, according to body parts:


General


Head


Chest


Abdomen/Pelvis

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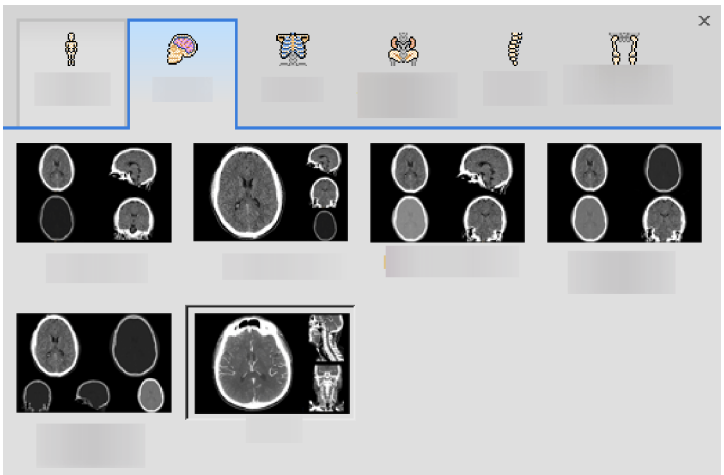
Spine

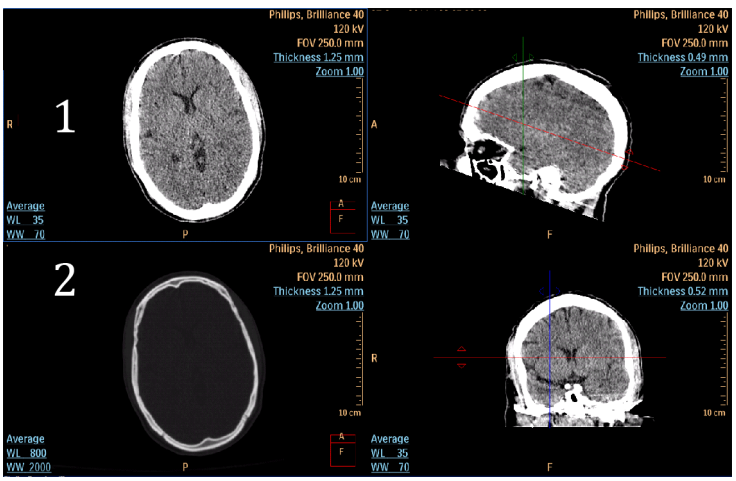
Extremities

Each group includes several review modes, identified by a thumbnail image depicting the review mode display. The following is an example of the Head group.



The name of each review mode represents the window settings that the series will be displayed in. For example, when selecting the first review mode in the Head group, the current series will be duplicated twice and will be displayed with brain windowing (the original windowing of the series) in one viewport and bone windowing (from Preferences) in the other.

1	Series 3 with brain window
2	Series 3 with bone window



- The geometry of the duplicated series is linked - zoom, pan, etc.
- Some review modes display the series in MIP, MinIP, and volume rendering modes, and with different thickness, based on the clinical need.

- The General group includes regular layouts, in which the series is not duplicated (same as in CT Viewer).
- Switching between the groups is done by hovering over the group name with the mouse.
- When clicking on a group name, the last review mode that was used in this group is selected by default.
- While in compare mode, the review modes menu will include compare-dedicated layouts only.
- The last review mode that was used in each group is saved and used as default in the next use of the application. The defaults are saved per user login info (each user may have his or her own defaults).

2D Mode

When a 2D series is selected from the series list, the Review Stage automatically switches to 2D mode.

Clicking on a volumetric series while in 2D mode will activate the Review stage 3D display.

Upper Toolbox (Review Stage)

Orientation

Select the orientation of the main MPR image and the VR image.

Review Mode

Use this button to select the Review mode.

Relate

Activate the common Relate tool, where you can access the “relate scenes” and “relate viewports” functions.

Next Series

Next series

Compare

Use this button to perform a side-by-side review of selected images (same as in CT Viewer).

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Link

When using the Compare function in the Slab viewing mode, the Link icon allows you to link images (“lock” together) to perform the same manipulation on the image(s) of your choice, such as manipulating, filming or saving.

Show Crosshair

The checkbox allows you to show or hide the crosshair,

Paddle Wheel

The paddle wheel function (see allows viewing images radially around a horizontal or vertical axis (same as in CT Viewer).

Rotation Center

The checkbox shows or hides the rotation center.

Reset Rotation Center

Resets the rotation center location.

Dynamic Viewer

This function allows switching between protocol presets available for currently loaded study. Press repeatedly if multiple presets exist (same as in CT Viewer).

Brain Processing Algorithm

Brain Processing Algorithm (same as in CT Viewer)

Vessel Stage

The Vessel stage allows quick review of vessels in contrast enhanced series.

WARNING

Verify the correctness of the vessel contours. If necessary, correct the contours using the tools provided in this application.

The Vessel stage includes two modes:

- Local Inspection

- Centerline Overview

When entering the Vessel stage for the first time in a study, the Local Inspection mode is selected by default.

Local Inspection Mode

The local Inspection mode allows placing a seed point on a coronal MIP/VR image to create a ring around the vessel lumen. Orientation is coronal by default, but you can change that from the layouts menu.

You can place a seed point when the **Select location** option is active.

In the Slab layout, when the **Select location** option is active, the mouse pointer changes to **place seed/scroll**.

In this mode:

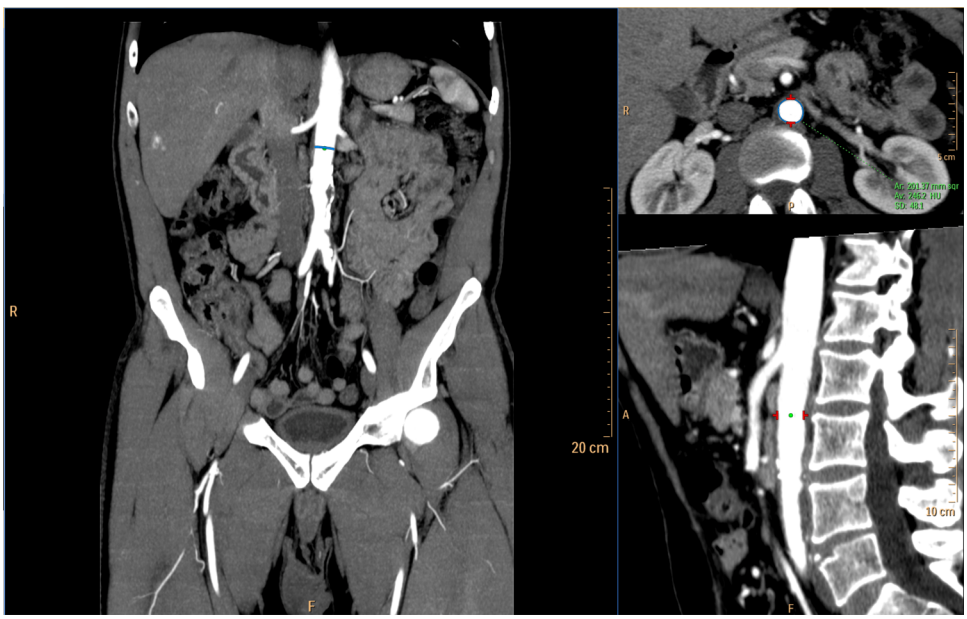
- Click and release the left mouse button to place a seed - this creates a ring.
- Click and drag the left mouse button to scroll through the images.

In the VR layout, the mouse pointer changes to **place seed/swivel**.

In this mode:

- Click and release the left mouse button to place a seed. This creates a ring.
- Click and drag the left mouse button to swivel the VR images.

In both layouts, placing a seed on a vessel creates a ring around the vessel.



When you create a ring, the upper right viewport displays the cross-sectional image of the vessel; the lower right viewport displays a longitudinal image, perpendicular to the cross-sectional image.

You can scroll through the cross-sectional images. While scrolling, the ring follows the vessel lumen.

You can rotate the longitudinal images or place a seed on them using the mouse cursor.

In this mode:

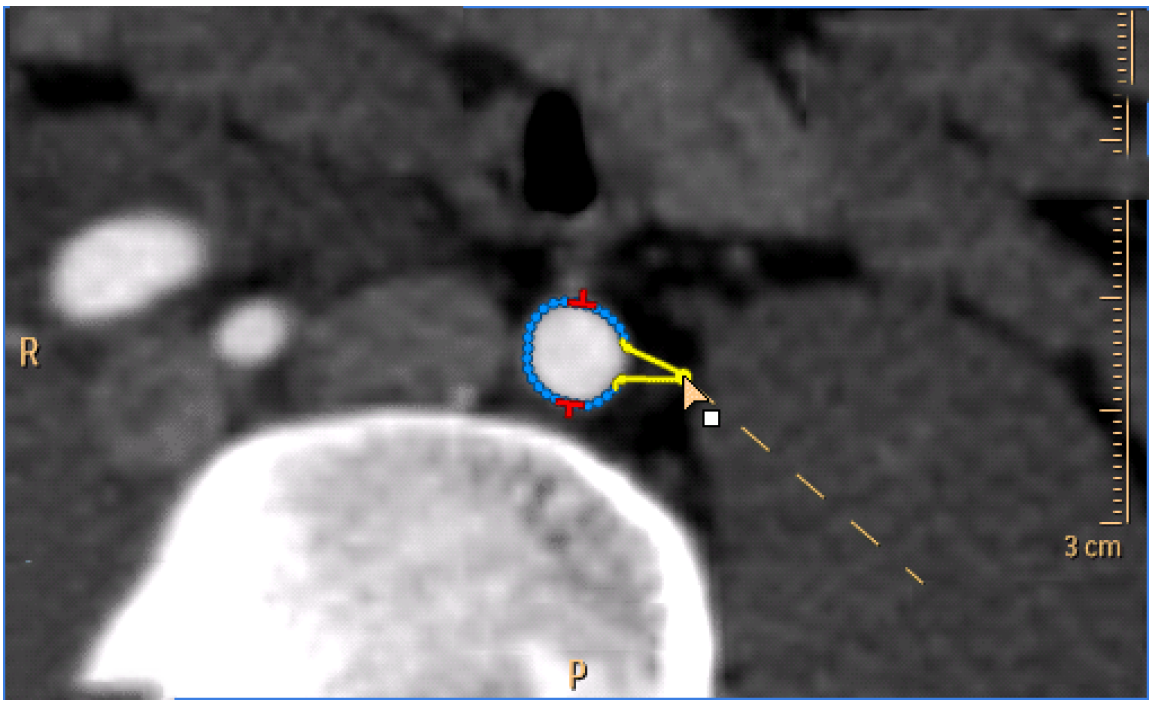
- Click and release the left mouse button to place a seed. This creates a ring.
- Click and drag the left mouse button to rotate the longitudinal image.

The following ring measurements appear on the cross-sectional image:

- Area
- Average HU
- Standard Deviation
- Max diameter
- Min diameter

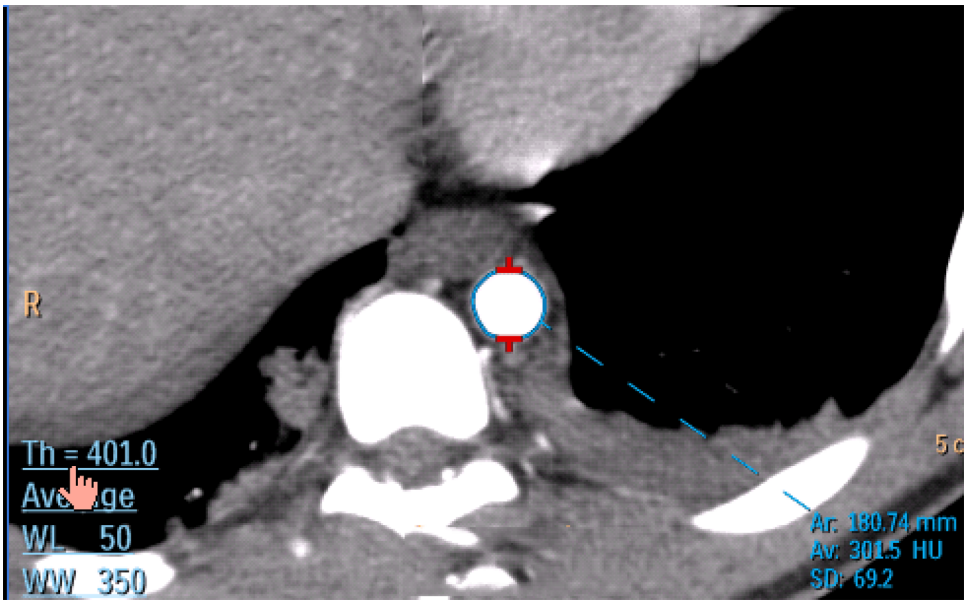
You can control the displayed parameters from the measurements annotation context menu.

You can edit a ring by hovering over it and dragging its control points. The measurements will update accordingly.



The local inspection algorithm provides calcium exclusion when needed. This can be activated by placing a checkmark in the **Exclude calcifications** checkbox in the upper toolbox.

When the checkbox is checked, the Threshold viewport control (Th) is added to the cross-sectional image.



This control sets the HU pixel threshold; pixels above the threshold are excluded from the ring.

Centerline Overview Mode

When the **Centerline Overview** mode is activated, you can use the **Create new centerline;** function to place seeds to create a centerline.

1. Activate **Centerline Overview** mode (#1 in image) in the **Inspection Mode** tool box.

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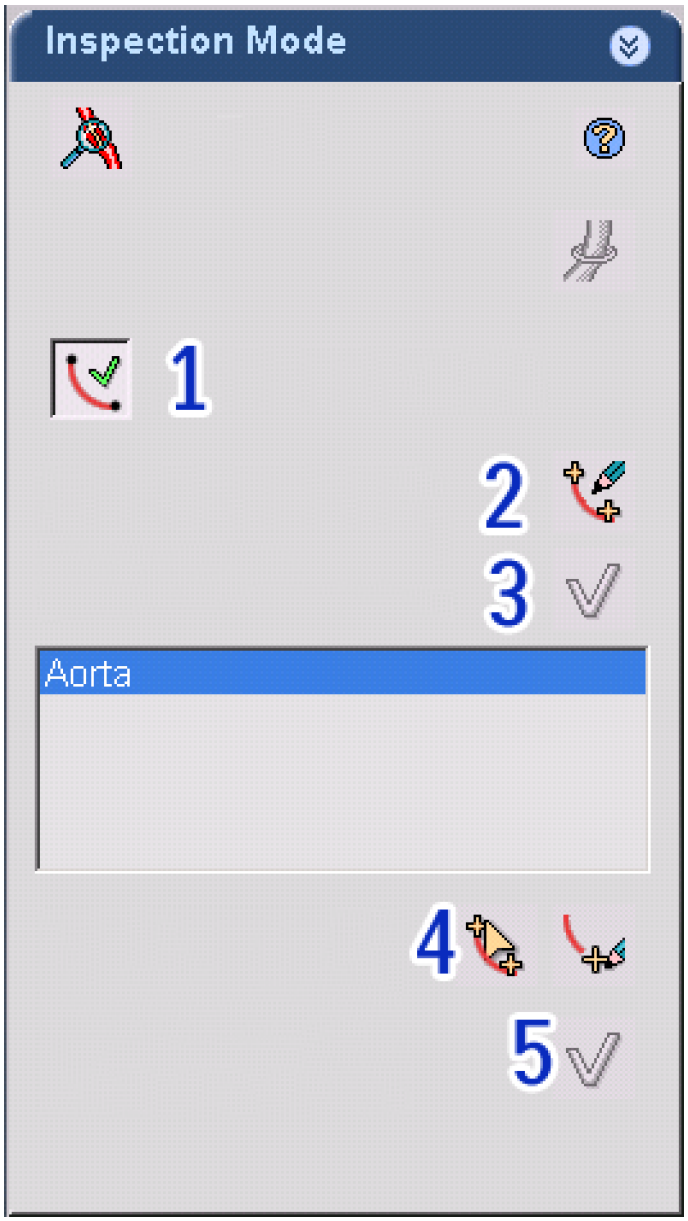


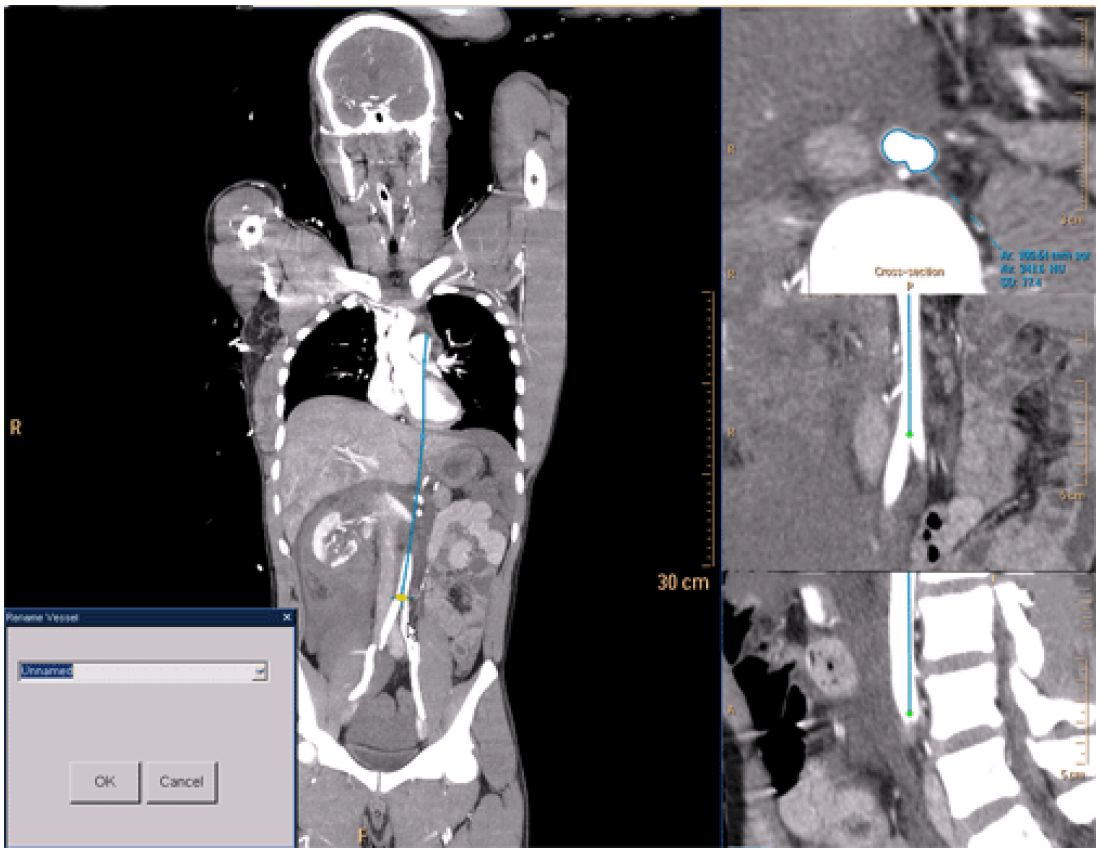
2. Place seeds on the slab images or on the VR image using the **Create new centerline** option (#2 in image) ; select the desired image type from the layout menu.

   At least two seeds are needed to create a centerline.

3. Finish creating a centerline and accept it by clicking on the **Finish centerline:** button (#3 in image), or double-click when placing the last seed.

   After the centerline is finished, a **Rename Vessel** dialog opens.

4. Select a name from the drop-down list or type in a name.



The new name of the vessel appears in the vessels list on the toolbox.

5. To display the created centerlines, select them from the vessels list. If the results from the AVA application are loaded, the centerlines will appear in the list. cMPR and sMPR images are available.

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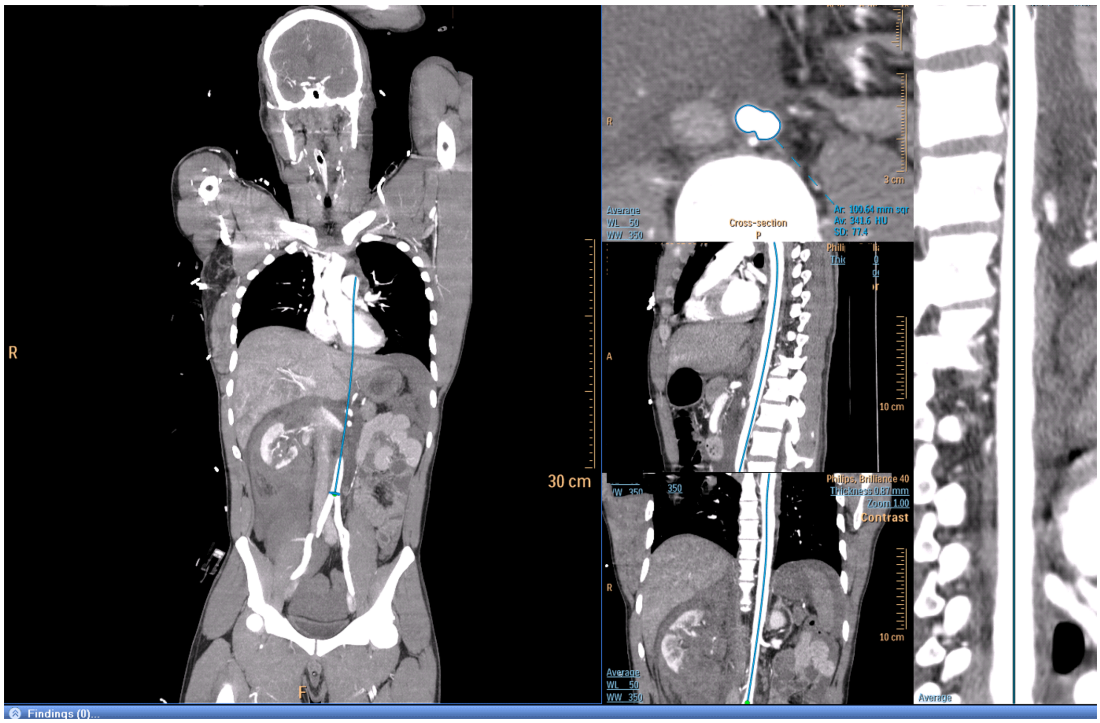

6. To add more centerlines, use the **Create new centerline** button (#2 in image) in the **Inspection Mode** tool box.
7. To modify existing centerlines, select a centerline from the list and click the **Edit centerline** or **Extend centerline** button (#4 in image) . To accept the change(s), click **Finish editing** (#5 in image) .

Upper Toolbox (Vessel Stage)

Select the orientation of the main MPR image and the VR image.

Flip the VR and MP images

Select screen layout

Next series

Activate the common **Relate** tool, where you can access the “relate scenes” and “relate viewports” functions.

Show centerline checkbox - Show or hide the centerline when in Centerline Overview mode.

Show measurements checkbox - Show or hide the ring measurements on the cross-sectional image.

Show ring checkbox - Show or hide the ring from the main viewport and the longitudinal image.

Exclude calcifications checkbox - Control the calcification exclusion option.

Bone Stage

The Bone stage includes two modes:

- Bone segmentation
- Virtual repositioning

Bone Segmentation

Limit Area

The first (optional) step before starting bone segmentation is to limit the volume on which the algorithm will run.

This can be done using the following tools:

- Bounding Box
- Sculpt (Include/Exclude)

Use the Bounding Box tool to locate a cube around the desired segmentation area.

Use the Sculpt tools to limit the segmentation area by including/excluding voxels.

When using these tools, the bone stage calculations are limited to the included voxels only. The operator's use of these tools may improve the performance of the bone segmentation algorithm.

Set Threshold

The second step is to set the high and low thresholds for segmentation calculations.

NOTICE

Setting the threshold accurately is essential for successful bone segmentation.

The threshold range controls the voxels that will be used for the algorithm calculation. Only voxels between the low and high HU threshold values are used for segmentation.

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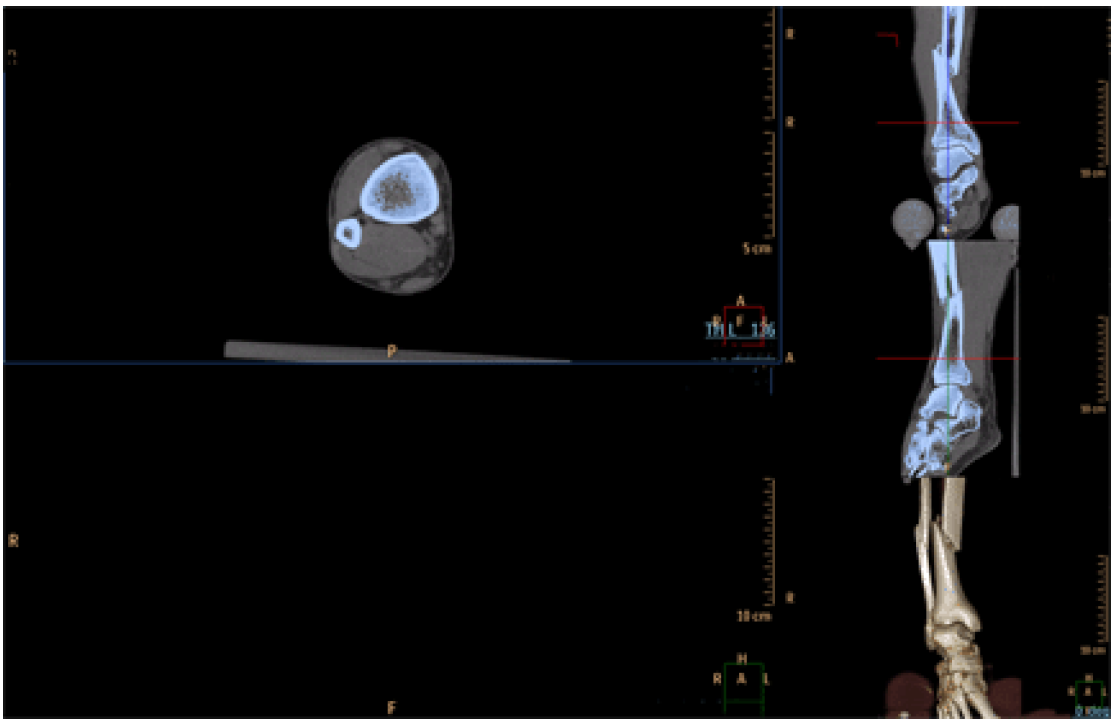
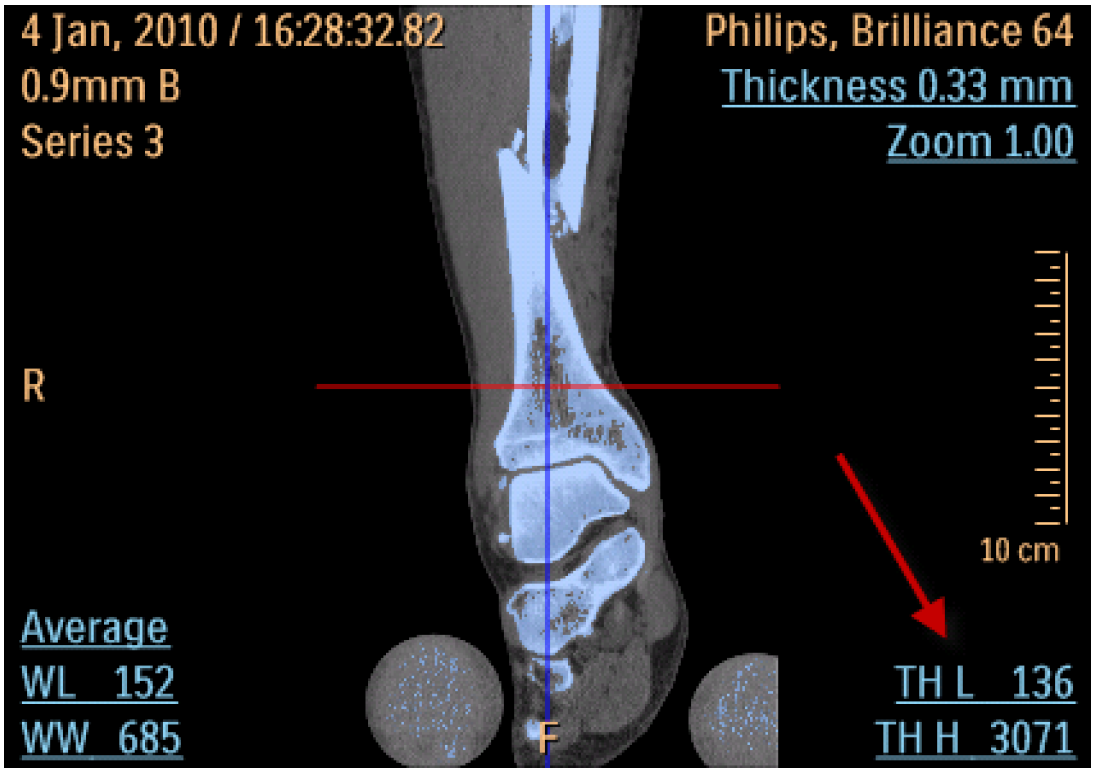
The voxels that are in the threshold range are displayed using a blue overlay on top of the MPR images.



When setting the threshold values, the goal is to include as much of the bone tissue as you can, without including other tissues around a bone and between bones.

There are three ways to set the threshold:

- **Toolbox** - Switch between the low and high threshold from the Set Bones HU Range drop-down list. Type-in the desired values in the HU textbox.
- **Viewport Controls** - Use the two viewport controls on top of the MPR images (TH L and TH H), which control the threshold values.



- **Mouse and Keyboard shortcut** - To change the **Low threshold**, hold down the **<Ctrl>** key and drag the middle mouse button. To change the **High threshold**, hold down the **<Shift>** key and drag the middle mouse button.

Place Seeds

The third step requires you to place seeds to verify individual bones and bone fragments on the MPR images. These seeds will be used as an input for the bone segmentation calculations.

To add a new bone to the bones list, click on the **+ New bone** button.

NOTICE

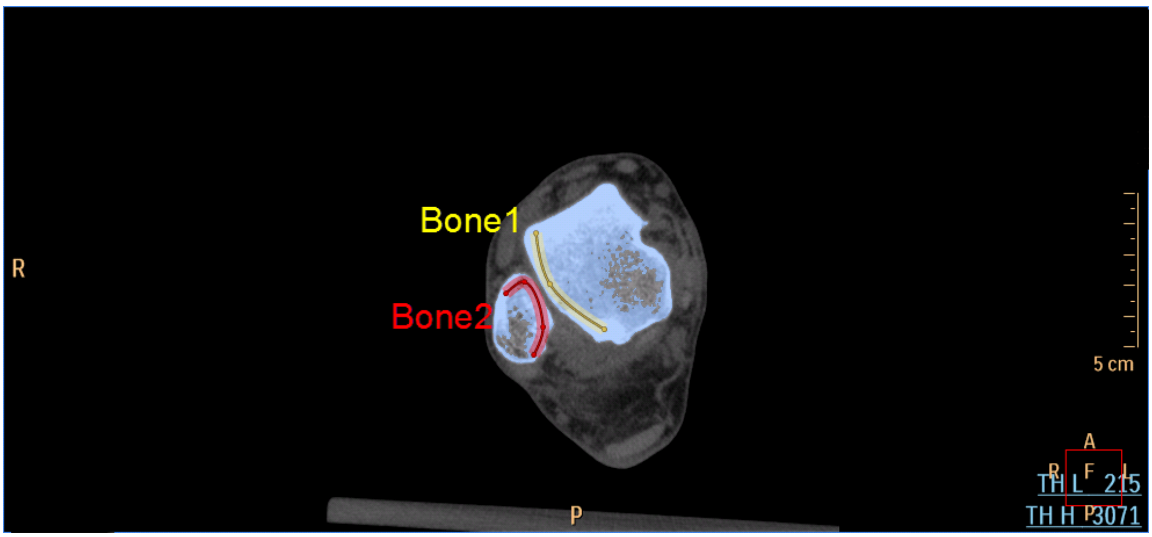
A new bone in the list is one that does not have seeds defined for it.

Seeds are added by selecting the **Draw seeds on selected bone** button. There are two options available to add seeds to a bone:

- The **Add seeds to bone using curve** option (the default method)
- **Draw seeds on selected bone using contour** - Adds seeds using contour (the “live wire” method)

NOTICE

It is recommended to locate the seeds near the areas of separation between two (or more) bones, as shown below.



You can place seeds on multiple slices and on the different MPR images.

Preview Results

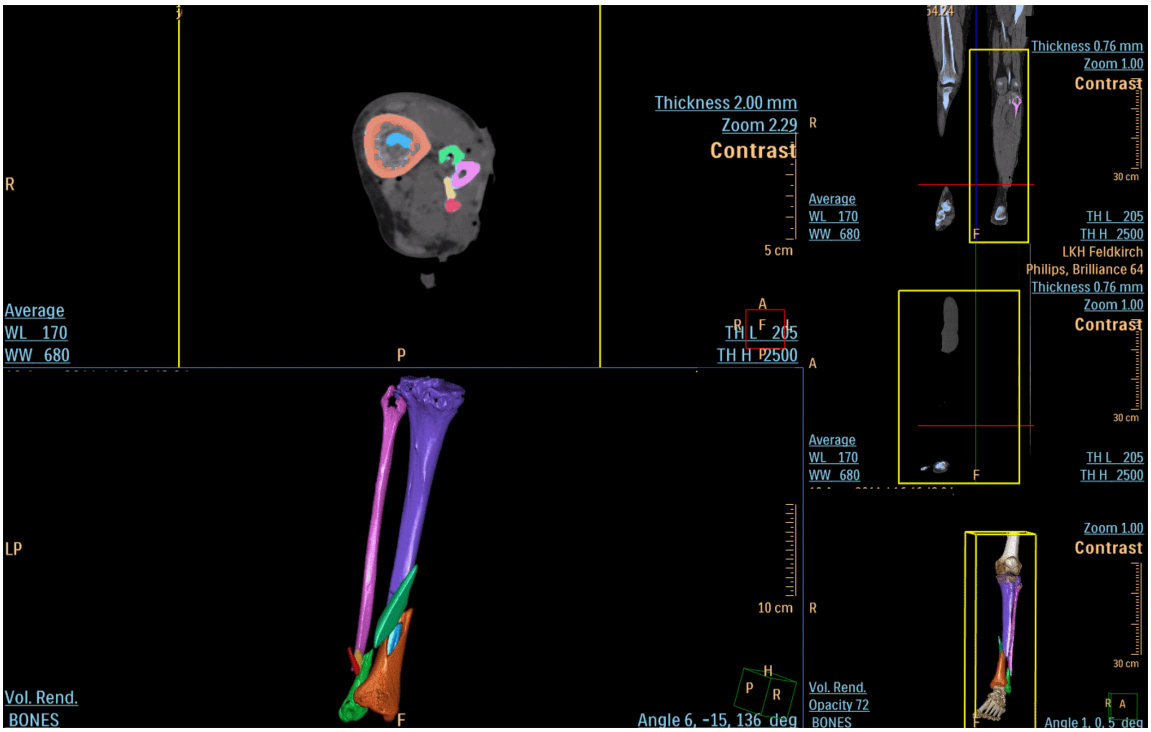
After placing seeds, click on the **Preview Results** button to run the bone segmentation algorithm.

When the segmentation calculation is complete, the segmentation results appear in the results viewport. In addition, the results appear on the VR image, and also as overlays on the MPR image.

WARNING

Verify volume segmentation correctness. Correct by editing the contours or adjusting the threshold, if required.

Each bone is segmented using the matching color from the bones list.



- To change a bone color, click on its colored box in the bones list.
- To rename a bone, right click on the bone and select the rename option from the context menu.

After the segmentation is complete, you can change the threshold values, add more bones, or add seeds to existing bones. After making the desired changes, click the **Preview** button again to re-run the segmentation calculation.

Accept Results

WARNING

The volume image displays the anatomy according to the segmentation quality and the defined protocol and should not be used as a SOLE basis for diagnosis.

When the bone segmentation results are satisfactory, click **Accept and lock bones**. This allows switching to the Virtual Repositioning mode.

NOTICE

The checkbox next to each bone fragment allows you to control the visibility of each bone fragment. This allows reviewing any areas that may be hidden between bones.

Splitting a Bone

You can split an already accepted bone into two or more fragments using the **Split selected bone** context menu option.

NOTICE

The **Split selected bone** option is only available when all bones are accepted (this prevents mixing two segmentation processes).

NOTICE

Only one bone may be split at a time.

After activating the **Split selected bone** function, a new empty bone list is created.

You can add bones to the list using the **New bone** button; you can add seeds on the original bone area using the same **Draw seeds on selected bone** function. For additional information see section “Place Seeds” on page 124.

Use the  **Preview Results** function to view the results.

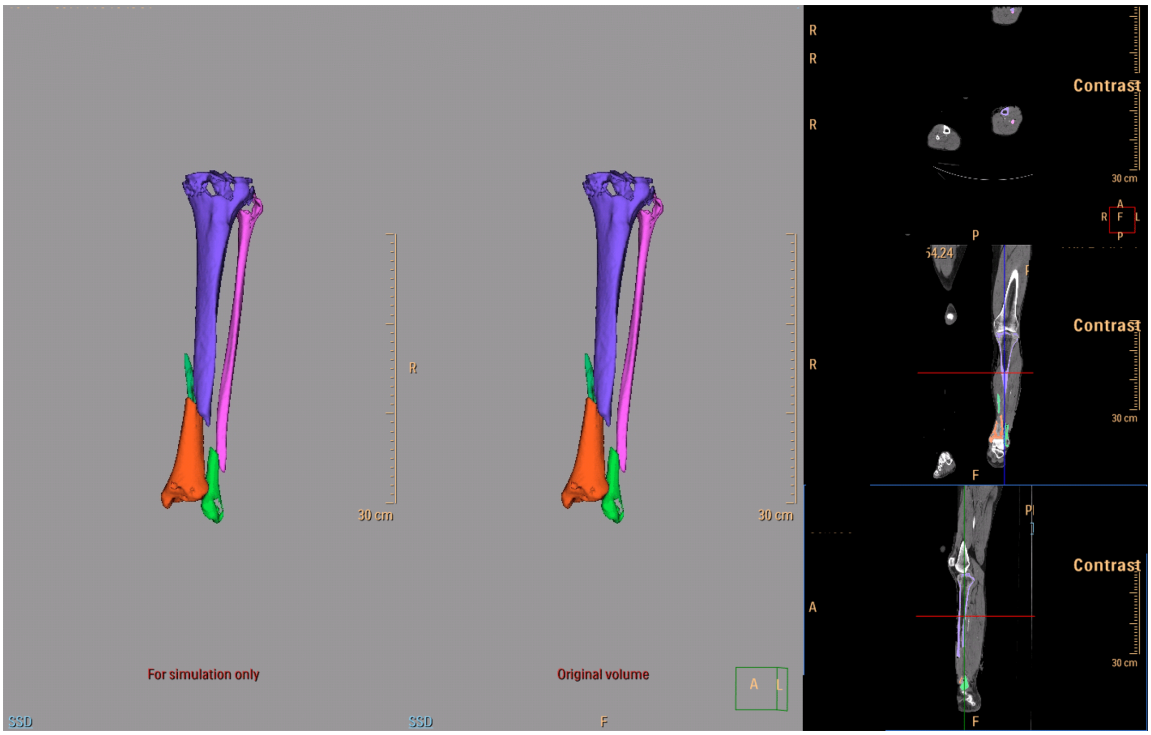
- When you use **Split selected bone**, segmentation is performed using the original bone’s area only (other segmented bones are not affected).
- When the new bones are accepted they replace the split bone in the original list.
- You can abort the split process and go back to the original list by clicking the **Exit Split Mode** button.

Virtual Bone Repositioning

Virtual Repositioning allows you to manipulate the segmented bones for surgery planning purposes.

Switching to the **Virtual Repositioning** tab is possible using the button at the bottom of the toolbox.

When switching to virtual repositioning, meshes are created to the accepted bones.



Each layout contains a viewport with the original segmentation results (labeled as **Original volume**) and a viewport with the segmentation results that allows you to manipulate the fragments (labeled as **For simulation only**).

You can perform these manipulations on each fragment:

- Move the fragment in X, Y and Z axes.
- Swivel the fragment around a rotation center located in the middle the bounding box of the fragment.
- Rotate the fragment in the screen plane.

Operations in Virtual Repositioning

Select - Select a bone for manipulation from the bones list. Or, select a bone by clicking on it in the viewport. When a bone is active, a bounding box is created around it.

Move - Click on the **Move** button. This adds three arrows in X, Y and Z axes, starting from the active bone's rotation center.

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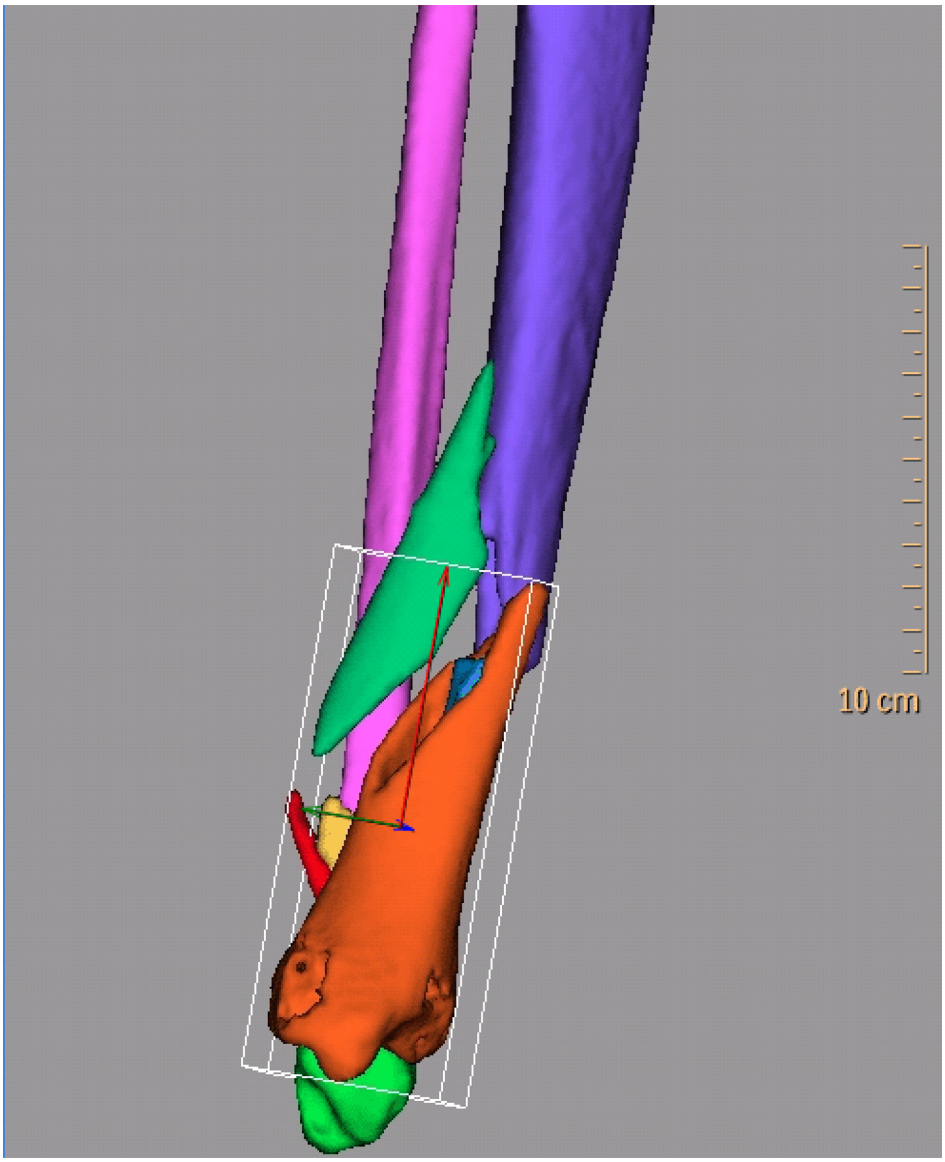
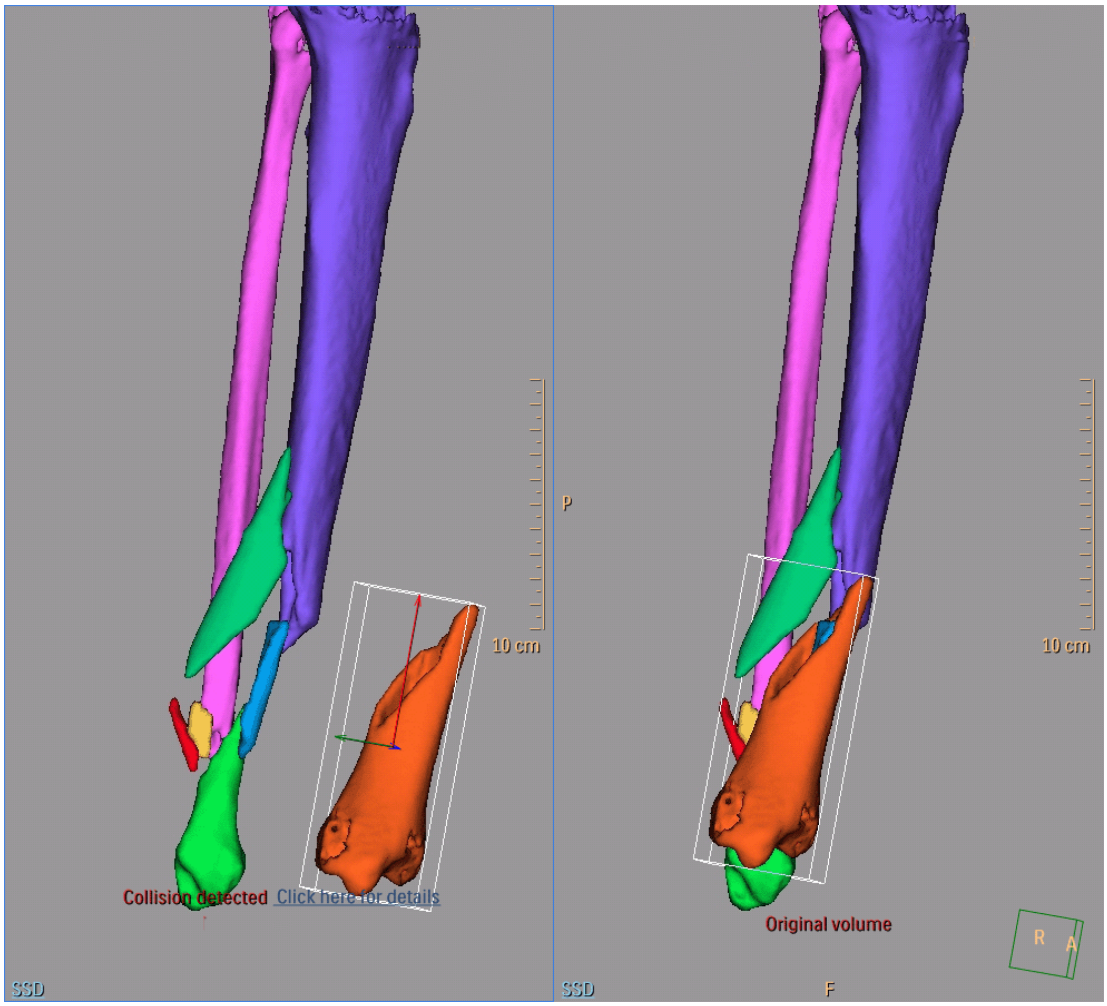
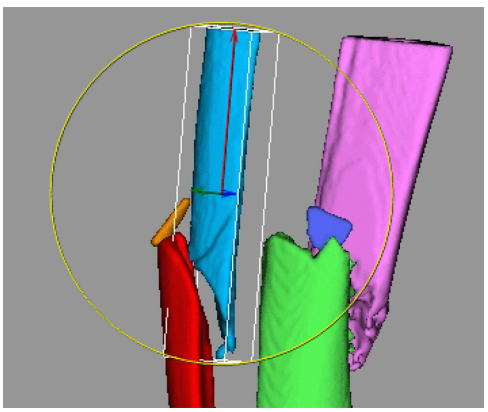


- **Repositioning a bone fragment** - Click and drag an arrow to drag the active fragment in the axis represented by the arrow.



- **Swiveling a bone fragment around its rotation center** - Click and drag inside the fragment's bounding box (but not while hovering on an arrow).
- **Rotating a fragment in the screen plane** - Locate the mouse cursor on the edge of the bounding box; a circle appears around it. Click and drag on the circle itself to rotate the fragment in the screen plane.



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- **Swiveling and rotating the active bone** - Click on the  button on the toolbox.
- **Manipulating a volume** - Click and drag outside the bounding box to manipulate the entire volume, according to the selected common tool from the toolbox . By default, **Swivel** is selected.

Collision

While manipulating fragments, collisions may occur between fragments.

Collision detection can be activated by placing a checkmark in the **Calculate collision** checkbox in the upper toolbox. When this option is activated, the application calculates whether collisions exist. If collisions exist, a message appears. In addition, in the label area, **Collision detected Click here for details** appears. Click on **Click here for details** for additional information.

Reset to original - You can reset all manipulations performed on a fragment and move it back to its original location. Select the bone fragment from the bones list (or from the viewport) and click the **Reset Bone to original** button (can also be done from the Bones list context menu).

Lock in original orientation - This function keeps one or more bones in a constant position and allows you to move the rest of the fragments around them. Select each bone you wish to lock and click the **Lock in original orientation** button (can also be done from the bones list context menu). A locked bone cannot be manipulated.

Orientation Annotations - When one or more fragments are locked in original orientation, orientation annotations appear on the manipulated results viewport. If no fragments are locked, the orientation annotations appear only on the original volume image.

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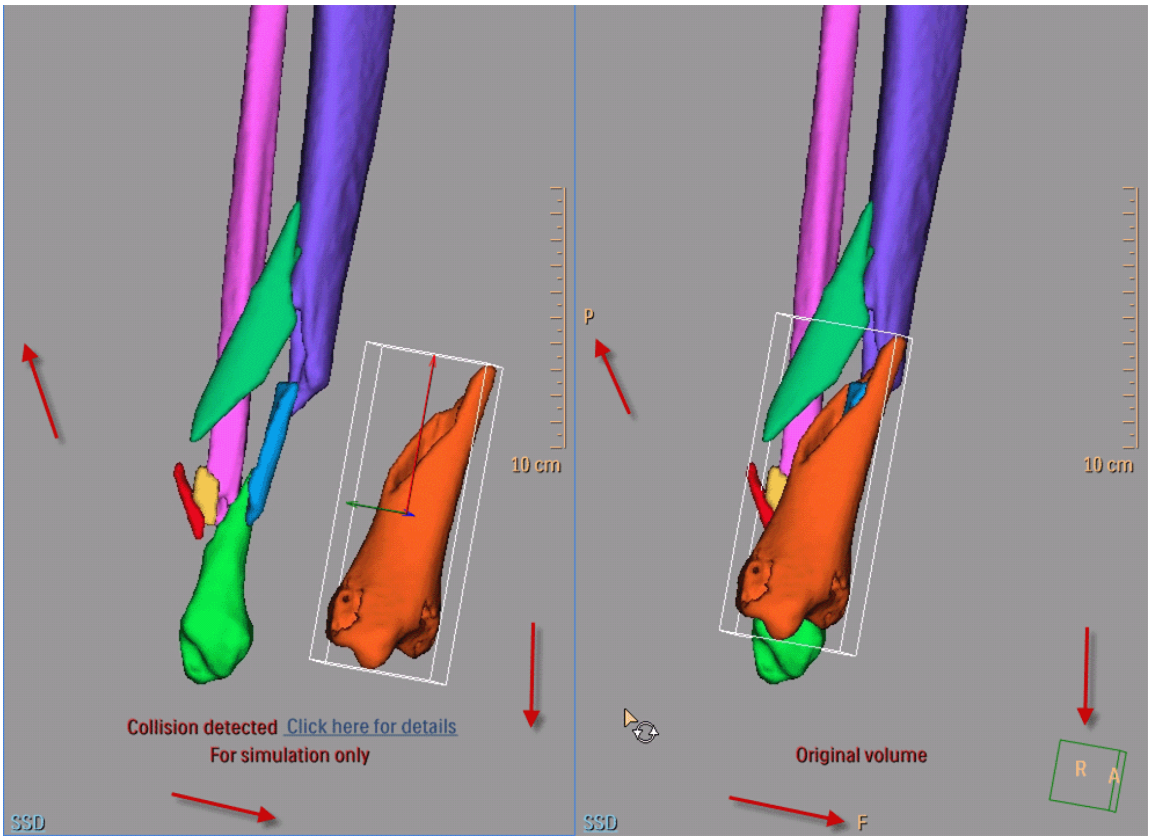


Other Virtual Repositioning Operations

- Control the visibility of each bone fragment by checking/unchecking the checkbox next to the bone.
- To remove the bounding box from around a fragment, use the **Clear selection** option from the context menu.
- If needed, moving back to the bone segmentation tab is possible using the **Segment Bones** button at the bottom of the toolbox.

NOTICE

Adding/deleting bones in the segmentation tab resets the manipulations done in virtual repositioning.

Upper Toolbox (Bone Stage)

Select the orientation of the main MPR image and the VR image.

Flip the VR and MP images

Select screen layout

Next series

Activate the **Relate** tool, where you can access the **Relate scenes** and **Relate viewports** functions.

Show crosshair checkbox - Show or hide the crosshair.

Show tissue overlays checkbox - Show or hide bone tissue overlays on the MPR images.

Show threshold overlay checkbox - Show or hide threshold overlays on the MPR images.

High quality (same as in CT Viewer)

Glass View / Show Transparent (same as in CT Viewer)

Click to center (same as in CT Viewer)

Bounding box, **Include**, **Exclude** - These tools can be used to limit the area of segmentation calculations.

Spine Stage

Automatic Centerline Detection

When a series is opened in the spine stage, the centerline of the spinal cord is automatically detected and displayed. The spine stage also detects the intervertebral disc planes.

You can continue working in other stages while the detection algorithm is running.

When centerline detection is running, its progress is shown by the progress bar at the bottom of the screen.

Edit Centerline Mode

After the centerline is calculated and displayed, the **Edit Centerline** mode is activated.

WARNING

Verify the accuracy of the automatic centerline extraction. If necessary, manually correct the centerline by dragging its control points.

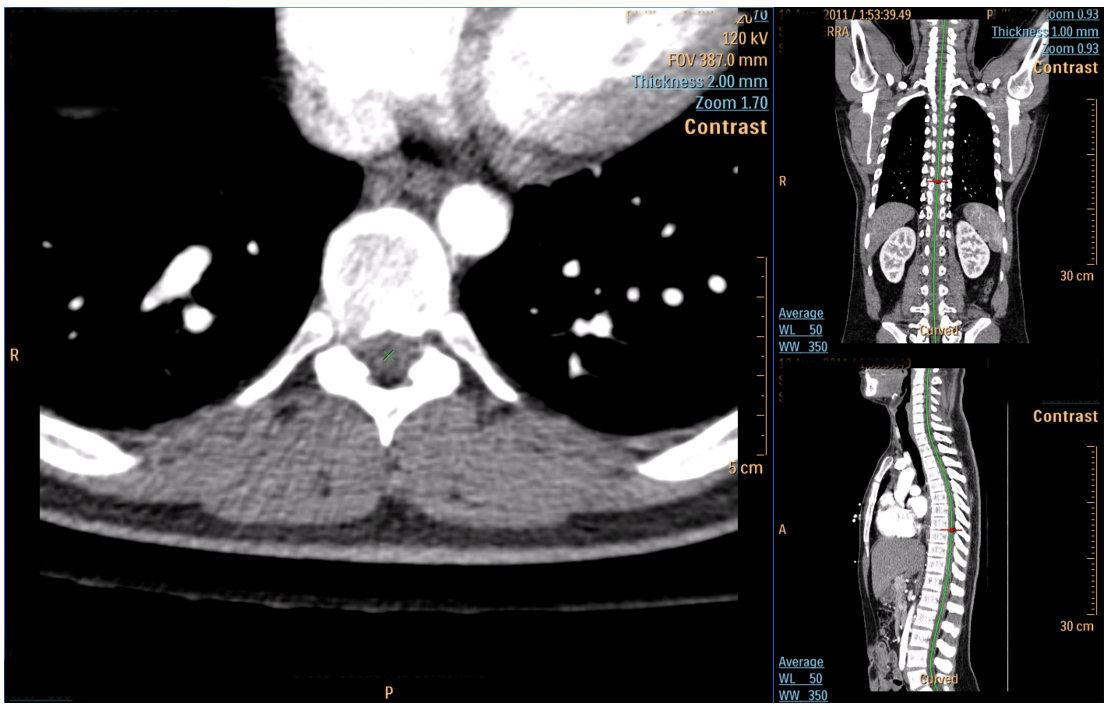
Review the centerline and edit it if needed. Editing can be done using the common curve editing tools (dragging control points, adding control points, and so on).

Review Along Spinal Cord

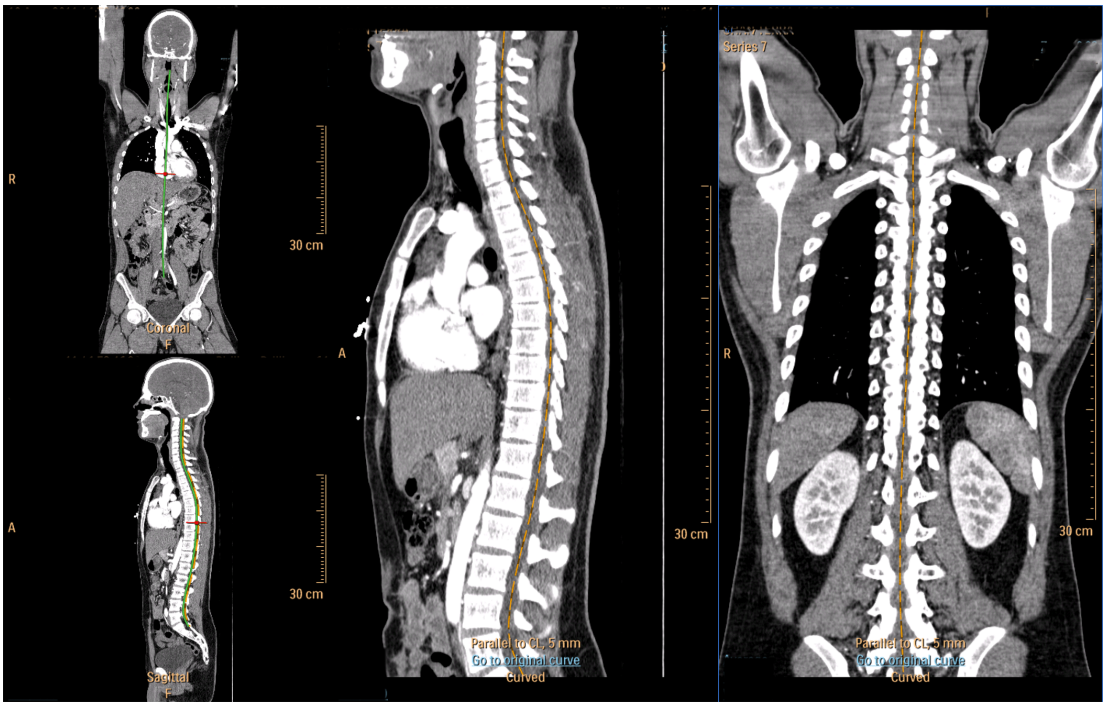
After the centerline is verified, you can review the spine along the spinal cord.

You can review in two ways:

- **Cross-sections** review option - shows the optimal viewports for reviewing the spine in planes that are cross-sectional to the centerline.



- **Parallel planes** review option - shows the optimal viewports for reviewing the spinal cord along curved-coronal and curved-sagittal planes, parallel to the centerline. In this mode, you can scroll through the cMPR images and swivel them. To return to the original centerline, click the **Go to original curve** viewport control at the bottom of the cMPR viewports.



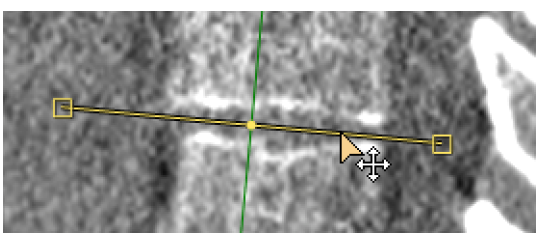
Edit Discs

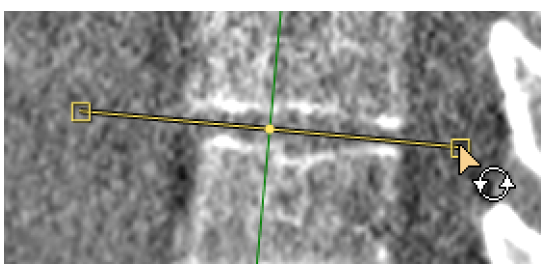
In the **Edit Discs** mode, the intervertebral disc planes are displayed on the different viewports, as they were identified by the algorithm.

WARNING

Verify the correctness of the disc planes location. Use the editing tools to correct the results, if required.

To edit the location and angle of each disc plane, drag the disc line (move) or drag its edges (rotate).





- To "jump” to the  **Previous/Next** disc (making it active), use the arrows on the toolbox.

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- To delete a disc line, use the  **Remove** button on the toolbox (or via the active disc line context menu).
- To add a disc line use the  **Add** button on the toolbox and click on the desired location on the centerline.

The newly created disc is placed, by default, between the disc above it and below it. The disc's location and angle can be edited.

WARNING

Verify that all disc lines are available and located correctly. This is crucial for correct labeling of the vertebra and for reviewing along vertebral body.

Apply Labeling

You can add labels to the vertebrae using the **Apply Labeling** mode.

WARNING

Verify the correctness of the vertebra labels. If required, delete the labels and start the labeling process again.

When selecting **Apply Labeling** for the first time, the **Set Spine Anatomy** dialog pops-up

- Selecting **Normal spine** closes the dialog.
- Selecting **Spine variants...** expands the dialog.

NOTICE

You must specify whether the anatomy of the spine is normal or abnormal (and the type of variant, if any exists) in order to continue with the labeling process.

WARNING

Wrong specification of the spine anatomy in the dialog may lead to incorrect labeling of the vertebrae.

After specifying the anatomy, and after closing the Spine variants dialog, examine the labeling results:

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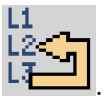
- If labels were automatically applied, you should review and confirm them.
- If labels were not automatically applied, you should hover the mouse over any unlabeled vertebra and from the context menu that appears, select the correct label for the active vertebra. This can be done on any of the viewports that display the vertebra lines.
- The labels will be propagated to the rest of the vertebrae, according to the manually selected label and the specified spine anatomy.

Propagation Failure

If the propagation fails, a message will appear. Propagation failure can be a result of:

- **Incorrect number of disc lines** - Return to the **Edit discs** mode, correct the disc lines and start the labeling process again.
- **Incorrect "first label" given by the user** - Relabel the vertebra that you tried to label before or label another one instead.
- **Incorrect spine anatomy specified in the "Set spine anatomy" dialog** - Open the dialog again from the labeling context menu and correct the specified anatomy. Continue with the labeling process.

After the labels are propagated, review the labels of all the vertebrae and select an option under **Apply Labeling**.

- If the labeling is correct, click on **Confirm Labels**  . The question marks disappear from the labels and the labeling is accepted.
- If the labeling is incorrect, click on **Clear Labels**  and start the labeling process again.
- To restart the labeling process, click on **Reset Labels**  . It is also possible to restart the process by selecting the **Reset Labels** option from the context menu while hovering over a vertebra.
- To delete any previously accepted labels, use the **Delete** options from the context menu while hovering over a vertebra

Review Along Vertebral Body

The **Review along Vertebral Body** function becomes available only after performing the **Edit Discs** operation (and after performing the optional **Apply Labeling** operation).

Review along Vertebral Body allows you to review the spine along the vertebral bodies in interpolated planes between the disc planes. If labeling was applied, the currently displayed disc/vertebra label appears at the bottom of the cross-sectional viewport.

Upper Toolbox (Spine Stage)

Select the orientation of the main MPR image and the VR image.

Flip the VR and MP images

Select screen layout

Next series

Show lines on: - Show or hide the display of Discs or Vertebra lines.

Show centerline checkbox - Show or hide the centerline curve.

Show crosshair checkbox - Show or hide the crosshair.

CT Acute Multifunctional Review Findings

Use the **Findings Repository** to gather and store images from the different stages of the application and send them to **Report** or **Film**.

NOTICE

See section “Findings Navigator and Findings Repository” on page 142 for more information.

Annotate Findings

To annotate a **Finding**, hover over it in the tray or use the **Preview**  button.

You can add the following information to each **Finding**:

- Finding Name (type-in or select from a drop-down menu)
- Criticality level (selecting from a drop-down menu)
- Findings location (selecting from a drop-down menu)
- Free text

Clip & Segment

You can access the **Clip & Segment** tools from a dedicated scene. The scene is identical to the Volume scene in CT Viewer.

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The scene is accessible from a drop-down menu on the **Review** stage button.

NOTICE

Tissues segmented in this scene will be added to the **Tissue Management** tab in the other scenes.

Results & Bookmarks

The CT Acute Multifunctional Review supports saving results and bookmarks.

- When saving a result, the results from all four stages are saved.
- When saving a bookmark, the states of all four stages are saved.

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