Aquarius iNtuition User Guide

Version 4.4.13.P4

English

US/EU | terarecon

Symbols used in the label:

Symbol	Meaning
	**Consult Instructions for Use.**
	**The CE 0197 mark applies to iNtuition and AquariusAPS Software.** The CE mark is affixed on the software containing the aforementioned software.
	**Manufacturer** The name and address of the manufacturer are listed next to this symbol.
	**Date of Manufacture** The year of manufacture is listed next to this symbol.
	**Authorized Representative in the European Community** The name and address of TeraRecon's authorized representative in the European Community are listed next to this symbol.

Notices

Copyright

This document contains important, helpful, usage, and precautionary information. Please review carefully all precautionary statements and advisories, whether onscreen or contained herein, as these are essential to the effective and authorized use of the products and applications discussed. Sample Screens in this document may differ from your installation, depending on installed versions, available functionality and configuration. Refer to the version number to ensure you are accessing the correct information.

Note: Any beta features extended are not to be used clinically, and can ONLY be authorized, obtained or accessed through an appropriate beta agreement.

General Description

iNtuition (also referred to as Aquarius iNtuition) is a medical device comprised of two stand-alone software components: a server software backend (iNtuition Server) which performs complex image post processing, and client viewer software (iNtuition Client Viewers) that provides a user interface, enabling the user to view medical image data and associated derived metadata.

The Aquarius iNtuition Client ("AQi") is one of the iNtuition client viewers with 2D/3D/4D (3D with dimension of time) image processing and advanced visualization capabilities to assist physician review of medical images. The base functionality of Aquarius iNtuition includes, but is not limited to, various tools for visualization and analysis, customizable workflow templates to deliver structured workflow, and support for the physician to write and store the report.

A fully-configured iNtuition system is capable of a comprehensive suite of image processing and visualization functions, including full-color Volume Rendering, Calcium Scoring, Time-Dependent Analysis (TDA), Time Volume Analysis (TVA), Segmentation Analysis and Tracking (SAT), Vessel Analysis, Flythrough, Multi-phase review, CT/CTA Subtraction, Lobular Decomposition (LD), iGENTLE, Maxillo-Facial, Volumetric Histogram, Findings Workflow, Fusion CT/MR/PET/SPECT, MultiKV. Results from the AquarisAPS Server module may be displayed in the viewer. Each of these features may vary by client viewer and offered as an independent upgrade option to the basic configuration.

IMPORTANT: Based on published literature and TeraRecon's analysis, any derived value results, while using AQi, have approximately 3% of uncertainties, depending upon the noises in the data, image acquisition and reconstruction techniques, and human interventions.

Indications For Use

iNtuition Indications For Use

To receive, store, transmit, post-process, display and allow manipulation of reports and medical images from acquisition devices, including optical or other non-DICOM format images, DICOM images with modality type XA, US, CR, DR, SPECT, NM and MG, and images from volumetric medical scanning devices such as EBT, CT, PET or MRI. To provide access to images derived data and derived images via client-server software, web browser and mobile technology.

Visualization in 2D, 3D and 4D are supported for single or multiple datasets, or combinations thereof. Tools are provided to define and edit paths through structures such as centerlines that may be used to analyze cross-sections of structures, or to provide Flythrough visualizations rendered along such a centerline. Segmentation of regions of interest and quantitative analysis tools are provided, for images of vasculature, pathology and morphology, including distance, angle, volume, histogram, ratios thereof, and tracking of quantities over time. A database is provided to track and compare results using published comparison techniques such as RECIST and WHO. Calcium scoring for quantification of atherosclerotic plaque is supported.

Support is provided for digital image processing to derive metadata or new images from input image sets, for internal use or for forwarding to other devices using the DICOM protocol. Image processing tools are provided to extract metadata to derive parametric images from combinations of multiple input images,

such as temporal phases, or images co-located in space but acquired with different imaging parameters, such as different MR pulse sequences, or different CT image parameters (e.g. dual energy).

iNtuition is designed for use by healthcare professionals and is intended to assist the physician in diagnosis, who is responsible for making all final patient management decisions.

Interpretation of mammographic images or digitized film screen images is supported only when the software is used without compression and with an FDA-approved monitor that offers at least 5Mpixel resolution and meets other technical specifications reviewed and accepted by the FDA.

iNtuitionMOBILE provides wireless and portable access to medical images. This device is not intended to replace full workstations and should be used only when there is no access to a workstation. Not intended for diagnostic use when used via a web browser or mobile device.

iNtuition-TDA, TVA and Parametric Mapping Indications For Use

iNtuition-TDA, TVA, and Parametric Mapping are software modules which supports assessment of time-dependent behavior of image intensity, density, dimensions or volume of regions of interest over time, for volumetric or planar dynamic image types such as CT or MR. Parametric mapping tools encode in color various parameters derived from the temporal or spatial characteristics of the planar or volumetric data.

Support is provided for digital image processing to derive metadata or new images from input image sets, for internal use or for forwarding to other devices using the DICOM protocol. Image processing tools are provided to extract metadata to derive parametric images from combinations of multiple input images.

iNtuition-TDA, TVA and Parametric Mapping are iNtuition based software features with dedicated workflows and basic tools and thus support post-processing, displaying and manipulation of reports and medical images from acquisition devices and visualization in 2D, 3D and 4D for single or multiple datasets, or combinations thereof.

iNtuition-TDA, TVA, Parametric Mapping are designed for use by healthcare professionals and are intended to assist the physician in diagnosis, who is responsible for making all final patient management decisions.

T1T2 Indication for Use

iNtuition T1 Mapping and T2/T2* Mapping are software modules that support the derivation and quantification of T1, T2, and T2* values from MR DICOM image pixel intensities and header information. The quantification of these parameters can be used to characterize tissues. Support is provided to overlay the T1, T2, and T2* values using color maps on related MR images.

Support is provided for using different color maps to overlay different ranges of T1, T2 or T2* values and restrict the overlay to region of interest on the images. The MR images can be of simple planar scan like a single slice or volumetric or 4D scans of a body part. iNtuition T1 Mapping and T2/T2* Mapping are iNtuition software features that can be used in multiple workflows or be used as basic tools for cardiac functionality. Additionally, the overlaid images can be captured and forwarded to other systems using standards such as DICOM or http protocol. Quantitative analysis is derived and available as text and graphical display.

iNtuition T1 Mapping and T2/T2* Mapping qualitative results and visualization can be used in a clinical setting on MR images of an individual patient and can be used to support the clinical decision making for the diagnosis of the patient. iNtuition T1 Mapping and T2/T2* Mapping are designed for use by healthcare professionals and are intended to assist the physician in diagnosis, who is responsible for making all final patient management decisions.

Safety Notifications

The iNuition Client is part of a Class II medical device regulated by the Food and Drug Administration.

Warning! Not intended for diagnostic use when used via a mobile device.

CAUTION! U.S. Federal Law restricts use of this device to trained physicians, or other suitably qualified and trained personnel on the order of a physician.

If you require training, please contact TeraRecon or a suitably qualified trainer. Please keep this documentation readily available near the Aquarius iNtuition Client (AQi) at all times, and please keep it updated with all corrections/addenda that may be released by TeraRecon.

Patient information is restricted, private, and extremely confidential, and subject to stringent legal regulations - you should control access to Aquarius iNtuition, and patient data contained therein should be protected accordingly.

Devices integrated to this product must comply with their own applicable safety standards.

Precautions Relating to General Use

Aquarius iNtuition software may allow images to be generated in which parts of the original scan data are obscured, removed (including but not limited to, through use of lossy compression), hidden, or modified. Similarly, output images and reports can be produced, saved, and annotated, with elements of the original acquisition omitted, obscured, modified, or hidden. Hence, careful and responsible use of the equipment and its output images requires that the user be aware of, and effectively communicate these important facts to, untrained or uninformed observers or recipients of the processed information.

Please ensure that all processing has completed (including completion of any final stage subsequent to an intermediate stage of processing) before formulating a final interpretative decision.

In certain situations, you may experience a delay in certain display processing. Please ensure that all processing has completed (including, for example, completion of any final stage subsequent to an intermediate stage of processing) before seeking to validate, or validating, a final interpretative decision.

Precautions Relating to Display Hardware

Aquarius iNtuition image display is limited in acuity and color or grayscale depth to that of the display device used. Display hardware characteristics can vary widely. **Interpretation of mammographic images or digitized film screen images is supported only when the software is used without compression and with an FDA-approved monitor that offers at least 5Mpixel resolution and meets other technical specifications reviewed and accepted by the FDA.**

If a monitor is not calibrated, image quality may vary. Monitors must be calibrated by the monitor vendor's calibration method.

Image quality is subject to the quality of the monitor. An image displayed on a color monitor can appear different from the same image displayed on a grayscale monitor.

A monitor may contain small defects on the surface, such as dust or scratches on the surface of the CRT, defects of LCD cell, and so on. A customer should understand this problem and not confuse the defects with a software problem.

The surrounding lighting conditions are critically important for optimal image viewing in Aquarius iNtuition. Lighting conditions can reduce the contrast of images being viewed, and may hinder your ability to distinguish subtle changes in the image. See Chapter 5: The Contrast Tool for instructions on how to use the Contrast Tool to configure the device for different lighting environments.

The judgment of the medical imaging professional is essential to reaching the appropriate conclusion from the results presented by Aquarius iNtuition.

Precautions Relating to Interpretation

Calculations relating to distances, measurements and other physical properties performed by Aquarius iNtuition are dependent in accuracy of the input DICOM images. It is the responsibility of the operator to ensure that the source DICOM images are correctly formatted and to heed any warnings that the software may display during operation relating to potential problems with the information supplied in those DICOM images.

Note further that, in certain instances, there may be problems or inconsistencies in the image information, Aquarius iNtuition will be unable to detect this, and erroneous image display will be unavoidable unless the user properly ensures the correctness of all input data in advance. Potential problems relating to errors in the DICOM information include incorrect dimensional readouts, incorrect orientation markings, and incorrect pixel value calibration. Three-dimensional imaging inherently offers a wide variety of different imaging views of any given dataset; it is an important responsibility of the operator to ensure that a proper visualization is achieved, and that a complete review of the data has been performed before reaching any diagnostic or interpretive conclusion relating to the dataset in question. Limitations present in the original input data (such as those relating to spatial and/or temporal resolution, pixel size, and slice thickness) remain valid even when Aquarius iNtuition processes the data, and these provisos should be considered when using the equipment for image review.

The image processing and display techniques offered by Aquarius iNtuition are only intended as an adjunct to, and not a substitute for, conventional diagnostic review of medical imaging data. **All results should be validated by qualified physicians trained in the subject matter.**

Aquarius iNtuition provides tools and protocols to quantify metrics and distances relating to structures in the CT, MR or other scans or images which are based upon the dimensions of the anatomy scanned or imaged at the time the images were originally acquired from the patient, and based on the measurement calibrations provided by the acquiring device. The suitability for any particular purpose, especially monitoring the progression of disease, or the sizing or planning of a device to be implanted in a patient, is dependent upon many factors, including, but not limited to, the accuracy of the original acquisition, the extent to which the images acquired still represent the patient's anatomy, and the way in which the actual device deployment may modify the anatomy into which it is introduced.

TeraRecon does not represent that the Aquarius products are suitable for such purposes — all such activities should always be cross-correlated with other techniques to ensure a complete understanding of the patient and contemplated procedure is obtained by the validating physician(s) in charge.

Precautions Relating to Magnetic Resonance Imaging Machines

Components of Aquarius iNtuition, including this document and its packaging or binding, may contain metallic or Ferro-magnetic components. Please ensure that no such component is introduced into the influence of magnetic fields from devices such as Magnetic Resonance Imaging Scanners, since injury or damage to equipment or property could occur.

Precautions Relating to Risk of Loss of Data

Neither Aquarius iNtution nor AquariusNet ThinClient are intended to be used as a primary archive for medical imaging data. A secure copy of any data should be maintained in a location separate from this software, for example, in the scanner, in a PACS archive, or on archive media. Please do not rely on Aquarius iNtuition and/or AquariusNet ThinClient as your primary archive.

In addition, do not rely on Aquarius iNtuition and/or AquariusNet ThinClient to convey data from its acquisition point to your primary archive, because in this configuration, a failure in Aquarius iNtuition and/or AquariusNet ThinClient could compromise your primary archive. Your primary archive should be maintained in a manner independent of, and not relying on, Aquarius iNtuition and/or AquariusNET.

Precautions Relating to Computer Software and Hardware:

Note that the installation and use of any additional software or hardware component without the specific direction and approval of TeraRecon may impair the safety and effectiveness of the product. No additional software or hardware component should be added to Aquarius iNtuition and/or AquariusNet, nor should the configuration be changed in any way, except under the express direction of TeraRecon personnel. Do not use the software if it is damaged, compromised, or if you in any way suspect that its safety may have been compromised; in such case, contact your customer service representative immediately.

Microsoft Windows Operating System Updates

Aquarius iNtuition software relies on the integrity of the Microsoft Windows operating system to perform as documented by Microsoft. In the event that a Microsoft Knowledge Base article is released that exposes a bug or defect adversely affecting specific hardware platforms documented for use with Aquarius iNtuition or AquariusNet ThinClient software, it is the customer's responsibility to remedy those defects using the steps outlined by Microsoft in its Knowledge Base Articles.

Aquarius iNtuition is not accessible without a network, including LAN and WAN. The availability of a network is the customer's responsibility. This includes accessibility to other devices on the network such as authentication servers, storage locations, and so on.

Precautions Related to Image Output Option

Aquarius iNtuition allows for Output of selected images and series to various computer standard file types. This technique does not maintain full image fidelity and may affect image quality. **JPG, PNG, BMP and AVI files are not intended for diagnostic purposes.**

Captured images for Output may contain patient information and use and distribution must be controlled to ensure that secure access to PHI is maintained pursuant to all applicable U.S. and International Laws, including but not limited to, the Health Insurance Portability and Accountability Act ("HIPAA") and the Health Information Technology for Economic and Clinical Health Act (“HITECH Act”).

Patent Information

U.S. patents apply to this product. For details, see http://www.terarecon.com/patents.

Welcome

Welcome to the Aquarius iNtuition Client Manual (AQi). This manual is intended for users performing and analyzing different studies using the AQi application. Please read all chapters to gain a complete understanding of the Aquarius iNtuition application. You can use the table of contents to navigate to your topics of interest.

Pay special attention to all Notices, whether presented onscreen, or contained herein, including all precautionary statements and advisories, as these are essential to the effective and authorized use of the products and applications discussed herein.–

Conventions

This manual uses the following conventions:

- The text that appears on buttons, menu items, dialog boxes and other elements of the Aquarius iNtuition user interface are printed in a bold font. For example, “Click the **Save** button.”
- Screen names are capitalized. For example, Patient List, 3D Viewer.
- The chapters are arranged based on the functions in the Aquarius iNtuition application.
- A NOTE contains supplementary information about a topic.

Contents

Chapter 1 Introduction to Aquarius iNtuition

Topics in this chapter:

Much of the repetitive work needed to prepare data for examination - such as bone removal, heart selection, centerline extraction, sphere finding, registration of images, and several other common tasks - can be performed automatically using AquariusAPS. Post-processed files are sent to the iNtuition server containing information about what kind of processing was done. When you view a series on Aquarius iNtuition, information about advanced processing is displayed in the Patient List. A technologist can perform further modifications to the data, to verify the advanced processing, and also to further prepare the data for examination by a radiologist or referring physician.

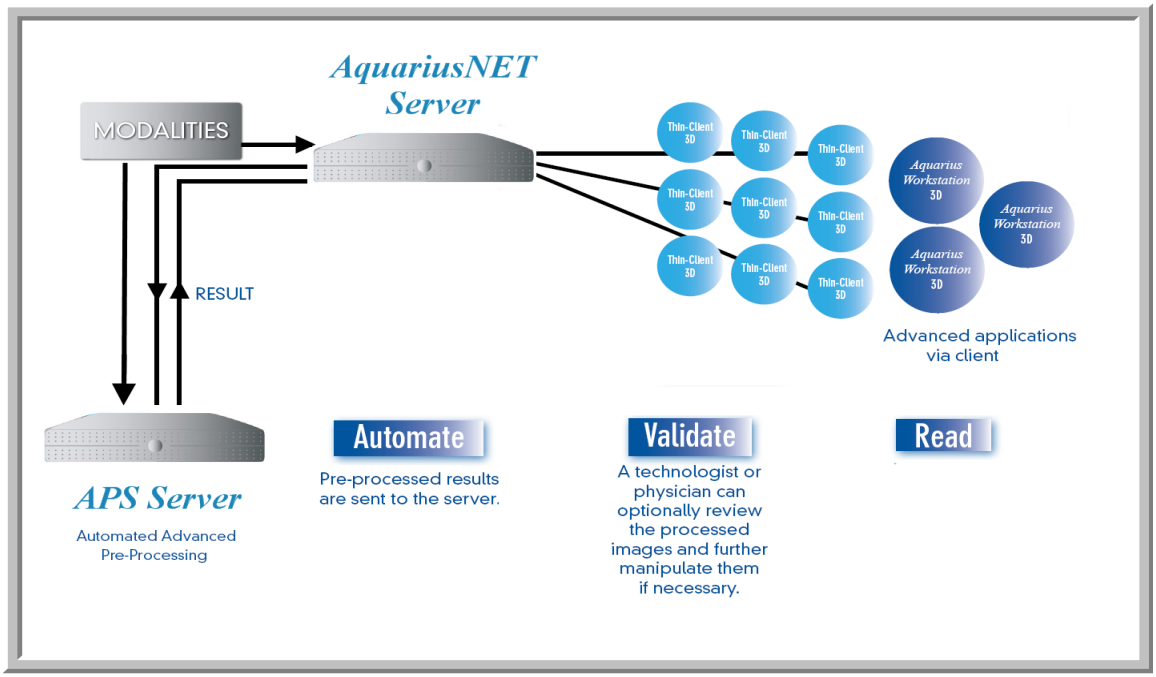


Figure 1-1: Aquarius iNtuition Architechture

Automate, Validate, and Read

The Aquarius iNtuition workflow is based on the concept of “Automate, Validate and Read”. AquariusAPS automates as much as it can. It automatically creates scene files after performing Advanced Processing on the original data. A technologist or physician opens a *workflow template*, which is a set of internal instructions on how to modify the data. For example, a workflow template for Runoff might contain instructions to remove bone from the data, help users clean the data and display images with certain options. When the study or series is opened, the technologist can activate this workflow template. This performs the function, removing bones from the data using results from AquariusAPS.

Common workflows are packaged together into *workflow templates*, which are templates for the sequence of steps you would perform on a particular type of study. iNtuition provides a number of sample Workflow templates, but you can modify them, as well as define your own templates. This is the automation step, which performs repetitive tasks the same way on all studies using the same template.

During the validation step, you can check the work done so far to validate its accuracy. When you are satisfied that the preliminary steps have been performed accurately, you can validate it for general usage. When validated, the template will become a *scene*. A scene is a snapshot that reproduces the images exactly as saved.

Once the study has been validated, you can save it as a workflow scene on the server. From there the doctor can reload the study, read the study, recheck the scene and modify it if necessary.

With the workflow scene now saved on the server, a referring clinician can launch the server, double-click on that scene, and have access to interactive workflow scenes that have been automated, validated and read.

Typical Scenario

Typically, workflows would be used by technologists, who would do a preliminary workup on the 3D image. A radiologist could then check the technologist's work, and if the workflow scenes for the study are acceptable, the radiologist would validate the scenes. If any of the scenes require extra preparation, the radiologist could modify them before validating them. Finally, a referring physician or surgeon would be able to analyze the data quickly and easily, because the images would already be in the format most needed for viewing.

TeraRecon provides several sample workflows by default, pre-designed by our clinical application specialists. Workflow templates are fully customizable. They can be used as they are, or modified to suit your specific needs.

See Chapter 4: "Workflows" for detailed instructions on how to use the workflows.

Note: If you are running the AQi Viewer on the iNtuition server itself, the server name must be "localhost".

Starting the Aquarius iNtuition Viewer

To start the Aquarius iNtuition (AQi) software, double-click the **Aquarius iNtuition Viewer** icon on your desktop. This launches the AQi Viewer and displays the login screen.

Logging In

Enter your username and password in the appropriate fields. Make sure that the **Server Name** field has the correct name or IP address of the iNtuition server.

Note: If you are running the AQi Viewer on the iNtuition server itself, the server name must be "localhost".

Figure 1-2: Login Dialog

1. Click the **Login** button.

   If the Aquarius iNtuition Client that is currently installed on your computer is the wrong version for the iNtuition Server you are logging in to, you will see a message asking whether you want to update AQi to match the server's version.

2. To download and install the correct version of AQi, click **Yes**. The client installer is downloaded automatically, and then the installer is launched.

   Follow the steps in the setup wizard to update the AQi client.

1. If **Show Last Login info** is enabled, the following dialog is displayed:

2. Click **OK** to close the dialog. See "Connection" on page A-48 to enable or disable this feature. When you have successfully logged in, the AQi Viewer is launched, displaying the Patient List:

Figure 1-3: The Patient List Screen

Chapter 2 The Patient List

Topics in this chapter:

When you log into your local server, the Aquarius iNtuition Client Viewer opens displaying the Patient List shown in Figure 2-1.

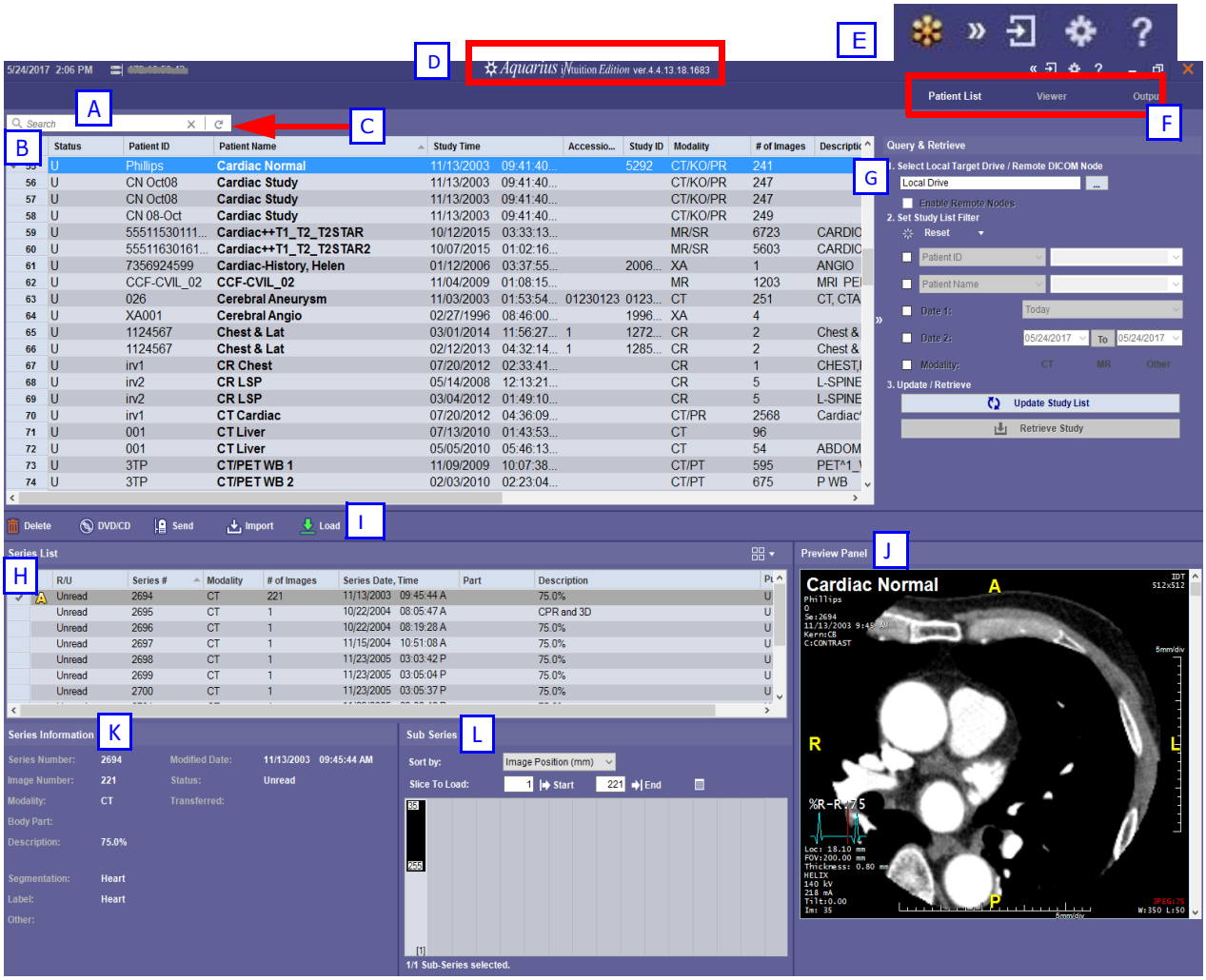


Figure 2-1 The Patient List Page

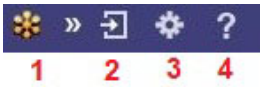
Elements of the Patient List

Note: Some of the following features apply only when the AQi Viewer is being run on the iNtuition Server localhost. These are noted within the context.

The Patient List View

Table 2.1 on page 2-3 lists each labeled area of the Patient List View shown in Figure 2-1.

Table 2.1: The Study List Fields and Menus

Label	Function	Description
A	**Filter (Search)**	You can filter the study list based on texts entered by users quickly.
B	**Study List**	This list displays the patient studies available on the system and displays the following information: Status, Patient ID, Patient Name, Gender, DOB (The patient's date of birth), Study Time (the time the scan was performed), Accession number, Study ID, Modality (CT or MR), Number of images (The total number of images in the study), Description (Optional information providing a fuller description of the study), Referring physician's name, AE Name, AE Title, Publish state, Age, Institution name Patient Other ID. You can sort the study list by clicking on the column headings. You can also change the relative location of these columns by LMB-hold, dragging, and dropping them on another column.
C	**Refresh Button**	Reloads the Patient List. This works exactly the same way as the **Update Study List** button in the **Query & Retrieve** panel.
D	**CE Mark and About Screens**	Right-click on the product name, and select either **CE Marking...** or **About...** to open the displays. • The CE Marking display shows an image of the product label found on all TeraRecon equipment. You can also see this label on the inside of the cover page of this manual. • The About display shows the current AquariusNet ThinClient Server version, the AQi Client version, the HASP ID number, and the Unique Device Identity (UDI) code. You can also click the clipboard icon (to the right of the HASP ID number) to capture this information to the Windows clipboard. You will need this information when contacting TeraRecon customer support.
E	**Top Left Toolbar icons**	See "Top Bar Functions" on page 2-21 for details.  1 2 3 4 1. Opens the Create a Conference window. (Arrows Hide or Show icon.) 2. Opens the Log file. 3. Opens the Preference Window. 4. Opens a browser for searching the Internet.
F	**Navigation Tabs**	These tabs give you quick access to the Patient List, 3D Viewer, and Output Panel.
G	**Search Filters**	This section allows you to list subsets of the Patient List according to various filters that you provide. For more information, see "Filtering the Patient List" on page 2-26.
H	**Series List**	This list displays the different series contained in the selected study. Here you will find more series-specific information, such as Series ID, Modality, number of images, part (body part examined), and Series description. If the patient were to have more than one series performed as part of the same study, you will see multiple lines of information in this box. Each line corresponds to one set of images (for example, pre- and post-contrast, or arterial- and venous-phase).

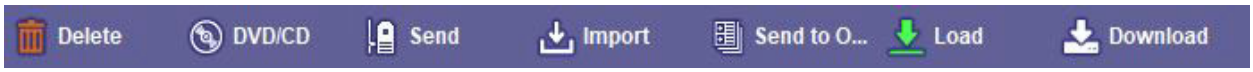
Label	Function	Description
I	**Data Management Tool Buttons**	These buttons allow you to **Delete** data, write data to a **DVD/CD**, **Send** files to other DICOM servers, **Import** DICOM files from your local hard drive or from the network, **Export** files to your hard drive (localhost only), and **Load** data into the 3D Viewer using your choice of workflow. For instructions on how to add remote DICOM preset buttons, see "Send" on page 2-24.
J	**Preview Panel**	In this panel, you can preview the original images of the current series before launching a module. Use the mouse wheel to scroll through the images, or left-click and drag to adjust the Window Width and Window Level. You can use the up and down arrow keys on your keyboard to change the slices. The Preview panel also has preset Window/Level values, as well as the **Cine** button to play the cine of the previewed image. If a study has %R- R information, it is displayed as an annotation on the Preview panel.
K	**Series Information**	This section contains detailed information about the series that is currently selected in the Series List. Much of this information is the same as what appears in the Series List, but is easier to read. In addition, the Series Information section provides information about any Advanced Processing (such as bone removal, CT table removal) that might have been done on the series, on Aquarius servers.
L	**Sub-series List and Slice Information**	Please refer to "The Series Information and Sub-Series Panels" on page 2-29 to learn more.

Note: Supported modality might vary by tool and feature.

Patient Study List Menus

You can use either the Data Management menu below the Study List window or you can RMB-click on a study and select an action from a pop-up menu window listing the appropriate actions for that particular study.

Data Management Menu Bar



When you select the Preference icon ( ), the **Preference window** opens. The options for the Data Management Menu Bar are selected within this window..

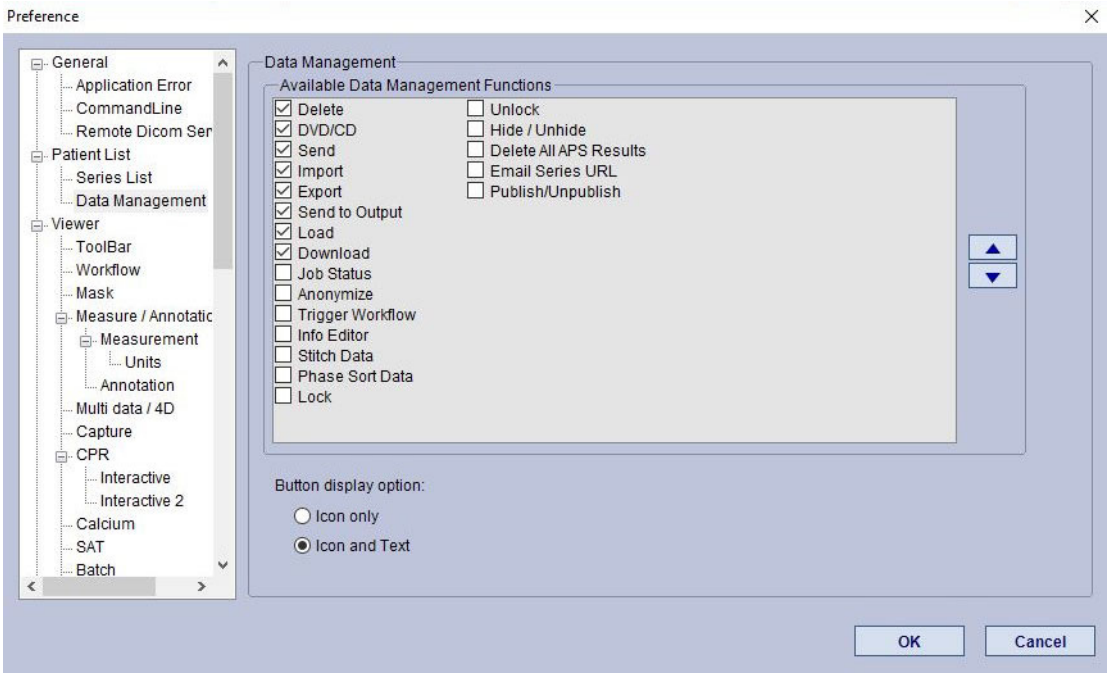


Table 2.2: Data Management Menu Bar Defined

Menu	Description
Delete	Delete the selected study
DVD/CD	Burn the selected study or studies to a DVD or CD (appears only when AQi is run on the localhost of the iNtuition Server).
Send	Send the study to a remote server.
Import	Import DICOM images from another folder.
Export	Export the selected study or studies to the selected drive, either local or on the network (appears only when AQi is run on the localhost of the iNtuition Server).
Send to Output	Send to another remote DICOM server.
Load	Load the selected study's images into the Viewer.
Download	Download the study to your local hard drive. When you select this option, a dialog is displayed that allows you to navigate to the desired folder to store the download.

Menu	Description
Job Status	This option allows you to check the status of the Trigger Workflow job. You can select this by RMB-clicking on the study and select **Job Status** as well. For more information, see XX.
Anonymize	If you want to anonymize the data that is being downloaded, check the box labeled **Download anonymized study/series**, located in the upper-left area of the dialog. When you click **OK**, another dialog is displayed, where you can to set anonymization parameters. See XX for more information.
Trigger Workflow	This feature allows you to run Advanced Processing on local data by triggering APS Clinical Protocols on a remote APS server. For more information, see XX.
Info Editor	This opens the Patient Info Editor window.
Stitch Data	Stitch (merge) and resample two or more series. The series might have different thicknesses prior to the stitch operation. However, they must all have the same orientation.
Phase Sort Data	Sort data in phases.
Lock	A study can be locked so that it cannot be deleted for a specified time period.
Unlock	Unlocks the study, canceling the selected time period.
Hide/Unhide	Does not delete a study - only hides or reveals a study.
Delete All APS Results	This deletes all scene files that have been created by Advanced Processing on this series.
Email Series URL	This feature allows you to email a link to another user, of images you have saved from a series. **Note**: Before you can use this feature, you must have Microsoft Outlook installed on your client computer, and you must have an email account on Outlook.
Publish/Unpublish	When you publish a study, the study is automatically locked in the database for 60 days. The study can be accessed directly using the Web Administrative interface. To unpublish a study, select this menu again. For more information, see the *Aquarius Web Admin iNtuition Edition* manual.

Study List Menu Options

When you RMB-click on a study or within the Study List, the following menu (dependent on the type of study) appears.

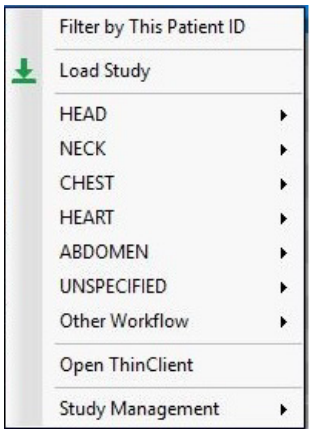


Table 2.3: RMB-click Menu List

Menu		Description
Filter by This Patient ID		Display only those studies belonging to the selected Patient ID in the Patient List.
Load Study		Load the selected study into the 3D Viewer.
Workflows	HEAD	Workflows specific to the HEAD.
	NECK	Workflows specific to the NECK.
	CHEST	Workflows specific to the CHEST.
	HEART	Workflows specific to the HEART.
	ABDOMEN	Workflows specific to the ABDOMEN.
	UNSPECIFIED	Workflows that don't focus on specific anatomical elements.
	Other Workflows	Any available and additional workflows.
Open iReview		See the Open iReview section on
Open ThinClient		This opens the iNtuition ThinClient. This is discussed in the Open iReview section on 2-7.
Study Management		Opens a menu window with additional management tools.

Study List Menu Option Details

Filter by This Patient ID

This selection displays only those studies belonging to the selected Patient ID in the Patient List.

Load Study

Load the selected study into the 3D Viewer.

Workflows

You can specify a workflow when opening a study or series. When you do so, iNtuition automatically opens the data using that workflow template in the 3D Viewer. The workflow menu items comprise the list of available workflows based on the study/series selected for you to use for analyzing.

Sample Workflows

The workflows listed in the RMB-click menu are sample workflows provided by Terarecon. The table below contains a brief description of each.

Table 2.4: Sample Workflows

Workflow	Description
Multidata VolBrowse	Provides Basic views when loading multidata
VolBrowse	Provides several basic views of a study
Angio	Provides standard toolsets used on most Angio studies
CTA Abd-Pelvis	For abdominal/pelvic area studies
ABD Tech	Provides technologist with a simple workflow for CTA abdominal studies
COW	Workflow for the Circle of Willis
COW Tech	Provides technologist with a simple workflow for CTA of the Circle of Willis studies
CTA Carotid	For studies of the neck region
Carotid Tech	Provides technologist with a simple workflow for CTA Carotid studies
Cardiac	For cardiac studies
Cardiac 1	Optional viewing methods for a cardiac
Cardiac Tech	Provides technologist with a simple workflow for Cardiac studies
Cardiac Measurements	Applies Customized measurements for Coronary Arteries
Bypass	Provides toolsets and viewing options for a bypass study
EP	Electro Physiology for Pulmonary vein diameters
Cardiac LSA	Lesion Specific Analysis
CTA RunOff	For full-body runoff studies
Runoff Tech	Provides technologist with a simple workflow for CTA Runoff studies
EVAR	Endovascular Aortic Repair
TAVR	Transcatheter Aortic Valve Replacement
LD2	Lobular Decomposition
Lobular Lung	Automatic lobular decomposition for the lung
Lobular Liver	Automatic lobular decomposition for the liver
Flythrough	Initiate Flythrough

Workflow	Description
TDA (Head)	Time-Dependent Analysis (Shown for TDA studies only)
SAT (Lung)	Segmentation, Analysis and Tracking for the lung
SAT (Other)	Segmentation, Analysis and Tracking for other organs
MT (Lung)	The same as SAT (Lung), with measurement tracking enabled
MT (Other)	The same as SAT (Other), with measurement tracking enabled
Orthopedic	Provides tools and viewing options for Orthopedic exams
LowAtt	Workflow for Low Attenuation scans
iReview	Open study in the iNtuitionReview (iReview) client
ThinClient	Open study in the Thin Client.
VEn	Duel Energy Workflow, requires multiple energy series
Fusion	Open studies of different modalities to perform Fusion.
New	Create a new workflow for this study

Note: The provided sample workflows are useful for specific types of procedures or protocols. They can all be modified according to your institution's needs, and you can also create new workflows. For instructions on how to modify and create workflows, see "Creating and Modifying AQi Workflows" on page 4-6.

To open a study with a workflow, select a study from the Patient List:

- Select a workflow from the RMB-click-click menu. This opens the study in the selected workflow, **OR**
- Click the **Load** menu in the Data Managment menu bar (see "Load" on page 2-26 for more information). Then RMB-click to select the appropriate workflow template for the selected study.

For more information about workflows, see Chapter 4: "Workflows".

Open iReview

This opens the iNtuitionReview (iReview) optional client viewer.

Open ThinClient

This opens the iNtuition ThinClient optional viewer.

Study Management

When you select Study Management from the RMB-click menu (in the Study List), you can choose other tools for managing the selected study.

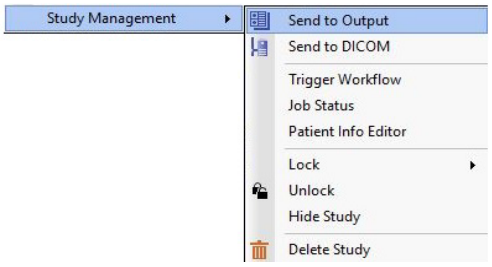


Table 2.5: Study Management Menu Options

Menu	Description
Send to Output	Send all images in the selected study to the Output Panel. If more than 500 images are sent at once, a confirmation dialog is displayed before the images are sent.
Send to DICOM	Push the selected study to a DICOM server. A dialog opens for you to select a DICOM server. Click **OK** to complete selection. For instructions on how to cancel a job once it has been sent, see "Cancel Send" on page 2-20.
Trigger Workflow	This feature allows you to run Advanced Processing on local data by triggering APS Clinical Protocols on a remote APS server. For more information on the functionality of Trigger Workflow, see "Trigger Workflow" on page 2-11 below. **NOTE:** You first must configure an AquariusAPS server as a remote DICOM node on the iNtuition server. Refer to the AquariusAPS Manual for instructions, or contact your system administrator.
Job Status	Gives the processing (AqAPS) job status.
Patient Info Editor	Allows you to editor patient information for processing.
Lock	Locks the study so that it can't be delete for a set time.
Unlock	Unlocks the study.
Hide Study	Hiding the study makes it invisible in the Patient List. The study is still on the server.
Delete Study	Allows you to delete only the studies you own.
Publish Study	When you publish a study, the study is automatically locked in the database for 60 days.

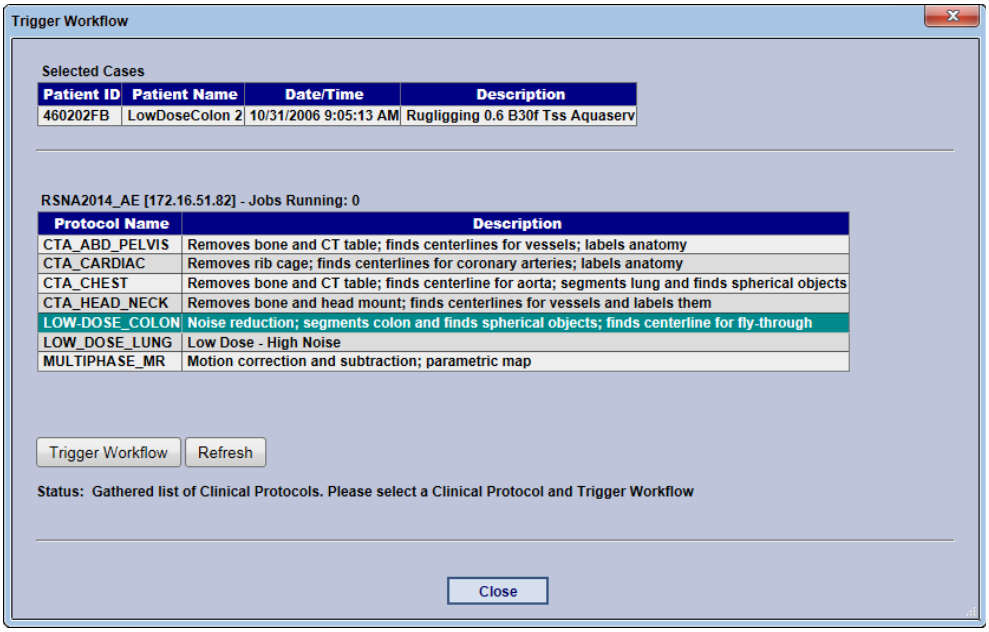
Study Management Menu Details

Trigger Workflow

This feature allows you to run Advanced Processing on local data by triggering APS Clinical Protocols on a remote APS server.

Note: You first must configure an AquariusAPS server as a remote DICOM node on the iNtuition server. Refer to the AquariusAPS Manual for instructions, or contact your system administrator.

When **Trigger Workflow** is selected, the following dialog is opened:



This dialog lists the clinical protocols on the APS server that are currently enabled.

Note: This dialog lists only those processors that have been enabled. Therefore, there might be other processors on the server that are not listed here.

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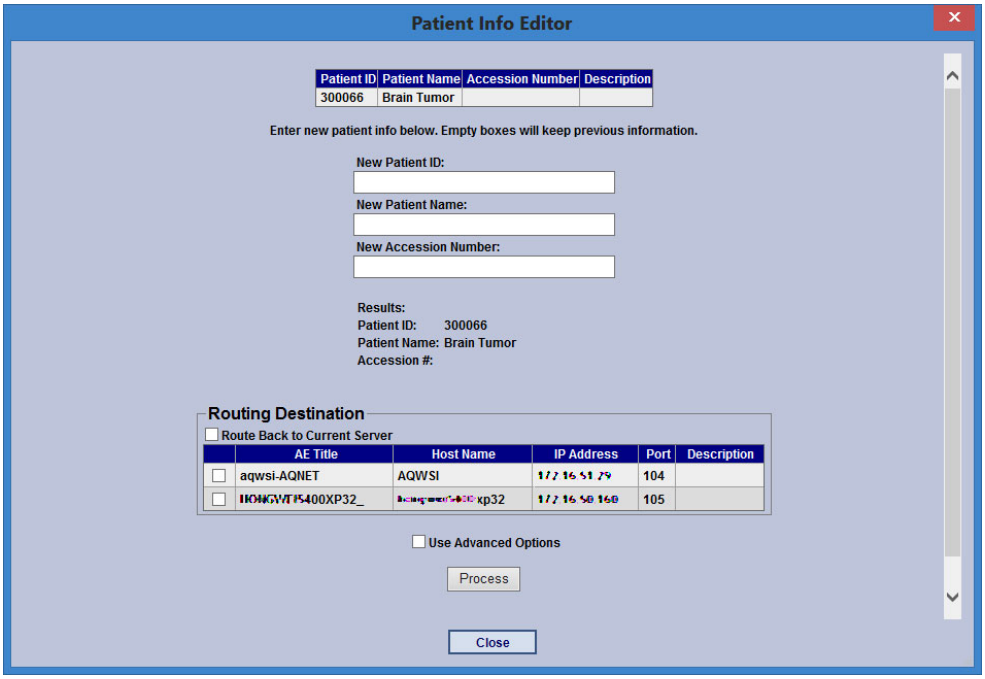
1. Select the protocol you want to run.

2. Click the **Trigger Workflow** button.



With this feature, you can change the following:

- Patient ID
- Patient Name
- Accession Number

Note: Tags that you would like to remain unchanged should be left blank.

You can then select routing destinations for the changed study, by selecting one or more of the remote servers in the Routing Destination list. You can also have the study rerouted back to the iNtuition server you are currently connected to.

Note: This feature makes a copy of the study and changes the tags of the copy. The original study is still on the server and still has the original tags.

When you have entered all the necessary information, click the **Process** button. This starts the process of creating a study having the new information.

To change other tags, click the **Use Advanced Options** checkbox, located near the bottom of the Patient Info Editor.

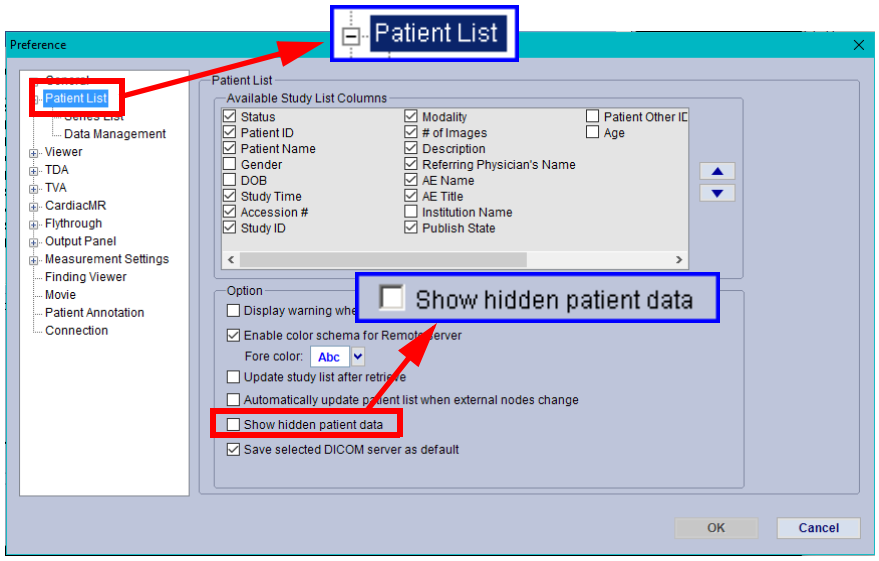
Lock/Unlock Study

A study can be locked so that it cannot be deleted for a specified time period. To lock a study, select **Lock** from the **Study Management** menu, and select a time period from the sub-menu. To unlock a study, select **Unlock** from the **Study Management** sub-menu.

Hide Study

When you hide a study, it becomes invisible in the Patient List. However, the study is still on the server.

To show studies that are currently hidden, open the user Preferences and click **Patient List** in the navigation panel. Then select the check box for the **Show Hidden Patient Data** setting.



Note: Enabling this setting will show *all* hidden data.

Delete Study

In order to delete studies, you must be given the right to delete studies that you own. If you do not have that right, contact your system administrator to configure your account or user group accordingly.

If you are allowed to delete your own data, select **Delete Study** from the **Study Management** menu. A confirmation dialog is displayed; click **OK** to delete.

Publish Study

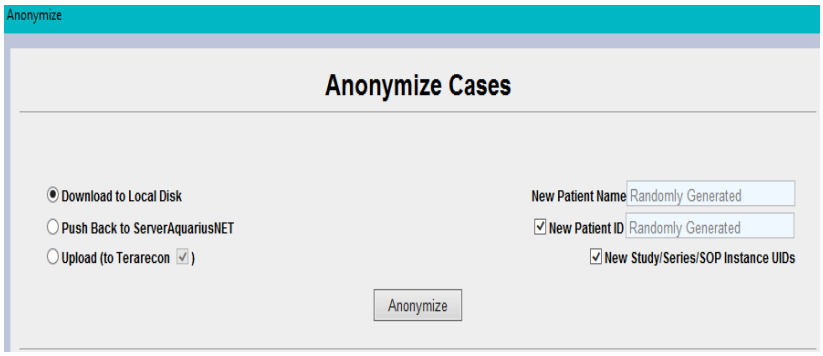
When you publish a study, the study is automatically locked in the database for 60 days. The study can be accessed directly using the Web Administrative interface. For more information, see the *Aquarius Web Admin iNtuition Edition* manual.

Download

Download the study to your local hard drive. When you select this option, a dialog is displayed that allows you to navigate to the desired folder to store the download.

Anonymizing Downloaded Data

If you want to anonymize the data that is being downloaded, check the box labeled **Download anonymized study/series**, located in the upper-left area of the dialog. When you click **OK**, another dialog is displayed, where you can to set anonymization parameters.



1. If you want to use a specific alternate for the patient's name, enter that name in the **New Patient Name** input box. Otherwise, the new patient name will be generated randomly.

2. If you also want to specify a new patient ID, check the box labeled New Patient ID. A text input box is opened, where you can enter the alternate patient ID. If a new patient ID is not specified, one will be generated randomly.

3. Check the box labeled New Study/Series/SOP Instance ID if you want the auto-anonymizer to generate UIDS for the study, series and SOP instances.

To Anonymize Your Data

1. Enter the new patient name in the **New Patient Name** field. If you do not enter anything in this field, a name will be randomly generated.

2. If you want to enter a new patient ID, check the **New Patient ID** checkbox. A field is then displayed for you to type in a patient ID of your choosing.

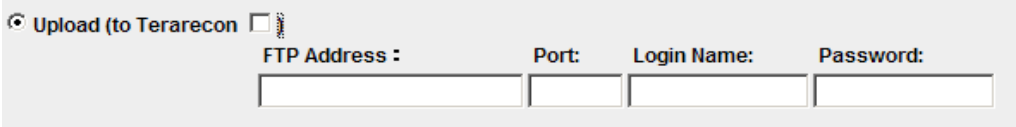
3. Check **New Study/Series/SOP Instance UIDs** if you want new UIDs to be generated.

4. On the left of the dialog, select the function to perform. There are three functions available for anonymized studies:

   - **Download to Local Disk** - Select this button and click **Anonymize**. A progress bar is displayed below during the download. It might take a few minutes, depending on the number and size of the data sets selected. Please wait for the **File Download** dialog to appear. When the dialog is displayed, click **Open** to open the study, and **Save** to save it to disk.

   - **Push back to Server AquariusNet ThinClient**- All anonymized data sets are pushed back to the server as new datasets.

   - **Upload to Terarecon** - The default FTP site is "Terarecon". Other FTP sites can be configured by unchecking the box and entering the FTP address, username, password and port (see the following figure).



Load Series

Load the selected series into the 3D Viewer.

Workflows

You can specify a workflow when opening a series. When you do so, Aquarius iNtuition automatically opens that workflow template. See the Workflows section under "The Study List Fields and Menus" on page 2-3.

Open TDA

This opens the Time Dependent Analysis (TDA) module for CT studies. For a full discussion of this module, please see the Aquarius Workstation iNtuition Edition.

Open ThinClient

This opens the iNtuition ThinClient. This is discussed in the Open iReview section on page 7.

Open MultiPhase

Open a multi-phase series, such as a series of phases in the changing volume of the of the heart. This opens the iNtuition Thin Client viewer.

Open Fusion

Open two datasets to be analyzed together, such as a CT and PET scan. This opens the iNtuition Thin Client viewer.

Series Management Menu Options

Send to Output

Send series images to the Output Panel. This is discussed under "The Study List Fields and Menus" on page 2-3.

Send to DICOM

Send series images to a DICOM server. This is discussed in the "Send to DICOM" on page 2-16 section under "Study List Menu Option Details" on page 2-7. For instructions on how to cancel a job once it has been sent, see "Cancel Send" on page 2-20.

Anonymize

This works exactly the same way the Anonymize study function works. See "Study List Menu Option Details" on page 2-7 for instructions.

Download

Download the study to your local hard drive. When you select this option, a dialog is displayed that allows you to navigate to the desired folder to store the download. This is discussed in the Download section under "Study List Menu Option Details" on page 2-7.

Stitch Data

Stitch (merge) and resample two or more series. The series might have different thicknesses prior to the stitch operation. However, they must all have the same orientation.

Select the series to be merged together and select **Stitch Data** from the **Series Management** menu.

A new series is created that contains the merged data. The series description is created by the software and has the following format: **APS_Stitch_S**, followed by a list of the original series that were stitched together. In Figure 2-2 (below), series numbers 5 and 6 were stitched together to create the new series.

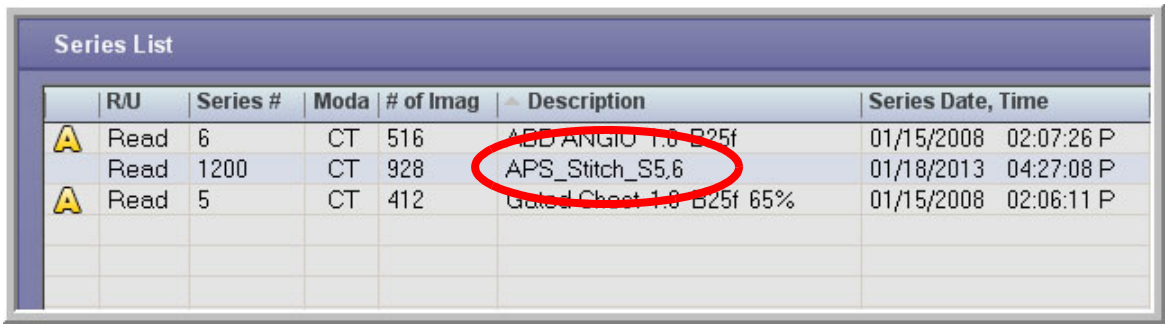


Figure 2-2: Newly Created Stitched Series

Below are images of each individual series, followed by the combined series:

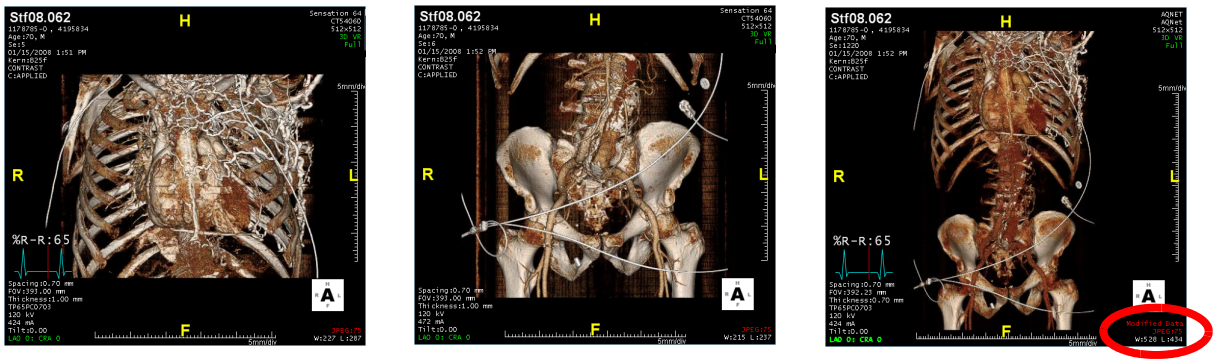


Figure 2-3: Left: Partial Series 5; Middle: Partial Series 6; Right: Stitched Series 1200

Note: The stitched series contains an annotation in the lower-right corner of the image, indicating that it is modified data (circled in green in Figure 2-3).

You can monitor the progress of the stitch processor in the **Input/Output Log**. (See "Input-Output Log" on page 2-22 for more information.)

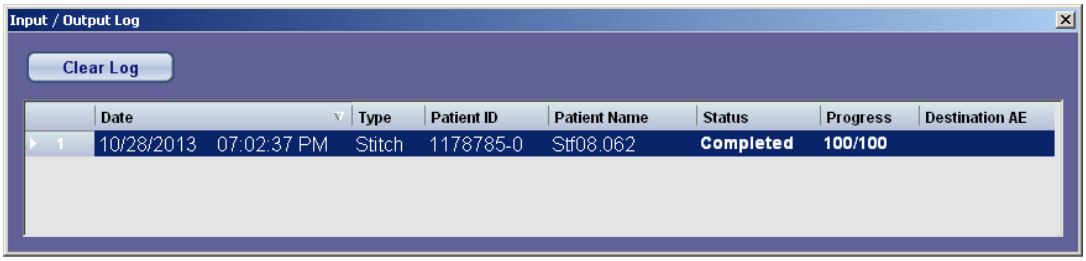


Figure 2-4: Stitch Data Progress in Input/Output Log

Lock/Unlock

Series can be locked so that they cannot be deleted for a specified time period.

To lock a series, select **Lock** from the Series Management sub-menu, and select a time period from the sub-menu.

To unlock a series, select **Unlock** from the Series Management sub-menu.

Hide Series

Hide selected series from the Series List. The data is still on the server. This feature is discussed in "Hide Study" on page 2-13.

Delete Series

This deletes the selected series. A confirmation dialog is displayed first; click OK to delete.

Note: You must have the right to delete series data. See "Delete Study" on page 2-14 for more information.

Delete All APS Results

This deletes all scene files that have been created by Advanced Processing on this series.

Email Series URL

This feature allows you to email a link to another user, of images you have saved from a series.

Note: Before you can use this feature, you must have Microsoft Outlook installed on your client computer, and you must have an email account on Outlook.

- Choose **AqClient Viewer** if the recipient can view the series using the iNtuition Thin Client.

Note: The recipient of this link must have the iNtuition (Thin Client) Viewer installed in order to open the link.

- Choose **AqNET WEB Viewer** if the recipient is not viewing the series with an Aquarius product. The series can be viewed using any Web browser.

  The password dialog box is displayed. If you enter a password, the recipient will need to enter the same password in order to access the selected series in the AquariusWEB Viewer. The password is optional; if you do not want to use a password, simply leave the input field blank.

Note: You can send only one series each time you select this feature.

If you need to require full authentication for the recipient, you can set a Preference that will make it necessary for the recipient to login to the server using both a username and password. To do this, follow these steps *before* emailing the URL:

a. Select the Preference icon () located on the right end of the top toolbar. The Preference window opens.

2. LMB-click **Patient List** in the navigation list located on the left side of the Preference window. This opens the Patient List Preference screen.

3. Check the box labeled, “Always use AquariusNET ThinClient account authentication”.

You can now email the URL.

For information on viewing a series using a Web browser, see Chapter 22: "AqWEB Viewer and AQiMobile".

- Choose **AQi Viewer** if the recipient can view the series using the Aquarius iNtuition Viewer.

Note: The recipient of this link must have the Aquarius iNtuition Viewer installed locally in order to open the link.

Each of these options opens an email in your default email client. The subject line contains series identification and the body of the email consists of the URL to the series, on the server you are currently logged in to. Address the email and send it.

When the recipient clicks on the link, the appropriate application is launched.

Note: If the recipient is unable to access the server from a remote location, this might be because access is blocked by a firewall or some other restriction. In that case, the Web server would need to be configured to make the hostname available to remote clients. For more information, please see the *Aquarius Web Admin iNtuition Edition* manual, or notify your system administrator.

- Choose **iEMV** if the recipient can view the series using iNtuitionEMV (iEMV).

Note: The recipient of this link must have access to the iNtuitionEMV Viewer in order to open the link.

Publish Series

When you publish a series, the series is automatically locked in the database for 60 days. The series can be accessed directly using the Web Administrative interface. For more information, see the *Aquarius Web Admin iNtuition Edition* manual.

View

Selecting the View option with the Series List brings up a sub-menu. You can choose whether to view the Series List in list form (the default), or view it in icon form:

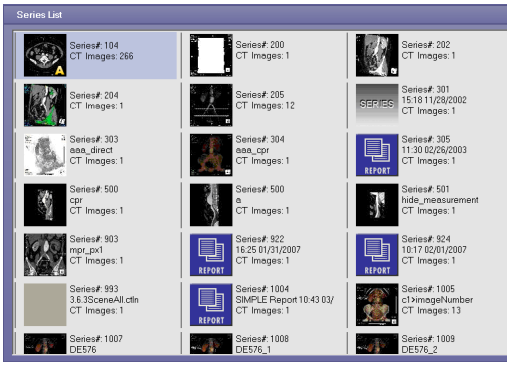


Figure 2-5: Icon View of Series List

Cancel Send

You can cancel a **Send to Dicom** that is in progress. The study being sent displays an icon in the left-most column (see figure at right), indicating that the transfer is still in progress.

1. Click the icon. A **Cancel** dialog is displayed.

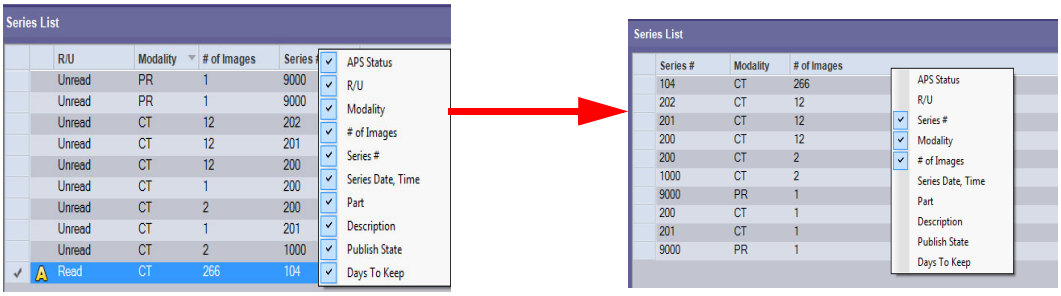
2. To cancel the send, click the **OK** button. The **Cancel** button will not cancel the send.

Note: Auto Selection of Series: Auto Select will work for CT, if you wish to configure your system to allow MRI, contact support to assist in this configuration change.

Customizing Series List Columns

You can customize which columns are visible/not visible two different ways.

1. By right-clicking the series list column header, you can select which columns you wish to be visible when viewing series options. For example, if you wish to only view the **Modality**, **# of images**, and the **Series #,** you can specify this as shown below:



2. You can also select which columns to be visible by going to **Preferences > Patient List > Series List > Available Series List Columns.** Here you can also re-order the arrangement of how these options appear in the Series List by using the click-drag method for additional customization

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Note: You cannot reorder the headers using the right-click method, you must go to the Preferences tab.

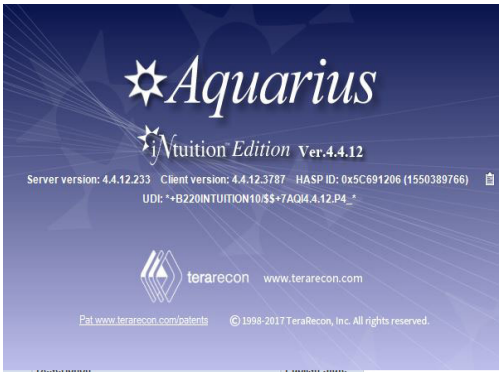
Top Bar Functions

The following section describes the functions of the buttons on the middle-to-right end of the top bar of the Aquarius iNtuition screen. For additional functioning, see"Chapter 3Top Toolbar Buttons" on page 3-143

CE Mark and About Screen

Right-click on the product name, and select either **CE Marking...** or **About...** to open the displays.

- The CE Marking display shows an image of the product label found on all TeraRecon equipment. You can also see this label on the inside of the cover page of this manual.
- The About display (pictured below) shows the current AquariusNet ThinClient Server version, the AQi Client version, the HASP ID number, and its Unique Device Identity (UDI) code. You will need this information when contacting TeraRecon customer support.



GoToMeeting

Prerequisites

In order to start a meeting using GoToMeeting, you must have the following:

- An active account with Citrix.
- The latest .NET Framework installed on the client computer where you are running AQi.

If you do not have the correct version of the .NET Framework installed, an error message is displayed when you click the GoToMeeting icon. To install the .NET Framework, do the following:

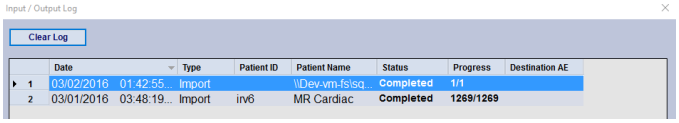
1. Use a search engine to find a download site for the .NET Framework.
2. Download and install the latest version on your computer.

To start a GoToMeeting conference session, click the GoToMeeting icon. In the **AqConferenceCenter** dialog, enter your Citrix **UserName** and **Password**. You can also enter a subject in the **Subject** text box (optional). Then click **Start** to begin the session.

Input-Output Log

The Input-Output Log monitors the transfer of data to or from other DICOM servers.

To open the log, click the log button, located in the upper-right corner of the Aquarius iNtuition screen. The Input-Output Log is displayed (see the following figure).



Preference

The Preference icon opens the Preference window for configuring the iNtuition GUI. For detailed information about preference settings, see Appendix A: "GUI Configuration". There are additional references to setting preferences in this window throughout this guide where applicable.

Online Help

The Online Help button opens the Online Help screen, from which you can obtain information about the User Interface, the workflows, various screens, and modules (see Figure 2-6).

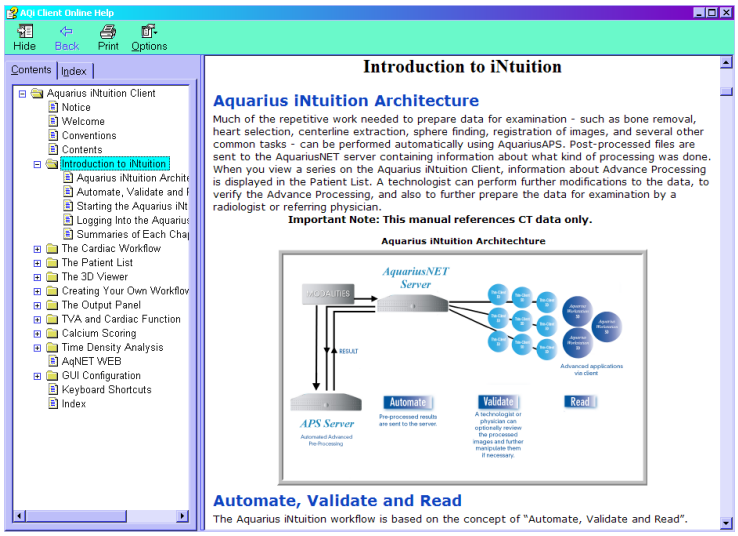


Figure 2-6: Online Help Screen

You can navigate around the Help system using the Contents list on the left. Each major topic can be opened to display lists of subtopics beneath it.

To display any of the topics in the main window click on the title in the Contents list.

Index

You can also search for Help topics using the Index tab.

- Double-click on any item in the Index list to display the topic in the main window.
- Type a word into the text box to search for that topic.

Switch User

This feature allows you to log out of AQi and log in as a different user. Once you have completed the login, the same data is loaded into the 3D Viewer.

Note: This feature is available only when the Aquarius iNtuition Client is launched from a command line. The Switch User icon is not visible when AQi is launched using the AQi icon on the desktop.

The **Switch User** icon appears on the top toolbar, just to the left of the **Input/Output Log** icon.

To log in as a different user, click the Switch User icon. The credentials dialog is opened, where you can enter the name and password of the new user.

When you click **OK**, you are automatically logged out of AQi, and then logged back in as the new user. The 3D Viewer is opened, loaded with the same data as before. However, the Patient List will not have access to any study on the server except the one that is currently loaded.

Data Management Tool Buttons

This panel is located on the left side of the screen, about halfway down from the top (see item **C** in Figure 2-1 on page 2-2).

Note: You can customize which Data Management functions are visible. See **Preferences > Patient List > Data Management** and select the functions you wish to see on the panel. Delete, DVD/CD, Send, Import, Export and Load are the default settings.

Delete

Delete the selected study or series. A confirmation dialog is displayed first; click OK to delete and Cancel to cancel deletion.

DVD/CD

Burn the selected study or series to a DVD or CD.

Send

Push the selected study or series to a DICOM server. For instructions on how to cancel a job once it has been sent, see "Cancel Send" on page 2-20.

You can add your own DICOM send button to the data management tool buttons. This will allow you to send DICOM files to single or multiple remote DICOM servers with a single click.

To add a user-defined DICOM send button, follow these steps:

1. Open the user preferences and select **General** -> **Remote Dicom Server** from the navigation panel on the left.
2. Click the **Enable Remote Dicom Server Preset** checkbox.
3. Click **Add preset button**. A dialog is opened for you to select a remote DICOM server.
4. Select one or more remote DICOM servers.
5. Enter the title you would like to be shown on the button into the **Button title** input box.
6. Choose where you want the preset buttons to be shown, by checking all appropriate checkboxes, and click **OK** to close the preference dialog.
7. In the **Remote Dicom Server** dialog, click **Preset buttons setting** to confirm that the preset buttons are displayed according to your configuration. A dialog (see Figure 2-7) is opened to show the current preset button configuration.

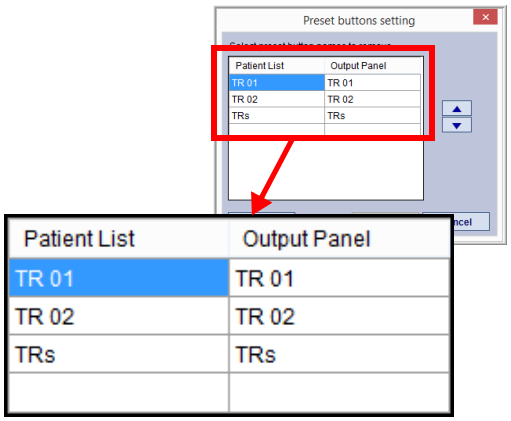


Figure 2-7: Preset Buttons Settings Dialog

Options

Access Privileges

- Private - The preset button settings apply to your account only.
- Group - Allows the preset buttons to be shown among users in the same user group. In this case, the other users in the group must also select the Group option to see the shared presets.

Preset buttons setting

Click the **Preset buttons setting** button to open the dialog. You can re-order the preset buttons using this dialog.

Select the preset button you want to move, and click the up or down arrow to move the button up or down, respectively, in the list. To delete the button, select the button and click **Delete**. To select multiple buttons, hold **Ctrl** and click on each one to select.

Note: If you want to hide the preset buttons without deleting them, you can disable the remote server preset feature by unchecking the **Enable Remote Dicom Server Preset** box. Configured preset button settings will remain, but the preset buttons will be hidden.

Import

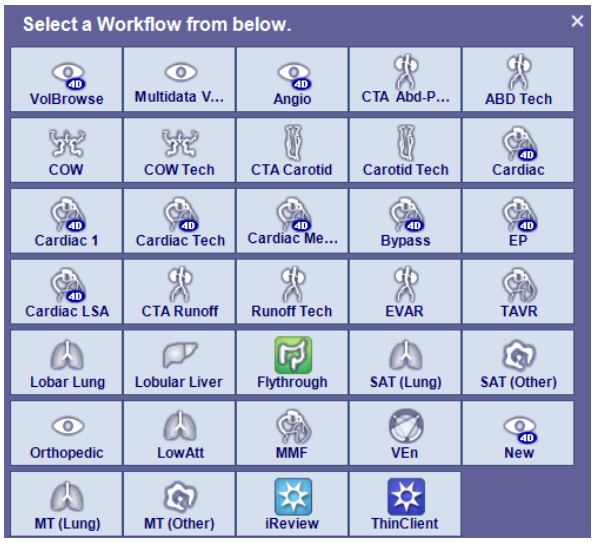
Import DICOM data from your server's hard drive or from the network. This is a drag-and-drop feature. Click on the study you wish to import, and then drag and drop it onto the Patient List.

Export  (localhost only)

Export data to the selected hard drive.

Load

Open the selected study or series. Selecting **Load** opens a set of templates for each workflow. You can then click the appropriate workflow to load the data.

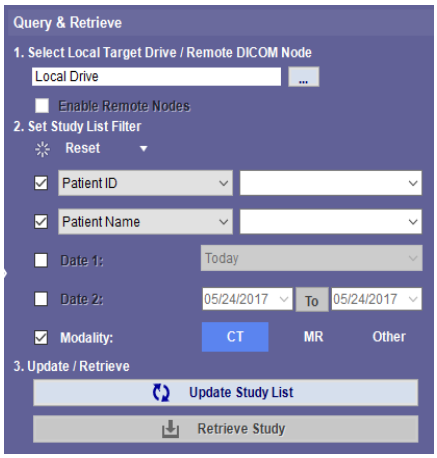


Multi-Data Workflow Selections

When multi-data studies are loaded, workflow templates for both modalities are displayed in the same menu, but on separate tabs, as shown below.

Filtering the Patient List

You can filter patient data to load by using the **Search** panel in the upper-right corner of the screen (shown below). You can query patients by ID, Name, Date, Modality or other criteria. You can also query remote DICOM devices.



Select Target

To target a DICOM server, or the hard drive on your local computer, do the following:

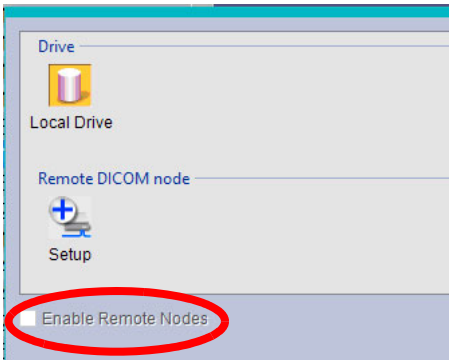
1. Open the pull-down menu located beneath "**1. Select Local Target Drive/Remote DICOM Node**"

Note: If clicking the pull-down menu does not open the select target node dialog (shown in the figure below), that means your user group does not have access to remote DICOM servers for query and retrieve. If this is something you require, contact your system administrator.

---

2. From the dialog that is displayed, select one or more servers to be searched.

   You can also enable remote nodes from this dialog. To do so, check the **Enable Remote Nodes** checkbox (circled):



   Click **OK** when done. Remote nodes are now enabled, and any remote nodes you have selected are listed in the searchable drives field of the filter panel.

Setting Up the Filter

To filter the patient database, perform the following:

1. Enter the node where you want to search.

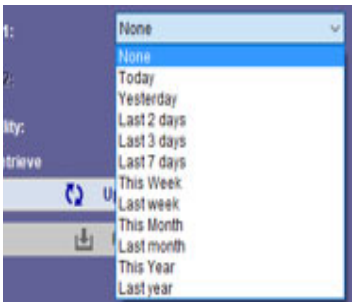
2. Enter up to two data fields from the pull-down menus, to narrow the search. The search fields available to choose from are Patient ID, Patient Name, Study ID, Accession Number, and Description, as shown in the figure at right:

3. Enter the date, to specify a single date or a period of scan. For example, if you are looking for a patient who has been scanned several times in the past 3 months, you can specify the start date and the end date, which narrows the search to studies occurring only between those dates.

   There are two different ways to specify a time period:

   - **Date 1**

     Date 1 specifies a **Time Period** dating back from the date of the search. For example, if you are looking for patient data that you know was scanned within the past 24 hours, you can select **Today** from the Time Period pull-down menu. The software will display the list of patients that were scanned in the last 24 hours.



   - **Date 2**

     Date 2 specifies a date range to narrow the search. To enter the starting date:

4. Click the down-arrow located to the right of the first date (circled in the figure below). A calendar image of the current month, day and year will appear.

5. If necessary, navigate to the required month, using the right and left arrows at the top of the calendar image.

6. Click on the start date.

7. To enter the end date, click the **To** button.

8. Repeat steps 1-3 for the end date.

After making changes to the filter you may use the drop down menu (next to reset button) to add new filter. The top three filter presets will display on the top of the search fields.

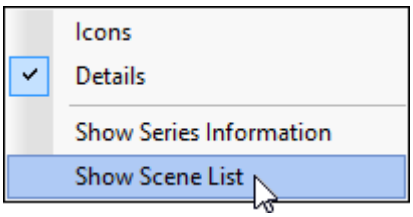
You can manage the filters using the same drop down menu, Manage Search Filter. Here you can delete or change order of the filter presets.

Update Patient List

When all search targets and criteria have been entered, click the **Update Study List** button to show only data meeting these criteria.

The Scene List

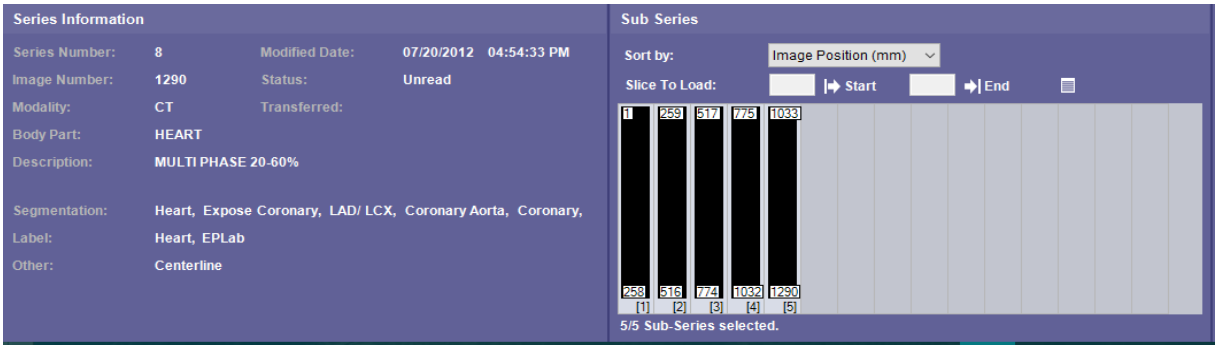
This panel is hidden by default, but can be displayed using the Series List pulldown menu (located in the upper-right corner of the Series List) and selecting **Show Scene List**.



The Series Information and Sub-Series Panels

These panels are located in the bottom-left and bottom-middle sections of the Patient List screen. If you do not see them (if, instead, all you can see is the Series List itself), you can display these panels by selecting **Show Series Information** from the Series List menu, located in the top-right corner of the Series List.

To display the menu, click on the down-arrow in upper-left corner of the **Series List**. This displays the **Series Information** and **Sub Series** panels:



The Series Information Panel

This panel is located in the lower-left corner of the Patient List screen. It contains the most frequently used information about the currently selected series. Much of the information in this panel can also be found in the Series List, but is grouped together here for your convenience. However, at the bottom of the panel there are three information fields not shown in the Series List, all of which pertain to Advanced Processing.

Advanced Processing Information

If Advanced Processing has been performed on this series, it is listed in this section. There are three subgroups:

- **Segmentation** - Any bone removal or CT table removal is listed here
- **Label** - Vessel labeling is listed here, by body part
- **Other** - Centerlines, spherical candidates and other processing are listed here

If AquariusAPS is not installed in your system or network, this section will not contain any values.

The Sub-Series Panel

The Sub-series Panel, located at the bottom of the Patient List screen, is a list of slice data information.

Sorting Options

- **Image Number** - You can combine sub-series data by selecting this menu item. This will allow you to load all the sub-series data into the same viewer.
- **Image Position** - When you select this item from the Sort-by menu, the list is sorted by the image position number. This is the default selection.

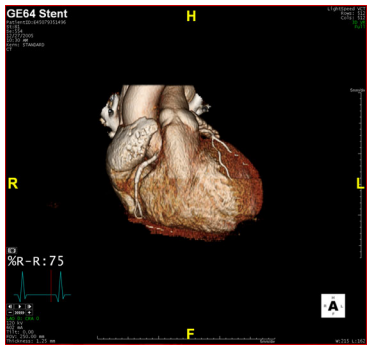
  When you sort by Image Position and then click the Slice Info tab at the top of the Sub-series Panel, you will see the slices sorted in order of position.

Note: They are sorted in reverse order.

- **Image Time** - The images are sorted in the order in which they were created (at scan time).
- **Every N Slices** - Displays one slice for every **N** that you specify. N can have a value from 2 to 5.
- **Preview** - Allows you to preview the selected series prior to loading.

Loading Sub Series

To load a sub-series, click the Sub-Series tab and right-click on the section or sections you want to see (see figure at right).



Selecting slice data to load

For situations where only some of the slice images in a series need to be examined, you can choose specific starting and ending slices to be loaded.

1. Click on the series you would like to review in the Series List.
2. Click the **Sub-Series** tab in the Sub-Series Panel.

3. Select the slice or range of slices to load from the range bars, right-click and select **Load Sub-Series** (see the previous image, shown at right).

Sending sub-Series to DICOM

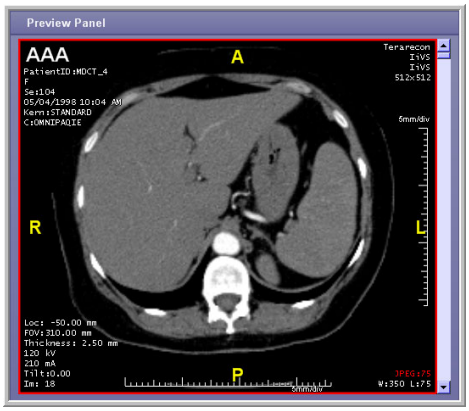
To send sub-series to DICOM, do the following:

1. Right-click on one or more sub-series and select Send to DICOM from the pop-up menu. A dialog box opens, for you to select a DICOM server.

2. Click **OK** to complete selection.

The Preview Panel

The Preview panel displays the axial images in the currently selected series. The Preview panel also displays annotation showing patient information and scan information. When you click on a series, the image is displayed in the Preview window. The annotation in the Preview panel displays the series date and series time. The series date and series time are also displayed in the main viewer. Use the scroll bar on the right to scroll through slice images.



To hide patient information in the annotation, use the Show/Hide Annotation menu. For details, see "Display Annotations Menu" on page 3-191.

The Quickview Window

The Quickview Window allows you more flexibility in how you can view the slice images that are in the Preview Panel.

To open the Quickview Window, do one of two things:

- Double-click on the Preview Panel

- Right-click on the Preview Panel and select **Show Quick View** from the pull-down menu.

The Quickview Window is opened. See Quickview Functions for a list of functions available in the Quickview window, along with a description for each.

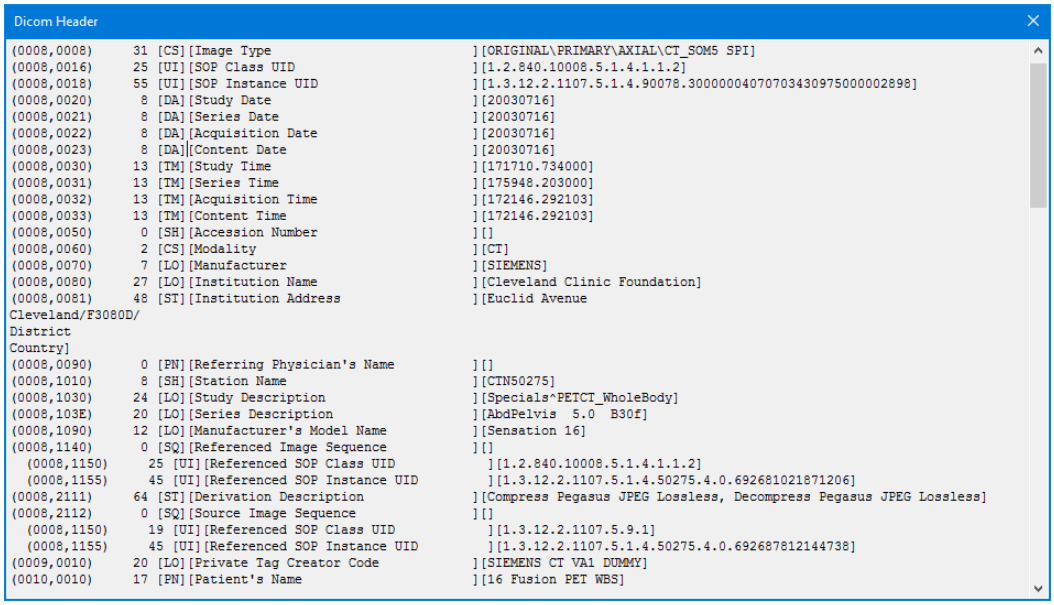
Quickview Functions

The following table shows the mouse or screen buttons used to perform various functions.

Function	Action Required
Scroll through the slices	Hold down left mouse button and drag mouse up or down.
Scroll without holding a button	Click middle mouse button (wheel) and then move up or down to control the direction and speed of the scrolling.
Zoom	Hold down middle mouse button and drag mouse up or down.
Pan	Hold down right mouse button and drag mouse up or down
Play batch cine of slices	Click the right-arrow located in the lower-left corner of the Quickview Window
Set the speed of cine	Use the minus (-) or plus (+) buttons to regulate the speed. (The right arrows in between indicate the speed currently set.)
View slice images in various window width/level modes	Use the preset window width and level buttons, located at the bottom of the screen.
Restore original zoom and pan locations	Right-click on image and select **Reset** from pull-down menu.
Exit Quickview Window	Either: Right-click on image and select **Hide Quick View** from pull-down menu; OR: Click the **X** box in the upper-right corner of the Quickview Window.

The DICOM Header

To display the DICOM header for the currently loaded series, right-click on the Preview Window, and select **DICOM Header**. The DICOM header is displayed.



Chapter 3 The 3D Viewer

Topics in this chapter:

This chapter describes the graphical user interface (GUI) of the Aquarius iNtuition 3D Viewer. The 3D Viewer screen GUI is divided into several areas, and each is described in a different section.

Opening the 3D Viewer

Select one or multiple series from the Patient List, and double-click the series, or click on the **Load** button. The image is loaded into the 3D Viewer and displayed as shown in Figure 3-1.

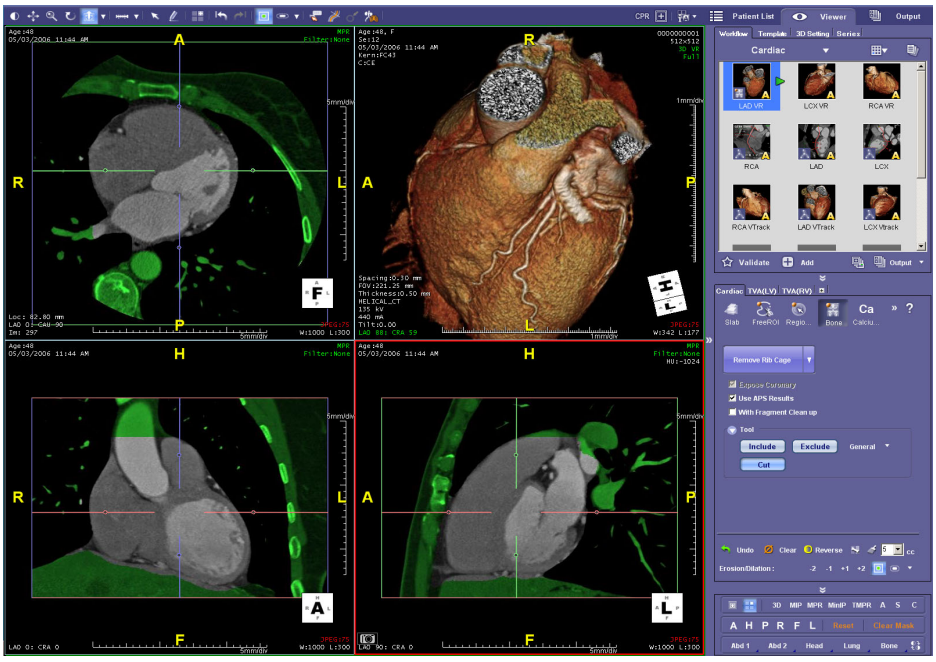
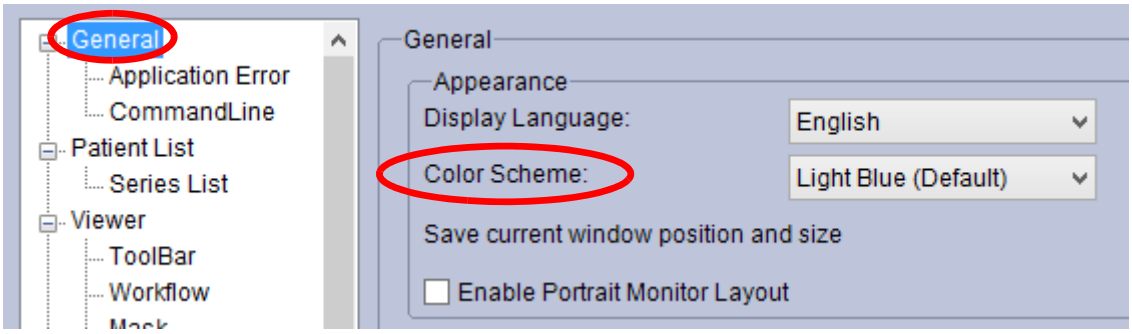


Figure 3-1: 3D Viewer

Portrait Layout

If you have a monitor configured for portrait mode display, you can also configure AQi for the portrait monitor layout.



Open the user preferences and click **General** in the navigation panel on the left. Then check the **Enable Portrait Monitor Layout** checkbox (see figure at right).

Note: This setting will not be applied until you restart AQi.

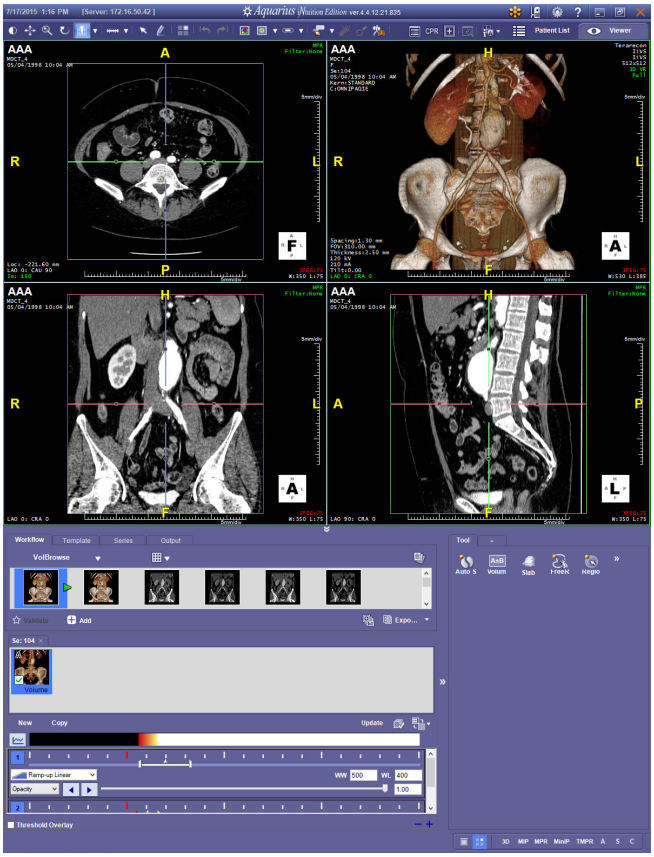


Figure 3-2: AQi Portrait Monitor Layout

Elements of the 3D Viewer Screen

The Main Window

The main window contains images rendered from the data that has been loaded. The typical main window display contains at least one 3D image and one or more 2D images. However, there are several different screen layouts and the one displayed depends on:

- The chosen image layout;
- The selected workflow; or,
- The diagnostic tool currently in use.

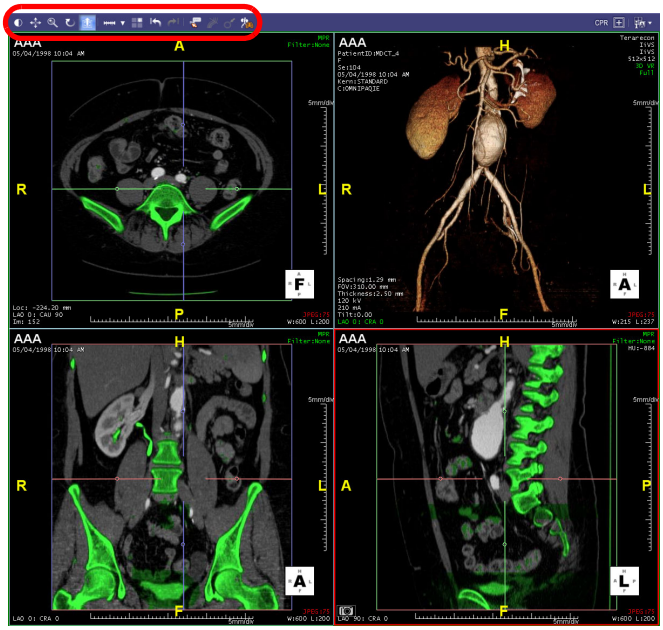
This is explained in greater detail later in this chapter. There are a number of tools available for manipulating images:

- Clinical tools

  These tools are accessed through the Tool Panel, which is discussed under "Clinical Tools" on page 3-21.

- Top toolbar functions

The toolbar located directly above the main window (circled in the figure below) contains several important tools for rotating, zooming (scaling) and panning an image, taking measurements, making notations, and several other functions. These are discussed under "Top Toolbar Buttons" on page 3-143.



- Right-click menu on the image

  When you right-click on an image, a pull-down menu is displayed showing a number of functions that can be performed on that image. The right-click menu is slightly different for 2D and 3D images. The table below lists each menu item, which type of image the feature is valid for (2D, 3D or both) and a description of the function.

Table 3.1: Menu Items and Image Features

Features	2D/3D	Description/Reference
Capture	Both	Capture the selected image.
Capture All	Both	Capture all images currently displayed in the viewer, and place each image in a separate cell of the Output Panel.
Capture All in One	Both	Capture all images currently displayed in the viewer, and place them all in a single cell of the Output Panel.
Capture to Folder	Both	Capture to a folder defined in the Capture preferences.
Capture to Clipboard	Both	Capture the image to the MS Windows clipboard. The image can then be pasted to another application, such as Word.
Batch Wizard	Both	See "The Batch Wizard" on page 3-75 for details.
Arrow/Text	Both	See "Arrows and Labels" on page 3-175 for details.
Rendering Modes	Both	These allow you to change the rendering mode of the image.
CPR	Both	Allows you to select a vessel and view it in CPR mode. See "The CPR Tool" on page 3-26 for details.

Features	2D/3D	Description/Reference
Segmentation	Both	Opens a sub-menu from which you can select one of the following segmentation tools: "Dynamic Region Growing" on page 3-53 "FreeROI" on page 3-49 "Bone Removal" on page 3-59
Measurement	Both	See "Measurement Tools" on page 3-146 for details.
Enable Measurement Tracking	Both	Allow measurements to be saved, tracked and viewed in the Finding Viewer. Measurement tracking is an optional feature. See Chapter 16: "The Findings Workflow" for details.
Show Magnifier	Both	Allows you to zoom into the area that you are examining, must be enabled in preferences.
Mouse Mode	Both	See "Magnifier Tool" on page 3-143 for details.
Layout	Both	See "Window Layout Modes" on page 3-179 for details.
Active FOV	Both	Left click on active annotation to change FOV or use preset. Note: Presets can be customized.
Smooth Surface	3D	Smooths out surfaces of image
Slab	3D	Display the 3D image in slab view. This menu item has the same effect as checking the Slab checkbox in the Slab tool panel. See "Slab and Cube View Tool" on page 3-22 or "Slab Thickness" on page 3-197.
Cube View	3D	Display the 3D image in cube view. This menu item has the same effect as checking the Cube checkbox in the Slab tool panel. For more information, see "Slab and Cube View Tool" on page 3-22.
Reset Orientation	3D	Reset the orientation of the 3D image to the orientation at load time.
Save Scene	3D	Save the 3D image as a scene. For details, see "Saving a Scene" on page 3-190.
Light Setting	3D	
Background color	3D	Changes the background color of the 3D image (default is black).
2D Filter	2D	Select one of the following filters to apply to any 2D image: • Median • Gaussian • Blur • Sharpen • iGENTLE Select **Filter Strength** to apply a strength from 1 to 5 on any filter.
Link to 3D	2D	When rotating the 3D image, perform the same rotation to the MPR images automatically. This also works in reverse and will rotate the 3D image if one of the MPR images is rotated.
Link the center of rotation	2D	All images rotate about the same location as their center.
Reset	2D	Reset the orientation to the original.

- Right-click menu on the crosshair

  Hover the mouse over the crosshair (also referred to as the cross-cursor) in any 2D image. The cursor changes to a double-arrow:

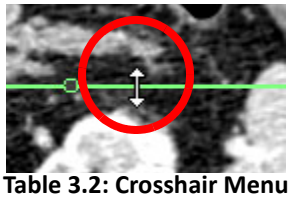


Table 3.2: Crosshair Menu

A menu is opened that contains the items listed in Table.

Table 3.3: Menu Items

Item	Description/Reference
Lock on the cross hair by 90 degree	When checked, the crosshairs are always perpendicular regardless of rotation angle. When not checked, one crosshair can move independently of the other. See Figure 3-3 below.
Reset	Reset the image slice to display the slice that is shown when the study is loaded, and place the crosshairs over the center of the image.
Re-center MPR crosshairs	If crosshairs are not centered in the image window, move them so that their intersection point is at the center of the window. If the crosshairs are already centered but the image has been panned, move the image back to the center of the window.
Hide	Hide the crosshair. To redisplay the crosshairs, right-click on the image window and select **Show cross hair**.
Create 3 Landmarks for Double-Oblique	Define an oblique plane on a 2D image. See "Create Three Landmarks for Double-Oblique" on page 3-195 for instructions.
Lock This Plane	Prevent the image in this view from being rotated.

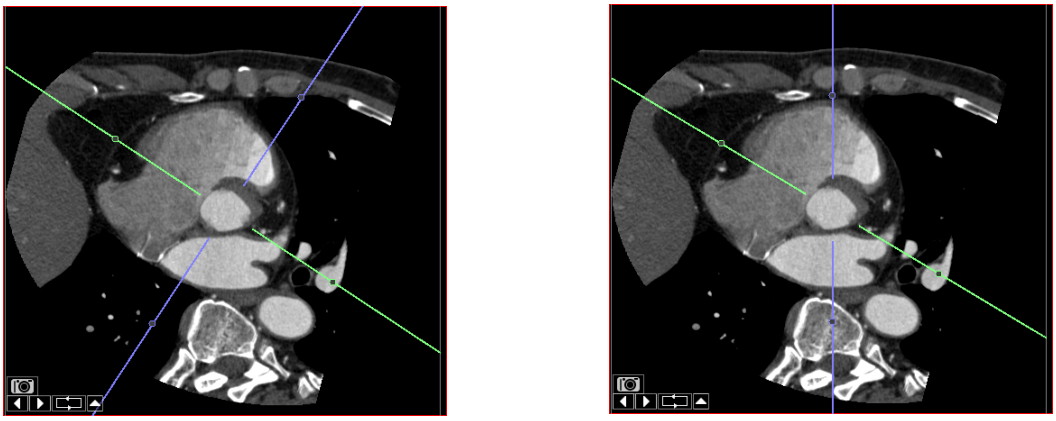


Figure 3-3: Left - Crosshairs Locked at 90 Degrees; Right - Unlocked

The Workflow Tabs

The workflow panel is in the upper-right section of the 3D Viewer screen. There are five tabs at the top of the panel, each contain a separate sub-screen: **Workflow**, **Template**, **3D Setting**, **Series** and **M/A**:

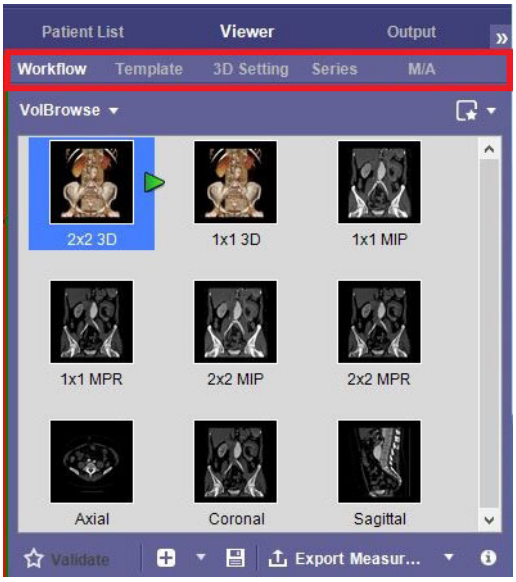


Figure 3-4 The Tabs in the Workflow Panel

These tabs are available dependent on the selected Workflow.

To view each of the screens located in this area of the 3D Viewer, click the appropriate tab. These screens are described in greater detail in the following sections:

- **Workflow** - Chapter 4: "Workflows"
- **Template** - "Workflows and Templates" on page 4-3
- **3D Settings** - "3D Settings Tab" on page 3-10
- **Series** - "Series Tab" on page 3-14
- **M/A -** "Measurement/Annotation Tab" on page 3-15

Template Tab

Aquarius iNtuition provides a set of templates containing color and window level information that can be applied to the currently loaded study data. They modify the 3D image display so that it is easier to see and examine the relevant ROI. You can access templates by clicking on the **Template** tab at the top of the upper-right panel (circled in the figure at right).

For example, if you have loaded a lung study into the 3D Viewer, you will see that the lung tissue is not visible. The lung template changes the color and window level settings so that the lungs become visible. To apply the template to the data, click the **Lung** template icon in the **Template** panel.

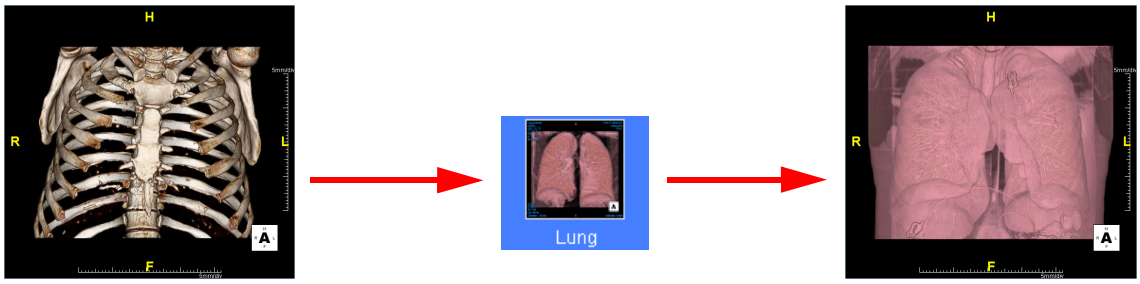


Figure 3-5: Left: Lung Data as Loaded; Center: Lung Template; Right: Template Applied

Adding a Template

You can create templates and add them to existing categories.

1. Click the **Add** button, which is located at the bottom of the template panel. A dialog is opened.
2. Enter a name for the template in the dialog and click **OK**.

Any changes in the color settings or window/level made prior to creating the template are saved in the template. Those changes can then be applied to any 3D image.

The new template is added to the category that is currently showing, referred to as the **current category**. (Template categories are discussed in the next section.)

Deleting a Template

To delete a template, first make sure it is selected (see the following figure) and then click the **X** button next to the **Add** button.

For details on changing the 3D color settings, see "3D Settings Tab" on page 3-10.

Template Categories

Template categories are groupings of templates that have a related function. For example, one of the the default categories is Flythrough. All of the templates in this category are designed to show images of the colon in the most effective way.

Selecting a Category

To select another category, select the category button located at the top of the template panel to open a pulldown menu. Category selections are listed in the top portion of the menu, above the horizontal line.

Creating a New Template Category

You can also create your own template categories, tailored to your specific needs. To add a category, select **Add New Category** from the menu. This opens a dialog box where you can enter the name of the category.

The empty category is shown in the template panel. You can now add templates to the category, as described in "Adding a Template" on page 3-8.

To delete a category (including any of the default categories provided by TeraRecon), select **Delete Current Category** from the menu, and click **OK** in the confirmation dialog.

CAUTION! When you delete a category, all templates belonging to that category are also permanently deleted.

Importing and Exporting Template Categories

Use the Export function to save template categories on the local hard drive, or on any storage device that is accessible to the Windows file system. The Import function allows you to add a template category stored on a computer storage device to the Template panel.

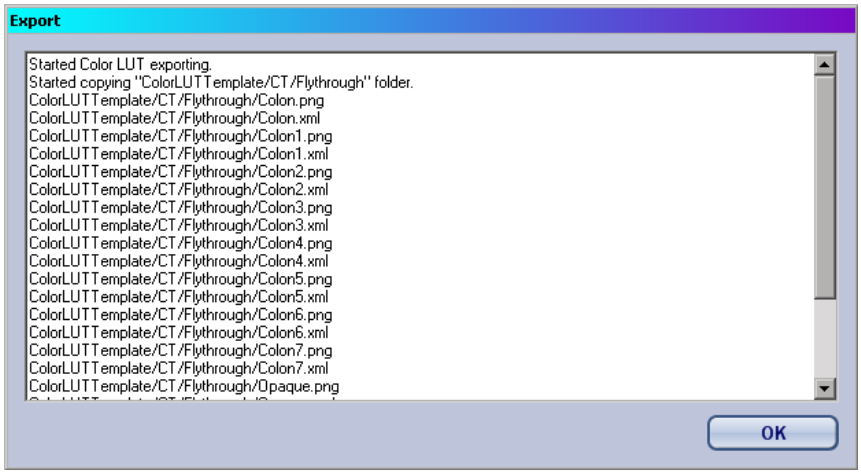
Export Current Category

The Export function saves the current category and all of its templates in a single folder. To export a template, do the following:

1. Click the category name at the top of the Template panel to display the pulldown menu.
2. Select **Export Current Category** from the menu. A Windows navigation dialog is opened.
3. Navigate to the folder where you want to store the templates.

Note: This folder must be empty. Only one category can be stored in a folder at one time. To export two or more categories, you will need to create folders for each of them.

4. Click **OK**. The **Export** status window shows a list of the files that were exported. Click **OK** again to close the status window.



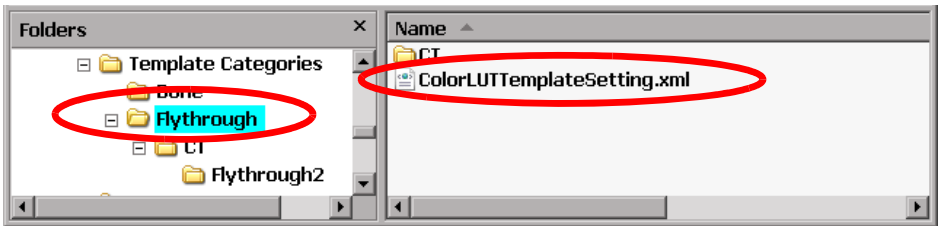
The template files are stored as XML documents, along with the icon images for each template. The category structure can be seen in the Folders panel below.

Import Category

To import a category that is stored on your computer or other local storage, select **Import Category** from the pulldown menu. A dialog is opened so that you can navigate to the folder where the category is stored.

Navigate to the folder that contains the file `ColorLUTTemplateSetting.xml`. This is not the folder that contains the template files, but is actually two levels above in the file structure.

Please see the following screenshot, of the Windows folder where template categories are stored. In this image, the **Flythrough2** folder contains the templates, but the **Flythrough** folder (highlighted in the image) is the one you need to navigate to. All template categories are similarly structured.



Click **Add** in the Import Color LUT Template dialog. The pathname of the folder is shown in the right panel. You can import multiple template category folders at the same time.

Click **OK** when you are ready to import.

3D Settings Tab

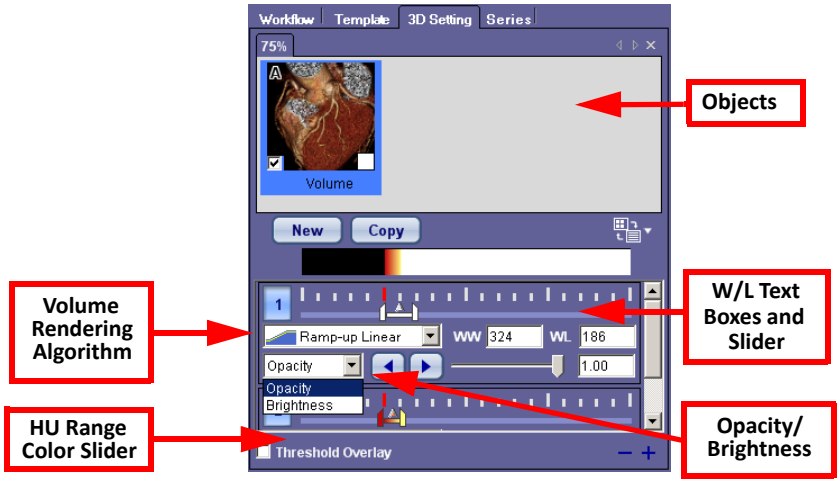


Figure 3-6: 3D Settings on Image Having Bone and CT Table Removed

The **3D Setting** tab, located in the upper-right corner (next to Workflow), allows you to adjust a 3D image for better viewing of critical sections under examination. You can adjust the opacity, window level, window width and rendering algorithm of the image. (See Figure 3-6.)

Objects represent different segments of the image, depending on whether mask operations have been performed.

For example, if bone has been removed from the 3D image, two objects are displayed in the 3D Setting area. One represents the main image in its current state (having the bone removed). The second object represents just the bone that has been removed.

If you then remove the CT table from the image, a third object is displayed. The first object represents the main 3D image in its current state (having neither bone nor CT table included), the second object represents the bone that has been removed, and the third represents the CT table that has been removed.

When you click on one of these objects, the image corresponding to it is displayed in the 3D window. If you check the box next to any object, the image in the 3D window shows pixels from both objects, superimposed. This way, you can temporarily re-display bone, if necessary, without needing to add and then remove it from the image. If you wanted to see only bone, for example, you would uncheck all the objects except the “Bone” object.

Configuring 3D settings

Table 3.4: 3D Icons and Functions

Icon	Function
W/L Slider	Slide this bar to set the new HU value or drag either end of this bar to adjust the HU range.
W/L Input Boxes	Enter the value directly to set the desired HU value.
VR Pull-down Menu	Select the volume-rendering algorithm for optimal 3D visualization.
Opacity Slider	Slide the slider bar to adjust the level of opacity of the object.
Opacity Input Box	Enter the direct value to adjust the level of opacity of the object.
Brightness Slider	Slide the slider bar to adjust the level of brightness of the object.
Brightness Input Box	Enter the direct value to adjust the level of brightness of the object.
HU Range Color Slider	Slide the slider bar to display portions of the image within different HU ranges.

Changing the Color

To change the color, perform the following:

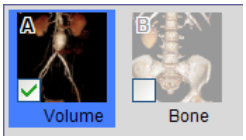
1. In the color slider bar, right-click one end of the slider (see image at right). A pull-down menu is displayed.
2. Select **Change Color**. This opens the Windows color palette .
3. Select a color from the color palette. You can also define a custom color. Click **OK** when done.
4. If desired, change the color of the other end of the slider bar. You can choose the same color for the other end, or a different color to create a blend.

   The colors on the image now reflect the new range of colors, as you slide the slider back and forth to display parts of the image having different HU values.

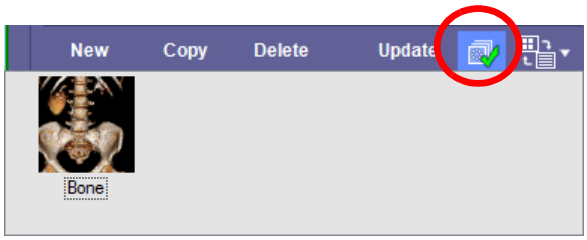
Excluded Masks

This feature allows you to create masks of unnecessary parts and register them as excluded masks. This means that if you perform other masking operations on an image, and then clear or reverse the masks, the excluded masks will not reappear.

1. Remove an unnecessary part, such as the bone. This creates a mask in the 3D Settings panel.

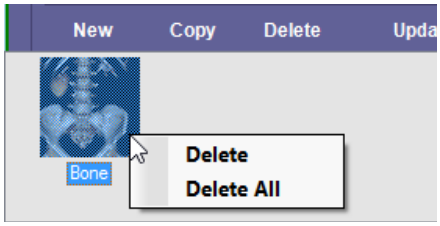


2. Right-click on the new mask and select **Register as Excluded Mask**. This mask now appears in the excluded mask panel. When there is at least one mask in the excluded mask panel, the checkmark on the excluded mask icon is highlighted in green (circled in the following figure). Click the icon to view the excluded mask panel.



3. Perform other segmentation tasks. If you need to clear or reverse the mask at any time, the excluded parts are not restored to the image.

An excluded mask will never be restored during a clear or reverse mask, as long as the mask remains on the excluded mask panel.



To remove an excluded mask from the panel, right-click on it and select **Delete** or **Delete All**.

Exporting a 3D Mask as a Mesh

You can output any 3D mask as a mesh to local storage.

IMPORTANT: This feature will export the boundary of the mask overlay, not the 3D VR image.

Note: Segment the object first before exporting. It is recommended that you use Region Grow as a segmentation tool. See "Dynamic Region Growing" on page 3-53 for instructions.

The following output file formats are available:

- STL
- Stanford Polygon
- Alias Wavefront
- AutoCAD DXF
- OpenInventor ASCII
- XML
- 3D Points XYZ

These files can be imported into compatible CAD and other 3D modeling software, as well as into 3D printers.

To start the exporting process, right-click on the desired 3D mask and select **Export as Mesh** (see Figure 3-7).

The **Export as Mesh** dialog is opened:

Figure 3-7Exporting as a Mask

- Filename

  a. Click the browse button (circled in the previous figure) to open a Windows navigation dialog.

  b. Navigate to the desired folder.

  c. Enter the name of the output file.

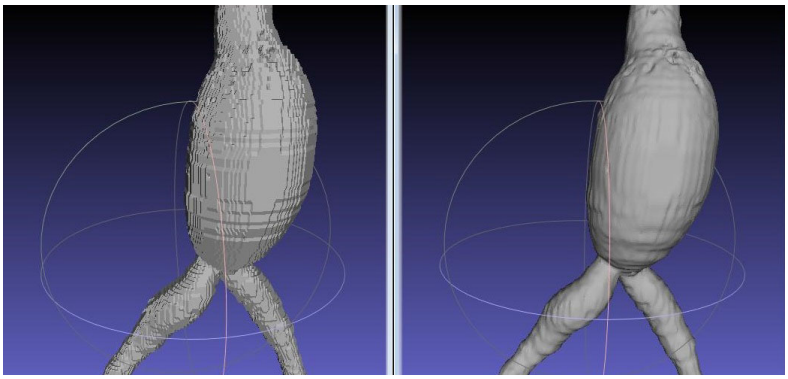
  d. Select a file format from the **Save as type** list.

  e. Click **Save**.

  The Windows dialog is closed and the full path filename is shown in the filename box.

- Smoothness

  Smooths out the polygon mesh surface by iterative calculations. A setting of 0% (the default value) means that no smoothing is applied. (See the following figure.)



Note: Increasing the smoothness will require more processing time to obtain the results.

- Decimate

  Polygon mesh decimation attempts to reduce the number of polygons on the final mesh. A setting of 100% (the default value) means that no decimation is applied. Decreasing the number might reduce the file size, and might affect the mask geometry.

When the file export is completed, the output file will reside in the designated folder.

Series Tab

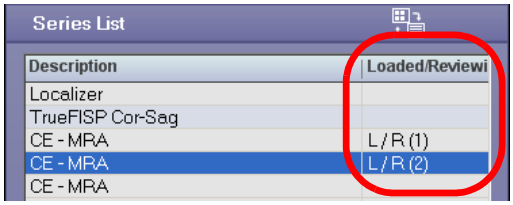
The **Series** tab is located in the Workflow panel, to the right of the **3D Settings** tab.

If a study has more than one series, or if you select multiple studies, the **Series** tab allows you to load and view several series at one time, from within the 3D Viewer.

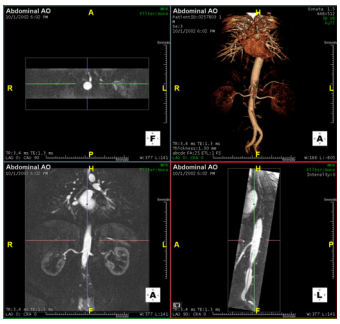
For example, suppose you load only one series out of several that are part of a study:

The **Series** tab allows you to load and view other series at the same time from the viewer, without any need to go back to the Patient List.

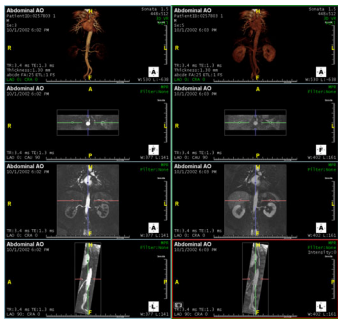
You can see which series is loaded in which column by scrolling the Series tab to the right, to see the **Loaded/ Reviewing** column:



A new viewer opens in a second column, displaying the second series:



One series loaded



Multiple series loaded

Figure 3-8: Loading Series

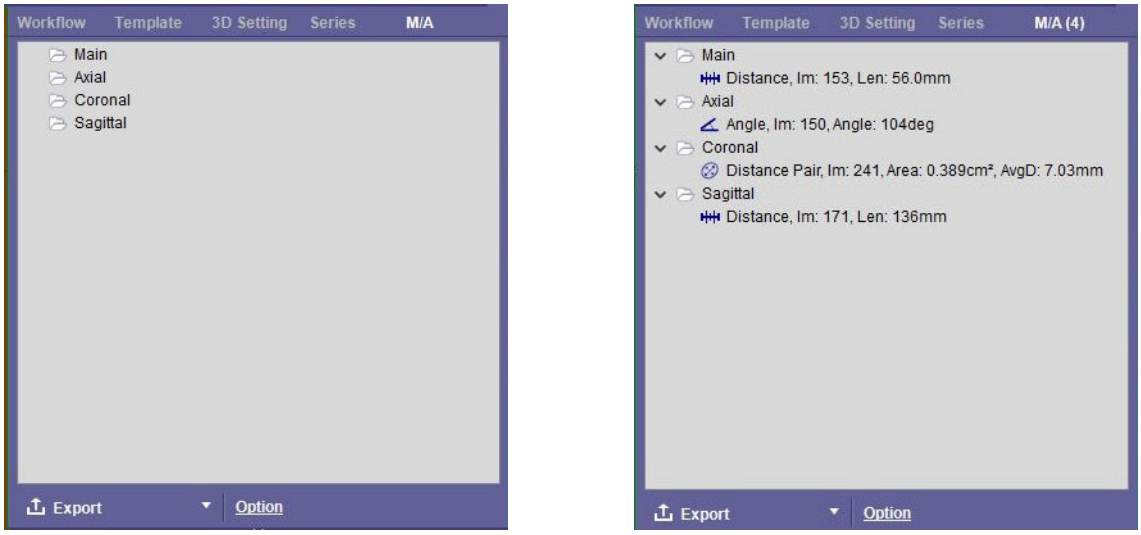
Right-Click Menu Options

When you right-click on any series listed in the Series tab, a pull-down menu is displayed, offering you other options:

- Show this series on new viewer - Opens a new viewing column in the main window to display the selected series.
- Load series - If the series has not been loaded, this item is activated so you can load it into the viewer.
- Switch to this series - Displays this series in the selected viewer column.
- Release this series - Unloads the series.
- Close the viewer - Closes the viewing column.

Measurement/Annotation Tab

The M/A tab is generally the last tab (farthest to the right) in the Workflow Panel, dependent on which workflow you choose. This tab displays any measurements and annotations you may have added to a series. (Figure 3-9)



Without Measurements **After Measurements are Taken**

Figure 3-9 Folders in the M/A Tab

When you use any of the Measurement tools under the measurement icon, or from the context menu, it is saved in the M/A panel under the type of image viewed.

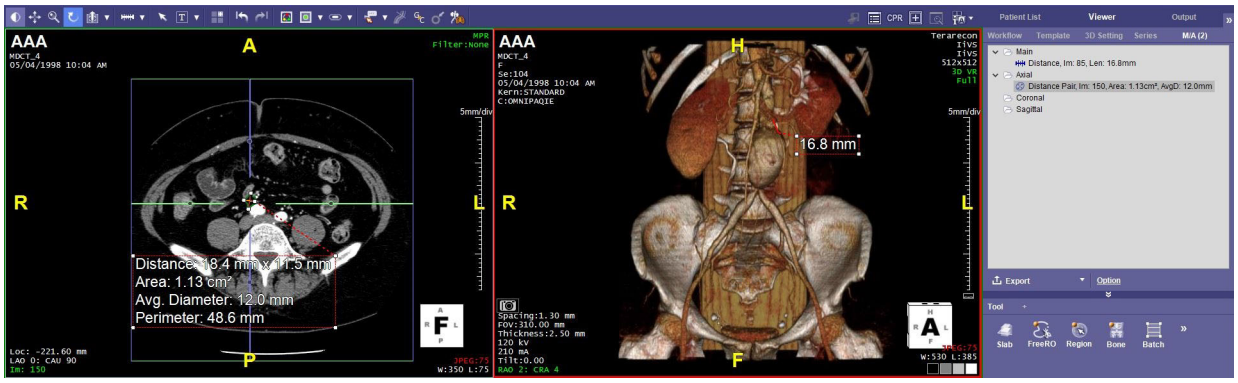


Figure 3-10 M/A Tab with Associated Measurements

The list is interactive. By clicking on the annotation or measurement, the selected viewer displays the corresponding slice location.

Export and Capture Options

On the bottom of the M/A tab panel are additional tools. Some additional options and settings are available in the Preference window or from the RMB-click context menu.

The Option tool lets the user select capturing configurations. With this tool, you can Export with images, Capture One or Capture All, or select from the Capture Options drop-down menu. You can set these selections as the Default setting.

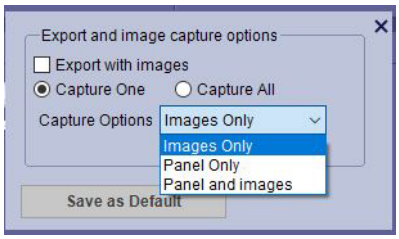


Figure 3-11 Option Tool and Capture Options

If you set these options to Panel Only or Panel and Images, The Export option allows you to export measurements, annotations, and/or images to a folder, to the Output Panel, to the series list in the Patient List page, or to both the Output Panel and Patient List.

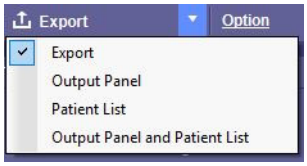


Figure 3-12 Export Choices

Selecting Panel and images in the Option tool and then Exporting to the Output Panel, you will see the M/A table of measurements and the corresponding images.

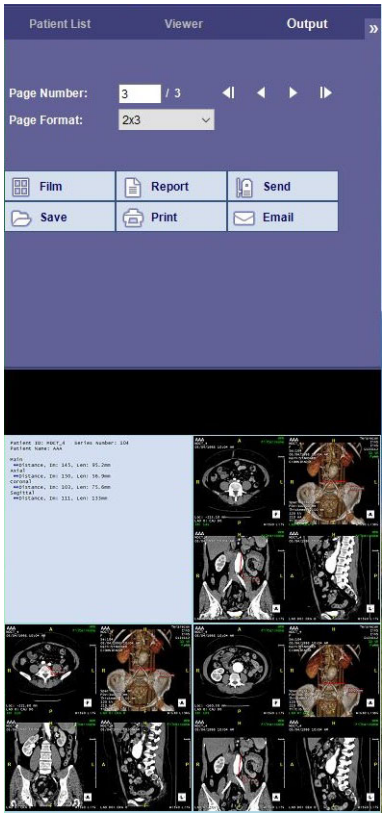


Figure 3-13 The M/A table and Corresponding Images in the Output Panel

You can save this information in several formats when you export. The information can be saved as .csv file as either single row or tabular form, as an .xml file, and as a plain text file. (Figure 3-14)

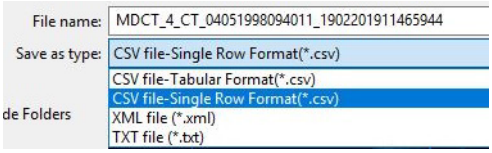


Figure 3-14 Export Formats

If you export to a .csv file in Single Row Format you see each measurement listed along one row in an Excel file (you might save this to a Excel workbook as well). (Figure 3-15)

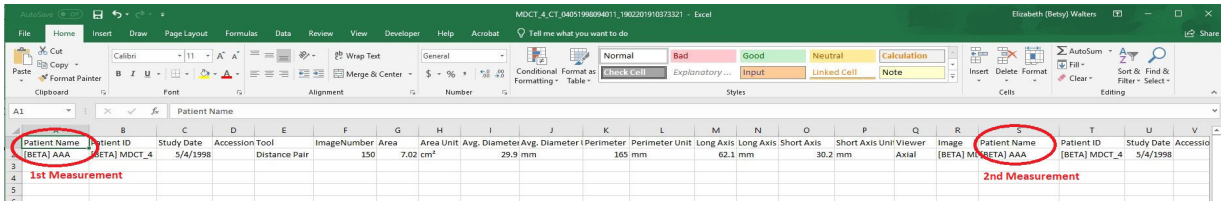


Figure 3-15 Exported Single Row Format

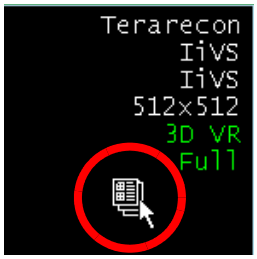
Floating the Workflow Panel

You can detach any of the tabs in the workflow panel so that it can be moved to another part of the 3D Viewer screen. This is called a “floating” panel. This would make it possible to see more than one tab in the workflow panel. When the panel is floating it can also be resized. This is useful when you need more room in the panel.

To float a panel:

1. Click on the tab name and hold down the mouse button.

2. Drag the mouse to another location on the screen. A small panel icon is displayed to indicate that the tab is being moved:



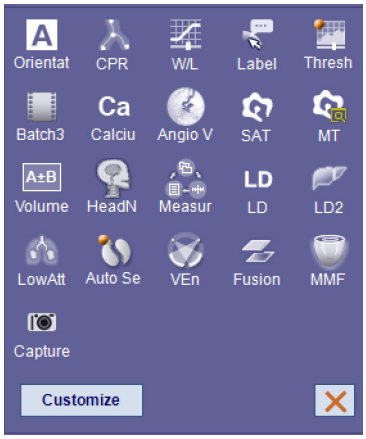
3. Release the mouse. The panel is now separated from its usual location in the upper-right corner.

You can now resize the panel and place it anywhere on the screen. To restore the panel to the workflow control panel, click the **X** in the upper-right corner of the floating panel, to close it.

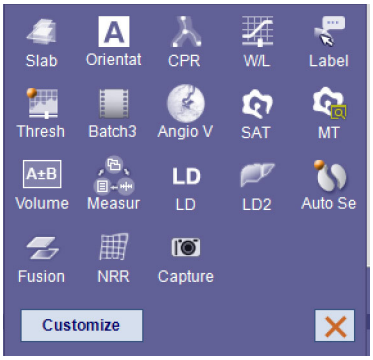
The Tool Panel

The tool panel contains the tools for viewing data and performing diagnostic tasks. It is located on the right, lower side of the 3D Viewer screen. The specific functions contained in the tool panel that you see when a study is loaded depend on which workflow was chosen to process the data.

The tool panel contains one or more tabs, each of which contains five visible tool icons and additional hidden tools. Figure 3-16 displays tool panels associated with the file type.



CT Tool Panel



MR Tool Panel

Figure 3-16: The Workflow-related Tools

To access additional tools in the hidden tool panel:

1. LMB-click the double right arrow located on the right side of the Tool Panel. (Figure 3-17) A second panel is opened above the main tab, containing the available tools that are hidden.

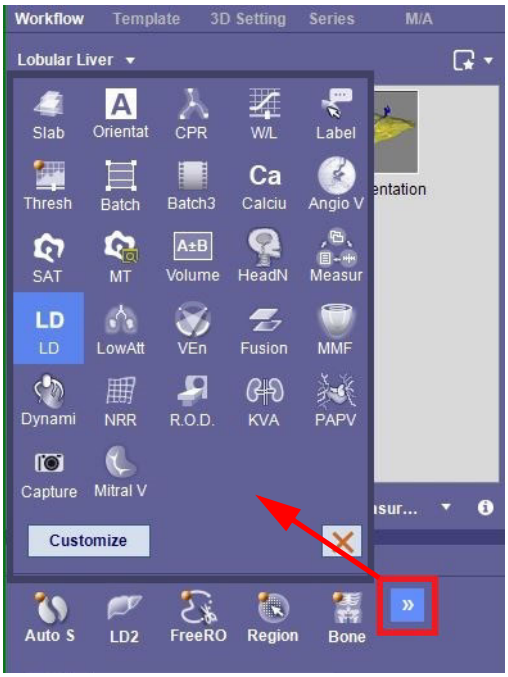


Figure 3-17: Hidden Tool Panel

You can select any of the hidden tools and drag them into the visible tool bar. The maximum number of visible tools is 5. Any additional tool added to the tool bar pushes the last tool up into the hidden tool panel.

To change the visible tools:

1. LMB-click the **Customize** button in the lower-left corner. (Figure 3-17)

2. LMB-drag the desired tool from the upper panel and position it on the visible tool bar. See Note below for more information.

Note: The maximum number of tool icons that can be showing at once is five. If you drag a sixth icon to the tab, the right-most icon in the tab is automatically moved up to the hidden panel.

---

3. Close the hidden panel by selecting the X in the lower right corner or move your mouse out of the panel.

For information on more ways to customize the Tool Panel, see "Customizing the Tool Panel" on page 3-141.

4D Workflow Hidden Tool Panel

Some tools are available only for 4D data. The hidden tool panel displays tools specific to 4D workflows.

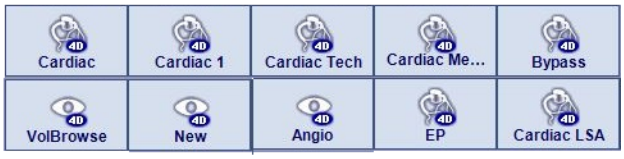


Figure 3-18 Example of Available 4D Workflows

The **NRR** tool is available in the hidden tool panel for this type of workflow data.

Selecting NRR opens a tool panel for register options for multiphasic data.

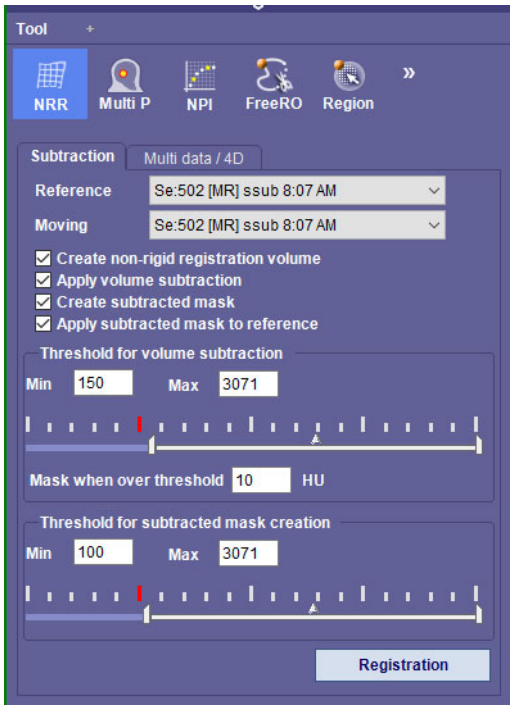


Figure 3-19 NRR Tool Panel with Subtraction Tab

The **Subtraction** tab provides registration settings including create non-rigid registration volume, apply volume subtraction, create subtracted mask, and apply subtracted mask to reference. It also has settings

for volume subtraction and subtracted mask creation thresholds. The **Multi data /4D** tab (Figure 3-20) allows you to select a reference data and moving data as well as the option to create a 4D Viewer.

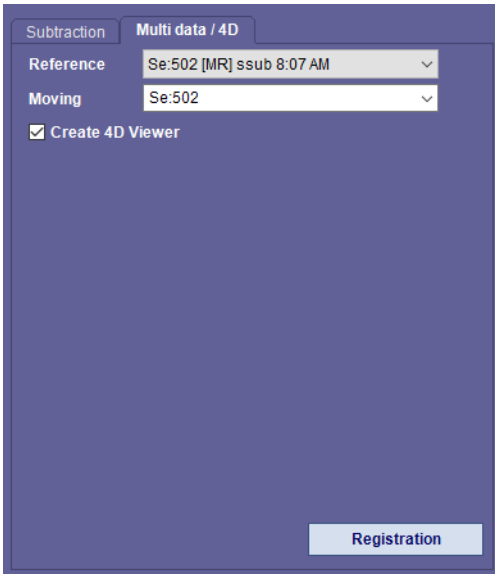


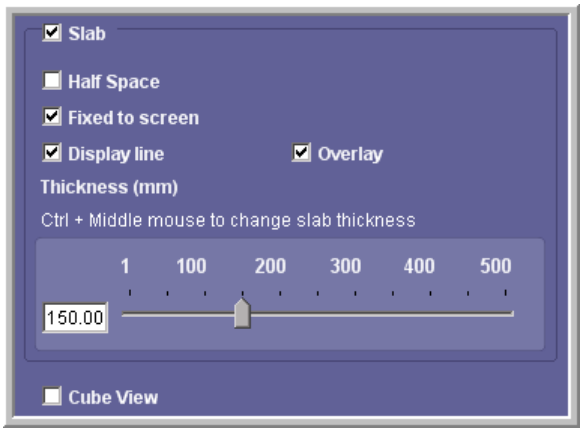
Figure 3-20 Multi data / 4D Tab

Clinical Tools

This section describes all the tools used to perform clinical and diagnostic functions in the 3D Viewer. To find the section you need, turn to the page listed below. If you are viewing this manual online, click the desired title:

Slab and Cube View Tool 

Click the **Slab** button from the tool panel. The Slab tool opens in the tool panel (see figure at right).



Settings

- **Slab** - Check this box to apply slab rendering.
- **Half Space** - Check this box to remove half of the volume on one side of the center of rotation.
- **Fixed to screen** - When this is checked, the cutplane is always parallel to the screen, and the rotations of the 3D image are linked to the rotations of the MPR images. When it is unchecked, the cutplane can be rotated to any orientation and does not necessarily face the screen. Rotations of the 3D image are not reflected in the MPR images. (See "Rotation" on page 3-24 for more information.)

- **Display line** - Show display lines (yellow) on MPR images. These lines delineate the slab boundaries. As you move them closer together (toward the center line), the slab thickness decreases. When the two outer lines are far enough apart that the entire MPR image is between them, the 3D window displays the full volume (see Figure 3-21 on page 3-23). The slider in the tool panel changes as you move the display lines closer or further apart.

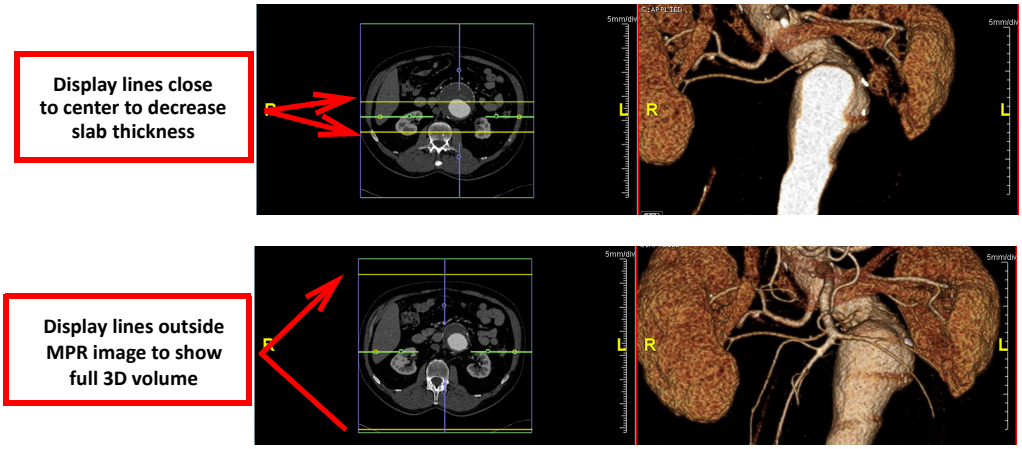
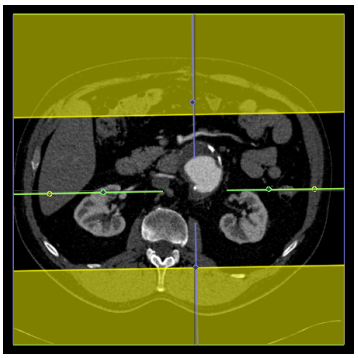


Figure 3-21: Moving Yellow Lines Apart Increases Slab Thickness in 3D Image

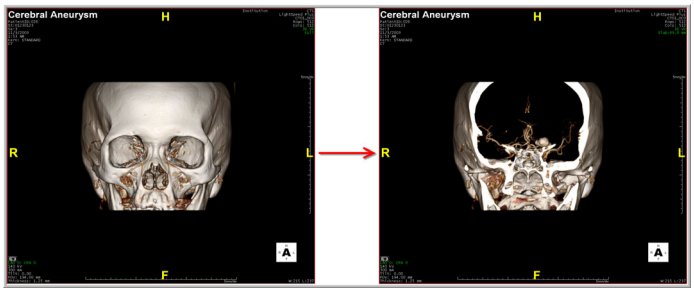
To move the display lines apart, click on one of the lines and move it away from the center. The other display line moves away from the center symmetrically. When you move the line toward the center, the other line comes toward the center from the other side. The cursor is circled in the figure below:

- **Overlay** - When checked, an overlay is shown on the parts of an image that have been cut out (see figure below).



- **The Slider** - Adjust the thickness of the slab using the slider in the control box, or by holding down the control (**Ctrl**) key and the middle mouse button, and then dragging the mouse up or down. The slider unit is in millimeters.

Note: When Half Space is selected, the slider is inactive.



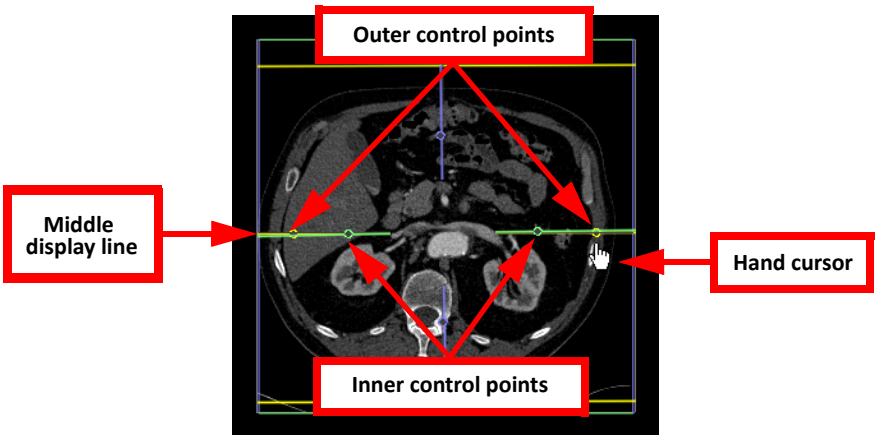
- **Cube View** - Check this box to display the image in cube view. To zoom in or out, hold down **Ctrl** key and the middle mouse button, and then drag the mouse up or down.

Rotation

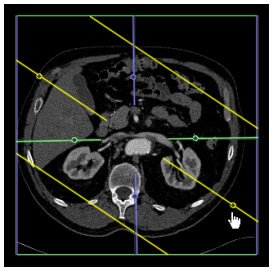
You can rotate the slab mask around the 3D image so that the only visible part of the volume is the section intersected by the rotating mask. The mask is rotated by manipulating the display lines in any of the MPR windows.

1. Make sure the **Display Line** box in the tool panel is checked.

2. Hover the mouse near one of the *outer* control points on the middle yellow line until the cursor is displayed as a pointing hand. See the following image:



3. When the cursor becomes a hand, left-click and drag the mouse up or down. The three display lines will rotate around the image in parallel.



As the slab region is rotated around the MPR image, a slab volume mask is rotated in the same direction around the 3D image. This is the most obvious when the MPR image being used to move the display lines is in the same orientation as the 3D image. (Figure 3-22)

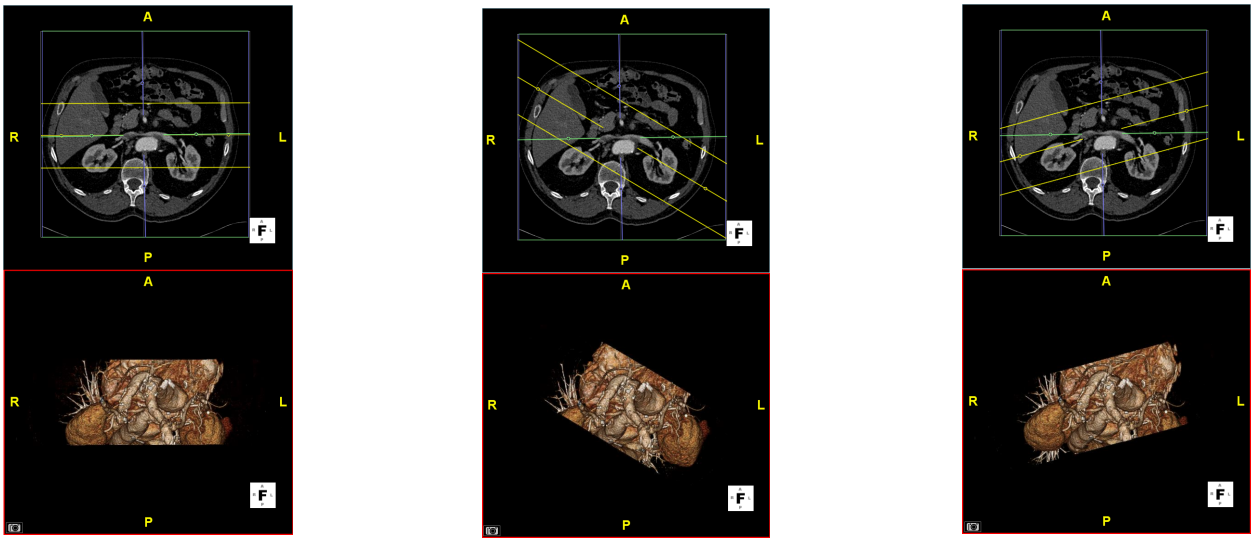
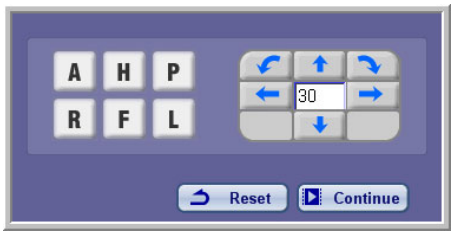


Figure 3-22 MPR image with Same Orientation

Note that the 3D image itself is not moving. Only the slab mask, through which the 3D image is shown, is being rotated. If you want the 3D image to rotate as well, check the **Fixed to screen** box in the tool panel.

Orientation Tool 



Use the positioning buttons to set the image to preferred viewing positions.

The six letters A,P,L,R,H,F can be used to switch the 3D view directly to the following orientations:

A	Anterior (view from the front, the patient is vertical).
P	Posterior (view from the rear).

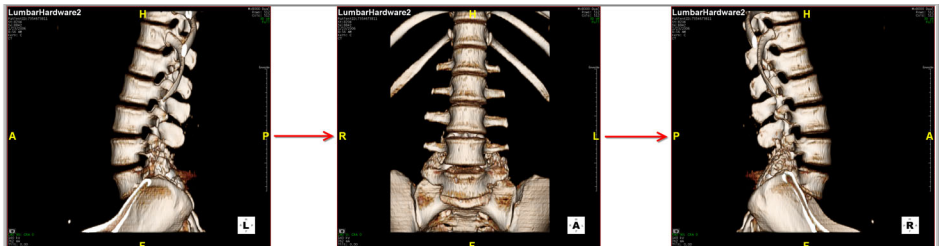
L	View from the left.
R	View from the right.
H	View from head towards feet, while the patient is lying face up.
F	View from feet towards head.

The **Reset** button resets the image to the default anterior position.

Continue mode

You may apply animation to the 3D image using the **Continue** button next to the angle setting controls. Click the **Continue** button, specify the angular increment in degrees, and select the direction of rotation by clicking one of the arrows. This moves the object in the direction specified. When you want to stop the cine mode, simply click the **Continue** button again.

For example, the following figure shows a continuous rotation rightward, in 90-degree increments. If you click the Continue button and then click the right arrow, the image rotates to the right in 90-degree increments, continuously.



The CPR Tool 

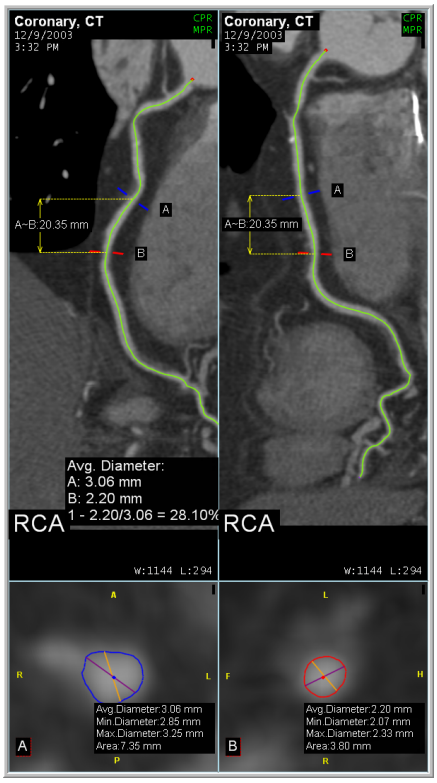
Centerlines allow you to view vessel paths. Centerlines can be added automatically by Advanced Processing, prior to being pushed to your server. You can also add centerlines manually using this tool, whether or not any Advanced Processing has been performed on the current data being viewed.

CAUTION! The embedded geometry is a mathematical model with limited capability. A real device can always have potential behaviors that embedded geometry is unable to predict or simulate. Be aware of this functionality, and ensure that you are verifying the results prior to use.

The CPR Tool displays two perpendicular CPR images and two orthogonal cross-section images by default. These windows can be viewed in other formats, which will be discussed further in this section (see "Right-Click Menu on CPR Window" on page 3-35).

If the data being viewed has not had centerlines added by Advanced Processing, the cross-section and CPR windows are initially displayed as empty, and a dialog box is posted to notify you that you must draw the centerlines manually.

If Advanced Processing has added centerlines to the data, the CPR view is displayed, as shown in the figure at right.



The CPR Tool Panel

When you click the CPR button, the CPR Tool Panel is displayed below the main Tool Panel.

Creating a Centerline Automatically

There are several predefined automatic centerline creation modes: Auto, Coronary, Normal, Head/Neck, Two Clicks, Multi-Click and Tree.

To create a centerline through a vessel automatically, hold down the shift key and left-click on the vessel. This works the same way in the Auto, Coronary, and Normal modes.

Creating a Centerline Manually

To create a centerline manually, do the following:

1. Click the **Manual** button.
2. Hold down the **Shift** key. Or, if you prefer, you can create a centerline without using the **Shift** key. To do so, open Preferences and click **Mouse Operation** in the navigation panel on the left. Then set the checkbox for **Operate FreeROI, DRG, Centerline tool without SHIFT key**.
3. Left-click at the start of the range.
4. Left-click *twice* at the end of the range.

Extracting Centerlines

To extract a centerline, highlight the centerline in the 3D window. You can do this by either clicking on it directly in the 3D window, or by clicking the forward or backward arrows in the toolbar at the bottom of the CPR window, to display each centerline individually. (For details on the CPR toolbar, see "Toolbars" on page 3-31.) Then click the **Extract** button.

Vessel List

You can also create a centerline by choosing from the list of predefined vessels in the Vessel List. The vessel list is displayed as a tree. When you click the name of the vessel in the list, the centerline for that vessel is highlighted in the viewer. If vessel labels were identified by Advanced Processing, those vessel names appear in the list. You can also add or modify other vessel labels from the image.

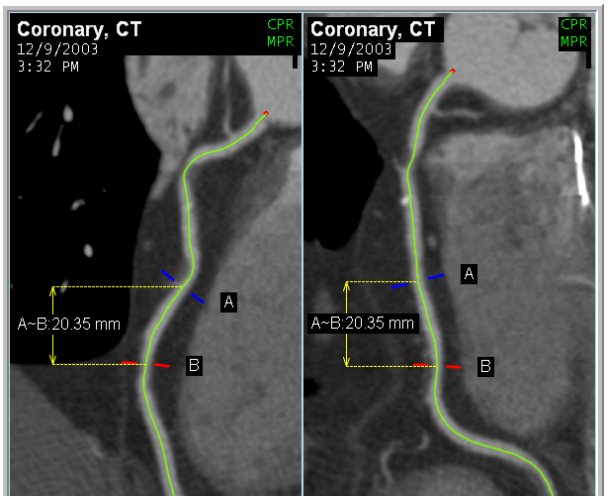
Deleting Centerlines

To delete all centerlines, click the **X** button located just above the vessel list:

CPR Tool Topic Links

This section describes the interface elements and functions of the CPR tool. To find the section you need, turn to the page listed below. If you are viewing this manual online, click the desired title.

The CPR Windows



The CPR Tool displays two perpendicular images that can be synchronized and rotated around the current stenosis.

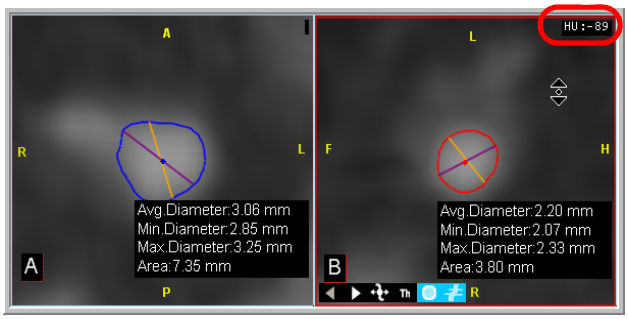
You can perform the following operations in the CPR windows:

- Edit the centerline, by moving the control points (dots) to change the path
- Show cross-section lines and measurements
- Display the vessel in straight view (sMPR)
- Perform measurements - Distance, Ellipse, and Profile measurements are enabled in the CPR window
- Perform stenosis calculations, using either the simple fraction method or QCA

For details about these features see "Toolbars" on page 3-31.

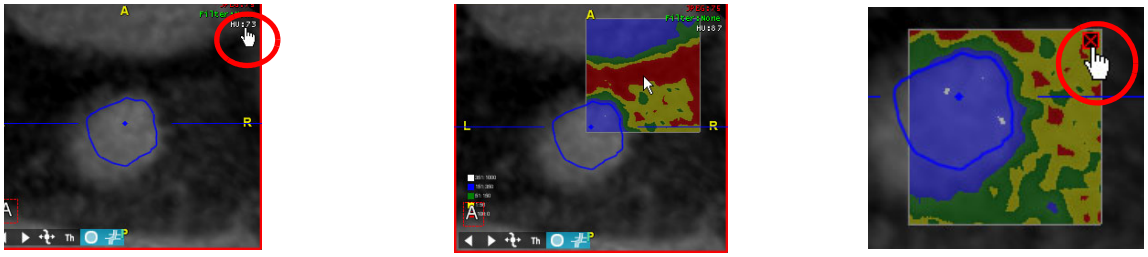
The Cross-Section Windows

The cross-section windows display two MPR images that are orthogonal to the CPR images. They can be synchronized and rotated around the centerline, as shown in the figure at right.



You can perform the following operations in the cross-section windows:

- Display the HU value as you move the mouse cursor (circled in the figure above)
- Show color map on MPR images. To do so, click on the HU display in the upper-right corner of the image and drag the mouse. The square color overlay is displayed and can be dragged around the image. To close the color map, click the X in the upper right corner. See the following figure.



- Display the average diameter and area of the cross sections in the CPR windows. These averages change as you move the cross-section lines along the vessel
- Show outline or cross-section lines of the vessel, or both
- Ctrl+left-click on the image to rotate the image around the center
    - Alt+left-click on the cross-section image to resize or reshape the outline (nudge tool).
- Shift+click and drag to redraw the outline. Redraws the outer wall and redefines stenosis calculation.

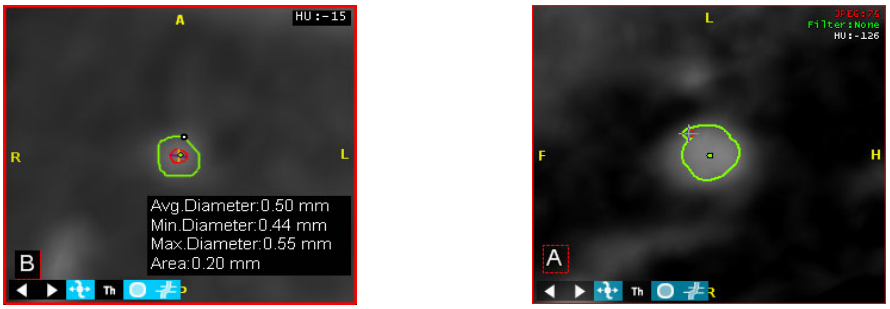


Figure 3-23: Left - Redrawing the outer boundary; Right - Nudge Tool

- Display a larger cross-section view (relative to the rest of the CPR display). To do this, open the Preferences menu by clicking the Preferences button located on the right end of the top toolbar.

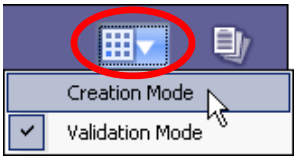
Select **CPR** from the navigation section on the left, and checkmark the box labeled **Larger Cross-section view**:

When this setting is enabled, the cross-section windows use a larger percentage of the entire screen.

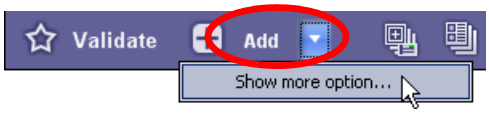
Multi Style Layout Options

CPR views can be displayed in multi style, giving you a view of up to four vessels in CPR mode. To use this feature, you must first create a Multi Style workflow element.

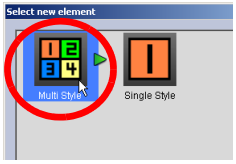
1. In the upper-right corner of the Workflow panel, select **Creation Mode**.



2. At the bottom of the Workflow panel, click the down-arrow to the right of the **Add** button, to display the pulldown menu:



3. Select **Show more option**. The **Select new element** dialog is displayed:



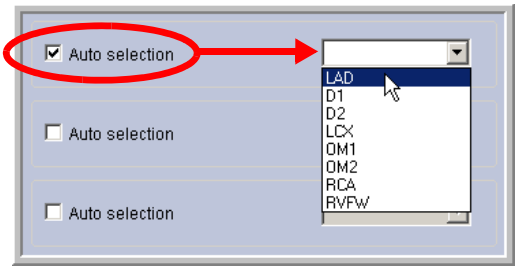
4. Click the **Multi Style** element (circled) and then click **OK**.

   The **Multi Style Setting** dialog is opened. This dialog allows you to choose how many vessels to display in CPR mode, and which vessels to select for the display. Up to four are allowed.

5. Type in a name for the workflow element. In this example, we will show three vessels in CPR mode: LAD, LCX and RCA, so we have named the element accordingly.

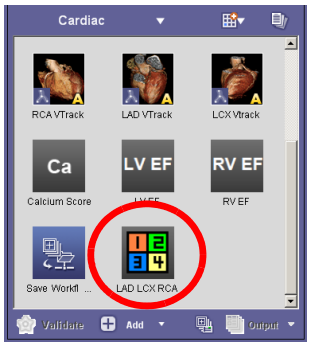
6. Check the box for **Change to CPR layout**.

7. For each vessel you would like to examine, check a box for and then select a vessel from the corresponding menu.

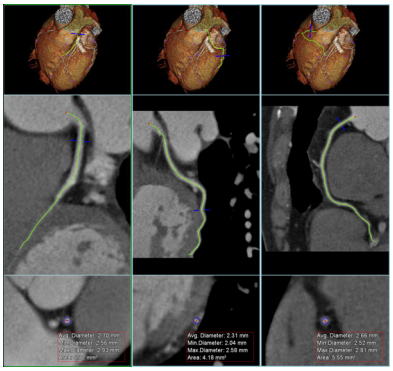


Three vessels have been selected for the multi style view: LAD, LCX and RCA. Click **OK** when finished.

8. The **LAD LCX RCA** element is now added to the workflow:.



9. Click the **LAD LCX RCA** element. The three vessels are shown in CPR mode:



Toolbars

When you move the mouse over any of the CPR or cross-section windows, a toolbar appears at the bottom of the window, as shown in the following figures.

CPR Window Toolbar

Cross-section Window Toolbar

Figure 3-24: Toolbars at the bottom of the Window

Description of the Toolbar Buttons

The following identifies and describes the buttons in the toolbars, from left to right:

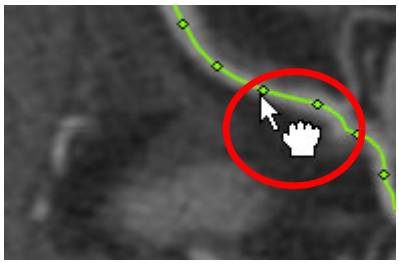
- Previous/Next Vessels (left and right arrows)

  Click the left and right arrows to show successive vessels from the 3D window. The vessel currently being displayed in the CPR window is highlighted in green in the 3D window.

- Edit Centerline 

  When this button is clicked, control points are added to the centerline in the CPR windows so you can edit the centerline. When you place the cursor close to one of the control points on the centerline, the curser turns to a “hand” sign (circled in the following figure, at right), indicating that you can move and stretch the centerline from its current position.

  When you have repositioned that section of the centerline, release the left mouse button and position the cursor on another section you want to change.



  You can also edit the centerline in the cross-section window. Click on the centerline in the center of the image and drag it to the desired location. Because this is a perpendicular view, the centerline appears as a dot.

The Redraw Tool

You can also edit the generated centerline manually by using the Redraw tool. The Redraw tool allows you to edit one section of a centerline without affecting the rest of the centerline.

There are two methods of redraw. You can drag the mouse along the path where the centerline should be, or you can click multiple times along the desired path.

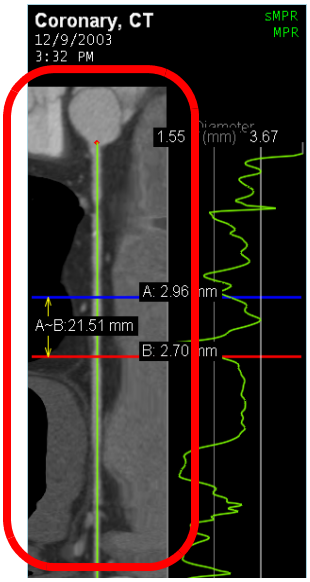
- To edit by drawing a line: Hold down the **Shift** key and the right mouse button simultaneously, and drag the mouse to redraw the section.
- To edit using multi-clicks: Hold down the **Shift** key and, using the left mouse button, click along the path you want to redraw.

Once the line has been manually redrawn, only the edited segment will be updated, leaving the rest of the centerline unchanged.

Note: If the redraw tool is not enabled, see "CPR Interactive 2" on page A-19 in the user preferences.

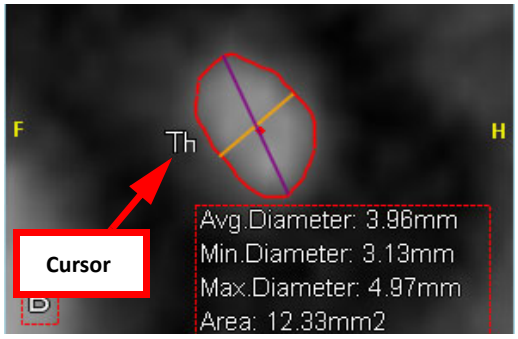
- Straight MPR View ("sMPR")

  Display the vessel in straight view, as shown at right.



- W/L Threshold - Cross-section windows only ("Th")

  Changes the W/L based on HU thresholds in the cross-section window:



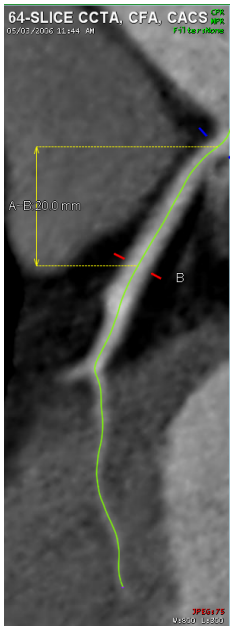
- Show/Hide Outline and Centerline (CPR view only)  - Toggle on/off display of the centerline in the CPR views.
- Show/Hide Contour (cross-section view only)  - Toggle on/off display of the cross-section contour.

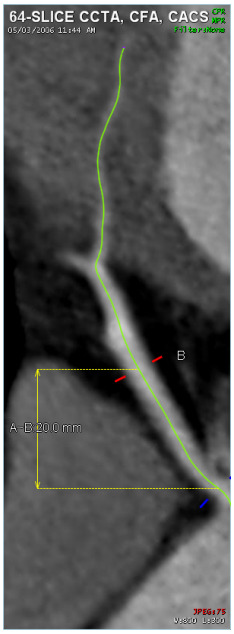
- Show/Hide Measurements 

  Toggle on/off display of the cross-section lines and measurements in the CPR views. This button has the same function whether it is accessed from a CPR or cross-section window.

- Flip Image - CPR windows only 

  Flip the image vertically. (See figure at right. Left: original image; Right: flipped image.)

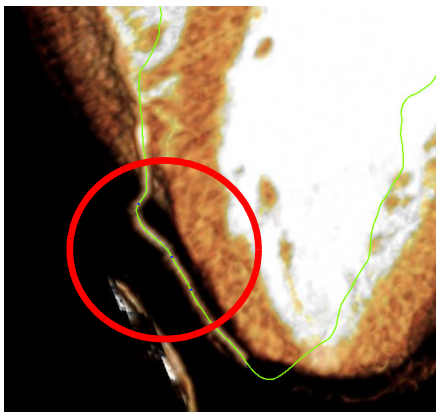




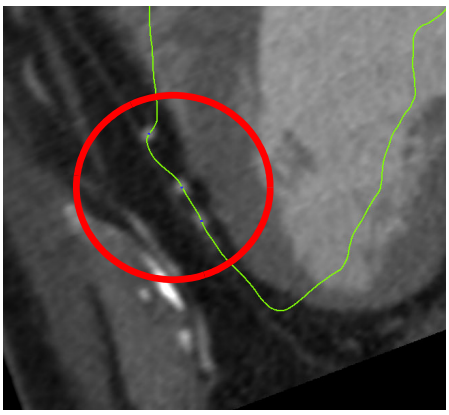
Viewing the Blue Dots in the Main View

The blue dots that appear in the axial view represent the places where the centerline intersects the 2D plane. These intersection points can also be accessed in the main view, if you prefer to read the study in an orientation other than axial. To see the dots in the main view, do one of the following:

- Change the slab mode to Half, or to a thickness that is less than or equal to 15mm. This allows you to view in 3D VR rendering mode.
- Change the rendering mode to MPR, MIP, MinIP or ThickMPR. If you select MIP, MinIP or ThickMPR, make sure the slab thickness is no greater than 15mm.



12mm Slab View



MPR Rendering Mode

Figure 3-25 Rendering Modes

Right-Click Menu on CPR Window

The right-click menu on the CPR window gives you an alternate way to perform functions described in the preceding sections. 2D Batch can also be performed on CPR windows through the batch tools or by utilizing the CPR batch layouts.

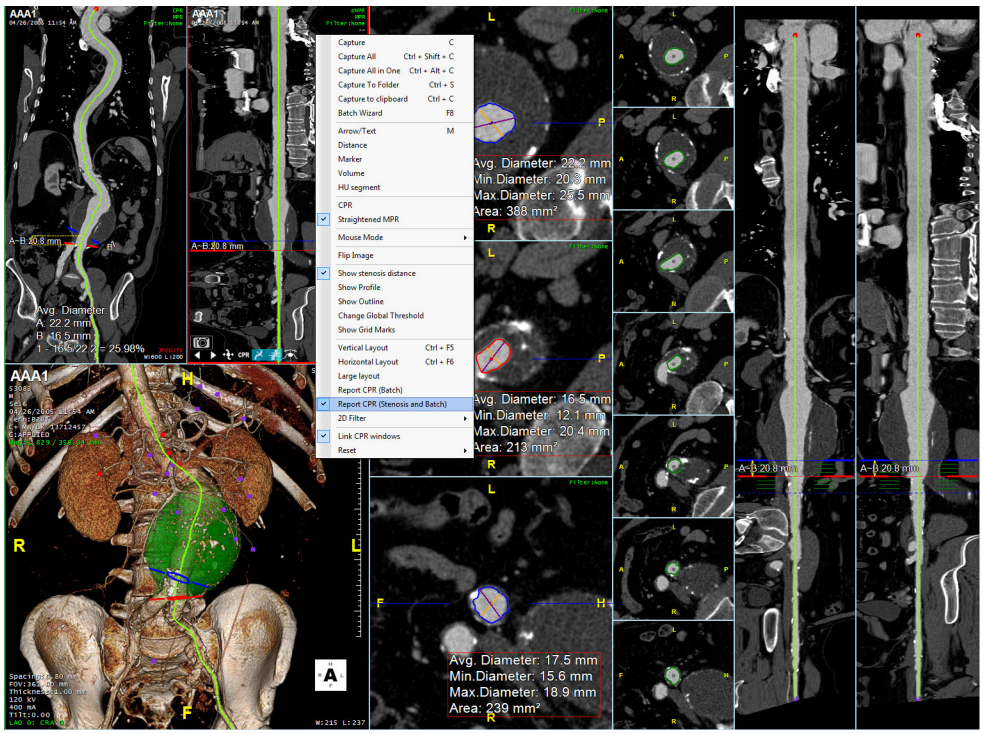


Figure 3-26 Right-click Menu

However, there are a few extra options in this menu:

- Plaque Analysis - Performs an analysis of plaque along a section of vessel. For a detailed description of this feature, see "Plaque Analysis" on page 3-38.
- Vertical Layout - Vertical layout shows the two CPR windows in vertical position with the two cross-section windows below them. The 3D image and axial views are shown on the right side of the window.

Vertical layout is the default layout of the CPR window.

- Horizontal Layout - Horizontal layout shows the two CPR windows in horizontal position, with the two cross-section windows below them. The 3D image and axial views are shown on the right side of the window.
- Large Layout - Large layout eliminates the 3D and axial windows so that the entire image display window is available for the CPR view. Both vertical and horizontal views can be displayed in large layout.
- Link CPR Windows - When this option is selected, operations performed on one CPR window are reflected in the other automatically. For example, if you rotate one CPR window, the other is automatically rotated to the corresponding position. When not selected, the CPR windows are independent of one another.

- Link to 3D - When this option is selected, operations performed on the 3D window are reflected in the CPR windows.
- Reset Orientation - Reset the position of the CPR windows to their original orientation.

Right-Click Menu on the Centerline

This menu allows you to modify a centerline itself. Right-click on any centerline to display this menu.

- Mark Here - Set a marker on the centerline.
- Delete to the Red Dot - Remove everything in the selected branch above the selection point (from the selection point to the red dot)
- Delete to the Purple Dot - Remove everything in the selected branch below the selection point (from the selection point to the purple dot)
- Delete branch - Remove the entire branch
- Edit - This is the same as the Edit Centerline icon in the toolbar at the bottom of the CPR window (see "Edit Centerline" on page 3-32).
- Smooth

  The **Smooth** feature allows you to adjust and then edit the CPR centerline. To use this feature, do the following:

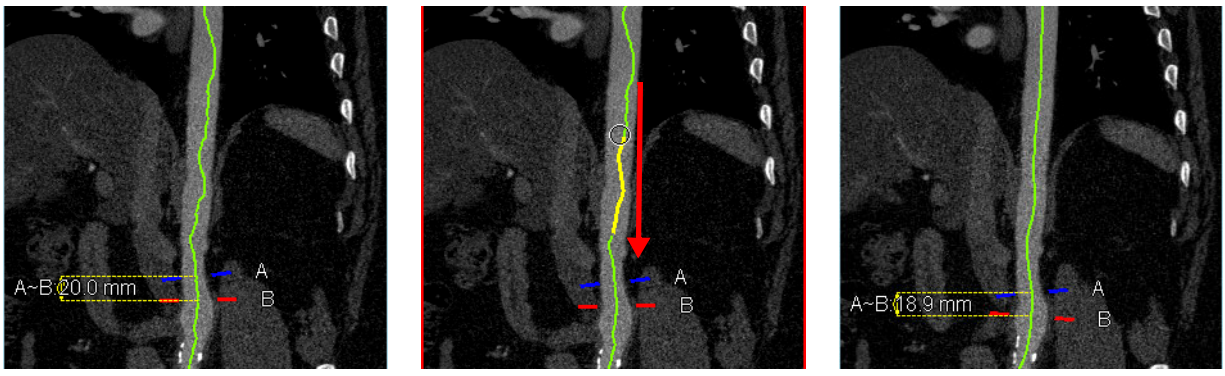
  a. After selecting **Smooth** from the menu, hold down the Control (**Ctrl**) key and click the centerline in an area that needs to be smoothed. A small circle cursor is displayed (see center image below).

  2. Drag the mouse along the rough section of centerline.

  3. When finished, release the mouse. The centerline is now in Edit mode.

  4. Edit the centerline as you normally would (see "Edit Centerline" on page 3-32

)



Rough Section of Centerline **Smoothing** **Corrected Centerline**

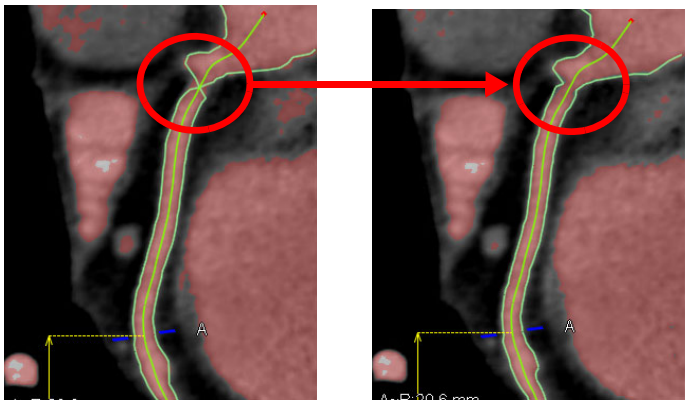
Figure 3-27: Managing the Centerline

- Embedded Geometry - Model and plan the manufacturing of a medical implant device. For a full description with instructions, see "Embedded Geometry" on page 14-4.

CAUTION! The embedded geometry is a mathematical model with limited capability. It is not intended to predict the implantation device's shape or location, and is not intended to be used as a decision-making tool for the procedure.

- Change root - The start point of a vessel determines its orientation in the CPR windows. The start point is indicated by a red dot. There is a blue dot at the terminating point of that vessel. When you select this menu item, the start and end points are switched. The CPR windows are updated to reflect the new orientation. You can also see that the start and ending points on the vessel in the 3D window have been switched.
- Get Greater Curve - Mark a section of the centerline, and then measure the length of the greater (outer) curve of the vessel along that section. For a full description with instructions, see "Get Greater/Lesser Curve" on page 14-21.
- Measure Curvature/Tortuosity - Find the tortuosity index of a vessel, defined as the distance between two points along the centerline, divided by the straight-line distance between those points. For a full description with instructions, see "Measuring the Tortuosity and Curvature of a Vessel" on page 15-13.
- Change Global Threshold from here

  If you are not satisfied with the outline drawn on the vessel under examination, this feature allows you to change the HU threshold levels along the entire centerline, so that the boundaries of the vessel will be recalculated.



- Export Centerline Data

  Export centerline coordinates to local storage.

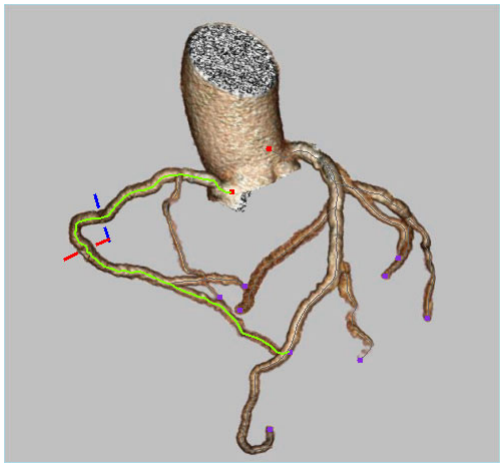
Note: The Enable Centerline Export preference must be enabled for this item to appear in the menu. To enable the option, open Preferences, navigate to the CPR screen, and check the box for Enable Centerline Export. See Appendix A: "CPR" on page A-16 for more information.

Segmenting the Aortic Root and Coronary Arteries

A segmented aortic root with coronary arteries is useful in various procedures. To do so, follow these instructions:

1. Click the **CPR** button in the Top Toolbar.
2. Select **Tree** from the vessel menu in the tool panel.
3. Follow the instruction at top of the 3D VR image that says "Please shift-click on the aortic root" (see image below).

4. Check all vessels to make sure that a centerline has been created for each. If any vessel does not have a centerline, shift-click on that vessel to create one.
5. Click the **Extract** button in the tool panel. The result is displayed as shown below:



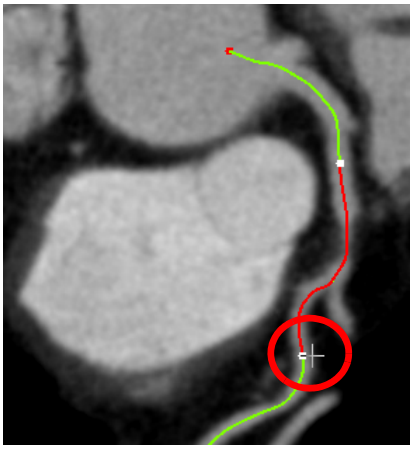
Plaque Analysis

Note: You are obligated to define the parameter ranges that are used in this procedure. When first accessed, the user interface for setting these parameters contains generic default values having no particular significance. You must acknowledge this by dismissing a warning message to this effect.

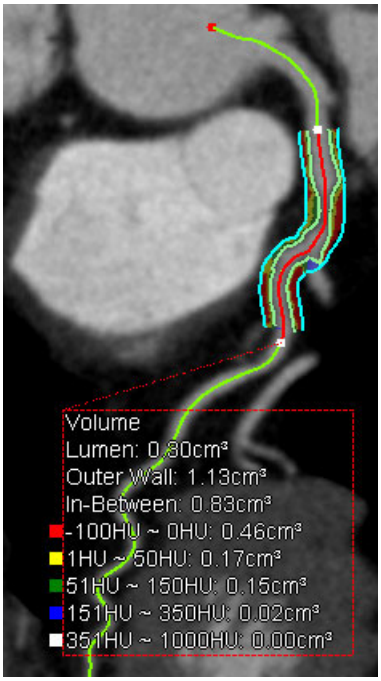
Note: Plaque Analysis measurements can be tracked in the Finding Viewer (see Chapter 16: "The Findings Workflow" for information about the Finding Viewer).

Right-click on one of the CPR windows and select **Plaque Analysis** from the menu. Then, by dragging the mouse, draw a line along the centerline, from the start to the end of the area of interest (see figure below, left). When finished, release the mouse.

The plaque analysis is displayed in the CPR window. (Figure 3-28, image on the right)



Drawing a Line



Plaque Analysis in CPR Window

Figure 3-28 Getting a Plaque Analysis

Display Plaque Analysis and Stenosis Analysis on One Screen

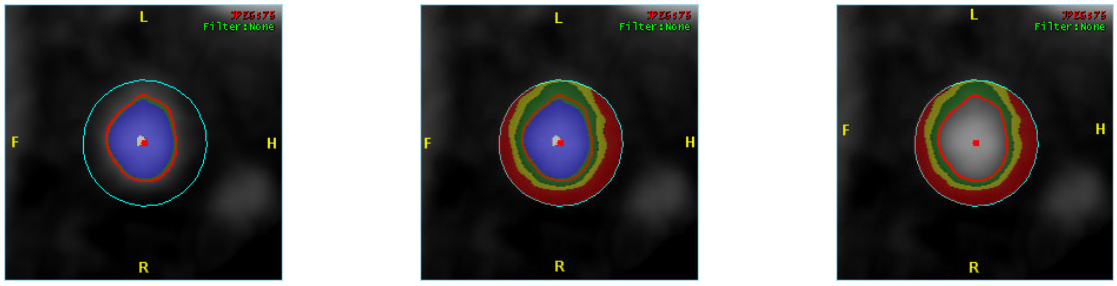
If you would prefer to see the plaque analysis results displayed along with the stenosis analysis, do the following:

1. Open Preferences.
2. Click the **CPR Interactive** link in the navigation panel on the left.
3. Check the box for **Analyze plaque and stenosis on the same screen**.

Color Maps

The cross-section windows can be displayed using a color map to show different HU ranges in and around the vessel. To show the color map, right-click on the measurement and select **Color map** from the menu.

Color maps are overlayed on the cross-section image to show three different views: lumen, outer wall or in-between (see Figure 3-29). These views are selected from the right-click menu, as shown in the previous image. Each color overlay represents the HU value range of that region, according to the colors shown in the measurement results (see Figure 3-29).



Lumen **Outer Wall** **In Between**

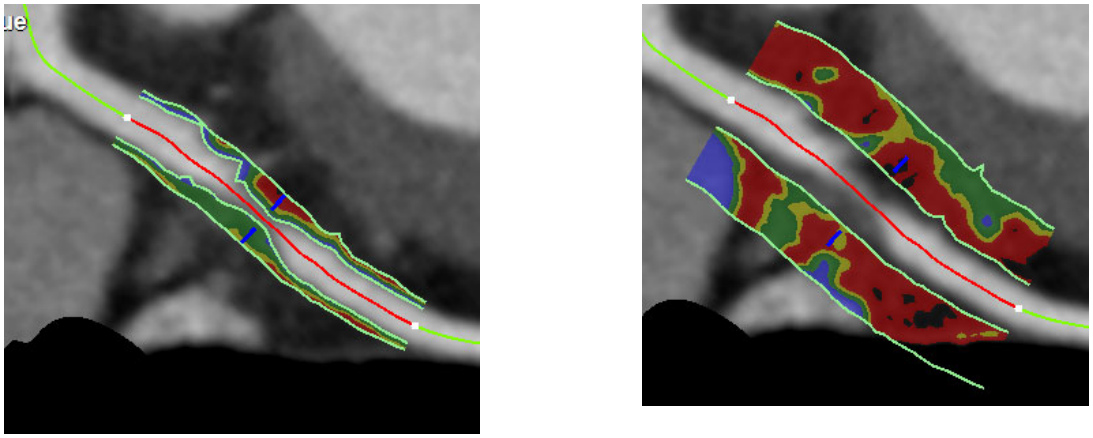
Figure 3-29: Color Maps

Extend Wall

You can configure the outer or inner wall to be extended by a fixed amount. This is useful for certain procedures, for example, performing a volume analysis of the tissue around a vessel.

Right-click on the measurement and select **Extend Wall** to open the Extend Wall dialog.

Select the values of the new outer and inner walls, first by selecting the start point from the pulldown menu, and then by entering the extension amount in the input box. The results appear as follows:



Normal Wall Boundaries **Extended Walls**

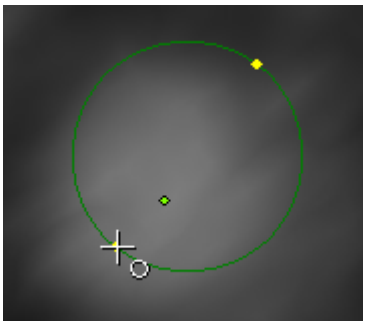
Figure 3-30: Extending Walls

Cross-section Image Editing Tools

If needed, you can edit the outer or inner wall by drawing a new circle around the wall, redrawing in freehand, or using the nudge tool.

Note: If you would like the outer wall to be interpolated, enter outline edit mode first (see "Edit Centerline" on page 3-32).

- **Draw Circle**



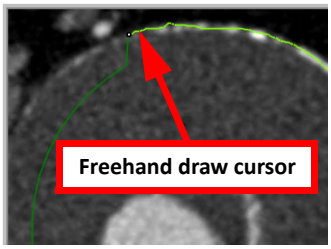
Use this tool when you need to redraw the outer wall completely. This tool draws a perfect circle, which may need to be corrected using one of the other tools.

a. Press and hold the **Ctrl** key.

b. Click the edge of the outer wall and drag across the cross-section image. A new circle is drawn on the image, which increases in diameter as you drag the mouse.

c. When the circle matches the outer wall, release the mouse.

- **Redraw**



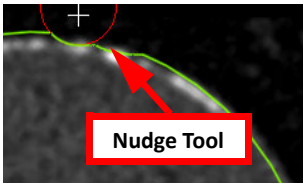
Use this tool to redraw the outer wall freehand.

a. Press and hold the **Shift** key.

b. Click on the edge of the outer wall, in an area that needs to be redrawn.

c. Drag the mouse along the correct circumference of the outer wall.

- **Nudge Outer Wall**



Use this tool to correct small areas of the outer wall.

a. Press and hold the **Alt** and **Ctrl** keys together. The nudge tool appears.

b. Click and hold down the mouse.

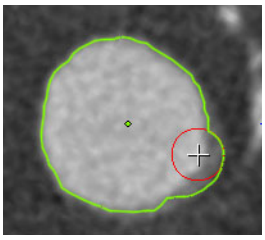
Note: When you click a location close to the outer wall, the nudge tool circle is small. The further away from the wall the image is clicked, the larger the circle.

---

c. Move the mouse along the outer wall to push the outline into the correct place.

- **Nudge Inner Wall**

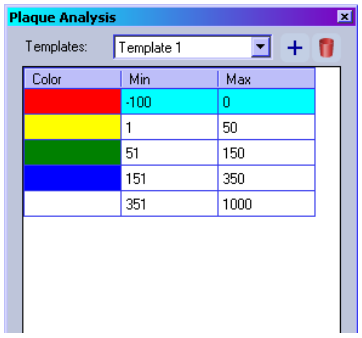
  This is the same as the outer wall nudge tool. The only difference is that you press the **Alt** key (instead of **Ctrl**) before clicking on the image.



Color Map Templates

The color map (which associates specific colors to HU value ranges) is defined by a template. When you first display the color map, one of the default templates is in use. You can change to another template, you can modify the default templates and you can also create your own.

To make changes in the color map templates, select **Edit color map** from the right-click menu. The template dialog is displayed:

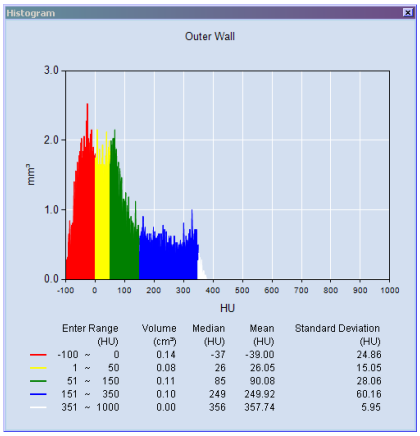


From this dialog, you can change the colors of the template. modify the HU ranges and create new templates.

To change any of the colors, click on the color. The Windows color palette is opened. You can then select a new color from the palette. To change any of the HU ranges, highlight the number to be changed and type in the new number.

Histograms

Select **Histogram** from the right-click menu. The graph and statistical data displayed on the screen refer to the section of the vessel cross-section selected at the time (lumen, outer wall or in-between).



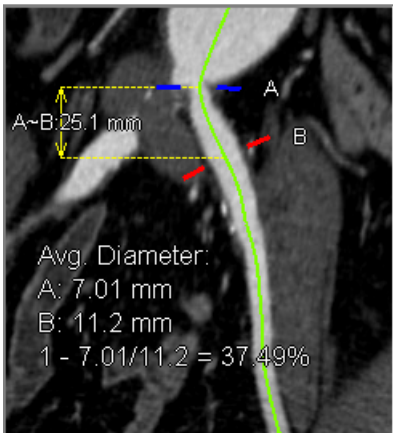
Display Stenosis

The stenosis calculation should be displayed on the CPR image. If it is not, you will need to enable **Show stenosis result** in the Preferences.

1. Open Preferences, and select **CPR** from the navigation panel on the left (see "Opening Preferences" on page A-1 for help with opening preferences).

2. In the upper-left section of the **CPR** Preference screen, there is a list of settings under the heading **CPR Initial view setting**. Make sure the box for **Show stenosis result** is checked.

The result is shown in the CPR window:



Changing the Stenosis Display

You can select different calculation methods for the display. To do so, right-click on the result and make another selection from the pulldown menu.

Default Stenosis Display

Stenosis results are displayed as the average diameter by default. If you would like to change the default stenosis results, you can do so in the Preferences.

1. Open the Preferences window.

2. Select **CPR** in the navigation panel on the left. Settings for the default stenosis display are in the upper-right section of the CPR screen.

3. To change the default, select the desired type from the right column and click **OK**.

Stenosis Calculation Algorithm

The top row in the **Stenosis Setting** section contains settings for the algorithm used to calculate the results displayed in the CPR window. Select either **Simple** (default) or **QCA** as preferred.

Snap-to-Stenosis

The Snap-to-Stenosis feature requires that you enable a Preference setting first.

1. Open Preferences.
2. In the navigation panel, expand the **CPR** list, and then click **Interactive**.
3. Under **Mouse Click**, check the box labeled “Click to set red cross-section to a stenosis nearby”.
4. Modify the three parameters underneath as needed:
+
5. Click **OK** to close the Preference window.
6. Click on one of the CPR images or on the 3D view near a stenosis. The red marker will snap to the stenosis. A confirmation message is displayed. The blue marker is placed at a near-optimal distance (defined by your preferences) from the red marker.

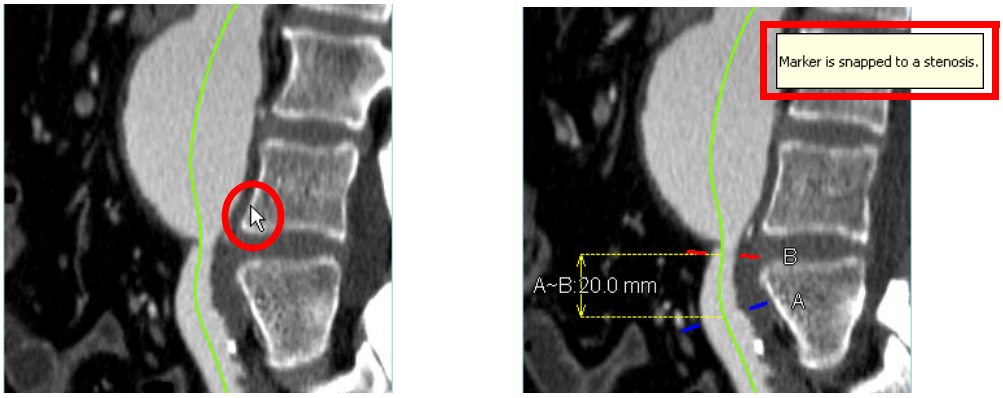
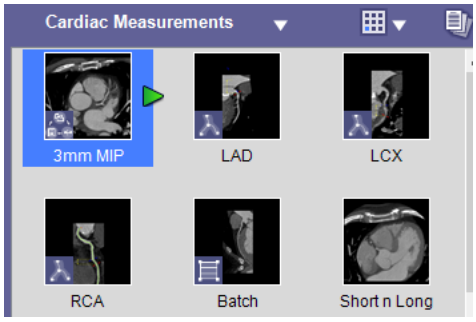


Figure 3-31: Left: Clicking on CPR near stenosis; Right: Red marker snapped to stenosis Upper right: confirmation message

Set Stenosis Grade

To set the grade of a stenosis measurement, load the study into the **Cardiac Measurements** workflow.



For each vessel under examination, do the following:

1. Click on the workflow element for that vessel.
2. Click the **CPR** button in the top toolbar to open CPR mode.
3. Measure the stenosis.

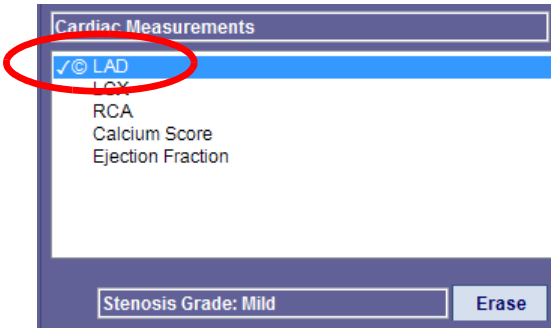
4. When finished taking measurements, validate the workflow element. The **Stenosis Grade** dialog is opened.

5. If needed, change the stenosis grade and then click **OK**.

Note: You are responsible for setting the stenosis grade. You are also obligated to define the parameter ranges that are used in this procedure. When first accessed, the user interface for setting these parameters contains generic default values having no particular significance. Click the **Configure** button to configure the default settings.

---

6. Click the **Measurement Protocols** tool button in the tool panel. The measurement will already be completed for that vessel.

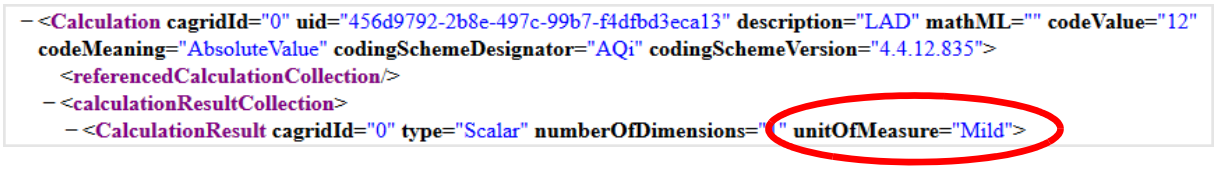


Export Stenosis Grade as AIM XML

7. At the bottom of the Measurement Protocols tool panel, click the down-arrow next to **Generate Report**, and select **Export Measurements as AIM XML**.

Note: This will not change the label on the button, and you will not see any visual indication that the measurements were exported. However, if you check the export folder for Export Measurements, you will see the AIM XML file.

The stenosis grade is found under **unitOfMeasure** in the AIM XML file:



Vessel Flythrough

Flythrough functions can be used to view the inside of a vessel. Before you can initiate the Flythrough, you must already have a vessel study open in CPR view.

To open the Flythrough main window, right-click on either of the cross-section views and select **Flying** from the menu.

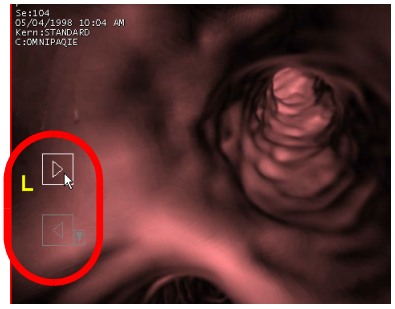
Note: The Flythrough always begins wherever the red marker is situated, regardless of which cross-section view is used.

The main window loads the 3D perspective view of the inside of the vessel.

To begin flying, do the following:

1. Hover the mouse near the left edge of the Flythrough window (circled in the figure below). This causes the cine buttons (directional arrows) to become visible.

2. Click the right arrow to start forward motion.



Navigating the Flight

Direction and Speed

There are two ways to control the direction and speed of the Flythrough.

- Cine Buttons - The right arrow begins a forward flight, and the left arrow begins a backward flight.
- Mouse movements - Drag the mouse upward on the image to increase the speed. Drag the mouse downward to slow the flight. As you move downward, the flight will eventually come to a stop and then reverse direction.

Starting and Stopping

- Directional arrows begin a flight in the appropriate direction (right arrow begins a forward flight, left arrow begins a backward flight).
- A mouse click on the perspective window stops a flight in progress, but does not initiate or resume a stopped flight.

Other Tools

When the two directional arrows are showing, you can also see a small down-arrow just below the left arrow. Click on the down arrow to display a menu containing more tools.

- Update all views while playing cine - When this is enabled, the two cross-section views and the axial view are automatically paged through the slices as the flight passes through the corresponding position.

- Record playing cine to AVI file

  When you select this option, a Windows navigation window opens so that you can create the AVI file that will contain the images from the Flythrough, and specify the folder where that file will be stored. The Flythrough then goes into recording mode (indicated by the down arrow turning red). You will not be able to select any other items in this menu until you stop the recording.

- Record playing cine to DICOM

  This records the Flythrough. When you complete the Flythough and stop the recording, a dialog opens where you can select a DICOM server to send the recording to.

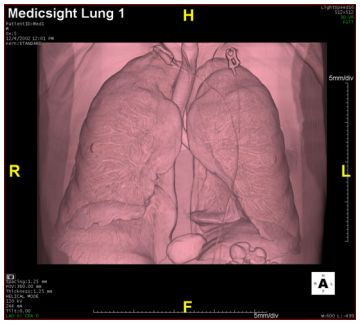
- Exit flying mode - Upon exiting flying mode, the 3D Viewer returns to the CPR view.

Airway CPR

You can use the CPR tool to create centerlines in the airway of a lung study, and view it in CPR mode.

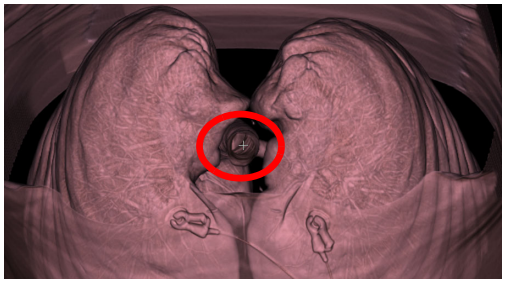
1. To begin airway CPR, open a lung study. To view it properly, use the lung template. The template panel is located in the upper-right area of the iNtuition Viewer. Click the **Template** tab to show the template panel. Then click the **Lung** template.

   The lungs are made visible in the 3D image window (see the following figure).

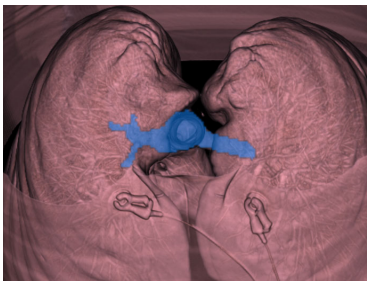


2. To isolate the airway, use the **Region Grow** tool in the Tool Panel.

3. To grow a region inside the airway, rotate the image to the Head orientation so that the opening is visible (see figure below). Then position the mouse right over the airway opening to begin the region grow. Otherwise, you will grow the region on the surface of the lungs, rather than inside the airway.



4. Hold down the **Shift** key and click. The masked area is displayed:



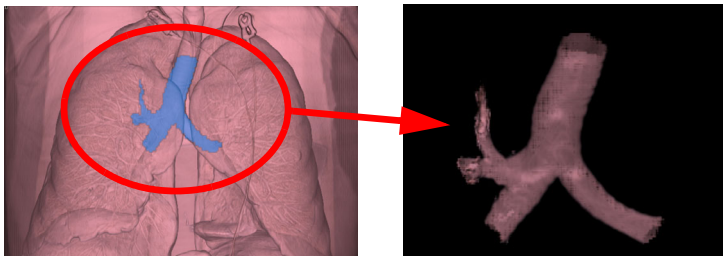
5. If too much of the lung has been masked, you can decrease the masked area by doing the following:

   a. Position the mouse over the area you want to remove.

   b. Roll the middle mouse button back (toward you).

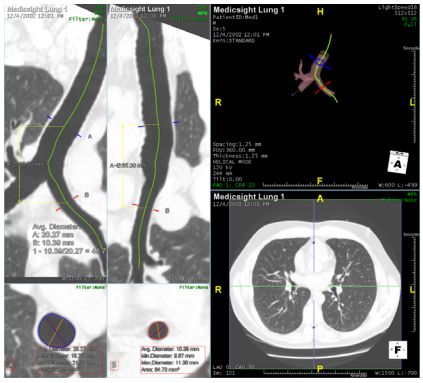
   c. Continue doing this until only the area under examination is masked.

6. Click the **Add/Select** button in the Tool Panel. Only the masked airway is displayed:



7. Now click the **CPR** button  in the Tool Panel.

8. To create centerlines, hold down the **Shift** key and click on sections of the airway where you want to draw centerlines. The centerline is automatically drawn, and the image is displayed in 2x2 CPR Vertical mode:

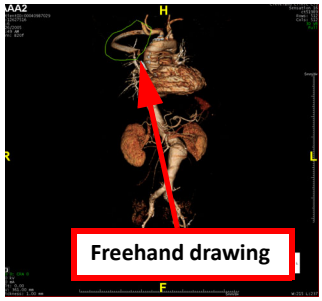


You can perform all of the same operations that are available for vessel CPR, such as centerline edits, viewing cross-section lines , performing measurements and displaying the airway in straightened view (sMPR). See "The CPR Tool" on page 3-26 for details on CPR mode.

FreeROI 

This tool allows you to define a Region of Interest within an image, using the hand drawing tool. You can then choose either to remove that area from the image, or to remove everything except that area.

Removing a Region of Interest



To remove a Region of Interest on an image, do the following:

1. Hold down the **Shift** key and click on the area where you want to begin drawing.
2. Draw a circle around the ROI. Continue holding down the **Shift** key as you do this.
3. When you have finished drawing the circle, release the mouse. The area you have circled is removed from the image (see Figure 3-32).

Adding In a Region of Interest

To add back a previously removed area, perform the above three steps, drawing with the *right* mouse button (shift + right-draw).

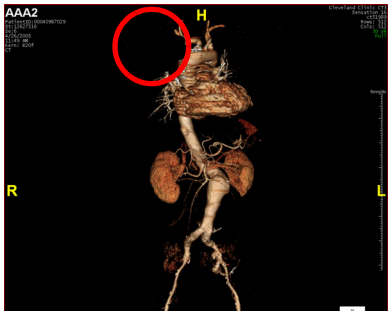


Figure 3-32: ROI Removed

Drawing an ROI Using Multi-Clicks

You can also draw a ROI using multiple clicks.

1. Hold down the **Shift** key and click along the edge of the ROI. Each click produces a green dot on the image in that spot.

   If you prefer, you can perform Multi-click FreeROI without using the **Shift** key. To do so, open Preferences and click **Mouse Operation** in the navigation panel on the left. Then set the checkbox for **Operate FreeROI, DRG, Centerline tool without SHIFT key**.

2. When enough dots have been placed to define an area, the 3D Viewer automatically draws a line from the most recent click back to the first click, making a closed area. You can continue clicking and the Viewer will redraw the final line.

3. When you have defined the ROI, release the mouse.

4. The FreeROI Tool Panel becomes enabled and contains buttons allowing you to remove, retain, and add in the Region of Interest.

The tool buttons have the following functions:

- Include - adds back any previously removed area inside the ROI
- Exclude - removes only the area inside the ROI
- Select - removes everything except the area inside the ROI
- Clear ROI - removes the most recent ROI outline that was drawn from the image. To remove previous ROIs, continue to click this button.

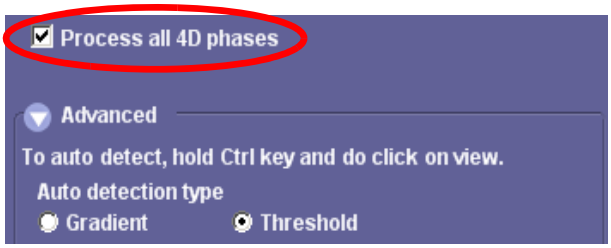
When the data loaded in the 3D Viewer is a multi-phase 4D series, you can process the changes performed on one phase to all phases by clicking the **Process all 4D phases** box.

Erosion/Dilation Dialog

This is a dialog that is displayed when **Select**, **Include**, **Exclude** or **Add/Select** is performed. See "Erosion/Dilation Dialog" on page 3-59 for more details.

Process All 4D Phases

Check this box to propagate the masking operation to all phases of a 4D study:

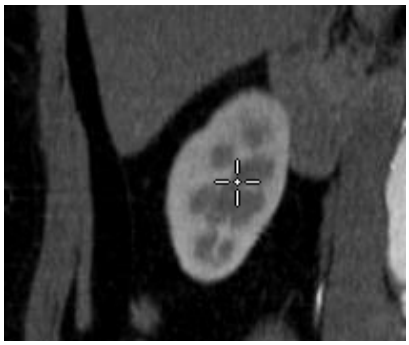


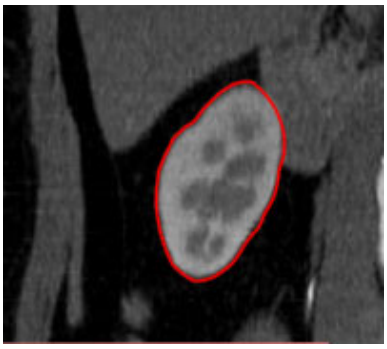
Auto Detection

The FreeROI function can automatically detect the edges of a region and draw an outline around it. To use auto detection, click the **Advanced** arrow in the tool panel.

Note: Auto detection can be performed only on 2D images.

Edge detection can be determined using the HU threshold or by gradient. Select the preferred algorithm by clicking the corresponding radio button. Then hold down the CTRL key and click on the anatomy to form the ROI.





Redrawing a Contour

To fix a poorly drawn contour, hold down the shift key and begin drawing along the edge where the problem exists. The contour will change shape according to the new outline drawn (see the following figures).

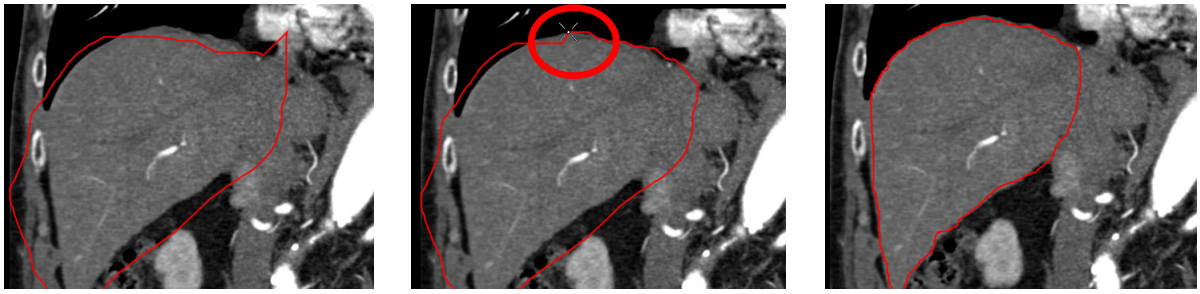


Figure 3-33: Left: Original Contour; Middle: Redrawing Contour; Right: Redrawn Contour

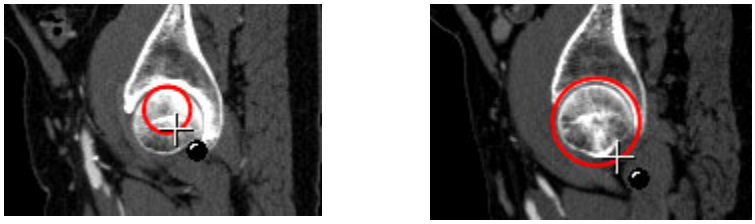
Sphere and Circle Drawing

The FreeROI tool can be used to isolate a spherical object such as a femur head.

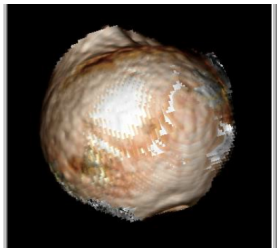
1. In the Sagittal image, page to a slice showing the femur head clearly.

2. Select the sphere mode for drawing a region.

3. On the image, place the mouse on the edge of the circular ROI, and then drag the mouse across the area. A circle is automatically drawn on the image. As you drag the mouse across the area, the circle becomes larger.



Click the **Select** button in the Tool Panel to segment the femur head. The segmented section is displayed in the 3D window:



Mask

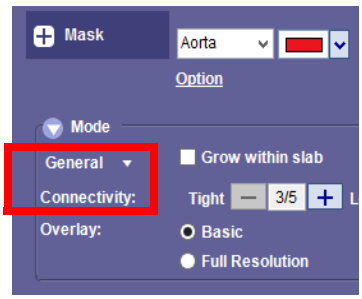
This feature allows you to segment regions of image data, create a mask for each region, and measure their respective volumes. See "Mask" on page 3-56 for instructions.

Dynamic Region Growing 

Automatically applies mask operations on the region to examine.

Masking a Region

1. Click on the **Region** button for mask operations.
2. If the tool panel underneath the word **Mode** is empty, click the arrow to the left of **Mode** to view the tools and settings.
3. Click the down-arrow to the right of the word **General**. The pull-down menu containing region-grow types is opened.



Each type of region-grow has its own algorithm, designed for the type of tissue or vessel being targeted.

Table 3.5: Region-grow Modes

Mode	Description
Auto	Auto-detect the type of tissue or vessel to be grown.
Bone	Use this for multiple bones (that is, entire rib cage).
General	Use this if the region you are growing has no special category.
Vessel	Use for all vessels except small vessels.
Small Vessel	Use for small vessels only.
Nodule	Use this for spherical type structures in lung, liver, and so on.
Bone2	Use this for single bones or small segments.
Airway	Use this for air filled structures such as the trachea or colon.
Carotid	Use for the carotid vessels.

4. Select the region grow mode that best suits the body part.
5. Choose the level of sensitivity or constraint you want for region growth, by selecting the appropriate value from the **Connectivity** scale (circled in dark blue in the figure above), ranging from 1/5 to 5/5.
   - **1/5** - This level grows the most slowly and is recommended for very fine vessels.

- **5/5** - This level grows the most quickly and is recommended for objects such as large vessels, bone, and other tissue.

The levels in between these two ends allow you to adjust the growth level more finely.

6. Hold down the **Shift** key, and then click and hold the mouse on the vessel you want to grow.

   If you prefer, you can perform Dynamic Region Growing without using the **Shift** key. To do so, open Preferences and click **Mouse Operation** in the navigation panel on the left. Then set the checkbox for **Operate FreeROI, DRG, Centerline tool without SHIFT key**.

7. When you have masked the region you want to grow, release the mouse.

Functions

The following functions are accessed through the buttons on the tool panel.

- **Include** - Adds back some of the tissue that was previously removed, such as with bone removal.
- **Exclude** - Shows everything except the masked area.
- **Select** - Shows only the masked area.
- **Clear Region** - Removes all masking from the image (does not change the image).
- **Cancel** - Cancels the operation in process. Once the masking is complete, it cannot be canceled. Click the **Clear Region** button to remove the mask.

Grow or Edit a Region with Freehand Option

You can use the Freehand tool to grow (“paint”) a region (Figure 3-34):

1. Select the **Dynamic Region Grow** icon.
2. Select the radio button next to **Freehand** (Figure 3-34, # 1). This allows you to “paint” a region larger.
3. Shift-drag your mouse in the selected area.
4. If you need to, you can change the size of the paint brush tool (Figure 3-34, # 2).

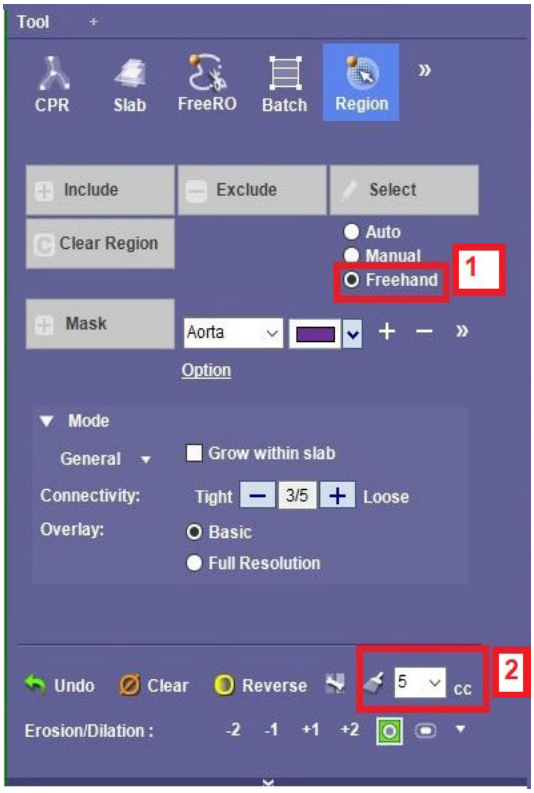


Figure 3-34Freehand Option and Paint Brush Size

5. You can select the **Include** button to include the new region.
6. If you “paint” a larger region than desired, use the same behavior to select the unwanted areas.
7. Select the **Exclude** button to remove the unwanted region.

Process All 4D Phases

Check this box to propagate the masking operation to all phases of a 4D study.

Add/Select

Add/Select (Figure 3-35) performs the functions of both **Include** and **Select** together. This feature is not shown in the **Region Grow** tool panel by default.

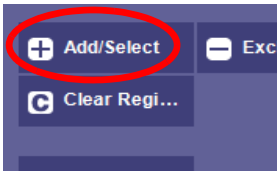


Figure 3-35Add/Select Button

To display it in the tool panel, do the following:

1. Open the Preference screen and select **Mask** from the navigation panel on the left.
2. Check the box for “Same button for Add/Select” (see "Mask" on page A-12).
3. Click OK. The Region Grow tool panel is displayed as shown in the image at right.

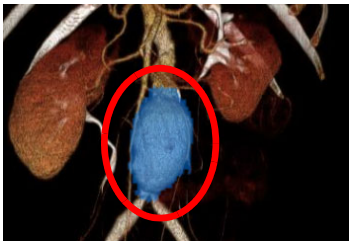
Mask

This feature allows you to segment regions of image data, create a mask for each region, and measure their respective volumes.

Note: If the *Mask* button is not visible, that means that Mask Template Mode is not enabled. Open the Preferences window, select Mask from the navigation panel on the left, check the box for Enable mask template mode, and click OK. The Mask button is immediately displayed. See "Mask" on page A-12.

---

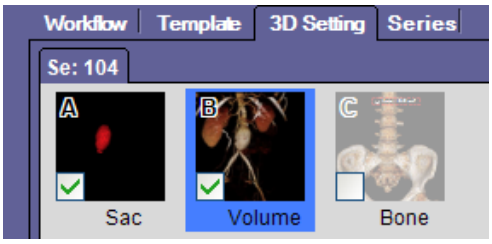
1. Apply Dynamic Region Growing to the area to be masked.



2. Use the pulldown menu to the right of the **Mask** button to select a name for the region. If an appropriate name is not in the menu, you can type in a name.
3. Select a color for the region.
4. Click the **Mask** button. The region is masked in the selected color, and the volume of the region is displayed in the measurement results.

5. To save the new mask name and color for later use, click the **+** button.

   The mask is automatically created in the **3D Setting** panel.



To save multiple mask templates configured as a single group, click the **>>** button and save as a multi-mask color preset.

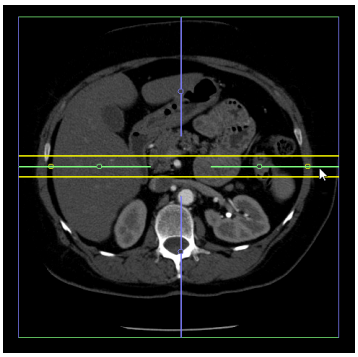
Grow Within Slab

To grow a region when the VR image is in slab mode, do the following:

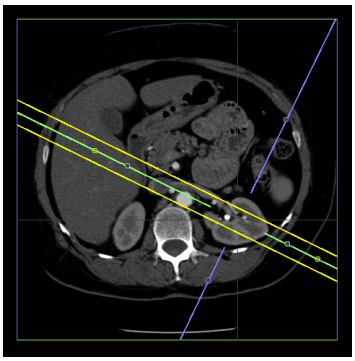
1. Check the box in the tool panel labeled **Grow Within Slab**.

   The MPR images show yellow display lines marking the boundaries of the slab in each dimension.

2. Move the display lines to the region of interest, and then rotate the slab area to include the desired area. (For instructions on how to move and rotate the display lines, see "Slab and Cube View Tool" on page 3-22.)



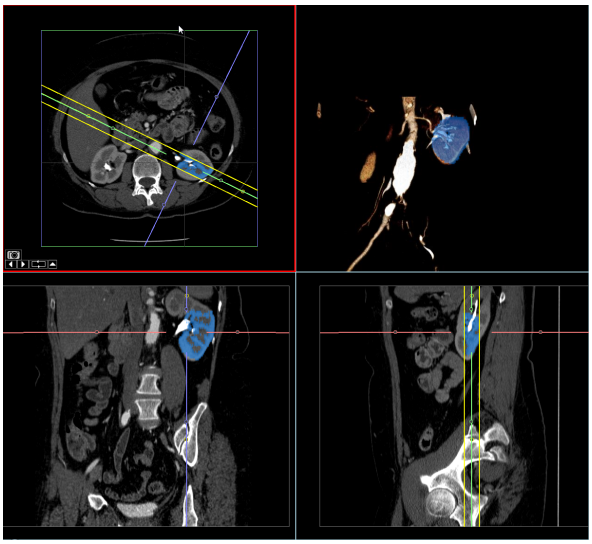
Display Lines Marking Off Slab



Display Lines Moved and Rotated

Figure 3-36: Grow within Slab

3. Pick on the main view and grow. The area is masked within the yellow line display boundaries in each MPR image (see the following figure).

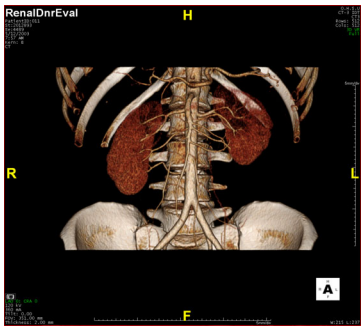


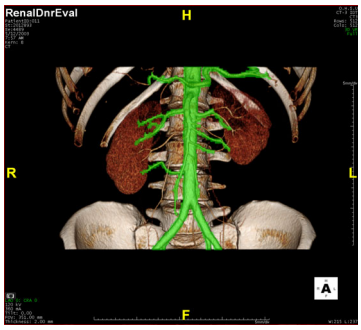
Use MPR Window Level Threshold

If you would find it easier to perform the region grow on an MPR image, you first need to make sure the **Region Grow** function can access the MPR image. To do so, click the Preferences button to open the Preferences dialog. Then click **Mask** in the navigation panel, and uncheck the box for **Use main view threshold for region growing**. See "3D Viewer" on page A-8. The Mask preferences are described in that section.

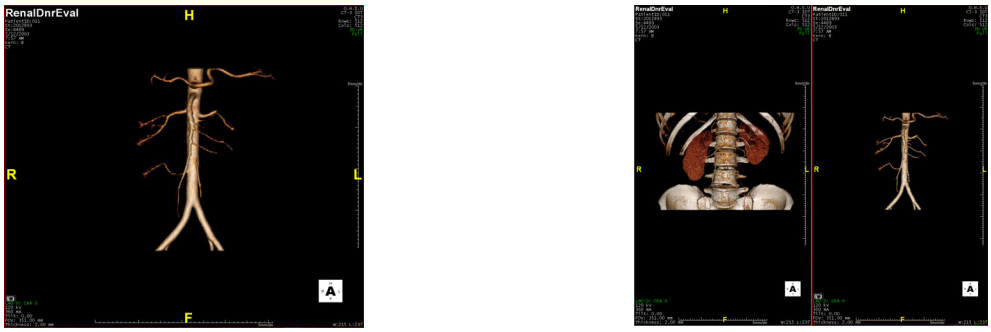
Example

1. Load an image into the iNtuition 3D Viewer, and click the **Region** button in the Tool Panel.
2. Mask the area of interest, following the instructions under "Masking a Region" on page 3-53.
3. Click the **Add/Select** button.
4. Select the **1x2 Bone Edit** window mode. (For information about window layouts, see "Window Layout Modes" on page 3-179.) The right panel of the window shows the included region, and the left panel shows all parts of the original image that were not included (the “Excluded” region).





Original Image **Masked Region**

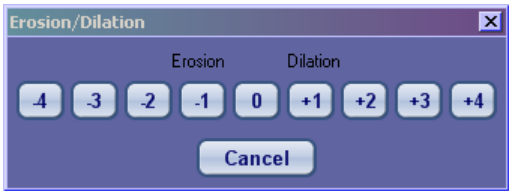


Included Region **Image in 1x2 Bone Edit Layout**

Figure 3-37 - Masking Regions

Erosion/Dilation Dialog

This dialog is displayed when **Select**, **Include**, **Exclude** or **Add/Select** is performed. The dialog allows you to fine-tune the amount that is added or removed (see "Masking a Region" on page 3-53):



Note: This dialog is not displayed by default, but must be enabled through the Preference screen. For details, see "Mask" on page A-12.

Single Click

You can mask a region with a single click by enabling it in the Preferences. When single-click region-grow is enabled, place the mouse over the area you want to grow, hold down the **Shift** key, and click once. The entire structure (such as a vessel) is masked.

For information on how to change the single-click Preference option, see "Mask" on page A-12.

Bone Removal 

There are several bone removal tools, each tailored to different parts of the body. Click the down-arrow to the right of the **Remove Body Bone** button to show a menu of bone removal options for different body parts. Select the mode that is most appropriate for the body part under examination.

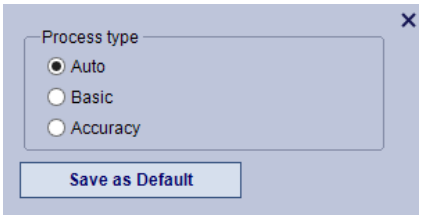
Note: You must validate the results and use the mask edit tools to adjust the image manually, if necessary.

- **Remove Body Bone**

  This is the most general bone removal tool. Use this tool when removing bone from part of the body except the rib cage, head, or neck.

  The Remove Body Bone tool allows you to specify the type of process used for bone removal and optimize the bone removal option in the case of urogram studies.

  Click the **Option** link located to the right of the **Remove Body Bone** button to open the **Process type** dialog (see image at right). The selections provide the following features:



  - Auto - The system chooses Basic or Accuracy automatically, depending on the data. This is the initial default.
  - Basic - This process runs faster.
  - Accuracy - This has a higher resolution and the results are more accurate.

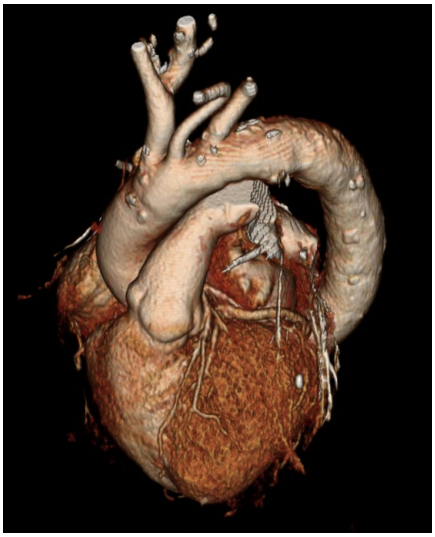
  If you want to keep your selection for future studies, click **Save as Default** before closing the dialog.

- **Remove Rib Cage (Excluding the Aorta)**

  Used for heart studies. The aorta is also removed.

- **Remove Rib Cage (Including the Aorta)**

  Used for heart studies. The aorta is not removed:



Note: The aorta might not be successfully extracted if it does not have contrast.

- **Remove Head Neck Bone**

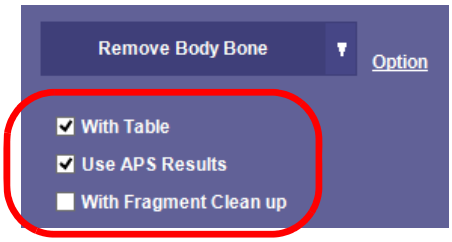
  Remove bone around the head and neck. Used for examination of the arteries connected to the brain. See Appendix A: "Mask" on page A-12 for head/neck settings.

- **Remove CT Table**

  Removes the CT table from the image without removing bone.

- **Remove CT Head Mount**

  Removes the head mount from the image without removing bone.



Options

There are options available for each type of bone removal. These can be set each time body removal is performed, by checking the desired boxes (see image at right).

- With Table - Remove the CT table along with the bone (Remove Body Bone only).
- Expose Coronary - Expose the coronary arteries (Remove Ribcage only).
- With Head Mount - Remove the head mount along with the bone (Remove Head Neck Bone only).
- Use APS Results - If there are any bone removal APS results included with the study, apply them here.

- With Fragment Cleanup - Remove any remaining bits of bone or other undesirable fragments from the image.

Head/Neck Bone Removal 

Click the **Head/Neck** button in the Tool Panel to display the Head/Neck bone removal tools. If the Head/Neck function is not already set for automatic bone removal, a dialog box is displayed first asking if you want the Aquarius iNtuition Client to remove the bone. Click **Yes** to remove the bone, find centerlines, and extract the centerlines. The Head/Neck tool is displayed in the Tool Panel (see figure below) as bone removal is being performed. See Appendix A: "Mask" on page A-12 for head/neck settings.

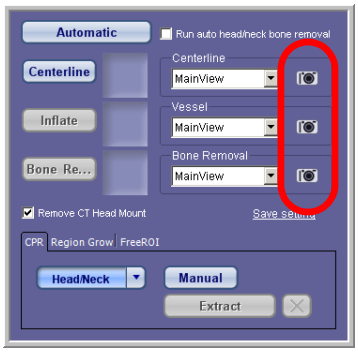
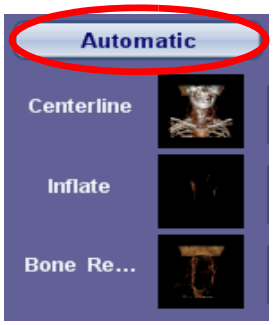


Figure 3-38: Camera Icons

As each function is performed, a small (“thumbnail”) image is displayed underneath the **Automatic** button:



Each thumbnail image corresponds with views of the centerlines, the vessels extracted and the anatomy with bones removed. Click any of the thumbnail images to display that image in the main window.

Use the camera icons (circled in Figure 3-38) to capture the corresponding image to the Output Panel.

Vessel Tools

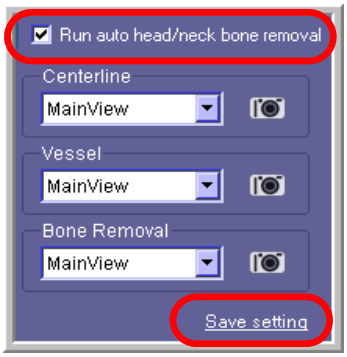
The **Head/Neck** tool allows you to analyze vessels using the **CPR** tool. You can grow vessels by using the "region grow" tool. You can cut out regions using the "Free ROI" tool. These are located in the lower portion of the tool panel. Options include Auto, coronary, normal, Head/Neck, Two Clicks and Multi-click

Figure 3-39: Vessel Tools

For instructions on using these tools, see the following sections:

- CPR: "The CPR Tool" on page 3-26
- Region Grow: "Dynamic Region Growing" on page 3-53
- FreeROI: "FreeROI" on page 3-49

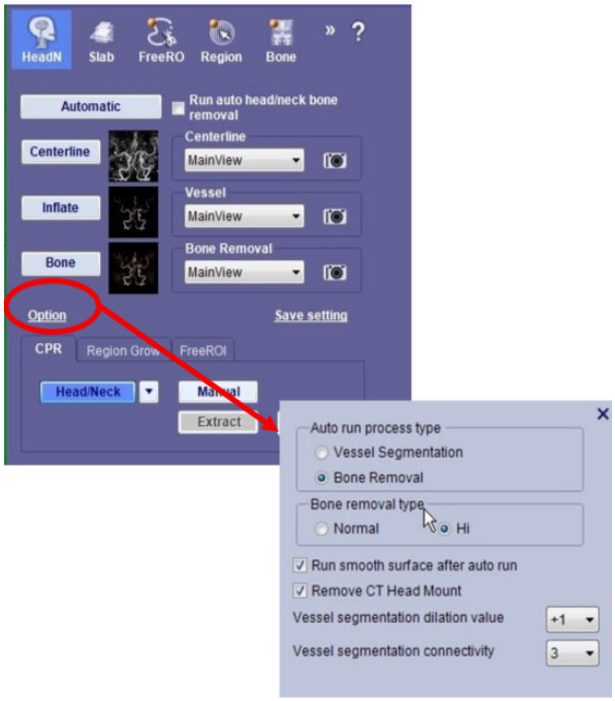
Saving Settings



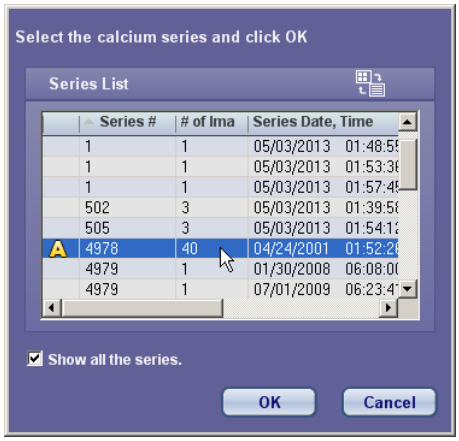
You can set an option to specify that the **Head/Neck** tool always removes the bone, finds centerlines and extracts the centerlines automatically, whenver the **Head/Neck** tool button is clicked. The checkbox for this option is located above the window pull-down menus. Enable, and then click the **Save Setting** link, located just below the camera icons (see figure at right).

Option Panel Settings:

Choose the Auto run process type by selecting the “Option” and specify if you would like to use Vessel Segmentation or Bone Removal. You can then select if you would like the bone removal engine to run at “normal” or “hi”. The “hi” bone removal option is a more effective way of conducting the bone removal function. Select the “run smooth surface after auto run” option in order to have the smooth surface function to be ran directly after bone removal. Lastly, you can specify the vessel segmentation dilation values and connectivity by using the drop down menu on the right. See figure below to view Option panel design.



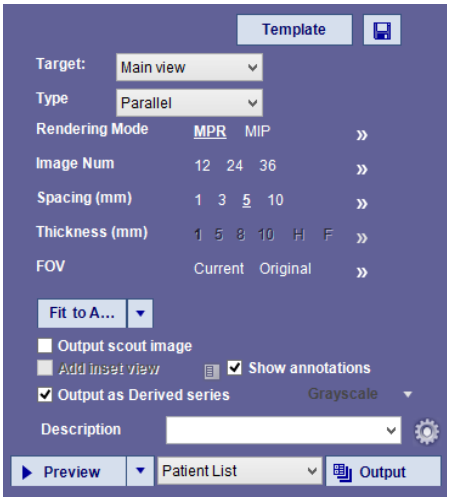
Calcium Score



When you click either the **Calcium** button in the Tool Panel or the Calcium Score workflow element, a window containing the series list for this study is opened (see image at right). Select the appropriate series and then click **OK** to open the Calcium module.

For a detailed description of the Calcium module, see Chapter 11: "Calcium Scoring"

Batch Tool



The Batch function allows you to display a series of consecutive images, taken from a defined area on an image. These can be 2D slices in MPR, MIP and other 2D rendering modes (Parallel mode), or they can be a succession of rotating 3D images (Radial).

To begin Batch mode, click the **Batch** button in the Tool Panel.

Figure 3-40: Batch Tool Panel

Parallel Batch

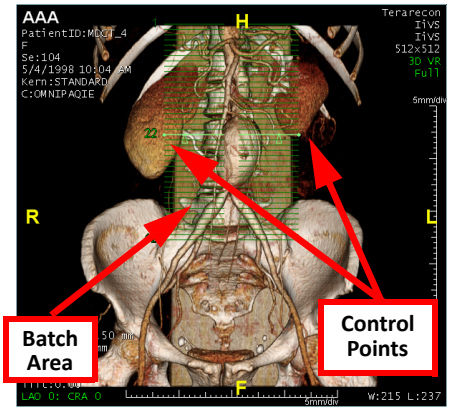
To make sure the batch mode is parallel, select **Parallel** from the pull-down menu labeled **Type** in the Tool Panel (see Figure 3-40).

Click on the image in the main window, and drag the mouse down along the image. A grid is drawn as you drag the mouse, defining the batch area from the first slice to the last.

Alternately, you can define the batch area by entering the batch parameters manually. In the **Batch** tool panel (see Figure 3-40), enter the rendering mode, number of images, spacing and field of view (FOV). To enter the FOV, do the following:

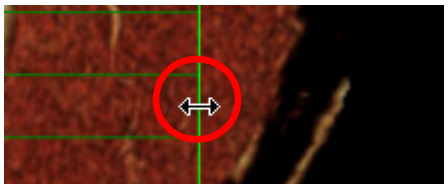
1. Click the double right arrow to the right of the **FOV** row.
2. Enter the width in the text box that appears. When you change the value of FOV, the width of the grid changes in the main viewer.

To adjust the size, location and rotation of the batch grid, note the circular dots in the corners and along the top and bottom edges of the grid. These are the *control points*, which allow you to change the size of the grid or to rotate it.



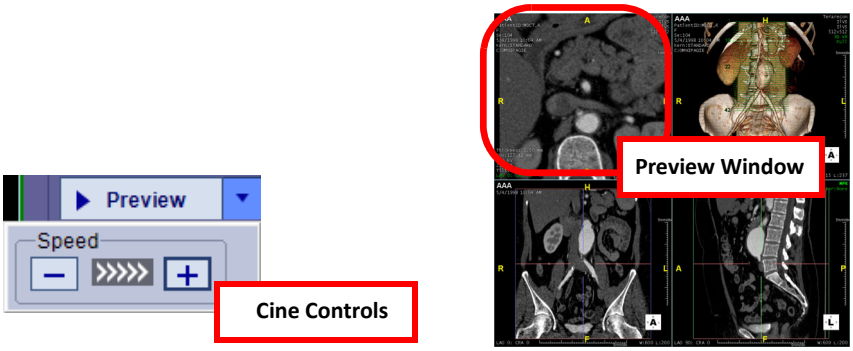
- **To adjust the height of the grid**, click on one of the dots in the center of the top or bottom edge, and drag it up or down.

- **To adjust the width of the grid**, place the mouse over the right or left edge of the grid. The cursor becomes a horizontal double-arrow (see the figure below). Click on the edge and drag the mouse right or left.



- **To rotate the grid**, click any one of the dots in the four corners of the grid.
- **To move the entire grid across the image**, click on any space inside the grid that is not part of the actual grid. Hold the mouse down and drag the grid to the desired location.

To play a cine of the slices, click the **Preview** button in the Tool Panel. The cine is played in the top-left MPR window in the 2x2 layout.



Note: You can set the speed of the preview cine by clicking the down-arrow to the right of the Preview button. A speed control box is opened.

To send the images to the Output Panel, click the **Output** button.

Fix to Axial

When this is selected, the parallel grid is automatically drawn perpendicular to the axial view. The grid can not be rotated.

Output Scout Image

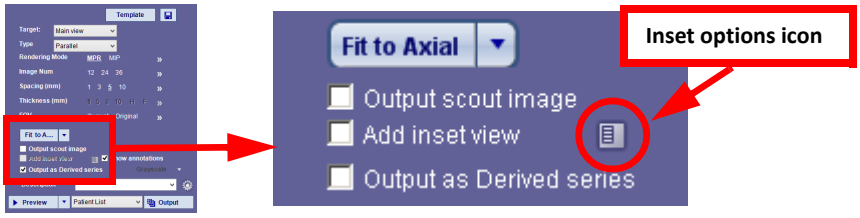
When this is checked, a scout image (the 3D image where the grid has been drawn) is captured to the Output Panel first, with the 2D slice images following.

Add inset view

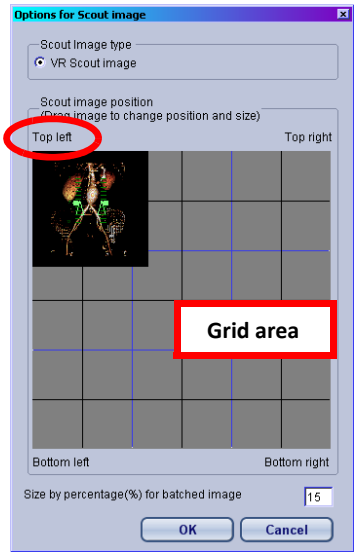
This feature allows you to place the scout image on each slice image captured in the batch process. The inset can be positioned and sized within the slice images.To add an inset view, do the following:

1. Check the **Add inset view** checkbox.

2. Click the inset options icon.



The options icon dialog is displayed. The grid area represents the slice image. Click the **Top left** link (circled in the figure below):



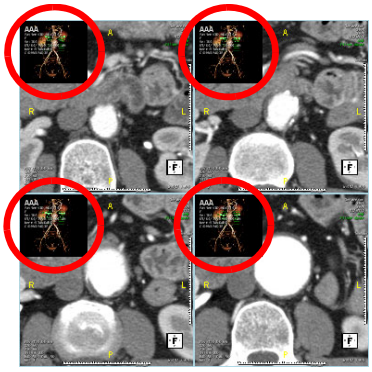
3. Click in the upper left corner of the grid and drag the mouse. The inset image appears on the grid.

4. Drag the inset image to where you want to place the inset, and then release the mouse button.

5. Resize the inset by clicking the bottom right corner of the inset image and dragging the mouse.

6. Click **OK** when finished.

When the slice images are sent to the Output Panel, they will appear as follows (inset image circled in each slice below):



Output as Derived Series

It is possible to create a derived series by outputting batched slices to the Patient List. To output the batched slices as a series:

1. Select either **Patient List** or **Output Panel and Patient List** from the output pull-down menu between the **Preview** and **Output** buttons.

2. Enter the name of the new series in the **Description** input field.

3. If you want to capture annotations into the slices, check the **Show annotations** box.

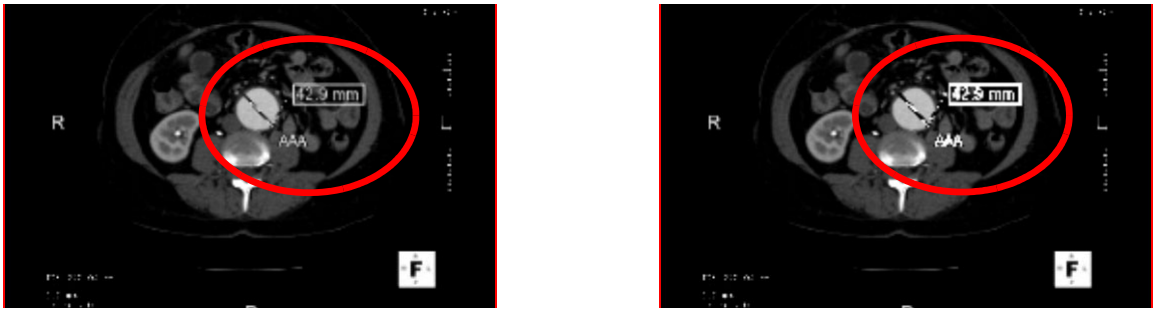


Figure 3-41: Captured Images in Patient List Preview
Left: Annotations Captured in Grayscale; Right: Not in Grayscale

---

Note: Annotations in derived series can be difficult to read, especially if they are small. To improve the quality of the annotations, set the Capture annotation in Grayscale preference (for more information, see "Output Panel" on page A-43). The following two images show a comparison between grayscale and non-grayscale annotations.

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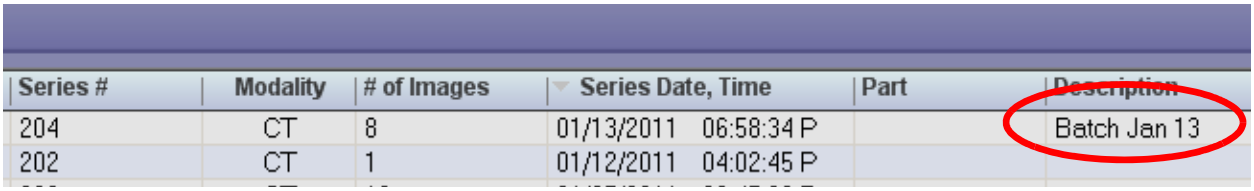
4. When finished, click the **Output** button.

5. To verify that the derived series has been created, go back to the Patient List and look for the series in the Series List.

In the example at right, the derived series had “Batch Jan 13” in the **Description** field. A series having this descripton will appear in the Series List:



Series #	Modality	# of Images	Series Date, Time	Part	Description
204	CT	8	01/13/2011 06:58:34 P		Batch Jan 13
202	CT	1	01/12/2011 04:02:45 P		

Note: Click another study in the study list and then click the current study again to refresh the Series List.

Parallel in 3 Directions

Parallel in 3 Directions allows you to create three batches in one step: front-to-back, left-to-right and head-to-foot.

1. Select **Axial**, **Coronal** or **Sagittal** from the **Target** menu.
2. Select **Parallel: 3 Planes** from the **Type** menu.

   A grid is automatically drawn on each 2D view. The grids are aligned to the cross hair.
3. Adjust any of the grids, by dragging the edges in the desired direction, to include all desired slices. The grids on all three views are synchronized, so the other two grids will be adjusted automatically.
4. Change the parameters (number of slices, FOV, spacing, and so on) in the tool panel in the same way that you would do so for the regular parallel batch.

Note: Parallel in 3 planes is not available through the main viewing window. You must choose Axial, Coronal or Sagittal.

Image Order to Output

Three-direction batch can be output in one series or thre separate series. The order in which the batched images are output is configurable. There are six different ways that the images can be ordered. For example, if you wanted the images to be batched starting with axial, followed by coronal, and then sagittal, you would select **Ax-Cor-Sag** from the Output order menu.

1. To select an output order, click the preferences icon in the lower-right corner of the **Batch** tool panel. The Batch preference dialog is opened. The configuration for **Parallel batch in 3 directions** is located in the lower-right corner of the dialog/
2. Select the output order from the drop-down menu.
3. To have the output saved as a single series, check the **Save as one series** checkbox. Otherwise, each set of images are output as three separate series.

Flip Order and Flip Orientation

Right-click on the batch grid to select these options.

- Flip Order - Output the slices in the opposite direction
- Flip Eye Direction - Flip the images horizontally in the output

Series Options

When the output destination includes the Patient List, series options are displayed on the tool panel.

- Series Description

  If the three batches will be output as one series, you can enter the description for that series in the **Description** text input box.

  If they will be output as three separate series, you can enter one description for all, or separate descriptions for each series.

  To enter separate descriptions, click the **Description** link. This opens a dialog in which you can enter the descriptions.

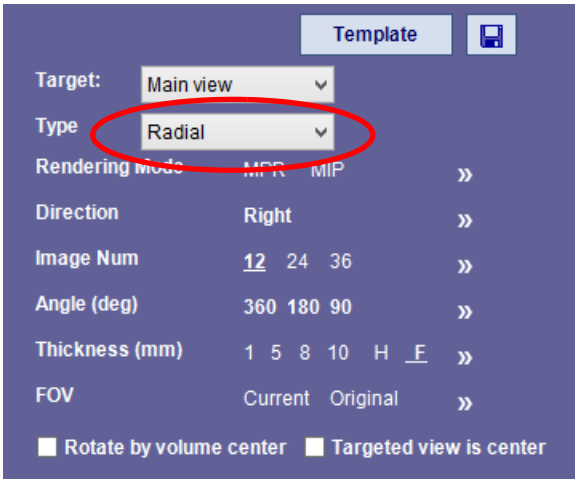
- Show Annotations

  To show the annotations on the batched images, check the **Show annotations** checkbox.

Radial Batch

Radial batch mode shows the image rotating around a central line. The image can be rotated to the left or right around the vertical center, and can be rotated up or down around the horizontal center.

To change to radial mode, select **Radial** from the pull-down menu labeled **Type** in the Tool Panel:



Parameters must be entered manually in the Tool Panel for radial batch mode.

1. Enter the Rendering Mode, Number of Images, Thickness and FOV as with Parallel Batch mode. All rendering modes are valid. Slab thickness applies only to 3D, MIP and Thick MPR rendering mode.

2. Enter the rotation **Direction** (right, left, up or down).

Note: If the **Rotate relative to the patient** setting is enabled, the rotations will go in the desired direction from *patient's* perspective. For more information, see Rotate relative to the patient below.

3. Enter the **Angle**, which defines the *total* angle of rotation. The total angle size will be divided by the number of images, to obtain the angle of rotation for *each* image.

4. Click the **Preview** button to see the batch movie.

Other Settings

- **Rotate by volume center** - Use the center of the *volume* as the axis of rotation, rather than the center of the image, regardless of where the volume is positioned within the image window.
- **Targeted view is center** - Begin the rotation at the halfway point between the current position and the final position.
- **Output as Derived series** - Send to the Patient List as a new (derived) series.
- **Rotate relative to the patient**

Note: This setting is accessed through the user preferences (see "Batch" on page A-21).

When this setting is disabled, the image is rotated toward the *screen* direction. For example, if **Right** is selected for the rotation direction, the image rotates toward the right side of the screen. Note the orientation cube in the bottom-right corner of each image in Figure 3-42.

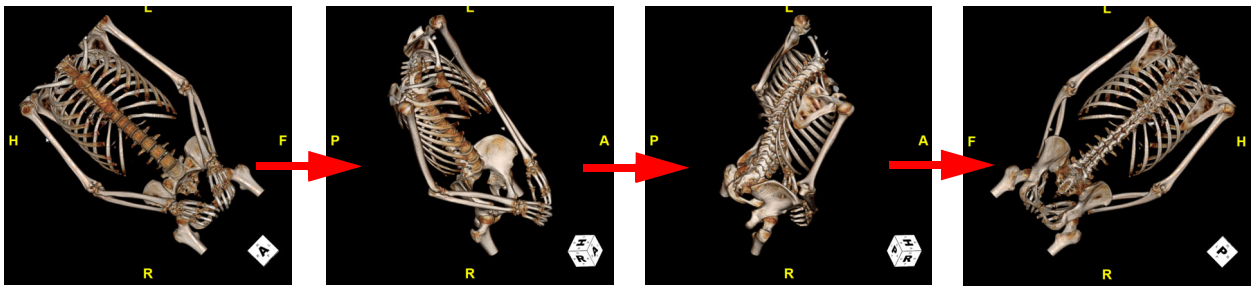


Figure 3-42: Normal Rotation, Right-rotation selected

When this setting is enabled, the image rotates in the selected direction from the patient's perspective, regardless of the image orientation seen on the main view. However, the image will always rotate about the center point of the screen. Note the orientation cube in the bottom-right corner of each image in Figure 3-43.

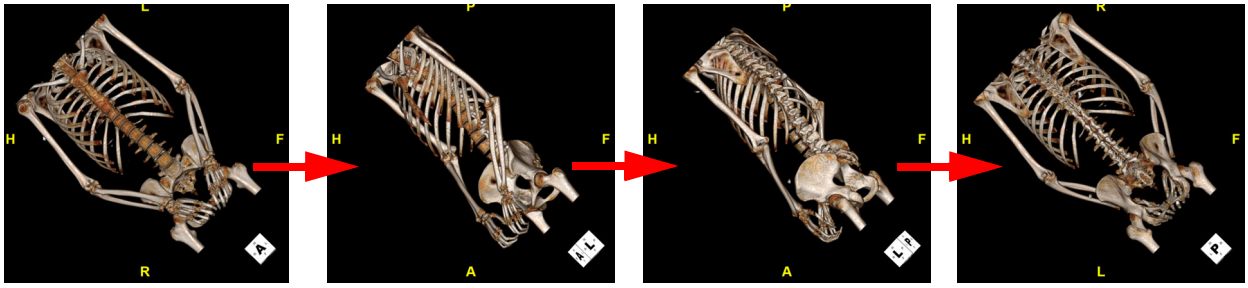


Figure 3-43: Rotate Relative to Patient, Right-rotation selected

CPR Batch

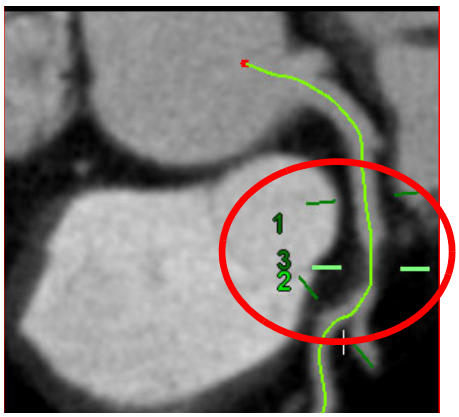
2D Batch can also be performed on CPR windows.

CPR Perpendicular

Perpendicular allows you to view perpendicular slices along the centerline of a CPR image.

To begin perpendicular batch, open the CPR view of a vessel and:

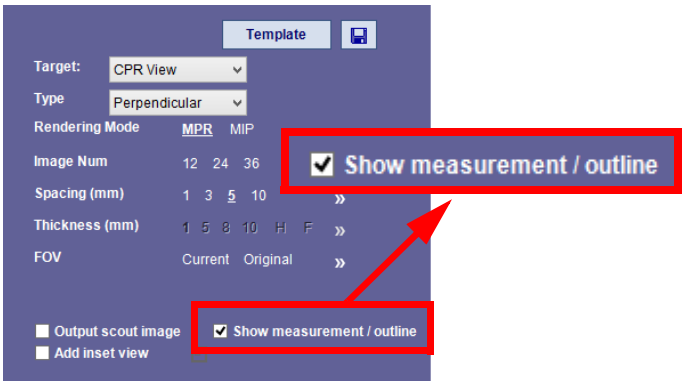
1. Click the **Batch** tool button. The **Batch** tool panel is opened, with **CPR View** as the target.
2. From the **Type** menu, select **Perpendicular**:
3. Click and then drag the mouse in the CPR window. The batch area is drawn along the centerline:

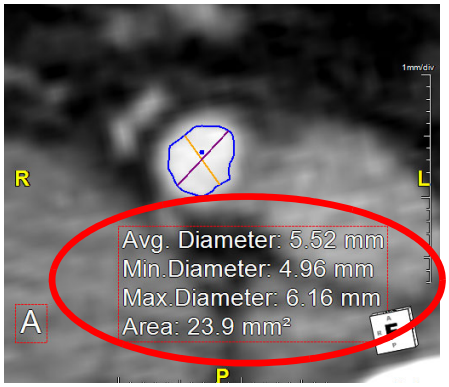


4. In the tool panel, select the rendering mode, number of images, and other values, as you would in parallel batch mode.

Other settings

- **Show measurement / outline** - Capture vessel diameter results and outline shown on the centerline cross section views.





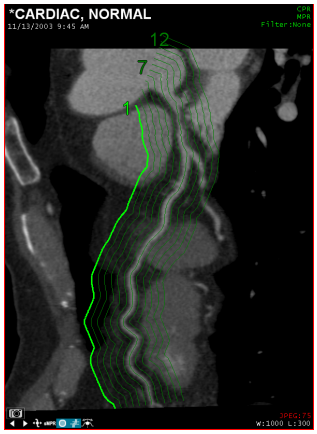
CPR Parallel

In parallel batch mode on a CPR window, the view of the slices is perpendicular to the centerline. To perform parallel batching on a CPR image, you first need to open the CPR view of a vessel. Then:

1. Select the **Batch** tool panel. The **Target** menu will already display “CPR View”.

2. Select “Parallel” from the **Type** menu.

The parallel batch grid is displayed on one of the CPR windows:

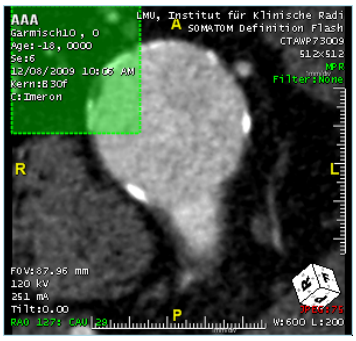


As with batch operations on a 3D window, you can change the grid using the Tool Panel. You can set the rendering mode, the number of images and the distance between each slice.

Slice output is viewed in the other CPR window. You can also change the output direction of the batch. To do so, right-click on any of the grid lines of the batch window, and select **Flip Output Order**.

Pan Preview Window

When the inset view is added to the preview window, it can sometimes block the view of the structure being examined, in which case, it would be useful to pan the image so that you can see the necessary area:



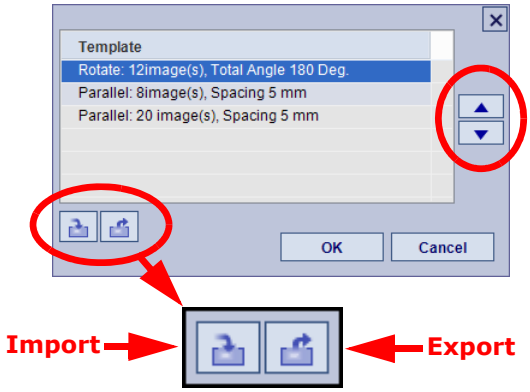
1. To enable panning of the preview window, open Preferences.
2. Under **Viewer** in the navigation panel (on the left), click **Batch**.
3. Under **CPR Batch**, check the box labeled **Pan image for perpendicular batch**, then click **OK**.

Templates

Templates allow you to save and then use the same batch parameters at different times or for different data. If you perform many similar batch operations on different studies, you can specify the spacing, number of images, angle, and so on, and can then use that same specification later for another study.

Importing/Exporting Templates

To import a batch template, click the import button in the Template tool panel (see figure below). A Windows navigation dialog is opened. Navigate to the folder where batch templates are stored.



To export one or more templates, first select the template or templates you would like to support. To make multiple selections, hold down the **Ctrl** key. Next, click the export button, and then navigate to the folder where you would like to store the template(s).

To sort the items in the template list, for example, to put the most frequently used templates at the top, select the template you want to move, and then use the up or down button to move the template in the desired direction.

Outputting Images

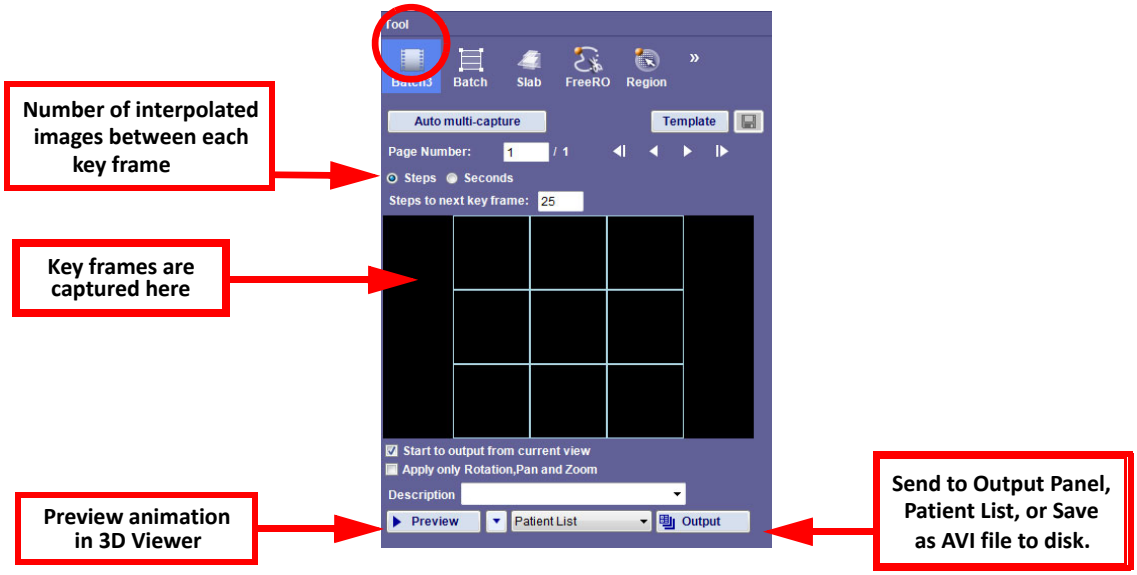
You can send batch images to the Output Panel, the Patient List, both, or as an AVI file. Use the pull-down menu between the **Preview** and **Output** buttons to select one of these four choices. Then click the **Output** button to send the images.

The Batch Wizard

If you need to use the entire screen to display the main image, you can open the Batch Wizard by pressing the **F8** function key on your keyboard. The Batch Wizard is the same Tool Panel as the one in the right panel, but it is displayed on the bottom of the image area. You can then hide the right panel to obtain maximum space for the image.

Batch3D 

Click the **Batch3D** button in the Tool Panel. The Batch3D tools are displayed:



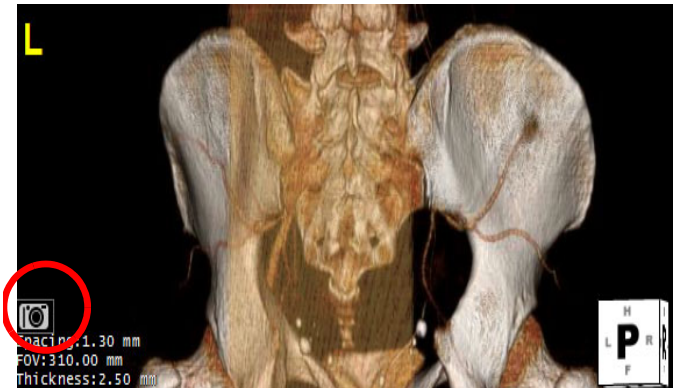
Batch3D works by taking snapshots that you have captured from the 3D window (known as *key frames*) and creating an animation of the image. The animation begins with the first key frame, ends with the final key frame, and passes through each of the intermediary key frames you have captured. The software is designed to insert interpolated images between each key frame to produce a smoother transition. For added customization, the user can set the number of interpolated images between every two key frames, and the total time of the generated movie is divided equally for transition from one key frame to the next. This feature allows you to set the transition time independently for each key frame.

If using a multi-phase series to create a 4D batch, the **Enable 4D phase changing** check box must be checked:

Note: This option does not appear for non-phased series.

---

1. Orient the 3D image to the starting point, and capture the image by clicking the camera icon in the lower left corner of the image:



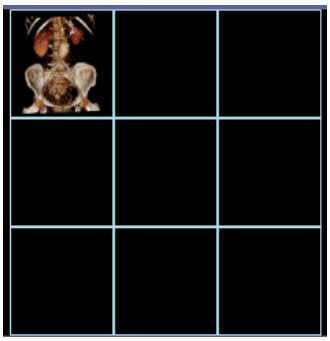
The first key frame appears in the first (upper-left) square of the Batch3D tool panel.

2. Modify the image as you wish (pan, zoom, rotate, change the rendering mode, or click to the next phase in the 3D window) and click the camera icon again to add the next key frame to the tool panel.

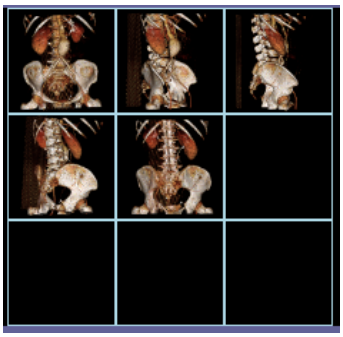
Note: If you are performing several operations on the image, but only want to see rotation, zoom and pan operations in the batch animation, click the “Apply only Pan, Rotation and Zoom” checkbox.

---

3. Repeat step 2 for all views you want to capture.



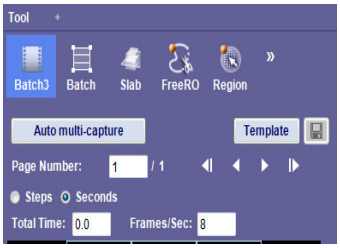
First Key Frame



Multiple Key Frames

Figure 3-44: Capturing Frame View

4. There are two options to choose from, **Steps** or **Seconds.** If you choose **Steps,** enter the number of images between each key frame in the input box labeled **Steps to next key frame**. This determines how many interpolated images will be inserted between each key frame. A higher number will produce a smoother transition as the image moves, but will also create more batch data. If you choose **Seconds,** you will input the **Total Time** desired and then the **Frames/Sec** you wish to view. The option is shown below:



5. If desired, preview the batch by clicking the **Preview** button. This does not output any images, but simply plays the animation in the main window.

6. Select the output destination from the pull-down menu located between the **Preview** and **Output** buttons.

7. Click **Output**. If you have selected **Save as AVI** as the output destination, a Windows **Save As** dialog is opened so that you can name the file and navigate to the folder where you want to save it.

   The AVI movie can be viewed in any video-playing software that supports the AVI format. Windows Media Player (standard with the Windows operating system) is one option (see image at right).

Batch 3D Templates

Batch 3D templates work the same way they do for Batch (2D). Please see "Templates" on page 3-74 for information and instructions.

Common Mask Controls

This control panel is used to fine-tune mask functions in each of the following tools:

- FreeROI
- Dynamic Region Growing
- Bone Removal
- Mask Threshold
- Angio View

The Common Mask Control Panel appears at the bottom of the Tool Panel for each of the above tools.

Description

- Undo - Nullifies the most recent mask operation, to take the process back one step. Up to 16 operations can be undone consecutively.
- Clear - Clears all operations that have been performed during this session and restores the original image.

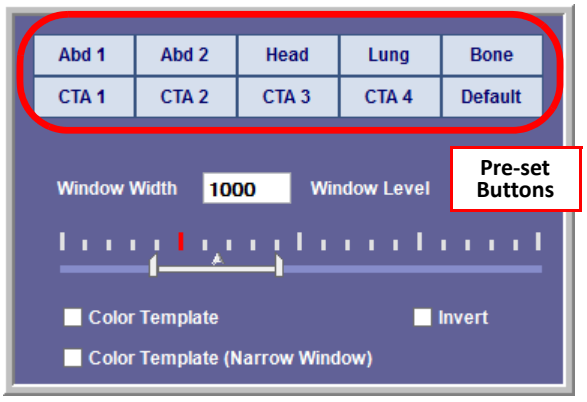
- Reverse - Most useful for the FreeROI tool, and is best seen in 1x2 layout (see "1x2 Bone Edit" on page 3-179). The left panel shows everything that has been removed, and the right panel shows everything that remains in the image. The Reverse button switches the two images.
- Bone Edit Mode - Opens 1x2 Bone Edit layout mode.
- Fragment Cleanup 

- Begins fragment cleanup. You can specify the level in the pull-down menu.
- Erosion/Dilation 

- Adds or subtracts pixels of data to/from the image.
- Turn Overlay On/Off - Toggles the green overlay on the MPR views, showing the masked area that has been removed.
- Show/Hide Mask Outline - Allows you to see the outline of bone mask on an image that has had bone removed. Click on the down-arrow on the right to display a slider. Moving the slider to the right shows more bone outline.

Window Level Tool

Adjust the window width/level from this tool panel. Use any of the preset buttons, or enter appropriate values in text boxes.



If you select **W/L** as the mouse mode, you can also adjust the W/L of the image by left-click and drag.

Changing a Preset W/L

To change an existing preset W/L to a new level, right-click on the preset icon. The following dialog box is displayed:

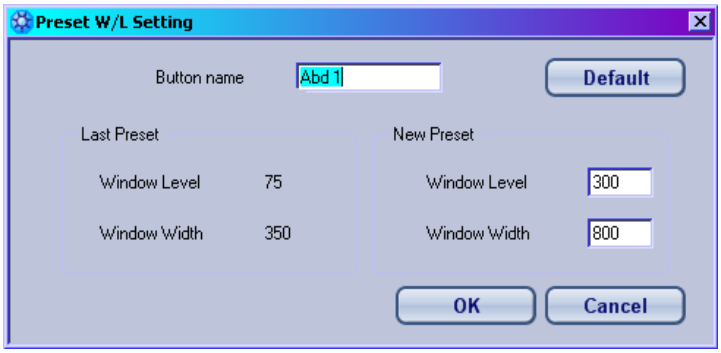
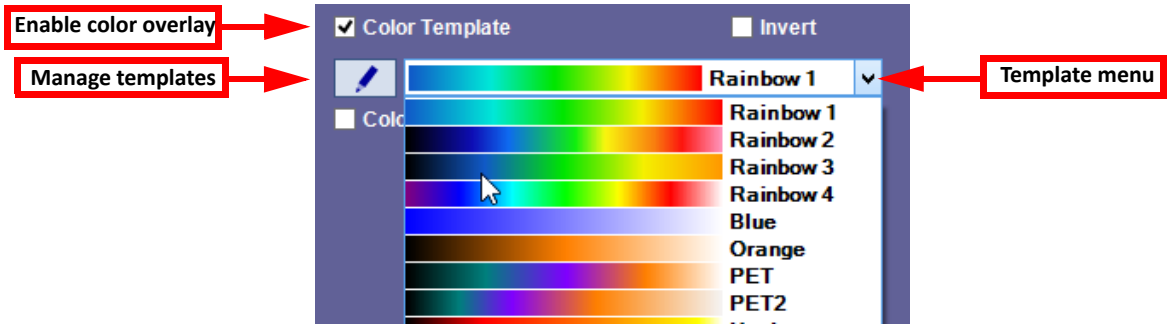


Figure 3-45: Change Preset W/L Dialog

The values on the left side, under “Last Preset”, show the current values for this preset button. The input boxes are on the right, where you can enter new values. You can also rename the preset button by entering the new name in the “Button name” input box at the top of the dialog. Clicking the **Default** button will restore the reset button to its original default values.

Color Template



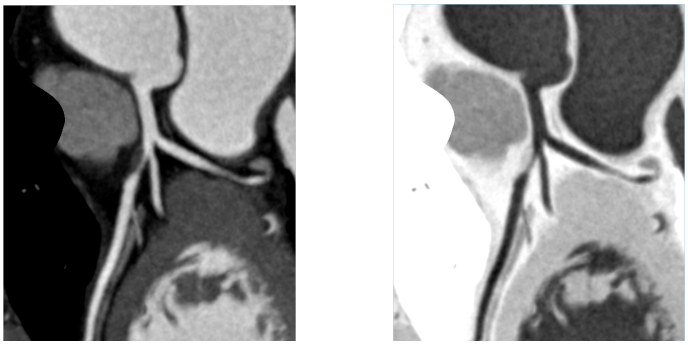
Check the **Color Template** checkbox to enable the color overlay.

Click the down-arrow on the right to show the pulldown menu. Use this menu to select a template.

Click the pencil icon to manage templates. The dialog allows you to create new templates, import templates, set a template as default, and export, delete, copy and rename templates. The following dialog is opened. See "Creating Color Map Templates" on page 9-5 for full instructions on using this feature.

Invert W/L

Invert W/L reverses the black and white values of the image. Click the **Invert** checkbox, in the bottom-right corner of the tool panel, to display the image in reverse.



Inverting an image with a color overlay produces an overlay having the opposite values, within the range of the selected color template.

Anatomy Label

Warning: The labels displayed by this function are suggestions resulting from an automated algorithm, and are not necessarily 100% accurate. The labels must be verified by a qualified person before being used.

Anatomy labels allow you to identify vessels or other body parts so that they can be found easily. Labels can be added automatically by Advanced Processing prior to being pushed to your server. You can also add labels manually using this tool, whether or not Advanced Processing has previously added labels.

If labels have been added by Advanced Processing, the list of vessels in the Anatomy List is displayed in regular text:

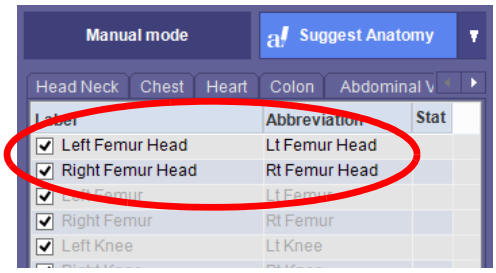


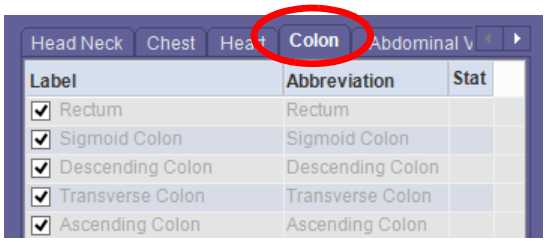
Figure 3-46Label Window

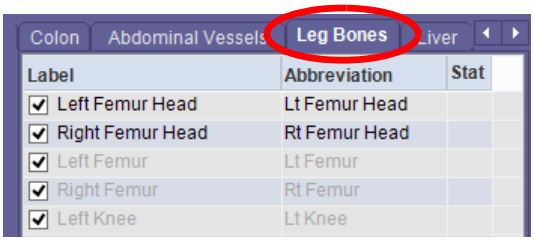
If labels have not been added to this data by Advanced Processing, the anatomy list initially appears in light-weight (grayed-out) text, as shown in the following figure. Grayed-out text indicates that a label has not been added to the data for that vessel or body part.

This feature allows you to examine each label in the image and validate it (if desired), to move the label to the correct place, to delete the label if that is appropriate, and to add new labels manually.

Anatomy Label Type

The anatomy label type tabs are at the top of the anatomy list. Each tab shows the set of labels that are relevant for the selected body part. When the **Colon** tab is selected, labels for the colon are listed (see image below, left). For anatomy label type **Leg Bones**, leg bone labels are listed.





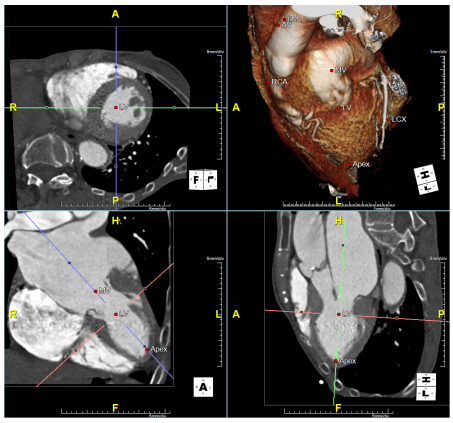
Orientation for Heart Data

When a cardiac or other heart-related study is loaded, the labels can be shown on images that have been rotated in different ways. The Orientation feature is used to select the rotation type.

For example, to view the label on images having an oblique rotation, do the following:

1. Select **Oblique** from the pull-down menu for **Orientation**.
2. Click in the label list.

The following image shows the label on images having an oblique rotation:



Finding a Vessel

When you click on a vessel name in the anatomy list, the image is automatically panned so that the vessel having this label is centered in the screen, making it easier to find.

Note that the name must be in regular type, showing that the vessel has already been labeled. If the type is grayed out, this means that the corresponding vessel does not have a label. You can label it manually. See "Adding New Labels" on page 3-82 for instructions on adding labels.

Validating a Label

To validate a label, select the desired vessel from the list and click the **Validate** button.

Moving a Label

There are two ways to move a label to another location on the image. The first is as follows:

1. Hold down the shift key.

2. Click on the label and drag the label to the new location.

3. Release the mouse.

The second way to move a label is as follows:

1. Right-click on the label dot. The Anatomy List menu is displayed. See Figure 3-46

Note: Be sure to right-click on the dot itself. If you right-click on anything else in the image, a different menu is opened.

---

2. Select **Cut anatomy label**.

3. Move the mouse so that the cursor points to the appropriate place for the label.

4. Right-click on that location.

5. Select **Paste anatomy label**.

Deleting a Label

To delete a label, do the following:

1. Right-click on the label dot. The Anatomy List menu is displayed.

2. Select **Delete anatomy label**.

Deleting All Labels

Right-click on any label dot and select **Delete all anatomy labels** from the right-click menu.

Note: APS label results can not be deleted.

Replacing a Label

To replace one label with another, do the following:

1. Hover the mouse over the label dot and right-click.

2. Select **Replace anatomy label** from the menu. A list of all the labels is opened.

3. Select the desired replacement label from the list.

Adding New Labels

You can also add labels to vessels that were not identified by the Advanced Processing module, or in the case where no Advanced Processing was done.

1. Scroll down the Anatomy List to the lower section of the list, where the text is displayed as grayed-out. These are the unidentified (unlabeled) vessels.

Note: If there has been no Advanced Processing on this data, all vessels in the list are unidentified and are displayed as grayed-out.

2. Click on the name of the unidentified vessel that you would like to add a label to.
3. Right-click on the vessel where you are adding a label to open a menu.
4. Select **Add [*Selected Label*] Anatomy Label**.

Note: The name of this menu item changes depending on which label was selected in the unidentified vessels list. In the example above, the Right Atrium has been selected, so the item displays as “Add RA Anatomy Label”.

The new label is added to the image and is automatically validated.

Manual mode

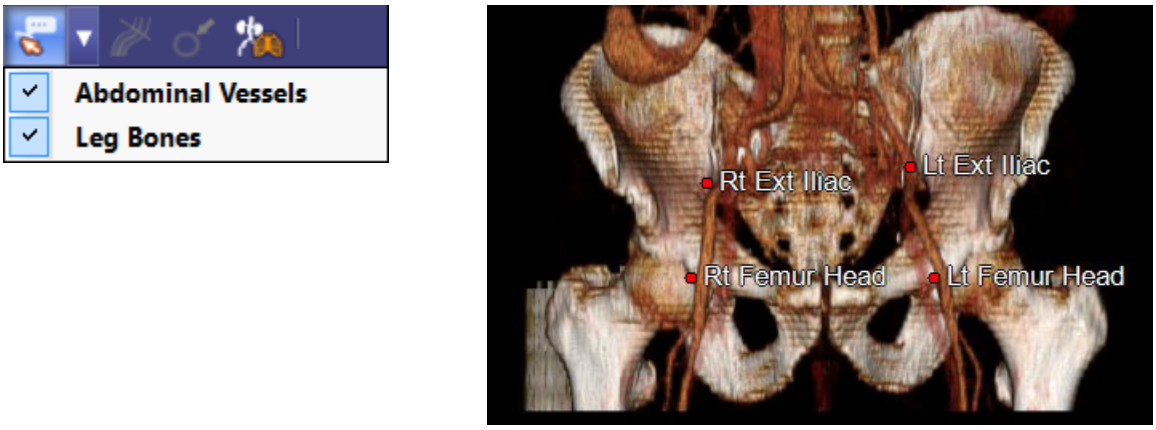
Manual mode allows you to add labels quickly. Click the **Manual mode** button in the upper-left corner of the tool panel to begin, and then select the desired undefined label name in the list. The viewer displays instructions for adding that label to the image.

For example, if you selected Left Atrium from the list, the viewer displays the following instruction: **Please shift-click on the Left Atrium**. Once you shift-click on the image, the label is added to that point.

After a label is added, the selection in the vessel list moves to the next unidentified vessel in the list. You can then continue to add vessel labels to the image.

Selecting Multiple Labeling Types

If your data has two or more types of labels, you can show labels of both types at the same time. For example, suppose your data has labels for both abdominal vessels and for leg bones. You can enable both types of labels to be displayed on the image at the same time. Select multiple label types from either the top bar or from the Anatomy Label tool panel.



Two Types Enabled in Top Bar Drop-down **Showing Both Selected Types**

Figure 3-47: Display Multiple Label Types

Vertebral Labeling

You can create labels manually or semi-automatically for vertebrae in a spinal CT scan. You can:

- Label the entire spine, based on a single validated label
- Create and extract the centerline of the spine
- Segment just the vertebrae.

To label vertebrae:

1. Load a spinal CT study in the **VolBrowse** workflow.
2. Click the **Label** tool icon in the Tool Panel. (Figure 3-48)

.

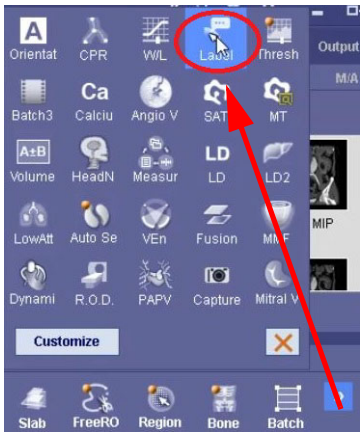


Figure 3-48 Label from the Tool Panel

3. Click the **Vertebra** tab at the top of the anatomy list:

4. Position the 3D, and sagital images to find the optimum view of the spine.

5. The tool panel then allows you to select the **Manual** button or the **Semi-automatic** button.

Figure 3-49 Vertebrae Tab opens Manual and Semi-automatic Buttons

6. Whether you select **Manual** or **Semi-automatic**, the view displays a prompt to select vertebra by using Shift+LMB-click.

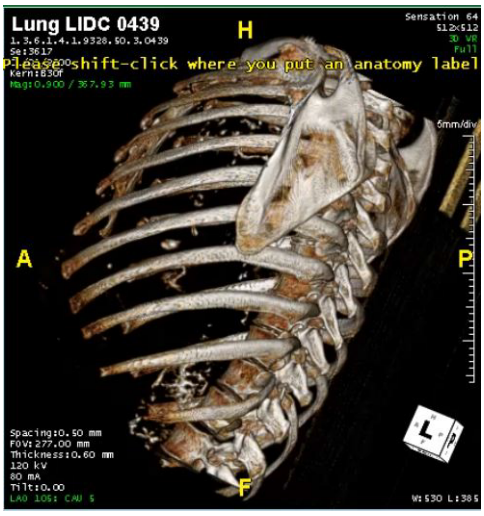


Figure 3-50 Prompt for Spine Labeling

7. If you select Manual labeling, you will need to Shift+LMB-click on the center of each vertebrae. If you select **Semi-automatic** labeling, a separate Vertebrae window opens.

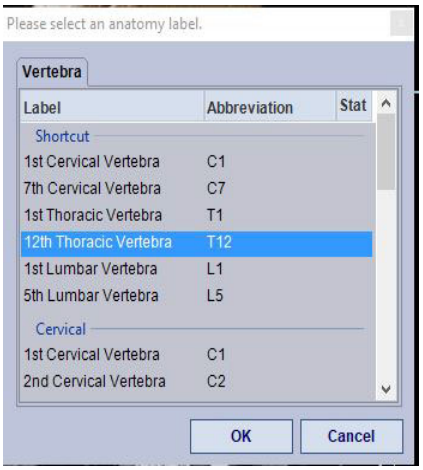


Figure 3-51 The Thoracic Vertebra T12 is Selected

8. Highlight the preferred vertebra and select **Ok**.

9. The viewer contains a labeled spine.

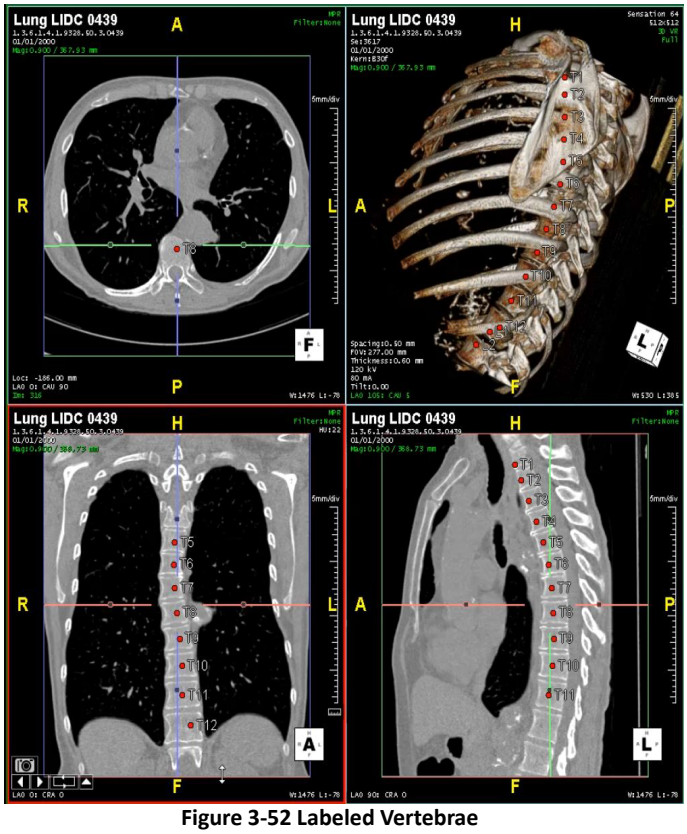
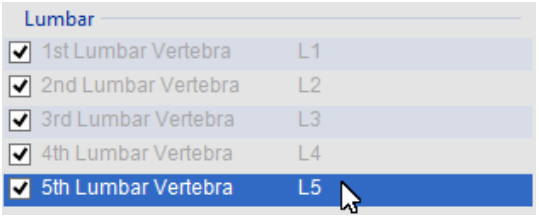


Figure 3-52 Labeled Vertebrae

Extract Labels from Validated Label

At first, the labels in the Vertebra table are grayed out because they have not been identified yet.

1. Click the name of the first vertebra in the spine that you want to identify.



2. The software instructs you to hold down the **Shift** key and click on the selected vertebra.

Note: Always click in the *center* of the vertebra.

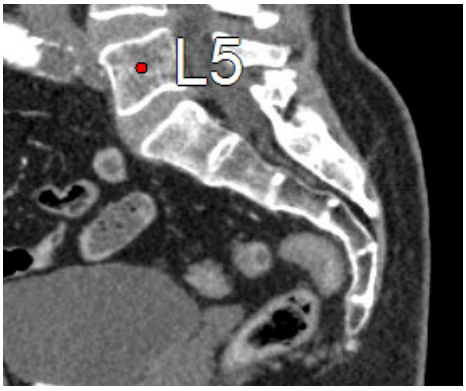


Figure 3-53: Vertebra Labeled

3. Once a vertebra is labeled, you can continue to shift+click along the spine to identify successive vertebrae.

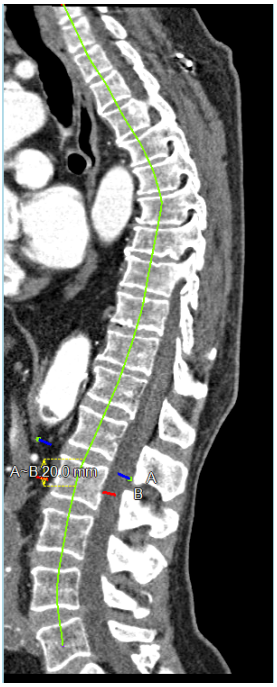
4. Follow the instruction at the top of the screen, which tells you which vertebra AQi is expecting you to click on next.

5. If you want to label a different vertebra, click on the name of that vertebra in the anatomy list in the tool panel. Vertebral labeling makes it easy to click on and label successive vertebrae, but you can label them in any order.

Extract Spinal Cord Centerline

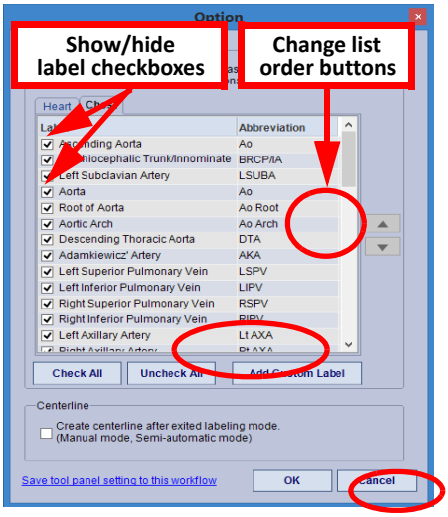
To extract a centerline, you first need to identify and validate at least two vertebrae. The two vertebrae do not have to be adjacent.

Click the **Create Centerline** button, at the bottom of the tool panel. A centerline is calculated and drawn from the first labeled vertebra to the last one:



There do not need to be any labeled and validated vertebrae in between them. However, the more vertebrae you label, the more accurate the centerline will be.

Show/Hide Labels



In the lower-right corner of the tool panel there is an **Option** link that opens a dialog for managing the label lists. Click the link to open the dialog. To show a label on the image, check the box next to the label name in the **Option** dialog. The label is listed in the tab for its type, such as **Heart** or **Chest**. To hide the label, uncheck the checkbox.

Changing the Display Order

To change the position of a label name in a list, select the label in the list and then use the buttons on the right side of the **Option** dialog (see image at right) to move the label name up or down in the list.

Custom Label

In the case where you need to label a body part whose name is not provided in any of the label lists, you can create a custom label. To do so, click the **Add Custom Label** button in the **Option** dialog. The **Add Custom Label** dialog is opened.

1. Enter a name for the label, to be added to the list for its Body Part type.
2. Enter an abbreviation for the name, to be displayed on the appropriate location in an image.
3. Select a body part category from the pulldown menu.
4. If the **Group** menu becomes active after the body part is selected, select the label group within the Body Part. In the example shown at right, the Body Part selected is **Vertebra**, and the Group is **Thoracic**.
5. Select the **Type** of tissue, such as vessel, organ or bone.
6. Click **OK**.

The custom label is added to the list:

Save Tool Panel Setting to This Workflow

Click this link (located in the lower-left corner of the Option dialog) to save the current settings in the Anatomy Label tool panel, including custom labels, to the current workflow. When future data is loaded into this workflow, these settings will be in effect.

Mask Threshold 

Set the mask threshold to display all points of an image whose HU values are between the numbers specified in the tool:

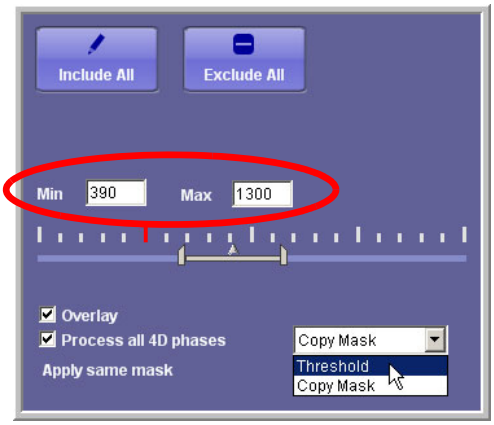


Figure 3-54: Threshold Tool Panel

1. Set the minimum and maximum HU values, either by entering them manually in the text boxes, or by using the sliders. (The values are reflected in the text boxes as the sliders are moved.)

2. To display all points of the image that fall within the threshold, click **Include All**.

3. To display all points that fall *outside* the threshold, click **Exclude All**.

Other Functions

The Threshold tool also includes the following functions:

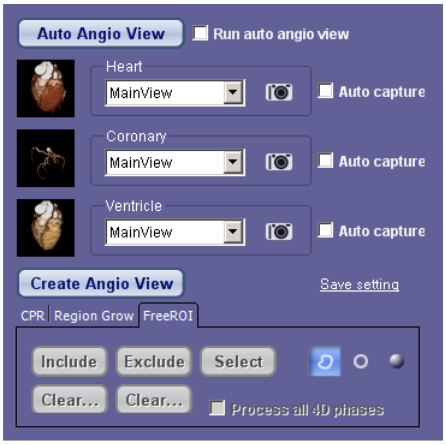
- Overlay - Show a color overlay on 2D images where the HU values fall within the threshold.
- Process all 4D Phases - Propagate Threshold operations to all phases of a 4D study.
- Threshold/Copy Mask - From the pulldown menu shown in Figure 3-54 on page 3-90, select **Threshold** to copy the current threshold setting to the other phases. Select **Copy Mask** to copy the mask in the current phase to the other phases.

Angio View 

Angio View allows you to display a MIP view of an image, with the focus on the vessels. To generate the angio view automatically, click the **Auto Angio View** button located at the top of the toolbar. The tool panel displays results as shown in the figure at right.

Each small (“thumbnail”) image along the upper-left side of the tool panel corresponds with views of the heart, coronary arteries and ventricle. Click any of the thumbnail images to display that image in the main window.

Use the camera icons to capture the corresponding image to the Output Panel.



The Angio View tool panel allows you to do region growing on the image to show more vessel tissue, and to cut out or add in sections of the image using the FreeROI tool. These are accessed by clicking on the **Region Grow** and **FreeROI** tabs located in the lower half of the tool panel.

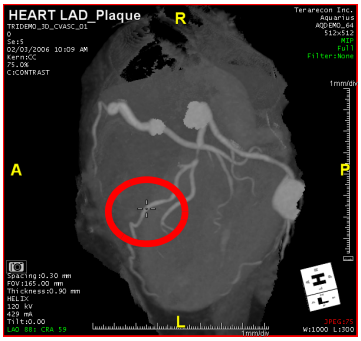
- For instructions on Region Growing, see "Dynamic Region Growing" on page 3-53.
- For instructions on using the FreeROI tool, see "FreeROI" on page 3-49.

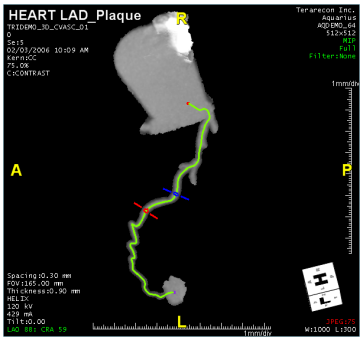
CPR in Angio View

The Angio View CPR tool allows you to extract coronary vessels without leaving Angio View. To use the CPR tool, click the **CPR** tab at the bottom of the Tool Panel.

Hold down the **Shift** key and click on the desired vessel. CPR mode is opened. From here, you can extract the vessel by clicking on the **Extract** button.

The extracted vessel is shown in the main window:





For more information about the CPR tool, see "The CPR Tool" on page 3-26.

SAT 

The Segmentation, Analysis and Tracking (SAT) module is started when you click the **SAT** Tool Panel button.

To perform SAT on a study:

1. Load a lung study or series into the 3D Viewer.

2. Click the **SAT** button in the Tool Panel.

For a detailed description of the SAT module, please see Chapter 8: "Segmentation, Analysis, and Tracking".

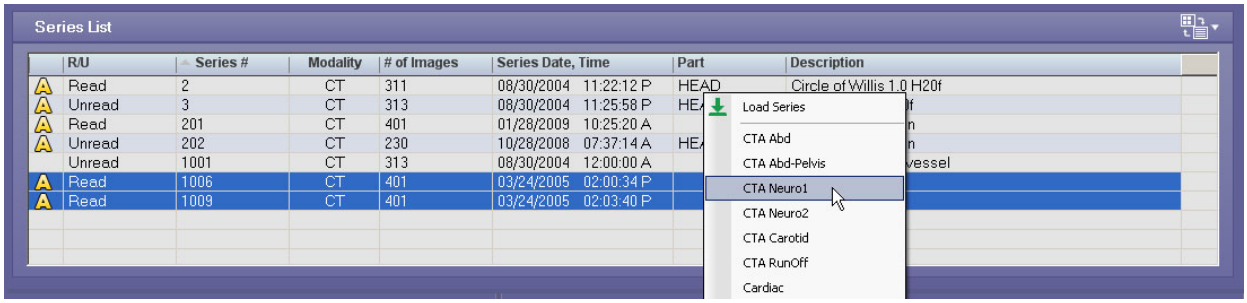
Volume Operation Tool 

Registration

In order to view an accurate overlay study, the series images have to be properly aligned or matched. This process is called *Registration*.

To register images, do the following:

1. Load two series from the same study.



2. Click the **Volume Operation** icon in the Tool Panel to open the Volume Operation Tool.

Note: If the Volume Operation icon does not appear in the Tool Panel, click the double right-arrow on the right to open the hidden functions (see "Customizing the Tool Panel" on page 3-141 for details).

---

3. Click the **Registration** button in the Tool Panel. The images are automatically registered so that they are aligned properly.

Registration Tools

Table 3.6: Registration Tools

Button or Menu	Description
Registration	Click this to perform automatic registration.
Precision	Click the down-arrow to open the menu to choose a level of precision vs. speed for the registration process. **Max precision** is the most precise, and **Speed** is the fastest.
Clear	Reset the overlay to its original position.
Enable Manual	Check this box to allow manual registration.
Volume A	The two volumes being registered. Either of these can be the base volume or the overlay volume.
Volume B	

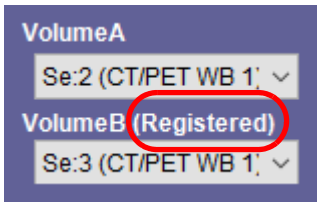
If you are not satisfied with the automatic registration, you can use the Manual registration option. For a complete description of manual registration, see "Manual Registration" on page 19-3.

Registering the Base to the Overlay

By default, the overlay study is always registered to the base study. However, you can can register the base to the overlay when needed. There are two ways you can enable this feature:

- Enable the setting in the User Preferences. See Appendix A: "Multidata/4D" on page A-14 for information.
- Change the behavior of the workflows that would be used for data that requires registration. See "Multi Data" on page 4-18 for details.

When registration is completed, the status is displayed on the tool panel, next to the volume that was registered. For example, suppose that Volume A is the base data and Volume B is the overlay, and also suppose that your preferences are configured so that the overlay data is registered to the base data. In that case, the word **Registered** appears next to the overlay data, which is Volume B:

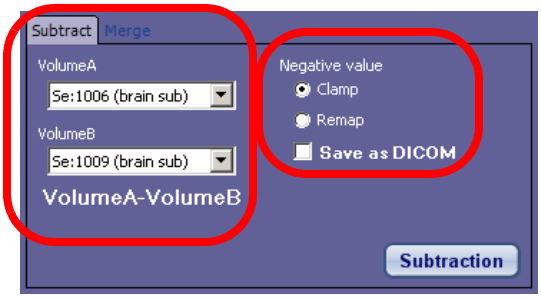


For a second example, suppose that Volume A is the overlay and Volume B is the base study. Also suppose that you have configured the preferences so that the base is registered to the overlay. In this case, the registration status is also displayed next to Volume B, because Volume B is the base and the base is the study that is being registered.

Subtraction

The Subtraction function performs a combination or superimposition of two series, which demonstrates the difference between them. Using this process, you can take a non-contrast image and subtract a contrasted image to result in a 3D image of the contrasted area of interest.

Note: The subtraction feature supports the following conditions only: 1) Volume A is a foot-view, supine, axial, non-gantry tilted scan or, 2) Both Volume A and Volume B are axial, non-gantry tilted scans, and have the same orientation, including supine, prone, decubitus L, or decubitus R.



Note: You are obligated to define the parameter ranges that are used in this procedure. When first accessed, the user interface for setting these parameters contains generic default values having no particular significance. You must acknowledge this by dismissing a warning message to this effect.

To perform Subtraction:

1. You first must decide which series is Volume A and which is Volume B. This is because the automatic Subtraction function in Aquarius iNtuition always calculates the result as Volume A - Volume B. Use the Volume pull-down menus to assign the volumes (circled in dark blue in the figure above).

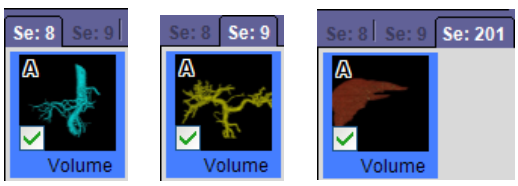
2. If the resulting values fall outside the specified range, select the **Clamp** option (circled in light blue). Data falling outside the range will be discarded.

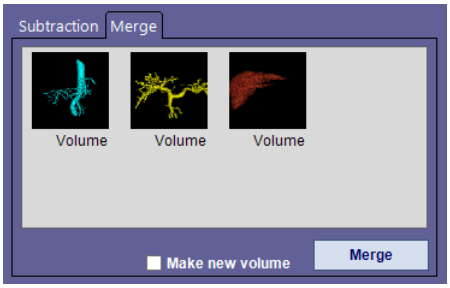
   If you select the **Remap** option, all values will be re-scaled to fit within the range. Data will not be lost but re-scaled.

   To save the subtracted images as DICOM files, select the checkbox labeled **Save as DICOM**.

Merge

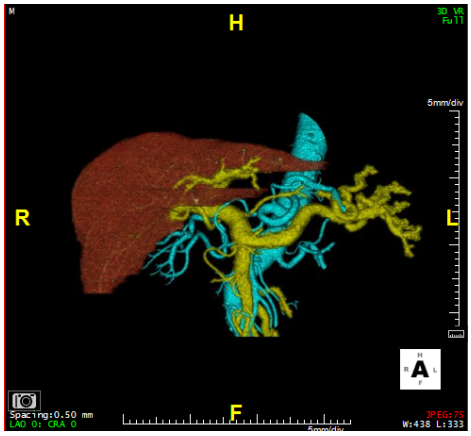
To merge two or more volumes, click the **Merge** tab. Masks that have been created by segmentation (shown in the following figure, left), done on different series should be visible in the Merge panel (below, right).





If not all the masks you want to merge are shown in the Merge panel, click on any of the missing masks in the appropriate series tab, and drag it to the Merge panel.

When all desired masks are in the Merge panel, click the **Merge** button. A new column is displayed in the main window, showing the result of merging the volumes in the individual series columns:



Measurement Protocols

The Measurement Protocols tool allows you to obtain the measurements required for a procedure or device, such as a stent.

1. To begin, click the down-arrow located in the upper-right corner of the Tool Panel:

2. The Measurement Protocols Dialog Box is displayed (see Figure 3-55).

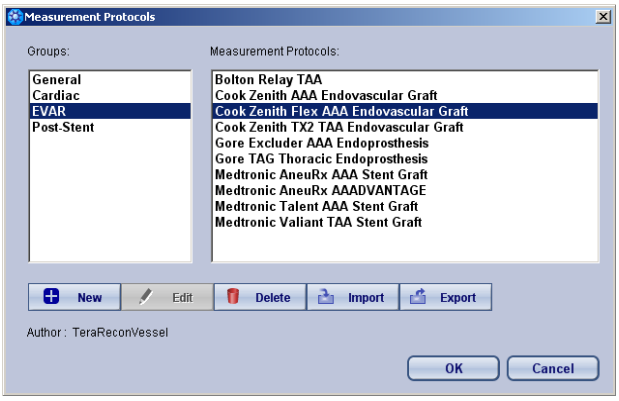
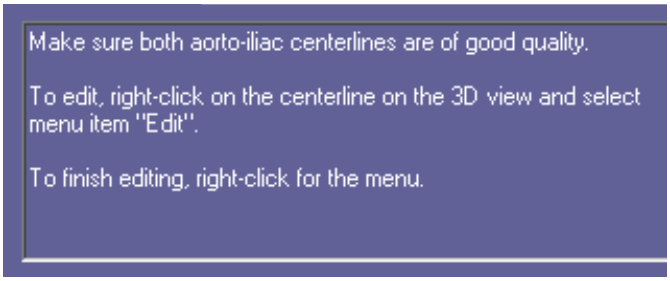


Figure 3-55: Measurement Protocols Dialog

3. Select a group from the left window, and then select a measurement protocol from the right window. The measurement protocol is displayed in the Tool Panel.

Each measurement protocol contains detailed instructions for obtaining the required measurements.



For more information, see Chapter 13: "Measurement Protocols".

Lobular Decomposition (LD) 

Lobular Decomposition allows you to measure the volume of each lobe of the liver. First you need to obtain the volume of the entire liver, and then the volume of the right lobe. The tool then calculates the volume of the left lobe. (Total volume - lobe 1 volume = lobe 2 volume).

To begin using the LD tool:

1. Select a liver study.
2. Load or RMB-click on the Lobular Liver workflow.
3. In the tool panel, select the **LD** icon. This icon is located in the hidden tools area (see Figure 3-16 on page 3-18).

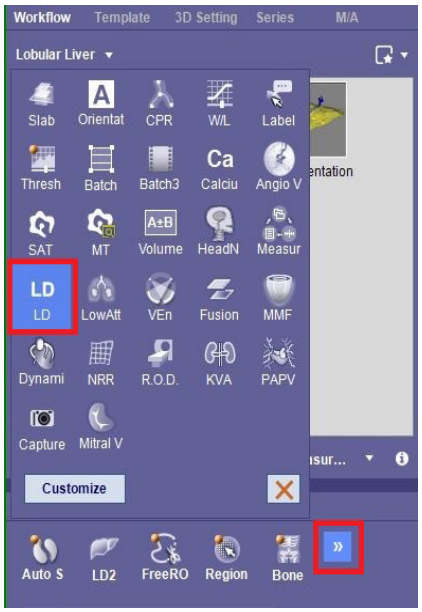


Figure 3-56 The LD Icon

4. The tool panel is opened.

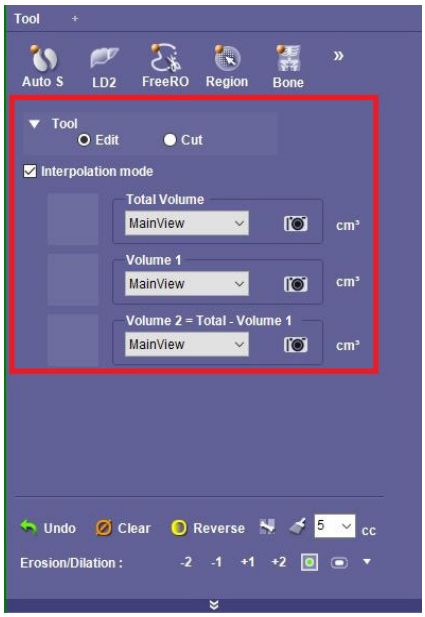
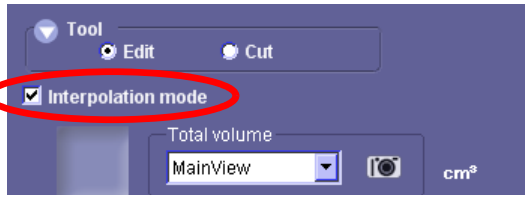


Figure 3-57 LD Tools

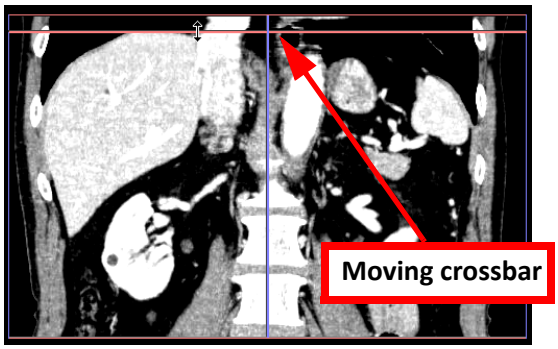
Step 1: Measuring the Total Volume

To get the volume measurement of the liver, first draw the outline of the whole liver on several slices throughout the entire volume, including the very top and very bottom of the structure. The LD tool will interpolate the area of the liver on each slice that comes between the ones where you have drawn outlines.



Note: The Interpolation mode must be enabled by checking the box, as shown above.

1. In the coronal MPR, position the crossbar at the very top of the liver.



2. In the axial image, draw an outline of the entire liver, as seen in that slice. To draw, hold down the **Shift** key and trace the outline with the mouse.

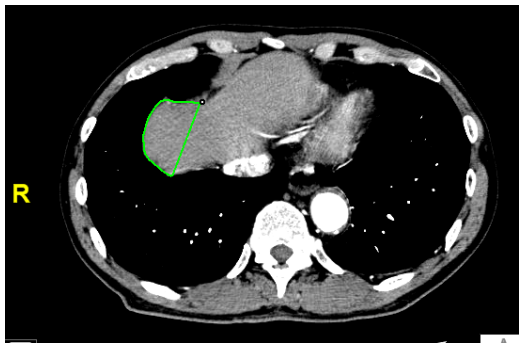


Figure 3-58 Beginning the Outline

3. When you have completed the outline, release the mouse. The outline appears as shown in Figure 3-59.

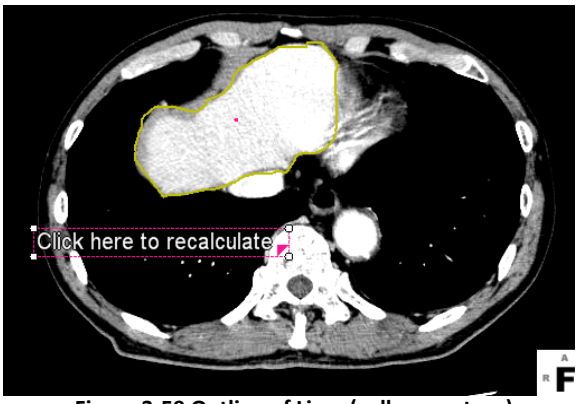


Figure 3-59 Outline of Liver (yellow contour)

4. Page through the slices on the axial image (or move the crossbar down a short way on the coronal image).

   Choose the next slice to outline of the liver on. There is no specific number of slices to advance between; however, the closer together the slices are, the more accurate the interpolation is.

5. Continue through the entire volume, drawing the area of the liver at selected slices. Be sure to draw an liver outline in the final slice in the volume.

6. When you are finished, calculate the volume by clicking the text on the image that reads **Click here to recalculate.** (Figure 3-60)

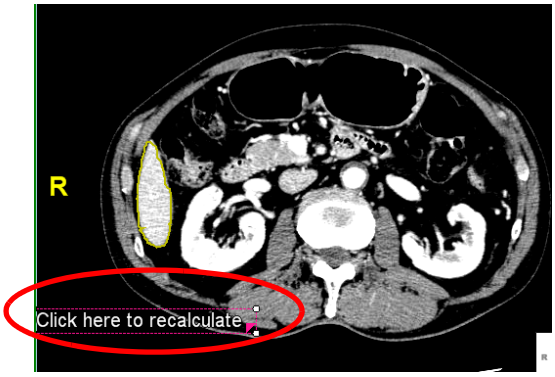


Figure 3-60 Calculated Volume

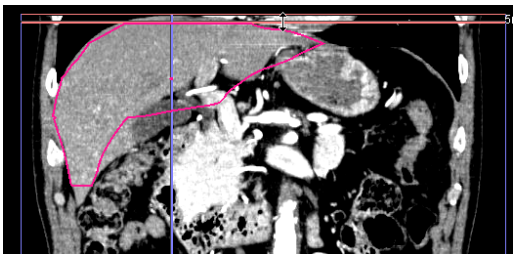
The volume is automatically calculated, and is displayed on the image.

7. To capture this volume in the LD tool, go to the tool panel, and click the camera icon in the first row of volumes, **Total volume**. The volume is displayed on the tool panel:

Step 2: Edit - Measuring the Right Lobe Volume

Measuring the right lobe's volume requires the same steps performed in measuring the total volume. However, you can modify the outlines already drawn around the entire volume so that only the area of the right lobe will be considered in the next calculation.

1. Reposition the crossbar in the coronal image back at the top of the liver:



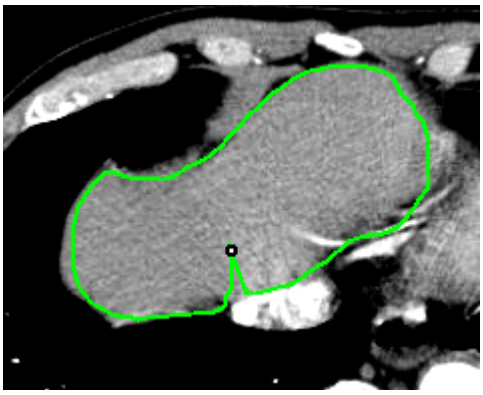
2. In the axial image, slowly scroll through the slices in the vicinity of the top until you find the first (topmost) slice having an outline.

Note: The interpolation that was done in the whole-volume calculation added an outline to every slice in the volume, so you need to begin at the topmost slice.

---

3. Continue paging through the volume, stopping at intervals of your choosing to modify the outline to include only the right lobe. Hold down the **Shift** key and draw along the edge of the area. When you

reach the point on the perimeter where the outline of the right lobe follows a different direction from what was previously drawn, follow the new outline. The shape of the area will automatically change to follow the new outline.

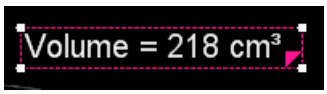


Note that the final slice for the right lobe is the same as that for the total volume, so you do not need to change that slice.

4. When finished, click the **Click here to recalculate** text. The volume of the right lobe is displayed in the tool panel.

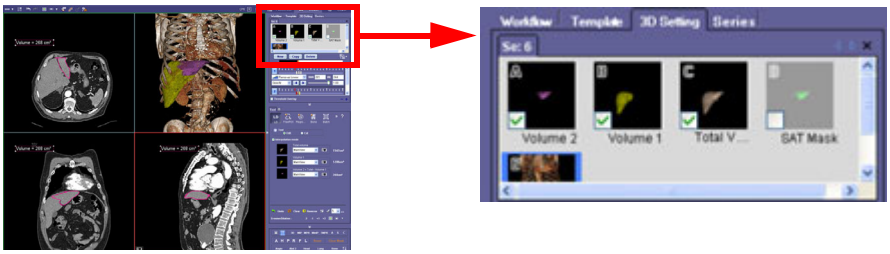
5. Click the camera icon in the second row of the tool panel to capture the volume of the large lobe. At this time, the volume of the small lobe is automatically calculated and displayed, along with the thumbnail image of the subtraction.

   The volume of the left lobe is displayed on the axial image:



3D Imaging

To isolate the liver in the 3D view, click the 3D settings tab to show the image mask thumbnails.



Select the thumbnails as desired. For more details about 3D settings, see "3D Settings Tab" on page 3-10.

Lobular Decomposition2 (LD2) 

This tool is optional. The Lobular Decomposition2 identifies tree-like structures within a volume of interest, for example, a scan region containing a vascular bed in an organ such as the liver or lung. The LD2 tool then identifies sub-volumes based on the proximity to a branch of the tree or a sub-branch(es).

To begin using the LD2 tool:

1. Select a liver (or lung) study. In this example, a liver study is selected.

2. Load or RMB-click on the Lobular Liver workflow.

3. In the tool panel, select the **LD2** icon. This icon is located in the hidden tools area (see Figure 3-16 on page 3-18).

4. The LD2 tool panel.

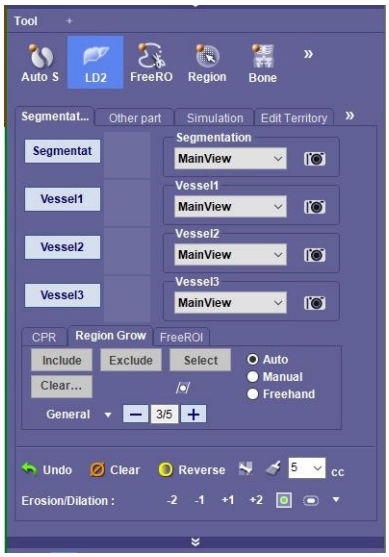


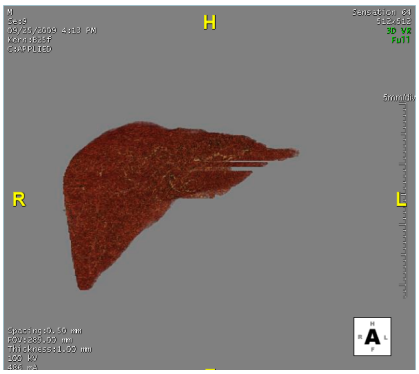
Figure 3-61 The LD2 Tool Panel

Segmenting the Liver

1. Click the **Segmentation** tab to bring the segmentation tool to the front.

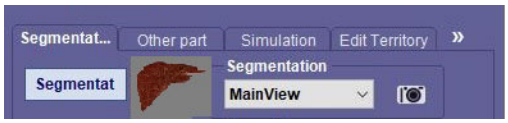
2. Before beginning the liver segmentation, adjust the window/level in the 3D image so that the liver is visible and dark.

3. Click the **Segment** button. The segmented liver is displayed as shown below.



4. If the segmentation is acceptable, capture the image by clicking the camera icon on the same row as the **Segmentation** button.

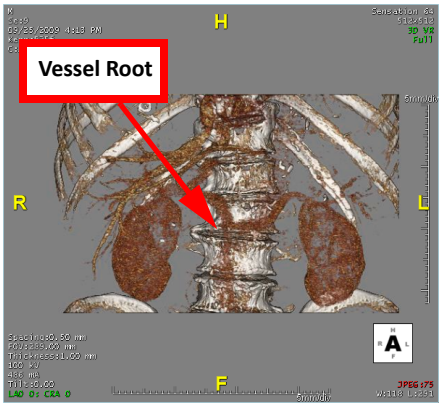
A thumbnail image of the segmented liver is shown in the small window (to the right of the **Segment** button), indicating that it has been captured.



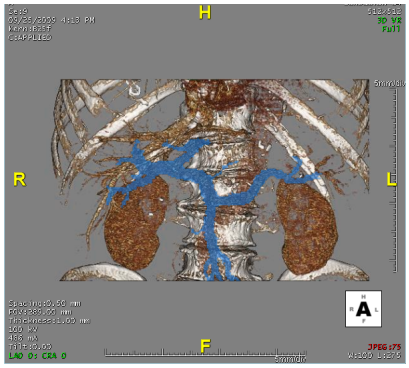
Segmenting Vessels

Use W/L to make the image very light so that the Region Grow function works properly.

1. While holding down the shift key, click on the vessel root:



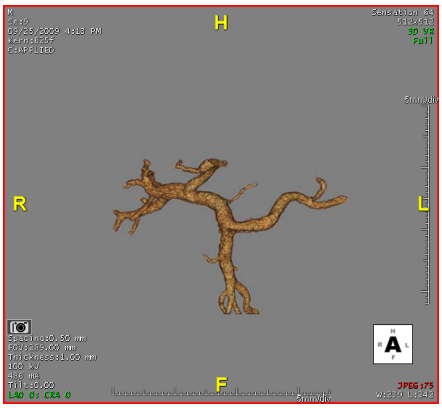
The entire vessel tree is masked (see the following figure).



Note: If the Region Grow operation does not fully mask the desired area, you might get better results using Manual Region Grow rather than Auto. Click the Manual button (see the following image) to switch to Manual Region Grow.

---

2. Click **Select** to segment the masked area. The vessel is displayed in the main window.



3. Capture the vessel by clicking the camera icon in the same row of the Tool Panel.

Note: The camera icon in the lower-left corner of the image captures images to the Output Panel and does not serve the same purpose as the camera icon in the Tool Panel.

Before the image is captured, you will be prompted to shift-click on the segmented vessel so that the software can find all the centerlines for the vessel tree. Click the vessel root for optimal results. When that is complete, the thumbnail image of the vessel is displayed in the tool panel.

4. If needed, click on one or more other vessels and follow steps 1-3 for each vessel.

   At the end of the segmentation step, the tool panel appears as shown in Figure 3-62.

Figure 3-62 Tool Panel after Segmentation

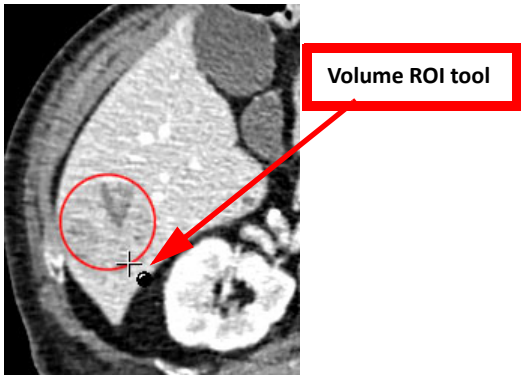
Other Parts of the Liver

This step allows you to segment and select other parts of the liver to be identified and measured separately. One example of this would be pathological tissue found in the liver, such as a tumor.

1. Use one of the MPR images to find and identify the pathology in the liver. On the axial, coronal or sagittal MPR, scroll through slices until you can see the pathology.

2. Select **FreeROI** in the Tool Panel to draw a boundary around the tumor. In this example, the Volume ROI icon is used (see the following image).

3. Press the shift key and drag the mouse across the tumor, so that a circle is drawn around the tumor:



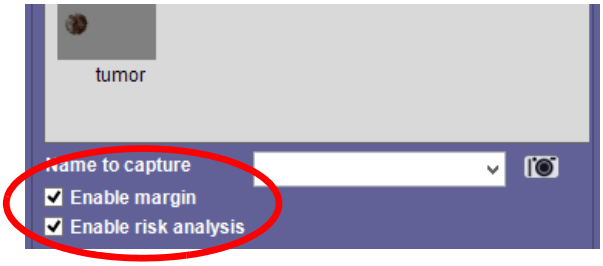
4. Click **Select**. If the tumor segmentation does not appear in the 3D window, use W/L to darken the image.

5. Click the camera icon in the Tool Panel to capture the image. If desired, type in a name to capture in the input field before capturing.

Distance Analysis and Margin

The LD2 tool assists you to visualize the proximity of the vessels to the ROI, by color coding the vessel based on the distance.

To enable risk analysis, click the **Enable distance analysis** checkbox in the tool panel:



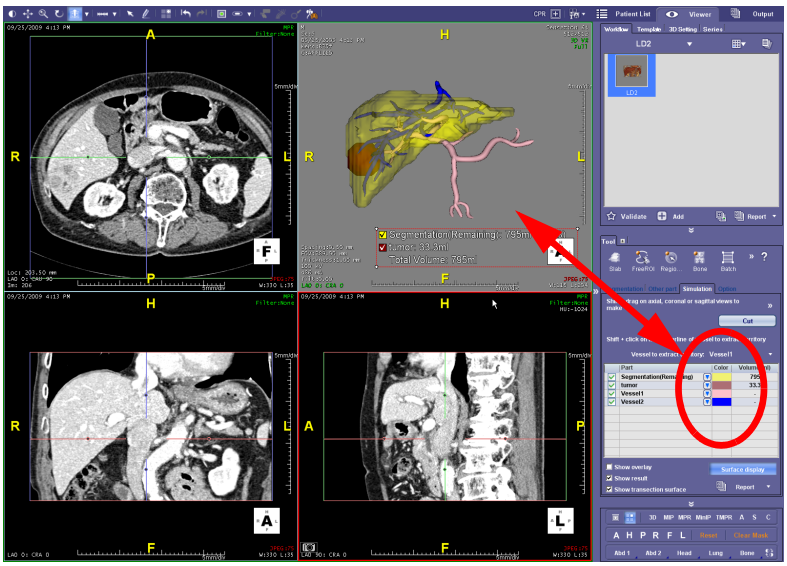
You can also display a margin around the diseased area that contains only healthy tissue. Click **Enable Margin** in the tool panel.

Simulation

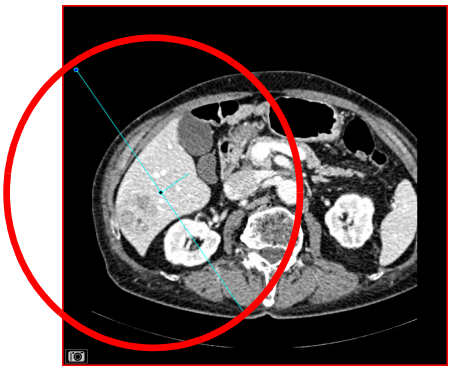
Click the **Simulation** tab. The segmentation result image is displayed, along with a table in the tool panel containing the name of each segmented part, the color mapping for each part, and the volume of each. This segmentation uses a surface rendering model, in which the software stacks multiple slices in order to provide a smoother appearance. However, if the number of slices is small, you may see a jagged image. The appearance can be improved by selecting **Smooth Surface** from the right click menu, or by using the shortcut key **Crtl+E**.

Note: The volume results shown in the viewer and table are calculated from masks. You can confirm this by enabling the Color Overlay on MPR views.

Making a Cut Line



To make a cut line, hold down the **Shift** key, and use the mouse to draw a line along the axial MPR image, so that the liver is divided into two parts: the cut part, which contains the pathology, and the remaining part.



Make sure that the line extends well beyond the boundaries of the liver, so that the cut line will be made through the entire organ. It can be difficult to see where the boundaries are when looking at only one slice. The cut section should contain all of the diseased tissue.

To freehand a cut line:

1. In the Simulation tab, select the drawing tool (“pencil”).

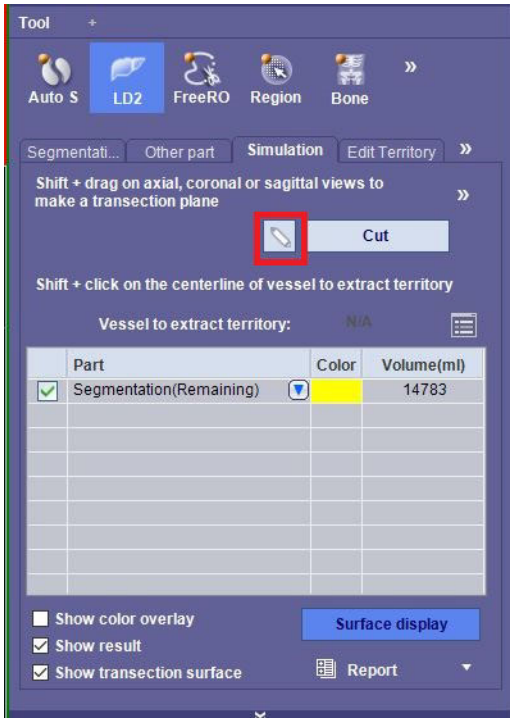


Figure 3-63 Pencil Tool

2. You can either hold-LMB and draw a multi-planar line or you can Shift LMB-click to create the line’s points.

3. You can edit the line with the LMB-click on a point and move it to the new location; or by using the nudge tool.

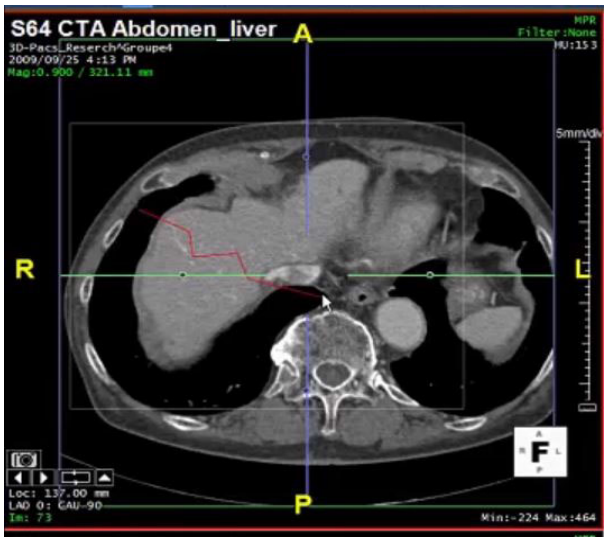
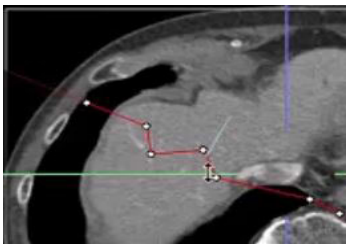
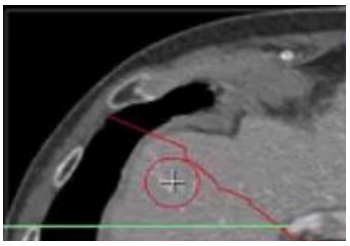


Figure 3-64 The Multi-planar Line



Moving Points of the Line



Nudge Tool

Figure 3-65 Editing Options

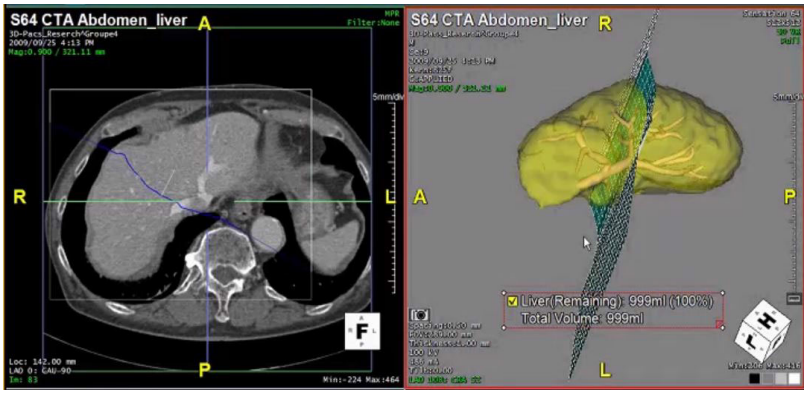
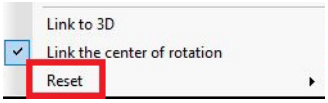


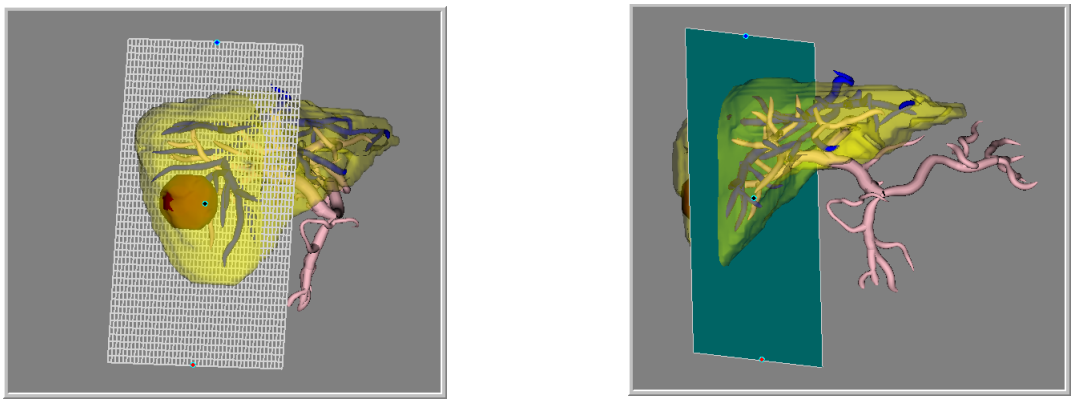
Figure 3-66 MPR and 3D View of Multiplanar Line

4. You can save this scene and then restore it. Select the Save Scene icon on the top, right toolbar.

5. To reset, select Reset from the RMB-click context menu.



The *transection surface*, a plane that cuts through the organ, is displayed in the 3D image. In Figure 3-67 on page 3-108, the smooth green side of the plane faces the part to be cut away, whereas the white mesh side faces the section that will remain.



Cut Side **Remaining Side**

Figure 3-67: Transection Surface

Note: Make sure the **Show transection surface** box in the tool panel is checked. (See "Other display options" on page 3-117 for more information.)

Manipulating the Transection Surface/Cut Line

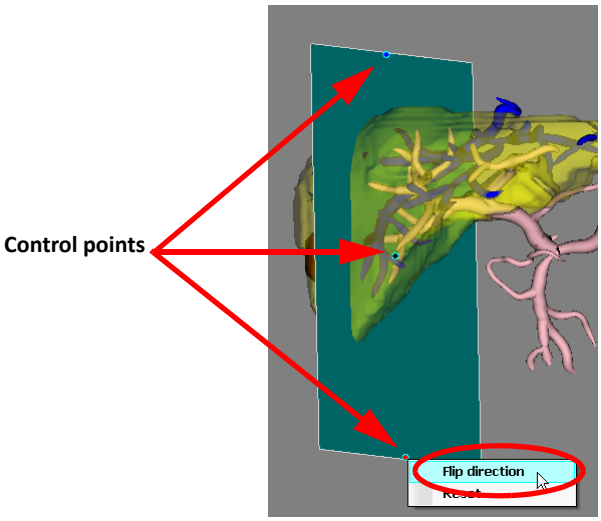
There are several tools available for manipulation of the transection surface (in the 3D image) or cut line on the axial image.

Note: The transection surface is the 3D representation of the two-dimensional cut line drawn on the axial MPR. Any function performed on the transection surface is automatically applied, two-dimensionally, to the cut line, and vice versa.

- Changing the direction of the transection surface

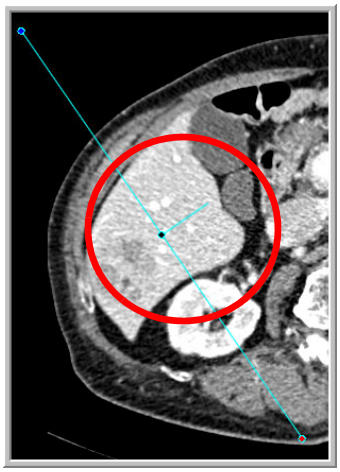
  Observe that, in Figure 3-67, the cut side (green) of the transection surface is facing away from the tumor. When this happens, you can reverse the transection surface so that it is oriented correctly.

  a. Right-click on one of the control points (dots located at the top, middle and bottom of the transection surface) of the transection surface to display a menu.



2. Select **Flip direction** from the menu.

   You can also flip the direction of the transection surface from the axial MPR image. In the middle of the cut line, a short perpendicular line is displayed on the image, pointing toward the portion of the organ that is assumed by AQi to be *removed*. If this is incorrect, you can change the direction.



   As with the 3D image, right-click on one of the end points or the middle point, and select **Flip direction** from the menu. Verify that the perpendicular line is now pointing in the correct direction.

- Rotating the transection surface/cut line

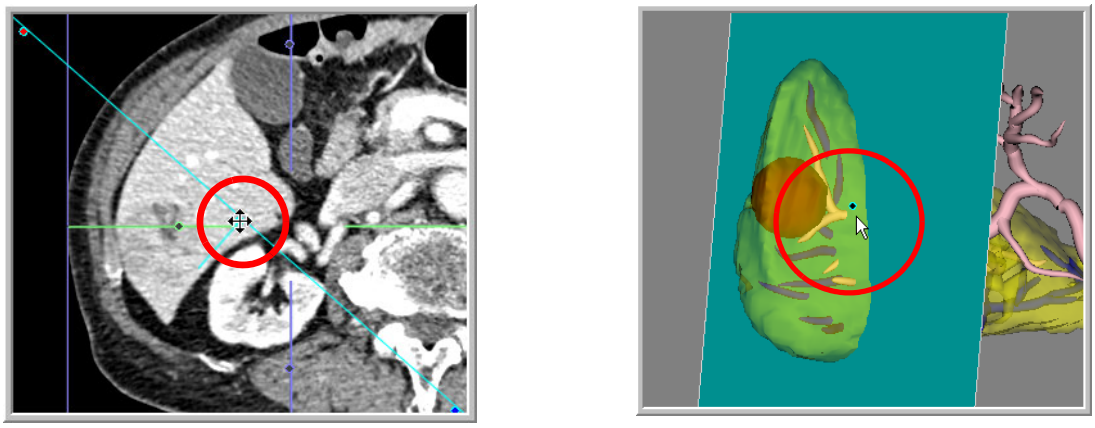
  To rotate the cut line, click one of the end points. The cursor changes to a horizontal double arrow. Drag the mouse clockwise or counterclockwise to rotate it. As the cut line is rotated, the transection surface is also rotated. You can rotate the three-dimensional surface around different axes by rotating the cut lines in the sagittal and coronal MPR images.

- Panning the transection surface/cut line

To pan the cut line, click the center control point (circled in the previous figure). The cursor changes to a cross shape (see Figure 3-68 on page 3-110). You can then drag the cut line to the desired location.

To pan the transection surface, click the control point in the very center of the plane, and then drag the surface to the desired location.

Panning the Transection Surface



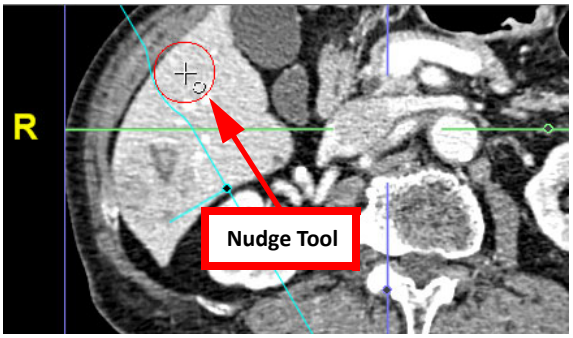
Panning the Cut Line **Panning the Transection Surface**

Figure 3-68: Panning the Transection Surface

- Editing the shape of the cut line and transection surface

  If desired, you can use the nudge tool to edit the cut line, and give it a curved shape more closely fitted to the diseased tissue. To do so, follow these steps:

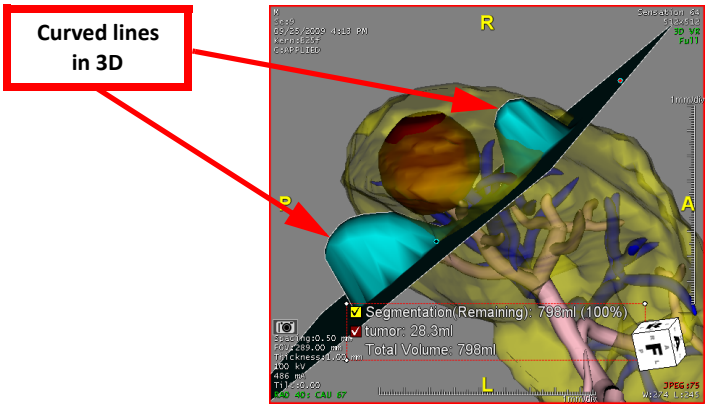
  a. Hold down the **Alt** key and click on the image. A circle appears on the image:



  2. As you move the circle closer to the cut line, the cut line will bend in that place. Push the line toward the tumor.

  Note that when you click on the image close to the cut line, the circle is relatively small. The further away from the cut line you start, the larger the circle.

  Curved lines on the axial MPR are represented in 3D as follows:



- Use the transection tool to draw a multiplanar cut.
- After cutting, Save Scene and restore Scene.

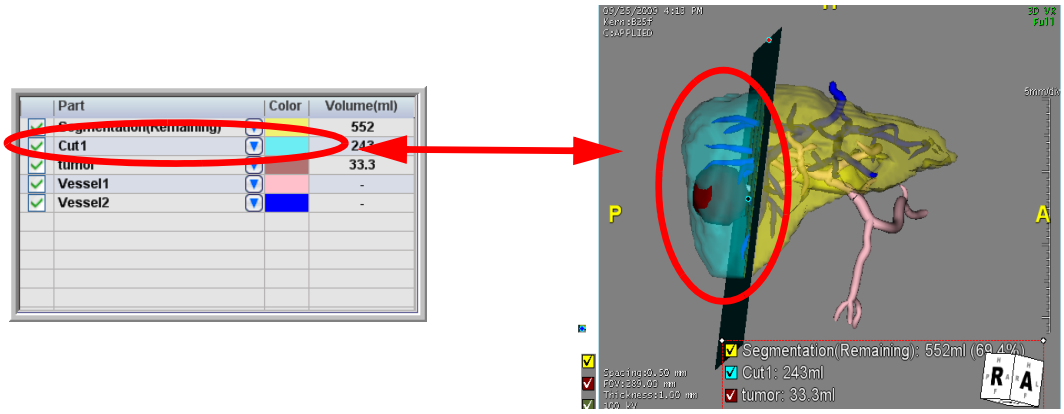
New features which I can't see in my AQi Viewer.

- Deleting the cut line and transection surface

  To delete the cut line, right-click on one of the control points and select **Reset** in the pulldown menu. This removes the cut line, the transection surface, and all work that has been done with them. You can then draw a new cut line.

Completing the Cut

Click the **Cut** button when finished. The **Cut1** part is added to the colormap table in the Tool Panel. The default color is light blue. In the 3D image, the section of the liver on the cut side of the transection surface is overlayed with the same color. See the following figure.



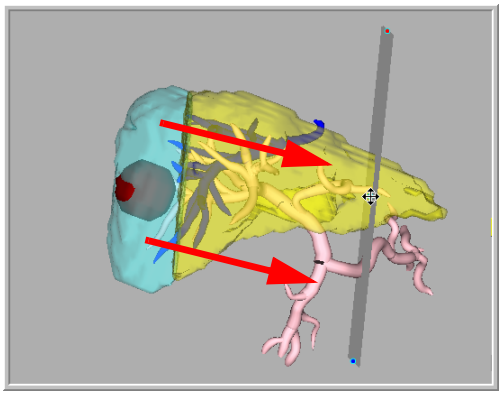
Making Additional Cuts

To make an additional cut, do the following:

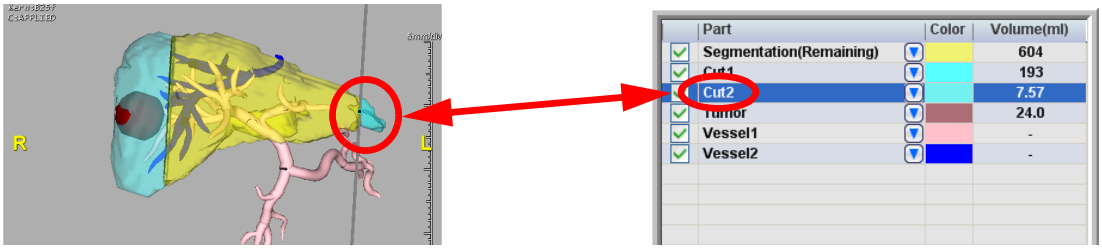
1. In the list of segments (the **Part** column), right-click on the previous cut ("Cut1" in this example, shown at right), and select **Restore transection**.

2. Flip the direction if the cut direction is incorrect.

3. Move the transection plane to the area of the new cut (see image below).



4. Click the **Cut** button.



Merge Cuts

To merge two cuts together, click and drag one cut in the table on top of the cut you want to merge it with.

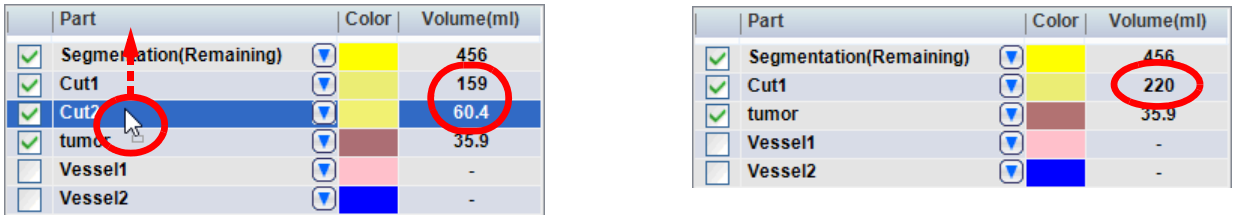


Figure 3-69: Merge Cut - Left: Move Cut2 on top of Cut1; Right: Cut2 Merged into Cut1

Note that the volume of the merged cut (circled in the figure above, right-hand image) is the sum of Cut1 and Cut2 in the left-hand image.

Distance Analysis

If you have not already enabled risk analysis or margins, you can do so in the **Simulation** tab. In the row that contains the ROI isolated in the **Other part** tab, click the down-arrow to the left of the color. Then check **Enable margin**, **Enable risk analysis**, or both.

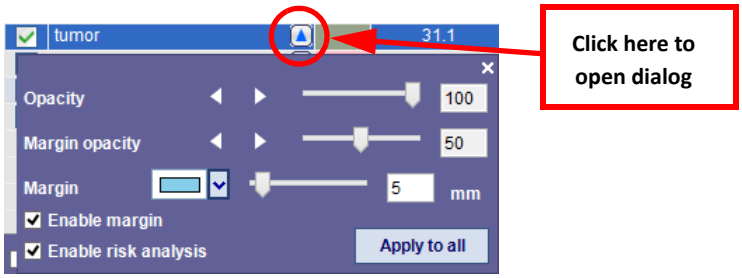
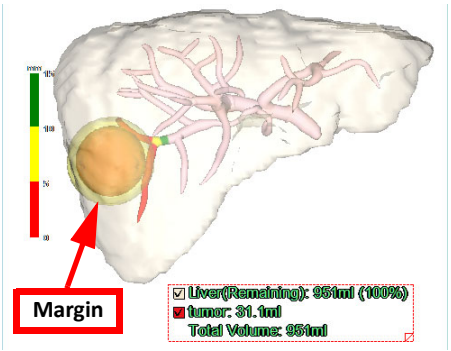


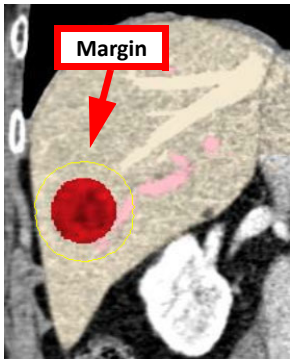
Figure 3-70: Margin and Risk Analysis Dialog

Viewing the Margin

When **Enable margin** is checked, a border around the ROI is created to show the tissue that surrounds the ROI.



The margin is also shown as an outline on the MPR images in the same color:

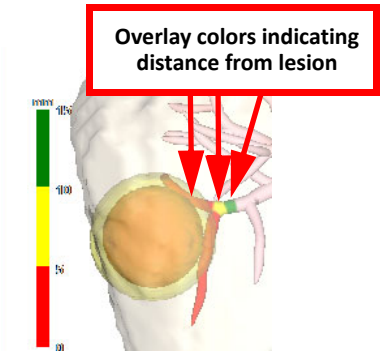


You can configure the width and color of the margin in the **Margin and Risk Analysis** dialog:

Note: The color of the margin will change the color of the ROI itself. You can adjust the opacity of each to maintain contrast between the two areas, by using the margin and risk analysis dialog (see Figure 3-70).

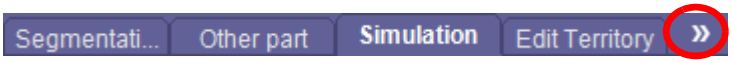
Distance Overlay Colors

When you make a cut line, the distance analysis feature helps you to see which vessels are within the cut region, which are close to the cut region, and which are well outside the region. Those parts of the vessels are overlayed with colors that indicate each level of risk shown by a color overlay on the vessels.



The colors, and the ranges used to determine which color to overlay, are configurable. To configure the distance-color template, do the following:

1. Click the double right-arrow located just to the right of the **Edit Territory** tab. This opens the **Option** dialog.



2. Click the **Edit distance color template** link in the lower-left corner of the **Option** dialog. This opens the **Color Distance Template** dialog.

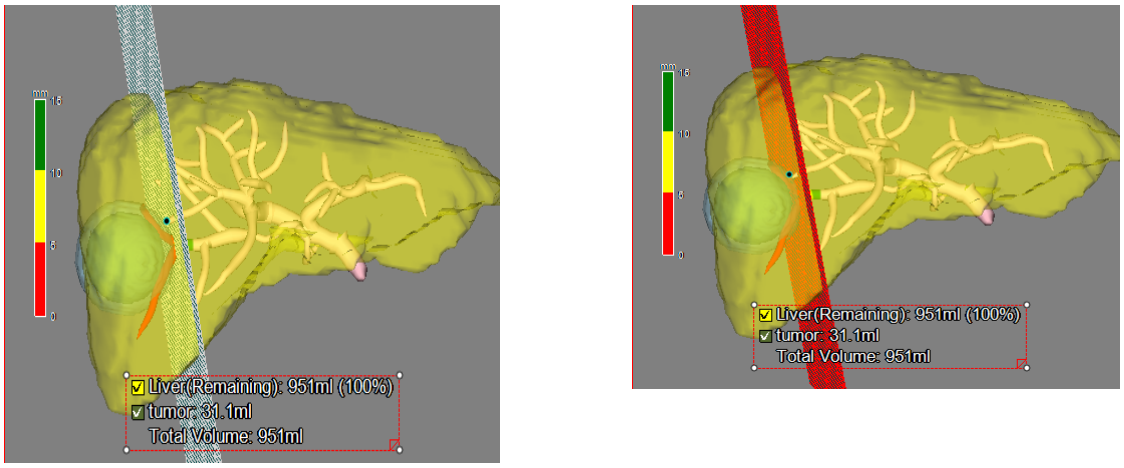
3. To change a color, click on it to open the Windows color palette.

   To change the range, double-click in the cell containing the number to be changed, and then type the new number over the old one.

Highlighting the Cut Line or Transection Plane

As you move the cut line (on an MPR image) or transection plane (on the 3D image) toward the margin, it is highlighted when it touches the margin. This alerts you that the proposed cut position is potentially too close to the margin.

Note: If the tissue enclosed in the margin has an irregular shape, the transection surface might not change color, even when the plane surface is close enough to the margin. Be aware of this functionality, and ensure that you are verifying the results prior to use.



Plane Outside Margin **Plane Touching Margin**

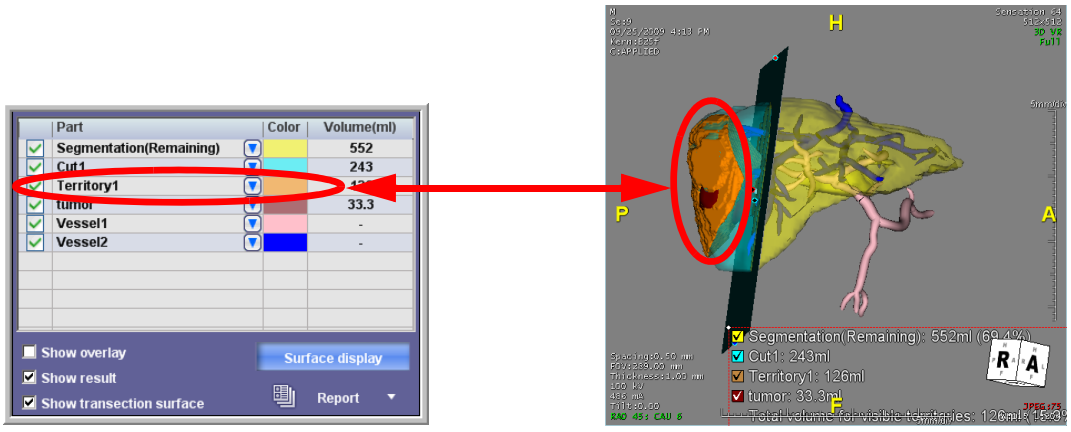
Figure 3-71: Transection Plane Touching Margin

Vessel Territories

You can use the Territory mask to see which sections of tissue within the cut area would be affected by vessels that extend across the cut line and into the cut area.

To find the territory related to a vessel:

1. Press the shift key to make the vessel centerlines visible.
2. Click the centerline of any vessel that crosses the cut line. The territory of that vessel is masked in a color corresponding to the **Territory1** color in the color table.
3. Select the target, either Segmentation or the cut.



4. Repeat this process for all vessels that cross into the cut area. Each new territory will be masked in a different color, and will have a separate entry in the segmented parts table.

3D Distance Spheroid Measurement

1. In the simulation tab, select **3D Distance** from the measurement menu in the top bar. The measurement tool posts the first instruction on the image window, **Please click target point**.

2. Continue following the instructions in the image window to complete the measurement. (For more information about the **3D Distance** measurement, see "3D Distance" on page 3-165). The **Edit Spheroid Template** dialog opens when the measurement is complete (see the following figure).

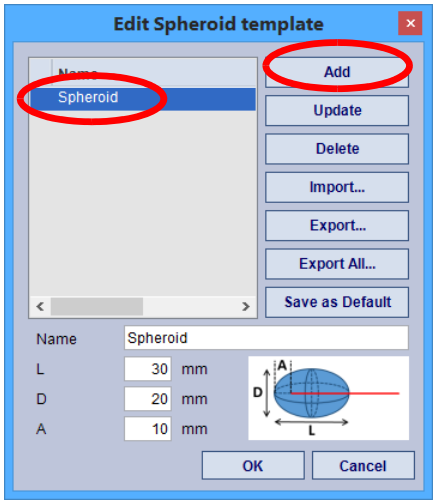
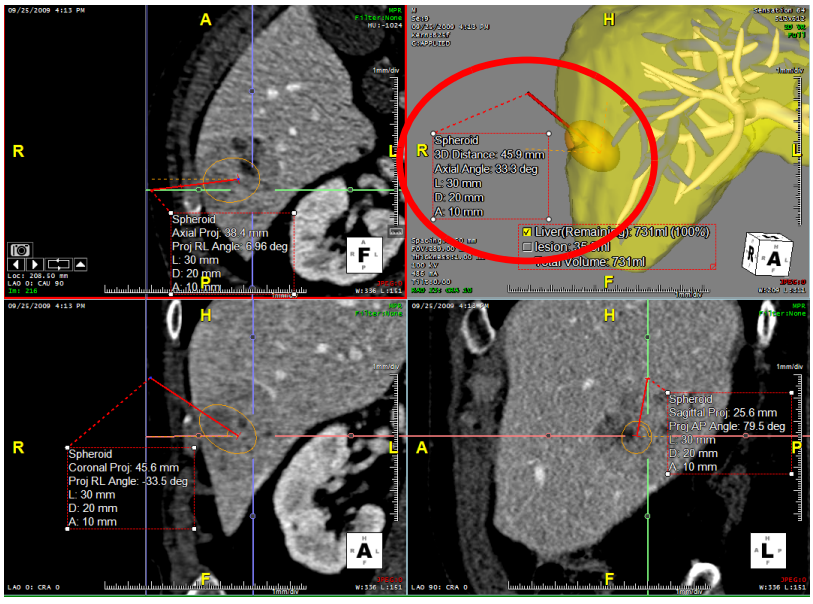


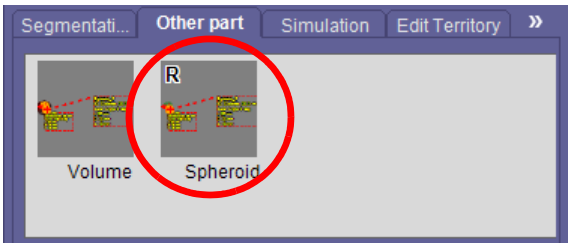
Figure 3-72: Edit Spheroid Template Dialog

3. Select **Spheroid** in the dialog, and click **OK**. The 3D measurement result is displayed on the image, with a spheroid outline and template dimensions (see the following figure).



Note: Approach view mode is not available with the spheroid template. (See "Approach View Mode" on page 3-167 for more information.)

The spheroid model is added to the **Other Part** panel in LD2:



Therefore, you can also use the **Distance Analysis** and **Margin** options. (See "Distance Analysis" on page 3-112.)

Edit Spheroid Template

The **Edit Spheroid Template** dialog (see Figure 3-72 on page 3-116) allows you to create a set of pre-configured templates or import/export templates to share with other users. Type in the name, configure the dimensions (L/D/A) and click **Add**.

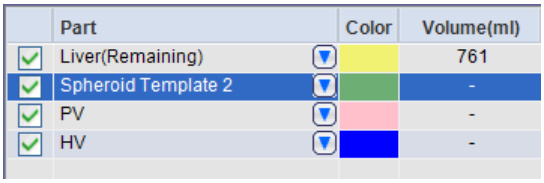
Right-click on the measurement in any of the image views to open the **Edit Spheroid Template** dialog.

Multiphase Data

For multiphase data review cases, the 3D distance spheroid measurement is copied to the other views so you can visualize synchronously.

Note: Location of the measurement depends on registration results. You must validate automatic registration before assigning any clinical significance. Please check the registration results on the axial, coronal, and sagittal views.

Each model (part) you created can be exported as mesh separately. Right-click anywhere on the list of parts, and select **Export as Mesh** from the menu.



(For information on exporting as mesh, see "Exporting a 3D Mask as a Mesh" on page 3-12).

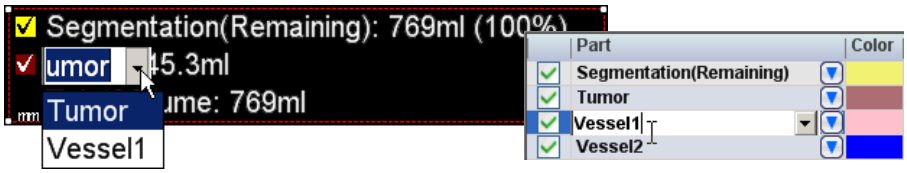
You can also select **Smooth Surface** from the RMB-click context menu on the 3D image, or use the shortcut key **Ctrl+E**, before exporting.

Other display options

In the bottom-left corner of the tool panel there are three options for displaying more information on the screen.

- **Show overlay** - Shows an overlay on the 2D images, whose colors are mapped to the segmentation list in the tool panel.

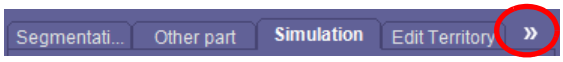
- **Show result** - Shows the volume information on the 3D image.
- **Show transection surface** - Shows the plane that cuts through the organ.
- **Changing the Names of Parts** - You can change the name of a segment, vessel, cut or territory at any time, in one of two ways:
  - Double-click on the name to be changed in the results text in the main window.
  - Double-click on the name to be changed from the part list in the Tool Panel.



In both cases, the selected text changes to a pull-down menu. If the name you want to use is in the menu, select it to change the name. If not, you can also type in a new name. Press **Enter** when done. A change in one of these places automatically changes the other. If you decide not to change the name, you can press **Enter** to close the menu.

The Options Dialog

The Option dialog allows you to set parameters for part segmentation, volume calculation and volume display. To open, click the double-arrow located to the right of the Edit Territory tab in the tool panel.

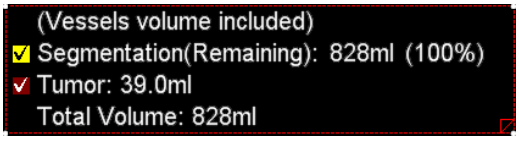


Description

Volume calculation:

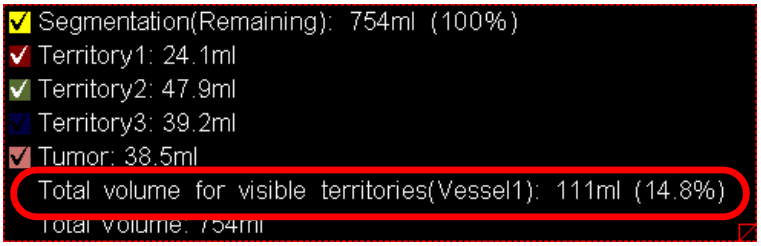
- Include vessels volume

  When enabled, the volume of the vessels is added to the Total Volume.



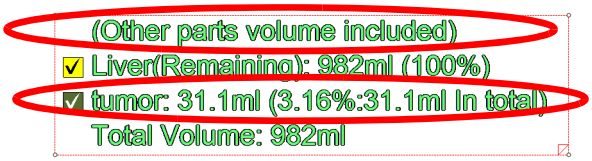
- Show total volume for visible territories

  When enabled, the total volume of all visible territories is shown in the results.



- Include other parts

  Include the volume of tissue isolated in the **Other parts** tab. Also display this volume's percentage of the total volume.



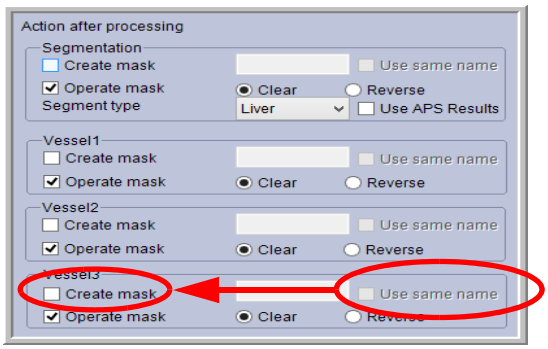
- Volume Unit

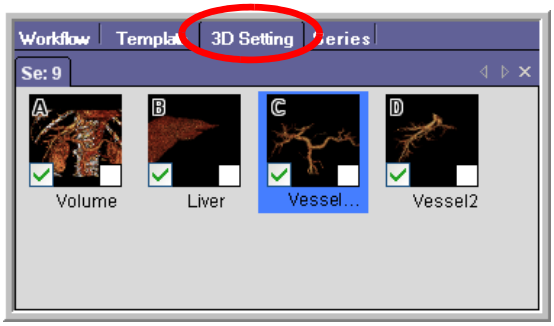
  Select measurement unit, cm^3 or ml.

Action after processing:

- Create Mask

  When you check the **Create Mask** box for a specific part, a mask is created from the segmentation of that part, and stored in the **3D Settings** tab. Enter a name for the mask in the text box. Check **Use same name** to give the mask volume the same as the name in LD2.





Mask Functions After Processing Masks

Figure 3-73:; Creating a Mask

For example, in Figure 3-73, the first mask created in **3D Setting** will be Liver, the second will be Vessel root, and the third will be Vessel2. After all masks have been selected and captured, check the **3D Setting** tab:

Note: The name of mask C has been shortened because there was not enough space for "Vessel root."

- Operate Mask

  Select **Operate mask** when you want the mask in the 3D window to change after a specific segmentation. You can then choose between:

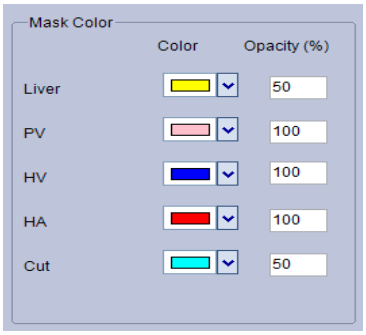
- **Clear**, which clears the mask that had been created for the segmentation
- **Reverse**, which reverses the mask in the 3D window to show everything except the segemented part

- Segment Type (Segmentation only)

  Select the desired body part from the pulldown menu. Check the **Use APS Results** box to apply Aquarius APS results to the segmentation, if any results are available.

- Mask Color

  Select a color and opacity value for each segmented part of the organ:



Lobular Liver

Load a liver series into the **Lobular Liver** workflow (see image below).

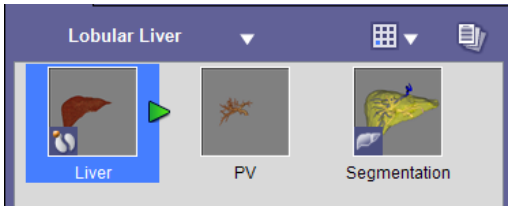
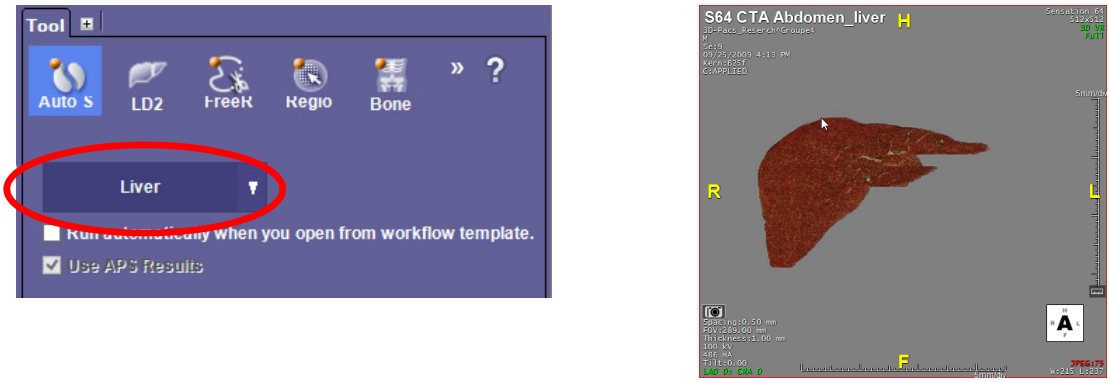


Figure 3-74: Example Lobular Liver Workflow

Segmentation

Liver

1. Click the **Liver** button on the Auto Segmentation tool panel to extract the liver.



Liver Button to Segment Liver **Segmented Liver**

Figure 3-75: Segmenting a Liver

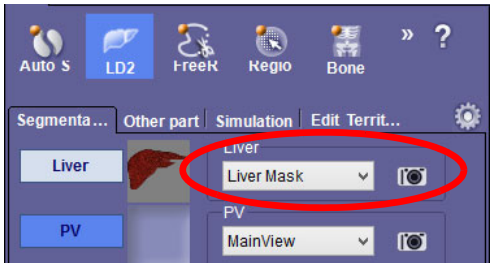
PV

2. Click the PV element in the Workflow panel (see Figure 3-74) to extract PV.

Figure 3-76: Extracted PV

3. Click the **Segmentation** workflow element (see Figure 3-74) to open the LD2 panel for segmentation:

4. In the first row (Liver), select **Liver Mask** from the drop-down list, and click the camera icon:



The liver mask is captured in the thumbnail window.

5. Click the camera icon for PV, and shift-click on the root of the vessel to create a centerline tree.

HV

6. Shift-click to **Region Grow** the HV on the viewer. Click **Select** when enough of the vessel is masked. You can continue to grow the vessel afterward using the **Include** button to show more masked area.

7. Click the camera icon for HV and shift-click on a lower part of the vessel to create a tree.

HA (Optional)

8. Shift-click to Region Grow the HA on the viewer, and click **Select** when done.

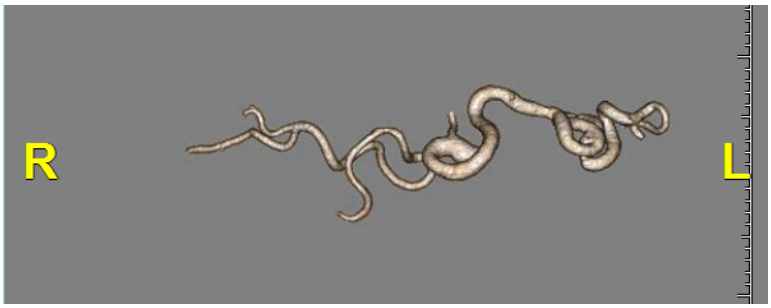
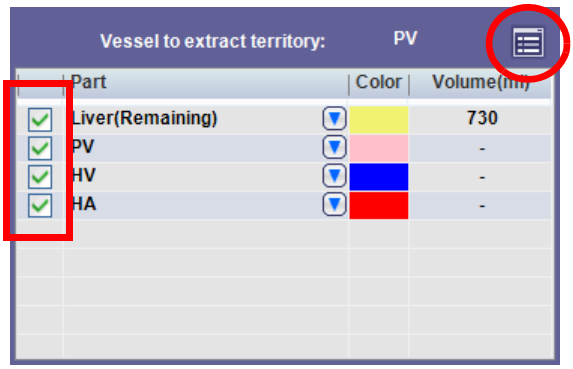


Figure 3-77: Segmented HA

9. Click the camera icon for HA, and shift-click on a lower part of the vessel to create a tree.

Simulation

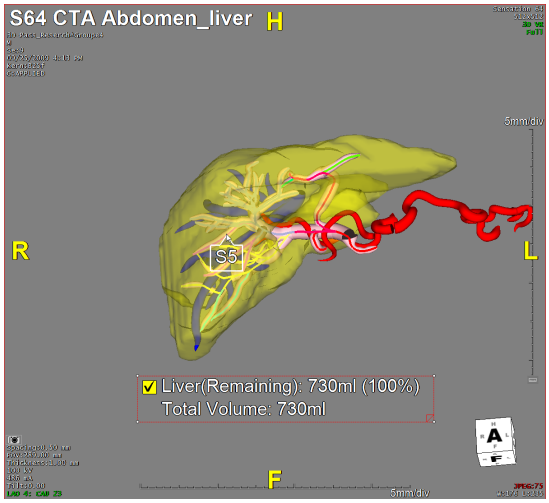
1. Click the **Simulation** tab in the LD2 tool panel. Wait for AQi to perform the simulation. When it is complete, a list of segmented parts and, when appropriate, their volumes is displayed (see below).



   Uncheck the **Liver**, **HV** and **HA** boxes from the list to see the PV more clearly in the viewer.

2. Click the **Auto Territory Segment** icon (circled in the previous figure) to open the Auto Territory Segment panel.

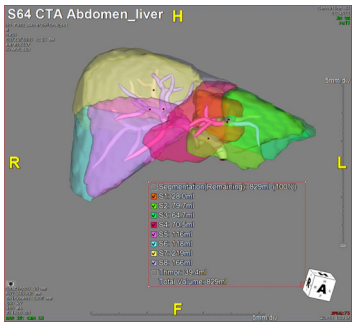
3. Select **PV-LobeLabeling01** from the drop-down list and click the **Auto Labeling** button. This creates proposed labels on the tree for subsequent review and validation.



4. If editing is required, edit the labeling result by shift-click on the centerline to display the Label Setting dialog. You can change the label name there.

5. Click the Decomposition button to create an eight-lobe segmentation result.

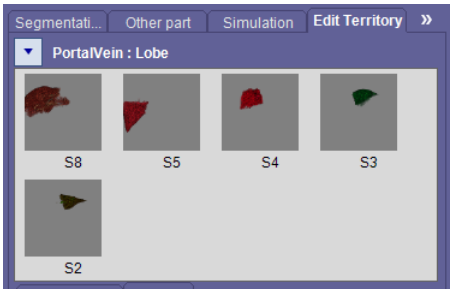
PRECAUTION: Decomposition results depend on the labels assigned to each segment. Please verify that the vessels are properly labeled, and edit the labels if you are not satisfied.



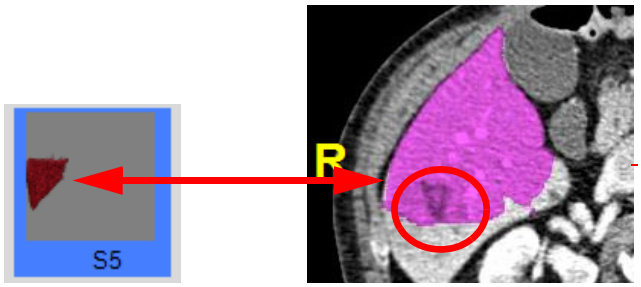
Territory Exclude

If the lobe segmentation did not separate the organ properly and there is a portion of tissue, called a "spilled area," that is labeled as belonging to the wrong lobe, it is possible to select that portion, remove it from the wrong lobe, and add it to the correct one.

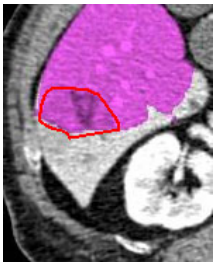
1. Click the **Edit Territory** tab. Thumbnail icons of each lobe are displayed in the tool panel:



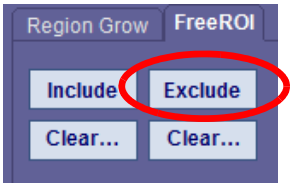
2. Click the icon of the lobe that has the erroneous portion. The corresponding area in the image is shown with an overlay (see images below):



3. Use Dynamic Region Growing or FreeROI to select the spilled area:

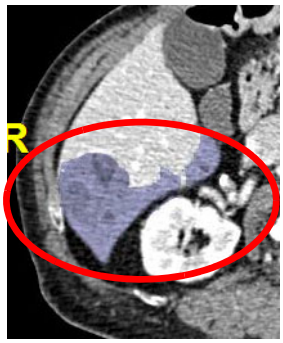


4. Click the **Exclude** button. A dialog is opened asking which lobe you want to add the spilled area to.



5. Select the appropriate lobe to add the spilled area to. The excluded area is removed from lobe S8 and is now part of lobe S5:

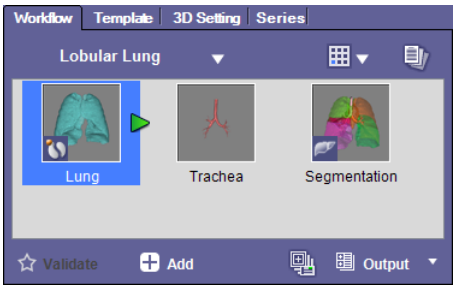
6. Select the appropriate lobe to add the spilled area to. The excluded area is removed from lobe S8 and is now part of lobe S5:

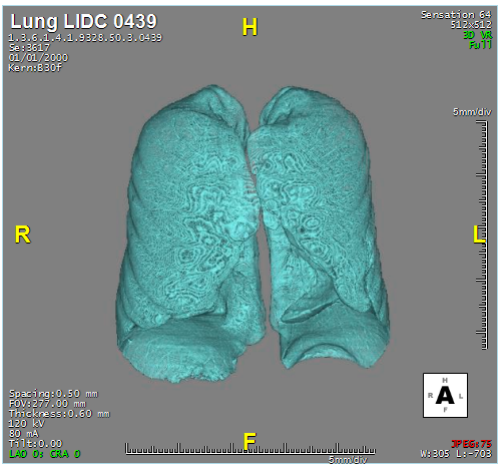


Lobular Lung (LD2 For Lung)

Lobular Lung uses the LD2 features to perform a five-lobe segmentation on lung data, identify which parts of the trachea extend into which lobes of the lungs, and obtain volume measurements for each lobe as well as the total volume of the lungs.

1. Load a lung study into the **Lobular Lung** workflow. The **Auto Segmentation** tool panel is opened and the lung is automatically segmented:





Example Lobular Lung Workflow **Segmented Lung**

Figure 3-78 Lung Workflow and Segment

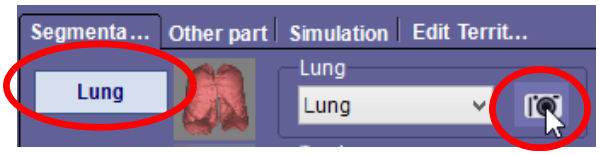
Note: If the lung is not automatically segmented, click the Lung button in the Auto Segmentation panel to extract the lung.

---

2. Click the Trachea Workflow element.
3. Click the Auto Segmentation tool panel button. The button in the tool panel should say "Trachea." If it does not, click the down-arrow to open the segmentation menu, and select **Trachea**.
4. Click the **Trachea** button.
5. Click the **Segmentation** Workflow element.
6. The **LD2** panel is automatically opened:

7. In the first row, which has the **Lung** button on the left (see image below, right), select **Lung** from the drop-down menu.

8. Click the camera icon on that row to capture the lung image (circled in light blue in the figure below).

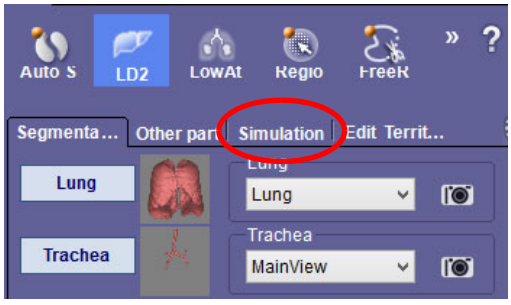


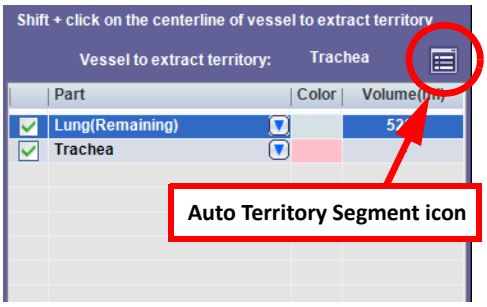
9. In the second row, which has the **Trachea** button, click the camera icon. The instruction, "Please shift-click on the vessel root" is displayed on the image.

10. Shift-click on the upper part of the trachea to create a tree.

    An image of the trachea will be captured onto the tool panel, just beneath the lung image.

11. Click the **Simulation** tab in the Tool Panel (circled in the figure below, left). The territory list (below, right) is created automatically.





12. Click the Auto Territory icon (circled in dark blue, in the previous figure, right) to open the **Auto Territory Segment** panel.

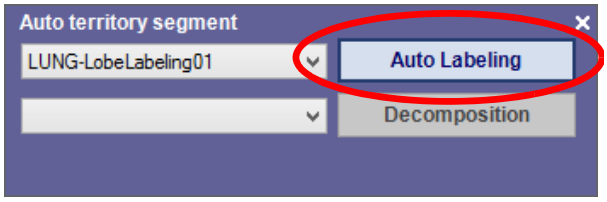


Figure 3-79: Auto Territory Segment panel

13. Select **LUNG-LobeLabeling01** from drop-down list.

14. Click the **Auto Labeling** button (circled in Figure 3-79) to create labels for different territories on the tree.

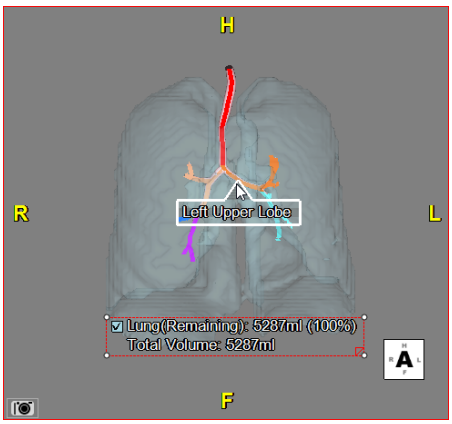
PRECAUTION: The labels displayed are suggestions which require review and validation by a qualified user prior to use. To accept this limitation and proceed, click *OK* in the dialog that is showing this message, to continue to the Decomposition step. Otherwise, click *Cancel*.

---

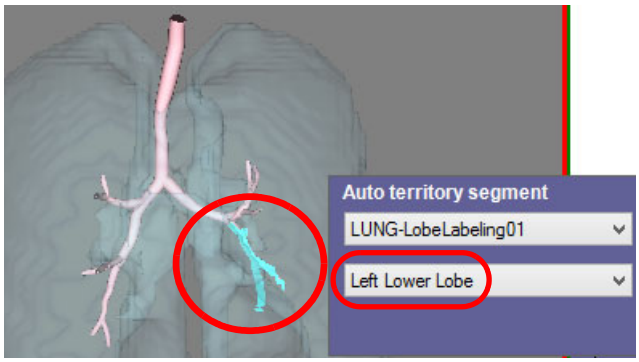
15. Hover the mouse over different segments of the tree, which are indicated by color, to display the label for each segment.

16. If editing is required, shift-click on the centerline to display the Label Setting dialog (shown at right). You can change a label name there.

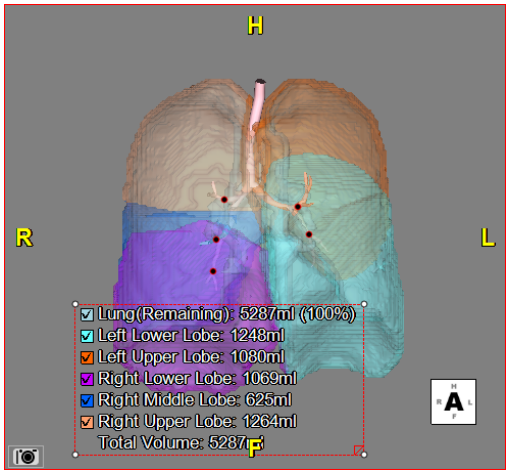
17. A Decomposition list is also created. When you select an item in the list, the corresponding segment of the tree is highlighted in its color.



Note: Decomposition results depend on the labels assigned to each segment. Please make sure to confirm that the vessels are properly labeled, and edit the labels if you are not satisfied.



18. Click the **Decomposition** button to create the segmentation result. To show just one lobe in the result, select that lobe from the Decomposition list. To show all five lobes, select **All** from the Decomposition list.



The LD2 feature offers other tools for making cuts and generating reports. For instructions on using them, see "Lobular Decomposition2 (LD2)" on page 3-100.

Low Attenuation Analysis 

(Optional)

Low-attenuation analysis is part of the Volumetric Histogram option. Volumetric Historgram allows a volume of interest to be segmented and analyzed for composition. The following applications are included:

- The analysis of low-attenuation regions of CT examination
- Threshold-based division of volumes of interest into voxel populations
- Investigation of scans of thrombosed vessels or aneurysms
- Other pathology

Threshold and Anti-Noise Parameters

PRECAUTION: The anti-noise option for the LowAtt feature removes isolated sparse voxels, using the erosion and dilation process. Therefore, utilization of this feature could impact the LowAtt volume measurements. Be aware of this functionality, and ensure you are verifying the results prior to use.

Setting and Displaying Threshold and Anti-Noise Parameters

Note: You are obligated to define the parameter ranges that are used in this procedure. When first accessed, the user interface for setting these parameters contains generic default values having no particular significance.

To set the threshold and anti-noise parameters, open the user preferences and navigate to the **Viewer>LowAtt** screen:

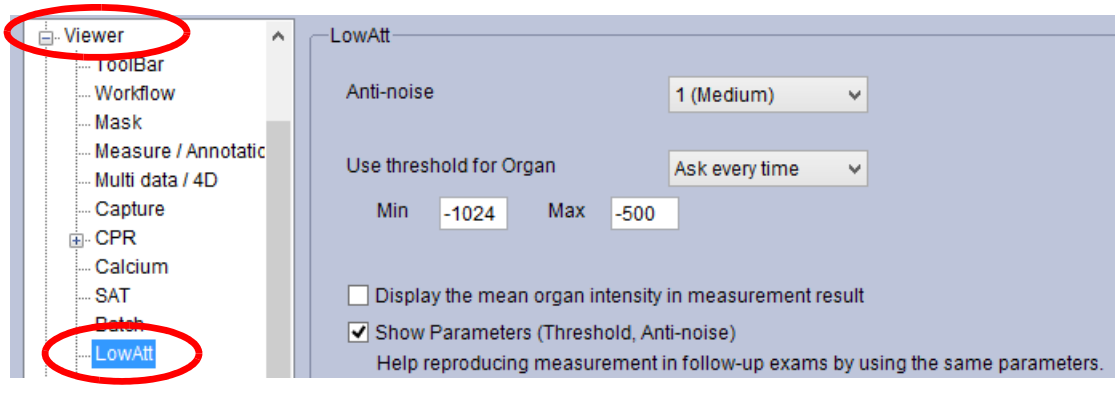
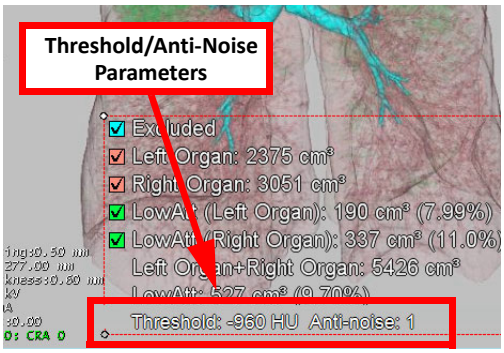


Figure 3-80: LowAtt Preferences Screen

To display these values in the measurement, you must enable the **Show Paremeters (Threshold, Anti-noise)** preference.

Followup Studies

When a patient comes for a follow-up exam, you will need to know the parameters (threshold, anti-noise level) used in the previous exam so that you can reproduce the measurement. These parameters are displayed at the bottom of the measurement (see figure below).



If you do not see the parameters, you can display them by setting the **Show Paramters (Threshold, Anti-noise)** preference in the LowAtt preference screen (see Figure 3-80, above).

Automatic Segmentation

If Advanced Processing has been performed on this study and there are files for any of these parts, all you need to do is step through the workflow elements.

1. To begin Low Attenuation Analysis, open a low-attenuation study in the **LowAtt** workflow. The study is loaded into the 3D Viewer using the **LowAtt** workflow

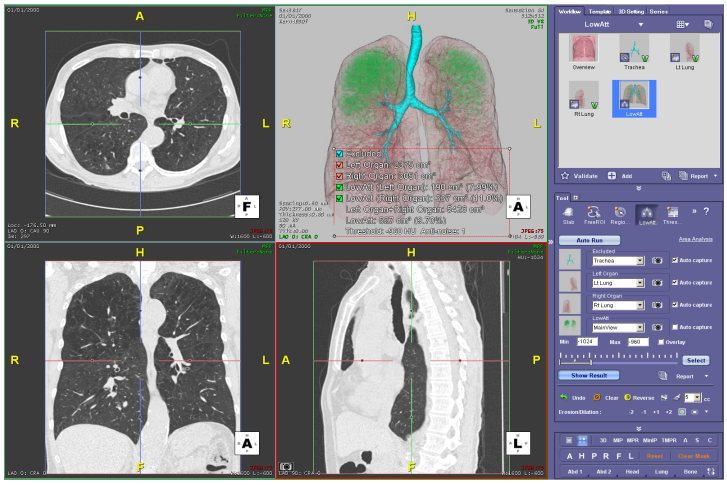
2. Click the final Workflow element (**LowAtt**). The **LowAtt** Tool Panel is automatically opened.

3. Click the **Auto Run** button in the Tool Panel.

   The LowAtt tool performs all the segmentation and captures. The volume of each segmented part is then calculated, and a segmented 3D image of the lung is built from the segmented parts.

   To see the volume results, make sure the **Show Result** button is active.

   The volume results are displayed on the 3D image.



4. Check each segmentation and the final result. If they are satisfactory, the analysis is complete.

   If there are any errors in the segmentations or if the results do not look right, you can do them over manually. For each part that contains an error:

1. Click the **Clear Mask** button to restore the original 3D image:

2. Using the **FreeROI** and **Dynamic Region Grow** tools as needed to isolate the part. (See "FreeROI" on page 3-49 and "Dynamic Region Growing" on page 3-53 for instructions on using each of these tools, respectively.)

3. When the part is displayed as a segmented image in the 3D window, click the **LowAtt** Tool Panel button.

4. Right-click on the thumbnail window of the part to be replaced, and select **Clear** from the menu.

5. Click the camera icon to capture the new image.

When finished correcting the segmentations, click **Auto Run** to recalculate the end result. When the dialog asking you whether you want to replace the thumbnail images, click **No**.

Manual Segmentation

Open a low-attenuation study in the **LowAtt** workflow. When the study has been loaded, click the **LowAtt** button in the Tool Panel to open the tool.

1. Validate the **Overview** workflow element. AQi automatically moves to the **Trachea** element.

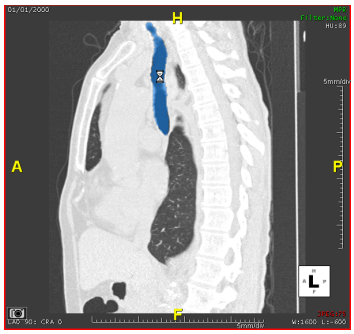
2. Segment the trachea.

   - If there is an APS file of the segmented trachea, the image is automatically loaded.

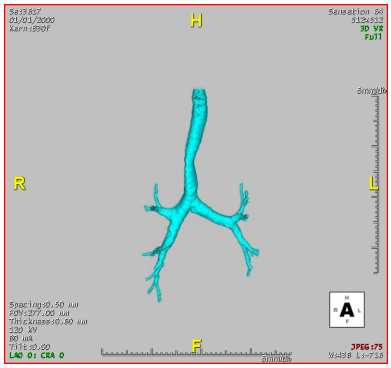
- If there is no trachea mask from APS, or if the APS segmentation was incorrect, segment the trachea manually:

3. Click the Region Grow tool in the Tool Panel.

4. In the sagittal image, shift-click and hold the left mouse on the trachea until the trachea is fully masked (see the following figure).



5. Click the **Select** button in the Tool Panel. The segmented trachea is displayed in the 3D window (shown below).



6. Click the **LowATT** tool in the Tool Panel.

7. Click the camera icon on the first line to capture the segmented trachea image as a thumbnail.

8. Validate the **Trachea** Workflow element.

9. Segment the left lung.

   - If there is an APS mask of the segmented left lung, the image is automatically loaded.

   - If there is no left lung mask from APS, or if the APS segmentation was incorrect, segment the left lung manually, using the **FreeROI** and **Region Grow** tools as needed to remove the right lung. (See "FreeROI" on page 3-49 and "Dynamic Region Growing" on page 3-53 for more information.)

10. Capture the segmented left lung to a thumbnail in the Tool Panel.

11. Validate the **Lt Lung** workflow element.

12. Repeat steps 5-7 for the right lung.

13. When all three parts have been segmented and captured, click **Auto Run** to calculate the volume of each segmented part, and build a segmented 3D image of the lung. The volume results are displayed on the 3D image.

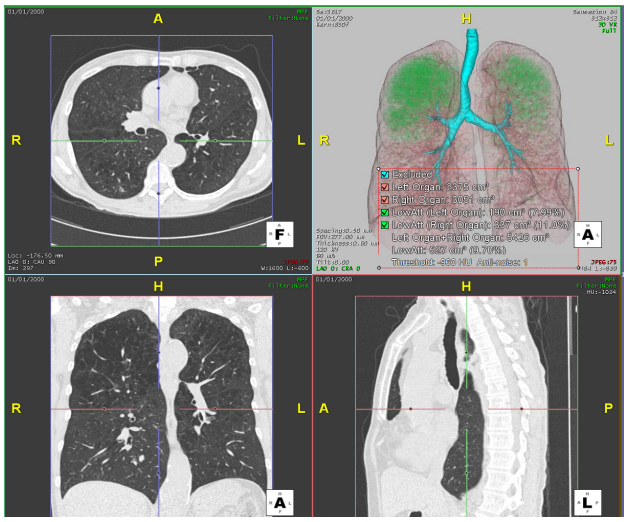


Figure 3-81: Completed Workflow

Note: To see the volume results, make sure the *Show Result* button is active (circled).

User-Defined Colors for Segmented Organs

You can configure a color template for LowAtt so that different colors are used to highlight each organ.

1. Click the **Template** tab, and create a new category called “LowAtt.” (See "Creating a New Template Category" on page 3-8 for instructions on creating a template).

Note: The template must be named “LowAtt,” using this exact spelling and capitalization. Otherwise, the LowAtt tool will not recognize it.

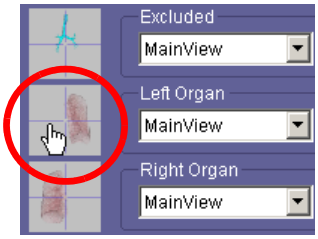
---

2. Load a LowAtt study.

3. In the LowAtt tool panel, click **Auto Run**. Wait until the results are displayed on the 3D image (see Figure 3-81).

4. For each organ whose color you want to change, do the following:

   a. Display a segmented organ by clicking that organ’s thumbnail image (see the following figure).



b. The corresponding organ is displayed in the main window (see the figure below).

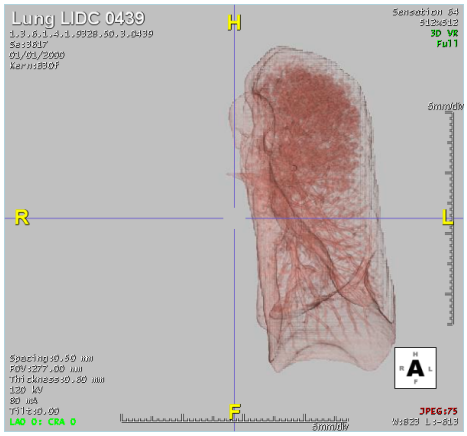
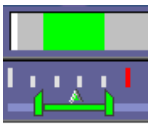


Figure 3-82: Left Organ Displayed

c. Click the **3D Setting** tab and change the color. (See "Changing the Color" on page 3-11 for instructions on how to change the color of an object in the main window.)

For example, suppose you chose a green color for the left organ. The color slider in the **3D Setting** panel and the corresponding image would appear as follows:



d. Click the **Template** tab, and select **LowAtt** from the pull-down menu.

e. Add the newly colored organ as a template. For instructions on adding a template to a template category, see "Adding a Template" on page 3-8.

Note: Elements in the template must be named exactly as they are named in the LowAtt tool. Otherwise, LowAtt will not be able to find them. For example, if you are adding the Left Organ to the template category, you must name that template “Left Organ” so that it will be recognizable to the LowAtt tool.

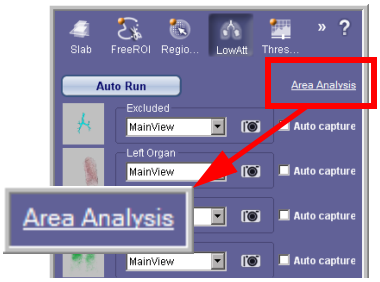
5. Repeat steps a-d for each organ whose color you want to change.

The next time a LowAtt study is loaded, the colors in the **LowAtt** template category, rather than the default colors, will be applied.

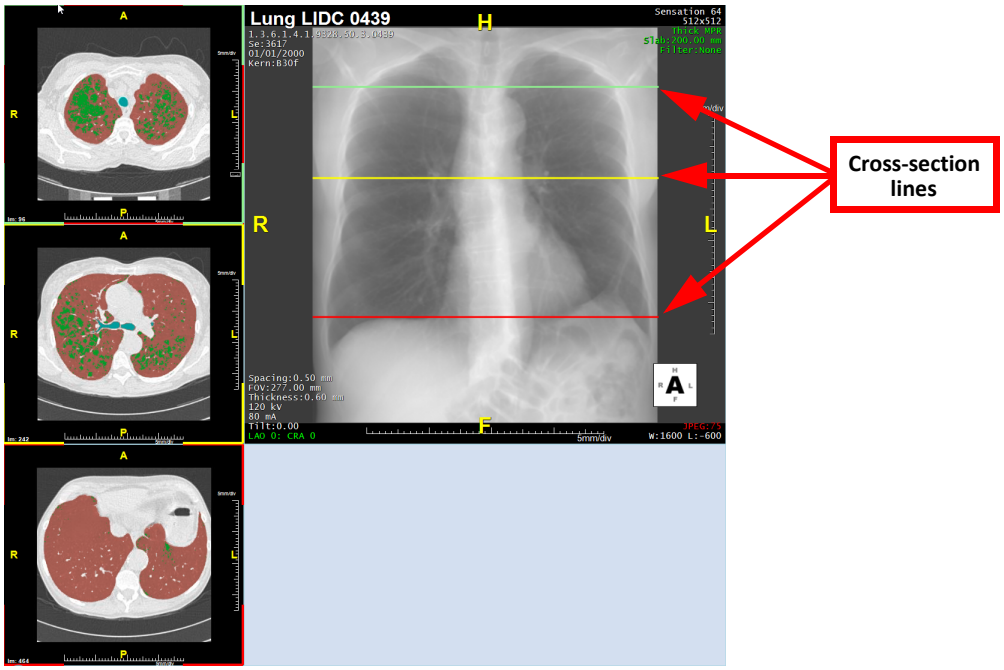
Area Analysis

Obtain area values on the axial image.

1. To perform the analysis, click the **Area Analysis** link in the top-right corner of the tool panel.



The LAA screen is displayed. The three cross-secton lines correspond to the top, middle and bottom axial images on the left.



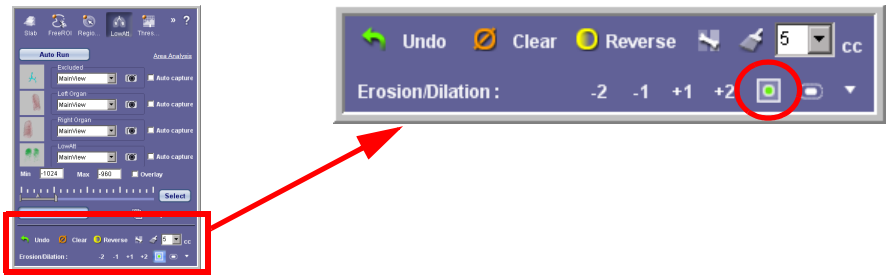
2. Adjust the cross-section lines to mark the top, middle and bottom slices for the measurement.

3. Click the **Show Result** button to calculate and display the area result (see the following image).

	Right Organ Area(cm²)	LowAtt Area(cm²)	(%)	Left Organ Area(cm²)	LowAtt Area(cm²)	(%)	Total Area(cm²)	LowAtt Area(cm²)	(%)
Top	82.6	30.6	37.1	87.2	20.4	23.4	170	51.1	30.1
Middle	146	8.09	5.54	120	6.06	5.05	266	14.2	5.32
Bottom	61.0	0.138	0.226	38.2	0.0585	0.153	99.2	0.196	0.198

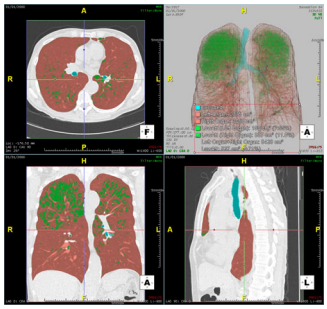
Other Features

- Click the mask overlay icon to see color overlay on the 2D images (see image below).

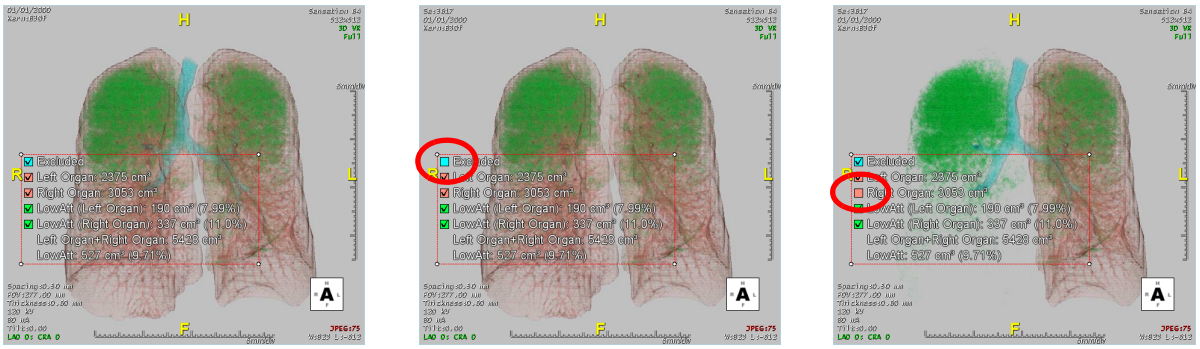


Note: The *mask overlay* icon is not the same as the checkbox labeled **Overlay** in the Tool Panel. The latter is used only to display a threshold overlay.

The Low Attenuation color overlay is shown on the 2D images:



- Click the color squares in the volume results to show or hide the corresponding segmented parts in the 3D image. When a part is hidden, the corresponding color box is hollow. 



All Parts Showing **Trachea Hidden** **Left Lung Hidden**

Figure 3-83: Show/Hide Corresponding Segments

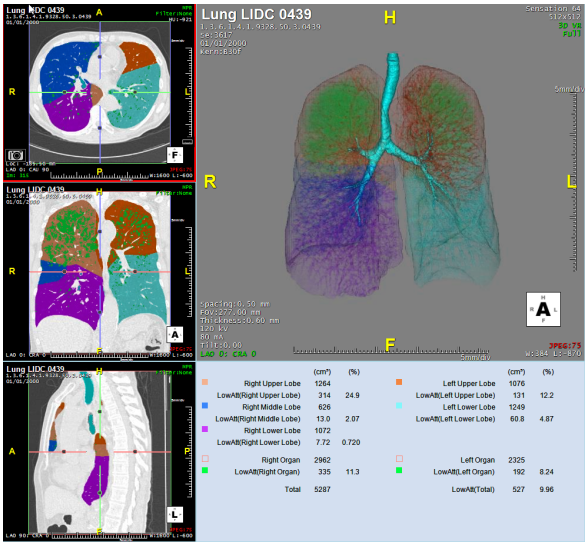
Low Attenuation Load Segment

After lung decomposition is completed, you can display the result of low attenuation volume analysis for each segment.

1. Click the **LowAtt** tool icon (circled in light blue, in the figure below).

2. Click the **Load Segments** button (circled in dark blue). The low attenuation volume analysis is performed automatically.

   Results are displayed in the main window:

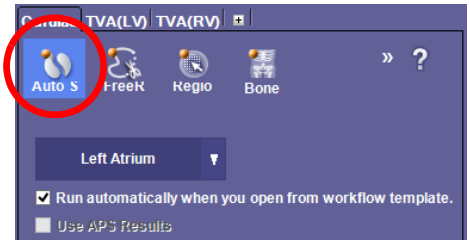


Auto Segmentation 

This tool automatically segments the selected organ. It can then be incorporated into a workflow template as an element.

PRECAUTION: You must validate automatic segmentation/mask results before assigning any clinical significance. Please check the model overlay on the axial, coronal or sagittal view. Use the Mask Edit tool to edit, or click on Clear Mask to re-do segmentation manually.

The Low Attenuation color overlay is shown on the 2D images:

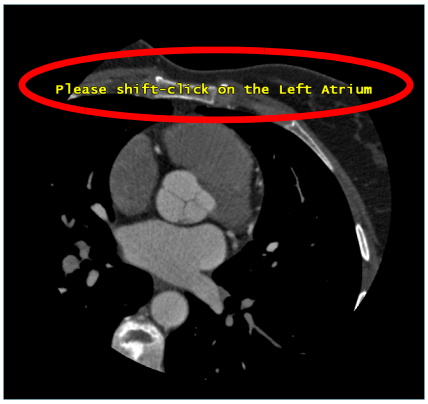


1. After loading a study that contains a heart, lung, liver,colon or Tumor, click the **Auto...** button. The Auto Segmentation tool panel is opened (see image at right).

Note: If you do not see this button in the Tool Panel, you must access it from the hidden panel. See ": The Workflow-related Tools" on page 3-18 for instructions.

The Auto Segmentation tool can detect which organs are present in the loaded data, and which organs, if any, can be segmented. In the example shown here, Auto Segmentation has detected a

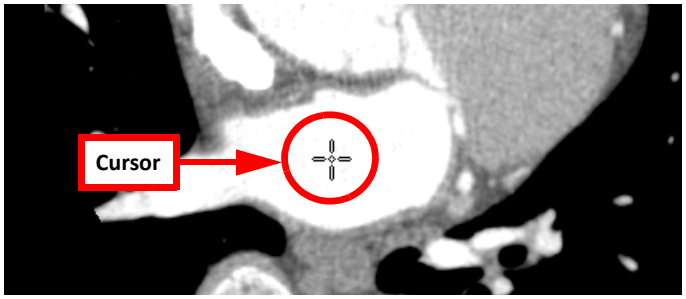
heart and has automatically displayed the **Left Atrium** button. In a different case, the button might show Liver, Lung, Colon, or Tumor.



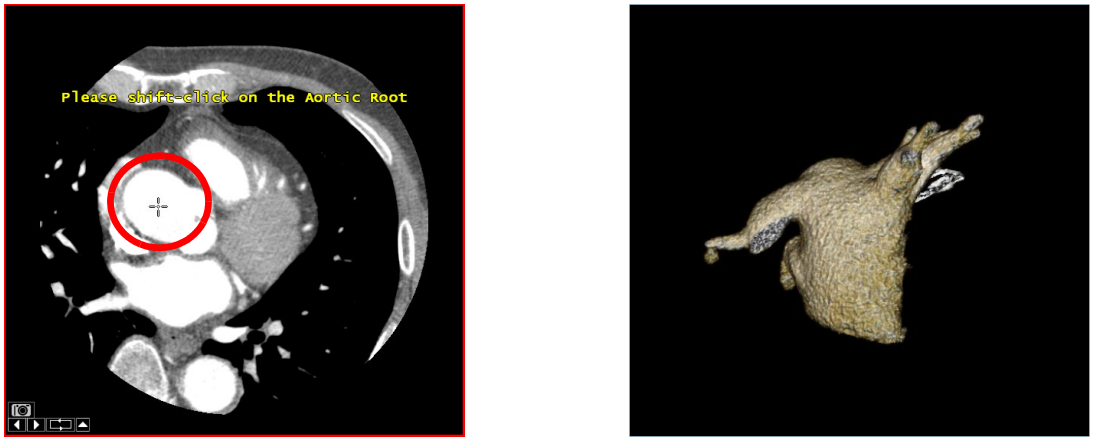
2. Click the button to begin segmentation. In this example, we are segmenting a heart and the **Left Atrium** button is visible. Instructions on how to perform the segmentation are displayed on each image.

3. If desired, slice through the axial image, adjust the WL, and otherwise manipulate the image to find the best view of the left atrium.

4. Shift and click on the left atrium (see the following image).



5. The next instruction is displayed: “Please shift-click on the Aortic Root.” Perform this step to start the segmentation.



Shift-click to Segment **Atrium Segmented**

Figure 3-84:Adding Auto Segmentation to a Workflow

Auto Segmentation is a useful tool to add to a Workflow. After performing the segmentation, you can create a new Workflow Element (WFE) to the current workflow, to be used with similar studies. Check the box labeled **Run automatically when you open from workflow template** to run Auto Segmentation when that element is clicked (see Figure 3-85 on page 3-140).

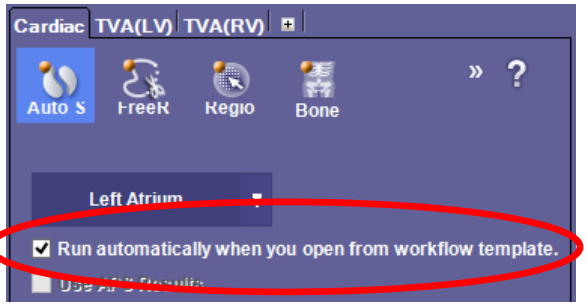
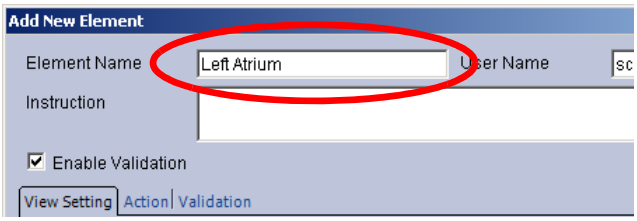


Figure 3-85: Auto Segmentation Tool

For instructions on adding a new WFE, see "Add the New Element" on page 4-9.

Please note that the instructions referenced in the above link use a different example. You should give this new element a relevant name for this operation:

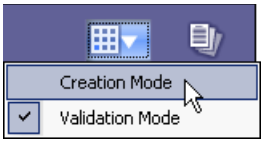


To preserve the changes made to this study data, you must check the appropriate boxes in the **Add New Element** dialog:

- Check the **Include Tool Panel Change** box to make sure the Auto Segmentation tool is opened when this WFE becomes active.
- If you made any changes to the layout, zoom, pan or rotation, check the appropriate box for each.
- Check the **Apply MPR W/L** box so that the W/L changes will be applied to future studies.

Click **OK** when done. The new element is added to the workflow.

To save the element to the Workflow Template, select **Creation Mode** from the menu at the top-right of the Workflow panel:

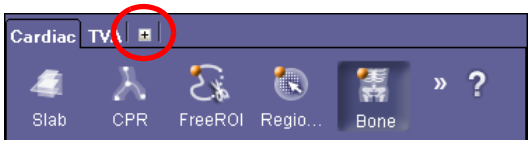


Then select **Save Workflow Template** from the Workflow pulldown menu.

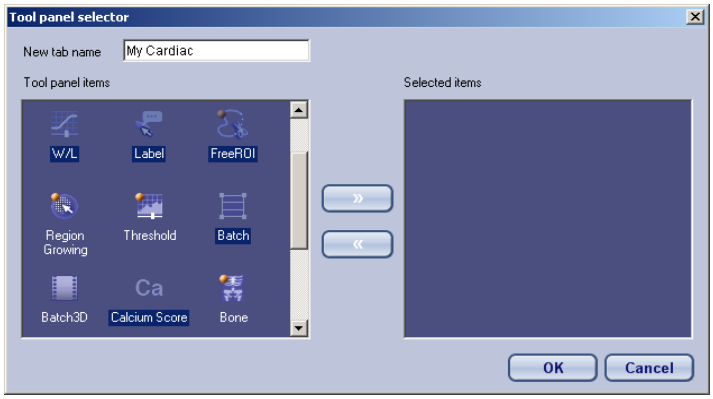
To save the current image as a scene, select **Save Workflow Scene** from the Workflow pulldown menu (circled in the figure at right).

Customizing the Tool Panel

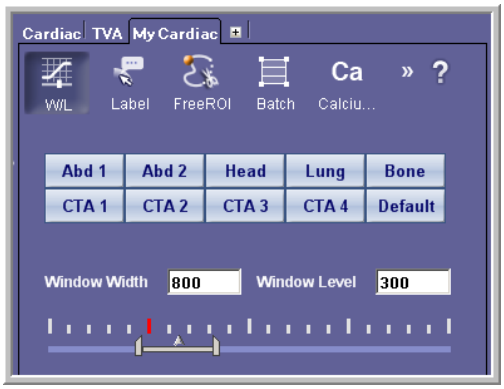
You can create your own Tool Panels that each contain the tools used most frequently in different types of studies or workflows. To create a new tool panel, do the following:



1. Click the plus sign (‘**+**’) tab, located to the right of other tool panel tabs such as the Cardiac tool panel. The Tool Panel Preference panel is displayed:



2. Click the **Add** button. The Tool Panel Selector dialog is displayed.
3. Type in a name for the new Tool Panel tab in the **New tab name** field.
4. Select up to five tools to be displayed in the tab.



5. Close the Tool Panel Selector by selecting another tab.

Note: All custom-created tool panels remain permanently in the Aquarius iNtuition 3DViewer, unless they are deleted.

Other Customizing Tools

Other functions of the Customizing tool include:

- Rename - Rename the selected tool panel. Select a tool panel from the list and click the Rename button at the bottom of the tool panel. (You can also rename by double-clicking the tool panel name slowly.)
- Delete - Delete by selecting a tool panel and clicking the Delete button at the bottom of the tool panel.
- Change Position - Move the position of a tab by selecting the name and then moving it up or down in the list with the up and down arrows located to the right of the list.
- Reset - Reset the tool panel to an earlier state, either to what it was at the time of the most recent login, or to the default state of the 3D Viewer. Click the Reset button at the bottom of the tool panel.

Floating Tool Panel

The tool panel can be detached from the right panel of the screen so that you can move it to a more convenient location.

To float the tool panel, click on the the active tab in the tool panel and drag it in any direction. To return the tool panel to its original position, click the **X** in the upper-right corner to close it.

Top Toolbar Buttons

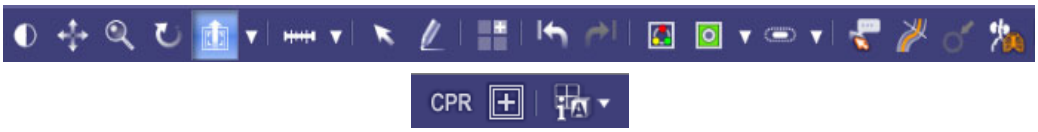


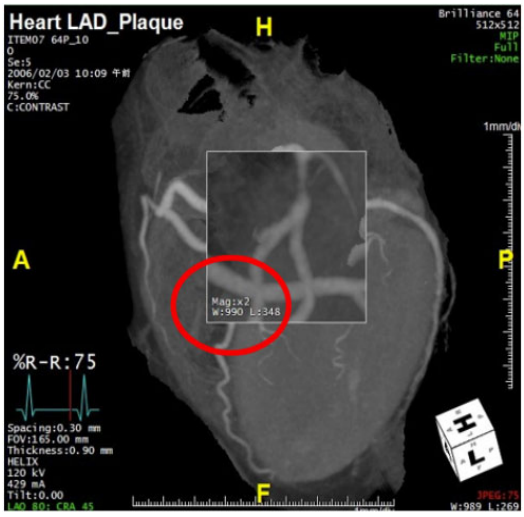
Figure 3-86: Top Toobar Buttons (Top: Left End; Bottom: Right End)

This section describes all the tools found on the Top Toolbar (located above the main 3D Viewer window). To find the section you need, turn to the page listed below. If you are viewing this manual online, click the desired title:

Magnifier Tool

To enable the Magnifier tool upon right-clicking an image, first you must go to Preferences > Viewer > Setting 2 tab and enable the “Show Magnifier area to context menu” option. When viewing an image in the viewer, right mouse click and select “Show Magnifier”. A Rectangle area will appear, drag to move the position.

- Change the zoom ratio (x1 - x3) by using the mouse wheel
- Adjust the W/L within the rectangle by using left and right mouse.
- Right-click the on the box to adjust the zoom ratio or to reset the WW/WL.



Note: When an area is resized, the viewer will return to the original size.

Mouse Modes

Each mouse button (left, right and middle) performs a different function when you hold it down while moving the mouse along an image. Combinations of mouse buttons also perform specific functions. Table 3-21 shows the default function for each mouse button or combination of mouse buttons.

Table 3.7: Mouse Button Functions

Mouse Button	Function
Hold down left Button	3D image: Rotate image 2D image: Page through slices
Hold down right Button	Pan the image
Left and Right Buttons held simultaneously	Change Window Level/Window Width
Hold down middle Button (wheel)	Zoom up or down
Roll Wheel (not held down)	(2D images only) Page through slices one at a time
Click wheel	Enter scroll mode. Up and down motions with the mouse control the direction and speed of the scroll. Click the middle or left button to stop the scroll. (Requires enabling a setting. See "Mouse Operation" on page A-24 for more information.)

Setting the Left Mouse Button

If you use one of these functions more frequently than the others, you can change the function of the left mouse button by clicking one of the following buttons on the top tool bar.

The first four buttons, from left to right, change the function of the **left** mouse button to window/level, pan, zoom, rotate (3D images only) and page through slices (2D images only):

Note: If you change the left mouse button to something other than rotation, the rotation function will not be available unless you change the left mouse button back.

Paging Speed

There are two modes available for paging through the slices of a 2D image.

- **Normal** - Scrolling up or down the 2D image while holding down the left mouse button (“slice mode”) causes the slice images to advance rapidly.
- **Control** - Scrolling on the 2D image causes the slice images to advance slowly, giving you more control over the viewing of each slice.

To toggle the paging mode between Normal and Control, click the down arrow to the right of the slice icon in the top tool bar and then select either Normal (left icon) or Control (right).

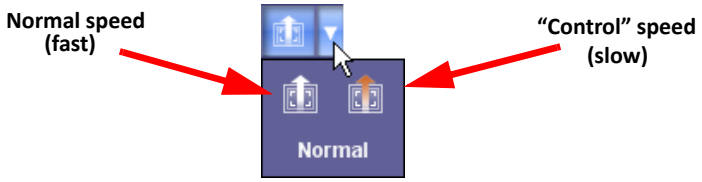


Figure 3-87 Paging Mode Controls

Measurement Tools 

All measurement tools for loaded data can be accessed from a pull-down menu that is located on the top toolbar. The menu shows each measurement with an icon, the measurement name and a shortcut key, if available. To find the section you need, turn to the page listed below. If you are viewing this manual online, titles are active links.

IMPORTANT:

If a measurement is made on an image and then the image is zoomed or the layout is changed, AQi keeps and displays the original measurement value. However, once a distance measurement or ROI is moved, a re-measurement is performed.

It is advised to first magnify the image before conducting measurements. Below are the error estimation values derived from testing conducted under controlled conditions against a digital phantom.

- **Error from length measurements such as distance, line, circumference, and so forth, is within 3%.**
- **Error from the intensity measurements is less than one.**
- **Error from angle measurements is less than 1 degree. Error from area measurements is within 2%.**

  The error estimation does not account for errors from the modality. You can reduce the risk of error by zooming in on the image before performing measurements.

  Supported for CT data only.

- **Distance**

  This feature calculates the distance of a line drawn on the image.

  To draw a line, do the following:

  a. Click on any point in the image.

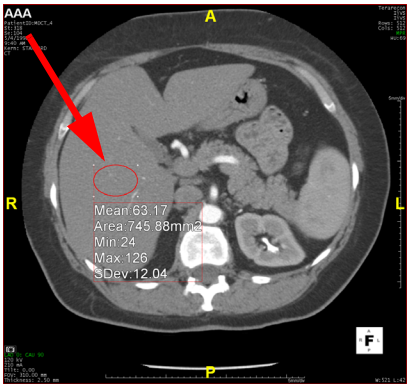
  b. Hold and drag the mouse across the image.

  c. Release the mouse to finish drawing.

  This tool can be used on MPR, MIP, MinIP and ThickMPR in any window. Distance measurements can be tracked in the Finding Viewer (see Chapter 16: "The Findings Workflow" for information about the Finding Viewer).

- **Ellipse**

  This feature calculates the average HU value within an area, defined by the ellipse drawn on the image (see the figure at right).



To draw an ellipse:

a. Click on any point in the image.

b. Hold and drag the mouse across the image.

c. Release the mouse to finish drawing.

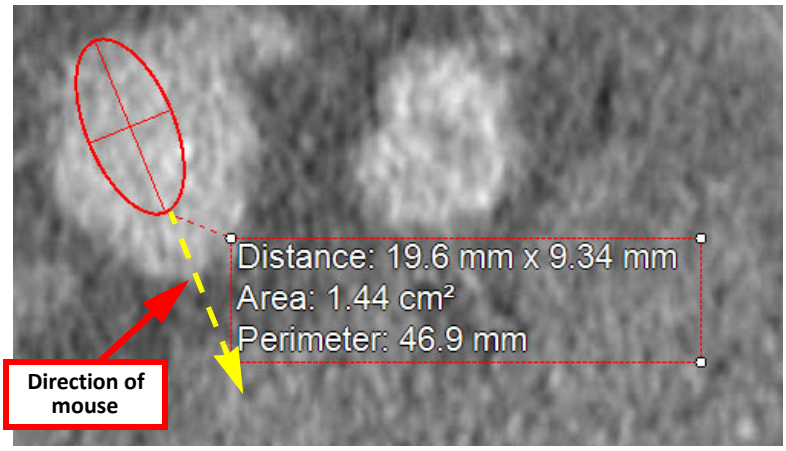
This tool can be used only on MPR images in the active (upper right) window. Ellipse measurements can be tracked in the Finding Viewer (see Chapter 16: "The Findings Workflow" for information about the Finding Viewer).

- **Oblique Ellipse**

This measurement calculates the distance of the major and minor axes, the area of the ROI and the perimeter of the ROI.

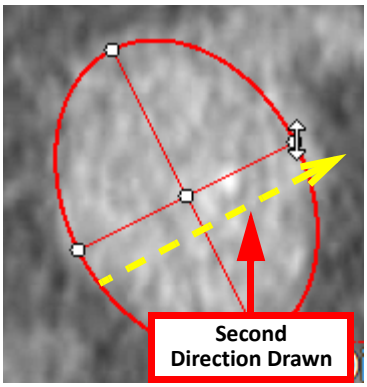
To draw an oblique ellipse:

a. Click on the edge of the area you are going to measure, and drag the mouse across the area to the opposite edge. An ellipse is drawn as you move the mouse.



b. Release the mouse when finished drawing the ellipse.

c. Click one of the endpoints on the axis that is perpendicular to the line just drawn. The cursor changes to a double-arrow icon (see figure below).



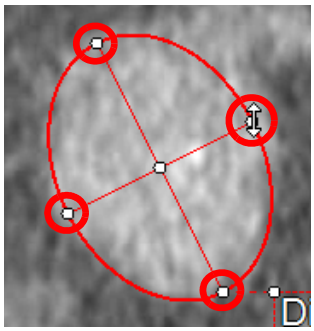
d. Drag the mouse away from the center. The ellipse expands in the perpendicular direction. You can also drag the mouse toward the center to contract the ellipse.

e. Release the mouse when done.

You can modify the ellipse after completing the initial drawing to get a more accurate measurement.

Resizing the Ellipse

There are four points on the circumference of the ellipse, two endpoints for each axis that crosses the ellipse (circled in the figure below). Click any endpoint and drag toward or away from the center to resize the ellipse lengthwise or width-wise.

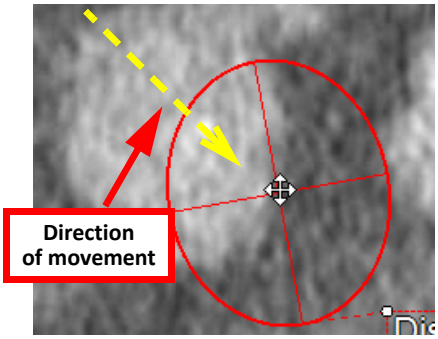


Rotating the Ellipse

Drag any of the four endpoints in a direction that is neither toward nor away from the center to rotate the ellipse.

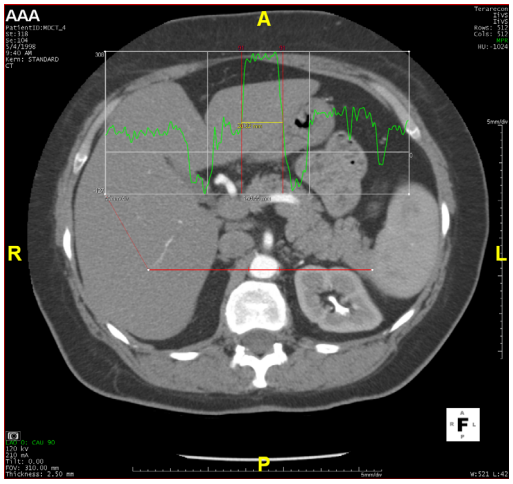
Panning the Ellipse

Click the center point (the place where the two axes intersect). The cursor changes to a cross-arrows image, indicating that the entire ellipse can be moved around on the image.



- **Profile**

  The Profile tool displays a graph showing an image's HU values, along the line drawn on the image.



  To draw a line:

  a. Click on any point in the image.

  b. Hold and drag the mouse across the image.

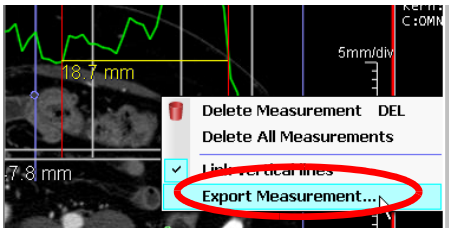
  c. Release the mouse to finish drawing.

- Exporting a Profile

  A profile can be exported to a text file and saved on your computer. To export a text file:

  a. Right-click on the profile graph.

  b. Select **Export Measurement**. A Windows **Save As** dialog is displayed.

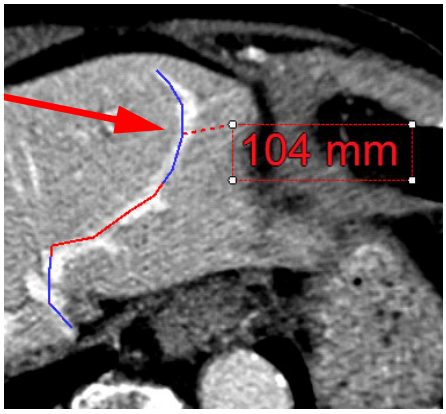


3. Navigate to the appropriate folder and save. The profile data is saved as a text file.

This tool can be used on MPR images in any window. Profiles can be tracked in the Finding Viewer (see Chapter 16: "The Findings Workflow" for information about the Finding Viewer).

- **Line Segment**

The Line Segment tool allows you to draw a series of connected line segments, through multiple planes, by clicking on the image, dragging the mouse along the image, and then repeating those actions as many times as required. The measurement given is the sum of the lengths of all line segments on the image.



Note: Blue line represent the active plane.

To place a **Line Segment** measuring tool onto an image:

a. Click on any point in the image.

b. Hold and drag the mouse across the image.

c. Release the mouse to finish drawing line segment.

d. Repeat steps 1-3 to draw a new line segment, as many times as needed.

e. Double-click to finish drawing.

In the active (upper right) window, this tool can be used only on MPR images. In the inactive windows, this tool can be used in MPR, MIP, MinIP and ThickMPR images. Line Segment measurements can be tracked in the Finding Viewer (see Chapter 16: "The Findings Workflow" for information about the Finding Viewer).

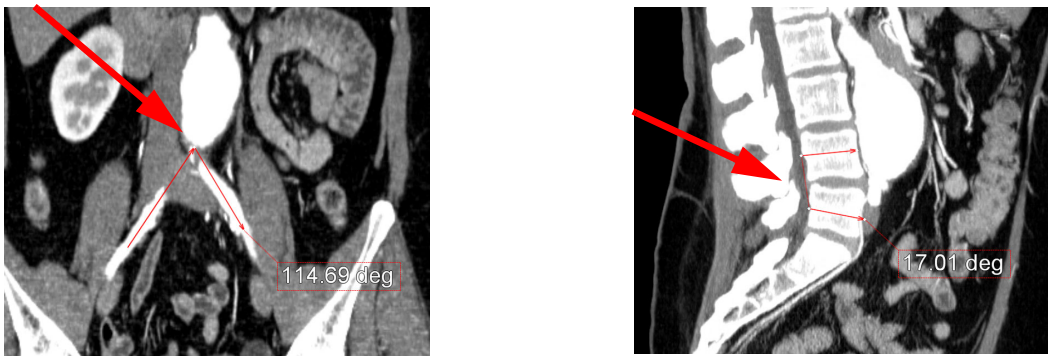
- **Angle**

The angle measurement tool displays the degree of the angle between two lines drawn on an image. The lines do not need to be connected.

To measure an angle:

a. Click on any point along one line of the angle.

2. Hold and drag the mouse along the line to the vertex of the angle.
3. Release the mouse to finish drawing the first line.
4. Click on any point along the other line of the angle. This may be right at the vertex of the angle, or it may be a disconnected line.
5. Drag the mouse along the second line, and then release to finish creating the angle. The angle measurement appears on the screen, with an input text box so that you can add information about the angle being measured.
6. Input text if desired.
7. Press the return button to finish.



Connected lines **Unconnected Lines**

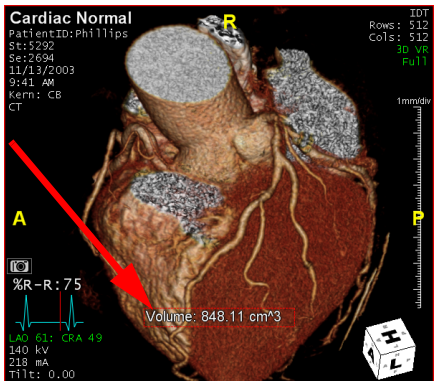
Figure 3-88: Angle Measurements

This tool can be used on MPR, MIP, MinIP and ThickMPR images, in any window.

- **Volume**

The Volume measurement finds the total volume (in cubic centimeters) of everything that is visible in the main window. For example, if you measure the volume, then remove bone, or cut out parts of the image using the FreeROI tool or slab rendering, and then measure the volume again, the amount displayed is less than the amount of the first calculation.

To measure the volume, select **Volume** from the measurement menu. The volume is displayed on the 3D image, as shown in the figure below:



Measurement Value Options

1. Right-click on the measurement to open the **Volume Options** dialog.

2. Select additional values to be shown in the measurement results. You can also set the current configuration to be the default.

Volume Classification

You can classify volumetric data into sub-volumes. The opaque and transparent portions of the volume reflect the visible and hidden segments of the 3D image, and can therefore be affected by any operation, such as masking or segmentation, that changes what is visible in the main window.

IMPORTANT:

If a measurement is made on an image and then the image is zoomed or the layout is changed, AQi keeps and displays the original measurement value. However, once a distance measurement or ROI is moved, a re-measurement is performed.

It is advised to first magnify the image before conducting measurements. Below are the error estimation values derived from testing conducted under controlled conditions against a digital phantom.

- **Error from length measurements such as distance, line, circumference, and so forth, is within 3%.**
- **Error from the intensity measurements is less than one.**
- **Error from angle measurements is less than 1 degree. Error from area measurements is within 2%.**

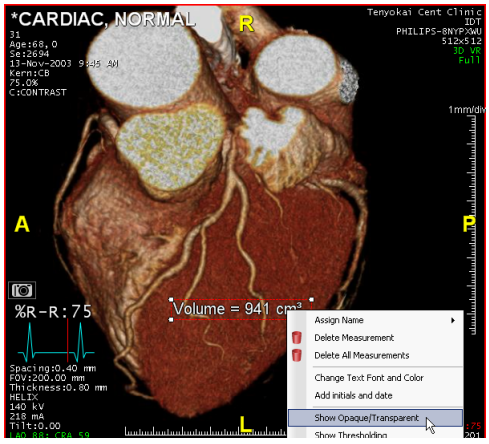
  The error estimation does not account for errors from the modality. You can reduce the risk of error by zooming in on the image before performing measurements.

  Supported for CT data only.

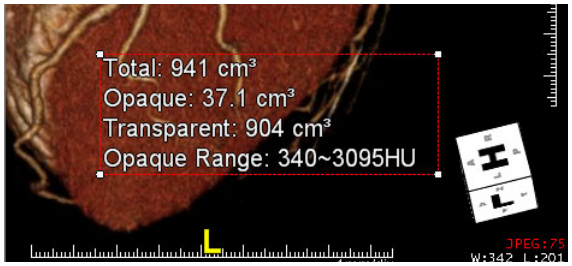
The Volume measurement can be tracked in the Finding Viewer (see Chapter 16: "The Findings Workflow" for information about the Finding Viewer).

Opaque/Transparent Volumes

To show the volume of the transparent and opaque portions of the data, right-click on the the measurement and select **Show Opaque/Transparent** from the pull-down menu:



The transparent/opaque values are displayed in the measurement:



These values can also be determined by the opacity threshold. In this case, the default threshold has been used. To adjust the opacity threshold, right-click the measurement and select **Settings** from the menu. The **Volume Classify Setting** dialog is displayed:

Enter a new threshold value in the input box and click **OK**. The opaque and transparent values shown in the measurement are recalculated and redisplayed.

HU Threshold Volumes

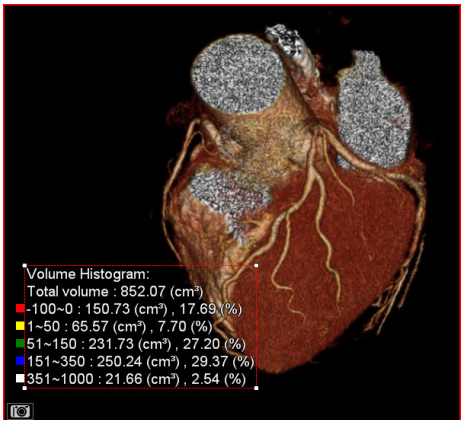
To set the HU threshold, click the **Thresholding** tab in the settings dialog. In the **Threshold** input box, enter a threshold value that will be used to separate the volume into sub-volumes of data having HU values above (or equal to) the threshold, or below the threshold.

Optionally, you can enter names for the higher and lower HU volumes, which will be displayed on the measurement. Click **OK** when done.

The HU threshold values (see figure below):

- **Volume Histogram**

  Volume Histogram, an optional module, calculates the same overall volume that the Volume tool does, but in addition, the total volume is broken down into HU value ranges. The volume and percentage of the total volume are displayed for each.



  The Volume Histogram measurement can be tracked in the Finding Viewer (see Chapter 16: "The Findings Workflow" for information about the Finding Viewer).

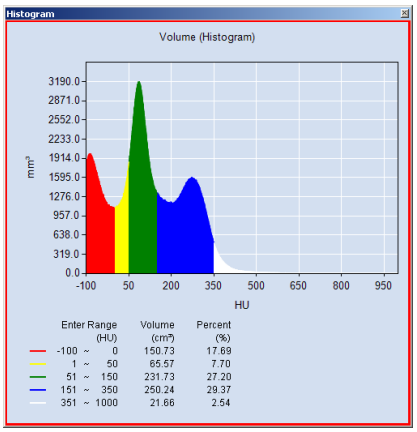
Note: You are obligated to define the parameter ranges that are used in this procedure. When first accessed, the user interface for setting these parameters contains generic default values having no particular significance. You must acknowledge this by dismissing a warning message to this effect

---

In the image below, the HU values are partitioned into five ranges. For each range, the volume of all data having HU values within that range is displayed, followed by that volume's percentage of the total volume.

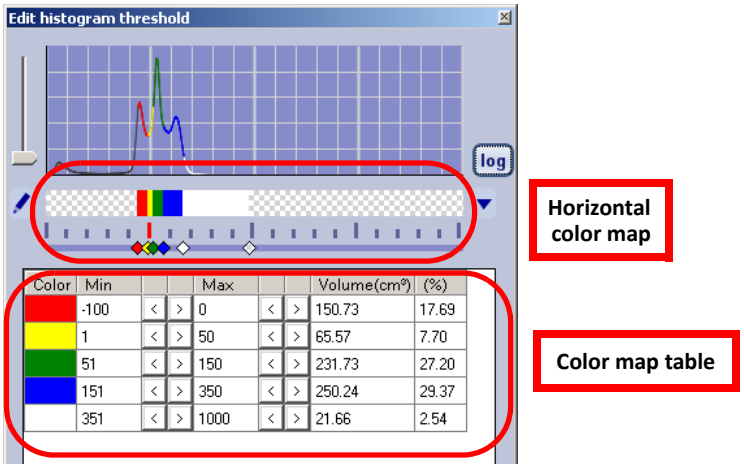
In this example, the volume of data having HU values between -100 and 0 comes to 150.73 cubic centimeters, which is 17.69 percent of the total (852.07).

Each HU range is associated with a color. These colors are used more extensively in the histogram graph. To see the graph, right-click on the measurement and select **Histogram**. The graph and color key are displayed as follows:



- Editing the Histogram Threshold and Color Map

  You can modify the threshold of an HU range and the color map in the **Edit histogram threshold** dialog. To open the dialog, right-click on the measurement and select **Edit color map**. The dialog is displayed as follows:



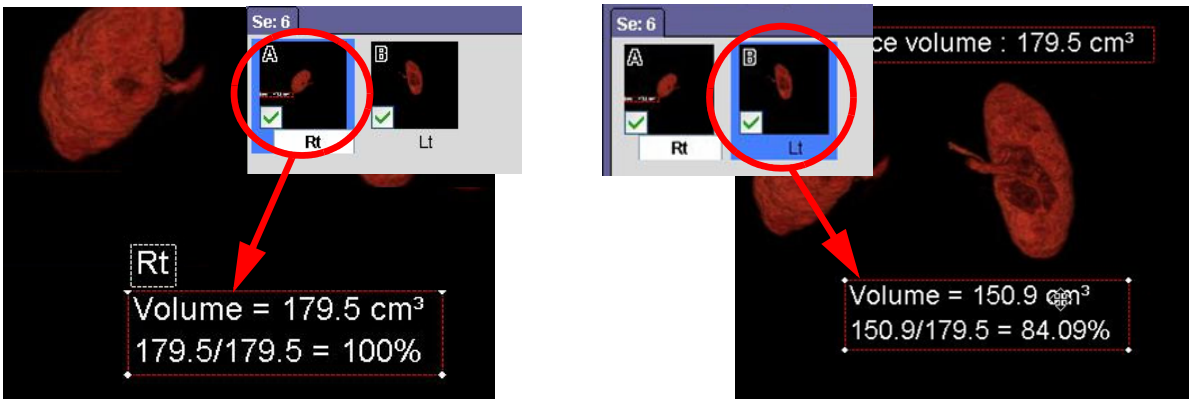
  The thresholds and color maps can be changed in two ways:

  - Horizontal color map - Add, delete, move, and change the color associated with the diamond markers below the horizontal color map.
  - Color map table - Click the left or right arrows in the table at the bottom of the dialog to change thresholds; click a color (left column) to change it.

Set the Reference Volume

a. Create or select a volume mask, and apply it to the volume.

b. Obtain the volume measurement.



c. To designate the measurement as the *reference volume,* right-click the measurement and select **Set Reference**.

d. Create or select a different volume mask, and apply that mask to the same volume.

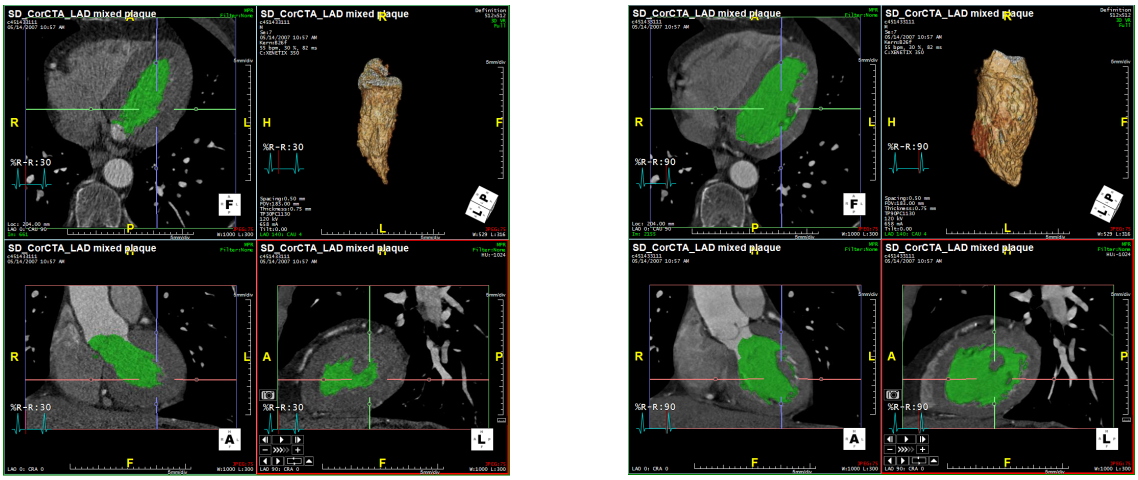
e. Obtain a new volume measurement. The measurement results will display the ratio of the new measurement to the reference volume.

- **Ejection Fraction**

This measurement tool allows you to calculate the ejection fraction in a 4D cardiac study from two user-defined LV volumes.

a. Load a 4D cardiac study. You can load as few as two phases. Including the end-systolic and end-diastolic phases will give the most accurate results.

b. Using the **Dynamic Region Growing** or **FreeROI** segmentation tools, segment the ventricle to be calculated in each phase.



Segmented **ED**

Figure 3-89: Segmenting the Ventricle

c. From the measurement tools menu, select **Ejection Fraction**. The EF value is displayed as a measurement on the 3D image:

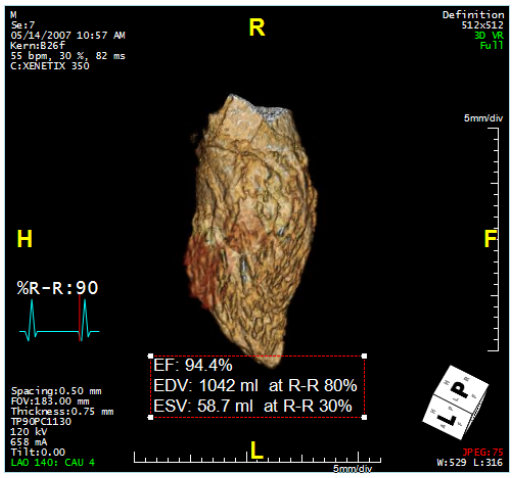


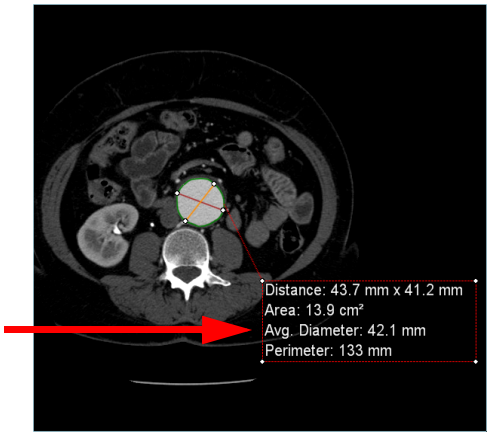
Figure 3-90: Ejection Fraction Result

- **Distance Pair**

  This feature calculates the maximum and minimum distances of an object, as well as its area.

  Click on an enclosed object (such as a vessel). The following items are calculated and displayed:

  - An outline around the object
  - The maximum and minimum diameters
  - The area
  - The average diameter
  - The perimeter length



  This tool can be used only on MPR images. Distance Pair measurements can be tracked in the Finding Viewer (see Chapter 16: "The Findings Workflow" for information about the Finding Viewer).

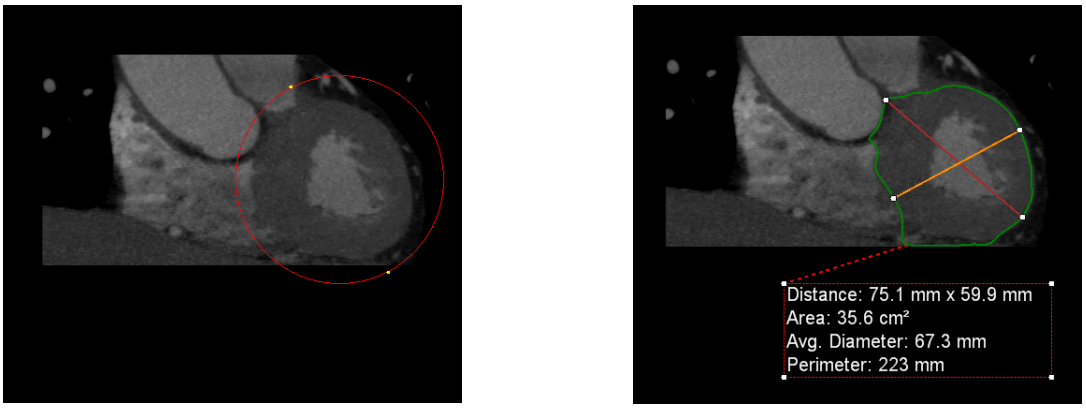
- **Assisted Distance Pair**

This tool calculates the maximum and minimum distances of an object, as well as its area.

Click just outside the edge of an enclosed object, and drag the mouse across the area. A circle is drawn around the area, growing larger as you drag the mouse. When the circle has reached a diameter that is larger than the largest diameter in the object, release the mouse. The circle will shrink to snap to the boundary.

The following values are calculated and displayed:

- An outline around the object
- The maximum and minimum diameters
- The area
- The average diameter
- The perimeter length



Drawing Circle Around Object **Circle Snapped to Boundary**

Figure 3-91: Assisted Distance Pair

Assisted Distance Pair can be used only on MPR images. Assisted Distance Pair measurements can be can be tracked in the Finding Viewer (see Chapter 16: "The Findings Workflow" for information about the Finding Viewer).

- Distance Pair Options

You can configure distance pair measurements to specify how the measurement is obtained and what information is displayed on the screen.

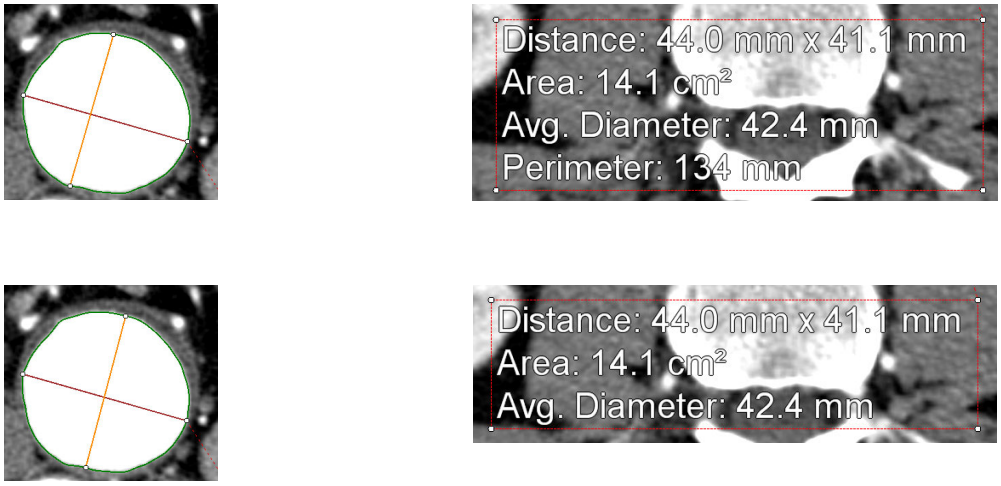
Note: These options apply to both Distance Pair and Assisted Distance Pair measurements.

Right-click on a distance-pair measurement and select **Option** from the drop-down menu. The **Distance Pair Options** dialog is displayed.

Table 3.8: Distance Pair Option Settings

Setting	Description
Calculate Minimum First	Find the smaller of the two diameters first.
Keep Perpendicular	Base the measurement on two perpendicular cross lines.
Through Center	Cross lines must go through the center of the area
Gradient/Threshold	Gradient: This method is recommended when the inside of the perimeter is smooth. Threshold: This is recommended when the inside of the perimeter is noisy.
Use existing contour on cross-section view	For distance-pair measurements on the cross-section view, use the contour that has already been calculated for the vessel diameter.
Show	Area - Area of the bounded region Average Diameter - The diameter of the circle that has the same area as the region bounded by the contour. Perimeter - The length of the boundary around the region Only if Smoothed - Show perimeter only if Smoothing is enabled Smooth - Apply smoothing to perimeter and calculate all values accordingly Scale - Scale factor for Smoothing Annotation - Show Smoothing scale factor in measurement result
Save as Default	Save current configuration as default
Update current	Show new measurement results immediately, while changing configuration
Default button	Revert to original default

The following images demonstrate examples of the **Keep Perpendicular** and **Show Perimeter** settings:



Top - Keep Perpendicular Enabled
Bottom - Disabled

Top - Show Perimeter Enabled
Bottom - Disabled

Figure 3-92: Keep Perpendicular and Show Perimeter Examples

- **Polygon**

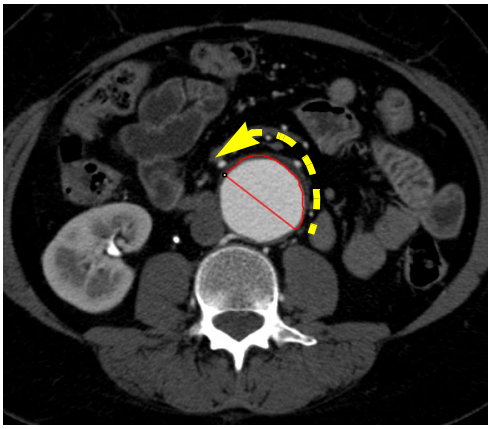
  Polygon is a free-hand ROI tool, allowing you to draw an outline around the region of interest, as you would do using the FreeROI tool. On most types of images, this feature calculates the area enclosed

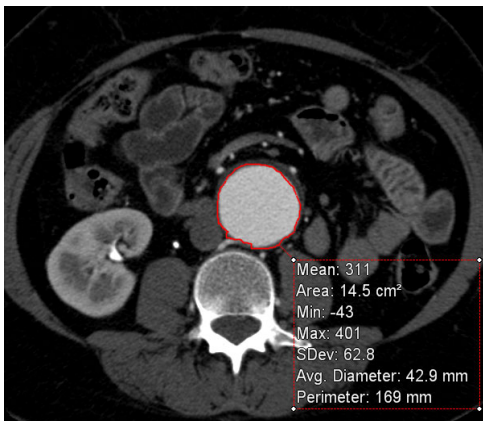
by the outline you have drawn. On MPR images, the average HU value within the area is also calculated and displayed.

To measure the region of interest:

a. Hold down the mouse and draw an outline around the region of interest.

2. When you are finished drawing, release the mouse. The area, mean, min and max, standard deviation, average diameter and perimeter length are displayed.





The Polygon tool can be used on any 2D image. Polygon measurements can be tracked in the Finding Viewer (see Chapter 16: "The Findings Workflow" for information about the Finding Viewer).

- **Circle ROI**

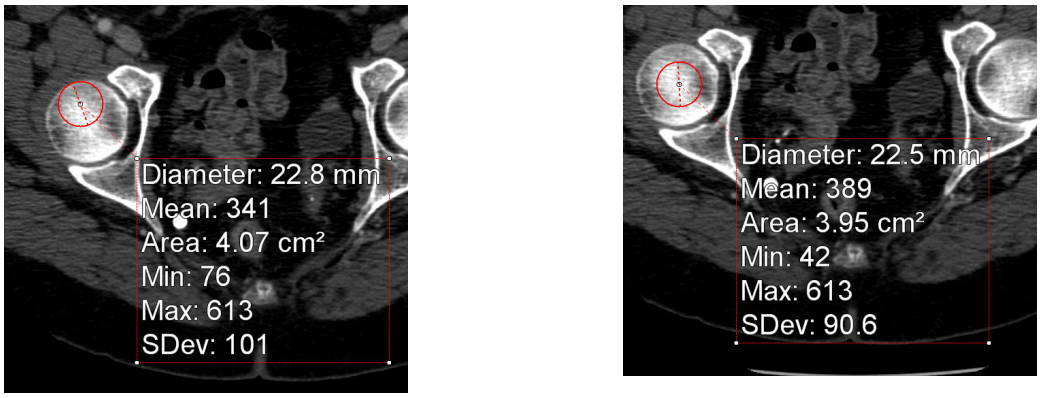
Circle ROI is a tool that allows you to draw an exact circle around the region of interest.

There are three ways to draw the circle:

- From the edge - Click on the edge of the ROI and drag the mouse across the area. The circle grows larger as you move away from the initial click point.
- From the edge, in incremental steps - Hold down the **Ctrl** key, click on the edge of the ROI and drag the mouse across the area. The circle grows larger by set increments as you move away from the initial click point.
- From the center - Hold down the **Shift** key and click on the center of the ROI. Then drag the mouse away from the center. The initial point becomes the center of the circle.

To move the circle, click on the center point and drag.

To change the radius, click anywhere along the edge of the circle and drag the mouse. Drag away from the center to make the circle larger, or toward the center to make the circle smaller.



Drawing Circle From Edge **Drawing From the Center**

Figure 3-93: Drawing Areas

The Circle ROI tool can be used on any 2D image. Circle ROI measurements can be tracked in the Finding Viewer (see Chapter 16: "The Findings Workflow" for information about the Finding Viewer).

- **Sphere**

  The **Sphere** measurement tool allows you to draw a 2D circle on a 2D image. A volume ROI is created from the drawn circle.

Note: The Sphere measurement tool is not supported for oblique or gantry tilt data.

PRECAUTION: To obtain results properly, do not include the edges of the volume when drawing the measurement boundary.

There are three ways to draw the ROI:

1. Draw from the edge of the circle.
   - Click the edge of the ROI and drag the mouse across the area to the opposite edge.
   - Release the mouse when the area is encircled.
2. Draw from the edge, increasing the diameter by steps of a set length
   - Hold down the **Ctrl** key and then draw from the edge, as described in the last bullet. As you drag the mouse, the size of the circle increases by a set increment.
3. Draw from the center of the circle

- Hold down the **Shift** key and click the center of the ROI, then drag the mouse in any direction.
- Release the mouse when the area is encircled.

Jump to Maximum Value

Right-click on a measurement and select **Jump to maximum value** from the menu. The volume measurement is displayed on the image when the mouse is released.

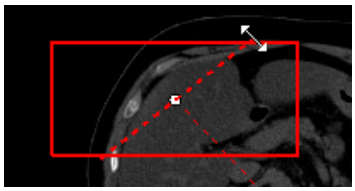
The Sphere tool can be used on axial, coronal or sagittal MPR images. Sphere volume measurements can be tracked in the Finding Viewer (see Chapter 16: "The Findings Workflow" for information about the Finding Viewer).

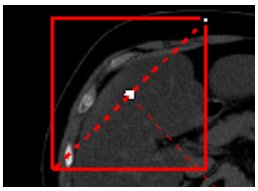
- **Cube**

The Cube measurement tool allows you to define a rectangular area on a 2D image. A volume ROI is created from the drawn rectangle, and the result shows the min, max and mean pixel values (HU, intensity or SUV, depending on the modality) for the volume contained in the ROI.

Editing Cube Size and Dimensions

To change the area or dimensions of the rectangle drawn on any of the 2D images, hover the mouse on any part of the rectangle's edges. The cursor turns to a double-arrow, and a dotted line is drawn from the hover point to its diagnonal opposite on the other side of the rectangle (see figure below, left). Click and hold the mouse, and then redraw the rectangle by moving the mouse around (below, right).

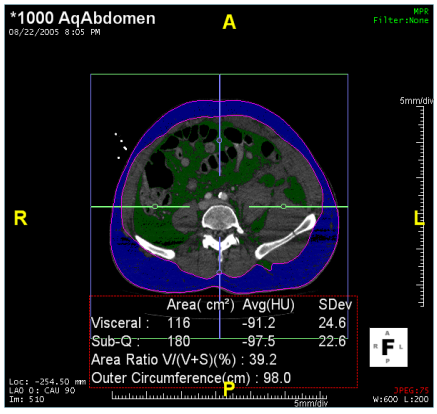




Cube measurements can be tracked in the Finding Viewer (see Chapter 16: "The Findings Workflow" for information about the Finding Viewer).

Fat Analysis

To obtain a fat analysis, select **Fat Analysis** from the measurement menu. The result is displayed on the axial MPR image:



The Fat Analysis tool can be used on axial MPR images only.

Options

To see fat analysis options, right-click on the measurement annotation and select **Option** from the menu. The options dialog is displayed.

HU Range

You can adjust the HU range used to detect fat in the region of interest. Use the slider to change the minimum or maximum ends of the range, or enter the desired values in the input boxes. To display the overlay colors, check the Overlay box.

Area Ratio Type

You can calculate the area ratio (V/[V+S]%), the visceral/subcutaneous fat ratio or neither. The selected ratio is displayed in the measurement annotation.

Color Map

The green and blue colors are default colors and can be changed. To change the color, click the down arrow to the right of the color you want to change. The color palette is displayed.

Select a new color from either the **Theme colors** or **Standard colors** group. To see the Windows palette, click **More colors**.

Default

- To make the new color map the default, click the **Save as Default** box.
- To reset the color map to the current default, click the **Default** button.

Fat Analysis measurements can be tracked in the Finding Viewer (see Chapter 16: "The Findings Workflow" for information about the Finding Viewer).

- **Fat Analysis 3D**

  Select **Fat Analysis 3D** from the Measurement Tools menu. The Start/End dialog is opened.

  - Scroll through the axial slices until you reach the start of the analysis range, and click **Start**.
  - Scroll through slices to the end slice of the range, and click **End**.
  - The 3D fat anaysis is calculated automatically. Results are then displayed in the image window.

  Fat Analysis 3D measurements can be tracked in the Finding Viewer (see Chapter 16: "The Findings Workflow" for information about the Finding Viewer).

Options

Right-click on the measurement and select **Option** from the menu to open the Options dialog. The following settings can be configured in this dialog:

- Min and max values for fat. Enter the numbers in the input boxes, or use the threshold slider to set the range.
- Color overlays for visceral and subcutaneous fat
- Min and max values for muscle. The values can be entered in the input boxes, or you can use the threshold slider to set the range. Use the menu to set the color.
- Min and max values for bone. The values can be entered in the input boxes, or you can use the threshold slider to set the range. Use the menu to set the color.

Note: Muscle and bone options are off by default. Check the Enable box to display muscle or bone values and to set options.

- Volume Ratio type

  Calculate the ratio in one of the following ways:

  - Volume ratio (V/[V+S]%)
  - Visceral/subcutaneous fat ratio
  - None

  The selected ratio is displayed in the measurement annotation.

- Defaults

  - Save current settings as default by checking the checkbox.
  - Click the **Default** button to restore original defaults.

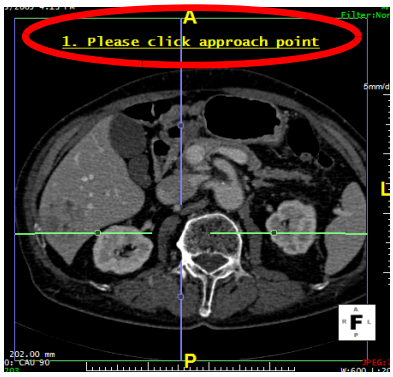
Contour Editing

- Nudge tool - Hold down **Alt** key and drag.
- Freehand draw - Hold down **Shift** key and drag.
- Polygon draw - **Shift** plus multiple clicks. Double-click to finish.

- **3D Distance**

  This feature calculates the distance of a line, drawn on an image, that might not lie in the display plane. It also calculates the length of the projection to the display plane and the angle between the distance line and the projection line.

  When you select the 3D distance tool, the images show an instruction step at the top of the view window:



Note: You can measure this distance on any image; in this example, the measurement is done on the axial MPR.

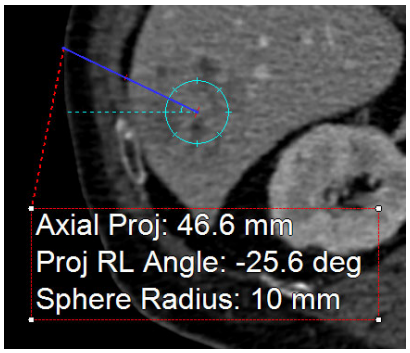
a. Click the approach (start) point of the line. For example, this might be the point at which a needle enters the body.

2. Click on the target (end) point of the distance line.

3. Release the mouse. The measurement is displayed on the image (see the following image).

Start Measurement at Target Point

If you prefer, you can start the measurement at the target point. To do so, click the instruction near the top of the image, “Please click approach point.” This changes the instruction to “Please click target point.” You can then proceed as above, beginning with the target point rather than the approach point. You can save this change by right-clicking on the instruction and selecting **Save as Default**.



Show Plane

In order to see the plane that contains both the approach and target points, right-click on the measurement and select **Show Plane** from the menu. The image is rotated so that the 3D distance line is parallel to the display plane.

Go To Target/Approach Point

This feature triangulates to the desired point without panning the orthogonal images.

- To place the target point in the center of the image:

  Right-click on the target endpoint of the 3D distance line to display the menu. Then select **Go To Target Point**.

Note: Be sure the mouse is pointing directly at the endpoint; if it is not, you will not see the desired menu.

- To place the approach point in the center of the image:

  Right-click on the approach point and select **Go To Approach Point**.

Approach View Mode

Approach View allows you to view the area along the 3D measurement line from different angles.

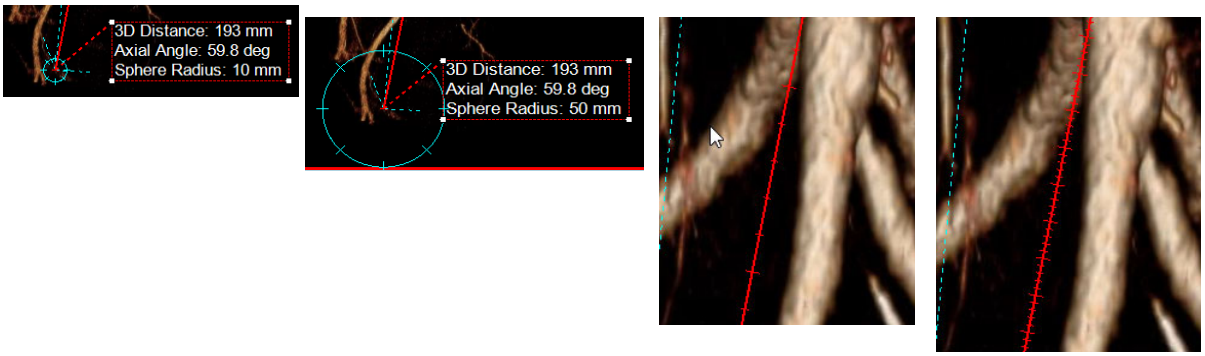
Right-click on the measurement in any of the image views, and select **Approach View Mode**.

In Approach View mode, you can scroll through the perpendicular images between the approach point and the target point. The tangent views can be rotated in two different ways. Hold down the left mouse button to rotate the image around the 3D distance line. Hold the **Ctrl** key and the left mouse button to rotate the image around the current position.

Right-click on the view and select **Exit approach view mode** to exit.

Options

To set 3D distance options, right-click on the measurement and select Option. The **3D Distance options** dialog is opened. It allows you to set the sphere radius and the length of the scale marks (see the following image). You can also save the new settings as the default.

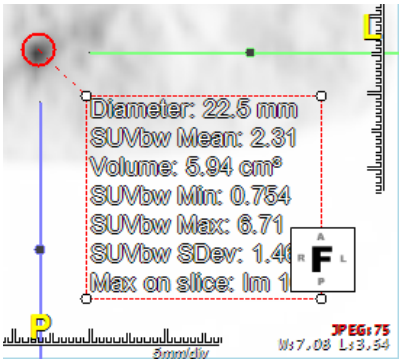


Sphere radius 10mm and 50mm Scale marks 5mm and 1mm

Figure 3-94: Selecting Options for Measurements

- **SUV Measurements on PET Studies**

  To obtain SUV measurements, draw a ROI around the target area using an area or volume measurement tool, such as **Ellipse** or **Sphere**. The image below shows the result of a sphere measurement:



  There are three SUV measurement types:

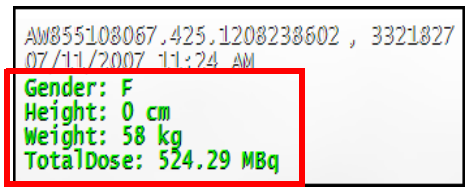
  - SUVbw - SUV body weight
  - SUVbsa - SUV body surface area
  - SUVlbm - SUV lean body mass

  You can change the type of SUV being displayed by selecting a different type from the following menu. Right-click on the measurement to see the menu.

  The default SUV type can be set in the User Preferences Measurement/Annotations screen. See "Measure/Annotation" on page A-13 for more information.

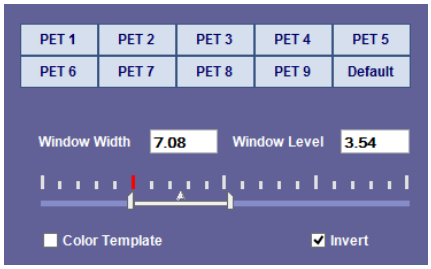
  Adding Patient Info For SUV

  If the annotation in the upper-left corner of the window does not have all the information needed to calculate the values properly (see image below), you can double-click the annotation to open the a dialog to input that information.



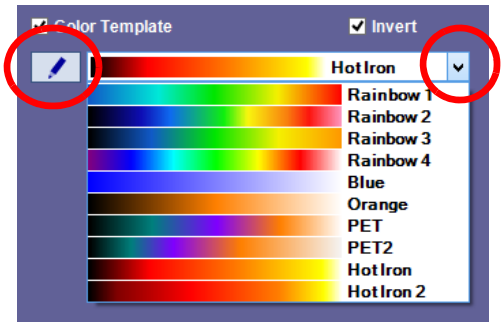
  W/L Settings, Color Template and Invert Image

  These settings are configured in the W/L tool panel. Click the **W/L** tool button to open the panel (see "The Tool Panel" on page 3-18 for information about the tool panel).



You can change the window/level directly on the images by holding down the left and right mouse buttons together and dragging the mouse in the desired direction (see "Magnifier Tool" on page 3-143). For a more exact setting, you can enter values in the input boxes, shown in the figure above.

- To invert the images, click the **Invert** checkbox.
- To enable the color templates, click the **Color Template** checkbox. The color overlay is disaplayed on the images, using the currently selected color template. In the figure below, the currently selected template is **HotIron**.
- To see or select other color templates, click the down arrow on the right of the current template (circled in dark blue, in the figure below). When another template is selected from this menu, the overlay on the images is immediately changed.



To edit the currently selected color template, click the pencil icon on the left side of the panel (circled in light blue in the figure above). The **Color Template Editor** dialog is opened. See "Color Template" on page 3-79 for instructions on using this editing tool.

Setting Defaults

- To use Min/Max instead of W/L as a default, the user preference setting must be changed. The setting is in the Viewer preference screen. For more information, see "3D Viewer" on page A-8.
- You can also configure the Viewer to open a PET study with the images already inverted, so that there would be no need to open the W/L tool panel to invert the images for each study you view. This is useful if you prefer to view inverted PET images all the time.

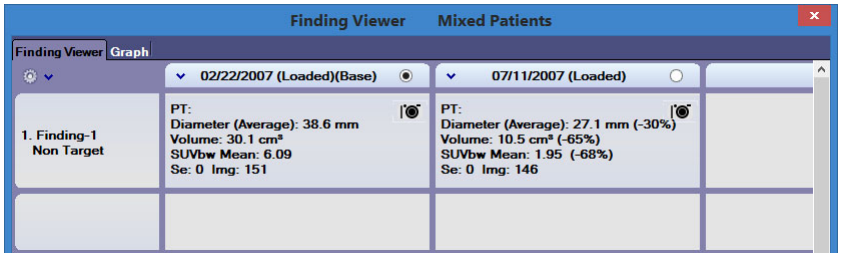
  There is no setting in the User Preferences to configure the default. Instead, this is done by changing a property in an element of the PET workflow. To see the properties, right-click on an element in the workflow and select Properties.

The Element Properties form is opened. You can not modify a workflow element using this form, but you can create a new element in the PET workflow that automatically inverts PET images in the Viewer. The **Apply MPR ColorTemplate/Invert** setting must be checked.

For detailed instructions on creating and configuring workflow elements, see "Adding a New Workflow Element" on page 4-8.

Findings Workflow

SUV measurements can be stored in the Finding Workflow and tracked using the Finding Viewer. To save measurements automatically, right-click on any image and select **Enable Measurement Tracking**. This setting is off by default.



You can change which properties of the measurement is displayed in each cell. Right-click on the cell and select **Show/Hide Details** from the menu. This opens a dialog that allows you to add or remove measurement properties from the Finding Viewer display.

To show a property of a the measurement, check the box next to it. To hide a property, uncheck the box.

For more information about the Findings Workflow, see Chapter 16: "The Findings Workflow".

Other Measurement Features

These features apply to some or all of the measurement tools.

Modifying Measurement Annotations

These options allow you some flexibility in the naming and manipulation of the measurement annotation. When you right-click on a measurement annotation, the menu is displayed.

- **Add to Finding Viewer**

  Open the Finding Details dialog to add this measurement to the Finding Viewer. For more information about the Finding Viewer, see Chapter 16: "The Findings Workflow".

- **Assign Name**

  Allows you to insert a name in the annotation text.

  To undo the assign name, click the Undo button in the top toolbar.

- **Delete**

  - Delete Measurement - Deletes the measurement that you right-clicked on.

- Delete All Measurements - Deletes all measurements from the series.

You can undo **Delete** or **Delete All Measurements** by clicking the Undo button.

- **Change The Font or Color**

  You can change both the font and the color of the annotations on any of the measurements described in this section.

  To change the font or the color, do the following:

  a. Right-click on the annotation you want to change.

  b. From the right-click menu, select **Change Text Font and Color**.

  c. From the **Font** pull-down menu, select the desired font.

  d. Select a color from the **Color** menu

  e. Click **OK** to change the font or color:

- **Change the Size**

  To change the size, click on one of the corners of the box surrounding the annotation, and drag the corner to change the size of the box. The text will change size correspondingly.

- **Add initials and date**

  Opens a text-input box where you can enter a set of initials or a name. The initials and the current date are then added to the annotation.

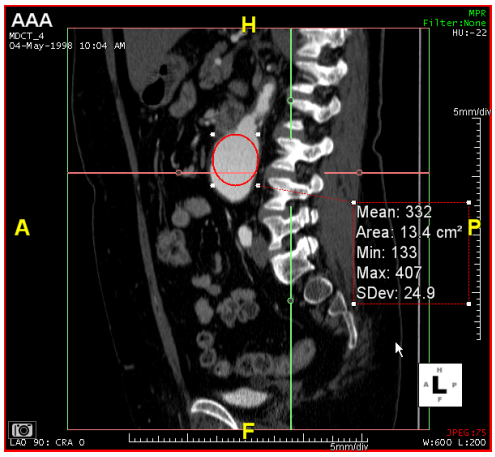
Copy Measurement Result

Copies the measurement to the clipboard, which can then be pasted to another application.

a. Right-click a measurement and select **Copy** from the pull-down menu.

b. On the window where you want to place the copy, right-click and select **Measurement>Paste (*Function*)**, where *Function* is the type of measurement copied (Distance, Ellipse, and others). Alternatively, you can select the window where the copy will be placed and type **Ctrl+V**.

The measurement is pasted on the second window. The area is the same as it is in the original image, but the Min, Max and Mean values depend on the HU values of the area encompassed by the measurement (see the following figure).

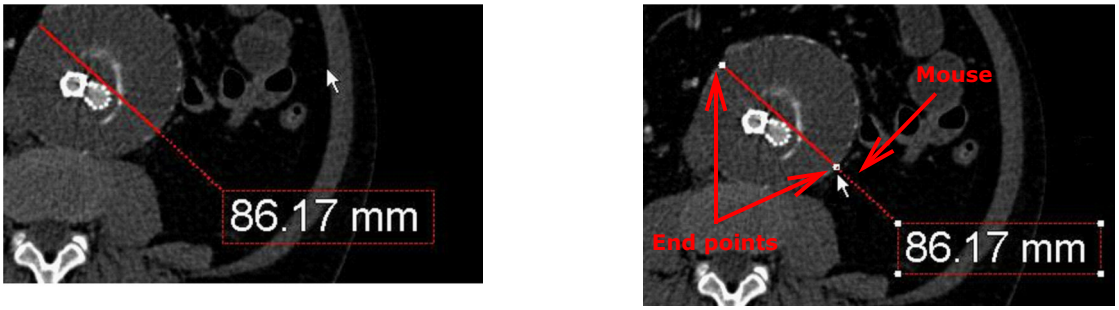


Significant Digits

You can set the number of digits with which to display a measurement annotation, to a value between 1 and 5. Regardless of the number chosen, the most significant digit(s) of the number will always be displayed. To change the number of digits shown, click the Preferences button and select Measure/ Annotation from the navigation list on the left. For more information, see Appendix A: "Measure/ Annotation" on page A-13.

Measurement Endpoints

When a measurement is made on an image, the dots that mark the end points or anchors do not remain visible. This allows the entire area being measured to be completely visible. The end-point dots of a measurement do not reappear when you click on the results of that measurement. However, they do reappear when you bring the mouse close to the measurement.



End Points Not Visible **Mousing over: End Points are Visible**

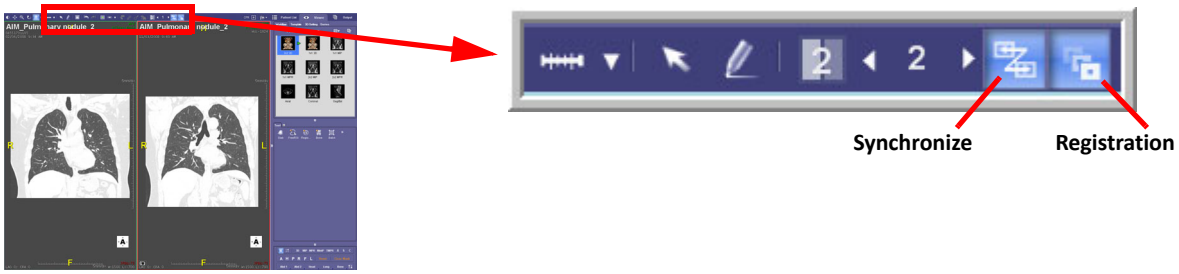
Figure 3-95: Viewing End Points

Synchronized Measurements on Multidata

When two or more datasets are loaded and synchronized, some measurements performed on one are applied to both. Ellipse, Polygon, Angle and Distance pair are supported.

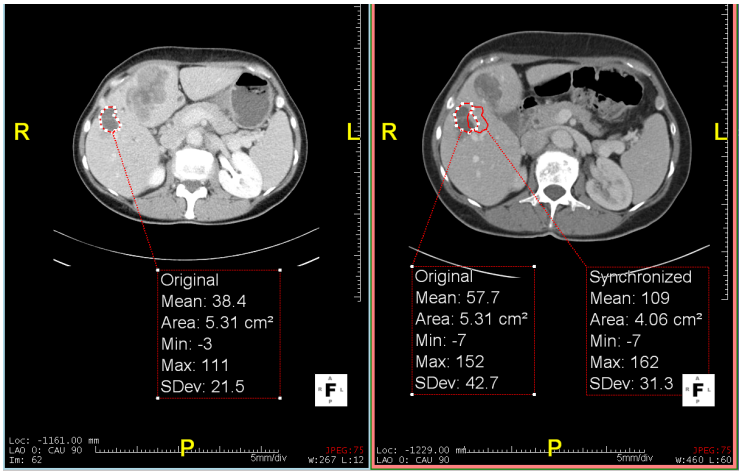
1. Click the **Synchronize** button.

2. Click the **Registration** button so the two studies will be aligned.



3. Obtain a measurement on one of the studies. The same measurement appears on the other study, but the results may be different because of differences in the two scans.

Compare synchronized measurements with a cut-and-pasted measurement from one study to the other, while the datasets are not synchronized:



In the image on the left, a measurement is taken while the two studies are in sychronization. This measurement is reflected in the measurement at right, labeled “Synchronized”. The measurement labeled “Original” in the right-hand image was cut and pasted from the left-hand image. The cut and pasted measurement is identical to the original, even appearing in the exact same place on the image.

Note: Synchronization is dependent on screen position. In order to maintain consistency, always be sure to check synchronized measurements.

Show/Hide Measurements

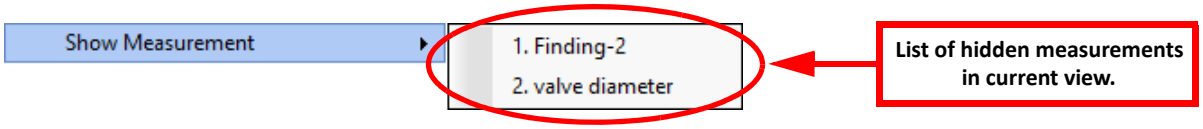
If a view becomes too crowded with images, you can hide some or all of them to make space for other measurements and better viewing.

- Hide Measurement - To hide an individual measurement, right-click on the measurement and select **Hide Measurement**.

- Hide All Measurements - To hide all measurements in the view, right-click on the view (not on a measurement) and select **Hide All Measurements**.

If some measurements are hidden on a view, you can show all the measurements again, or you can show just one of the hidden measurements, using the following features:

- Show Measurement - To show just one measurement, right-click on the view and hover the mouse over **Show Measurement**. A sub-menu shows a list of the hidden measurements. You can select the one you want to show from that menu.

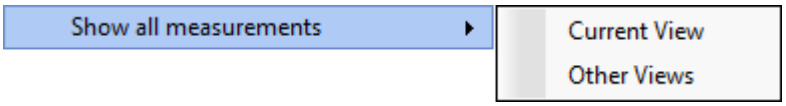


If the measurements are named, their names are listed in the sub-menu, to distinguish each measurement. You can also hover the mouse over any measurement in the sub-list to see see a tool tip containing more details about that measurement.

- Show All Measurements - When you hover the mouse on the **Show All Measurements** menu, one of two menus is displayed, depending on whether measurements are hidden on the current view or on another view:

  - Current View - All hidden measurements on the current view are shown.
  - Other views - All measurements on all other views are shown.

The **Current View** menu selection is visible only if the current view has hidden measurements. The **Other View** menu selection is shown only if another view has hidden measurements. If there are hidden measurements on multiple views, both selections are shown.



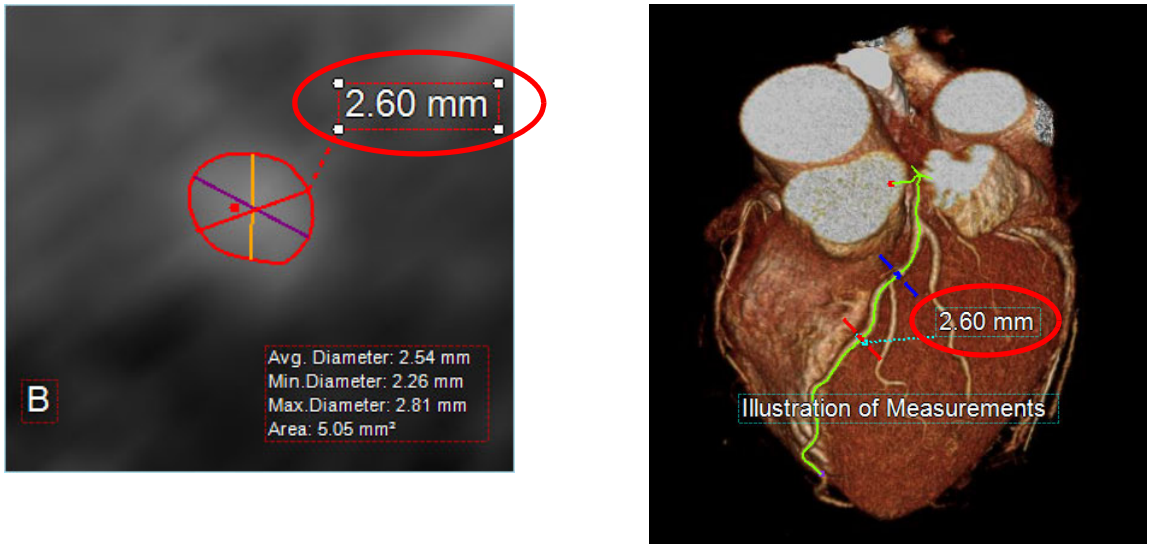
The **Show All Measurements** selection is shown in the context menu on a view when there are any hidden measurements on either the current view or on another view.

In order to use this feature, the **Enable Show/ Hide measurements** setting must be checked in the preferences. It is disabled by default. See "Measurement Options" on page A-46 for details.

Note: If you disable the **Show/Hide Measurements** setting while there are hidden measurements on any view, all hidden measurements will be shown. However, re-enabling the setting does not hide them again.

Measurement Illustration

When certain measurements are performed on the cross-section view of a study in the CPR display, they are also displayed in the 3D VR image.

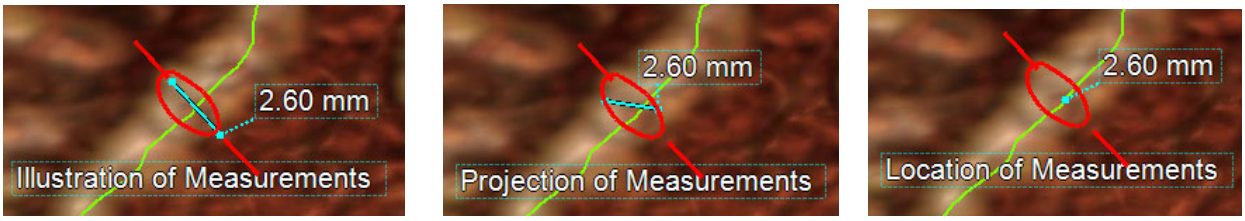


Distance Measurement on Cross-Section **Illustration on 3D VR Image**

Figure 3-96: Measurement Illustrations

There are three types of measurement illustrations shown on the 3D VR image: Illustration, Projection, and Location (Dot). To switch from one to another, right-click on the text (shown as “Illustration of Measurements” in Figure 3-96, image on right) and select the desired illustration from the drop-down menu.

The following figure shows a closeup of each type of display:



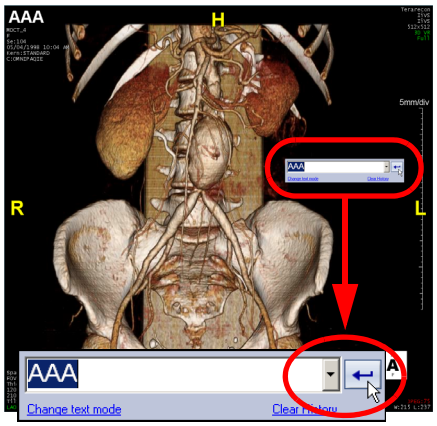
The Illustration view is supported for the **Distance**, **Distance Pair** and **Assisted Distance Pair** measurements.

Arrows and Labels

Adding Text

You can annotate the images. To do this, click the **Text** button in the top tool bar, or right-click on the image and select **Arrow/Text**. A text window opens on the image, where you can type in the annotation

you want to add (see figure below). If you have previously entered annotations that start with the same letter or letters, those annotations appear in a drop-down list below the text input box.



You can also click the down-arrow at the right end of the text input box to show a drop-down list that contains *all* previously used labels. If the label you want to use is already in the list, you can select it rather than typing it on the keyboard.

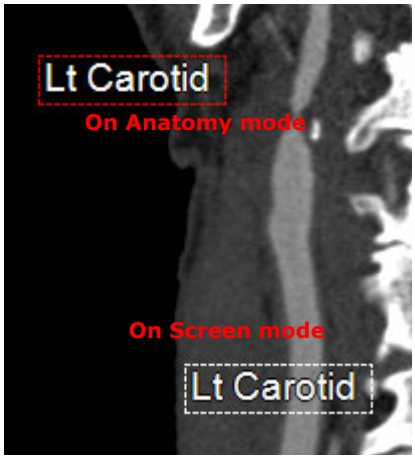
When you are finished typing the text, press the **Enter** key to complete the annotation, or click the Enter symbol using the mouse.

Text Options

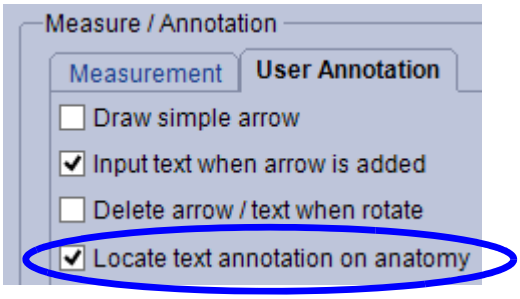
You can change how to place text annotation on the image by clicking the drop-down arrow to the right of the text tool.

- On Anatomy - Text is placed using patient coordinates. For example, in the case of radial CPR batch, the text will remain attached to the location on the image where annotation was placed, and will move along with the CPR image rotation during preview or capturing.
- On Screen - Text is placed using the screen position. For example, in the case of radial CPR batch, text can be placed in a static position on the screen, and will not move with the CPR image rotation during preview or capturing.

Text placed on an image in **On Anatomy** mode is surrounded by a red box. Text placed in **On Screen** mode has a white box around it (see figure below).

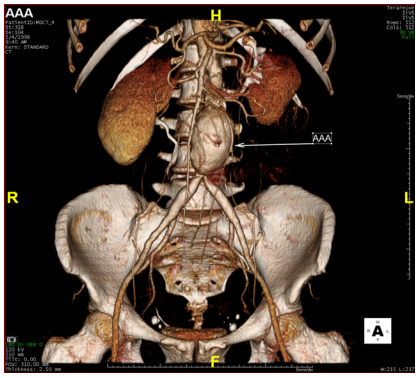


The default mode is On Anatomy. To change the default mode, open the user preferences and click on **Measure/Annotation** in the navigation panel. Then click the **User Annotation** tab.



Adding an Arrow and Text

You can add an arrow with text to an image by clicking the **Arrow** button in the top tool bar, or by right-clicking on the image and selecting **Arrow/Text** from the menu. The cursor appears on the image as a plus sign ('**+**'). To add the arrow and text, place the cursor over the area you are pointing to, and drag the cursor away from it. The arrow and text box appear (see the following image), and you can input your text in the box as above.



Changing the Font and Color of Label Text

You can change the font and text size of the label text. For instructions, see "Change The Font or Color" on page 3-171.

Changing the Arrow Appearance

To change the appearance of an arrow, right-click on the arrow and select **Settings**.

The **Landmark Settings** dialog is displayed.

Table 3.9: Landmark Settings

Setting	Function
Thickness	Changes the length and angle of the arrowhead and the thickness of the stem.
Dotted Line	Changes the length of the dotted line that starts at the tip of the arrowhead, and ends at the object the arrow is pointing to.

Setting	Function
Head Length	Changes the length and angle of the arrowhead.
Stem Width	Changes the thickness of the stem.
Etched	Changes the amount the arrowhead is filled.

Show Arrow Off

To show a dotted line instead of the arrow, uncheck the **Show Arrow** setting, located in the upper-left corner of the **Landmark Settings** dialog.

Figure 3-97: Left - Show Arrow enabled; Right - Show Arrow disabled

Fill Color

Click the **Fill Color** menu to change the color.

Note: To disable this feature, check the Draw simple arrow box in the User Annotation tab of the **Viewer>Measure/Annotation Preference** screen. For details, see "Measure/Annotation" on page A-13.

Window Layout Modes 

Window layout is controlled with the Layout button at the top of the screen. Click the down arrow to the right of the button to see the pull-down menu of layout choices.

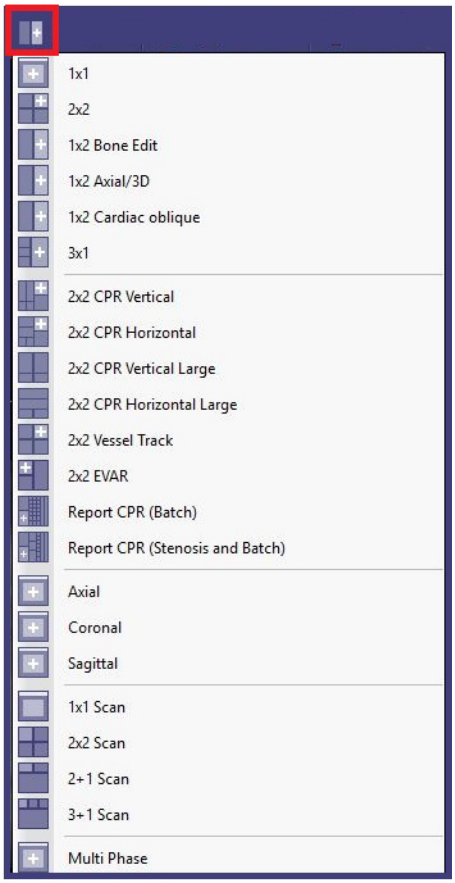


Figure 3-98Available Layout Windows

Layout Icons

The following table lists the default positioning and content of each screen layout.

Table 3.10: Screen Layout Positioning and Content

Layout	Description
1x1	The 3D image fills the entire screen in this layout.
2x2	The default 2x2 layout shows a 3D image in the upper-right panel, with MPR images in the other 3 panels, seen from different orientations.
1x2 Bone Edit	This layout shows the 3D image in the right panel. The left panel displays any part of the 3D image that has been removed, such as in bone removal, or any section taken out using the FreeROI function). Sections from the left panel can be selected and put back into the 3D image on the right.

Layout	Description
1x2 Axial/3D	This layout shows the 3D image in the right panel. The left panel displays the Axial image in MPR format.
1x2 Cardiac oblique	This layout is available for single data only. This layout allows the user to interact interchangeably between the two viewers. When first loading, the images are isocenteric with the left image as the short axis. For more information on this layout and its options, see the "1x2 Cardiac Oblique Layout" on page 3-181.
3x1	This is similar to the 2x2 in that it shows the image in 3D and 3 MPR views, but the 3D image is much larger in relation to the others.
2x2 CPR Vertical	The right side of the screen contains the 3D image on top, and the axial MPR view in the panel below it. On the left side are CPR and MPR views of selected vessels. Nothing is shown in these windows until a centerline has been drawn and the vessel has been selected. This view is best for examining vertical vessels.
2x2 CPR Horizontal	This view is best for examining horizontal vessels.
2x2 CPR Vertical Large	Similar to 2x2 CPR Vertical, but without the 3D or axial images, which give maximum space to the CPR view.
2x2 CPR Horizontal Large	Similar to 2x2 CPR Horizontal, but without the 3D or axial images, which give maximum space to the CPR view.
2x2 Vessel Track	This view displays the image in MIP mode.
2X2 EVAR	3D image (upper left), MPR cross-section view (lower left) and straightened MPR view (right), used for taking measurements for stent planning.
Report CPR (Batch)	See illustration below.
Report CPR (Stenosis and Batch):	See illustration below.
Axial	MPR view of the image in the foot orientation.
Coronal	MPR view of the image in the anterior orientation.
Sagittal	MPR view of the image in the left orientation.
1x1 Scan	Used for SAT.
2X2 Scan	Used for SAT.
2+1 Scan	Used for SAT.
3+1 Scan	Used for SAT.
Multi Phase	Used for SAT.

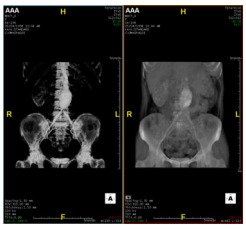
Multi-Style Layouts

Multi-Style layouts can be accessed from the right-click menu on any image. Select **Layout** from this menu to display the sub-menu shown in Figure 3-98.

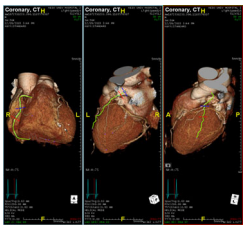
There are three types of Multi-Style layouts: 2 Multi-Style, 3 Multi-Style and 4 Multi-Style. Each of these makes identical copies of the original images. You can then change individual copies of the 3D images image-manipulation tools such as rotation, panning, zoom, W/L changes or color templates.

Note: Multi-Style layouts affect 3D images only.

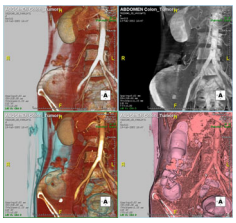
To go back to single layout style, right-click on an image, select **Layout**, and then select **Back to Single Style** from the submenu.



2 Multi-Style



3 Multi-Style



4 Multi-Style

Figure 3-99 Multi-Style Layouts

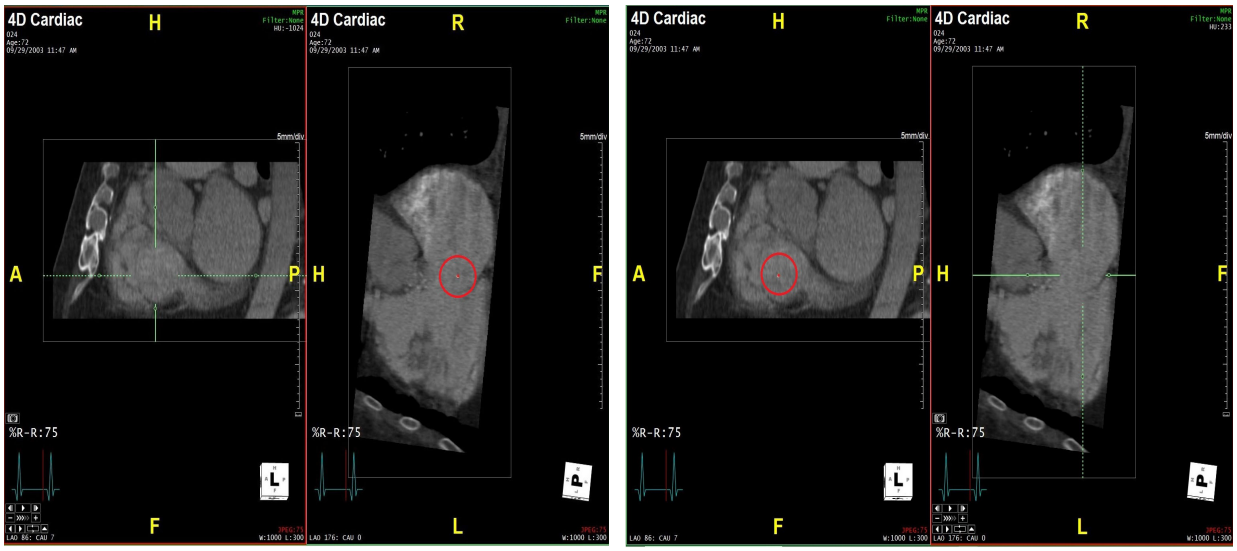
1x2 Cardiac Oblique Layout

The 1x2 Cardiac Oblique layout allows the user to interact between the two viewers interchangeably. If the user rotates the image on the left viewer, the result displays on the right viewer. If the user rotates the image on the right viewer, the result displays on the left viewer (see Figure 3-100). The images load into the viewers in isocenter positions with the left image displayed as the short axis.

Available, synchronized functions include:

- Cine functions which acts the same as the 4D viewer Cine functions.
- Zoom/pan
- Scrolling
- Window level

Note: This layout is available for single data only.



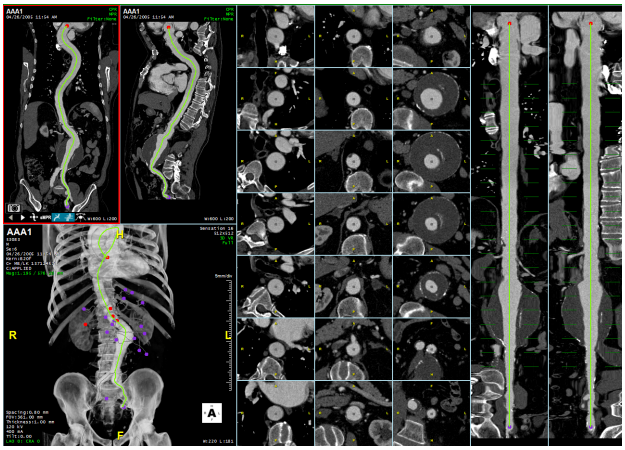
Active Viewer on the Left; Location Dot on Right **Active Viewer on the Right; Location Dot on Left**

Figure 3-100The 1x2 Cardiac Oblique Layout

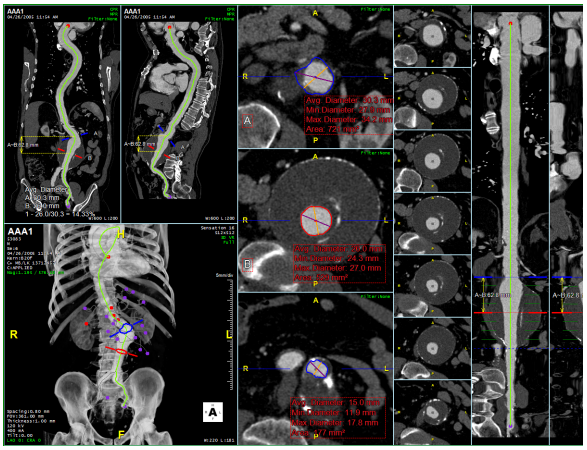
Report CPR Layouts

Report CPR (Batch) layout: The left top viewers include curved and straight MPR, bottom left includes main (3D VR), middle section includes cross section batch images, right viewers include SMPR and sMPR 90 degrees.

Report CPR (Stenosis and Batch) layout: The left top viewers include curved and straight MPR, bottom left includes main (3D VR), middle section includes stenosis viewers with measurements and cross-section batch images, right viewers include SMPR and sMPR 90 degrees.



Report CPR (Batch) Layout



Report CPR (Stenosis and Batch) Layout

Figure 3-101 Report CPR Layouts

Undo and Redo 

Undo the last operation. Redo the last operation to be undone.

Show or Hide Color Overlay 

Toggles the color overlay on the MPR views

Show or Hide Mask Overlay 

Toggles the green overlay on the MPR views, showing the masked area that has been removed

Show or Hide Mask Outline 

Allows you to see the outline of the bone mask on an image that has had bone removed. You can also set the **Outline Level** and color of the outline. To do so, click the down-arrow on the right to display a dialog.

Move the **Outline Level** slider to the right to show more bone outline. To show mask outlines in the same color on every image, check **Constant Color** and select a color from the menu.

Note: The **Constant Color** feature is supported only on VP2000 processors.

Advanced Processing Functions

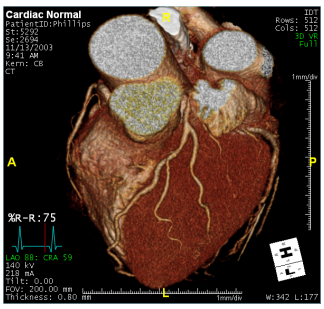
If you have AquariusAPS (Advanced Processing), the next group of tools can be very useful and time-saving Advanced Processing is performed on incoming data before it is available on your iNtuition server.

The tool icons in the figure above, from left to right, perform the following functions, respectively: Label, Centerline, Find Candidates and Mask. To display the image with AquariusAPS results, click the desired processor from the toolbar shown in the figure above.

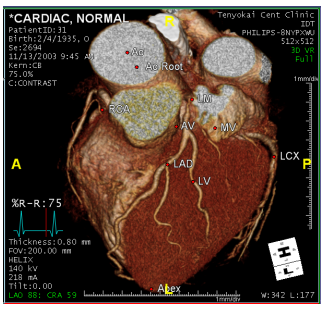
Label

Display the labels that have been identified by Advanced Processing.

Warning: The labels displayed by this function are suggestions resulting from an automated algorithm, and are not necessarily 100% accurate. The labels must be verified by a qualified person before being used.



Without AquariusAPS



Labels Identified by AquariusAPS

Figure 3-102: With and Without AquariusAPS

Centerline

Display centerlines that were created by Advanced Processing.

- To highlight a specific vessel, move the cursor over it.
- To open a CPR window displaying that vessel, click on the vessel.

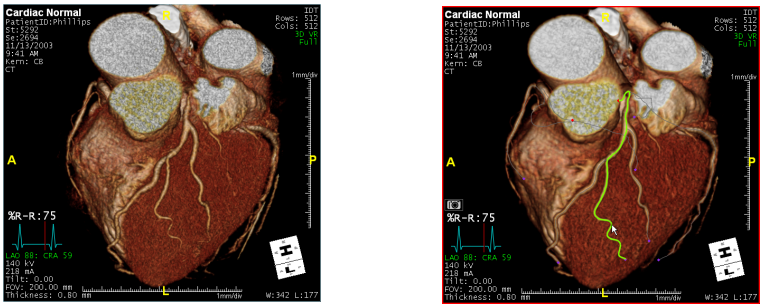


Figure 3-103: Without AquariusAPS (left); Centerlines Created by AquariusAPS (right)

Candidate Marker

Display candidates for spherical nodules that were found in Advanced Processing. AquariusAPS places a blue dot at the location of the candidate.

Figure 3-104: No APS (left); Candidates Identified by APS (right)

Masks

Add, subtract or isolate vessels or other areas that have had masks created in Advanced Processing.

For example, suppose you want to isolate the aortic root, lad/lcx and rca vessels, to examine them more closely. You can do the following:

1. Click the **APS Mask** button (shown at right). The Mask pull-down menu is displayed this study.

Note: The items in the pull-down menu depend on which APS operations were applied to the loaded study. Another study with Advanced Processing might show more, fewer, or different vessels in the list.

---

2. Select **Aortic Root** to apply the mask for the aortic root. The **Load Mask** dialog is displayed.

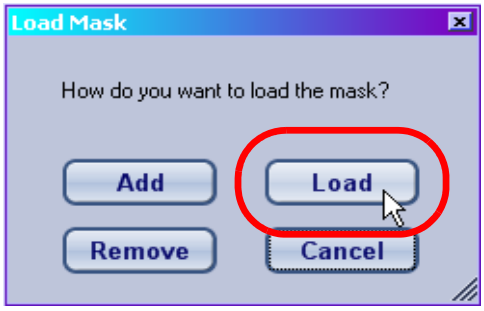
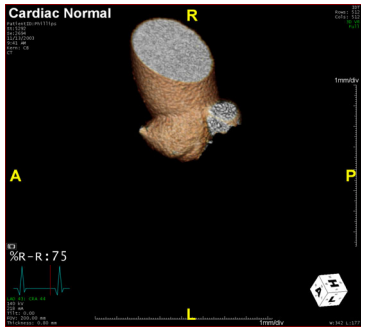


Figure 3-105: Load Mask Dialog

3. Select **Load** to load the *masked area only*, which is the aortic root. The aortic root is displayed in the main window (see image below).



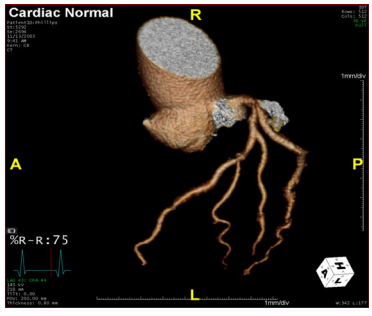
4. Click the **APS Mask** button again to display the mask menu.

5. Select **LAD/LCX** to apply the **LAD/LCX** mask. The **Load Mask** dialog is displayed again.

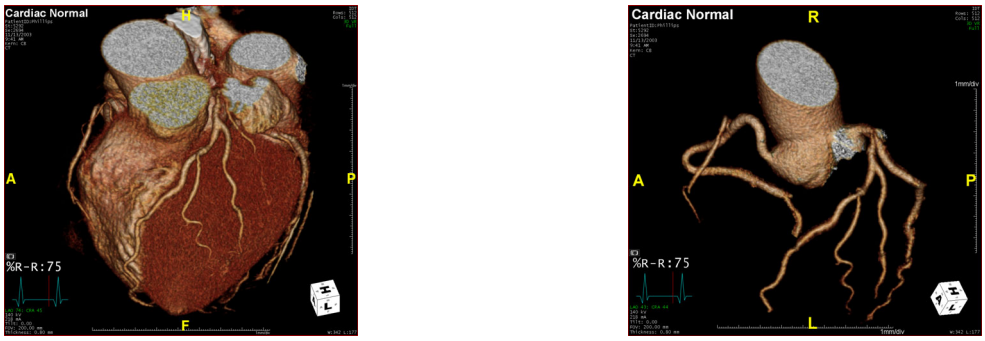
6. Click **Add** this time, to add the **LAD/LCX** vessel to the aortic root image. The **LAD/LCX** vessel is added so that both are displayed together.

7. Click the **APS Mask** button again, and select **RCA** from the menu.

8. In the **Load Mask** dialog, click **Add**. The **RCA** vessel is added to the image (see below).



9. Rotate the image as needed for the best view.

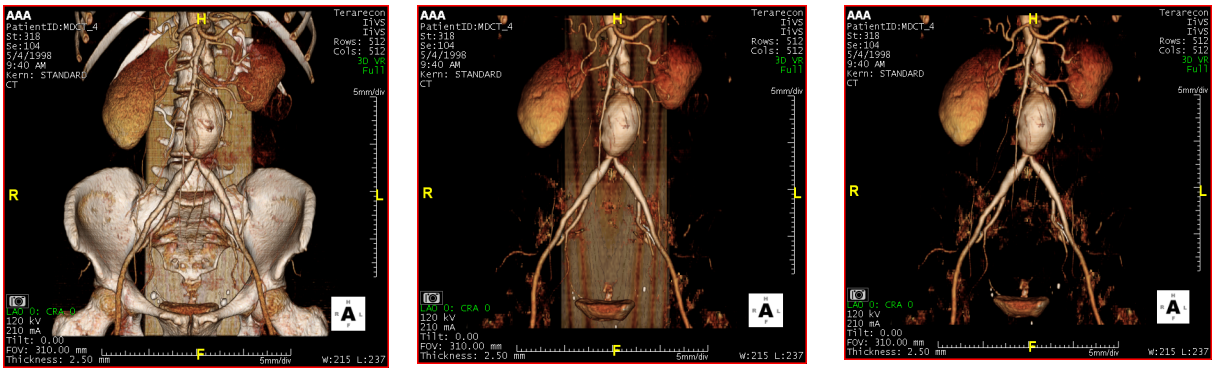


Without AquariusAPS **Isolated Vessels**

Figure 3-106 Example of the Study Without AquariusAPS and Isolated Vessels

Bone Removal

This removes bone or CT table automatically. To remove bone, click the mask button and select **Remove Bone** from the pull-down menu. To remove the CT table, select CT Table from the menu. The result of each operation is shown in Figure 3-107.



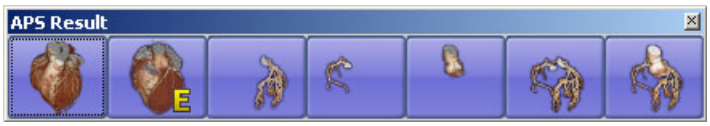
Without AqauriusAPS Bone Removed CT Table Removed

Figure 3-107 Bone Removal

Applying APS Masks Using Drag-and-drop Icons

As an alternative to the pull-down menus described above, you can apply masks generated by advanced processing using a set of APS result icons that represent each mask. This feature is enabled through a preference setting, “Enable to apply APS by drag and drop”. See "Toolbar" on page A-10 for details on setting the preference.

When you click on the mask icon in the top toolbar, a set of APS result icons is displayed on the screen:



To apply a mask to an image, right-click the desired mask and drag it onto the image. The **Load Mask** dialog is displayed, asking whether to Load, Add or Remove a mask (see Figure 3-105 on page 3-186). This works the same way as it works with the pull-down menu.

The previous image shows a sample icon for each of the masks. These are generic images. You can also display the APS Result icons using real images from the currently loaded study. This feature is disabled by default. To enable it, click the checkbox for the preference setting, “Do not use sample icon”. See "Toolbar" on page A-10 for details. When this feature is enabled, the APS Result icons are displayed as follows:

If You Do Not Have AquariusAPS

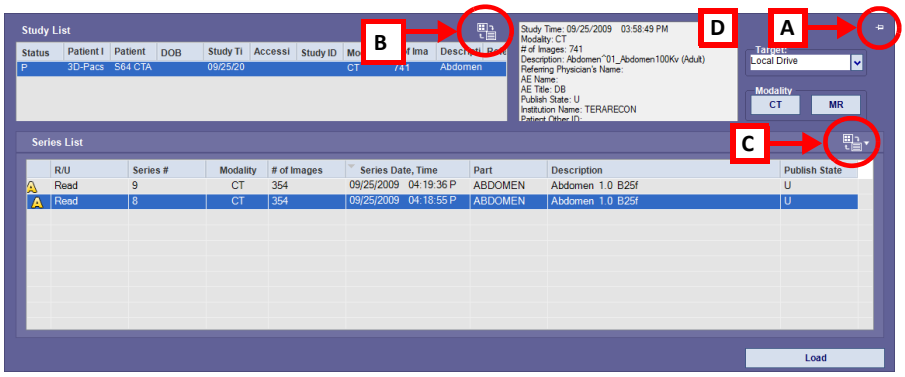
If you do not have AquariusAPS, the Advanced Processing tool icons in the upper bar are displayed as grayed-out. You can still perform some of the functions, such as labeling, masking, and creating centerlines, but you will need to perform them manually.

Note: The remaining Top Bar Tool Buttons are located on the right end of the bar.

Mini Patient List 

The **Mini Patient List** allows you to access some of the features of the full Patient List from the 3D Viewer, without going back to the Patient List. Instead, a smaller version of the Patient List is opened in a separate window. Only the currently loaded study is shown in the **Mini Patient List**. From this list you can load additional series, use the **Preview Panel** and **Quickview Panel** and do a search from your local drive or another DICOM node.

Elements of the Mini Patient List



The following items describe the corresponding sections of the Mini Patient List pictured above.

A Pin

The Pin (upper-right corner) keeps the Mini Patient List from closing automatically. When the Pin is horizontal, the Mini Patient List is not pinned down, and will close automatically *a few seconds* after it is opened. When the Pin is vertical, the Mini Patient List remains on the screen until it is unpinned. To pin or unpin the list, click the Pin icon 

B Study List Display Menu

Click this button in to toggle the Study List display between icons and details.

C Series List Display Menu

Click this button to toggle the Series List display between icons and details, and to toggle the sub-series List, Scene List, and Preview Panel on and off.

Note: When the Sub Series List, Scene List or Preview Panel is toggled on, the Series List is shortened horizontally to make room for it. The menu button stays in the far right corner of the Series List, so it might appear in a different place within the Mini Patient List, depending on the length of the Series List.

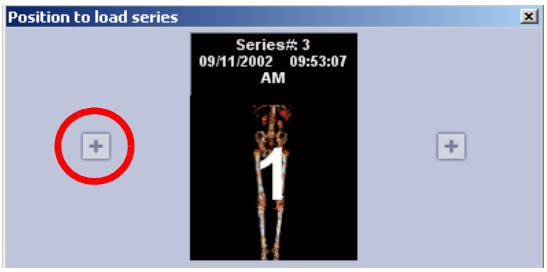
D Study Information

This contains the same information found in the columns of the Study List. Because the Mini Patient List is smaller than the full Patient List, this information is duplicated for easy reference.

Loading a Series

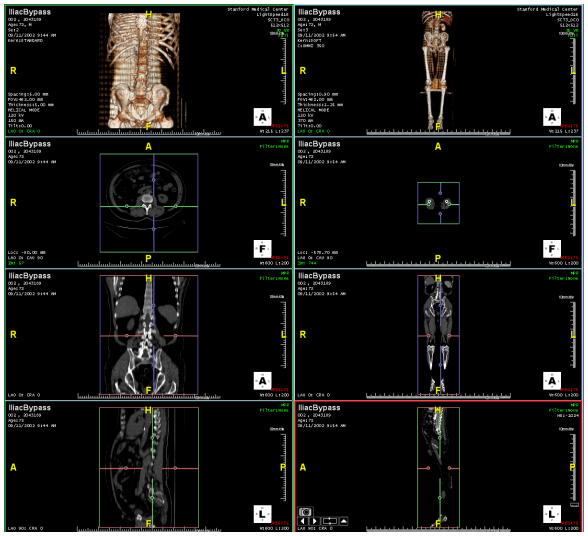
To load additional series from the Mini Patient List, right-click on the desired series. A popup menu is displayed. If the selected series can be loaded, the **Load series** item is shown in black text. If the item is shown in gray text, this indicates that Load Series is not available for the selected series.

When **Load series** is selected, the following dialog is opened:



To load the series on the left side of the currently loaded data, click the plus ('+') sign on the left of the image in the dialog (circled in the previous figure). To load the series on the right side, click the plus sign on the right.

The following example shows the result when the plus sign on the *left* side is clicked:



In the figure at right, the series shown in the right column is the main series, which was loaded initially from the full Patient List. The second series to be loaded (from the Mini Patient List) is shown on the left.

Other Features of the Mini Patient List

In addition to loading series, you can do the following in the Mini Patient List:

- Select a target to search for study data
- Filter the Study List by modality
- Page through slices in the Preview Panel
- Use the Quickview Panel

These all work in the same way they work in the full Patient List, with the exception that the search feature in the Mini Patient List can use only the modality as a filter.

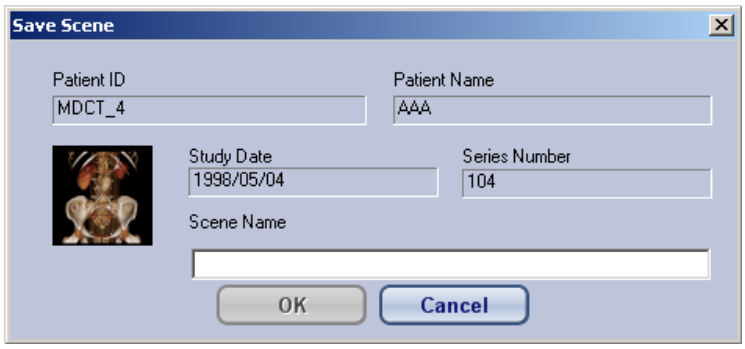
CPR Button 

The CPR button allows you to select a vessel in the image to open a CPR view of the vessel. It is the same as using the **CPR** tool in the Tool Panel. (See "The CPR Tool" on page 3-26, in The Tool Panel section for more information.)

Saving a Scene 

To save an image as a scene, do the following:

1. Click the **Scene** button (shown above). This opens the **Save Scene** dialog (see below).



2. Change the name of the scene if desired, and click **OK**. The scene is saved in the Series List, and can be loaded directly from there.

Display Annotations Menu

The Display Annotations menu allows you to choose which information or display elements will be superimposed on the images in the 3D Viewer. You can display one or any combination of annotations and display elements.

The menu items are as follows:

- **Scale Bar** - Calibrated lines at the bottom and right sides of each image, showing the proportions of the image (labeled in Figure 3-108).
- **Orientation** - The white cube in the bottom right corner, showing the orientation of the image. Also, the letters on the sides and top, indication orientation (A, P, L, R, H, F) (circled in light blue in Figure 3-108).
- **Annotation** - The text describing the image, plus links and buttons. The white text provides information about the study. Green text items are function buttons that you can click on to change the image (circled in dark blue).
- **Hide Patient Information** - You can hide patient information even when showing all other annotations. To do this, select **Hide Patient Information**. While this item is checked, the patient information is removed including from the Finding Viewer title bar, even when **Show All Annotations** is selected.
- **Show/Hide Annotations** - If you want annotations displayed on images, select **Show All Annotations** from this menu. To hide annotations, select **Hide All Annotations**. The image is displayed as shown in the right-hand image in Figure 3-108.
- **Use recommended W/L for each image** - Preview window uses the Window/Level values found in the DICOM header of the data.
- **Cross Cursor** - The cross cursor allows you to place an area of a 2D image into the center of the window. You can make the cross-cursor very small, for better visibility of the images. To do so, you need to change a setting in the preferences. See "3D Viewer" on page A-8 for information.
- **Mask Overlay** - Mask overlays show mask areas where bone or other tissue has been removed (see the right-hand image below). You can also set a preference so that a single click on the 2D image will move the cross cursor to the clicked location. The preference is located on the **Mouse Operation** screen. (See Appendix A: "GUI Configuration" for a description of preferences.)

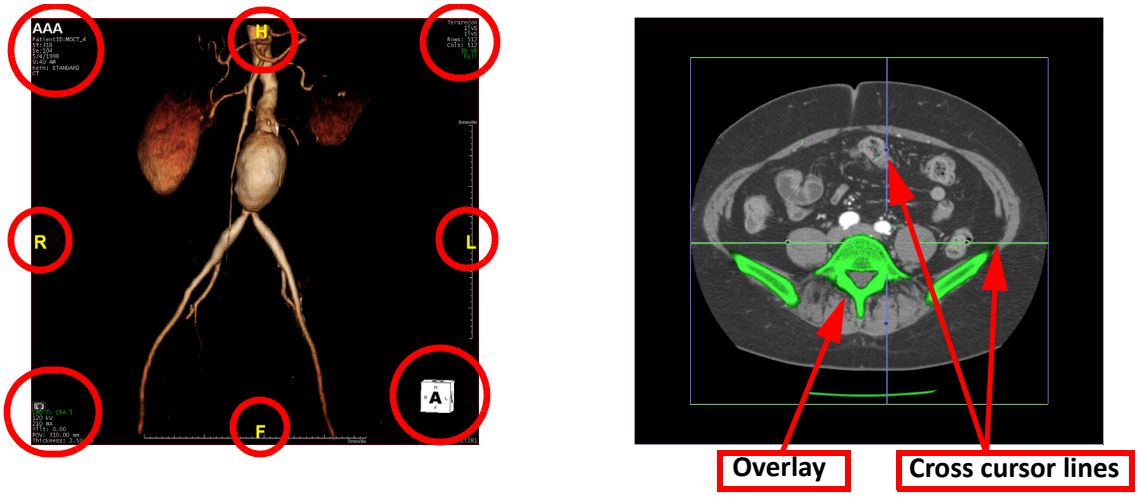


Figure 3-108: Annotations

- **Save as Default** - When **Save as Default** is selected, the current display status (either “show” or “hide”) for the scale bar, orientation, annotation, mask overlay and patient information is saved. The next time a study is loaded, the same defaults are in effect. You can change the display status during that session, but when a different study is loaded, the status is reset to the default.

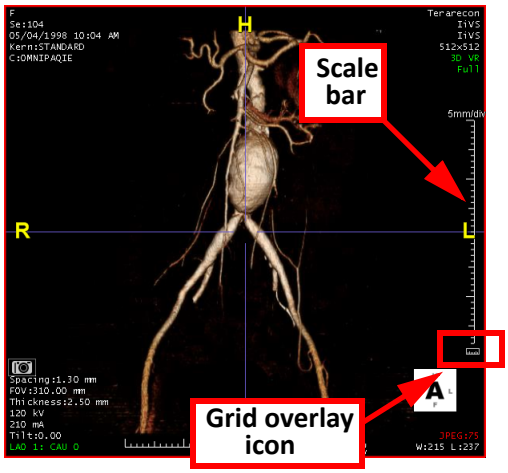
  Example

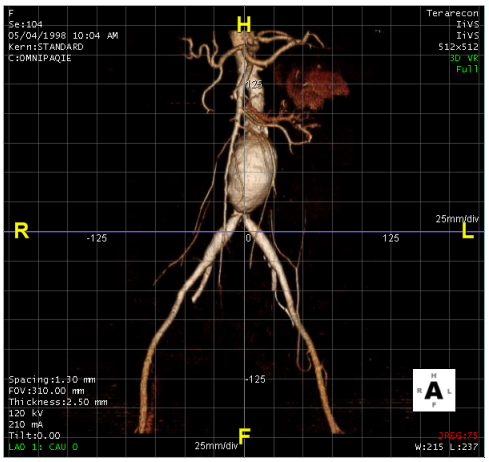
  Suppose all annotations are hidden, and that is saved as the default. You can select **Show All Annotations** and the annotations are redisplayed on the image. However, when you load a different study, annotations will be hidden, because that is the default.

Warning: If “Hide All Annotations” has been set as a default status, it is possible that you, or another user if your account is shared, are unaware that the annotations might contain critical information that is not visible. Missing this information might change the way the images are viewed, possibly causing a different diagnosis. If no annotations are showing when a study is first loaded, it is recommended that you temporarily show the annotations to be sure nothing important is missed. You can then hide annotations again if desired.

Grid Overlay

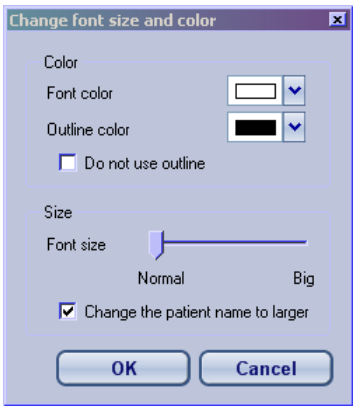
You can display a grid overlay on an image by clicking an icon on the screen. The icon is located just below the vertical scale bar on the right, and looks like a small ruler.





Changing the Size and Color of Patient Annotation

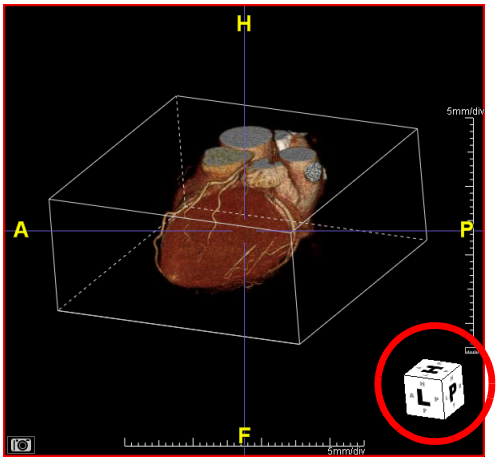
You can change the patient annotation's color and size from the default values. To do so, right-click on the patient annotation to display a small menu. Then select **Change font size and color**. The following dialog is displayed:



To change the color, select a new color from the **Font color** pulldown menu. You can select a contrasting color for the text outline. This allows the text to be visible on any background. The default outline color is black. If you do not want an outline on the text, check the box labeled **Do not use outline**.

To change the font size, use the slider. If you want to display the patient name in a larger size, check the box labeled **Change the patient name to larger**.

Wire Box



The wire box allows you to rotate images more easily.

Double-click the orientation cube in the lower-right corner of the image to enable the wire box. You can also right-click on the cube to display a menu, which contains the following choices:

- **Wire Bounding** — The wire box encloses the image, and grows larger or smaller as you zoom the image in or out. It also moves with the image when the image is panned.
- **Wire Cube** — The box is a cube shape that stays in the center of the main window, and does not change size when the image is zoomed.
- **Wire Box Option** — Open the options dialog.

- **Hide** — Hide the orientation cube.

Wire Box Options

- **Wire color** — The color of the visible edges of the box. (The internal edges, which would be invisible in an opaque box, are drawn as dotted lines in a light color.)
- **Hilight color** — The color of the edges selected for rotation.
- **Outline color** — An extra outline around the edges of the box for better visibility.
- **Visible hidden wire** — Draw the internal edges (that would be invisible in an opaque box).
- **Enable hidden wire** — Show circle on visible hidden wire when mouse hovers over.
- **Hide wire box automatically** — Hide wire box when the cursor is dragged outside of the main window.
- **Always show arc handles** — Show an arc on the middle point of each wire edge that indicates the axis and plane of rotation, when rotating from that point.
- **Show Cross Hair at the center of Wire Cube** — Show a small plus-sign (‘**+**’) cursor in the center of the cube.
- **Wire cube size** — When **Depend on Screen Size** is checked, the size is set to a percentage of the window size. If the window size changes (for example, if you change from a 2x2 layout to 1x1), the box is resized to retain the same percentage of the window size. When the checkbox is unchecked, the box is set to a specific size (in pixels), which does not change.
- To rotate about the center point of the image, hover over one of the corners of the box. A circle appears on that corner. Click and hold down the mouse to rotate.
- To rotate about an axis in the center of image, hover over one of the edges (see Figure 3-109). A circle appears the center point along that edge. Click and hold down the mouse to rotate.

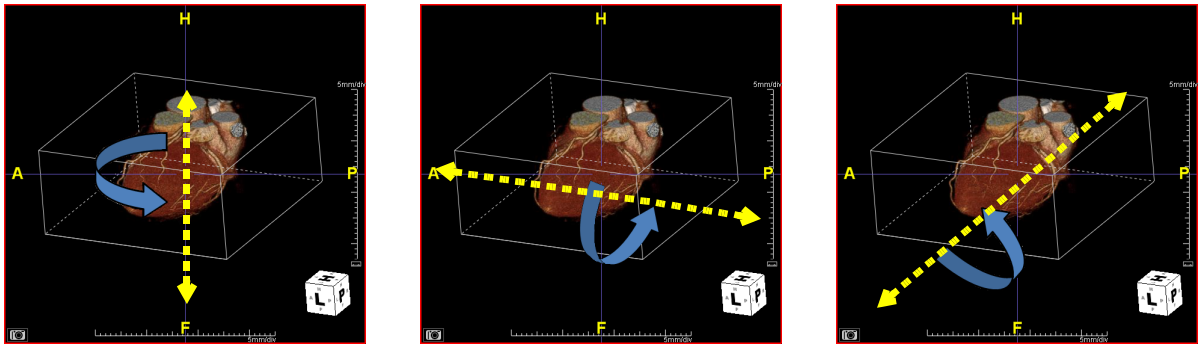


Figure 3-109: Rotation About Axes

You can also rotate MPR, MIP and slab images using the wire box.

Note: To use the wire box on a 2D image, it must be displayed in the main window that is normally used for 3D VR images. The wire box is not shown in any other window.

Create Three Landmarks for Double-Oblique

This feature allows you to mark three points on a 2D image that are not all on the view plane. The points are then connected to create a triangle, which lies on a plane within the volume. It requires two rotations to show the triangle on the viewer and is called a double-oblique plane.

When **Create 3 Landmarks for Double-Oblique** is selected from the right-click menu on an image crosshair, a dialog window opens.

The dialog allows you to select a default preset (either **TAVR** or **Orthopedic**), or one of the three user-defined presets. Each of these presets has its own configuration of the settings in this dialog. These settings can be changed.

Table 3.11: Create 3 Landmarks Settings

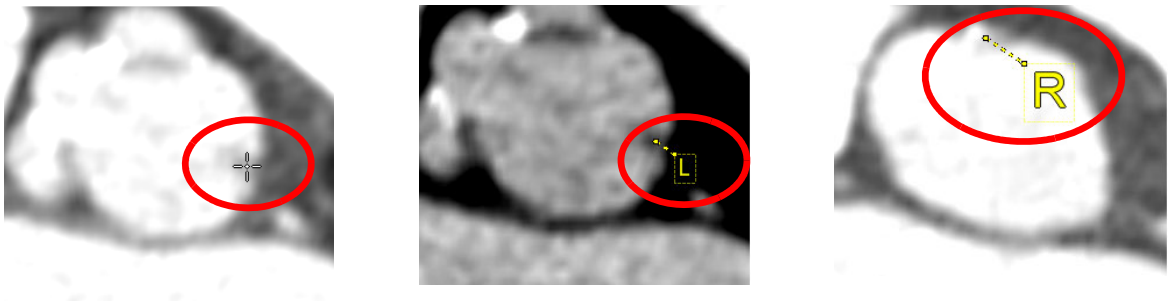
Setting	Description
Preset Name	Assign a name to the preset. The name on the currently selected present will change to the new name.
View to display result	Select Axial, Coronal or Sagittal, or select **Where Menu is Shown**, which means the result will be displayed in the same window where you opened the menu to select this dialog.
Lock this plane	When this is checked, the plane where the menu is opened cannot be rotated.
Landmark Names	Specify the labels for each landmark
Color	Select a color for the landmark points, labels and triangle lines, if a triangle is shown.
Keep the crosshair straight	When the crosshair is straight, the volume is oblique. This is the default for Orthopedic studies.
Keep the volume straight	The crosshair is oblique. Default for TAVR studies.
Show Triangle	Display the triangle formed by joining the three landmark points.
Show Angle	This angle is determined by the 3 landmarks, where the first landmark is on one arm, the second landmark is on the turning point, and the third landmark is on the other arm. The angle appears on the image as a measurement result.
Delete landmarks afterwards	Rotate the images to show the double-oblique plane, but remove the landmark labels.
Link to 3D	Use the pulldown menu to select one of the MPR images to be rotated to the same position as the 3D image, after the double-oblique rotation is completed. You can also choose **None**.
Show C-Arm angle measurement on 3D view	The C-arm angle is shown as a large text measurement on the 3D view.
Apply	Being creating the three landmarks.
Save Preset	Save any changes to the preset configuration, and begin creating the three landmarks.

The following instructions use a TAVR study as an example. The landmark dialog is used to make three landmarks (on the left, right and non-coronary cusps) to define the plane that is perpendicular to the aortic root.

1. Click the **Apply** button in the dialog. The cursor switches to a plus (‘+’) sign, indicating that a mouse click will be interpreted as a selection of a landmark. Click on the left cusp.

2. Scroll the mouse wheel on the axial image until the left cusp begins to disappear. At the point where it is almost invisible (see image below, left), click on it. The cusp is then labeled **L**.

3. Scroll until the right cusp has almost disappeared, and click on that. The cusp is labeled **R**.



Marking Left Cusp | Left Cusp Marked | Marking Right Cusp

Figure 3-110: Marking Cusps

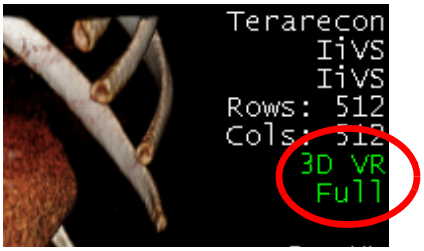
4. Do the same for the non-coronary cusp.

   You have now marked three points, which define a plane. The three points should lie along a straight line in the 3D image.

Buttons in the Image Annotations

Some of the annotations on an image are displayed in bright green. This indicates that it is an active button allowing you to change that image attribute. The three attributes that allow changes in this manner are the rendering mode (all images), the slab thickness (3D images only) and the heart angle (main image only).

Rendering Mode



The rendering mode button is located in the upper-right corner of each image panel. In a 3D image, this annotation is displayed as “3D VR”; in an MPR image, it is displayed as “MPR”, and so on.

To change the rendering mode in this panel, point the cursor directly on the annotation and right-click. A pull-down menu of other rendering mode options is displayed.

Slab Thickness

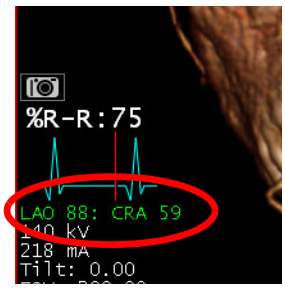
The slab thickness annotation is located just below the rendering mode annotation. This is active only in a 3D image. If the image is not 3D, the annotation is displayed in white text and does not activate a pull-down menu.

To change the slab thickness, click on the green annotation to display the pull-down menu, and then select a new thickness.

Heart Angle Setting

This annotation is located in the lower-left corner of the image. It is active only in the main window.

When you click this annotation, the Angle Setting dialog box (see Figure 3-111) is displayed. Enter the desired angles and click **OK** to change the setting.



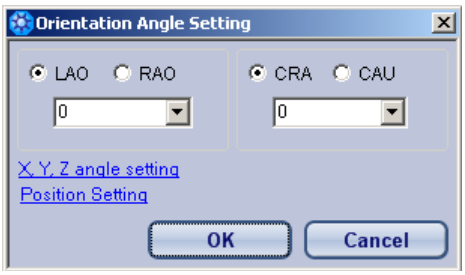
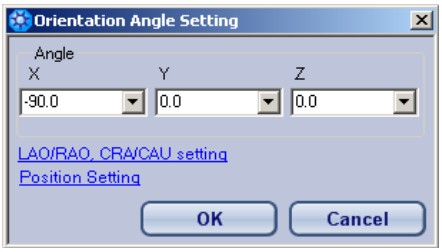


Figure 3-111: Heart Angle Settings

XYZ Angle Setting

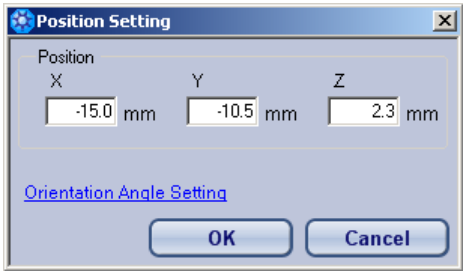


The XYZ angle setting dialog allows you to change the viewing angle of the heart in one dimension at a time, or more than one at once. To use XYZ settings, click the **X, Y, Z angle setting** link (see Figure 3-111). The XYZ dialog is displayed:

Using this dialog, you can change the heart's viewing angle in the horizontal, vertical, and/or depth direction. Click the **LAO/RAO, CRA/CAU setting** link to display the original dialog.

Position Edit

This dialog allows you to change the position of the image in the main window along the X, Y or Z-axis.

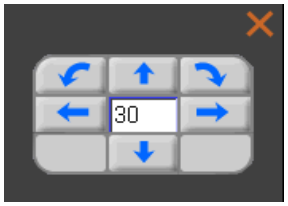


To access the Position Setting dialog, click the **Position Setting** link on the **Orientation Angle Setting** dialog. The Position Setting dialog is displayed (see right).

The direction an image will move for each axis depends on the initial orientation. When the 3D image is in the axial (Foot) orientation, the X-axis runs from left to right, the Y-axis runs from top to bottom and the Z-axis runs forward to back. However, changes to values in the Z box will not result in a visible change on the screen. In order to see positional changes on the Z-axis, rotate the image 90 degrees to the left or right.

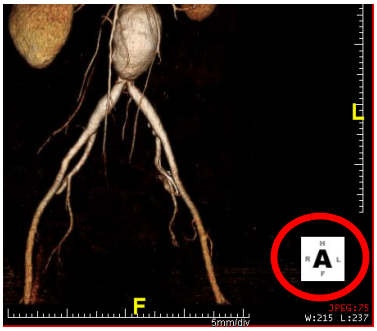
When the initial orientation is rotated from the axial position, the position setting tool works the same way, except that the axes have also been rotated the same amount and direction. Therefore, the image will move left, right, up, down, back and forward in relation to the *rotated* axes.

Image Rotation Form



The image rotation form allows you to rotate an image by a specified number of degrees:

To display the rotation form, click the Orientation cube in the bottom-right corner of the 3D image:



The rotation form works similarly to the way it works in the Orientation tool (see "Orientation Tool" on page 3-25). You can specify an angle of rotation, and then click one of six directions in which to rotate the image.

Autoscroll (2D Images Only)

The Autoscroll feature pages through the slices of a volume without any need to use the mouse. The tools, located in the lower-left corner of the image, allow you to page forward and backward, set the repitition mode, and finally, set the speed and cine interval of the autoscroll.

Play Forward/Play Backward 

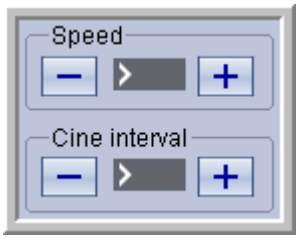
Click the left-arrow to scroll through the volume slices from head to foot, and the right-arrow to scroll in the opposite direction. During autoscroll, the selected directional arrow becomes a stop button. Click that button to stop scrolling.

Repeat  or Sweep 

Autoscroll runs continuously until it is stopped manually. This button toggles the mode of repetition between Repeat (represented by a rectangular image) and Sweep (represented by two parallel lines). In Repeat mode, when the scolling is completed, it begins at the start point and continues in the same direction. In Sweep mode, the scroll starts again from the current position and pages through the slices in the opposite direction.

Set Speed/Cine Interval 

The up-arrow opens the Speed/Cine interval dialog.

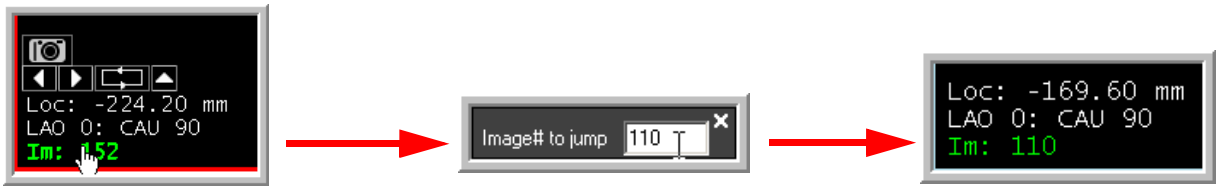


Speed refers to how many slices are skipped between each step. A higher speed means more slices are skipped. Change the speed by clicking either the plus ('+') or minus ('-') buttons. Increasing speed is indicated by additional right-arrows in the middle box.

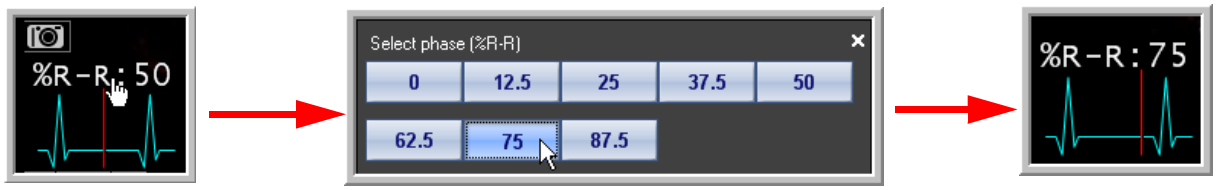
Cine interval refers to how quickly the cine is played. A higher cine inteval means the cine is played more quickly. It is changed in the same way as the speed, using the plus and minus buttons.

Jump to Slice and Jump to Phase

You can jump directly to another slice in a series if you know the image number. To do so, click the green annotation that shows the image number, located in the lower-left corner of the image. A small dialog is opened where you can enter the desired image number. Press **Enter** to jump to the image slice.



In a multi-phase study, you can access a non-contiguous phase directly from the currently showing phase. To do so, click the phase annotation on the left side of the image. A small dialog is opened where you can select the desired phase by clicking on the number. The new phase is then displayed.



Shortcut Key

The shortcut key for autoscroll is the backquote (‘), located in the upper-left corner of the keyboard, just below the escape (‘Esc’) key. First select the window to be used for scrolling, and then press the backquote key. To stop autoscrolling, press the backquote key again.

Mini-Toolbars

These tools are located in the lower-right corner of the 3D Viewer screen. They provide different ways to change the appearance of the images on the screen.

Rendering Mode Mini-Toolbar

These features change the rendering or viewing mode of the main window.

- Layout buttons - These select 1x1 and 2x2 layout, respectively
- 3D - Shows the 3D Volume Rendering image
- MIP - Shows the image in MIP mode

- MPR - Shows the image in MPR mode
- MinIP - Shows the image in MinIP mode
- TMPR - Shows the image in ThickMPR mode
- A, S, C - Shows the image in axial, sagittal and coronal view, respectively

Orienatation Mini-Toolbar

A, H, P, R, F, L

These are the Orientation buttons. When you click one, the selected image is redisplayed from the point of view of the corresponding orientation (Anterior, Head, Posterior, Right, Feet, Left).

Reset

This button redisplays the image in the original orientation, prior to any edits done in the 3D Viewer.

Clear Mask

Restores all parts of the image that have been masked out.

Window/Level Mini-Toolbar

These are preset window/levels that are best for viewing different types of studies. These settings can be changed if desired. See "Changing a Preset W/L" on page 3-78 for instructions.

Invert W/L

The rightmost button in the Mini-Toolbar (circled in the figure above) allows you to invert the W/L values of the currently loaded 2D images. See "Invert W/L" on page 3-79 for more information.

Chapter 4 Workflows

Topics in this chapter:

Workflows

A workflow is a process by which a physician or radiologist examine images in a patient's study. A study is made up of a series or several series of each slice of an image captured as a CT or MRI. Workflow templates are available based on the type of selected patient study.

AQi offers several workflow templates for this examination process. Workflows can be changed, customized, and then saved without effecting the original template.

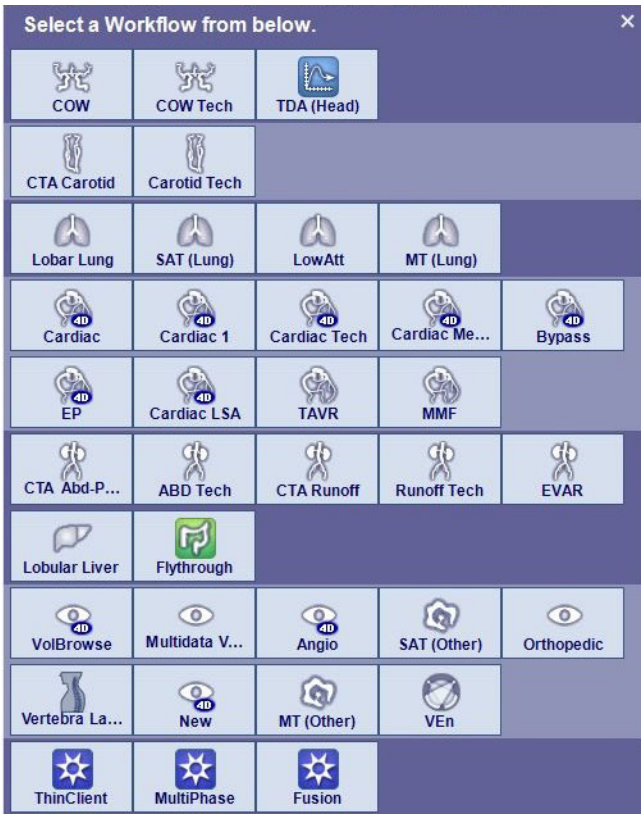


Figure 4-1 Example of available Workflow Templates

To access a workflow template:

1. Within the Patient List select a study and select **Load**.

2. The Workflow Template window opens. The window displays templates that are appropriate for the type of images or part of the anatomy in the study.

3. Left-click to select a template.

4. The viewer opens.

A workflow is a collection of operations to be performed on the loaded study data. The Tool Panel displays all these operations, called Elements, in that template. The Elements, or steps, of a workflow provide a variety of information and manipulations that helps a physician or radiologist to determine a diagnosis. They also provide a way to visually focus on the area to examine.

For example, one workflow element might remove bone from the data and then zoom in on a critical area. Others might rotate the image, cut away a section of an organ, or change the viewing mode.

Note: If more than one study is loaded in multi-data mode, the workflow element is applied to both or all, if they are synchronized.

The Workflow Template

To apply the selected workflow to a new study or series, first open the study or series into the 3D Viewer. The Workflow and Elements appear in the Tool panel is located in the upper-right corner of the 3D Viewer screen (see Figure 4-2).

Each element within a workflow represents a different view of the image, related to the type of study being examined.

Note: You have the option to display 3 or 4 workflow elements in a row. The default is 3 however, you can change this by going to **Preferences > Viewer > Workflow** and selecting your preference underneath the **Number of workflow elements to display in a row** option.

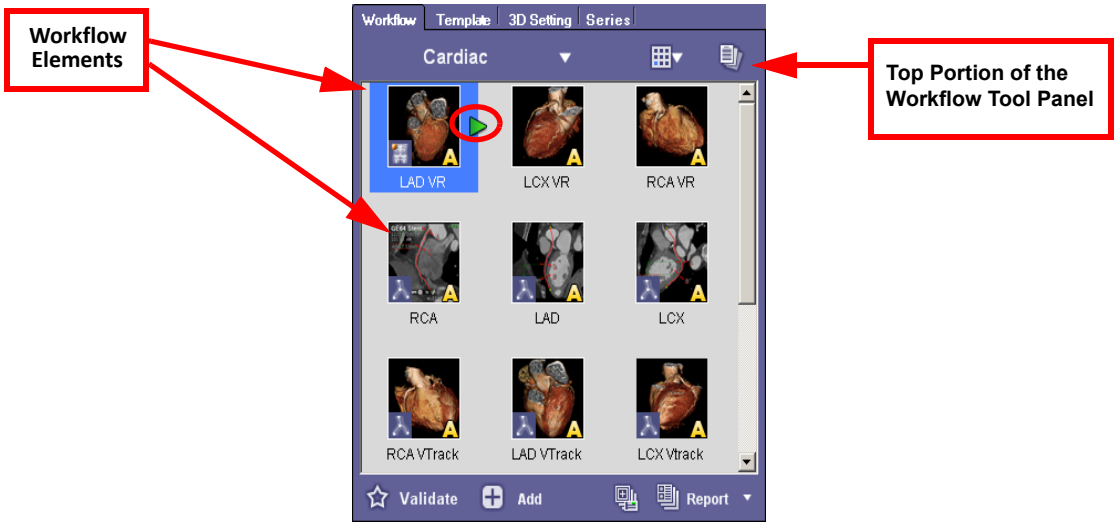


Figure 4-2: Workflow Elements within the Tool Panel

To apply a workflow element to the data, left-click on that element to activate it.

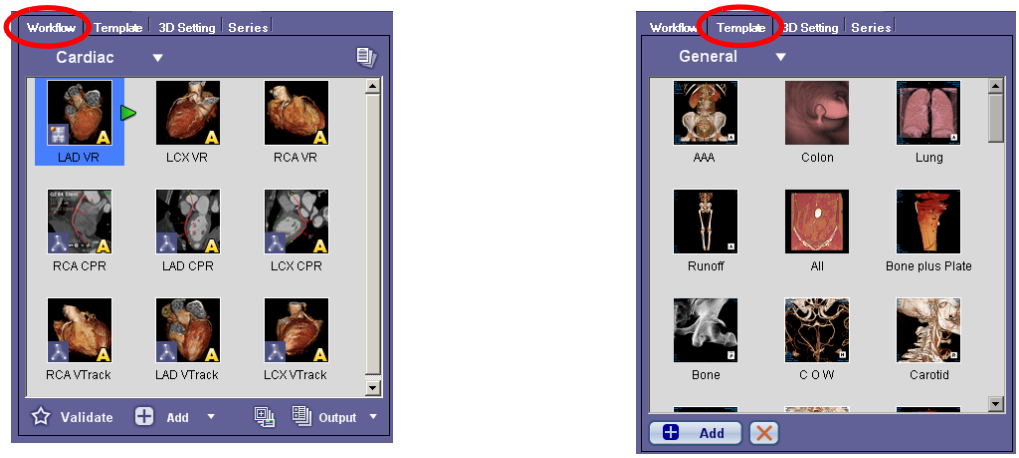
The small green arrow pointing rightward (circled in Figure 4-2) indicates which workflow element is next to be processed. You can apply the workflow elements in any order you prefer; this is only the suggested order. However, the green arrow is a good way to determine which workflow element was most recently applied to the image, because the arrow directly follows that element.

When the most recent workflow element to be applied is the last one (rightmost) on a row, a small green "return symbol" indicates that the next element to be applied is the first one on the following row.

The Aquarius iNtuition Client provides a set of default workflows, which you can use or modify to fit your needs. You can also create your own workflows. This is discussed further on in this chapter.

Workflows and Templates

A Workflow is not a Template. Aquarius iNtuition provides a set of Templates which you can access by clicking on the **Template** tab at the top of the Workflow panel. Templates contain color and window level information that can be applied to any image. Workflows allow much greater flexibility in the type of modifications you can store. For example, you can store zoom, rotation, application of masks, removal of parts of images, CPR mode, and much more, as well as color and W/L information.



Workflow Tab **Templates Tab**

Figure 4-3: Finding Workflows and Templates

Validation

Validation of a workflow element means that the element, *applied to the current data*, has been reviewed by a radiologist or referring physician and found to be accurate. The validation is for the current data only; each element must be validated separately for each study or series.

To validate an element, click the **Validate** button at the bottom of the Workflow panel (see Figure 4-2 on page 4-2). The letter "V" appears in the lower-right corner of the element icon to indicate that it has been

validated. When this study is opened again, the V will still be there. However, when a different study is opened using this workflow, the element will not show a V until it has been validated for that study.

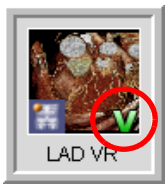


Figure 4-4 Validate Icon

Selecting a Workflow for a Study

1. Click the down arrow in the upper bar of the Workflow panel (circled in the figure below). A pull-down menu displays a list of workflows to choose from.

2. Select the workflow that is most appropriate for the study.

3. Click on any of the workflow elements to apply the operations in the element automatically to the image.

Note: You can see what the image will look like after the operations of an element have been applied, by rolling the mouse over the element icon. The actual operations are not applied to the 3D image until you click on the element icon.

Changing to another Workflow

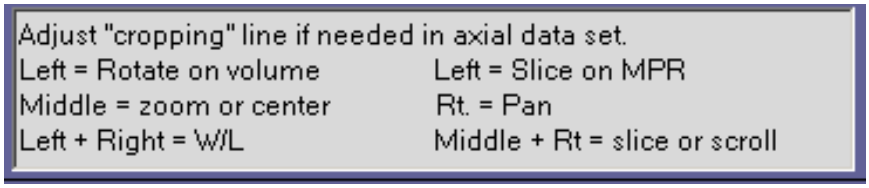
It may be necessary to switch from one workflow to another during the examination of a single study. This is easy to do - just open the pull-down menu shown in the previous figure and select the new workflow.

If you have validated any workflow elements in the current workflow, the iNtuition Viewer posts a dialog asking whether you want to copy the validated workflow elements to the new workflow.

If you click **Yes**, the new workflow will contain all workflow elements from the current workflow that have been validated.

Instructions for Workflow Elements

AQi provides instructions or comments in the Instruction Panel of many Workflow elements. When you click on, or merely hover the mouse over, a different Workflow element, the set of instructions provided for that element are displayed. In some cases, the Instruction Panel is empty. Not all Workflows or Workflow elements have instructions.



Entering Your Own Instructions

When you add a new Workflow element, the **Add New Element** dialog is opened, allowing you to set all the parameters of the new element. One of these is the **Description/Comment** field, in which you can write instructions, reminders or other comments. Whatever is entered in the **Description/Comment** field is displayed in the Instruction Panel when that Workflow element is made active. See "Adding a New Workflow Element" on page 4-8 for more information.

Generating Reports

To generate reports, do the following:

1. Locate the button in the lower-right corner of the Workflow panel. It says either **Output**, **Output All**, **Report**, **Send to DICOM** or **Export Measurements**.

2. If it does not say **Report**, click the down arrow located to the right of the button (circled in figure at right). This opens the pull-down menu.

3. Select **Report** from this menu. The button changes to say “Report”.

4. Click the **Report** button. The **Report Templates** dialog is displayed.

Cardiac Report

If your report is for a cardiac study, you can select **Cardiac Report** to generate a heart-specific report template. See page Figure 4-7 on page 4-34 for an example of a Cardiac Report.

Cardiac Report (Compliancy with SCCT guidelines)

This report follows the SCCT guidelines for cardiac reports.

Calcium Report

The Calcium Report contains information about calcification of coronary arteries, and is obtained by doing a Calcium Score. See "Generating a Report" on page 11-21 for details.

Simple Report

The **Simple Report** template is a general-purpose report template. Choose the Simple Report template to generate reports that are not for a specific module or body part.

Creating and Modifying AQi Workflows

You can create your own workflows and modify their settings. You can add, modify and delete new elements to an existing workflow, including to the pre-defined workflows provided by Aquarius iNtuition.

Creating a New Workflow

To create a new workflow, do the following:

1. Click the down-arrow located to the right of the current workflow name, in the workflow panel (see figure at right).

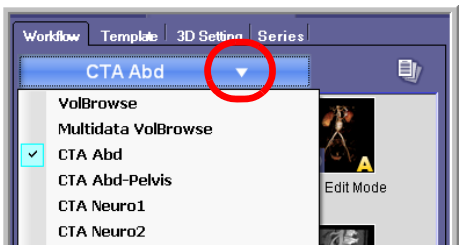
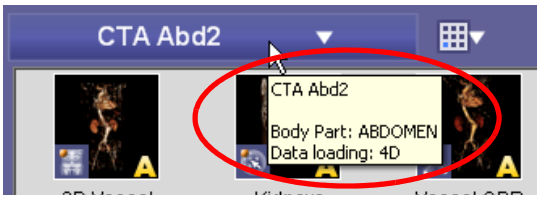


Figure 4-5: Workflow Drop-Down Menu

2. Select **Add New Workflow** from the pull-down menu. The **Add New Workflow** dialog is opened.
3. Enter the name of the new workflow in the **New Workflow Name** text box.
4. Optionally, add a description of the workflow in the **Description** text box.
5. If you would like this workflow to be displayed as a button on the Patient List, check the **Show on Patient List** checkbox.
6. If this workflow is associated with a particular body part or clinical protocol, select the appropriate **Body Part** from the pull-down menu.
7. Select the **Data Loading** type from the pulldown menu. This setting allows you to decide how multi data and multi-phase studies are loaded. For details, see "Multi Data" on page 4-18.
8. If you would like the **Validate Element** dialog to open when validating an element, enable the **Show finding form when Validating**. This dialog is the same as the **Add New Element** dialog, but it allows the opportunity to change any of the settings before validation.
9. Click **OK** to create the workflow. The new workflow is then displayed in the workflow panel. The workflow is empty initially, because you have not added workflow elements to it.
10. Open the Workflow drop-down menu (see Figure 4-5 on page 4-6) and select **Save Workflow Template**. This saves all the workflow elements permanently in this workflow.

Note: Once the Workflow Template has been saved, you can see a brief summary of the properties that were chosen for this Workflow by hovering the mouse over the name of the Workflow (at the top of the Workflow panel). The summary appears as a tooltip.

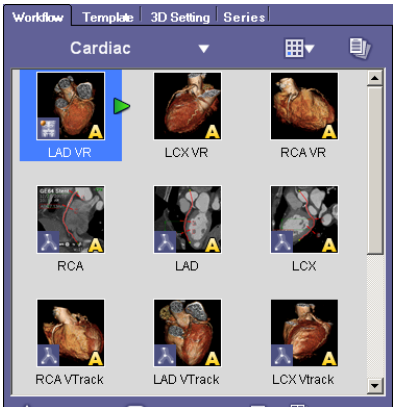


You can now start adding elements to the workflow, as described in the following section.

Adding a New Workflow Element

This section shows how to add a new element to a workflow.

To illustrate the procedure, we will use the Cardiac workflow as an example. The Cardiac workflow has eleven workflow elements by default: nine for finding and examining vessels, and two for performing calculations.



Suppose you regularly examine the short axis of the heart, in several studies per day. Because that view of the heart is not included in the standard Cardiac Workflow, that is a view that you would need to set up manually, each time you reviewed a heart study.

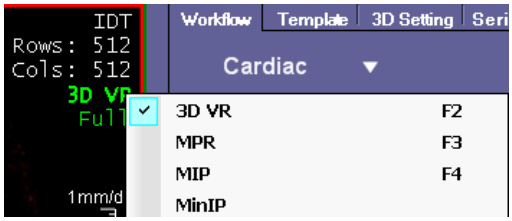
However, you can add new elements to existing workflows, including to the default workflows, such as the Cardiac Workflow. You can create an element to apply the operations to the image that would display the short axis on any heart study.

Perform Image Manipulation

Perform the image manipulation necessary to create the desired image in the main (upper-right) window. For example, to add a short axis element, do the following:

1. Open a heart study in the Cardiac Workflow. Bone is automatically removed because it is the first workflow element. The default window layout for opening a heart study is 2x2 layout.

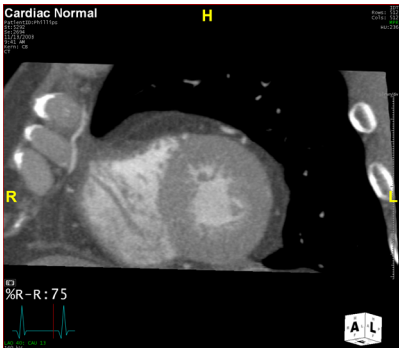
2. Change the 3D image (upper-right quadrant), to an MPR view. To do this, click on the green annotation in the upper-right corner of the 3D image which says “3D VR”.



3. Rotate, pan and zoom in or out on the image to obtain the best view of the short axis.

   - **To rotate** the image, click on it with the left mouse button, and drag it along the image.
   - **To pan** the image (move it around), click on it with the right mouse button and drag it.

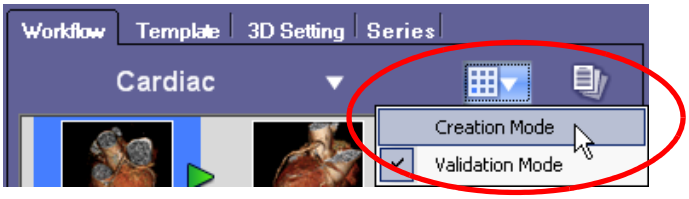
- **To zoom in**, click on the image with the middle button and move up. To zoom out, move down.



Add the New Element

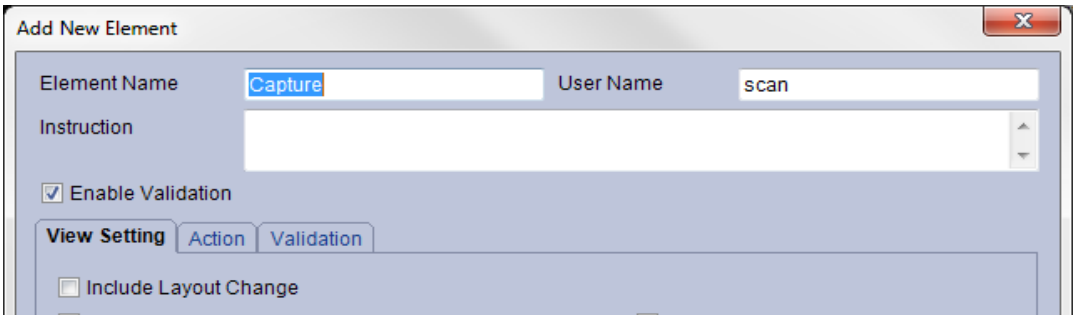
When you are satisfied with the image, you can save the operations just performed as a new workflow element. These operations can then be applied to many other heart studies when you need to see the short axis.

1. Make sure the workflow is in Creation mode. To do so, click the Validation/Creation mode button to display the pulldown menu:



2. Select **Creation Mode** if it is not already selected.

3. Click the **Add** button at the bottom of the Workflow panel to open the **Add New Element** dialog.



By default, the **View Setting** tab is shown when the dialog is opened.

View Setting Tab

1. Type the name of the workflow element (“Short Axis” in the previous example) in the top text box (circled in above image).

2. Optionally, add a description, instructions on how to use the Workflow element or any other comments, in the **Description/Comment** text box. Anything you enter here will be displayed in the Instruction Panel when this Workflow element is made active. See "Instructions for Workflow Elements" on page 4-4 for more details.

3. Check the appropriate boxes, depending on which properties you want to be applied to future studies. The selections are described below:

   Include Layout Change - Save the current layout, and then apply the same layout to future studies.

   Include Tool Panel Change - Save the currently open Tool Panel, and then open the same tool in future studies.

   Do Not Update View - Do not change the images when activating this element. All checkboxes related to image manipulation are disabled.

   Annotate Text on CPR View - Show text on the CPR views as an annotation. Enter the annotation text to be shown in the input box below.

   Reset View - Reset the image to the state at load time.

   Apply VR W/L - Apply the current W/L values of the 3D image to the 3D image in future studies.

   Apply MPR Color Template/Invert - Apply the current invert state and currently selected color template of the MPR images to the MPR images in future studies.

   Applying Mode for Multi Data - This applies the synchronization mode according to one of the following selections:

   - Follows current sync mode - Follows synchronization status of top bar. (Default).
   - Applies to all data - Even if synchronization is disabled in the top bar, all multi data loaded will be synchronized in this workflow element.
   - Applies to current view only - Even if synchronization is enabled in the top bar, synchronization will be applied to the multi data displayed on current view in this workflow element.

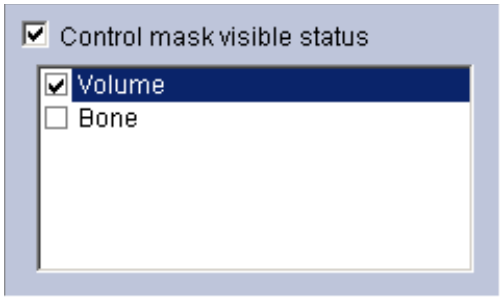
   Label Matching - Future studies will be repositioned so that the labels in the new study match the positions of the labels in the original study.

   Apply Zoom, Pan, Rotation and 2D Filter - Save all image manipulations done to this study since it was loaded for zoom, pan, rotation and 2D filters. These will be applied to future studes.

   Apply MPR W/L - Apply the current W/L values of the MPR image to the MPR image in future studies.

   Apply MPR Zoom - Apply the current zoom factor of the MPR image to the MPR image in future studies.

   Control Mask Visible Status - When the study has multiple masks, created manually or by APS, this setting allows you to decide which masks to show or hide when you step to this element. When this box is checked, a list is shown below of volume masks currently present. Check the boxes for the masks you want to show (see image below).



Action Tab

Enable Validation - When unchecked, you can not validate the element.

Run Smooth Surface - Apply the smooth surface function. This removes any rough edges that are exposed by removal of part of the image.

Exclude Mask - Determines what should be done with current masks, as well as masks that are currently excluded.

- None — no action related to excluding masks.
- Add — add current mask to the excluded mask list, but do not reverse the current mask.
- Clear — clear all masks from the excluded mask list.

For more information on excluded masks, see "Excluded Masks" on page 3-11.

Mouse Button Setting - Apply a change in the function of the left mouse button.

Sections

- Action after processing:

  Apply Only When Element is Validated - Performs mask operations only when the element is validated.

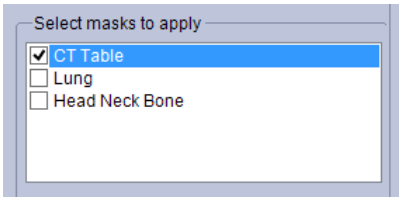
  Create Mask - Creates a volume mask in the 3D Settings panel.

  Operate Mask - Apply the mask to the image in the main window. If **Apply only when element is validated** is checked, the mask is not applied until the WFE is validated. Otherwise the mask is applied when the user clicks on the following element. Select **Clear** to remove the mask and display the original volume. Select **Reverse** if you want to see everything except the masked area.

  Move to Next Element - This setting is accessible only when **Enable Validation** is unchecked. It allows you to hide the element.

- Select masks to apply

  This is a list of APS masks that might apply to the loaded data. Check the box next to any masks that you want to be applied when this workflow element is stepped-to or clicked on.



- Output Panel

  Include Output Panel Change - When enabled, the current configuration of the Output Panel is saved in this workflow element.

  Page Format (Format) - Indicates which page format is in effect.

Validation Tab

Auto Validate - The WFE is validated automatically when another WFE is selected.

Validate after having added Element - The WFE is validated when it is created.

Measurement Results - Measurement results are copied to the clipboard.

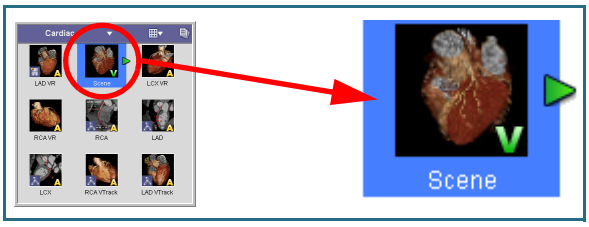
When finished, click **OK** to save the workflow element.

Validation Mode

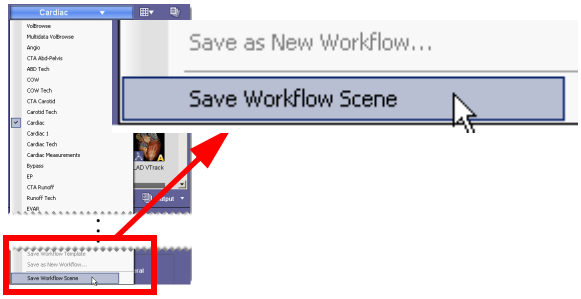
Validation mode is used when you want to save work that applies to the current data, but is not needed for any future data loaded into the same workflow. In that case, it is not necessary to create and add a new workflow template. Instead, you can save your work as a workflow scene. The workflow scene is saved in the Series List (you can find it in either the Series List or the Scene List). The workflow itself is not changed, and the workflow element will not appear with any other data loaded into the same workflow.

To enter Validation mode, do the following:

1. Click the **Validation/Creation Mode** button to display the pulldown menu.
2. Select **Validation Mode** if it is not already selected.
3. Click the **Add** button at the bottom of the Workflow panel. A new Workflow Element is created and displayed in the Workflow panel (shown below).

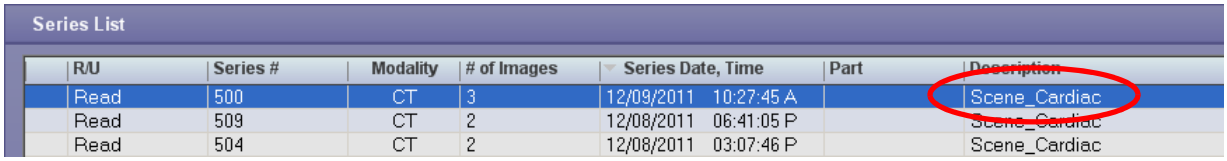


The workflow scene is automatically validated. To save the scene, select **Save Workflow Scene** from the pulldown menu.

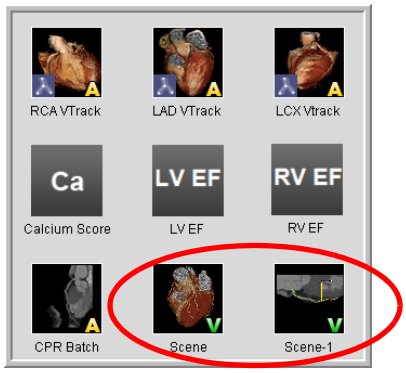


The workflow scene is saved in the Series List of the currently loaded data.

The Description column contains an identifier that says “Scene_<*workflow-name*>”. For example, if the workflow where you created the scene is the Cardiac workflow, the name **Scene_Cardiac** appears in the Description column of the scene.



To load the workflow scene along with the series, select the workflow scene and load it in the same way you usually load a series. When the series is loaded, the workflow panel will contain the workflow scene.



Multi-data Studies

Please note that when multi-data studies are loaded, there are some limitations on which functions are available.

- **Validate** - You cannot validate a workflow element on multi data.
- **Validate after Having Added Element Setting when Creating a New Element** - This setting, in the **Validation** tab of the **Add New Element** dialog (see "Add the New Element" on page 4-9), is disabled for multi data.
- **Save Workflow Scene** - This can be done in **Validation** mode with single data, but not with multi data.

Default Workflow Elements

Default workflow elements are included with AQi and

To access the default workflow elements, do the following:

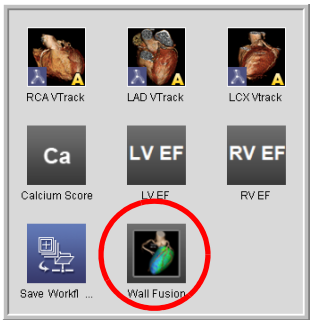
1. Select **Creation Mode**.

   If the current workflow has any more default workflow elements, a down-arrow will appear to the right of the **Add** button at the bottom of the workflow (see the following figure).

2. Click the down-arrow to display the pull-down menu. Select **Show more option...**: from the menu.

   The **Select new element** dialog is opened. This dialog contains default workflow elements, which can be added to the workflow if desired. To add a workflow element to the current workflow, click on it and then click **OK**.

   The workflow element is now added to the workflow (as shown below).



Editing Workflow Elements

To edit a workflow element, right-click on the element and select **Properties** from the menu.

The **Edit Element** dialog is opened. This dialog is identical to the **Add New Element** dialog, except that the data fields contain information about the existing element. Any of this information can be changed. See "Add the New Element" on page 4-9 for a full description of this dialog.

Editing a Default Element

You can edit a limited number of a default element's properties. This example shows how to edit the Calcium (Ca) default element. Each default element's properties are slightly different.

1. Make sure the workflow is in Creation mode. See "Add the New Element" on page 4-9 for instructions.

2. Right-click on the default element and select **Properties**.

Note: Some default elements can not be edited. If that is the case with the element you are trying to edit, the Properties item does not appear in the menu.

The **Edit Element** dialog for this element is opened. You can edit the following properties of the Calcium default element:

- **Load data automatically if only one data matches filter**

  When unchecked, the series list dialog is always opened (see the following bullet point).

- **Show Series List Dialog**

  Display a dialog that contains the Series List. This allows you to select a series to be loaded into the calcium score module.

- **Set Filter**

  - Minimum number of images

    List all series with this number of images or greater in the series list dialog.

  - Maximum number of images

    List all series with this number of images or fewer.

Note: When both of these are set, they define a range of the size of the series. Typically, a calcium series has between 45-65 slice images.

- **Series Description (contains)**

  List all series that contain the word or words in the series description.

3. When finished, click the down-arrow to the right of the workflow name and select **Save Workflow Template** from the menu.

Note: If the workflow is shared, a dialog is posted asking whether you want to update the shared workflow as well as your personal copy of the workflow.

Deleting Workflow Elements

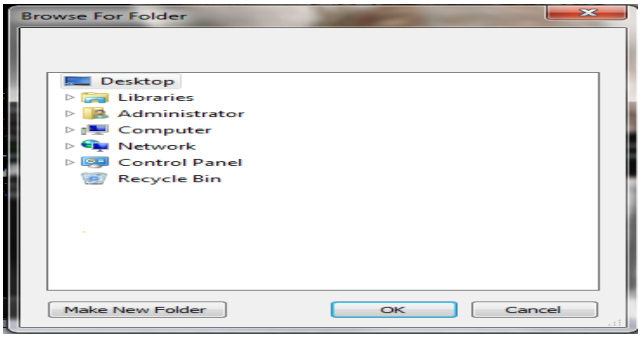
To delete an element from a workflow, right-click on the element you want to delete, and then select **Delete**. A dialog pops up asking you to confirm; click **OK** to confirm deletion, and **Cancel** to cancel deletion.

Editing Workflow Settings

After you create a new workflow, you can change some of the settings you specified at the time of creation. (You can also modify the AQi default workflows.) To edit a workflow, do the following: Click the down-arrow located to the right of the workflow name.

4. Select **Edit Workflow** from the pull-down menu.

   The Edit Workflow dialog is displayed, as shown below:



This dialog allows you to change the following settings:

- **Assigned body part**

  On the row containing the Workflow you want to change, click under the **Assigned Body Part** column. A pop-up menu is displayed, from which you can select the desired body part.

- **On Patient List**

  Choose whether to display the current workflow in the Patient List. On the row containing the Workflow you want to change, click under the **On Patient List** column. A pop-up menu is displayed, from which you can select **Yes** or **No**.

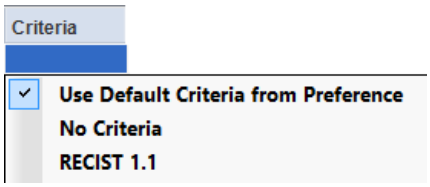
- **Load Condition**

  The **Load Condition** setting determines the workflow to be opened when a study is double-clicked in the Patient List or launched from PACS. The **No setting** selection allows the user to select a workflow manually.

  To change the load condition, click the cell in the **Load Condition** column and select the desired item from the pulldown menu.

- **Criteria**

  Associate measurement criteria with the selected workflow. These criteria will be used when measurements are tracked in the Findings Workflow. If this setting is not used in the selected workflow, any measurements tracked in the Findings Workflow that are performed in this workflow will use the default criteria that have been set in the preferences.

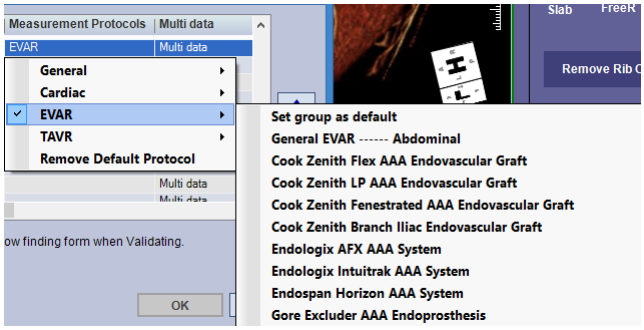


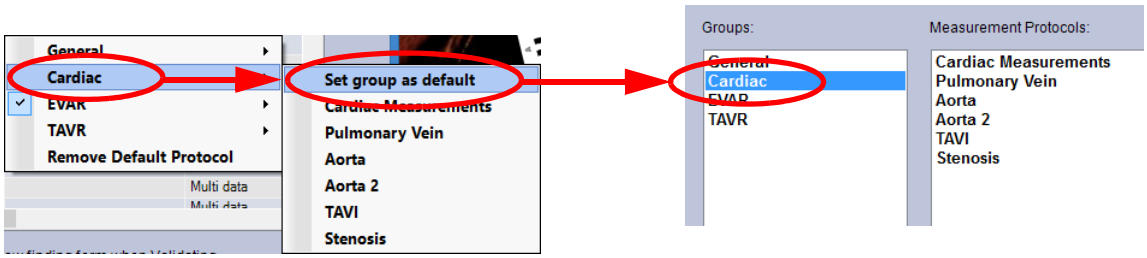
- **Measurement Protocols**

  This setting allows you to associate a default measurement protocol with the selected workflow. When a study is loaded into the workflow and the **Measurement Protocols** tool panel is opened in the 3D Viewer, that measurement protocol is loaded automatically.

  When you click in this column, the pulldown menu shows the list of all the measurement protocol *groups* currently defined on the server. Each group has a sub-menu listing the protocols in that group (see the following image). You can select a group as the default for this workflow, or you can select a specific measurement protocol.

  To associate a measurement protocol *group* with this workflow, select **Set Group as Default** from the sub-menu. That group then becomes the default group in the Measurement Protocols tool panel, as shown in the following image. For more detailed information about measurement protocols, see Chapter 13: "Measurement Protocols".





To remove the default measurement protocol, select **Remove Default Protocol** from the group menu.

- **Multi Data**

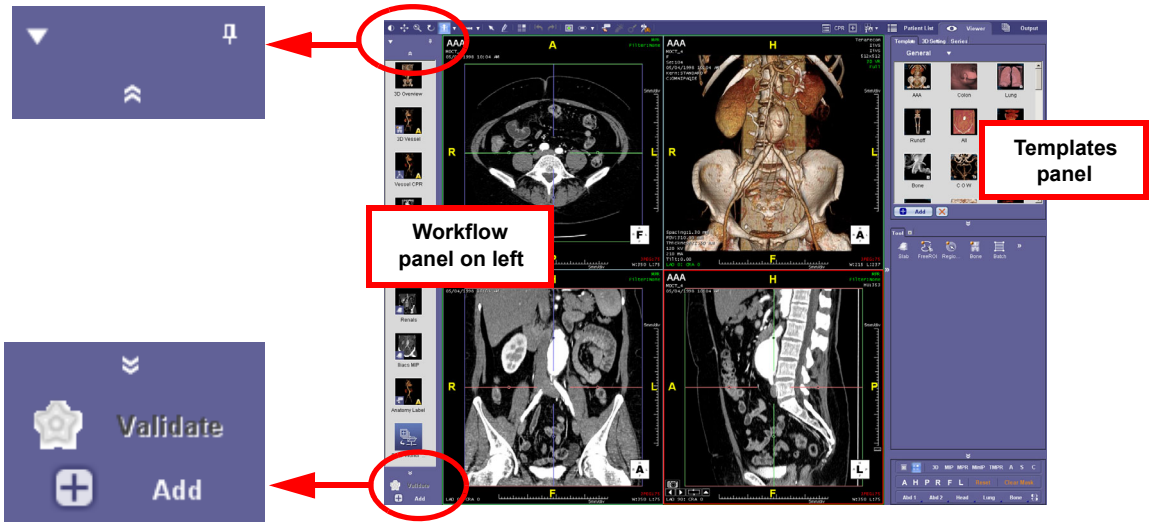
  This setting allows you to decide how multi data or multi-phase studies are loaded. When it is set to multi data, all multi data or multi-phase studies are loaded as multi data. When set to 4D, all multi data or multi-phase studies are loaded as multi-phase. Single data studies are loaded normally whether this setting is 4D or multi data. However, if it is set to 2D, all types of data are loaded as 2D.

- **Style**

  The **Style** setting allows you to move the Workflow panel to different locations in the AQi Viewer. The options are **Left** (left side of the AQi Viewer), **Bottom** and **Tool Panel**, which is the default location. The changed location is valid only for the workflow in which the Style setting has been set.

  In the following example, the **CTA Abd-Pelvis** workflow is being edited. The **Style** is set to **Left**:

  The next time a study is loaded into the CTA Abd-Pelvis workflow, the viewer will appear as shown in the following image:



The panel in the upper-right corner is still there, but the Workflows are no longer located there. Instead, the **Templates** panel is now visible. The Workflow panel's function buttons are arranged differently to accomodate a different location and shape.

The following functions are found at the top of the panel:

- **Down-Arrow** - Click on this to display the pulldown menu used for workflows.
- **Thumbtack Icon** - When this is upright (as it is in the previous image), the workflow panel is locked in place. When it is on its side, the workflow panel is hidden when the cursor is moved elsewhere. You can redisplay the workflow panel by moving the mouse into the edge of the panel that is showing.
- **Double Up-Arrows** - These scroll the workflow panel up when there are more workflow elements than can be visible at the same time.

These functions are found at the bottom of the panel:

- **Double Down-Arrows** - These scroll the workflow panel down when there are more workflow elements than can be visible at the same time.
- **Validate Button** - This is the same **Validate** button that is found in the Tool Panel when the Workflow panel is there.
- **Add Button** - This is the same **Add** button that is found in the Tool Panel when the Workflow panel is there.

Note: There is an Add button in the Tool Panel, but take care not to mistake this for the Add Workflow Element button. This Add button is for Templates.

When the Style selected is Bottom, the top functions described here are found at the left end of the workflow panel, and the bottom functions are found at the right end.

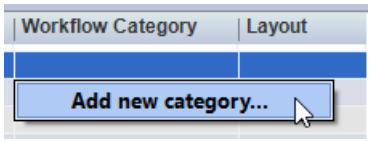
- **Monitor**

  Select Single or Dual monitor, to match your system configuration.

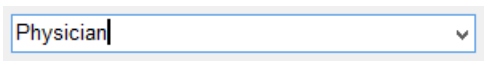
- **Workflow Category**

Create or select a category that you want this workflow to belong to. This is not a body-part category, as described in "Workflow Categories" on page 4-26. This feature allows you to define a category based on whatever criteria are relevant to your needs. For example, you can create categories for different work groups at your institution.

Click the cell under Workflow Category, in the row of the workflow you want to change. A menu is displayed. If any categories have already been defined, they will appear in the menu. You can also create a new category by selecting Add new category...

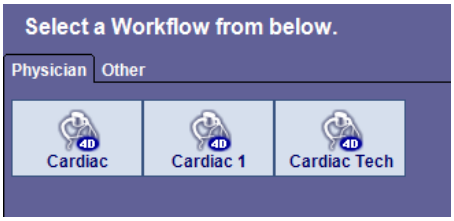


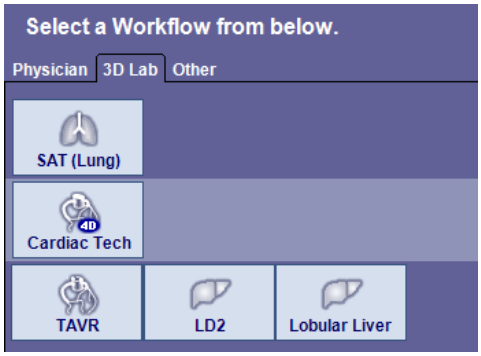
Enter the desired name in the text input box.



The category name is shown in the column.

Each category is displayed on a different tab on the **Load** menu. This can be combined with body-part categories, as shown in the image below, at right. The first row contains workflows in the chest category, the second row is in the heart category and the third row is in the abdomen category. All are part of the 3D Lab category.

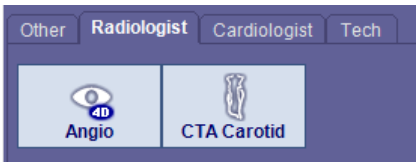




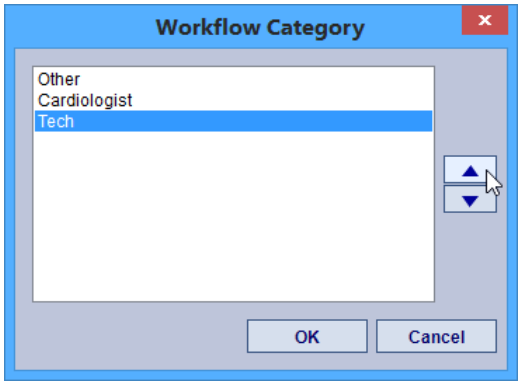
Reordering the Category Tabs

You can reorder the category tabs at the top of the workflow button panel, so that, for example, you can place frequently used categories in front.

Suppose your workflow categories are arranged as shown below, with the **Radiologist** category at the beginning of the tabs, and you would prefer to have the **Tech** category at the start. You can reorder the categories by doing the following:

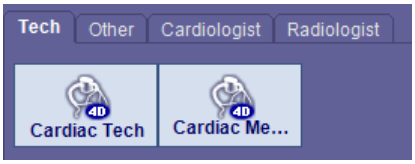


1. From the drop-down menu in the workflow, select **Edit Workflow**, to open the **Edit Workflow** menu.
2. Click in any cell in the **Workflow Category** column. This opens a menu.
3. Select **Order category tabs**. This opens the **Workflow category** dialog:



4. Select the category you want to move, and then click the up or down button on the right to move it. Each click moves the category one step in the list.

5. Click OK when done. The desired category tab has been moved to the new position:

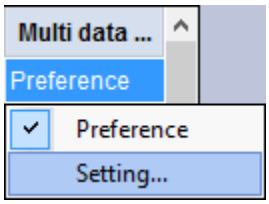


- **Layout**

  Select a single or multi-data layout.

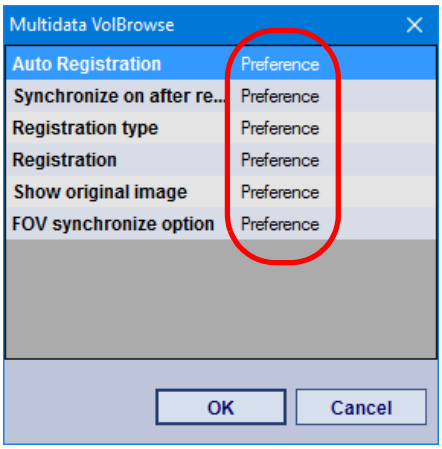
- **Multi Data Setting**

  There are several settings under the Multi data column. By default, these contain the values that were configured in the user preference settings. However, you can override those values for specific workflows. Click the cell in the desired workflow's row, and a menu (shown at right) is displayed.



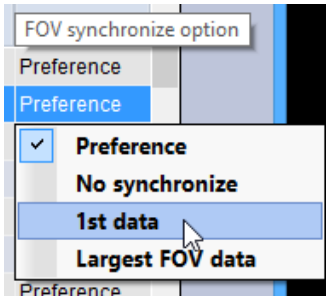
  - **Preference** - Use the setting in the User Preferences (see "Multidata/4D" on page A-14).

  - **Setting** - Open a dialog to set preferences for multi-data 4D settings. The following dialog is opened:



Click the right-hand column to show a menu where you can select the option for each of these settings. For further descriptons of these settings, see "Multidata/4D" on page A-14.

- **Auto Registration** - Select **Yes** to enable Auto Registration for this workflow, **No** to disable it, and **Preference** to use setting in the User Preferences.
- **Synchronize on After Registration** - Select **Yes** to enable synchronization for this workflow, **No** to disable it, and **Preference** to use setting in the User Preferences.
- **Registration Type** - Select **Translation Only**, **Translation + Rotation**, or **Preference** to use the setting in the User Preferences.
- **Registration** - **Select Overlay** to register the overlay study to the base study, **Base** to register the base to the overlay study, and **Preference** to use the setting in the User Preferences.
- **Show Original Image** - When **Yes** is selected, the base or overlay image registers only the position (and not rotation). The axial view always shows original slices.
- **FOV Synchronize Option** - This option is used for a multi-data side-by-side display, when the images in one study are zoomed larger than the other (or others). This setting determines whether their sizes will be synchronized in the display, and if so, how they will be synchronized.



  - **Preference** - Use the setting in the User Preferences (see "Multidata/4D" on page A-14).

- **No Synchronize** - Do not synchronize the FOVs.
- **1st Data** - Synchronize the FOV of all data with the first study loaded.
- **Largest FOV Data** - Synchronize the FOV of all data with the study having the greatest zoom factor.

Other Functions

Other functions of **Edit Workflow** are as follows:

Reorder the list of workflows

1. Select a workflow from the list.
2. Using the up/down arrows on the right side of the dialog, move the workflow up or down the list.

Delete the workflow

1. Select the workflow to be deleted.
2. Click the **Delete** button.

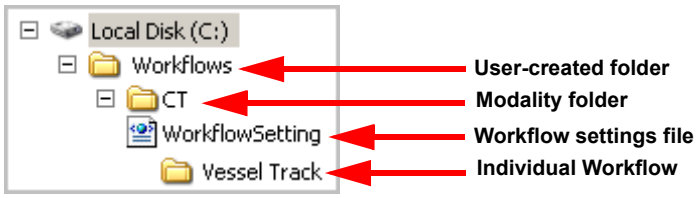
Note: There is no confirmation dialog box for this deletion. The workflow is simply deleted. Contact TeraRecon customer support if you have questions or need assistance.

Importing, Exporting, and Sharing Workflow Templates

You can make AQi workflow templates available to other AQi users. This is particularly useful for sharing workflow templates that you have created yourself. Workflow templates are shared through the Export Workflow Template feature of the AQi 3D Viewer.

Exported Workflow Structure

When a workflow template is exported from AQi, it is created on storage media in a specific structure, as shown below:



The Export feature requests the name of the folder where you would like the workflow template to be saved. In the diagram above, that folder has been named “Workflows”, but you can choose any legal name in Windows. The folder can be created anywhere that is accessible from the AQi client.

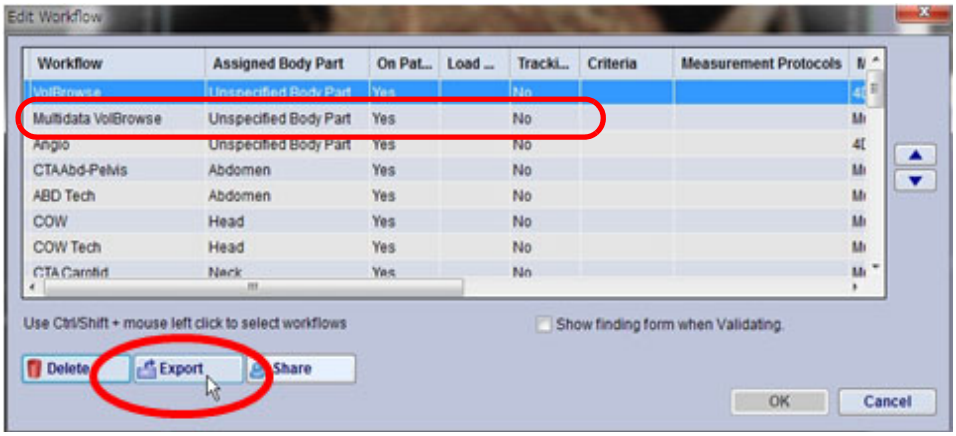
Inside the folder, a subfolder is created for the modality of the workflow. In addition, an XML file, **WorkflowSetting**, is created. This file contains all the information about the workflow templates that have been exported to this folder.

In the modality folder are folders for individual workflow templates. The XML files for each workflow element are stored inside the workflow template folders.

Exporting Workflow Templates

To export a workflow template, do the following:

1. In the Workflow panel, click the down-arrow located to the right of the workflow name.
2. Select **Edit Workflow** from the pull-down menu. The Edit Workflow dialog is displayed:

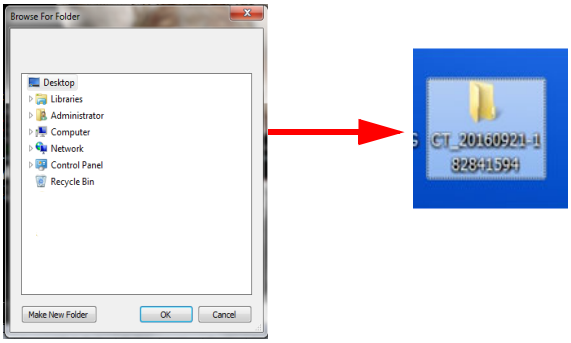


3. Select the name of the workflow to be exported by clicking on the name.

4. Click the **Export** button. A Windows navigation dialog is opened.

5. Navigate to the folder where the workflow template will be exported, and click **OK**. The workflow template is saved to the target folder.

    - If the current folder you are trying to export to is not empty, a new folder will be created and named using its Modality_Date_Time. The workflow will then be exported to the new folder.



Importing Workflow Templates

In addition to creating new workflow templates, you can add workflow templates that have been created and exported by another Aquarius iNtuition Client.

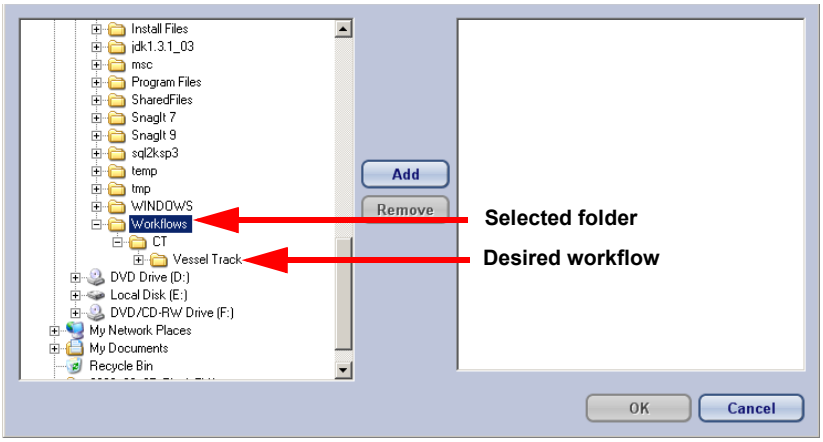
To import a workflow template, do the following:

1. From the workflow pull-down menu, select **Import Workflow Template**. A navigation dialog box is displayed.

2. Navigate to the folder where the workflow template is stored.

3. Click **Add** to select the folder.

Note: Do not select the folder for the desired individual workflow template. The selected folder *must* contain the XML file "WorkflowSetting". This file is stored two levels above the individual workflow template in the Windows file structure. Please see the diagram of the file structure in the figure below.



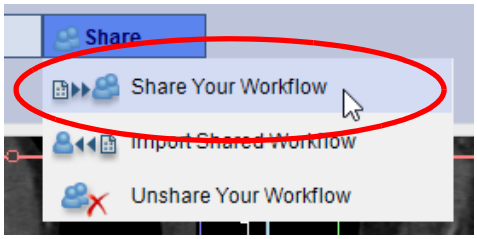
4. Click **OK**. The new workflow template is added to the workflow. The icon will now appear in the workflow panel.

Sharing Workflow Templates

You can make your workflow templates available to all users who connect to the server.

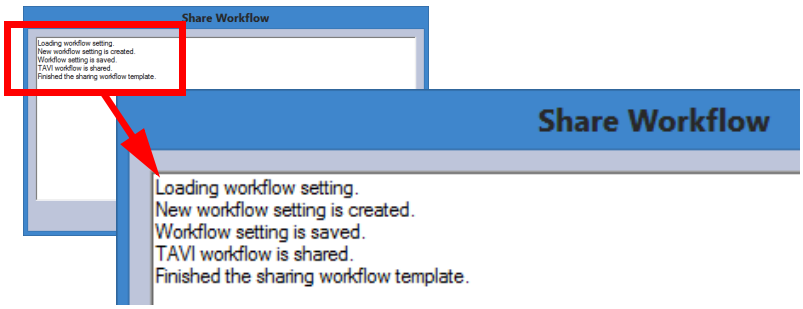
1. Select a workflow from the list.

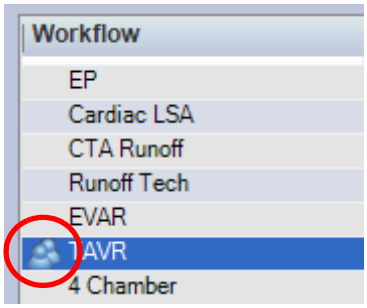
2. Click the **Share** button. A menu is displayed below the button.



3. Select **Share Your Workflow** from the menu.

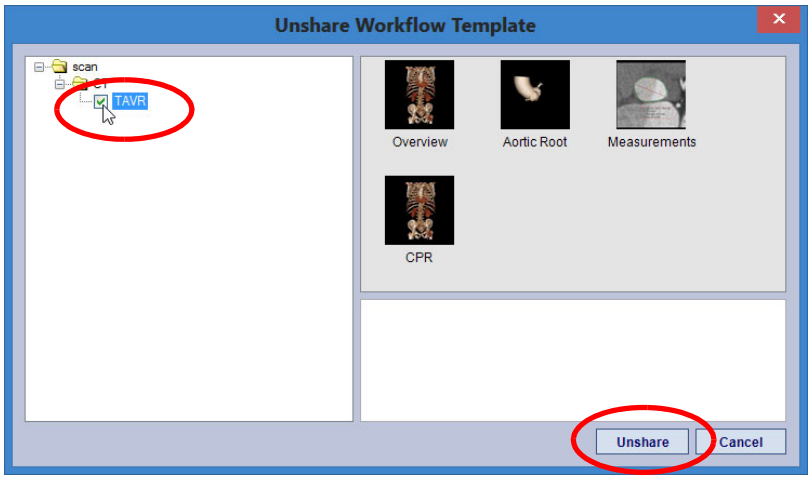
   The workflow is automatically converted to shared. This process is logged and the log is displayed when it is completed (see below, left). The shared status is indicated by an icon next to the workflow name (below, right).





Unsharing Workflow Templates

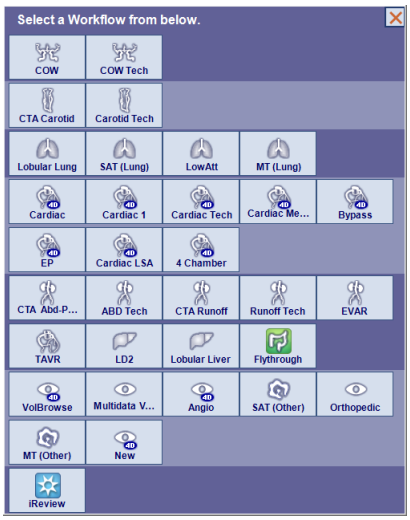
To discontinue sharing a workflow, click the **Share** button, and then select **Unshare Your Workflow** from the pulldown menu. This opens a dialog that shows the file structure containing your shared workflows. Check the box next to the name of the workflow to unshare, and then click the **Unshare** button.



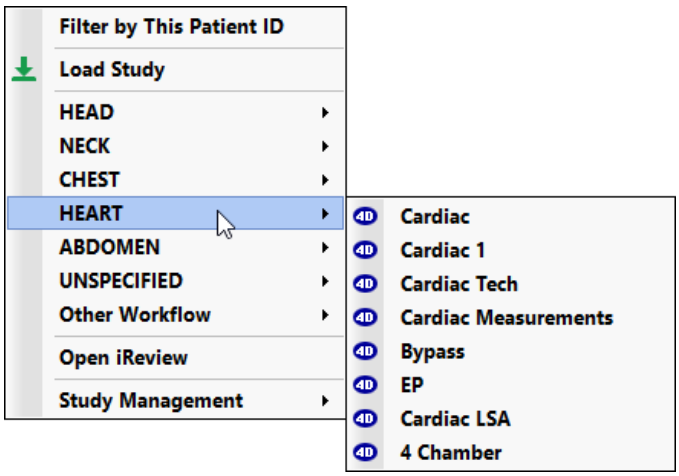
Workflow Categories

Workflow templates can be categorized by body part so that they are grouped by category in the workflow **Load** menu and the right-click on study/series menu. To enable categorization, check the **Categorize for body parts in workflow** setting in the Workflow Preference screen. (See "Workflow" on page A-11 for more information.)

By default, the workflow templates appear in a single group on either menu. When categorization is enabled, the menu is displayed as shown below:



The right-click menu is also categorized:



Example: The Cardiac Workflow

This section demonstrates the way workflows are designed to work, by showing you how to perform an example cardiac study using the default AQi Cardiac workflow. The purpose is to give you an opportunity to become familiar with AQi workflows, by providing step-by-step instructions to take you through the entire process.

Opening a Cardiac Study

To open a cardiac study, do the following:

1. Select the patient study from the Study List.
2. Right-click and select the Cardiac workflow (see the following figure).

   This opens the Aquarius iNtuition 3D Viewer with the Cardiac Workflow (see Figure 4-6).

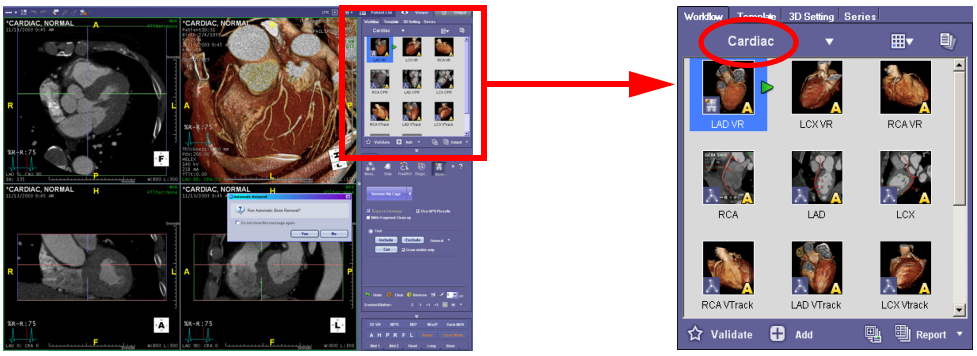


Figure 4-6: The Aquarius iNtuition 3D Viewer with Cardiac Workflow

For more details about the Aquarius iNtuition 3D Viewer, please see Chapter 3: "The 3D Viewer".

Automatic Bone Removal

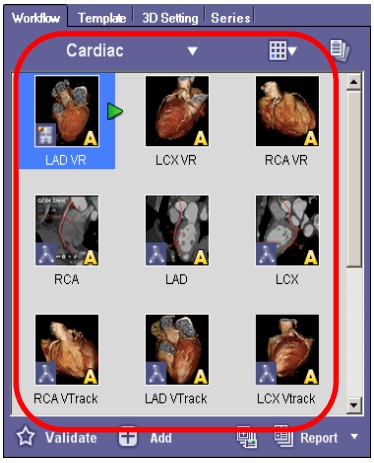
When a study is opened in a specified workflow, Aquarius iNtuition automatically applies the first workflow element to the image. In the Cardiac Workflow, the first element does bone removal. When you load a study into the Cardiac Workflow, a dialog is displayed asking whether you want the bone to be removed automatically from the image.

If you know that you will always want the bone to be removed automatically, check the box labeled “Do not show this message again” before clicking **Yes**. From that time on, whenever you open a Cardiac Workflow, the bone will automatically be removed, with no inquiry.

Using the Cardiac Workflow

The Cardiac workflow contains a series of icons, called *workflow elements*, each of which represents a different view of the study image. Together they make up a standard analysis of the cardiac vessels. Each workflow element is actually a set of instructions to Aquarius iNtuition to modify the image so that you can examine specific vessels in differerent image formats (such as CPR or MIP) or at different angles, levels of magnification, or with different parts removed (such as bone) or exposed.

Each element of the Cardiac workflow is focused on a specific vessel, viewed in a different rendering mode.



Nine of the Cardiac Workflow elements consist of three different views each of the RCA, LAD, and LCX vessels. The top row contains 3D Volume Rendering views of each vessel, the middle row contains CPR views, and the bottom row contains Vessel Track (MIP) views.

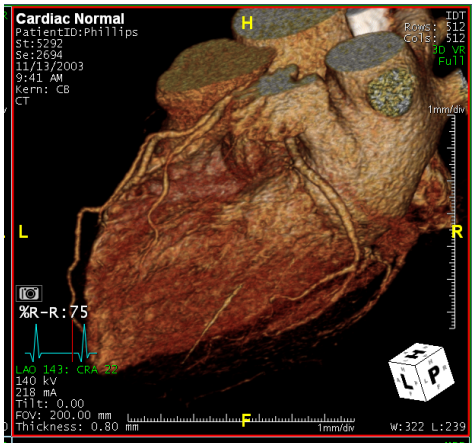
Description of Each Element

- **3D Volume-Rendering Mode** - These workflow elements show an overview of the heart so that you can see where the arteries are, where they originate, and what the relationships are among the arteries.
- **CPR Views** - A CPR view gives the best diagnostic view for stenosis, calcium, soft plaque, and so on.
- **Vessel Track** - This gives the MIP view, which allows you to track the vessel along the centerline.

When you click on one of these nine elements, the image in the main window changes so that the selected vessel is prominently shown, displayed in the rendering mode indicated on the workflow element icon.

Example 1: LCX VR

Click the **LCX VR** workflow element. The image in the main window changes to display the heart in 3D Volume-Rendering mode, showing the LCX vessel prominently (see the figure below).



Example 2: LAD CPR

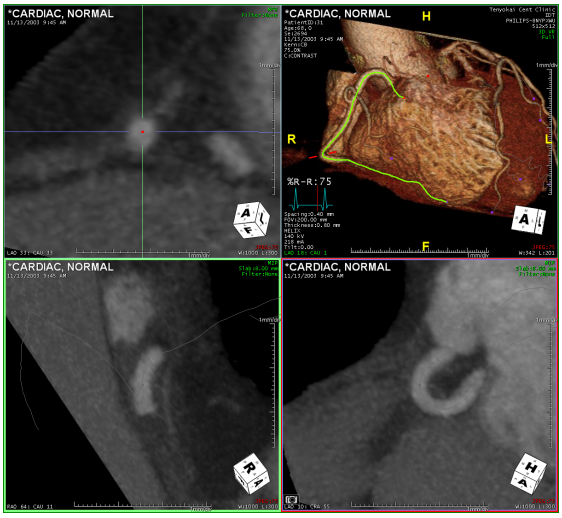
Click the **LAD CPR** workflow element. If centerlines have already been found by Advanced Processing, this creates a centerline on the LAD vessel and opens a CPR window in the main viewing area. Otherwise, centerlines must be created manually.

To create a centerline manually, hold down the shift key and click on the vessel of interest.

Example 3: Vessel Track

Click the **RCA VTrack** workflow element.

Vessel track view uses MIP images to show the vessels more clearly. The two bottom images are the tangent views of the RCA vessel, and the image in the upper-left is the cross-section view.



As you page through the slices in the cross-section window, corresponding parts of the tangent images become visible. You can also move the cross-section line along the centerline in the 3DVR window to page through slices.

To rotate the tangent images, click on the image, hold down the mouse button and drag it around the image. This is called “free rotate” because the tangent image can be rotated in any direction. To rotate around the central vertical line in the image, hold down the control (**Ctrl**) key while rotating.

The Calcium Scoring Module

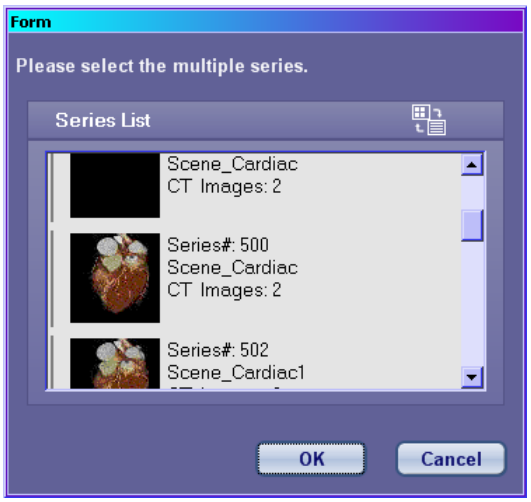
The next workflow element opens the Calcium Scoring module. This module is described in detail in Chapter 11: "Calcium Scoring".

Ejection Fraction

The final elements in the Cardiac Workflow perform the Ejection Fraction functions. To find the ejection fraction of the , use the **LV EF** workflow. For the right ventricle, use the **RV EF** workflow. This example will show LV ejection fraction.

Note: This function is relevant for multi-phase series only.

You can calculate the LV ejection fraction by clicking on the workflow element shown inthe figure above. A small window displaying the Series List opens beneath the Workflow panel, asking you to select multiple series for TVA (see figure below).



Results are displayed in the Tool Panel, located just below the Workflow panel. The LV EF result is also displayed on the LV EF workflow element itself.

Note: You must validate the EF Workflow Elements before generating a report, or the EF values will not be populated in the report.

Automatic and Manual EF

By default, the Aquarius iNtuition Client calculates the Ejection Fraction automatically. However, if you prefer to step through manually to provide parameters, you can change your preferences so that the desired TVA module is invoked in manual mode.

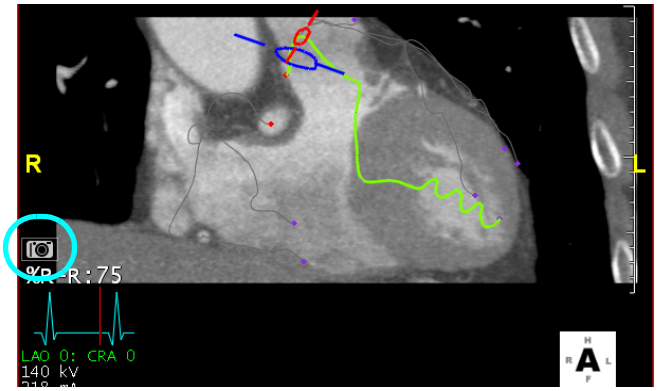
To change the preference, click the Preferences button at the right end of the top toolbar, and set the **Analysis Method** to Manual on either the **TVA(LV)** or **TVA(RV)** screen, or both of them, depending on your needs. For detailed instructions on changing the TVA preferences, see "TVA(LV)" on page A-35 (for left-ventricle TVA) or "TVA(RV)" on page A-35(for right-ventricle TVA).

Outputting Images

You can send Workflow images to the Output Panel or to a PACS server, and you can also generate a report.

Sending Images to the Output Panel

You can send images to the Output Panel from the 3D Viewer, to be included in a report that will be generated from the Output Panel. Do either of the following to capture images:



- Click the camera icon in the image to be sent (see image at right). This sends the image that the cursor is currently pointing to.

- Right-click on the image and select one of the following from the pull-down menu:

Capture	Capture the selected image.
Capture All	Capture all images currently displayed in the viewer, and place each image in a separate cell in the Output Panel.
Capture All in One	Capture all images currently displayed in the viewer, and place them all in a single cell in the Output Panel.
Capture to Folder	Capture to a folder defined in the Capture preferences.

Sending Workflow Views to the Output Panel

You can send views of the current study, as determined by the workflow elements, to the Output Panel.

To send the currently selected element to the Output Panel, do the following:

1. Locate the button in the lower-right corner of the Workflow panel (see figure at right). It says one of the following: **Output**, **Output All**, **Report**, **Send to DICOM** or **Export Measurements**.

2. If it does not say **Output**, click the down arrow located to the right of this button. This opens a pull-down menu for output options:

3. Select **Output**. The button is now set to **Output**.

4. Select a workflow element so that it is applied to the image. The image with the workflow element applied to it is called a *workflow scene*.

5. Click the button to send the workflow scene to the Output Panel.

Output All

To send all elements in the current workflow to the Output Panel, do the following:

1. Follow steps 1, 2 and 3, and then select **Output All** from the pull-down menu.

2. Click the **Output All** button. All validated workflow scenes are automatically sent to the Output Panel.

To see the Output Panel, click the **Output** tab. The tabs for **Patient List**, **Viewer** and **Output** are just above the Workflow panel, and the **Output** tab is the rightmost:

The Output Panel shows the images that were captured during the Cardiac workflow.

Generating Reports from the Cardiac Workflow

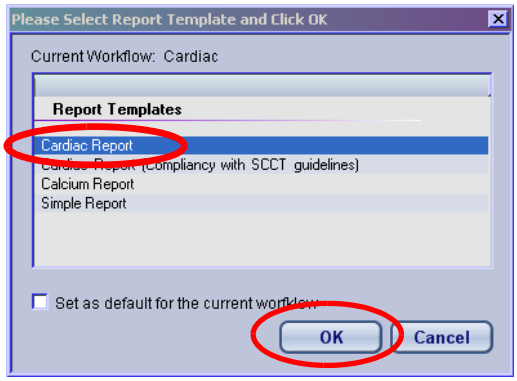
To generate reports, do the following:

1. Locate the button in the lower-right corner of the Workflow panel (see Figure 4-2 on page 4-2). It says either **Output**, **Output All**, **Report**, **Send to DICOM** or **Export Measurements**.

2. If it does not say **Report**, click the down arrow located to the right of this button. This opens the following pull-down menu:

3. Select **Report** from this menu.

4. Click the **Report** button. The **Report Templates** dialog is displayed (see figure below).



5. Select “Cardiac Report” and click **OK**. This creates and opens the report in a Microsoft Word file.

   The first page of the report contains findings from calcium scoring, perfusion, stenosis analyses, and other information (see Figure 4-7 on page 4-34). The second page (along with any pages thereafter) contains the images that have been captured to the Output Panel (see below).

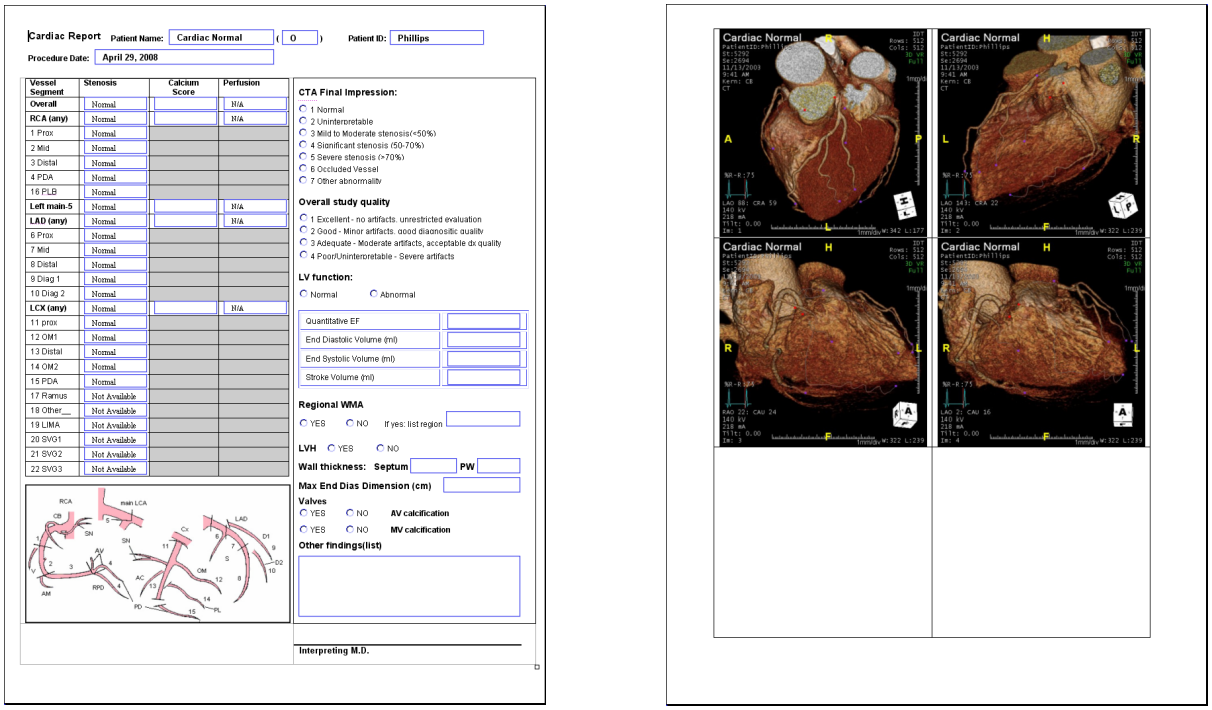


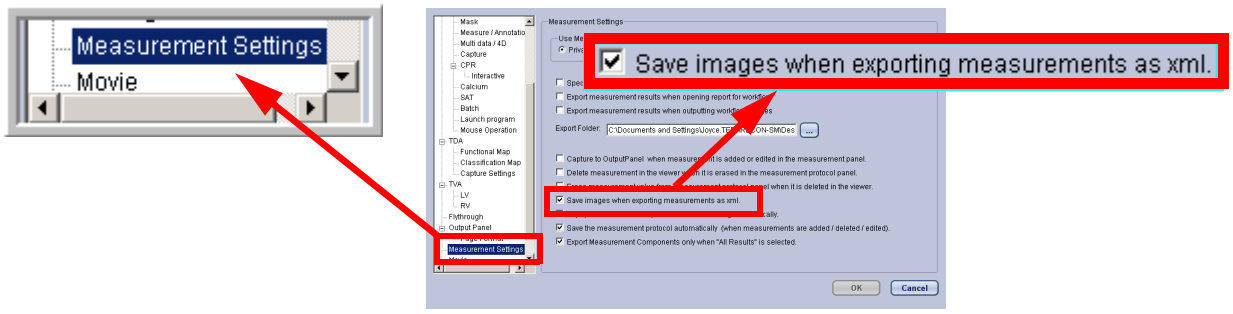
Figure 4-7: The Cardiac Report

Capturing Cardiac Measurements and Images for a Report

You can associate a Measurement Protocol with a cardiac Workflow, so that measurements obtained while stepping through the cardiac Workflow are automatically captured to the protocol. These results can then be exported to an xml file and incorporated in a report. In addition, you can set a preference so that images from the Workflow are saved and included in the report.

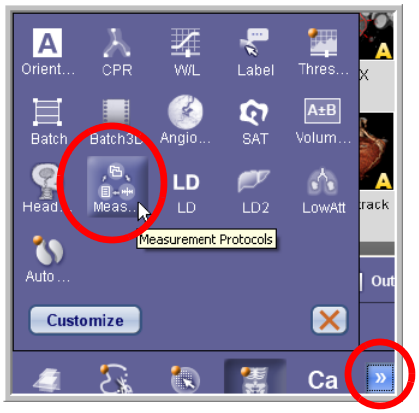
Create a Measurement Protocol

1. Open Preferences and click **Measurement Settings** in the list on the left. Make sure that the box for **Save images when exporting measurements as xml** is checked.

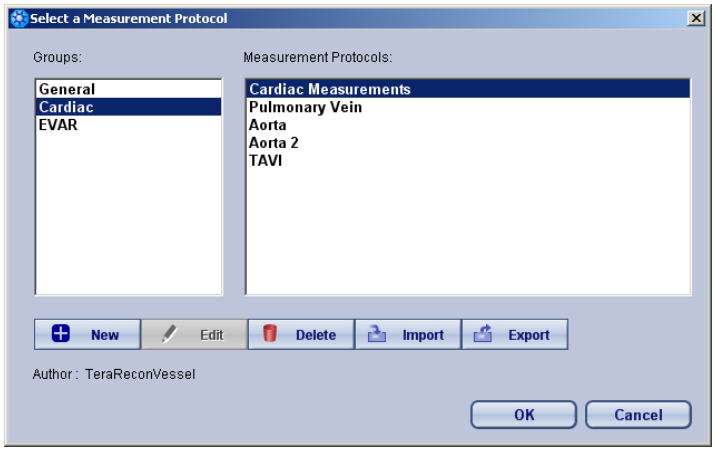


2. Load a cardiac study.

3. In the 3D Viewer, open the **Measurement Protocols** tool panel (circled, at right).



4. Open the **Measurement Protocols** dialog (see "Opening a Protocol" on page 13-1).



5. Select **Cardiac** from the **Groups** list on the left.

6. Create a new protocol called Stenosis (see "Adding Measurements to a Protocol" on page 13-8).

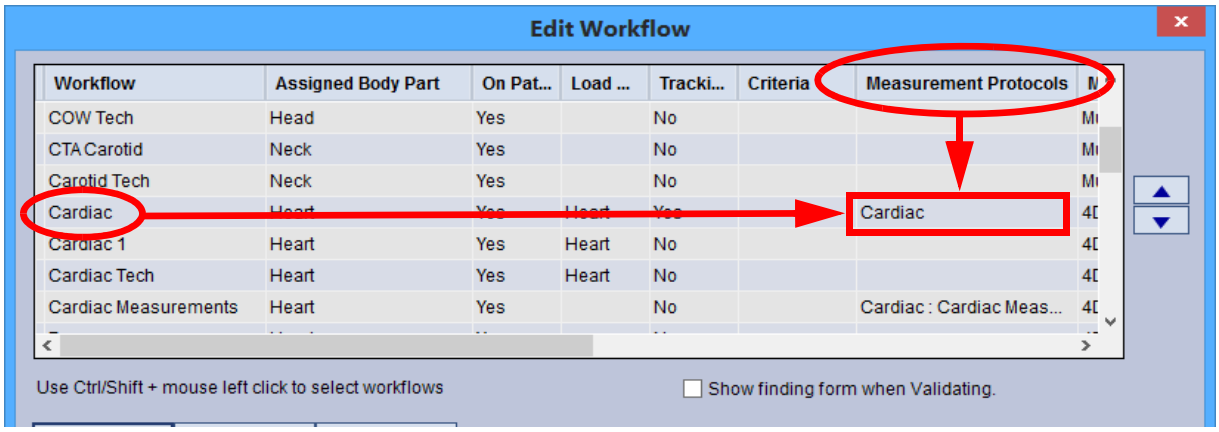
Note: The only settings you need to configure for this protocol are the protocol name ("Stenosis") and the report template (AqSimpleReport2.doc, which is the default).

When you have finished, the new (but empty) protocol is loaded into the tool.

7. Add measurements to the new protocol. In this example, we will add measurements that contain stenosis results from the RCA, LAD and LCX vessels. In the **Long Name** box, type RCA, and type the same in the **Short Name** box. In the **Type** box, select stenosis. (See "Adding Measurements to a Protocol" on page 13-8)

Editing a Workflow

1. From the Cardiac workflow pulldown menu, select **Edit Workflow**. The **Edit Workflow** panel is opened.



2. In the **Workflow** column, find the "Cardiac" row. In the **Cardiac** row, find the “Measurement Protocols” column. Click in that cell to open a menu.

3. Select **Cardiac**->**Stenosis** from the menu/sub-menu, to associate the Cardiac workflow with the Stenosis Measurement Protocol. (See "Measurement Protocols" on page 4-17 for instructions.)

Note: For convenience, you can also add a workflow element to this workflow that loads the Measurement Protocols tool into the Tool Panel. Make sure to open Measurement Protocols first, and then add the new workflow element. (See "Adding a New Workflow Element" on page 4-8 for instructions.)

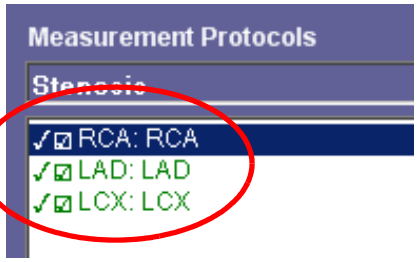
Using the Measurement Protocol in Other Studies

1. Load a cardiac study.

2. Open the **Measurement Protocols** dialog and select the **Cardiac** from the left column, if not already selected. Select the **Stenosis** protocol from the right column, and click **OK**.

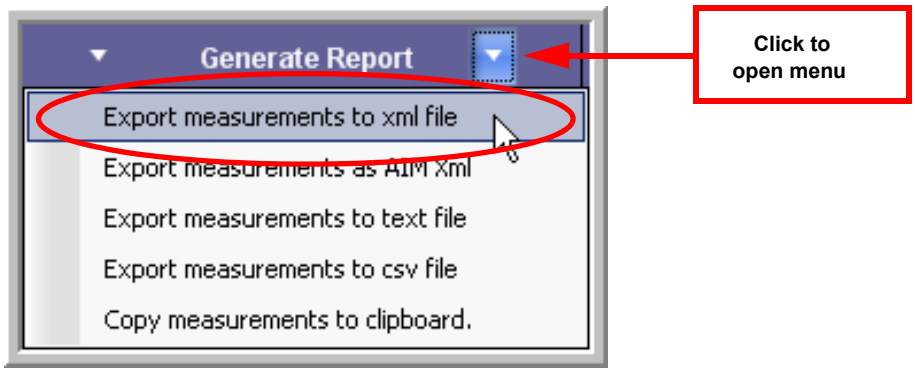
3. Validate the RCA, LAD and LCX workflow elements. Stenosis measurements are obtained automatically.

4. Verify that each step of the protocol has been completed.



5. Find the **Generate Report** button located in the lower-right corner of the Tool Panel.

6. Click the down-arrow on the right (see the following figure).



7. Select **Export measurements to xml file**.

8. Generate a report and verify that the measurements and images have been included in the report.

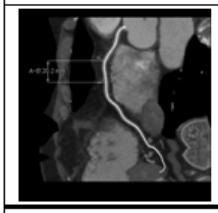
Report
AnyScan Medical Imaging Center
1234 Road Street
South Medical Plaza, AB 13240
Tel: 663-132-0231

terarecon

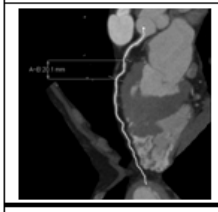
Patient Name:	HEART LAD_Plaque		
Patient Age:		Referring MD:	
Patient Gender:	O	Scan Date:	3//20/02/0
Date of Birth:		Patient ID:	TRIDEMO_3D_CVASC_01

Measurements:

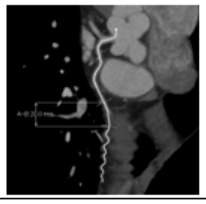
Measurement Name	Value
RCA:RCA	19.42 %



LAD:LAD	44.94 %



LCX:LCX	47.58 %



HEART LAD_Plaque — 02/03/2006 — Page 1 of 1

Chapter 5 The Output Panel

Topics in this chapter:

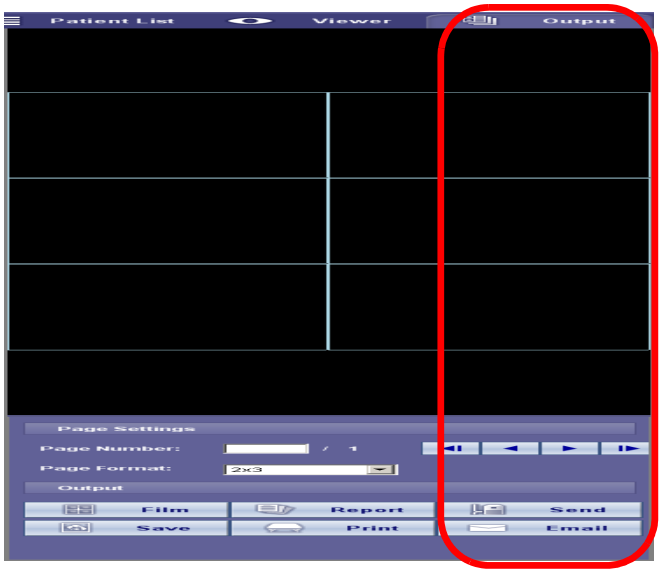


Figure 5-1: The Output Panel (circled)

The Output Panel allows you to generate reports, send images to a DICOM server, email images, print images to paper and film and save images to a disk.

Images are captured from the 3D Viewer or other module during examination and analysis. They are saved until you are ready to perform the necessary output tasks that make the images available to other physicians or technicians.

Page Settings

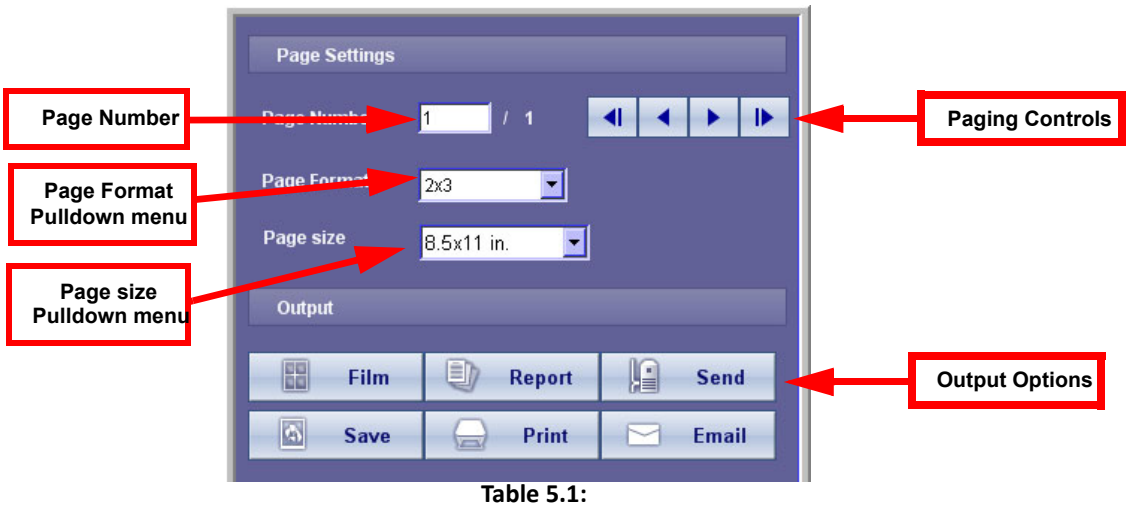


Table 5.1:

Page	Settings
Page Number	If there are more images than can be displayed on one screen, the number in the text window shows the page currently being displayed. To the right of that is the total number of pages for all the images. You can skip around to different pages, either by typing the desired page in text window and hitting **Enter**, or by using the buttons on the right.
Paging Controls	These buttons allow you to page through all pages of images in the Output Panel. From left to right: go to the first page, go back one page, go forward one page, and go to the last page.
Page Format (pulldown menu)	This allows you to choose the layout of images on the Output Panel screen. The choices in the pull-down menu represent the layout, width by length, of the images displayed on an Output Panel page. For example, a 1x2 layout displays up to 2 images on one page, a 2x3 layout displays up to 6 images, and so on (see Figure 5-2 on page 5-3).
Page Size	The page size determines the dimensions of the paper when printing the contents of the Output Panel. The Page Size menu is visible only when two or more page sizes have been selected in the Preferences menu. (See "Page Format" on page A-44 for details.)
Output Options	**Film** - Print to printer containing film **Report** - Generate a medical report **Send** - Send to DICOM server **Note: For instructions on adding user-defined remote DICOM preset buttons, see** "Send to DICOM" on page 2-16**.** **Save** - Save to Hard drive **Print** - Print to network printer **Email** - Send images via email

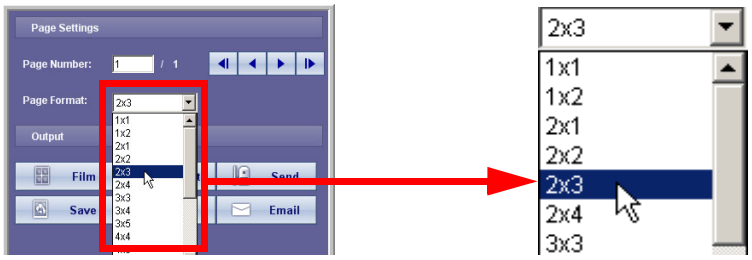


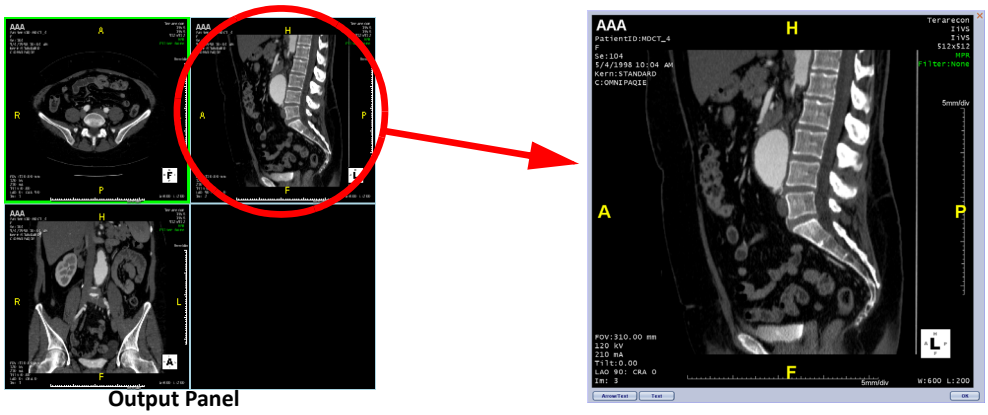
Figure 5-2: Page Format Options Pulldown Menu

The Right-Click Menu

The Output Panel offers more functions in the right-click menu. Point the mouse on one of the images in the Output Panel and right-click to show the menu.

Edit Selected Images

You can open an image in the Output Panel to edit it. To do so, right-click on the image and select **Edit Selected Images** from the menu. The image is displayed on the screen in a separate window.



Output Panel

The edit window provides the following functions:

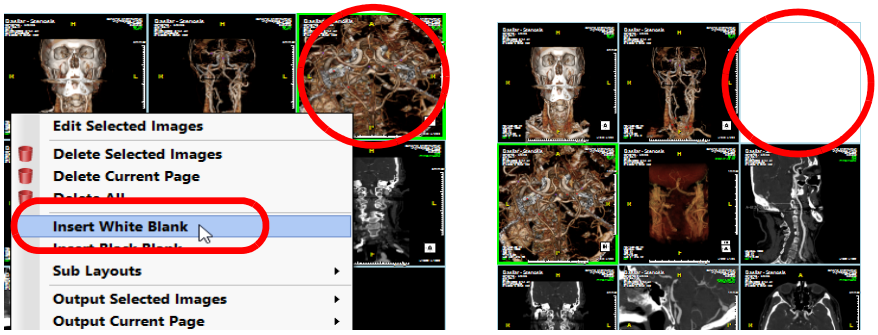
- **Pan** - Right-click on the edit window and hold down the mouse to pan the image.
- **Zoom** - Click on the middle mouse button and hold it down, then move the mouse upward to zoom in and downward to zoom out.
- **Window/Level** - Click on the left and right mouse simultaneously, and then move the mouse up or down to change the Window/Level.
- **Add Annotation** - To add text only, click the **Text** button in the lower-left corner, and then click on the image where you want to place the annotation. A text-input box is displayed at that location, where you can enter the annotation. To add text with an arrow, click the **Arrow/Text** button and then click the image to place the annotation. A text-input box is displayed, connected to an arrow, where you can enter the annotation. In both cases, you can move and resize the annotation after it has been added.

Delete Images

- **Delete Selected Images** - Deletes only the images previously selected. You can select any images on the page. To select two non-contiguous images, hold down the **Ctrl** key while selecting.
- **Delete Page** - Deletes all images on the page currently being viewed.
- **Delete All** - Deletes all images in the Output Panel.

Insert Blank (White or Black)

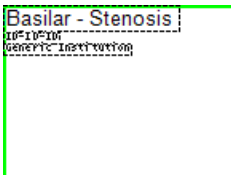
Inserts an empty cell before the image you have right-clicked on. Select either **Insert White Blank** or **Insert Black Blank**. The following images show the insertion of a white blank cell in the Output Panel. All captures that follow the inserted cell are shifted down by one.



Insert Black Blank inserts an empty black cell in the same way.

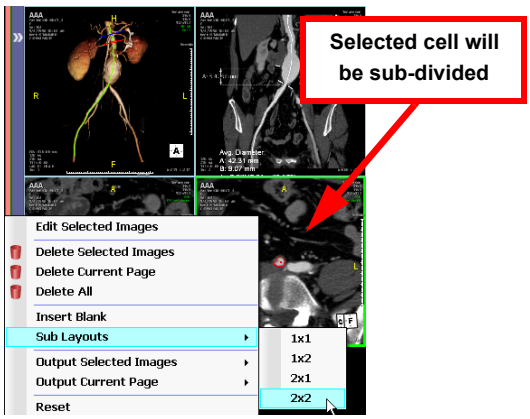
Show Annotations on Blank Image

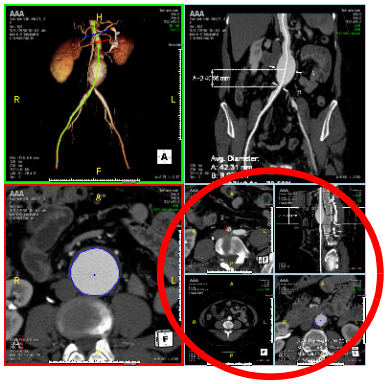
If a blank cell has been inserted, you can show annotations on it. Right-click on the blank image and select **Show Annotations on Blank Image**.



Sub Layouts

Sub layouts allow you to divide an individual cell into sub-cells.



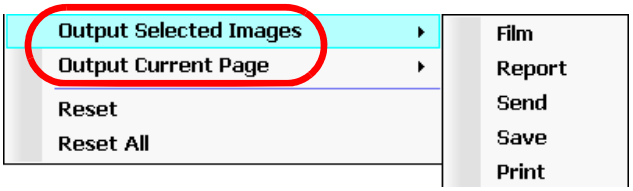


In the figure above, the Output Panel has 8 captures. Only 4 are showing because the layout is in 2x2 images per page.

In the left-hand image, the bottom-right cell is selected to be sub-divided into a 2x2 sub-layout. In the right-hand image, the bottom-right cell has been sub-divided into a 2x2 sub-layout. The images which occupy 3 of these cells came from the second page of captures. If there had not been any more images, 3 of the sub-cells would be empty.

Output selected Images and Output Current Page

These two functions allow you to perform the Output functions on a subset of images, rather than on all the images. The functions are: Film, Report, Send, Save, Print and Email. They correspond to the buttons in the Output Panel's control panel.



- **Output Selected Images** - Performs the Output functions on selected images only.
- **Output Current Page** - Performs the Output function on the current page only.

Reset Images

The **Reset** functions undo any zooming, panning or window-level changes performed during this session.

Note: Annotations that you have added are not removed with the reset. These must be removed manually.

- **Reset** - Resets only the image you have right-clicked on.
- **Reset All** - Resets all images in the Output Panel

Output Functions

The remainder of this chapter describes the output functions.

Generating Reports

Note: Before you being generating reports, make sure that MS Word is installed in your computer, and that the security settings in Word are properly configured, to allow the auto-formatting feature to run. For information about the security settings in Word, see "Setting the security in MS Word" on page 5-11.

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iNtuition offers a highly customizable report template for general reporting purposes. The report template utilizes MS Word. You can send the report to other physicians as an e-mail attachment, print it, or file it back to the DICOM server as part of the patient record. You can capture the images displayed on the 3D Viewer (or other module) and use them for your interactive report. The interactive report is saved on the server and you can retrieve it any time by accessing the patient data.

Pre-requisites

Before using the report generation function, please note the following:

- In order to use the report function, your computer must have Microsoft Word (98 or above) installed.
- Microsoft Word security settings must be properly configured. (For instructions, see "Setting the security in MS Word" on page 5-11.)
- If you wish to e-mail the report created, you must have an E-Mail program installed on your computer. In addition, you also need to have an access to the mail server from within your network.
- You may not overwrite the original report that is saved on the server. You will need to save a new report after you manipulate the image on the existing report.
- You may not delete a report that has been previously saved on the server. If you have created an unnecessary report and wish to have it deleted, please contact your server administrator.
- The image on the report comes alive only when the recipient of the report has access to the iNtuition server where the patient data resides.

Create The Report

To create a report, perform the following:

1. Select the Page Format from the **Page Format** pull-down menu (see Figure 5-2 on page 5-3). The images are redisplayed in the selected format. This is the format in which they will appear in the report.
2. Click the **Report** button from the Output Options (see "Page Settings" on page 5-2).

The report page opens in Microsoft Word (see Figure 5-3 on page 5-7).

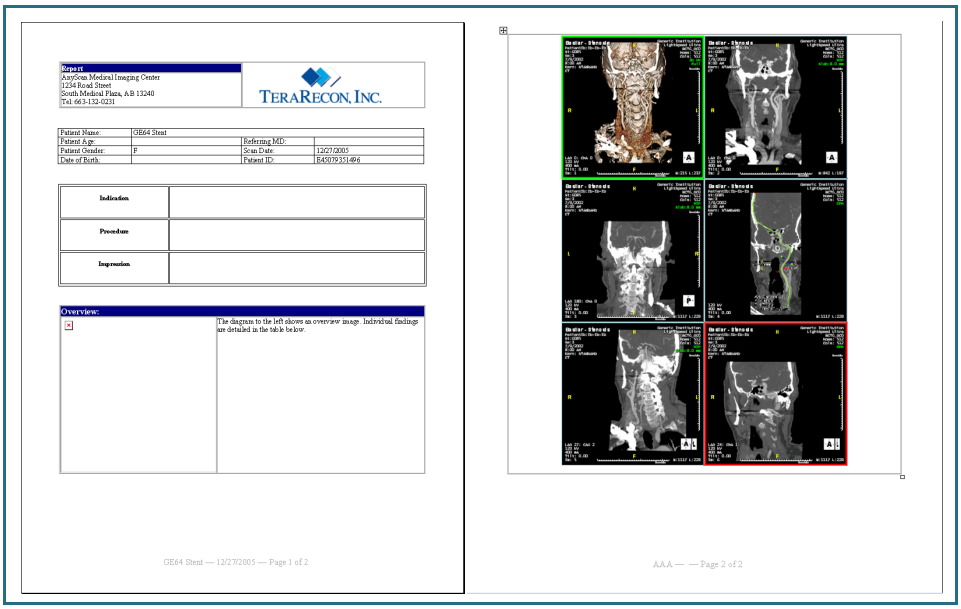


Figure 5-3: Simple Report

Note: Before exiting Word, be sure to save the report.

Web-based Reports

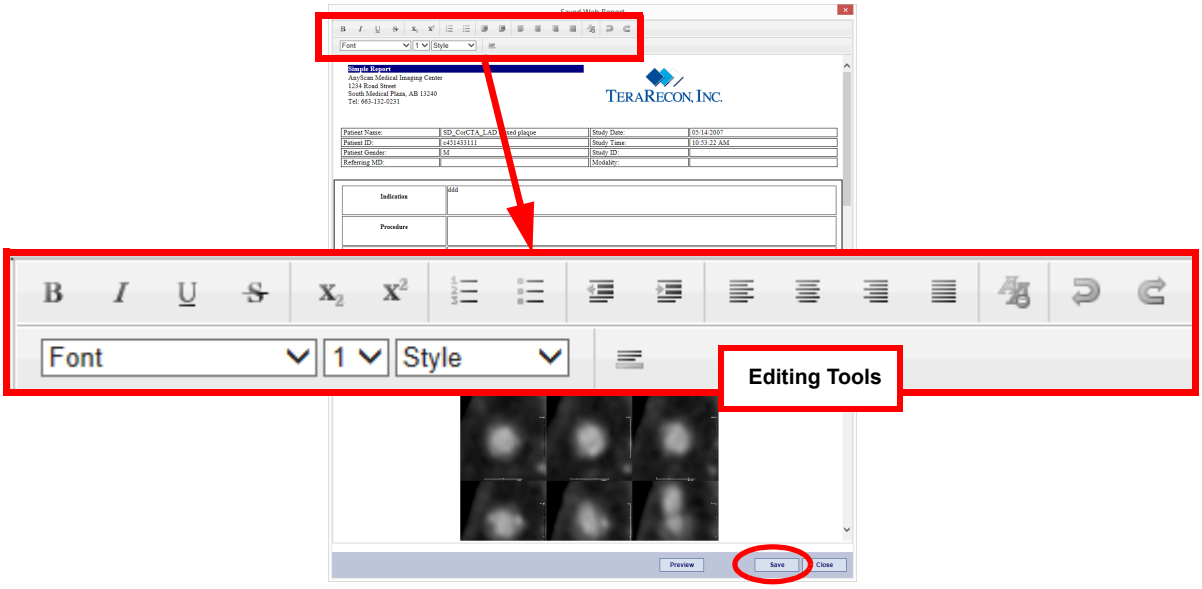
AQi also supports web-based reports, which make it possible to generate reports without having MS Word installed on the client system.

Requirements:

- Internet Explorer, version IE 7 or later, fully updated, installed on the client system.
- Connection to an iNtuition server with IIS 7 or later.

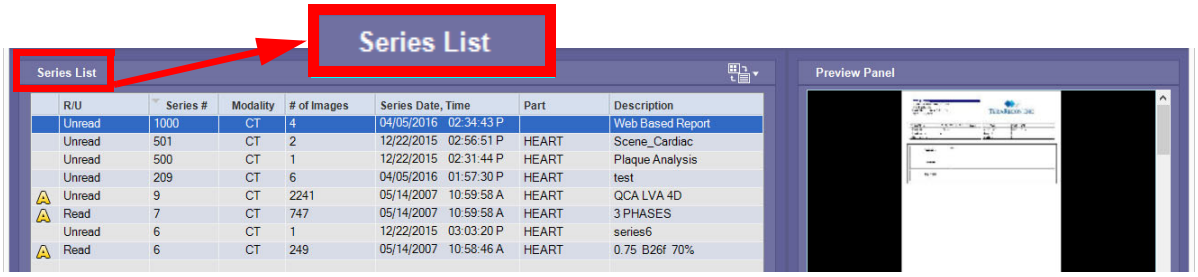
Note: Before you can use this option, it must be configured on the iNtuition Server. Please contact TeraRecon customer support for more information, or to enable the option.

Once configured, a web-based report will be opened, as shown below, when you generate a report. The report templates and languages supported will vary, depending on your software version. If you use a report template that is not supported in web-based reports, AQi will use MS Word to generate the report.



Editing tools are provided on the top (see the previous figure). Click the **Save** button after completion.

Note: The report will be saved as a DICOM file in the Series List.



If you want to edit the report again, double-click the series to open, edit and save again. The revised report will be saved as a new series and will not overwrite the existing one.

Sending Images to a DICOM Server

To send the image to a DICOM Server, do the following:

1. Click the **Send** button. The **Send to Remote Server** dialog opens.
2. Select the desired server, and click **OK**.

Emailing Images

To email the captured images, do the following:

1. Click the **Email** button. This opens a new message in your default email client. The captured images are inserted as attachments to the message.

Note: All images in the Output Panel are sent in the email.

2. Address the message, enter any desired text in the body, and send.

Printing Images

To send captured images to regular or DICOM printers, perform the following:

1. Open the Output Panel, and choose a display format (see Figure 5-2 on page 5-3).
2. Click the **Print** button in the Output Panel. This opens a Windows Print dialog.
3. Set the printer name to any standard printer name on your network**.**
4. Set other desired printing options and click **OK**.

Saving Images to the Hard Drive or External Drive

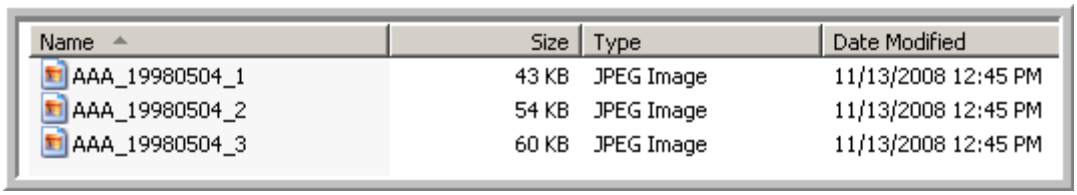
1. Click the Save button in the Output Panel. This opens a Windows folder navigation window.

2. Navigate to the appropriate folder.

3. Choose an output format from the **Save as type** pull-down menu. Formats supported are .JPG, .BMP, .PNG and .AVI.

4. Click **Save** in the Windows dialog.

Note: Each saved file consists of all the images on a single page. Therefore, the total number of saved files equals the number of pages in the Output Panel. The file names are automatically appended with the date stamp and a number to give them distinct names.



Name	Size	Type	Date Modified
AAA_19980504_1	43 KB	JPEG Image	11/13/2008 12:45 PM
AAA_19980504_2	54 KB	JPEG Image	11/13/2008 12:45 PM
AAA_19980504_3	60 KB	JPEG Image	11/13/2008 12:45 PM

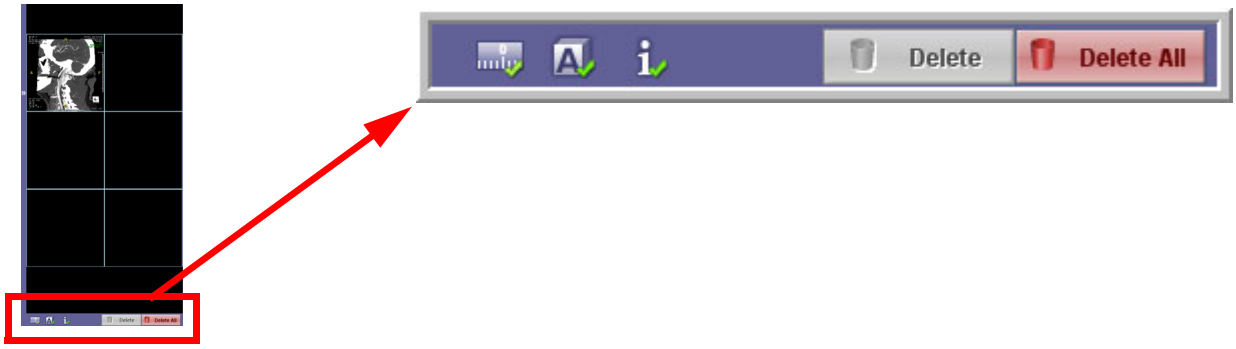
Figure 5-4: Saved Image Files

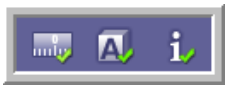
Printing to a Film Printer

This feature allows you to print images to film instead of paper.

Bottom Bar Tools

These buttons duplicate the functionality of menu items found elsewhere in the AQi interface.



Annotations 

- Scale Bar - show or hide the calibrated lines (rulers) at the bottom and right sides of each image.
- Orientation - show or hide orientation information (white cubes in the lower right corner, letters appearing at the top, bottom and sides of each image).
- Annotation - show or hide the annotation text (patient and study information).

When you use these buttons, the symbols or text are shown or hidden on the images in the main viewer as well as those in the Output Panel. For more details, see "Display Annotations Menu" on page 3-191.

Delete Selected Images/Delete All Images 

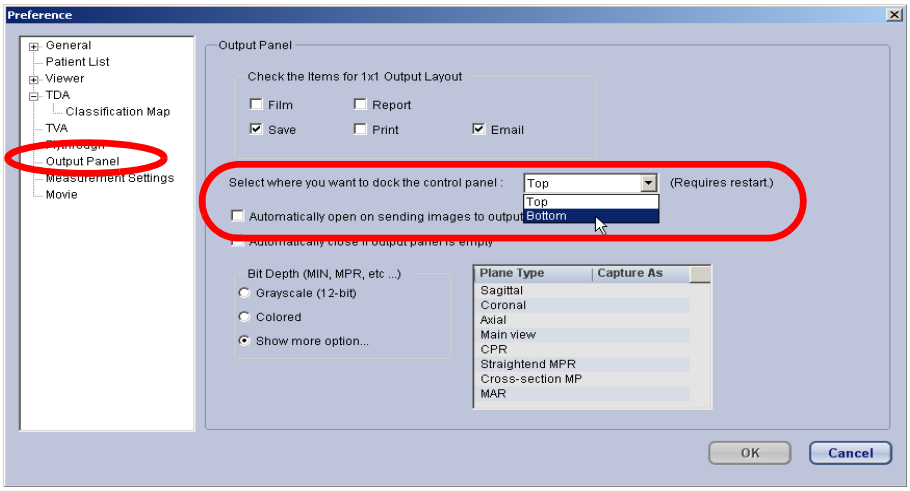
These are the same functions as corresponding items in the image right-click menu. See "Delete Images" on page 5-4 for descriptions.

Positioning the Control Panel

You can choose where the control section of the Output Panel is displayed (at the top or bottom) by changing the setting in the Preferences file. To open the Preferences menu, do the following:

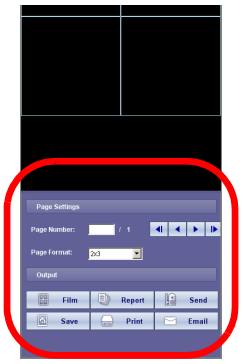
1. Click the Preferences button located on the right end of the top toolbar.

2. In the Preference menu, click **Output Panel** on the left to display the Output Panel preferences.



3. Select the preferred position in the pull-down menu labeled “Select where to dock the control panel”.

   The control panel is now at the bottom (see the image at right).



Note: You must restart the AQi Viewer in order for this change to take place.

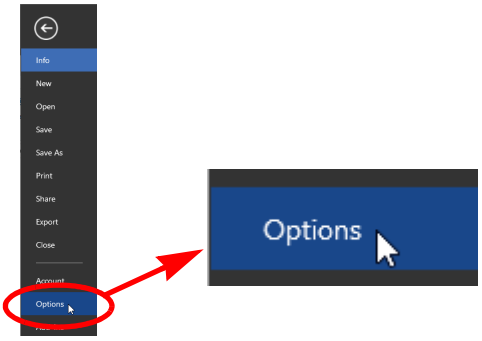
Setting the security in MS Word

Note: These instructions apply to MS Word 2013. If you have a different version of Word, please refer to the user documentation, or contact TeraRecon customer support for help.

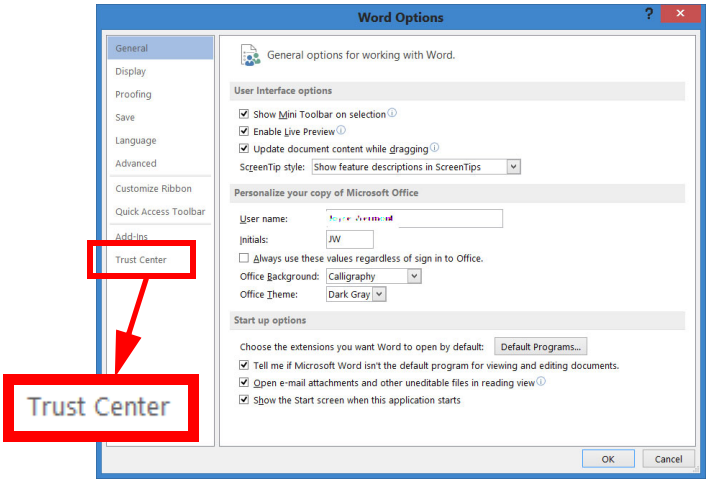
To configure security settings in MS Word, do the following:

1. Open MS Word.

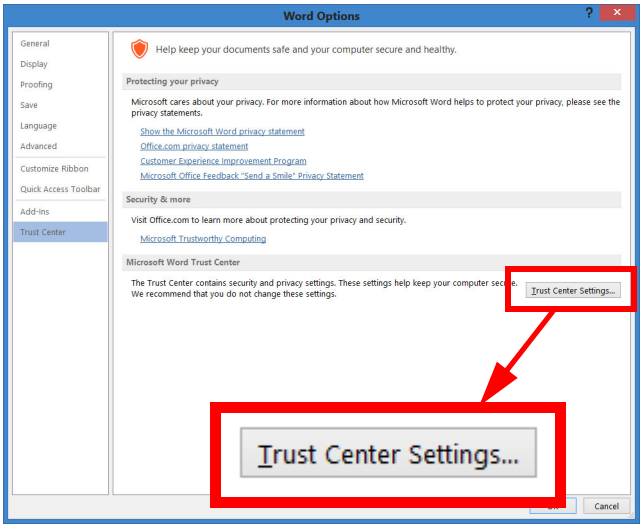
2. Click **File** and select **Options** from the menu (circled in red, in the image at left). This opens the **Word Options** dialog.



3. Click the **Trust Center** item in the menu on the left (circled in green, below).

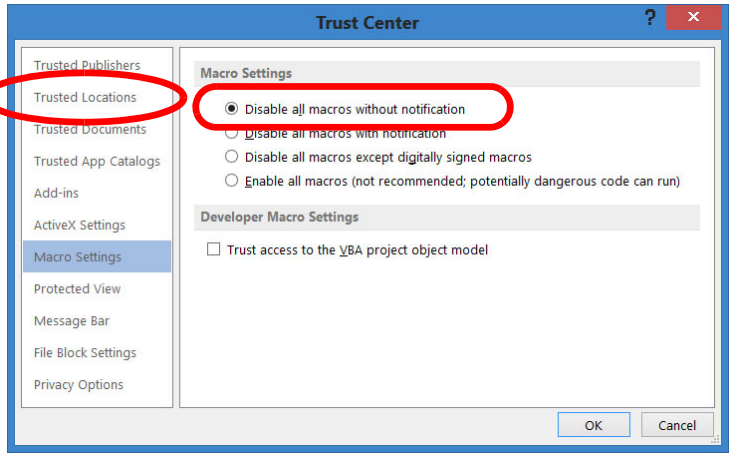


4. Click **Trust Center Settings** in the lower-right corner of the screen shown below:

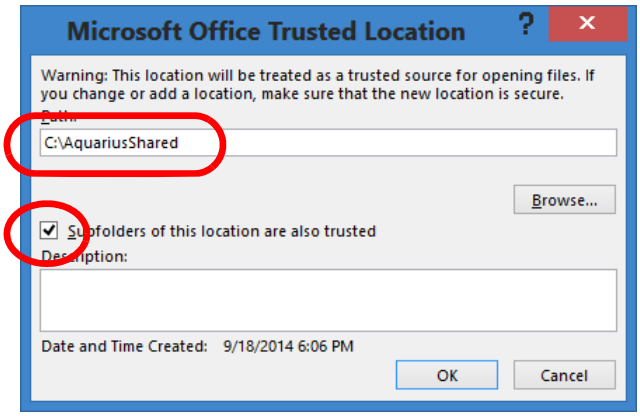


5. Under **Macro Settings**, select **Disable all macros without notification**.

6. In the panel on the left, click **Trusted Locations** (see image below).



The following dialog is opened:



7. In the text input box near the top of the **Microsoft Office Trusted Location** dialog, enter:

   `C:\AquariusShared`

8. Check the box labeled **Subfolders of this location are also trusted**.

9. Click **OK** in this and in any previous dialogs to close them.

10. Exit MS Word.

Chapter 6 TVA and Cardiac Function

Topics in this chapter:

The **Time-Volume Analysis** (TVA) optional module calculates time-dependent behavior of volumes in multi-phase studies from CT. An example of a time-dependent behavior is the change in the volume of the left ventricle of the heart.

Note: The user is obligated to define the wall boundaries in question. Also note that when first accessed, the user interface for wall boundary outline holds generic default values with no significance. You must acknowledge this by dismissing a warning message to this effect.

Starting Time Volume Analysis (TVA) for CT Studies

To load a study for TVA, do the following:

1. From the Patient List, select an appropriate CT study comprised of multiple series or sub-series.
2. Highlight multiple series/sub-series in the Series (or sub-series) List by clicking the desired series or sub-series with the left mouse button, while holding down the **Ctrl** key.

Note: Each series that you select should have the same number of images.

---

3. Load the series/sub-series into the Cardiac Workflow by doing one of the following:
   - Right-click on the desired series and select **Cardiac** from the pull down menu.
   - Click **Load** in the Data Management Tool Buttons (located in the middle-left of the screen), and then click **Cardiac** from the workflow buttons.

TVA of the Left Ventricle (LV)

Click either the **TVA(LV)** tab in the Tool Panel or the **LV EF** Workflow element.

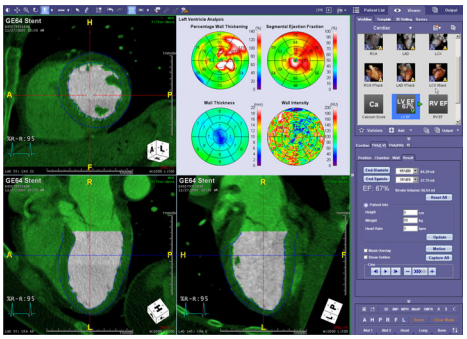
Automatic vs. Manual EF

Ejection fraction on the left ventricle is calculated automatically by default. The measurements are verified to be accurate with artificial digital phantom data. However, clinical data is more complex. You are responsible for verifying the automatic segmentation (overlay and outlines) in both the end-systolic and end-diastolic phases. During this verification process, if the results do not meet expectations, TVA (LV) should be redone manually. The results correlate with the segmentation and will be updated with user specified changes.

Note: It is your responsibility to verify the phases automatically chosen. If the preselected phases do not meet your expectations, proceed to perform TVA manually.

If in general you prefer to perform TVA(LV) manually, you can set a preference so that manual TVA(LV) is started by default. To set the preference, do the following:

1. Click the Preference button in the top bar on the right.
2. The Preference window is displayed. Click on **TVA** in the navigation list and then **LV** in the sub-list to display the TVA(LV) preferences.
3. Check either the Manual, Automatic or Automatic (All Phases) checkbox. (Each selection is explained in the Preference screen.)

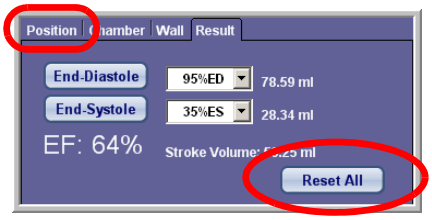


The change will take effect the next time you start TVA(LV). For more details about TVA(LV) preferences, see "TVA(LV)" on page A-35

In automatic TVA(LV), the LV EF value is shown on the **LV EF** Workflow element when the calculation is completed.

Performing Manual TVA(LV)

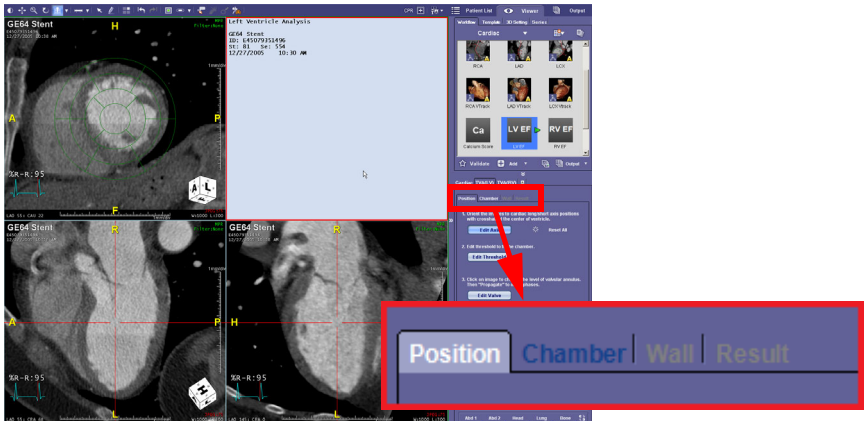
The Ejection Fraction on the left ventricle is calculated automatically when the module is invoked. However, you might prefer to perform TVA manually so that you can supply the positioning, threshold and segmentation data yourself.



Manual TVA(LV) is comprised of the following steps:

- Positioning the images and defining the threshold.
- Segmenting the volume of interest.
- Making sure that the wall of the structure under analysis is correctly marked.
- Viewing and interpreting the results.

To begin manual TVA(LV), click the **Position** tab or the **Reset All** button at the top of the Tool Panel (see the image below).

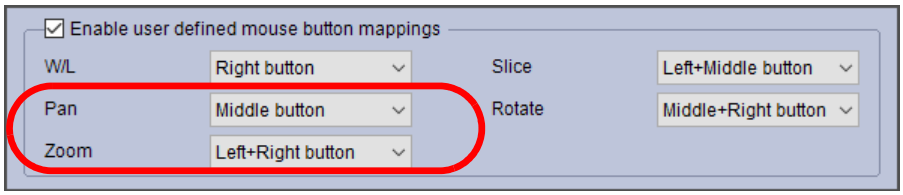


Mouse Operations in TVA

In the following steps of TVA, you can pan and zoom images:

- In the Position tab, in Edit Axis mode only
- In the Chamber, Wall and Result tabs

When the pan and zoom functions are defined in the user-defined mouse button settings, they also work in the above tabs.



In the previous example of user-defined mouse button settings, you can hold down the middle mouse button to pan the image, and you can use the left+right button combination to zoom, when working in the appropriate tabs.

Step 1 - Positioning and Threshold

The **Position** tab allows you to do the following:

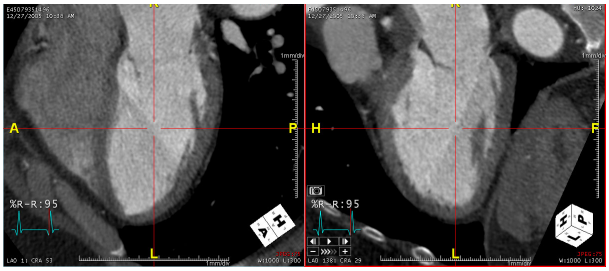
- Position the axis
- Edit the threshold of the contrast area
- Position the valvular annulus

Positioning the Axis

1. Click the **Edit Axis** button in the Tool Panel.

2. Move the mouse over one of the two long-axis views. The cursor changes to a rotation icon to indicate that you can now rotate the image.

3. Rotate the image so that the long-axis image displays the standard position, with the crosshairs at the center of the left ventricle (see the following image).

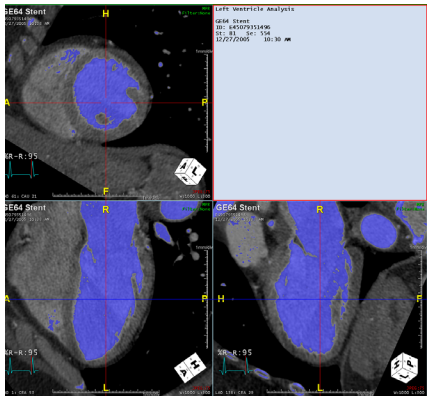


When you are satisfied with the positioning, click the **Edit Threshold** Button.

Editing the Threshold

The Aquarius iNtuition Client automatically applies the threshold to all the frames. Examine the threshold to make sure it is applied properly, and that the mask best fits the chamber.

To adjust the level of overlay, click in the box labeled **Min**, and use the mouse wheel to change the value. The following figure shows the threshold properly adjusted.



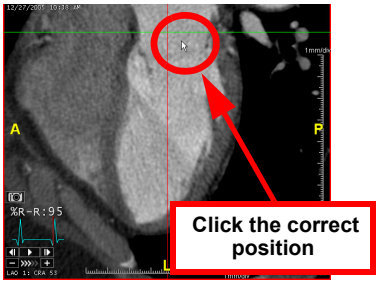
When the threshold has been properly adjusted, click the **Edit Valve** button.

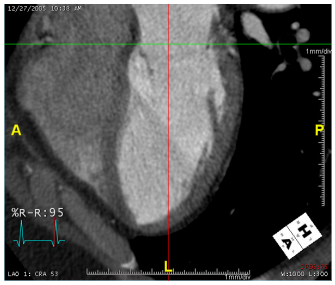
Positioning the Valvular Annulus

The position of the valvular annulus is calculated internally, and is then displayed on the long-axis views with a horizontal green bar.

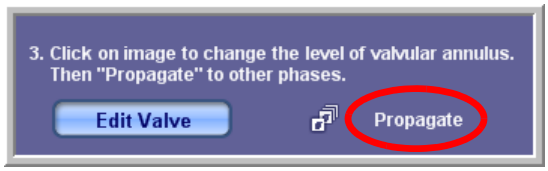
1. Examine the position of this bar in every phase to verify that it is correct.

2. If any is incorrect, adjust the level of valvular annulus by moving the mouse over the long-axis view that contains the error, and clicking on the place where the bar should be (see the following figure). The bar moves automatically to the selected position.





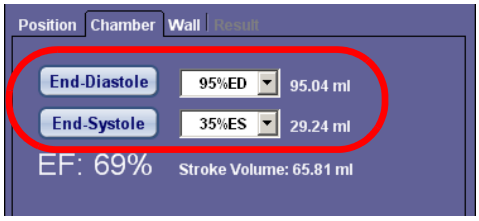
Click the **Propagate** button (shown at right) if you want the valvular annulus to be adjusted automatically in all phases.



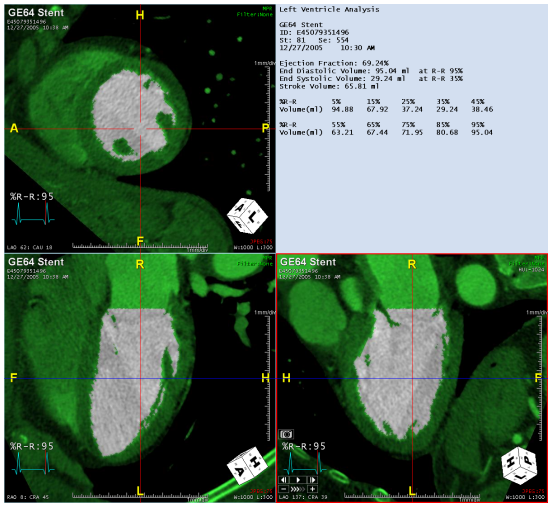
3. When you are ready, click the **Next** button located at the bottom of the Tool Panel, to advance to the **Chamber** tab.

Step 2 - Chamber Segmentation

The **End-Diastole** and **End-Systole** phases have been identified automatically and are displayed at the top of the tool panel (see the following figure). The Ejection Fraction value has also been calculated and is displayed just beneath.



The images are displayed in the main window, as shown below:



By default, the green overlay shows areas that have been removed by previous functions. If you would prefer to see the overlay on the areas inside the chambers, you can change that in the Preferences menu.

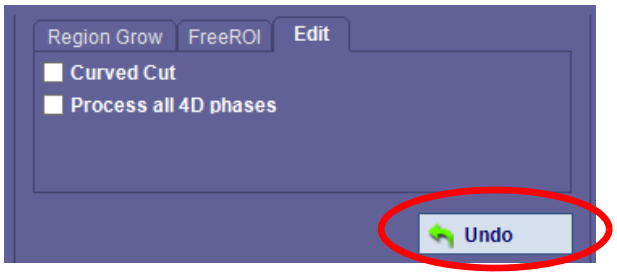
1. Click the **Preferences** button in the top bar (see 6-2).
2. When the Preferences window opens, click **Viewer**, which opens a sub-menu underneath.
3. Click **Mask** in the sub-menu.
4. In the Mask preference window, *uncheck* the box that says **Overlay on Removed Area**.
5. Click **OK**.

For more information about TVA(LV) preferences, see "TVA(LV)" on page A-35.

When this box is unchecked, the overlay displays only on the remaining area, after segmentation.

1. Check each phase of the series to verify that the segmentation was performed correctly.
2. If you are not satisfied with the automatic segmentation on any phase, you can do one of two things:
   - Perform manual mask operations using the editing tools. These include **Dynamic Region Growing** (DRG), **FreeROI** and the **Edit** panel, as shown below. For instructions on DRG, see "Dynamic Region Growing" on page 3-53. For FreeROI, see "FreeROI" on page 3-49.

Note: Free ROI can be performed only on the short-axis view. However, you can perform DRG on any of the images.



There is a keyboard shortcut for region growing: **Shift**+**Ctrl** and left-mouse. Hold down the mouse to grow the desired region.

The **Undo** button (see image above) undoes any mask operation.

- You can also recalculate the segmentation by adjusting the valvular annulus again on that phase. Do this by clicking the **Previous** button at the bottom of the tool panel. The Position window is displayed.

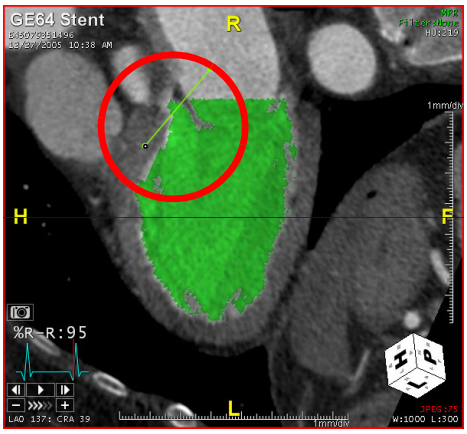
  Adjust the valvular annulus on any phase that was not correctly segmented, and click **Next** to come back to the Chamber window.

3. If the segmentation included any part of the heart that should not be considered part of the chamber, you can cut it out manually by doing the following:

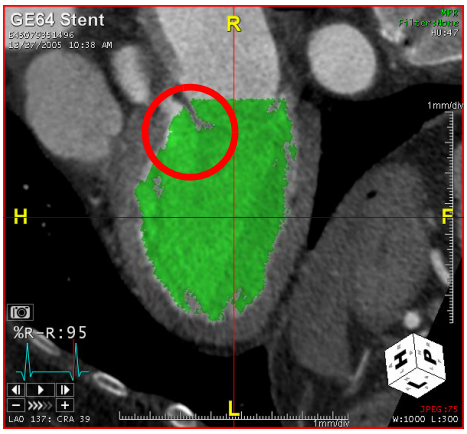
   a. Hold down the shift key and click on the image.

   b. Draw a line along the image so that it separates the part you want to keep from the part you are cutting out.

   c. Release the mouse to begin the cut.



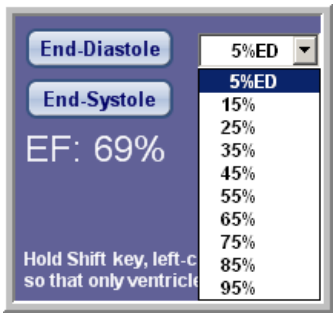
Drawing Cut Line



After Cut

Figure 6-1: Cutting

4. Check each phase of the series to verify that the end-diastole and end-systole are correctly identified. If they are not, you can change them by selecting the correct value from the pull-down menu beside the current value (figure image below).



5. When you are ready, click **Next**.

Step 3 - Wall Correction

The LV chamber from the Chamber stage has been wrapped and smoothed to generate the inner surface. The papillary muscles have been filled out in order to calculate the myocardial thickness. The software automatically expands the inner surface to fit the next contrast change, and the result is the outer surface. It may be incorrect when there is not enough contrast, in which case it needs to be corrected manually.

In this step, perform any corrections necessary to ensure that the ventricle wall has been properly segmented. You need do this only for the End-Diastole and End-Systole phases, as those are the only phases needed for calculations that are done from this point on.

In addition, corrections made in this step affect the wall thickness/thickening and the myocardial volume only. Ventricular volumes and ejection fraction have already been determined in the previous step.

To perform corrections in the wall, do the following:

1. Use the End-Diastole and End-Systole buttons to display these phases.

Note: The end-diastole and end-systole phases cannot be changed in this tab.

---

2. Rotate the image to examine the wall, to verify that it was correctly drawn. If some portions are not correct, you can redraw this sections manually.

Figure 6-2: Left: Boundary Lines Not Correct; Right: Redrawing Wall

Hold the **Shift** key and do multiple clicks along the edges of the wall to redraw the wall in the correct place (see the image on the right in Figure 6-2).

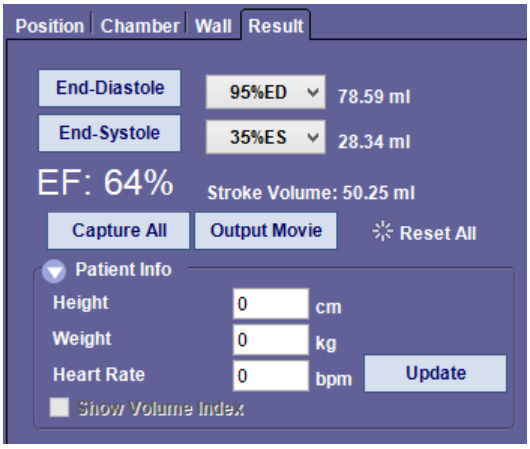
3. When you have finished placing correction dots along the incorrect section of wall, release the shift key to trigger the automatic redraw.

Note: You might need to do this several times to get the boundary lines in the exact place you need it to be.

4. Click **Next** to proceed to the final step.

Step 4 - Calculation and Result

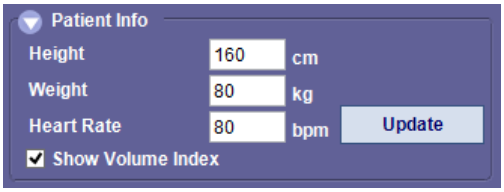
In this step, the cardiac function is calculated and the results are displayed by the software (see figure below).



Presentation of TVA(LV) Results

You can now view tables, graphs, and polar maps of the segmental ejection fraction, wall thickness, and other parameters.

1. To generate these displays, first enter the patient's height, weight, and heart rate into the Patient Info fields.



2. Click the **Update** button. The manual TVA(LV) result window is displayed.

Volume Index

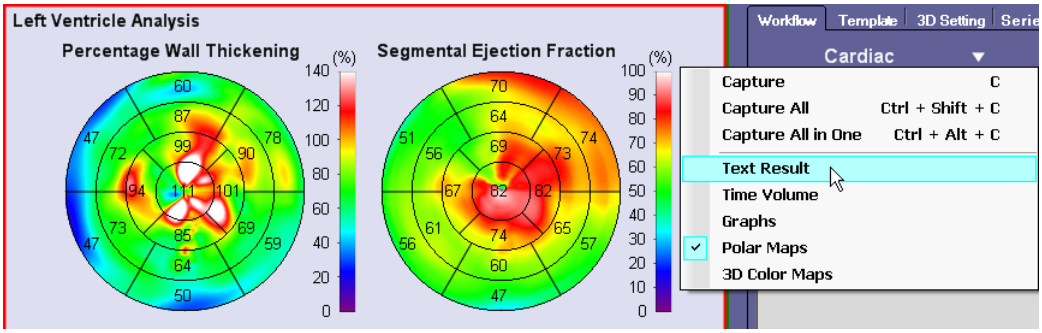
The volume index is the volume (in ml) divided by the total body surface area (BSA). BSA is calculated from the height and weight of the patient, and expressed in square meters.

To show the volume index, click the **Show Volume Index** checkbox in the **Patient Info** section of the tool panel. The results are updated in the tool panel, which show the volume index for the end-diastole and end-systole phases. Volume index values are also shown in the text results in the main window:

```
Ejection Fraction: 63.94%

End Diastolic Volume: 78.59 ml  at R-R 95%
End Systolic Volume: 28.34 ml   at R-R 35%
Stroke Volume: 50.25 ml
Cardiac Output: 4019.93 ml/min

End Diastolic Volume Index: 42.87 ml/m²  at R-R 95%
End Systolic Volume Index: 15.46 ml/m²   at R-R 35%
Stroke Index: 27.41 ml/m²
Cardiac Index: 2193.06 ml/min/m²
```

You can review different TVA(LV) results in different formats, including text, as a time-volume curve, as a graph, or as a polar map. To change the format for displaying data, do the following:

1. Right-click on the polar map, displayed in the upper-right corner of the main window (see the following figure). This displays a pull-down menu.



2. Select a display format from the menu.

Note: The results vary for each frame. Click on each frame using the Cine buttons to view the corresponding data.

Polar Maps

A polar map shows the distribution of an index on the surface of the left ventricle. The middle corresponds to the apex and the border corresponds to the base. Orientation is the same as the short axis image. Only slices containing myocardium in all 360° are selected. The polar map is divided into 17 segments and an averaged value is labeled on each segment. The segmentation of the polar map conforms to AHA's standard. See the following article for details:

- *AHA Scientific Statement: Standardized Myocardial Segmentation and Nomenclature for Tomographic Imaging of the Heart (Circulation 2002;105:539-542*).
- http://circ.ahajournals.org/cgi/content/full/105/4/539

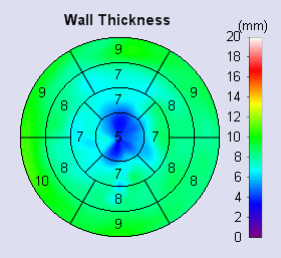
The following are views of different TVA(LV) results in polar maps.

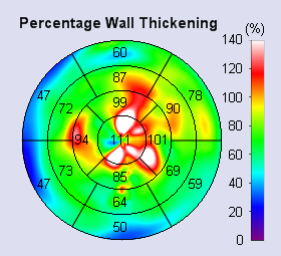
Wall Thickness and Wall Thickening

With the ventricular wall segmented, the wall thickness can be measured automatically, anywhere on the wall. The percentage wall thickening is calculated from the end-systolic wall thickness (Ws) and end-diastolic wall thickness (Wd), as follows:

Percentage wall thickening (%) = (Ws - Wd) / Wd X 100

This formula is valid anywhere on the wall.

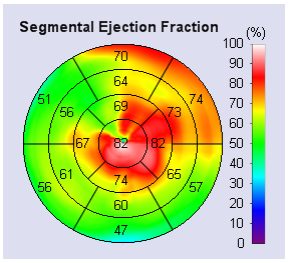


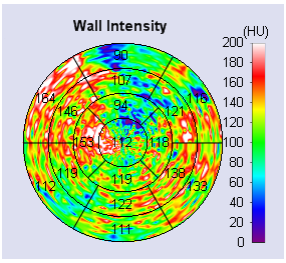


Segmental Ejection Fraction and Wall Intensity

On the short-axis image, the chamber is divided into many sectors in which segmental ejection fraction is calculated. Compared with global ejection fraction, segmental ejection fraction is a regional property that reveals how much blood under a piece of muscle is pumped out.

The wall intensity is sampled at the middle layer between the inner wall and the outer wall. Voxels away from the middle are not sampled because they are subject to partial volume effect and do not reflect the true intensity of the myocardium.





Note: Double-click on the Polar Map display to toggle between single-image view (1x1) and 4-in-1 view.

3D Polar Maps

To view any of the polar maps in 3D, right-click on the desired map and select **3D Color Maps**. The polar map is displayed in 3D. (Figure 6-3)

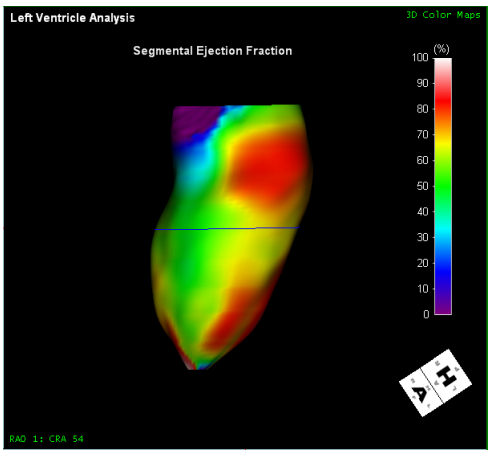
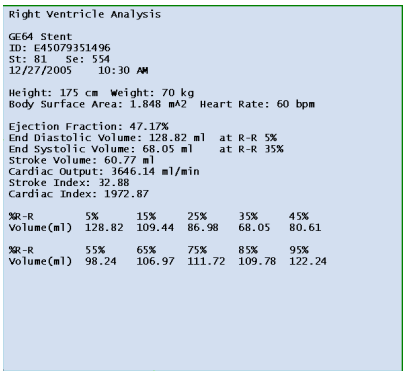


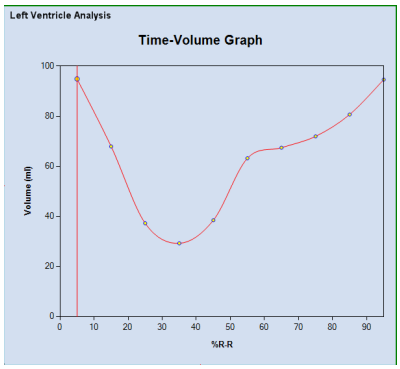
Figure 6-3 3D Polar Map

To return to the 2D polar maps, right-click and select **Polar Maps**.

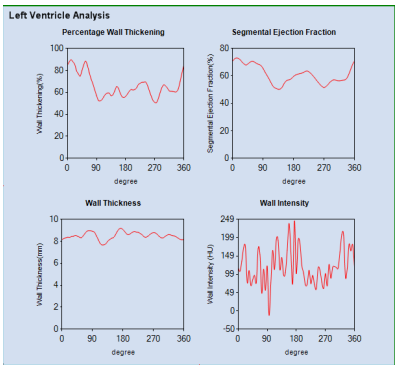
Text and Graphs



Text of TVA(LV) Values



Time-Volume Graph



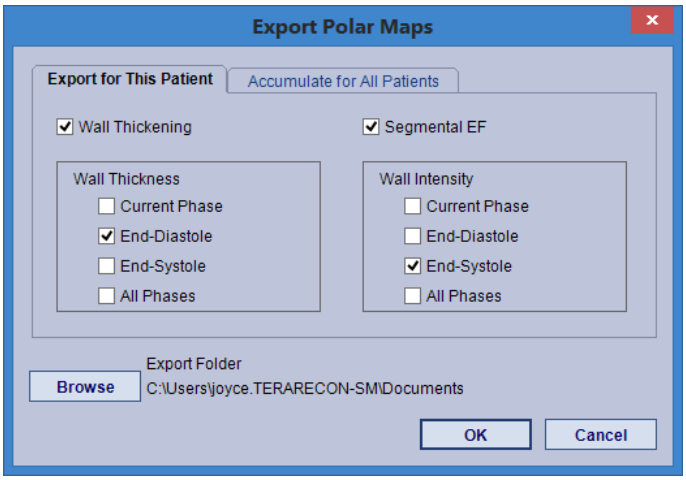
The Four Graphs in TVA(LV)

Figure 6-4:Viewing Text and Graphs

Export Polar Map Values to File

This feature allows you to export the numerical values in any of the AHA-17 segmented maps to a .csv file.

1. Right-click on the polar maps view and select **Export Polar Maps** from the menu. A dialog is opened where you can select maps, phases and types of data.



2. To export data related to this patient only, click the **Export for This Patient** tab.

3. To export Wall Thickening or Segmental EF values, check the boxes for those results.

4. For Wall Thickness or Wall Intensity values, you can chose to export data from one or more phases. Check any combination of **Current Phase**, **End-Diastole** or **End-Systole** as desired. You can also choose **All Phases**.

5. To select an export folder, click the **Browse** button and navigate to the desired folder. The default export folder pathname is displayed on the dialog. If that folder is acceptable, you can skip this step.

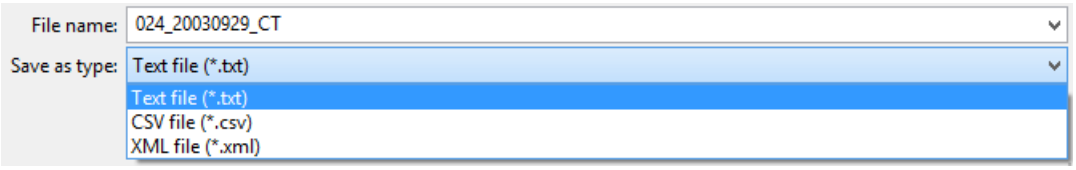
6. Click **OK** to export. Each polar map selected for export is saved in a separate file. In addition, all exported maps are saved in one composite file, named *patient-ID_study-date_modality*.csv.

64-SLICE CCTA	CFA	CACS															
ID: CARDIAC																	
St: 17106 Se: 14																	
5/3/2006 11:20																	
	Segment:	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
WallThickening		30		29	103	132	107	110	27	38	136	113	94	133	39	113	90
SegmentalEF		56	55	53	55	62	64	54	58	64	65	56	56	57	68	64	53
WallThickness	at R-R 0%	6	13	11	5	5	5	6	13	12	5	5	5	5	10	4	5
WallIntensity	at R-R 40%	118	114	104	110	124	133	112	109	110	120	126	119	113	124	138	108

To export accumulated data for all patients, click the corresponding tab in the dialog. The selections in this tab are the same as for single-patient exports, so you can follow the same instructions as above. The output will show aggregate values based on other files previously exported into the same folder.

Export Text Result to File

You can save the text results in text format, or as a CSV or XML file. To do so, right-click on the text display and select **Export Text Result to File**. A Windows dialog is opened for you to select or enter a file name, navigate to the save folder, and select the file type. Click **Save** to create the file.



Captures

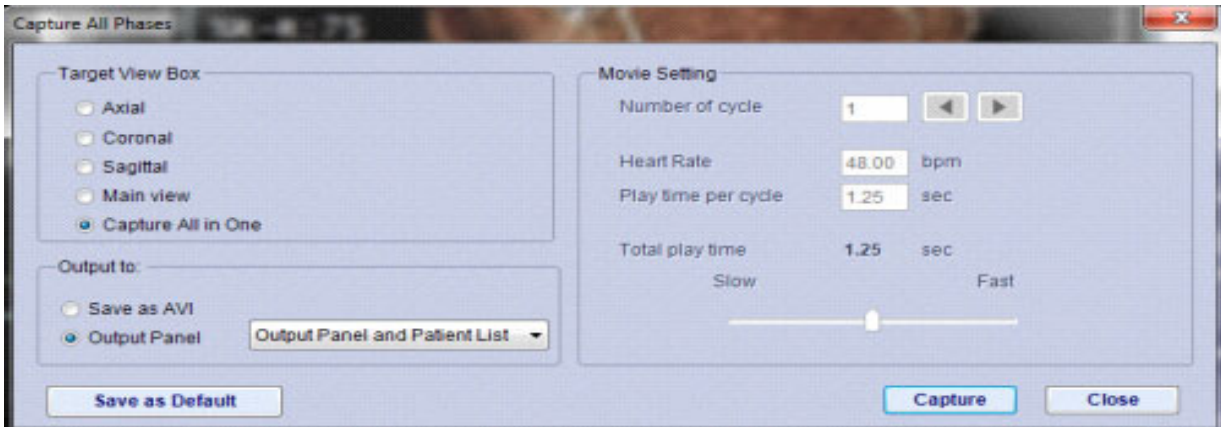
Right-click on the image to open the pulldown menu. The following table describes each type of capture in the menu.

Table 6.1: Capture Menu

Menu Item	Function
Capture	Capture the selected image.
Capture All	Capture all images currently displayed in the viewer, and place each image in a separate cell in the Output Panel.
Capture All in One	Capture all images currently displayed in the viewer, and place them all in a single cell in the Output Panel.
Capture All Phases (4D only)	Capture all phases of the selected view. The images can also be exported as an AVI movie. See "Output Movie" on page 6-14 for a full description.
Capture to Folder	Capture to a folder defined in the Capture preferences.

Output Movie

You can export a captured set of images showing all phases of a view, and save it as an AVI movie. To do so, click the **Output Movie** button in the tool panel. The **Output Movie** dialog opens:



1. Under **Target View Box**, select the view to be captured: the axial, coronal or sagittal 2D image, the result window (the upper-right quadrant of the main window), or all images in one.

Note: The movie will contain some or all of the images that are on the screen at the time you begin the capture.

2. To output a movie, select **Save as AVI** in the **Output to** section.

Note: You can also use this dialog to send the images to the Output Panel. This does not create a movie.

3. Set the number of cycles and the speed of the movie in the **Movie Setting** section. The play time per cycle means the length of time it takes to play a full cycle, and the total play time is calculated from those inputs. For example, if you set the number of cycles to two and the play time per cycle to 1.25, the total play time will be 2.5 seconds. However, you can use the slider to shrink the total play time, without chaning the time per cycle. This will also shrink the amount of time that each cycle takes to play.

4. Save this configuration as the default, if desired.

5. Click **OK** to begin capture.

Calculation Algorithms

The values calculated are defined as follows:

Left Ventricular Volume: The Left Ventricular chamber is segmented using the threshold, the level of valvular annulus, and the cutting. Next, the Left Ventricular volume is calculated by multiplying the number of voxels in the chamber with the volume of a single voxel.

Table 6.2: Formulas for Other TVA(LV) Values

Value	Formula
Left Ventricular Stroke Volume	LV End Diastolic Volume - LV End Systolic Volume
Left Ventricular Stroke Index	(Stroke Volume) / (BSA)
Left Ventricular Cardiac Output	(Stroke Volume x Heart Rate) / (1000)
Left Ventricular Cardiac Index	(Cardiac Output) / (BSA)
Ejection Fraction	((LV End Diastolic Volume - LV End Systolic Volume) * 100) / LV End Diastolic Volume

Myocardial Volume - The myocardial volume is calculated at the end diastolic phase using the total volume from the outer surface minus the ventricle volume (by threshold and cutting).

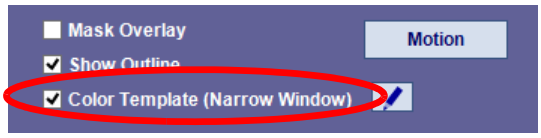
To perform wall analysis, open the **TVA(LV)** Preferences window and check the box labeled **Perform Wall Analysis (for myocardial mass, wall thickening, etc.)**. You can also enter the Myocardial Density in a text-

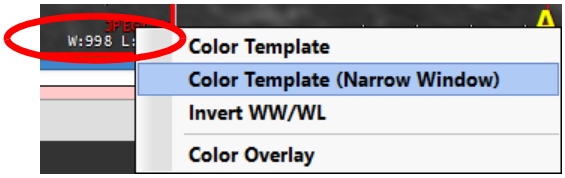
input box in the same window. (For instructions on how to open the TVA(LV) Preference window, see "TVA(LV)" on page A-35.)

Color-Coded Intensity Visualization

After TVA of the left ventricle has been completed, you can view the wall intensity on the 2D images. There are three ways to access the color template:

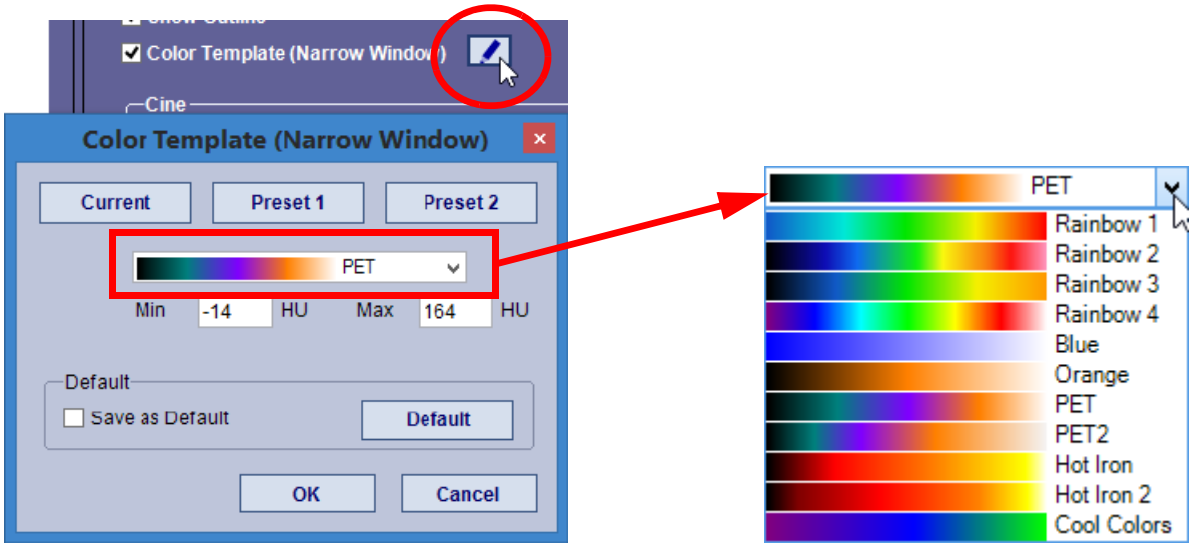
- Check **Color Template (Narrow Window)** checkbox in the TVA Result panel
- Check **Color Template (Narrow Window)** checkbox in the W/L tool panel
- Right-click on the W/L annotation on the image and select **Color Template (Narrow Window**)





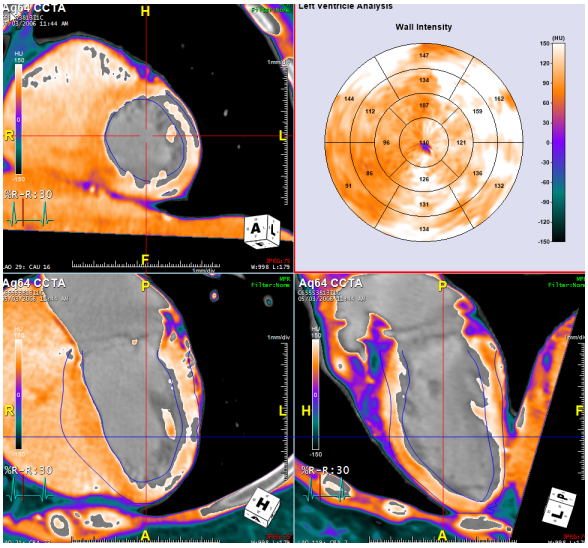
Selecting a Different Color Template

To use a different color template for this overlay, click the edit icon next to **Color Template (Narrow Window)** in the tool panel (circled in the following figure). The Color Template dialog is opened:



This dialog allows you to change the color template to one of the Preset templates, or to a template in the pulldown menu. You can also reset the HU range using the input boxes in the dialog.

Click **OK** to display the color overlay on the images (see figure below).



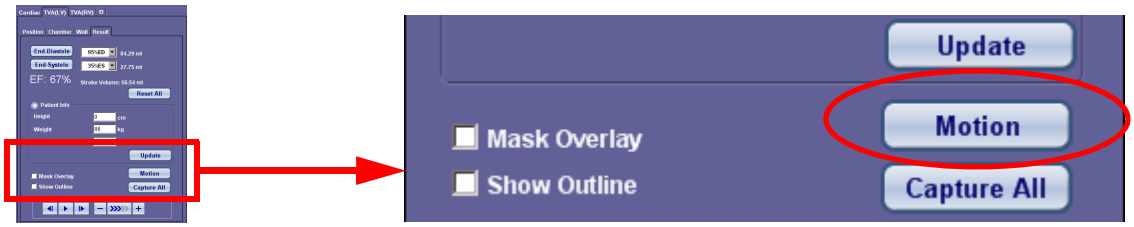
Colored Motion Maps

Colored motion maps show the motion of blood at the systolic and diastolic phases. This feature is most useful for capturing images to send to a colleague who does not have access to a 4D cine of the study.

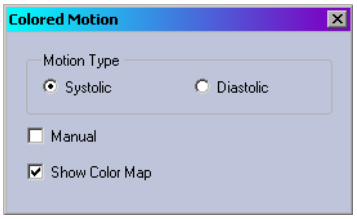
Note: This feature should be applied after TDA (either manual or automatic) has been performed.

---

1. To show colored motion, click the **Motion** button in the Tool Panel:

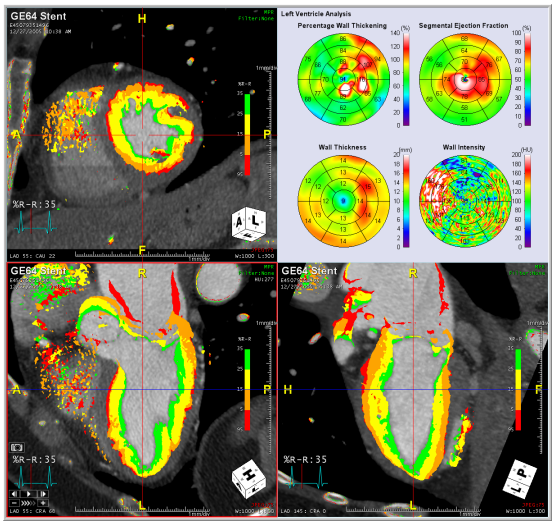


The **Colored Motion** dialog box is displayed, as shown below:



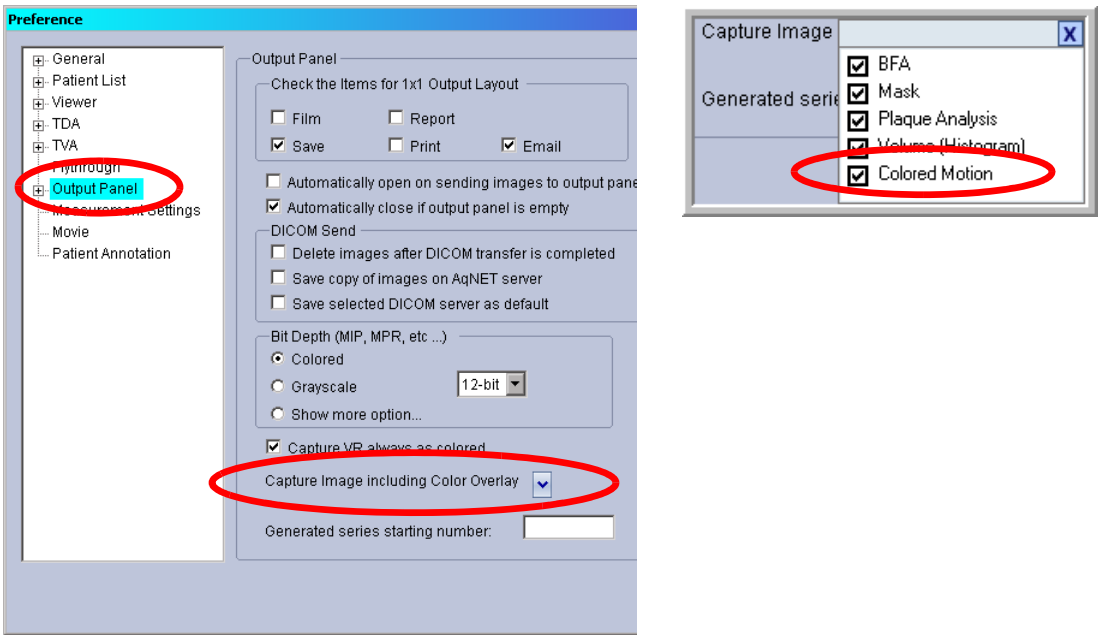
Systolic motion is selected by default. The cine is played automatically, stepping through each phase of the study until the end-systole phase is reached. At that point, the cine stops and the color is overlaid.

Note: To show crosshairs during cine, enable this in Preferences in Viewer > Setting 2 by checking "show crosshairs and bounding box during cine".



2. Before capturing images to the Output Panel, verify that colored motion overlays are included with captured images.

    1. Open the Preferences tool.
    2. Click **Output Panel** in the navigation panel on the left.
    3. Click the down arrow just to the right of the text reading **Capture image including Color Overlay**.
    4. Check the **Colored Motion** box, if it is not already checked.
    5. Click **OK** to exit Preferences.



6. Capture images to the Output Panel.

You can show the colored motion overlay for the end-diastole phase by clicking **Diastolic** in the **Colored Motion** dialog. To hide the color overlay, uncheck **Show Color Map** in the **Colored Motion** dialog.

TVA of the Right Ventricle (RV)

A different procedure is needed to analyze the volume change of the heart's right ventricle.

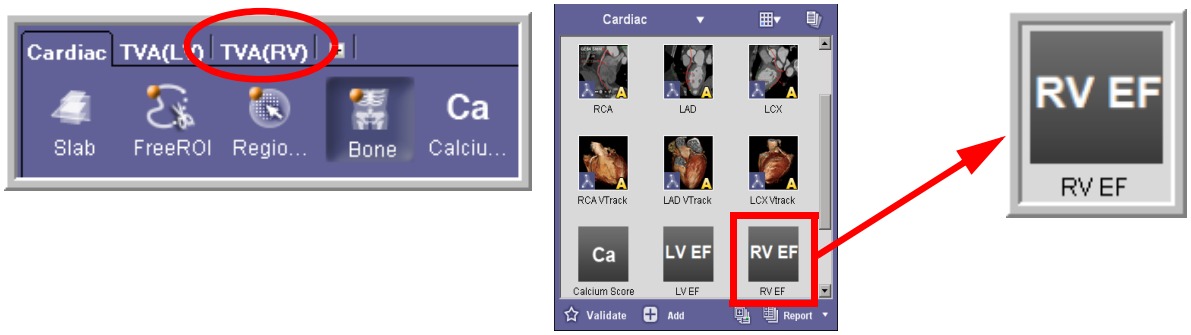
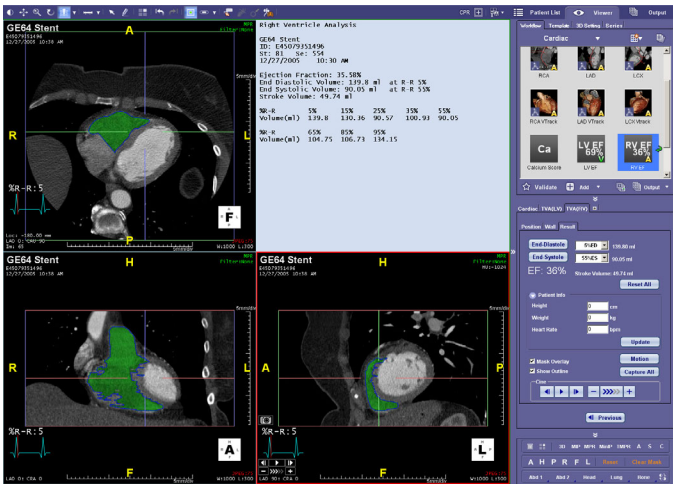


Figure 6-5: Left: TVA (RV) Tab in Tool Panel; Right: RV Ejection Fraction Workflow Element

The right-ventricle ejection fraction is calculated automatically when the RV EF or TVA(RV) module is invoked.



You are responsible for verifying the automatic segmentation (overlay and outlines) in both the end-systolic and end-diastolic phases. During this verification process, if the results do not meet expectations, TVA (RV) should be redone manually. The results correlate with the segmentation and will be updated with user specified changes.

Note: It is your responsibility to verify the phases automatically chosen. If the preselected phases do not meet your expectations, proceed to perform TVA manually.

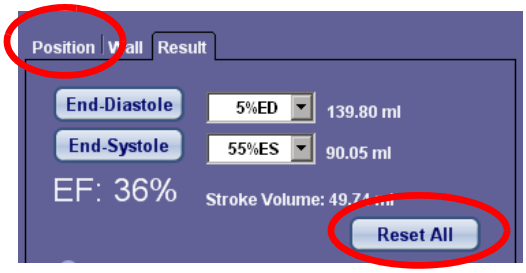
Performing Manual TVA(RV)

In some cases, you might prefer to perform TVA(RV) manually so that you can supply the positioning, threshold and segmentation data yourself.

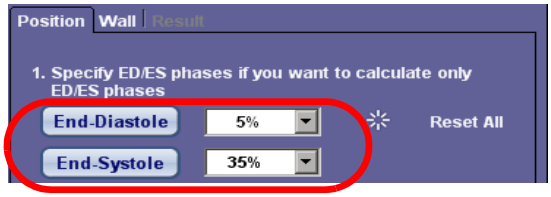
Manual TVA(RV) is comprised of the following steps:

1. Positioning the images and defining the threshold.
2. Segmenting the volume of interest.
3. Making sure that the wall of the structure under analysis is correctly marked.
4. Viewing and interpreting the results.

To begin manual TVA(RV), click the **Position** tab or the **Reset All** button in the tool panel (see figure below). The Manual TVA(RV) window is displayed.



Step 1 - Positioning and Threshold



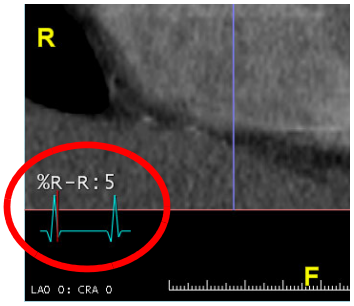
The **Position** tab allows you to do the following:

- Select the best phases to mark as end-diastole and end-systole.
- Mark the positions of the aortic root, the left ventricle and the proximal RCA.
- Edit the threshold of the contrast area.

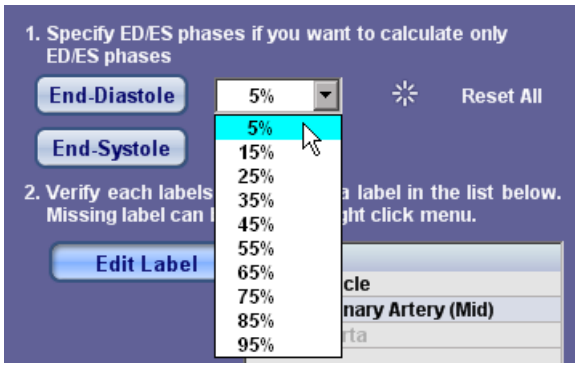
Selecting End-Diastole and End-Systole

1. Choose an MPR image that has the best view of the chamber wall and hover the mouse over that image so that the cine buttons are showing. (Alternatively, you can use the cine buttons in the tool panel, as shown in the image at right.)

2. Using the step-forward cine button, examine the chamber wall in each phase to determine which one is largest (the most full). This should be the end-diastolic phase. (See the following image.)



3. If the phase designated as **End-Diastole** in the tool panel (see buttons circled in red in the image above) is different from the phase you have determined to be end-diastole, select the correct value from the pulldown menu beside the **End-Diastole** button (see the following image).



4. Repeat steps (2.) and (3.) to verify the end-systole phase.

5. When you are satisfied with the positioning, click the **Edit Label** Button.

Editing Labels

This section allows you to verify that the labels placed on the images are correct. If they are not, you can move them to the right place.

For example, to verify the RCA label and, if necessary, move it, do the following:

1. Click the **Right Coronary Artery (Mid)** item in the **Label** list (see the following image).

2. The right coronary artery is labeled **RCA** on the lower-left MPR image. If it is correct, you are finished with this step.

3. If the RCA is incorrectly labeled, move it by doing the following:

   a. Hold the **Shift** key

   b. Click on the label and drag it to the right location.

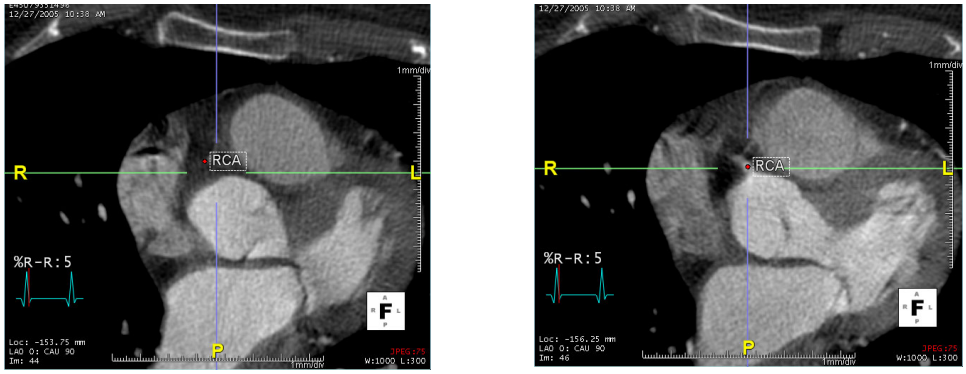


Figure 6-6: Left: Label in Incorrect Place; Right: Label Corrected

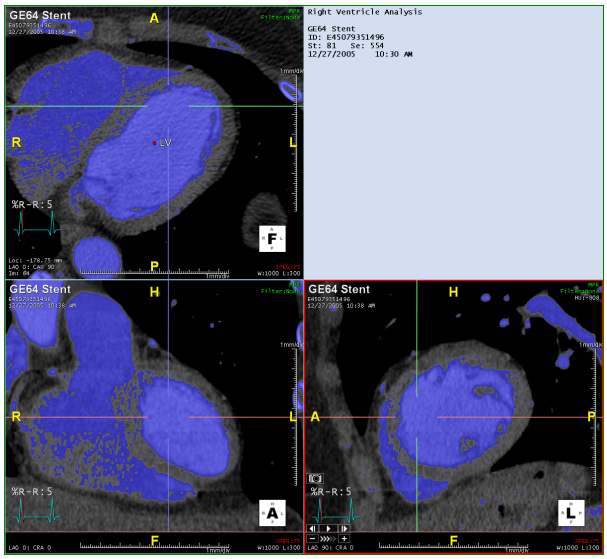
4. Repeat the previous three steps for the **Left Ventricle** and **Aortic Root** labels.

Editing the Threshold

The Aquarius iNtuition Client automatically applies the threshold to all frames. Examine the threshold to make sure it is applied properly, and that the mask best fits the chamber.

Click the **Edit Threshold** button. To show the overlay, check the **Overlay** box. Use the slider to change the mask area on the images. You can also enter minimum and maximum HU values in the **Min** and **Max** input boxes.

In the figure below, the threshold has been properly adjusted:



When you are satisfied with the threshold coverage, click the **Next** button in the tool panel.

Step 2 - Wall

If there is insufficient contrast, the segmentation may be incorrect. If so, you will need to make corrections manually.

You can make corrections in every phase, but only the end-diastole and end-systole phases are required for the ejection fraction calculations. However, for each phase in which you do make corrections, you

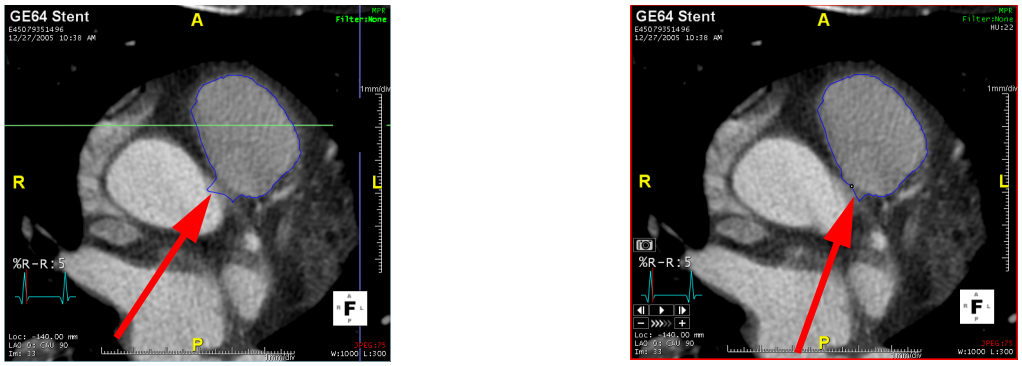
must correct **every slice** that has segmentation boundaries drawn. The right ventricle is too irregular for slice interpolation.

To perform wall corrections in the end-diastole and end-systole phases, do the following:

1. Click the **End-Diastole** button to display that phase in the MPR windows.
2. Find the first slice in the phase that has a segmentation boundary drawn on the image.
3. Correct each slice in that phase by doing the following:

    a. Hold down the **Shift** key and, using the mouse, redraw the wall along the correct boundary (see the image on right in Figure 6-2).

    You can make as many corrections as needed on a single slice. Release both the mouse and the **Shift** key between each line you redraw.

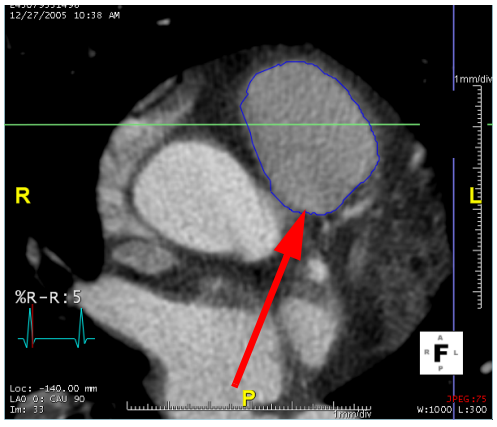


Incorrect Boundary Line Redrawing Wall

Figure 6-7: Left: Correcting Slices

    b. When you have finished redrawing the slice, use the middle mouse button to advance to the next slice.

    c. Repeat steps (a.) and (b.) until all slices in the phase have been corrected.



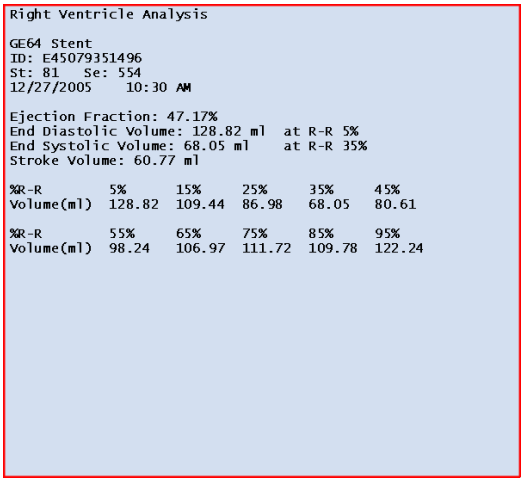
4. Click the **End-Systole** button, and repeat steps (2.) and (3.) to correct all the slices in the end-systole phase.

Note: If you choose to correct the wall boundary in every phase, you will need to step through the phases using the cine buttons in either the tool panel or in lower-left corner of the image window (see the previous image).

When finished with all corrections, click **Next** to proceed to the final step.

Step 3 - Calculation and Result

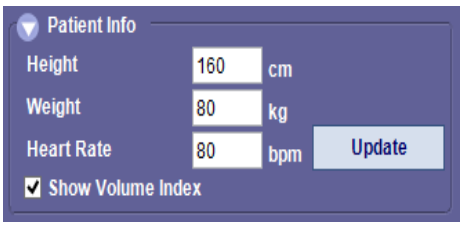
In this step, the cardiac function is calculated and the results are displayed in the tool panel. More detailed results are displayed in the upper-right portion of the main window (see the following figure).



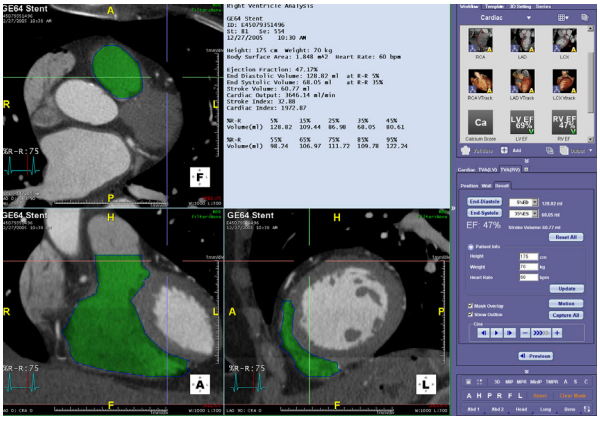
Presentation of the TVA(RV) Results

You can now view a more complete table and a graph of the segmental ejection fraction, wall thickness, and other parameters.

1. To generate these displays, first enter the patient's height, weight, and heart rate into the Patient Info fields.

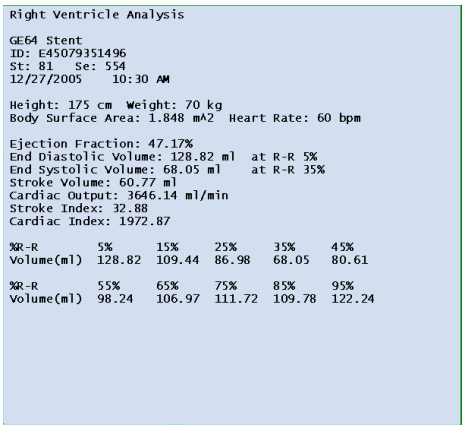


2. Click the **Update** button. The manual TVA(RV) result window is displayed:

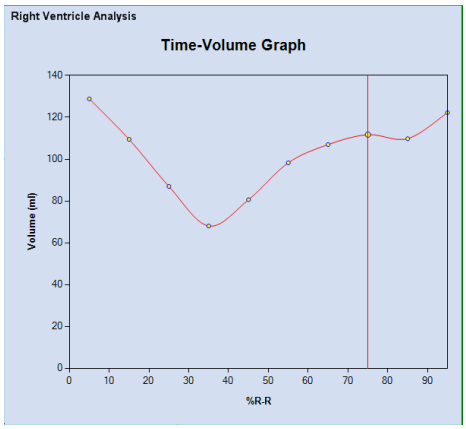


Formats for Reviewing Results

Results can be viewed in two formats, text and a time-volume graph.



```
Right Ventricle Analysis

GE64 Stent
ID: E45079351496
St: 81   Se: 554
12/27/2005    10:30 AM

Height: 175 cm  Weight: 70 kg
Body Surface Area: 1.848 mA2  Heart Rate: 60 bpm

Ejection Fraction: 47.17%
End Diastolic Volume: 128.82 ml  at R-R 5%
End Systolic Volume: 68.05 ml    at R-R 35%
Stroke Volume: 60.77 ml
Cardiac Output: 3646.14 ml/min
Stroke Index: 32.88
Cardiac Index: 1972.87

%R-R        5%      15%     25%     35%     45%
Volume(ml)  128.82  109.44  86.98   68.05   80.61

%R-R        55%     65%     75%     85%     95%
Volume(ml)  98.24   106.97  111.72  109.78  122.24
```



Text Results **Graph Results**

Figure 6-8 Formats for Reviewing Results

Generating a Report

You can generate a cardiac report, which will include the TVA results.

To generate a TVA calculation report, capture the images that you require, and click the **Generate Report** button. In this case, the report is directly generated without going through the Output Panel. Following is an example of a TVA report, including analyses on both the left and right ventricles:

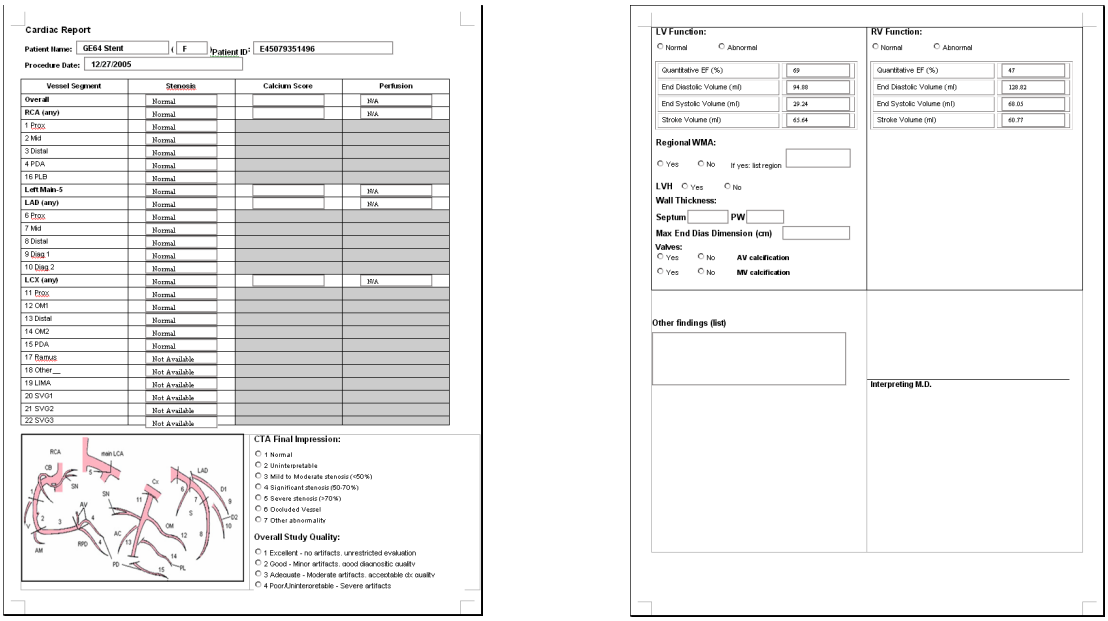


Figure 6-9: The First and Second pages of the Generated Report

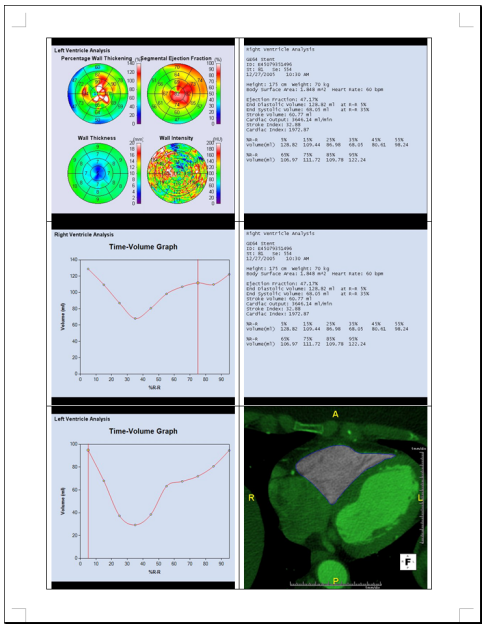


Figure 6-10: Third Page of the Generated Report

Lesion-Specific Analysis (LSA)

Please read the following section before using the LSA feature.

Lesion-Specific Analysis adds physiological information to anatomical images.

After the mycardium is segmented, the software can calculate a territory specific to a given lesion or branch on the coronary tree. A territory is the set of all the points that are closest in distance to the given branch. Because every patient has a different coronary tree structure, a territory calculated in this way is specific to this patient and this lesion. The AHA 17-segment territories are not specific.

The intensity value displayed is an average of mid-wall samples within the territory. Because of the limited resolution of the scanner, the "partial volume effect" makes the sampling inaccurate at near-endocardium and epicardium. Mid-wall is the least affected and has the most reliable samples.

Precaustion! *Beam-hardening artifact of the scanner affects the intensity read. This tool should not be used when there is any strong beam-hardening artifact. Some scanners have a reconstruction algorithm that suppresses the beam-hardening artifact.*

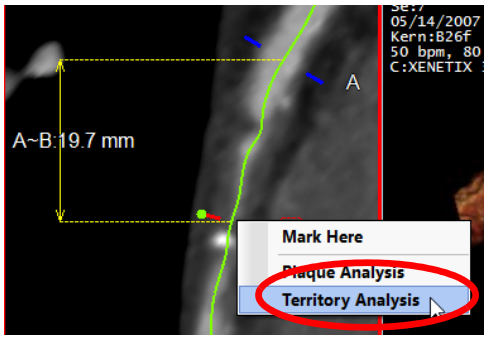
The territory volume or total volume displayed here does not include the volume of papillary muscles. This is different from the myocardial volume displayed in the cardiac function result, which includes papillary muscles.

Mark the Vessel

1. Open a coronary CTA study in the **Cardiac LSA** workflow.

2. Open CPR mode for the vessel having the stenosis. (In this example, the LAD vessel is being examined.)

3. Right-click on the centerline in the vertical 2D image and select **Territory Analysis** (see figure below).



   The results of the territory analysis become available when the LV wall is segmented in TVA. At that time, the values will be displayed in the measurement.

Perform EF

4. Scroll down in the workflow panel and click on the **EF** workflow element. Allow automatic EF to calculate results and display the segmented images and polar maps.

Now that the wall has been segmented, you can view the territory using the 3D polar map.

View the Territory

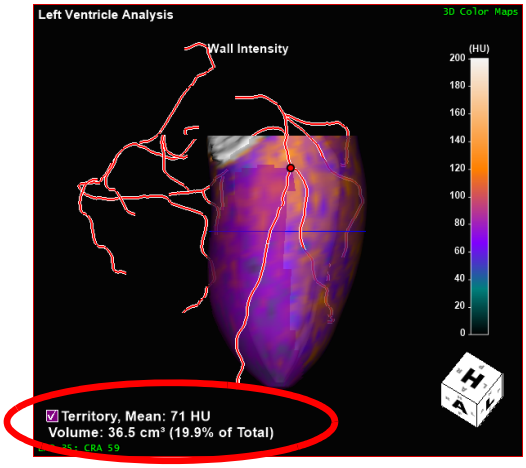
5. To view the territory, right-click on the **Wall Intensity** polar map, and select **3D Color Maps**.

CAUTION! Click the APS button in the top toolbar (see below) to overlay the centerline.

6. Click the **CPR** button in the top toolbar to display the territory analysis measurement, which has been filled in with calculated values. Then click the CPR button again to show the 3D polar map.

   The territory analysis results are displayed in the lower-left corner of the 3D polar map view, as shown below. The mean HU value and the percentage of the entire wall's volume that is part of the territory are also displayed.

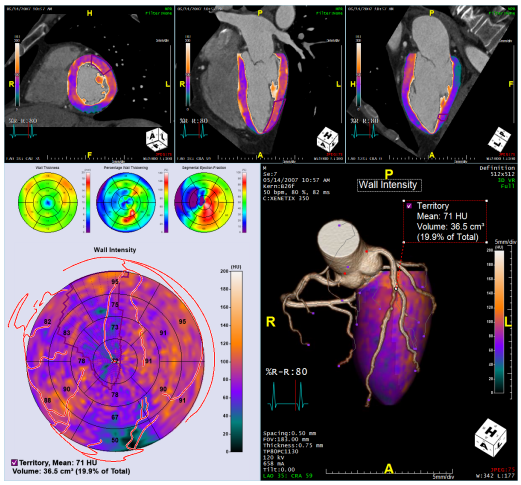
7. To show or hide the territory overlay, click the checkbox for **Territory** in the lower-left corner of the 3D image (see figure below).



Wall Fusion

8. Click the **Wall Fusion** workflow element.

   A combined layout, including the volume rendered coronary artery, three MPR views with a color overlay and the polar maps from EF, is displayed (see image below).



Other Features

Multi-style Layout

To view the data in multi style, right-click on the polar maps display and select **Multi Style**. The maps are displayed in multi style, as shown in the following image:

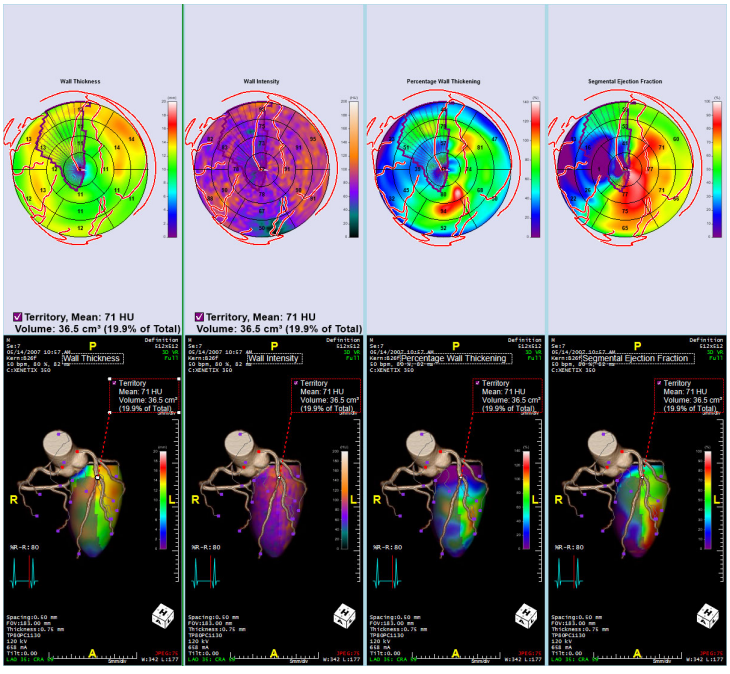
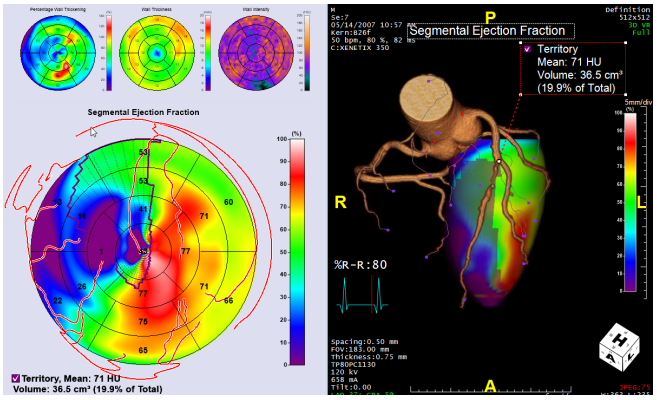


Figure 6-11: Multi-Style

To view the data in single style again, right-click on any of the polar maps and select **Back to Single style**.

Switching Polar Maps

To focus on a differerent polar map, double-click on the desired map. The selected polar map is then displayed in a larger size, in both 2D and 3D forms (see below).



Changing the Overlay Color Template

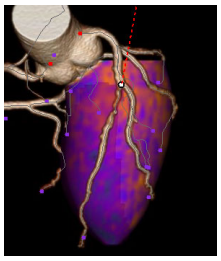
The overlay color template is changed in the Window/Level (W/L) tool panel. To open the W/L tool panel, click the double right arrow on the right side of the panel to show all tools. Then select the W/L tool.

See "Selecting a Different Color Template" on page 6-16 for instructions on changing the color template.

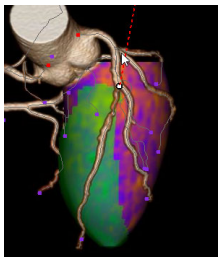
Changing the Territory Color

To change the color of the territory under examination, do the following:

1. Right-click on the territory measurement.
2. Select Change territory color. This opens a Windows color dialog that allows you to select standard themes and colors or to create custom colors.
3. Select another color, for example, green. The territory is then overlayed with the new color (below, on right):



Before Color Change



Color Overlay Change

Figure 6-12 Example of Overlay Color

Cardiac Function Measurements

Inter-Observer Difference, Cross-Product Difference, and Reading Time

This section describes testing that was done to compare results among the automatic TVA module included in the Aquarius iNtuition (AQi) Client, manual TVA in the AQi Client, and the Classic Workstation's TVA module.

Objective

TeraRecon's Time-Volume Analysis (TVA) module has been widely used to measure cardiac function from 4D cardiac CT data on the Classic Aquarius Workstation for many years. The AQi-TVA documented in this chapter has added a fully automatic mode in order to speed up reading, while still allowing the user to switch to manual mode when automatic TVA does not meet requirements. The Classic TVA has manual mode only.

The objective of this test is to compare the cardiac function measurements made on AQi-TVA to those made on Classic TVA, to see if the difference is significant. We are also testing to determine whether AQi-TVA cuts down reading time.

Material and Method

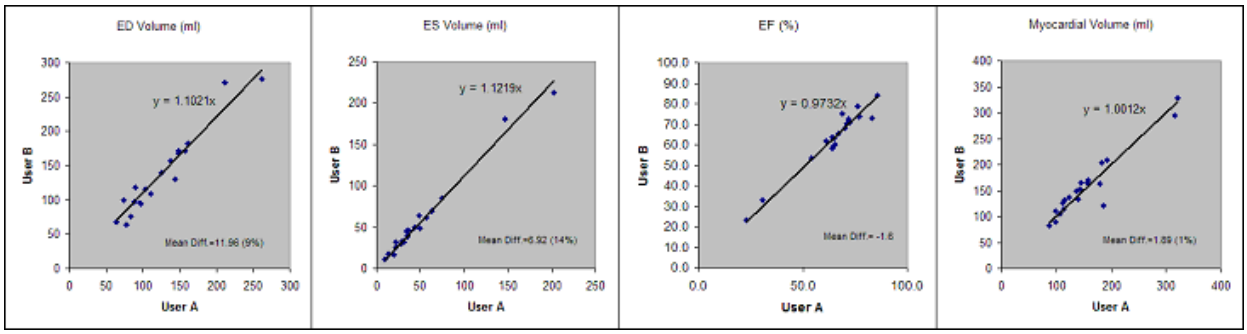
Twenty Cardiac CT datasets were randomly chosen from a hospital. The acquisition was using the ordinary protocol that served the reading in the department of radiology.

Two experienced technicians (both having 6 or more years' experience processing cardiac CT data) processed the data using classic TVA and AQi-TVA. For each dataset being processed, the entire chamber analysis and wall analysis were performed. Values of the End-Diastolic (ED) phase, End-Systolic (ES) phase, ED volume, ES volume, Ejection Fraction (EF), and myocardial volume were captured. The time was measured from the beginning, when the patient data was selected, to the display of the results.

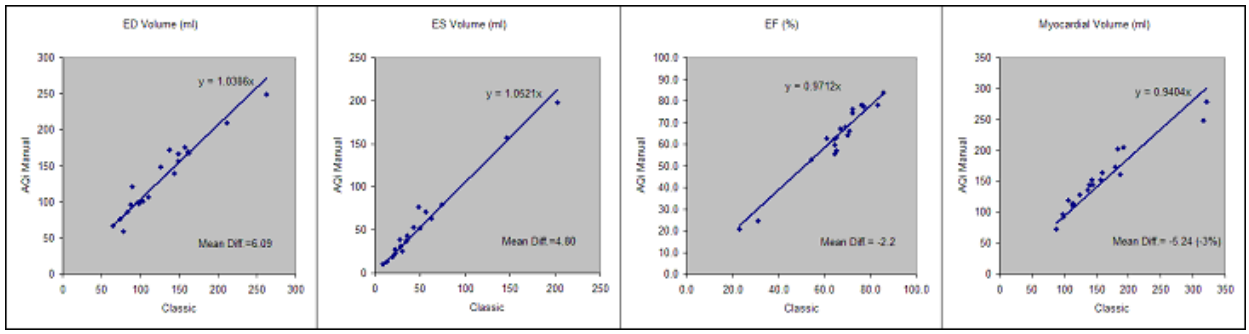
Linear regression (from Microsoft Excel) was used to process the measured values, for the purposes of comparison. The values from user A and user B, using classic TVA, were compared for the inter-observer difference. The values from user A using AQi-TVA manual mode were compared with the values from user A using classic TVA for the cross-product difference. And the values from user A using AQi-TVA automatic mode were compared with the values from user A using classic TVA for the cross-product difference.

Results

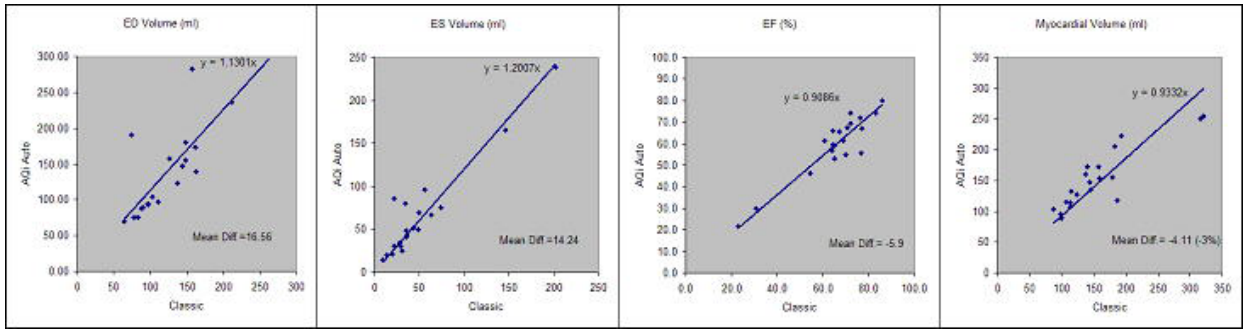
Classic TVA Inter-Observer



AQi-TVA Manual Mode vs. Classic TVA



AQi-TVA Automatic Mode vs. Classic TVA



Time Spent

The average time spent in Classic TVA for each case was 3.8 minutes for user A, and 6.4 minutes for user B. The average time spent in AQi-TVA manual mode for each case was 5.2 minutes for user A. The automatic mode in AQi-TVA took 1 minute for every case (mostly on loading the data).

Conclusion

For the measurements of ED volume, ES volume, EF, and myocardial volume, there is no significant difference between AQi-TVA manual mode and classic TVA. The difference is comparable to the inter-observer difference with classic TVA itself. AQi-TVA manual mode can replace classic TVA in these measurements.

For these measurements, AQi-TVA automatic mode has a significantly larger difference than AQi-TVA manual mode when compared to Classic TVA. AQi-TVA automatic mode can not replace Classic TVA or manual mode.

The time spent in automatic mode is significantly shorter than manual mode or Classic TVA.

Discussion

There were two cases where the automatic mode showed a very large difference in ED volume. These datasets were noisy, and noise in data affects automatic processing more.

If a site consistently has low-noise high-contrast data, we recommend using automatic mode in AQi-TVA by default. Be sure to follow the instructions to check the overlay for the segmentation result on both ED and ES phases. If any of them is wrong, go back to edit them manually.If a site consistently has high-noise data, or is experiencing errors too frequently in automatic mode, we recommend changing the default to use manual mode.

Chapter 7 Magnetic Resonance (MR) Cardiac

Topics in this chapter:

Cardiac MR Imaging is a noninvasive medical test used to diagnose and treat medical conditions pertaining to the heart and its structures. It evaluates the anatomy and physiology of the heart chambers and valves, the size and flow of blood through vessels, and the surrounding structures. It is used to determine whether a patient is suffering from any form of cardiovascular disease such as limited cardiac or valvular related functional outputs.

Cardiac MR Imaging Options

Time Volume Analysis (TVA)(MR)

The **Time-Volume Analysis** (TVA) optional module calculates time-dependent behavior of volumes in multi-phase studies from MR. An example of a time-dependent behavior is the change in the volume of the ventricles of the heart.

Note: You are obligated to define the wall boundaries in question. **Also note**: When first accessed, the user interface for wall boundary outline holds generic default values with no significance. You must acknowledge this by dismissing a warning message to this effect.

TVA of the Left Ventricle (LV)

To perform TVA of the LV separately, highlight the cine series in a cardiac MR study, click the **Load** button and then select **Cardiac MR2** from the Workflow menu.

Note: You can also perform TVA of the left and right ventricles together in one workflow, CardiacMR. For more information, see "The Combined LV/RV Workflow" on page 7-24.

The default layout shows all slice images from the same phase. The TVA(LV) tool panel is opened first, and the initial Workflow element is LV EF.

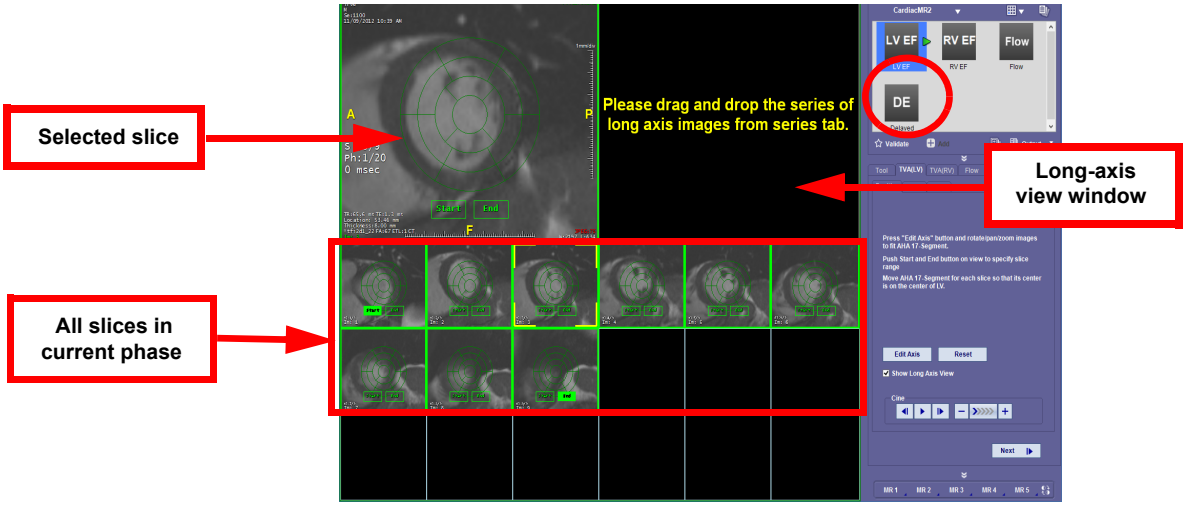


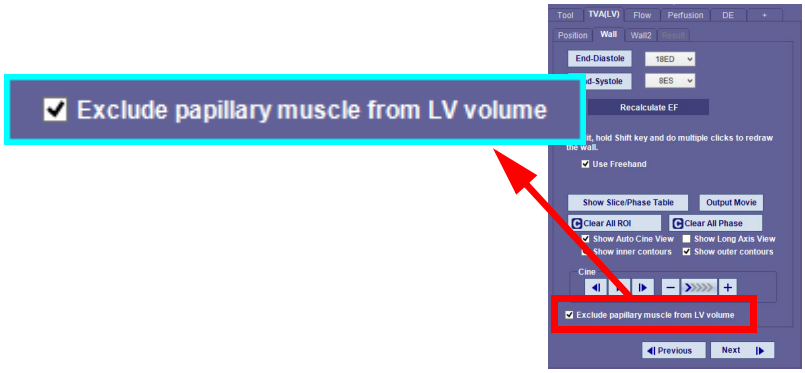
Figure 7-1: Cardiac MR of LV

Note: For processing only, highlight a cine series in a cardiac MR study, click the *Load* button, and then select the *Cardiac MR3* workflow sample from the Workflow menu.

Excluding Papillary Muscle in LV Results

This option allows you to obtain a more accurate measurement of the ejection fraction in the Left Ventricle by manually editing the contours and removing the papillary muscle from the results.

1. Enable the **Exclude papillary muscle from LV volume** option in the **Wall** tab (see the following figure).

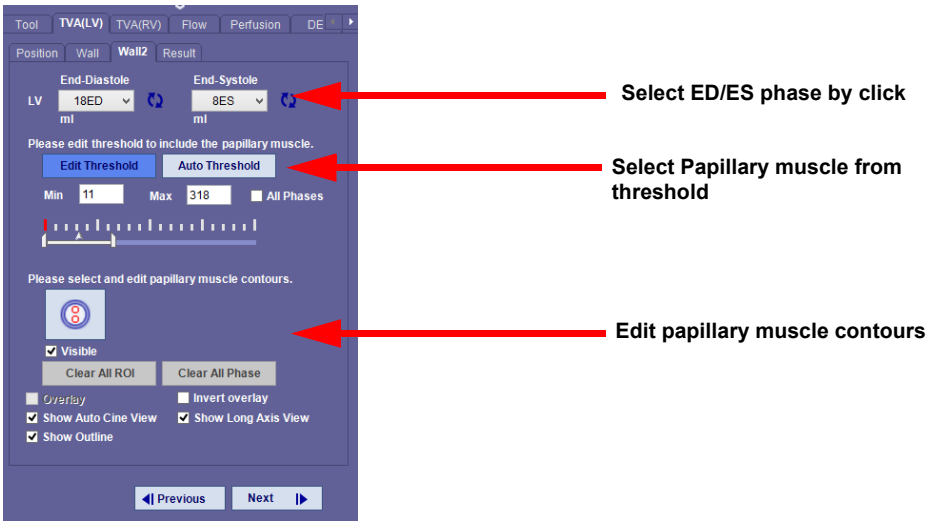


2. The system then proceeds to **Wall2** tab, which contains more detailed information about papillary segmentation.

3. Select the end-diastolic or end-systolic phase.

4. In order to manually edit, highlight the papillary muscle using the threshold, and edit the contours of the papillary muscle for a more accurate reading.

These options are shown in the figure below.



When you select the papillary muscle from the threshold, the **Exclude papillary muscle from LV volume** option is enabled. The threshold of the papillary muscle is calculated for each phase.

Note: This option applies only to the LV Volume and related results. This will not have an effect on results from wall calculations.

You can also include the papillary muscle volume even when **Exclude papillary muscle from LV volume** is enabled. If you would like to see the papillary muscle volume (or mass) in the analysis, you can specify this in the Preferences > CardiacMR > MRTVA tab. For more information see Appendix A: "CardiacMR - MRTVA".

Note: Volume of papillary muscle is dependent upon segmentation results of the papillary muscle. It is up to the qualified user to review papillary muscle segmentation to verify volume accuracy.

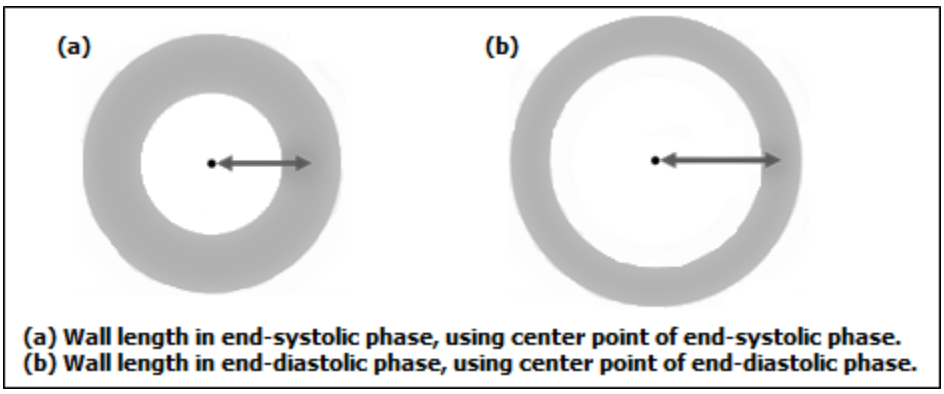
Wall Motion Polar Map

Wall motion analysis can be calculated from both inner and outer ROI.

The wall motion can be calculated by determining the difference between the length of the wall in the end-diastolic phase and the length of the wall in the end-systolic phase, as follows:

Note: Wall Motion (mm) = Wall Length (ED) - Wall Length (ES),

---



(a) Wall length in end-systolic phase, using center point of end-systolic phase.
(b) Wall length in end-diastolic phase, using center point of end-diastolic phase.

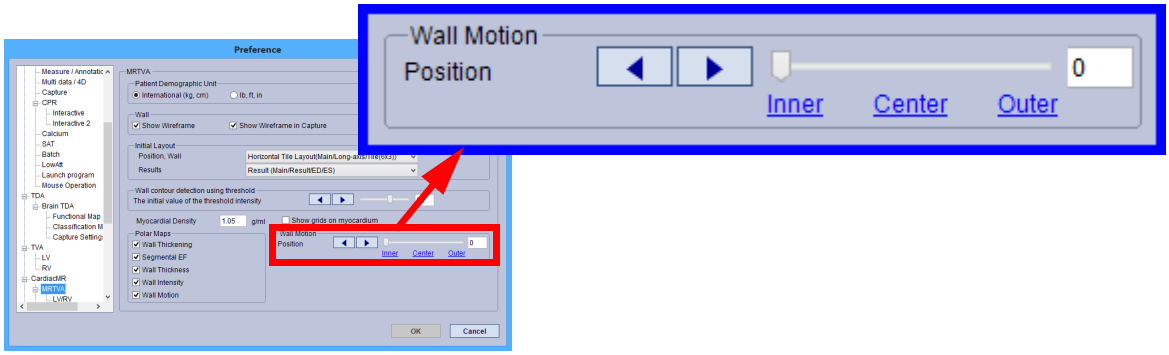
Where the value for the wall length is determined using the following equation:

```
Wall Length = Length (LV center point to inner wall) + Length (inner wall to
outer wall) X Wall Offset
```

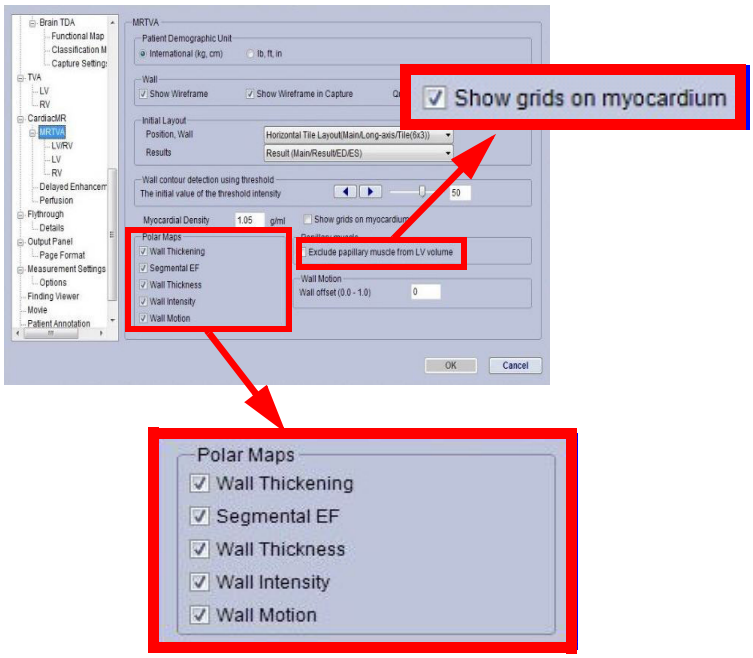
Where the Wall Offset is calculated by the following:

```
Wall Offset (0.0 - 100) = Preference Value

                                    0: Inner wall

                                   50: Center of Myocardium

                                  100: Outer Wall
```

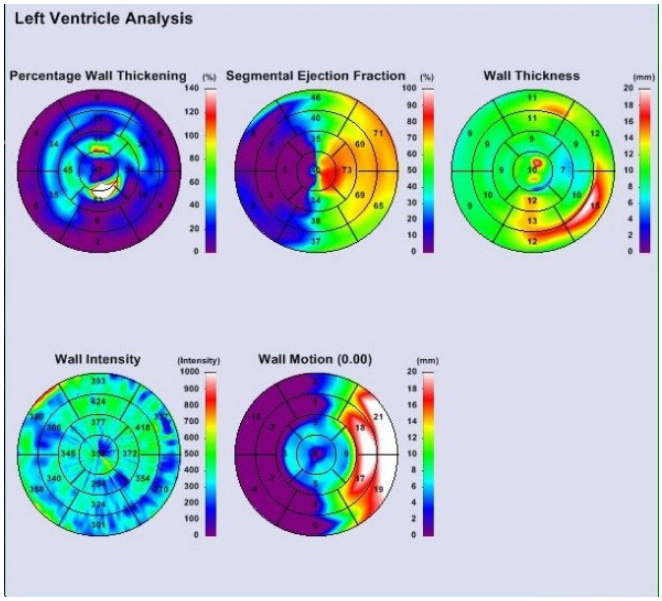
To customize the position of the Wall Motion, open **User Preferences** and select **Cardiac MR** -> **MRTVA** from the navigation panel on the left.



When the result is generated, you can select which polar maps to display. Additionally, to show how the myocardium is moving, make sure that the **Show grids on myocardium option** in the MRTVA tab is enabled.



Analysis maps:



The figures below show the myocardium grid on (left) and off (right):

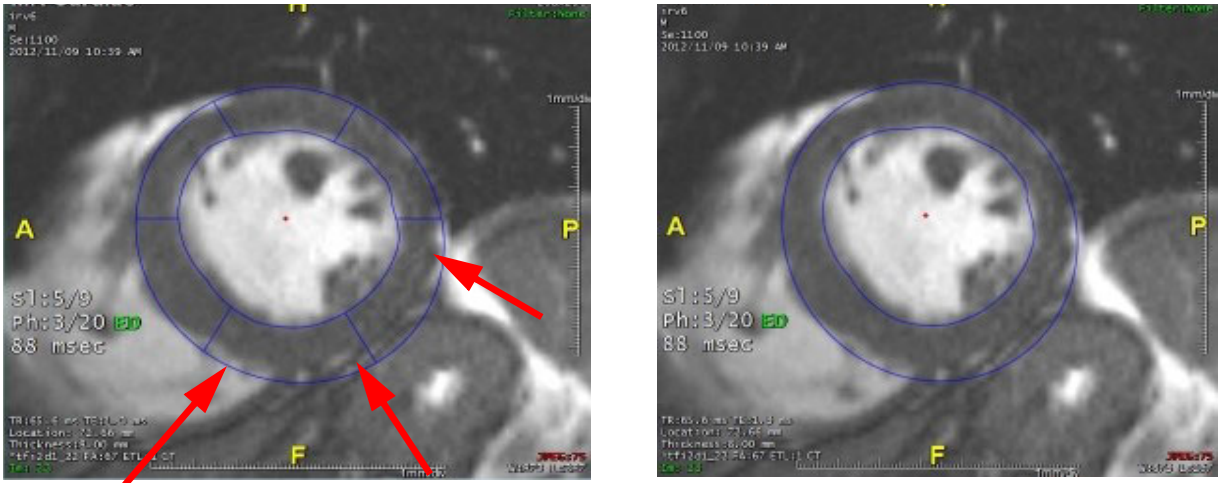


Figure 7-2: Left - Grid Enabled; Right - Grid Disabled

Note: You can select the type of results you wish to view initially upon calculating TVA for Left Ventricle including: Text Results, Time-Volume, Graphs, or Polar Maps depending on your preference. See Appendix A: "CardiacMR - MRTVA" on page A-36

Phase Sorting Data

When multiple series level data is loaded to Cardiac MR, it is loaded in a multi-data layout:

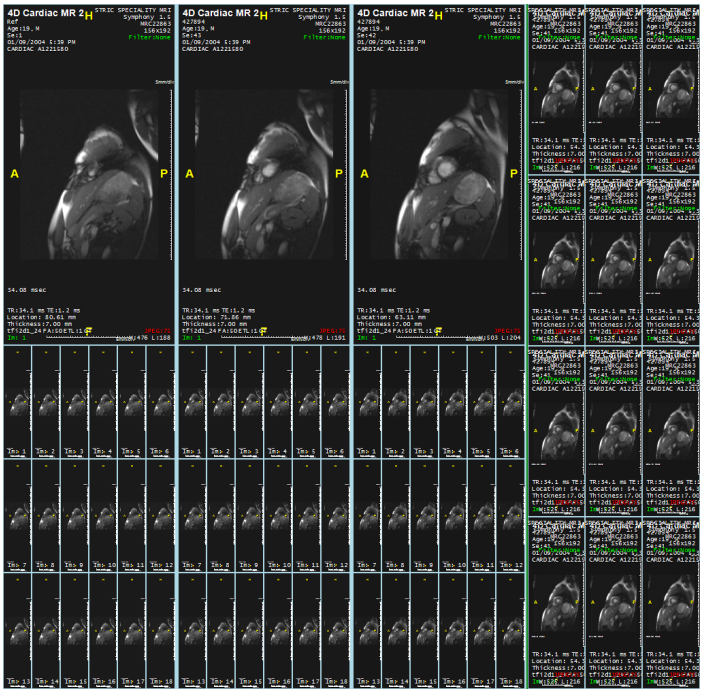
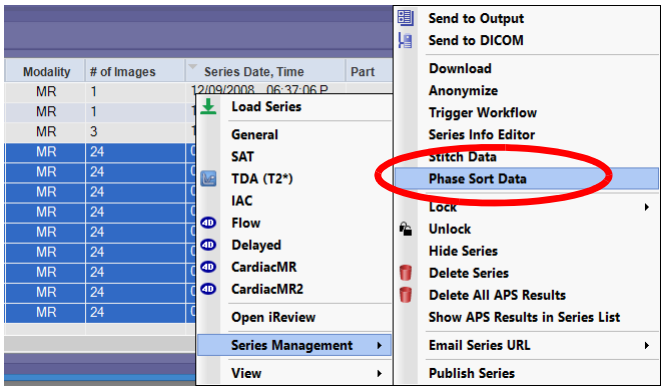


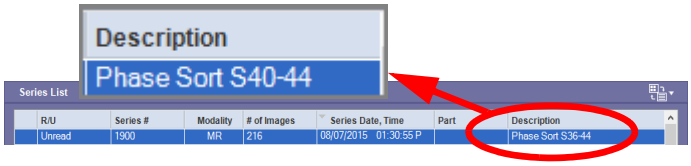
Figure 7-3: Unsorted Multi-Series Level Data

The data needs to be sorted first. Phase Sort takes scanner-generated multiple series level data and converts it into a single series, with each sub series as one phase.

1. Select all phases of the data to convert, and right-click.
2. Select **Series Management**, and then select **Phase Sort Data** from the sub-menu.



The sorted series is routed back to the Series List.



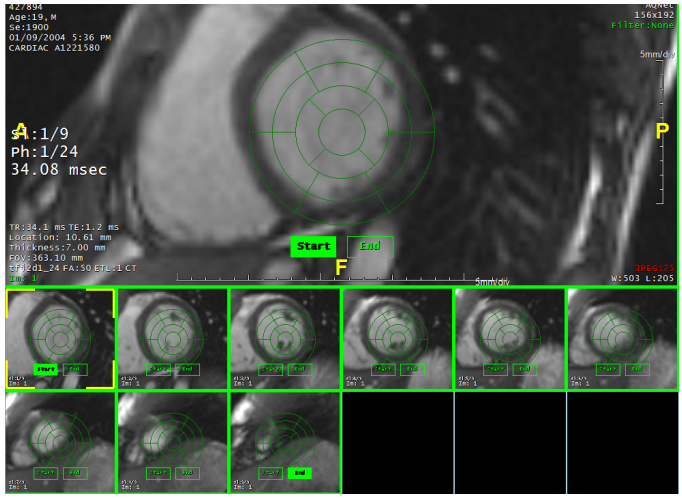


Figure 7-4: Sorted Data Loaded

Note: Non-uniformly spaced volumes are not supported.

Cine Tools

Click any of the images in the main window to display the cine tools:

Figure 7-5: Cine Tools

There are two sets of cine tools. The upper set controls the direction of the cardiac motion through each phase in a single position. From left to right, the buttons in this row do the following: go back one phase (left arrow), play cine (middle button), go forward one phase (right arrow).

The lower buttons allow you to page through the slice images of a single phase. The third button in this row determines whether, after reaching the last image, the cine will begin again at the first image or will play the cine in reverse. The fourth button opens a small dialog where you can set the speed and cine interval. The middle row also controls the cine speed. Use the zoom and pan tools to fit the images in the view areas.

Note: To show crosshairs during cine, enable this in Preferences in Viewer > Setting 2 by checking "show crosshairs and bounding box during cine".

The Tool Panel

When the series is first loaded, the TVA(LV) tool opens in the **Position** tab. This tab contains brief instructions for preparing the images for the ejection fraction (EF) process.

You can use the Cine buttons at the bottom of the tool panel to preview the phases of all images at once.

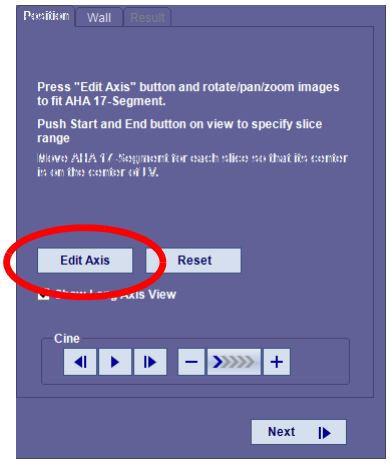
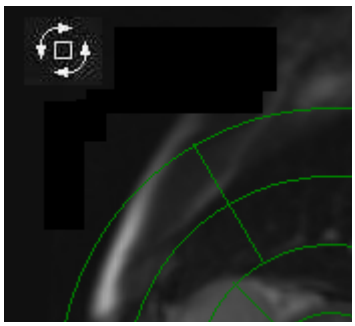


Figure 7-6: Edit Axis

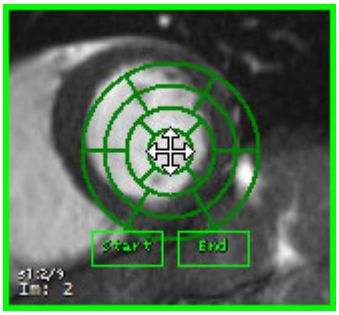
Editing the Axis

Rotate the short axis images so that they are displayed at the correct angle. To do this, click the **Edit Axis** button in the tool panel (circled in Figure 7-6). The cursor changes to a rotation image. You can then rotate short-axis images around the center of the image window (see image at right).



The AHA-17 Segmented Map

For each slice, move the AHA map so that the center of the map overlays the center of the ventricle, in the short-axis view.



1. Click the first slice to center the map in, from the slice images. This slice is displayed in the upper-left quadrant of the screen.
2. Hover the mouse over the center of the AHA map to highlight it. Highlighting is indicated by darker and thicker lines of the AHA map. The cursor changes to a double-arrow cross-sign (see image at right).
3. Click and drag the AHA map so that the center of the map is positioned directly over the center of the ventricle. You can perform this operation in the upper-left display of the current slice, or directly on the slice image below.
4. Center the AHA map on each slice image in the current phase.

When finished, you can check the other phases by playing the phase cine (see Figure 7-5 on page 7-8). If any image is not centered properly, you can move the AHA segmented map again to center it.

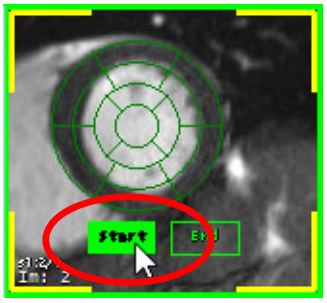
Setting the Start and End Positions

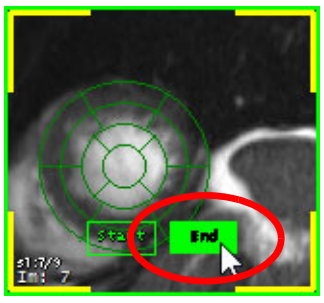
After previewing the images, select the range to be used for the calculations. You can do this in one of two ways:

- Clicking the **Start** and **End** buttons of the slice images you want to designate as the start and end slices of the volume to be used in the calculation. You must do this for each phase.
- Using the long-axis view to select start and end slices.

Start and End Buttons

1. Choose the slice that gives the best view of the ventricle and wall in all phases as a start position.
2. Choose the best slice for the end position.
3. Use the **Start** and **End** buttons to select the range.





Click **Next** to continue to wall calculations. When calculations are completed, the following screen is displayed:

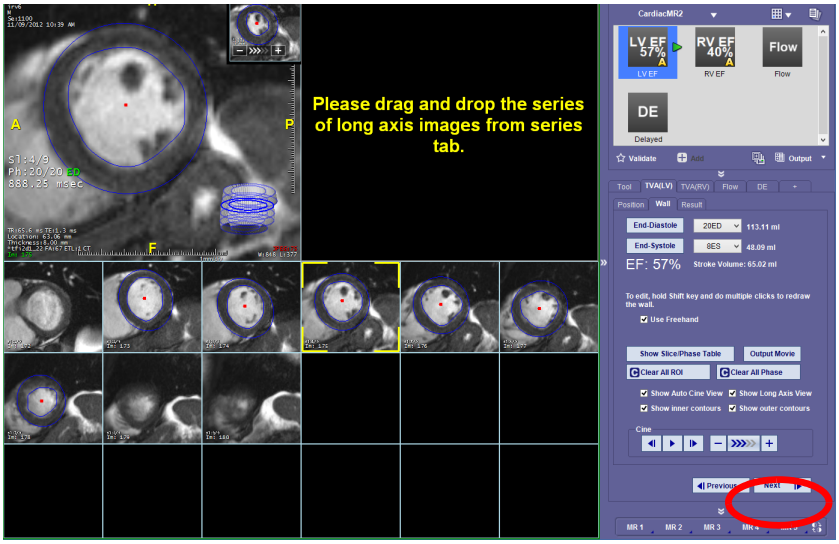
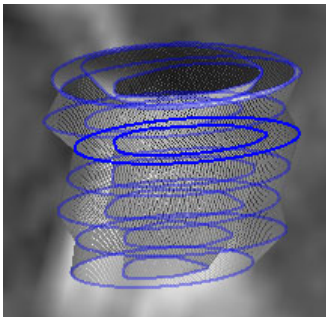


Figure 7-7: Wall Calculation

The Wire Frame

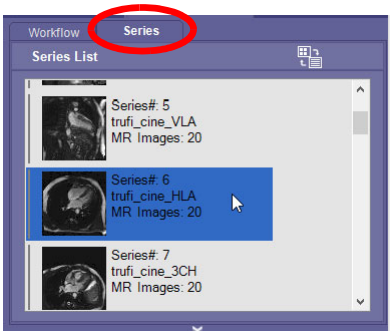


The 3D Wire Frame is displayed in the lower-right corner of the large short-axis view. It is provided to give you a 3D view of the slices in the currently displayed phase. When a slice is selected within the rows of short-axis images, it is displayed in the large window in the upper-left corner, and the corresponding slice is highlighted in the wire frame. In the image at right, the third slice from the top is highlighted, meaning that the third slice is currently selected.

The wire frame can be rotated so that you can view the shape of the ventricles from different angles.

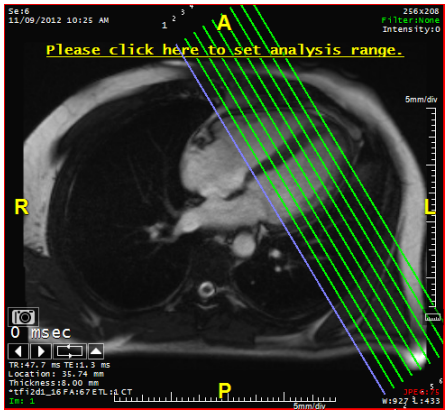
The Long-Axis View

You can also select the start/end slices from a long-axis view of the data.



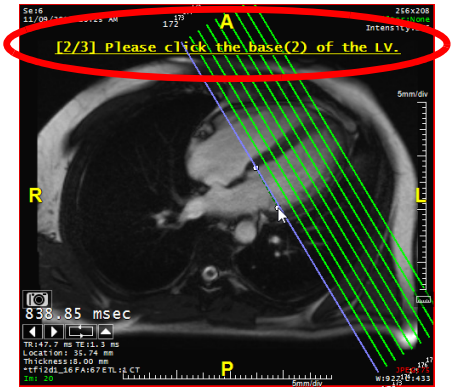
1. Click the **Series** tab in the Workflow panel to select a series to load (see figure at right).

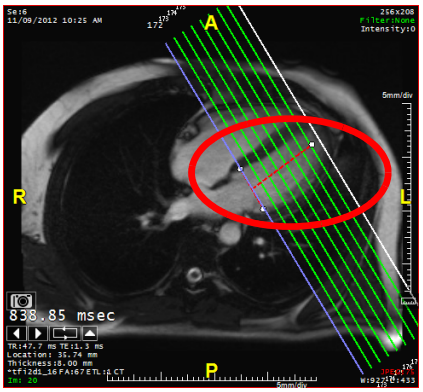
2. Drag the desired series to the upper-right window to load it. See the following image:



The parallel lines on the image represent each slice in the current phase. When you click on any of the slice images, the corresponding line is highlighted in blue.

3. At the top of the long-axis image, click on the instruction “Please click here to set analysis range.” The second instruction, “Please click the base of the LV,” is displayed at the top of the long-axis window.





4. Click one edge of the ventricle, along the slice that you want to designate as the base.

5. Move the cursor to the opposite edge along the base, and click that point. The third instruction, “Please click the apex of the LV,” is displayed above the long-axis image.

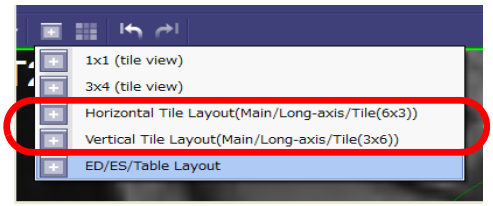
6. Click the line that falls on the apex of the range. This defines the full analysis range of the ventricle (see image above, right).

   If you wish to hide the scout lines while having the ability to adjust the analysis range, simply right-click and unselect **Show scout line** and select **Show analysis range**. This provides better viewing capability.

Long-Axis View Layout Options

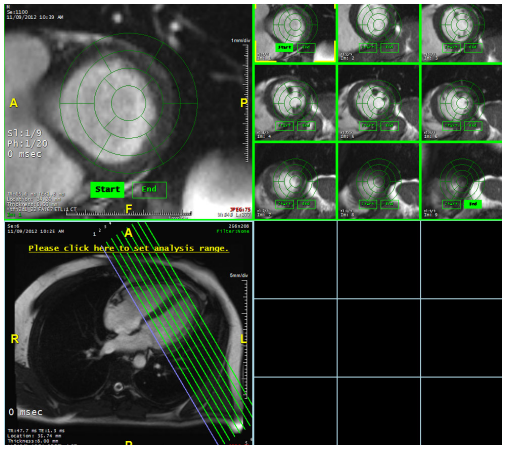
There are two layouts available for displaying data that contains the long-axis view: horizontal and vertical.

Click the layout button in the top toolbar to open the menu (see the following figure).



The horizontal long-axis layout is the initial default, but the layout can be reconfigured in the user preferences (see "CardiacMR - MRTVA" on page A-36).

Long-axis vertical layout:



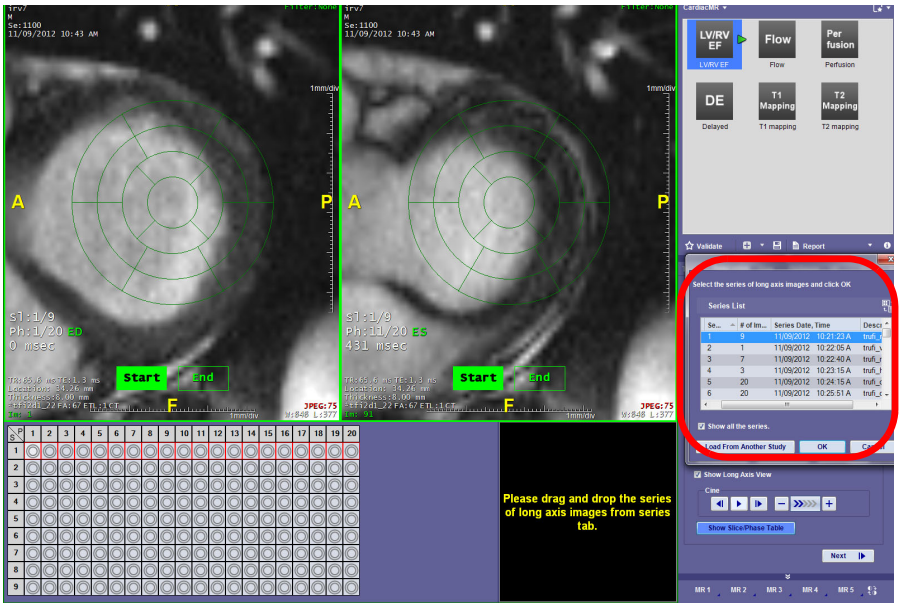
Note: If you are in the long axis view and you wish to switch over to short axis view, simply click directly on the scout line and it will switch from long axis to short.

ED/ES Table Layout

First, load a Cardiac MR study into the Cardiac MR workflow and the viewer will show both phases together so you can select the slice range efficiently.

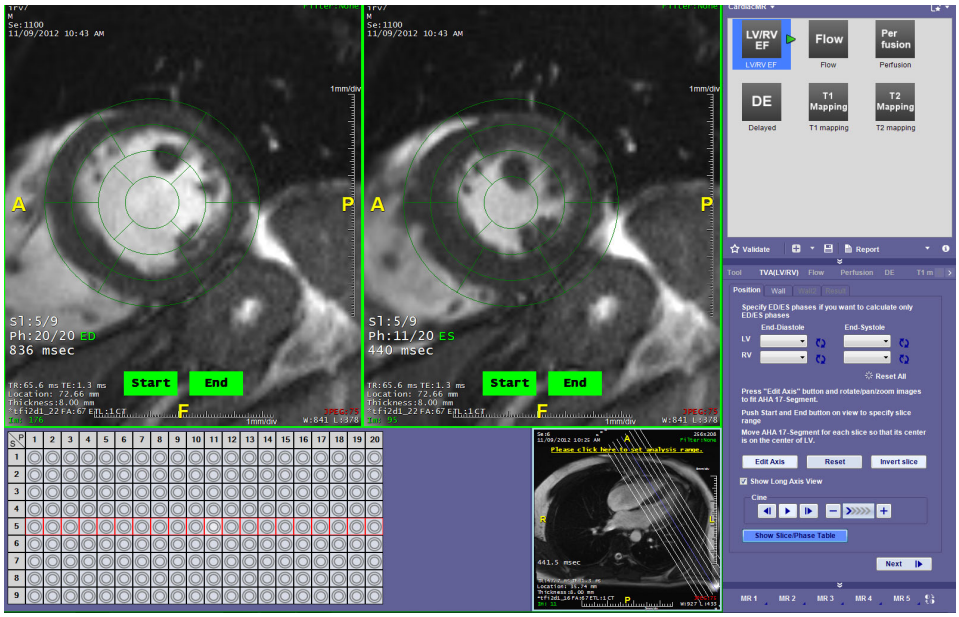
You can view the End-Diastolic and End-Systolic phases side-by-side. **I**f you wish to view this option, select **Show Slice/Phase Table** in the right tool panel. For more information, see "The Slice/Phase Table" on page 7-15. To view the long axis view, check the **Show Long Axis View** checkbox right about the cine controls in the tool panel.

ED/ES Layout:

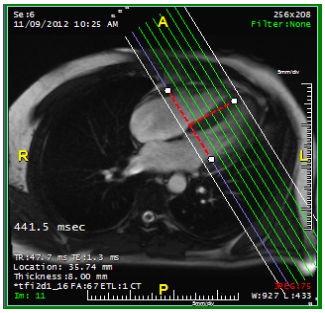


Next, you will be prompted to select the series of long axis images. You can do this by either going to the series tab (circled) in the right tool panel and dragging the series to the long axis viewer, or by selecting the series in the pop-up window circled above.

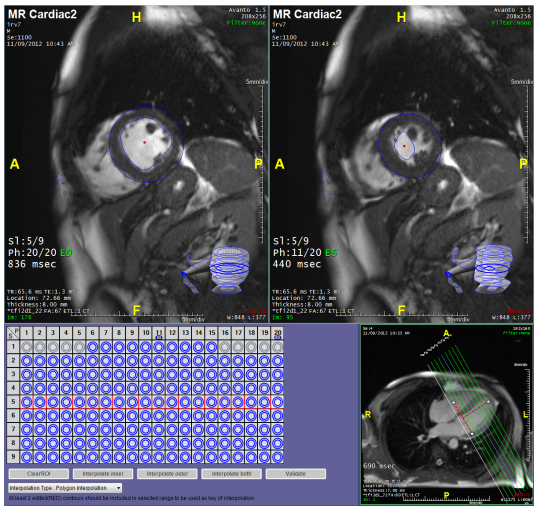
Start by selecting your start and end points with the ED phase, you want to be sure to select the slice/phase where the ventricle is at its largest. Line the AHA-17 segmented map up with the inner and outer walls of the ventricle. Next you will go to the ES phase and do the same, except you want to select the slice/phase where the ventricle seems to be at its smallest size.



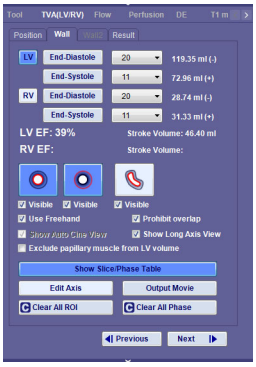
Once you have determined the start and end points for the slice range of each phase, you need to choose the analysis range on the long axis viewer.



Click Next to begin the calculation of the Inner/Outer wall and the EF. The result will look similar to the image shown below:

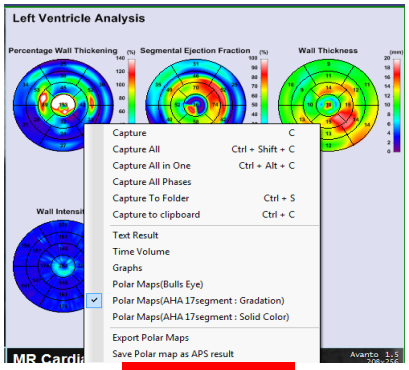


In the right tool panel, you will see the values for the LV and RV analysis. The (-) sign next to the values indicates that there the value chosen was not the largest value and that there is another value larger in the selection that you can choose to use. The (+) indicates the opposite, meaning there is a smaller value in the list that you can use to continue with the analysis.

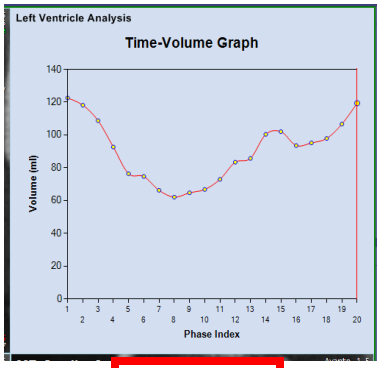


Once you are satisfied with the results, click Next.

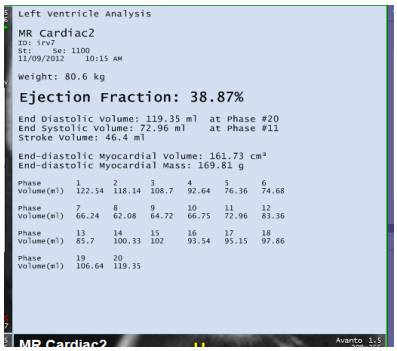
The Polar Maps for the Left Ventricle Analysis will appear, however you can change the results view by right clicking on the upper right-hand viewer. The options are shown below:



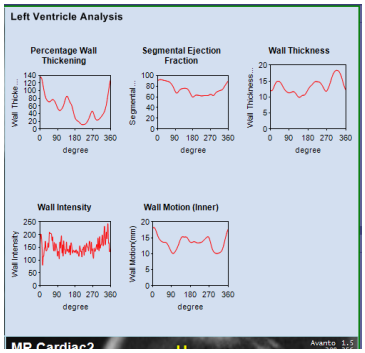
Polar Maps



Time Volume



Text Results



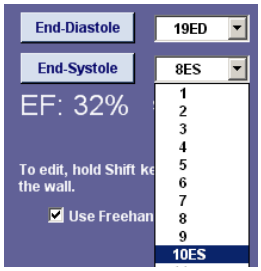
Graphs

If you wish to specify which layout appears on the initial result, see Appendix A: "CardiacMR - MRTVA"

Automatic vs. Manual EF

Ejection fraction on the is calculated automatically by default. The measurements are verified to be accurate with artificial digital phantom data. However, clinical data is more complex. You are responsible for verifying the automatic segmentation (overlay and outlines) in both the end-systolic and end-diastolic phases. During this verification process, if the results do not meet expectations, TVA (LV) should be redone manually. The results correlate with the segmentation and will be updated with user specified changes.

The end-diastole and end-systole phases are automatically selected by the software. It is your responsibility to verify the phases automatically chosen. If the preselected phases do not meet your expectations, proceed to select the correct phases from the pull down menus (see figure at right).



The Slice/Phase Table

This table contains a matrix of the wall boundaries for each phase within each slice in the selected range. It is automatically generated when the start and end positions are set.

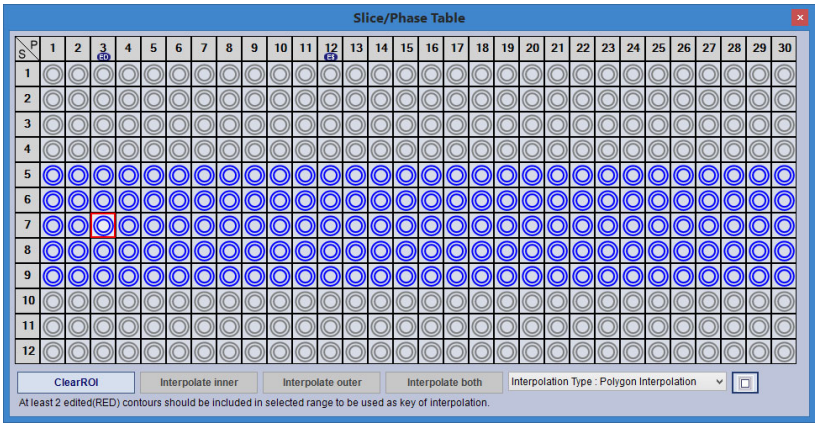


Figure 7-8: Slice/Phase Matrix

Each row represents a slice that lies within the range you selected using the **Start** and **End** buttons. Figure 7-8 above shows five slices. Each column represents one phase of the scan. (This scan has 30 phases.) You can add to or remove slices or phases from the selection.

Note: If the table is not automatically displayed, click the Show Slice/Phase Table button in the tool panel.

The slice/phase table allows you to select a set of images whose wall contours are to be reinterpolated after editing. To access individual images quickly. Click on any of the blue circles to display the image that corresponds to it. You can then review the wall boundaries drawn by the software on specific images and edit the boundaries, if necessary, in preparation for interpolation.

Color Codes in the Slice/Phase Table

The following table describes the meaning for each of the circle colors in the table.

Icon	Description
	Wall contour was interpolated by AQi algorithm.
	Wall contour was edited by user.
	Wall contour was re-interpolated by algorithm after user edit.
	Wall contour was removed from the table using **ClearROI**. **Only contours in the inner slices are turned yellow when removed. If the removed contour was in the first or last slice, the color turns gray instead.**

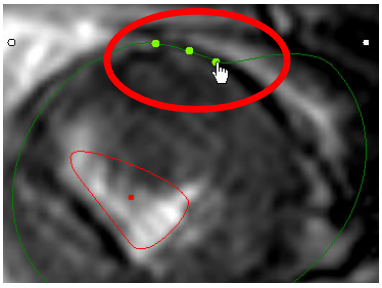
Icon	Description
	Unselected images (outside the slice and phase range under examination).
	Inner wall was interpolated by AQi algorithm. Outer wall was re-interpolated by algorithm after user edit.
	**Outer** wall was interpolated by algorithm. **Inner** wall was re-interpolated by algorithm after user edit.
	(Box around circles is red and cell is highlighted.) This is the image currently selected and displayed in the main window.

Editing the Wall

If the wall has not been drawn correctly on any of the images, you can edit the inner and outer walls. There are several tools you can use to edit the boundaries:

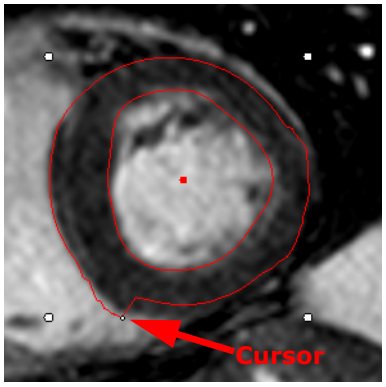
- **Multi-Click**

  Hold the shift key and click multiple times along the wall boundary where the contour should be drawn:



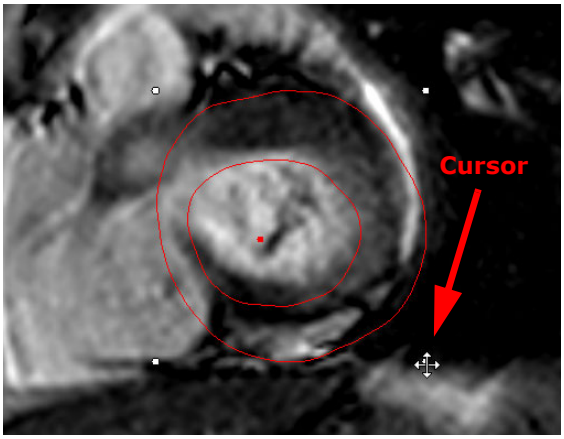
- **Freehand**

  Check the **Use Freehand** box in the tool panel to change the edit mode from multi-click to freehand. After editing, the contour color will change to red:



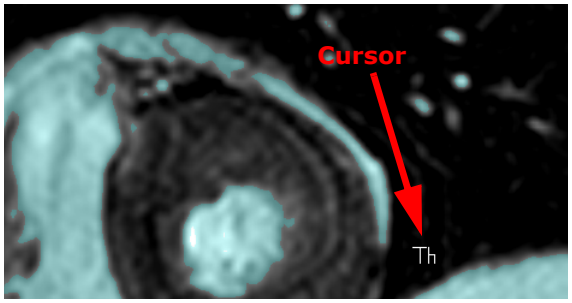
- **Pan Wall Boundary**

  You can also pan the entire wall boundary across the image to move it to a more accurate position. The cursor takes the shape of a cross (see figure below).



- **Threshold**

  Hold down the CTRL key and move the cursor up and down to show a threshold mask on the image. The inside of the ventricle should be completely covered with the mask, while the wall should not have any mask. Release the CTRL key to redisplay the wall boundary.



Interpolation

Whenever you have edited the wall on an image, the entire selected data set must be interpolated again, to take the new values into account. Therefore, it would be most efficient to do editing on a few key images first - for example, the first and last phases in a slice, and one or two in the middle - and then run the interpolation again. You can interpolate all phases in a single slice (a horizontal row in the slice/phase table) independently from the interpolation of all slices in one phase (vertical).

To begin interpolation, select all the circles in the table corresponding to the phase or slice to be recalculated. Selected circles show as highlighted in the slice/phase table.

Note: At least two images in the selection must be edited before interpolation.

It is recommended that you calculate the phases within each slice first, and then calculate the wall boundaries in all images. This is because the change in wall boundaries between consecutive phases is much smaller than between adjacent slices, so the interpolation is more accurate. After recalculating the walls for each slice, you can then recalculate the selected data set.

When you are satisfied with the wall boundaries, click **Recalculate EF** to update the EF value.

The updated EF and related values are displayed as shown below:

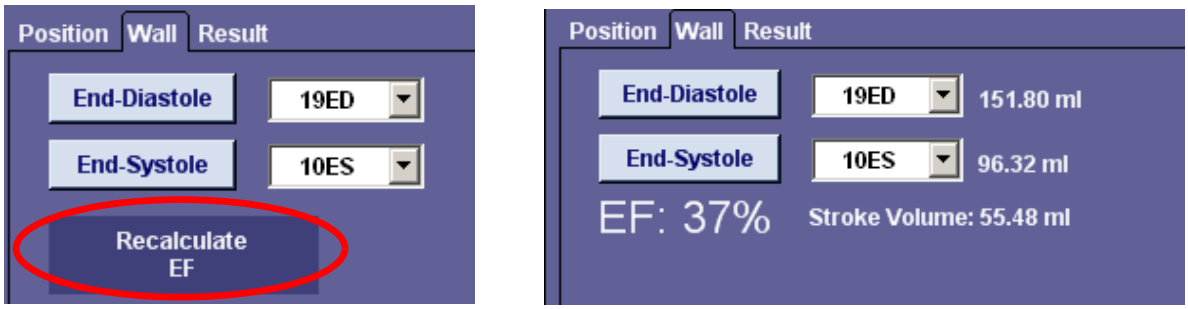
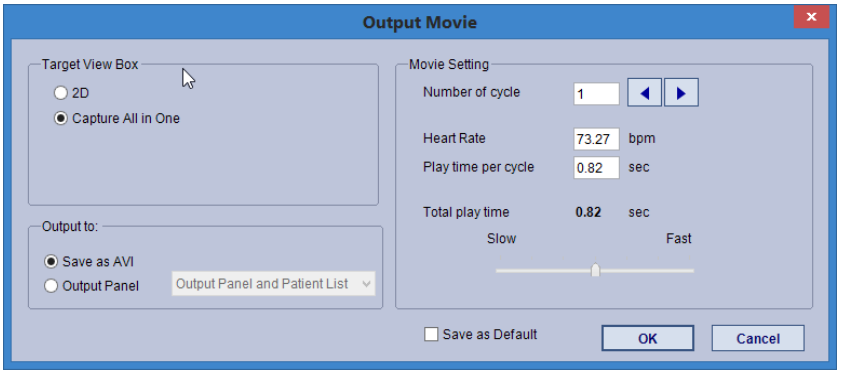


Figure 7-9: Left - Recalculate EF; Right - Updated EF

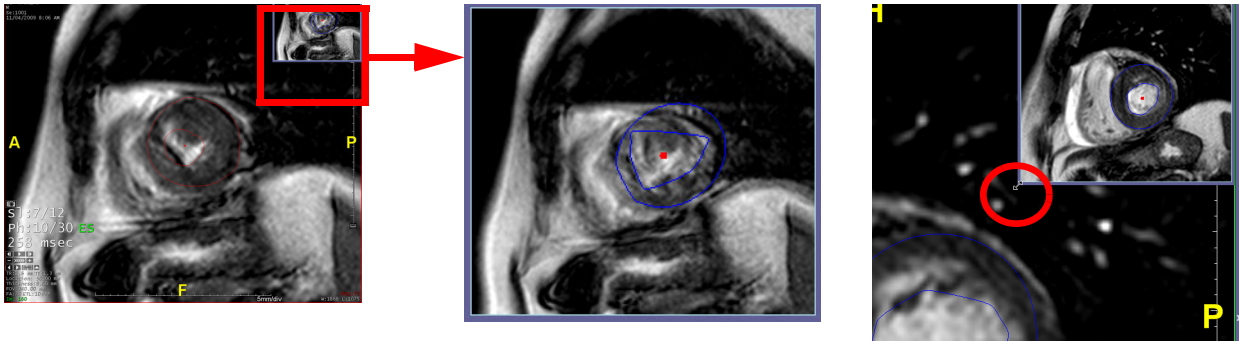
Other Tools

You can view images in the following ways, using some of the other tools on the Wall tab:

- Output Movie



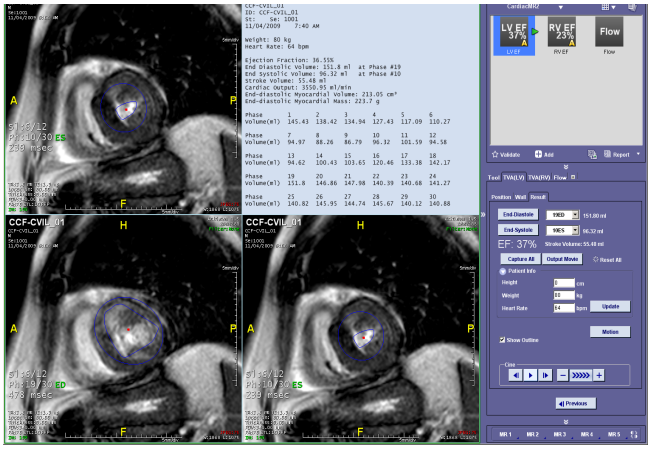
- Clear All ROI - Clear all ROIs drawn in the current phase.
- Clear All Phase - Clear all ROIs in all phases.
- Show Auto Cine View - Show the cine image in the top-right corner of the main window (visible only in 1x1 layout).



You can also resize the auto cine view by clicking on the lower-left corner and dragging it (above, right).

- Show inner contours /Show outer contours - Show or hide the contours of the inner or outer walls.

When you are finished editing walls and updating the EF values, click **Next**. The resulting images and result table are displayed:



Text Results

The text results section display results for Ejection Fraction, End Diastolic and End Systolic volume, stroke volume, cardiac output and End diastolic myocardial volume and mass. The text results include a reference ranges which can be edited in Preferences.

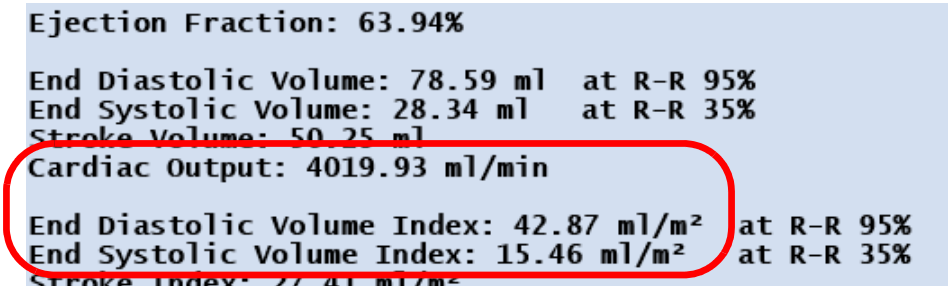
The reference range database information can be found here:

> Kawel-Boehm, N., Maceira, A., Valsangiacomo-Buechel, E. R., Vogel-Claussen, J., Turkbey, E. B., Williams, R., et al. (2015). Normal values for cardiovascular magnetic resonance in adults and children. J. Cardiovasc. Magn. Reson. 17. 10.1186/s12968-015-0111-7.

Volume Index

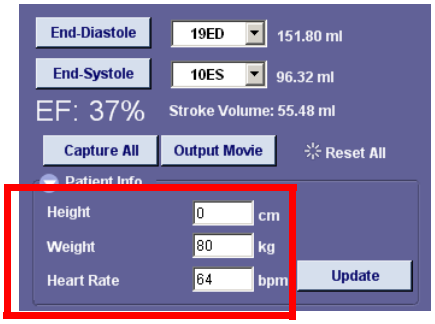
The volume index is the volume (in ml) divided by the total body surface area (BSA). BSA is calculated from the height and weight of the patient, and expressed in square meters.

To show the volume index, click the **Show Volume Index** checkbox in the **Patient Info** section of the tool panel. The results are updated in the tool panel, which show the volume index for the end-diastole and end-systole phases. Volume index values are also shown in the text results in the main window:



Note: The cardiac output can also be expressed in l/min units. The unit is configured in the user preferences. See "CardiacMR - MRTVA" on page A-36 for more information. Scroll down to the bottom of the table to find the settings. Cardiac Mass can be represented in grams with default cardiac density of 1.05 g/ml. This can be configured in the user settings.

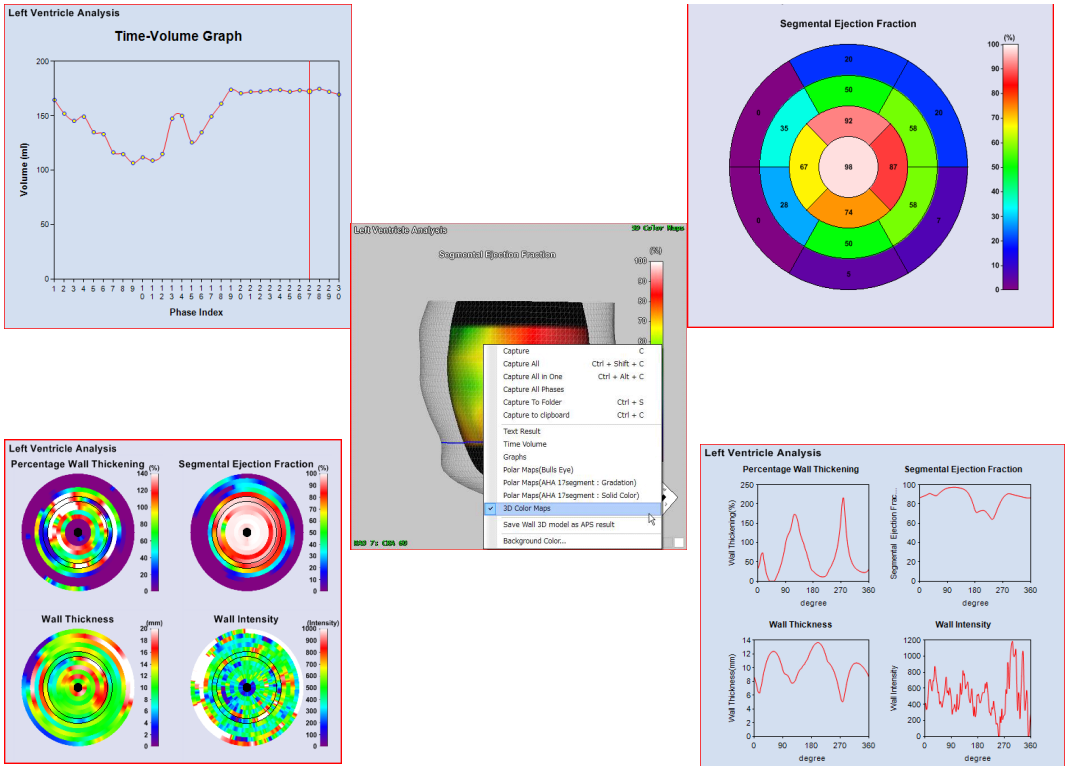
To show additional parameters, enter the height, weight and heart rate in the input boxes and click **Update**. The cardiac output parameters are displayed in the text portion (upper right quadrant) of the main window.



Text Results

Graphs

To view presentations of the data in other graphs, right-click on the graph currently displayed.

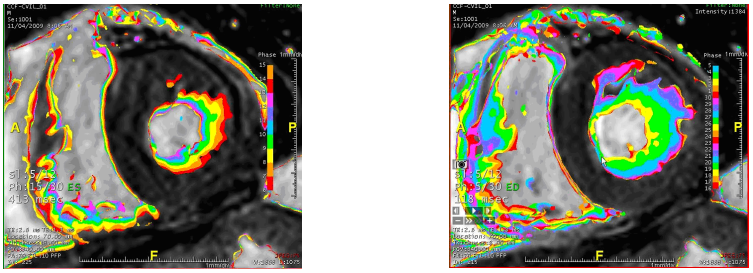


Exporting Polar Map Values to File

This feature allows you to export the numerical values in any of the AHA-17 segmented maps to a .csv file. For instructions on how to export polar map results, see "Export Polar Map Values to File" on page 6-12.

Colored Motion

Click **Motion** to see colored motion images in either the systolic or diastolic phase.



For details on colored motion, see "Colored Motion Maps" on page 6-17.

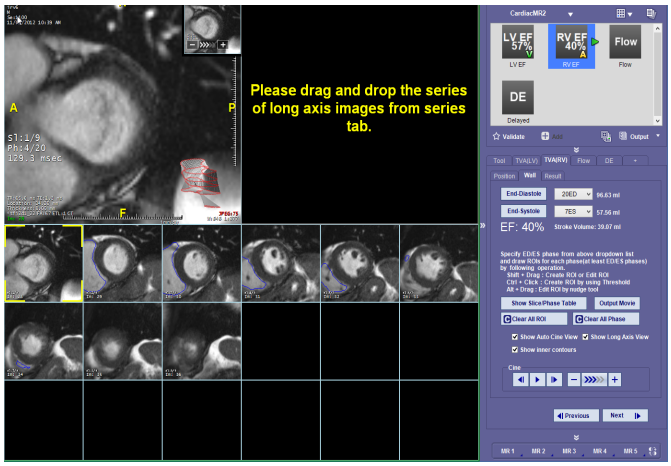
TVA of the Right Ventricle (RV)

If you have not performed TVA on the LV, load data into the **CardiacMR2** workflow. If you have already completed LV EF in the **CardiacMR2** workflow, click the **RV EF** workflow element. The software automatically detects the RV contour. You are responsible for verifying the automatic segmentation

(overlay and outlines) in both the end-systolic and end-diastolic phases. During this verification process, if the results do not meet expectations, TVA (RV) should be redone manually. The results correlate with the segmentation and will be updated with user specified changes.

It is your responsibility to verify the phases automatically chosen. If the preselected phases do not meet your expectations, proceed to perform TVA manually. Click the **Position** tab to start over and then follow the instructions on the control panel to manipulate the images.

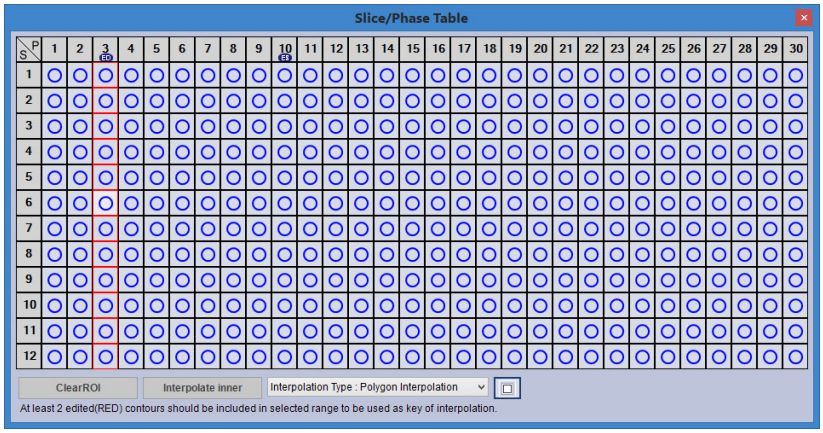
When finished, click **Next** to go to the **Wall** tab.



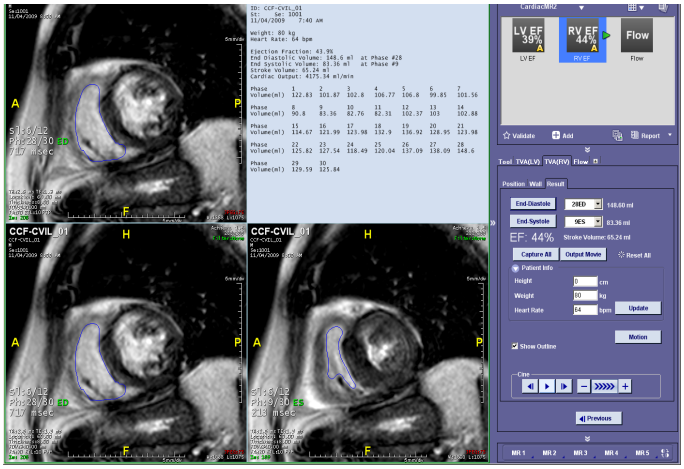
If the ROIs are incorrect, use the tools described in "Editing the Wall" on page 7-17 to edit them.

The Slice/Phase Table for RV TVA

The slice/phase table for the right ventricle is slightly different because only the inner contour is calculated. However, this table works the same way it does when performing TVA on the . See "The Slice/Phase Table" on page 7-15 for the complete description.



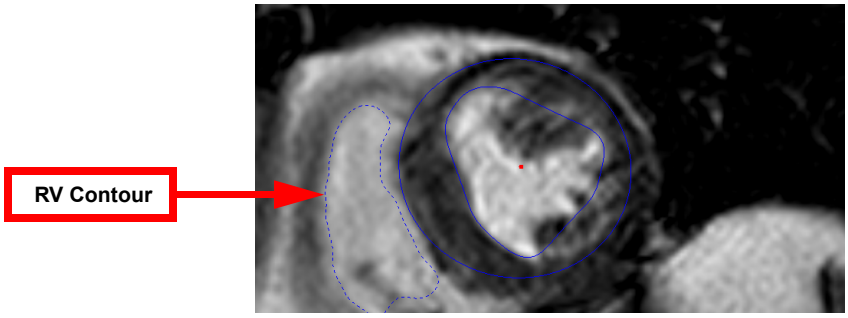
Click **Next** when finished.



As with LV EF, you can input patient information (height, weight and heart rate) and use the colored motion features.

The Combined LV/RV Workflow

You can perform TVA on both ventricles in one step by selecting the **CardiacMR** workflow. The LV/RV workflow is loaded. Both sets of contours are calculated at the same time:



The process of editing the wall contours is the same as it is in the **CardiacMR2** workflow. However, the tool panel interface is somewhat different.

The CardiacMR tool panel has buttons for editing the inner and outer walls, and for showing or hiding contours on images. You might want to hide the contour on an image if it is blocking a section of the image that you want to examine.

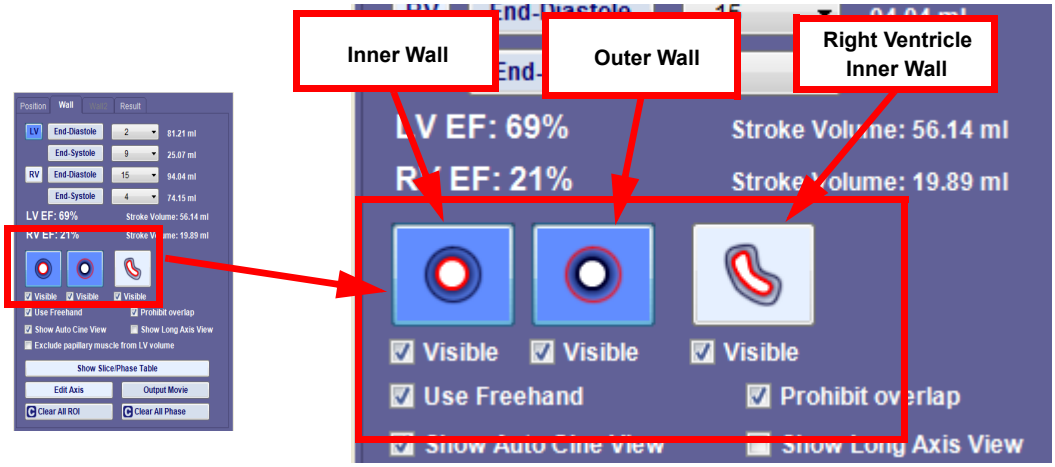


Figure 7-10: Tool Panel Buttons

Editing Buttons

The two large buttons on the left (see Figure 7-10 on page 7-25) are for editing the inner and outer walls. The button on the right is for the right ventricle inner wall. Click the appropriate button to edit the corresponding contour.

When a button is selected, it is blue, and the contour is displayed as a solid line, indicating that the contour can be edited. When the button is not selected, it is gray and the contour is displayed as a dotted line, which indicates that the contour cannot be edited.

You can also edit the walls manually by choosing **edit axis** in the tool panel. See Figure 7-10

Visible Checkbox

Beneath each button is a checkbox labeled **Visible**, which allows you to show or hide the corresponding contour.

Prohibit Overlap

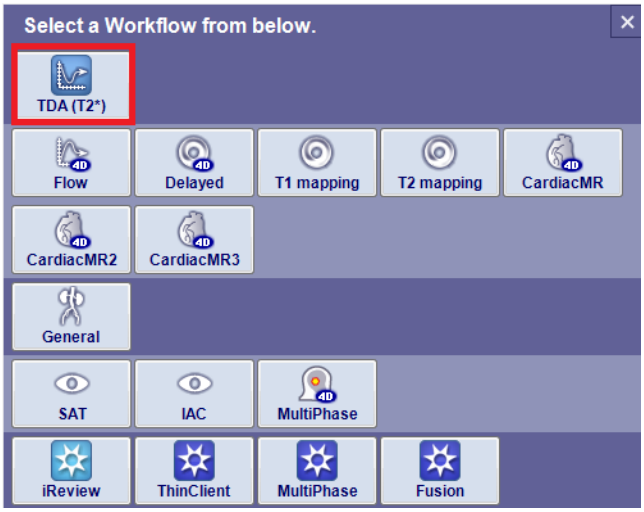
Check the **Prohibit overlap** checkbox to prevent the software from drawing contours on either ventricle that overlap contours on the other ventricle.

For complete instructions on editing a wall contour, see "Editing the Wall" on page 7-17.

Flow Dynamic - MR

The optional Flow workflow performs quantitative flow analysis on phase-contrast MR images. It provides semi-automatic contour detection for the analysis of the blood flow in vessels. The parameters calculated include stroke volume, forward and backward flow volume, regurgitant fraction, absolute stroke volume, mean flux/velocity and stroke distance.

Select an anatomical series and velocity series from a cardiac MR study, click **Load** and select the **Flow** workflow.



Note: When multi data is loaded into the Flow workflow, you have the ability to run a comparison between the series, this comparison data can then be exported. **Also note,** when non-supported flow data is loaded, a error message is displayed.

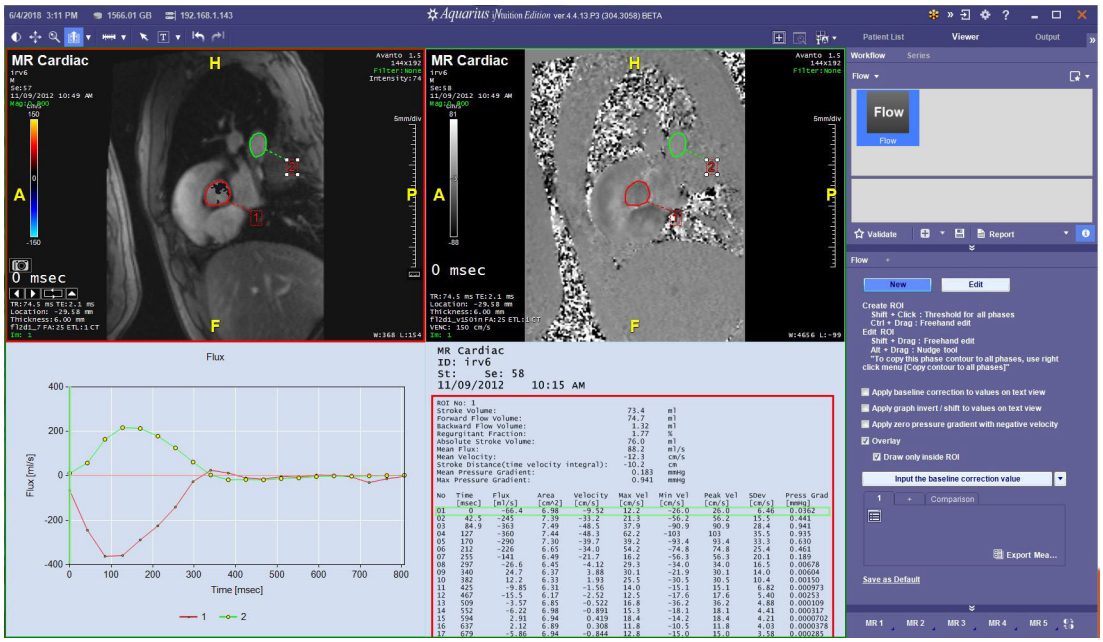
Measuring the Flow in a ROI

Draw a ROI on the anatomical data in one of the following ways:

- Create ROI
  - Create threshold for all phases: Shift+click on the image.
- Edit ROI
  - Freehand edit: Shift+drag, starting from the edge of the ROI, drag mouse across the area.
  - Using the Nudge tool: Alt+drag

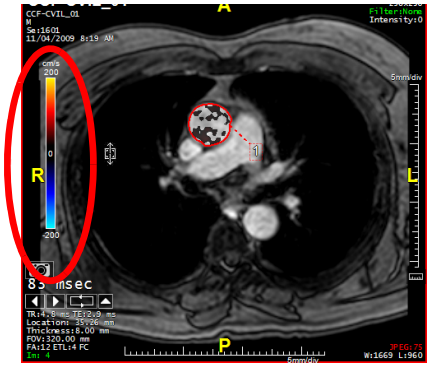
The Flow Viewer Layout

The top-left view shows the anatomical image. In the top-right view, the velocity map is displayed. ROIs in the velocity map correspond directly to the ROIs in the anatomical image. The bottom-left view shows a graph of the velocity inside each ROI, and the same values in text form are listed in the bottom-right view.



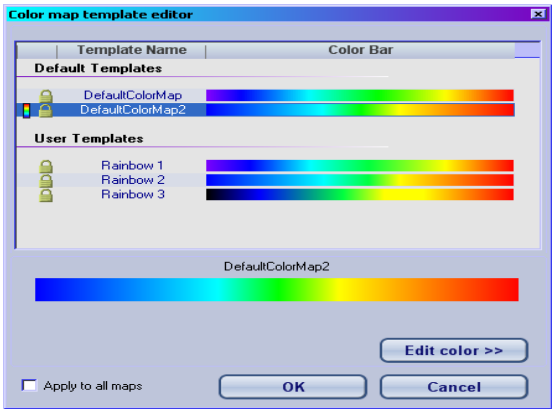
The Color Bar

The color appears on the left side of the anatomical image. It shows which colors, when laid over on the ROIs, represent velocity values at different phases. To see each phase, hold down the left mouse button and scroll up or down.



Customizing the Color Bar

To change the color map or create a customized color map, right-click on the color bar and select **Load Color Map**. The Color Template Editor is opened:



For instructions on using the color template editor, see "Changing Color Maps" on page 9-5.

Window/Level Bar

The window/level bar is located on the left side of the velocity map view. It shows the range of velocity values for the W/L setting.

Capturing Text Results

To capture the text results, right-click on the text view and select one of the capture options.

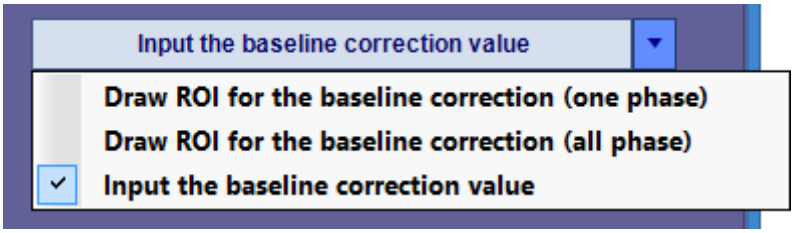
If the results for all of the phases in the series can fit in the text view, the capture is complete. If there are more phases than can be displayed in the view, a dialog is posted asking what you want to do. Click **Yes** if you want the entire text table to be captured into one image. The font size is decreased to the size necessary for all of it to fit. Click **No** if you want the text size to stay as it is. In this case, the text table is captured into more than one image.

Features of the Graph

You can display several kinds of information, and present it in different ways using the following features:

Baseline Correction

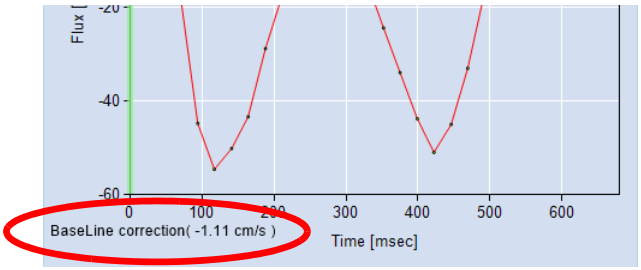
Baseline correction can be done in several ways. Select the preferred method from the baseline input menu at the bottom of the tool panel.



Drawing the ROI for baseline correction (one phase)

1. Make sure that the menu item selected is **Draw ROI for the baseline correction (one phase)**, and then click the button. It changes to a dark blue color to indicate that it is selected.

2. Hold down the **Shift** key and draw a small ROI on an area of the anatomical image that has uniform color. The baseline is displayed at the bottom of the graph window:



The same baseline correction is used for all phases.

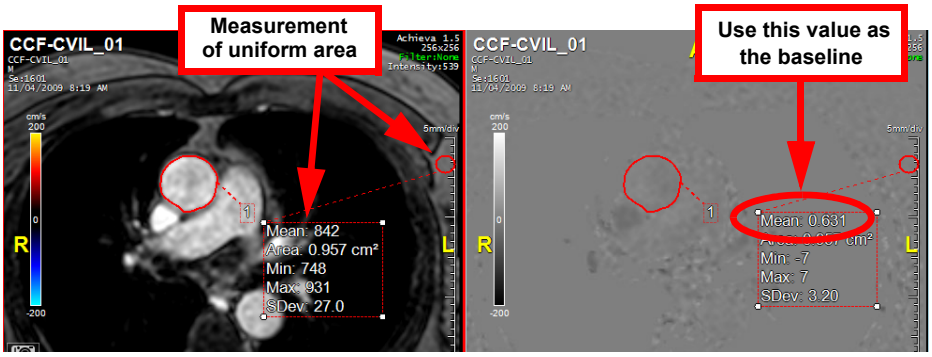
Drawing the ROI for baseline correction (all phases)

This is performed the same way as you would to draw an ROI for baseline correction in one phase, but in this case, the baseline correction is calculated separately for each phase.

To verify, scroll through the anatomical images. The vertical line in the graph view steps through each phase, and the baseline correction displayed at the bottom of the graph changes for each phase.

Inputting the baseline correction value

1. Obtain an ellipse or other area measurement on a small area of the anatomical image that has uniform color.



2. Use the **Mean** value in the *velocity map* view as the baseline. In the image above, that value is 0.631.

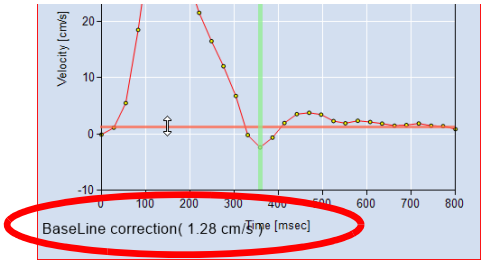
3. Select **Input the baseline correction value** from the menu at the bottom of the tool panel. Or you can right-click on the graph and select **Baseline correction**. Either will open the **Baseline Correction** dialog.

4. Enter the mean value in the dialog.

To apply the baseline correction to the text table, check the box labeled **Apply baseline correction to values on text view in the tool panel**.

Moving the line on the velocity graph manually

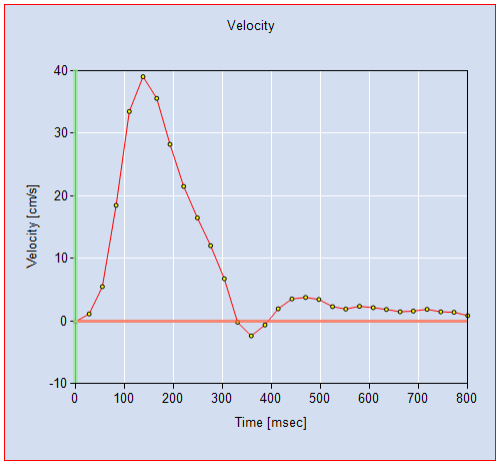
On the Velocity graph, click the horizontal pink line to move it up or down. The baseline correction appears in the bottom-left of the graph view (circled):

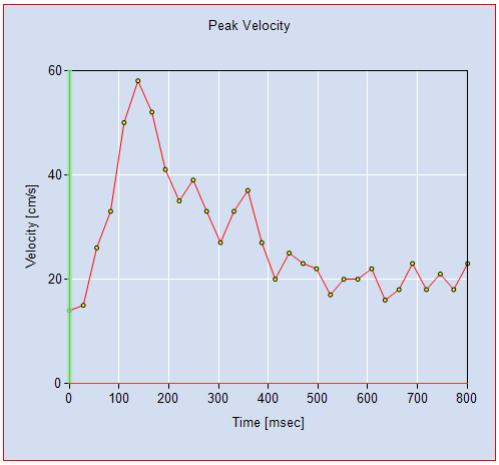


Note: One baseline correction value is applied to all phases.

Displaying Different Graphs

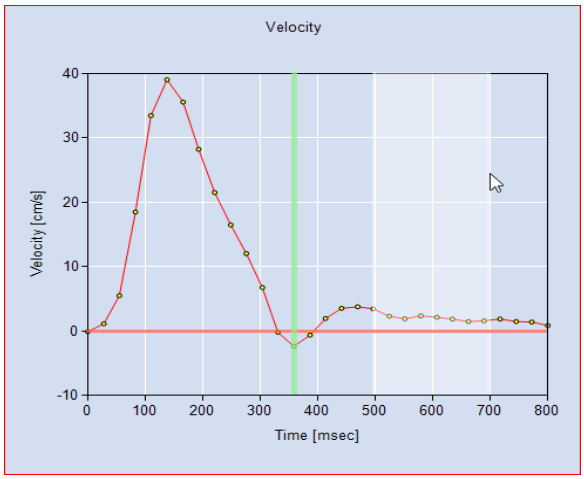
You can display the following graphs in the graph view: Flux, Area, Velocity, Max Velocity, Min Velocity, Peak Velocity and Standard Deviation.





Zoom

To zoom in the graph, click anywhere on the graph and drag the mouse in a horizontal direction. The area selected as you scroll turns white to indicate the zoom amount. The graph zooms in by a factor inverse to the width selected, so the more area selected, the smaller the zoom factor.



To reset he graph to its original size, click the icon in the lower-left corner.

Invert Graph

To invert the graph, right-click on one of the data points in the graph curve, and select **Invert** from the menu.

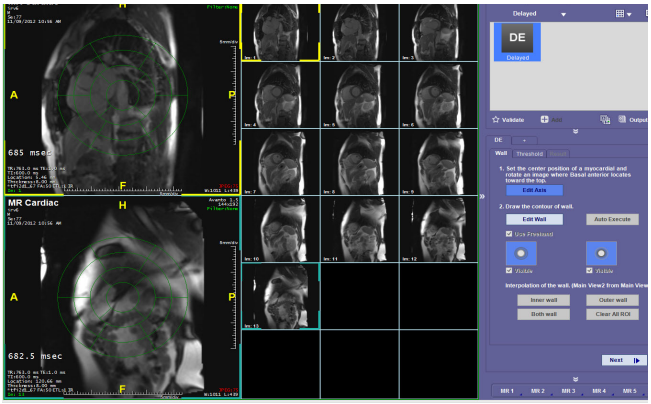
Note: You can select the type of results you wish to view initially upon calculating TVA for Right Ventricle including: Text Results & Time-Volume depending on your preference. See Appendix A: "CardiacMR - MRTVA" on page A-36 for more information.

Delayed Enhancement

Introduction

The delayed enhancement procedure calculates the volume of the part of the ventricle wall being examined.

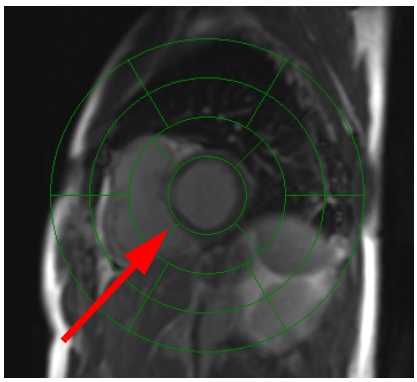
Load a single, short-axis DE series.

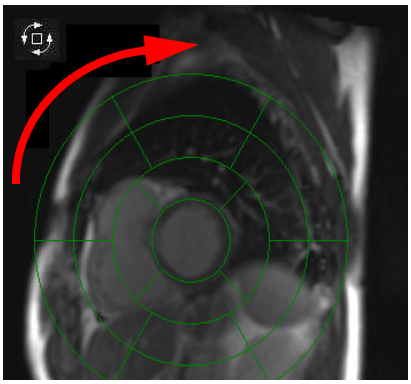


Workflow

Step 1: Define the Center Position and Correct Image Orientation

1. Click the **Edit Axis** button in the tool panel to display the AHA map, and to allow rotation.
2. Pan the image so that the center of the ventricle short axis is directly beneath the center of the AHA map.
3. To correct the image orientation, click and drag the cursor in a circular motion.





Step 2: Define the Wall

There are a few ways to draw the wall contour: freehand, multi-click, and auto execute. To draw the contour in freehand, make sure the **Use Freehand** box is checked. To use the multi-click method of drawing, uncheck the **Use Freehand** box.

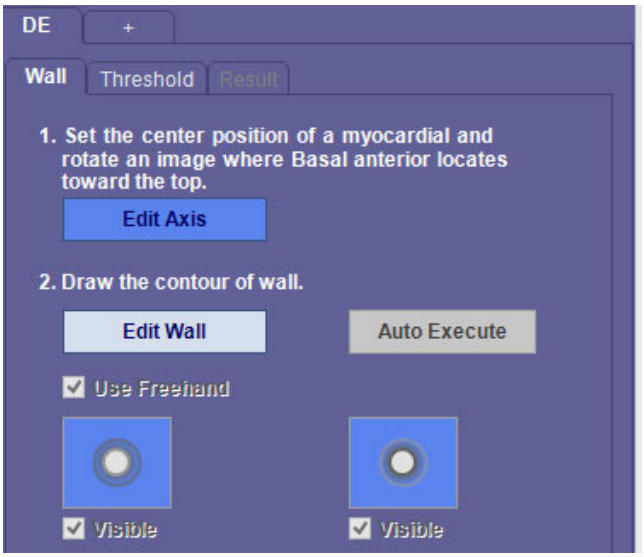


Figure 7-11: Tool Panel - Wall

Note: It is recommended that you zoom in on, and, if necessary, change the window/level of the image, to give you the best view.

Auto Execute

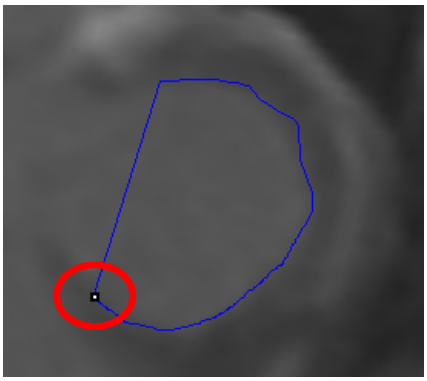
Click the **Auto Execute** button (see Figure 7-11 on page 7-32) to have the contours calculated automatically.

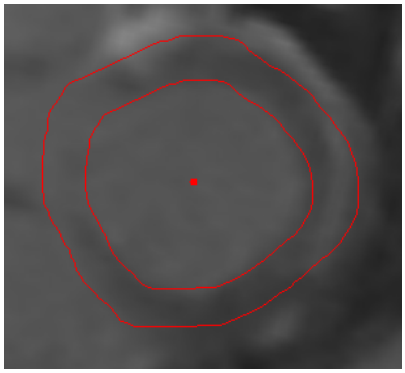
When finished, click **Next** in the lower-right corner of the tool panel.

Calculate the Contours Manually

Drawing Freehand

Hold down the **Shift** key and draw with the cursor around the inner wall. The cursor is displayed as a small white dot (see image at right). When you are finished, release the mouse. AQi will draw the outer wall (see the following figures).

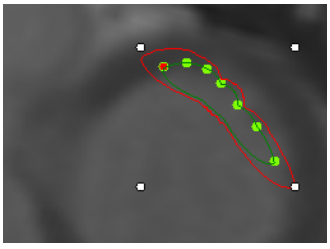




Drawing Using Multi-Click

To draw using multi-click, deselect the **Use Freehand** box. Hold down the **Shift** key and click the mouse along the inner wall. In the figure below, the red contour is being supplied by AQi as you enter clicks. It is drawing the outer wall. When you have drawn the full contour of the inner wall, the outer wall will have the correct shape.

Note: This is supported for both LV and RV.



Step 3: Select the Threshold

There are three options provided for threshold selection within the myocardium ROI:

- Full Width at Half Maximum (FWHM) - Auto
- FWHM - Manual
- Semi-Automated ("n"+ Standard deviation)

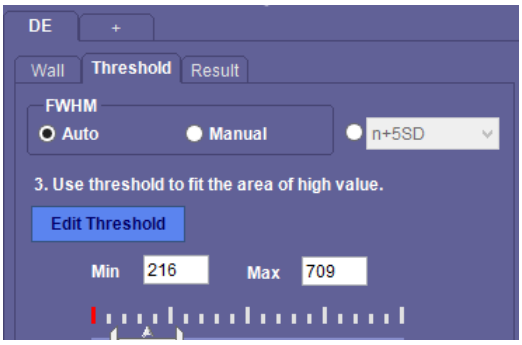


Figure 7-12: Edit Threshold Panel

FWHM Auto

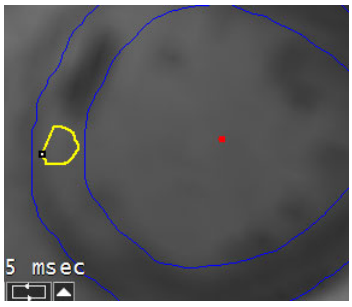
The threshold is calculated automatically from the myocardium in all slices, using the following formula:

$Th = MaxSI_{all} * 0.5$

Th:	Threshold
$MaxSI_{all}$:	The max signal within the myocardium of all slices

FWHM Manual

1. Select the **Edit ROI** button in the tool panel.
2. Draw an ROI within an *abnormal* lesion of the myocardium to define the reference value.



Note: If there is no abnormality found in this series, click the N/A button.

The threshold is calculated and overlayed in each slice, using the formula:

$Th = MaxSI_n * 0.5$	
Th:	Threshold
$MaxSI_n$:	The maximum signal of the lesion ROI

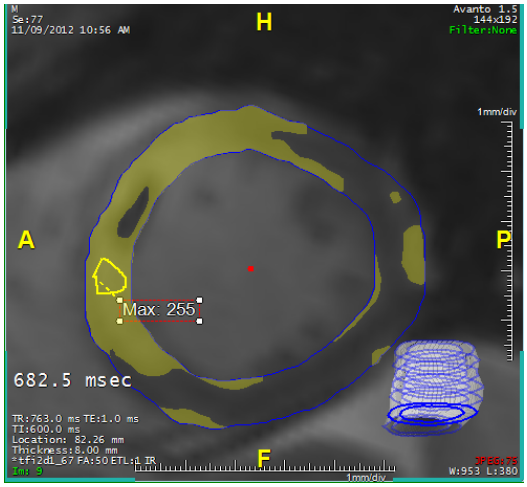


Figure 7-13: Manually Selected Threshold

Note: Make sure to check the Overlay checkbox in the tool panel to see the overlay (see Figure 7-11 on page 7-32).

"n" + SD

1. Select the **Edit ROI** button in the tool panel.
2. Draw an ROI around normal tissue in the myocardium.

The threshold is calculated automatically from the following formula:

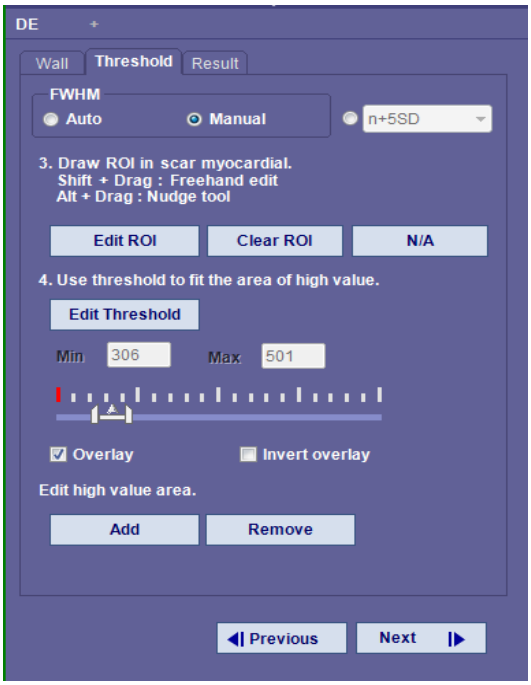
Th = n + xSD (2<=x<=6)	
Th:	Threshold
n:	The mean signal of a normal ROI
SD:	The standard deviation of the normal ROI

Invert Overlay

You can invert the threshold overlay so that the normal area is highlighted rather than the abnormal areas. This way, the color will not obstruct your view of the tissue you need to examine.

Check the **Invert overlay** checkbox at the bottom of the **Threshold** (see Figure 7-12 on page 7-34), or at the top of the **Result** (see) tabs of the tool panel.

To edit areas of enhanced myocardium, use "Add" button to add a new mask for the high contrast area. Use shift-left mouse click and drawn on each slice. Use "remove" button to delete masked areas by utilizing the shift-left mouse button. When "next button" is selected the value will be recalculated.



Proceed to Results

Click **Next** when finished.

Step 4: Results

The result is an analysis of the abnormal area of the ventricle wall that is under examination.

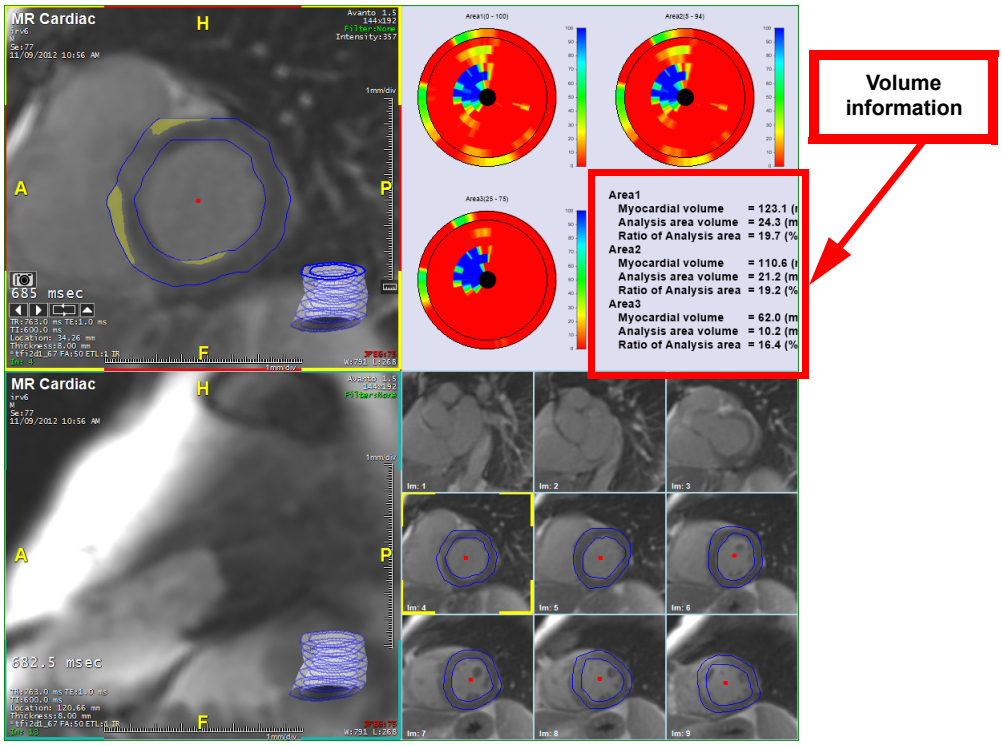


Figure 7-14: Results

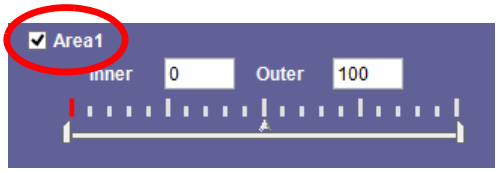
You can display up to three polar maps in the upper-right window. Each polar map illustrates the following information:

- The ventricle wall volume
- The volume of the area under analysis (the area defined by the threshold, and indicated with the overlay)
- The percentage of the threshold volume within the whole polar map

Areas of the Wall

You can decide how the information is displayed in each polar map. There are three slider bars in the **Result** tab of the tool panel, each of which allows you to define the inside and outside boundaries of an area, based on thresholds. The area boundaries also determine the size and position within the wall that will show an overlay in the main views and slice views.

To display the polar map and volume information for a specific area, click the checkbox next to the area name (circled in the figure below). In Figure 7-14 on page 7-37, all three areas are checked, so all three polar maps and volume information are displayed on the screen.



To display specific sections of the wall, you can set the slider boundaries to wide or narrow ranges. The **Inner** value represents the percentage of the entire wall width where the inner boundary is set. The Outer value represents the position of the outer boundary, by percentage of the wall width.

The following shows two examples of areas defined by the sliders, as shown in the overlay on the Main 1 image and the corresponding polar map.

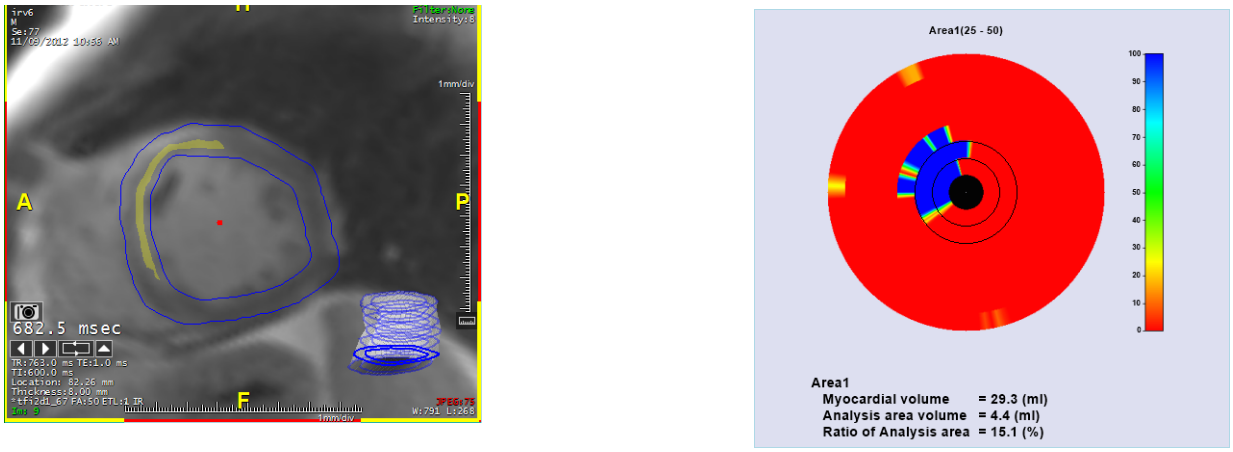


Figure 7-15: Inner Boundary Percentage of Wall - 25; Outer - 50

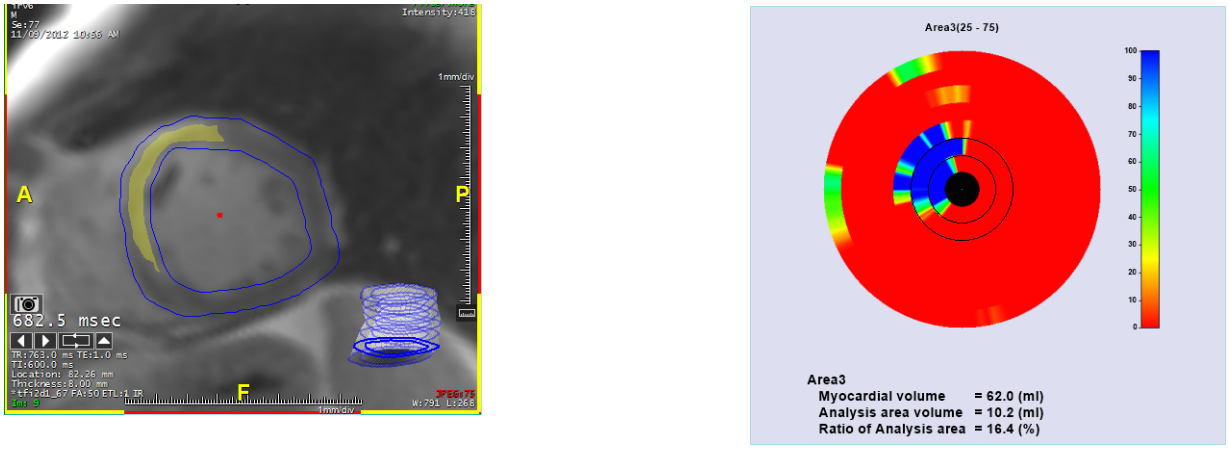


Figure 7-16: Inner Boundary Percentage of Wall - 25; Outer - 75

Whenever these settings are changed, click the **Update** button to redisplay the images and maps.

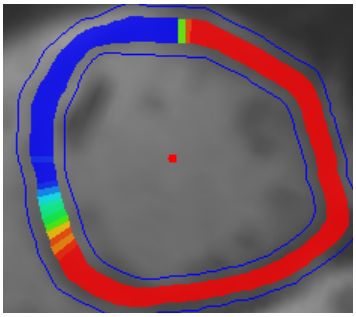
Other Settings

- Threshold Overlay

  The overlay showing the abnormal area of the wall on an image (see bottom left, in Figure 7-16).

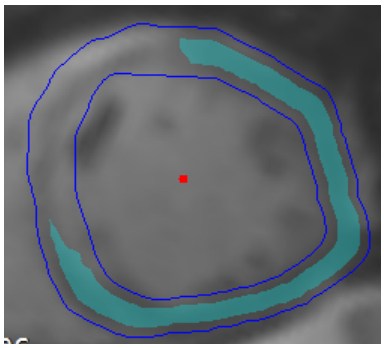
- Polar Map Overlay

  An overlay showing the entire section of the wall that is defined by the area slider. The overlay shows volume values in polar map form. See image at right. The thin blue lines represent the inner and outer boundaries of the wall. The strip inside, which has the polar map overlay, is the area defined by the slider for that area.



- Invert Overlay

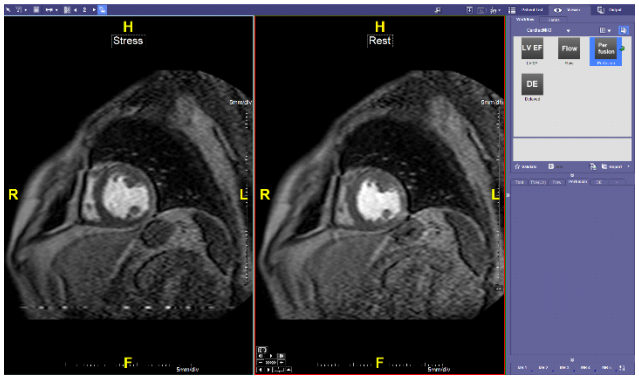
  An overlay on the normal tissue within the ventricle wall, rather than on the abnormal tissue.



MR Cardiac Perfusion

Cardiac MR Perfusion determines whether there are perfusion defects in the myocardium of the left ventricle caused by narrowing of one or more of the coronary arteries. You can generate a side-by-side view of both the rest and stress views of a particular series for qualitative analysis, by following the steps below:

1. Load the study in the **Cardiac MR** Template.
2. Select the Perfusion workflow element. The **Series** dialogue is shown
3. Drag-and-drop perfusion series to stress and rest view.
4. Confirm the Slice/Position Navigation overlay is displayed on the image by hovering over bottom left corner of image.



To change the orientation of the rest/stress views and the layout of the series, see "CardiacMR" on page A-36.

Chapter 8 Segmentation, Analysis, and Tracking

Topics in this chapter:

The **Segmentation, Analysis, and Tracking (SAT)** optional module is used to segment, analyze, and track lesions over the course of time. The goal of the study is to analyze a volume in its present state, as well as track its rate of growth over time. A prime example of such a study is to analyze and track the growth of lung masses.

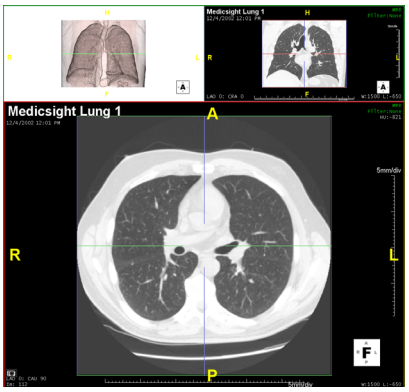
Note: Gantry tilt is not supported in SAT.

Starting the SAT Study

To start SAT, do one of the following:

- Right-click a lung study or series and select **SAT (Lung)** from the menu.
- Select a lung study or series and select the **Load** button in the Data Management Tools. The Workflow menu opens, then select the **SAT (Lung)** button.

The SAT module is started, and the selected data is loaded into the SAT main viewer. The SAT main viewer is displayed on the left of the screen, and appears in **2+1 Scan** layout, as shown in the following figure:



The three images in the **2+1 Scan** layout are described in Table 8.1.

Table 8.1: 2+1 Scan Layout

Area	Description
Top Left	Global view. Findings are marked with a small red dot on each location containing a suspected lesion.
Top Right	Coronal MPR view of the scan.
Bottom	Axial MPR view.

You can also choose 2x2 layout from the layout menu in the top tool bar.

This shows the three views described for 2+1 Scan layout, but also displays a 3D volume rendered image, as shown in Figure 8-1.

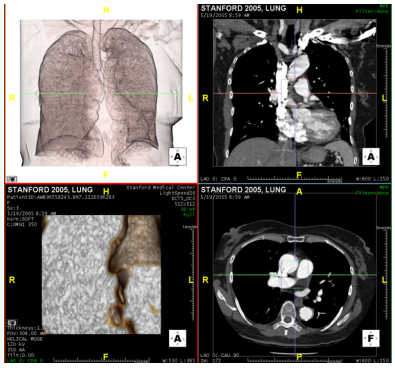


Figure 8-12x2 Layout

The Tool Panel

To begin performing SAT, click the SAT tool button, located in the Tool Panel on the right side of the screen.

The SAT Tool element is displayed.

Right-click Menu Options

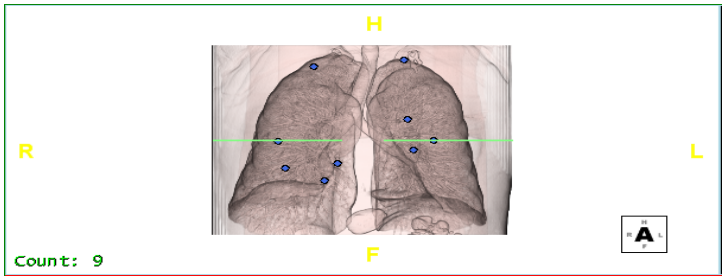
The right-click menu options work the same way in the SAT module as they do in the 3D Viewer. Please see "Right-click menu on the image" on page 3-4 for a complete description.

Performing SAT with Advanced Processing

If Advanced Processing (APS) has been performed on this data to find lesion candidates, you can see the locations of the candidates by clicking the **Candidate** button in the APS section of the Top Toolbar. (Figure 8-2)

Figure 8-2: Show Lesion Candidates Found By APS

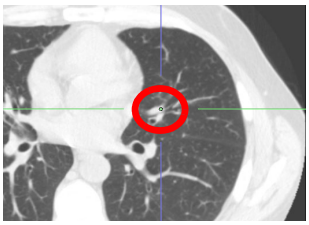
This feature displays the lesion candidates in the Global View image:

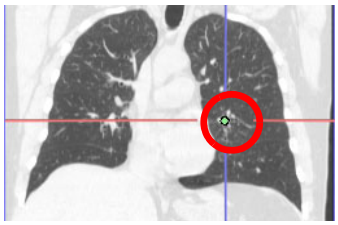


Elements of the Global View

- **Blue Circular Dots** - Indicate locations of lesion candidates found by Advanced Processing.
- **Horizontal Green Bar** - The vertical position indicates which slice is currently displayed in the axial view.
- **Blue Diamond** - When a candidate is selected, it becomes *active*, which is indicated by the blue circular dot changing to a diamond shape (not shown above).
- **Number of Candidates** - Located in the lower-left corner of the global view, shows the number of candidates found by Advanced Processing.

Click on one of the blue dots, and the corresponding location of the potential lesion is displayed in the axial and coronal views.





Note: The lesion candidates found by APS are only possibilities. Each candidate must be checked and verified by a doctor or technician.

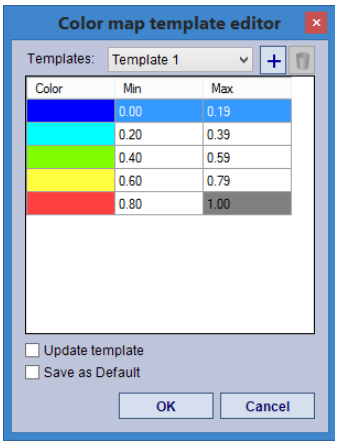
Colorizing the Candidate Markers

You can display the candidate markers in various colors according to their score.

Note: You are obligated to define the parameter ranges that are used in this procedure. When first accessed, the user interface for setting these parameters contains generic default values having no particular significance.

To enable color markers, open the user preferences and click **SAT** in the navigation panel, to open the SAT preferences screen. Check the **Colorize candidate markers by score** box.

To configure the colors, right-click on the color bar, on the left side of the Global view. Select **Load Color Map**. The Color map template editor is opened:



The **Color** column shows the color that is appled to candidates that fall within the **Min** and **Max** values on the same row.

To change the color, double-click it, which opens the Windows color palette, and select a new color.

To change the range for a color, click twice (with a slight pause in between clicks) to highlight just the min or max value to be changed, and then type the new range.

Check the **Update template** box at the bottom of the dialog to save the change. You can also save the change as the new default by checking **Save as Default**. Then click **OK** to finish.

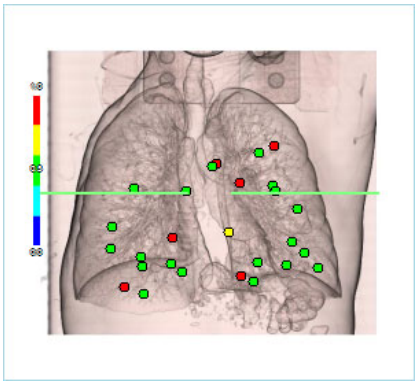
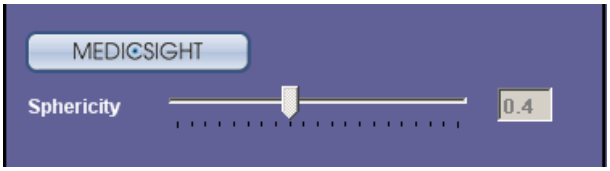


Figure 8-3: Candidate Markers Colored by Score

Medicsight APS (Optional)

If the data has been processed by the Medicsight Lung APS module, the tool panel will contain a button for displaying the suspected lesions as found by Medicsight. This behaves exactly like the **Candidate** button in the APS section, shown in the following figure. You can use either button to display the lesion candidates.

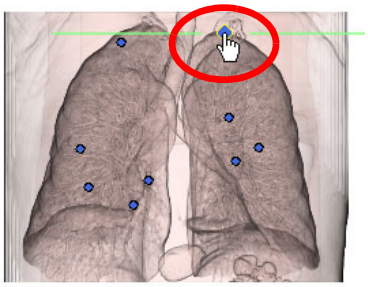


The Sphericity scale allows you to determine how sensitive the display of potential lesions should be. A *lower* number in the box means that the display is more sensitive, and therefore, that more candidates

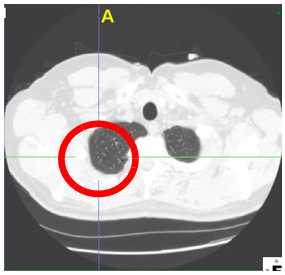
will be considered potential lesions, whereas a higher number means that fewer candidates will be displayed.

Examining Lesion Candidates

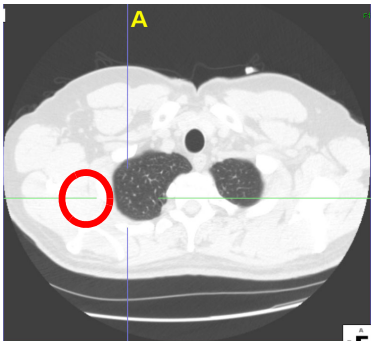
1. Use the candidate markers on the global view to locate the corresponding suspected lesions in the axial or coronal view.

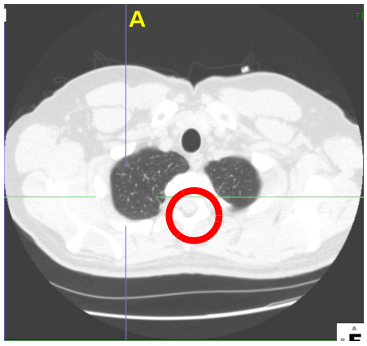


2. Click the marker for the first lesion to be examined (see image at right). The suspected lesion is displayed in the axial and coronal views (see the following image):



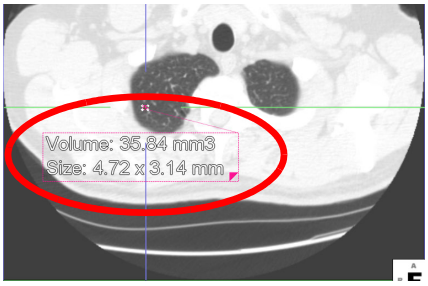
3. Scroll through the slices using the middle mouse button, to examine the spot in other slices.



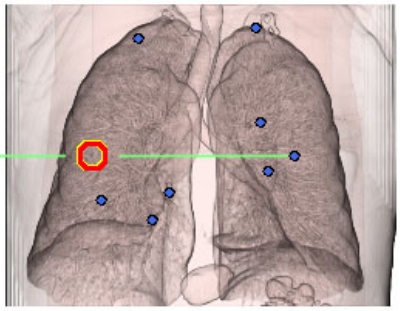


4. If you determine that this candidate is a lesion, you can confirm it by using the **Confirm** button in the tool panel.

   The volume and area of the lesion are displayed on the MPR view, as shown below:



In the global view, the confirmation is marked with a red circle:

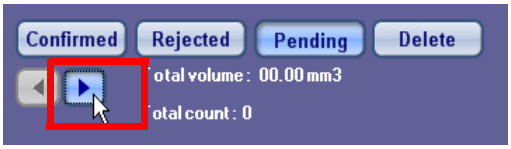


To reject a lesion candidate, click the **Rejected** button. The blue dot is then displayed as a green dot. The lesion also appears in the Findings list as Rejected (**R**) (see "The Findings Window" on page 8-14 for more information about the Findings list).

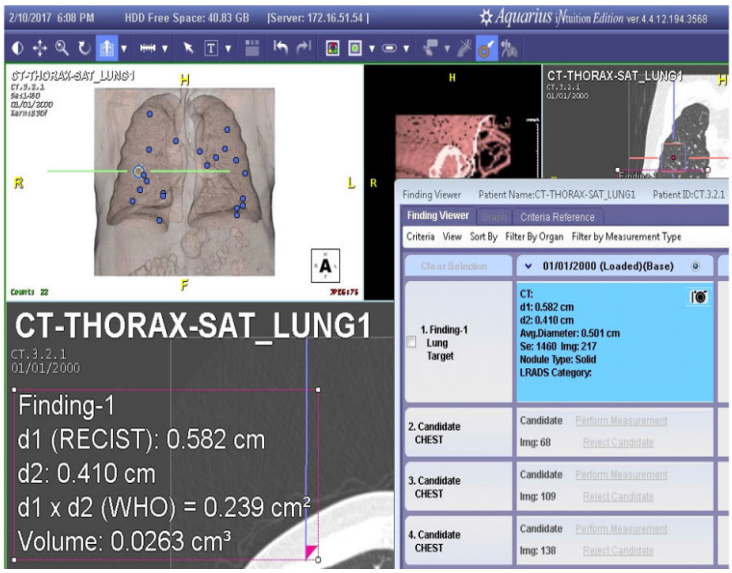
To delete a lesion candidate, click the **Delete** button when that candidate is selected.

Next Lesion Candidate

To examine another candidate, click the blue dot in the global view directly, or click the right-arrow button in the tool panel (circled in the following figure).

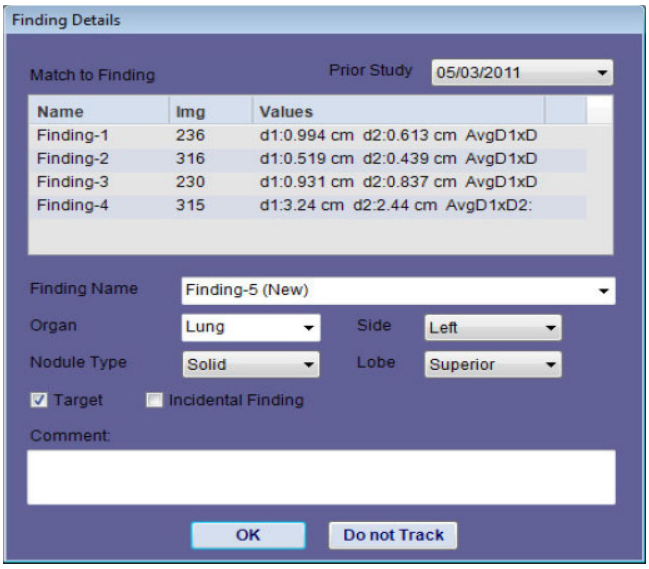


The candidate markers will display and list in order of this priority from Superior to Inferior: Right Lung, Left Lung, Indeterminate. The Findings Viewer will also be in the same order.

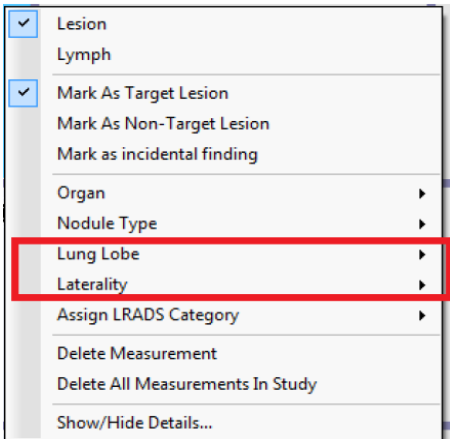


In Finding Details, you can confirm the location of the findings. If anything is incorrect, you can change from right or left lung.

\



Also, in the context menu, you can define the lobe and laterality of the identified findings.



Adding Your Own Findings

You can, of course, add your own findings to the report, in addition to or instead of those found by Advanced Processing. The procedure for performing SAT manually is the same regardless of whether Advanced Processing has been performed on the data. This procedure is described in the following section.

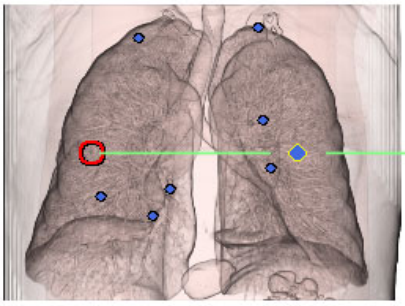


Figure 8-4: Next Candidate

Performing Manual SAT

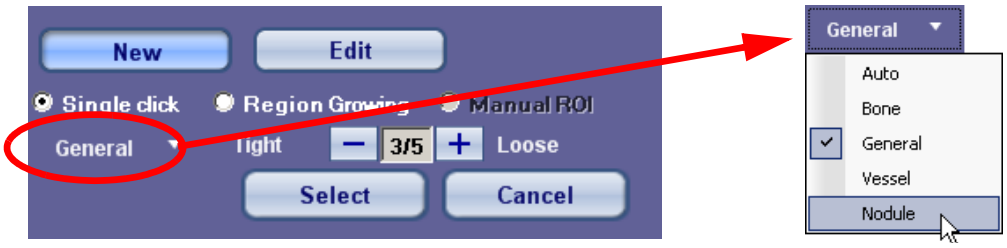
New Lesions

1. In the main SAT viewer, left-click on the axial image to scroll through the slices.

2. When you view a potential lesion, click the **New** button located in the tool panel. A new panel is displayed beneath the **New** And **Edit** buttons.

3. To highlight the lesion on the axial view, check the **Single click** button on the tool panel (circled in the figure above).

4. Select **Nodule** from the region type menu.



Hold down the **Shift** key and click on the suspected lesion in the axial view. The area and volume of the lesion are automatically calculated and displayed on the image:

Figure 8-5: Left - Shift+click on Candidate; Right - Result Displayed

Editing Lesions

If the region included in the automatic area and volume calculations is incorrect, you can edit the lesion to add to, remove from or redraw the region.

Note: ManualROI and Sphere are both disabled when Gantry Tilt data is loaded for SAT. **Also note:** You are obligated to define the parameter ranges that are used in this procedure. When first accessed, the user interface for setting these parameters contains generic default values having no particular significance.

To begin editing, click the **Edit** button. The Edit menu is displayed:

There are three ways to edit a lesion: by a single click, by region growing, and by drawing around a region of interest (ROI).

Single Click

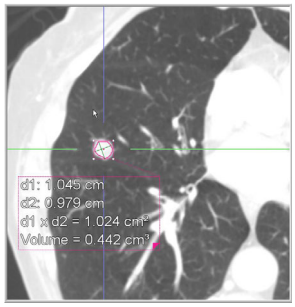
Single Click allows you to click once on the area of the lesion candidate, and the SAT Lung module will calculate the appropriate area and volume.

Click the **Single click** button in the Edit tool panel. The Single Click tool is displayed in the tool panel:

1. Select **Nodule** from the pull-down menu.

2. Adjust the sensitivity of the region drawing. **Tight** means a smaller area will be drawn, while **Loose** means a larger area will be drawn.

3. Hold down the **Shift** key and click on the lesion in the main axial view. The area of the lesion is drawn automatically:



Region Growing

Editing a lesion using the Region Growing feature is done exactly the same way as with the Single Click feature, except that the end result is a mask region, rather than a drawn boundary. Furthermore, you can continue to grow a region if the first click has not resulted in a large enough area.

To edit a lesion using Region Growing, click **Region Growing** in the Edit tool panel, and then follow the instructions listed under **Single Click**.

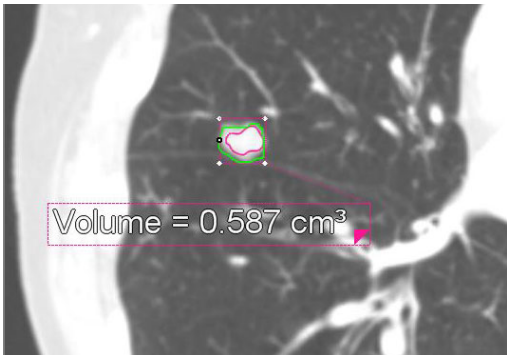
Manual ROI

The Manual ROI feature allows you to redraw the boundary around the region, to add to it if the original calculation did not include the entire lesion, and to cut out extraneous regions that might have been included.

1. Click the **Manual ROI** button in the Edit tool panel. The **Redraw**, **Add**, **Cut**, and **Edit** functions are displayed below it.

2. Click whichever tool is needed to correct the lesion area, by clicking the radio button to the left of each tool.

    - **Redraw** - Draw a new boundary around the lesion area to replace the boundary that was drawn by the software. The redrawn boundary is shown in green:



- **Add** - You can also draw a boundary around an adjacent region to add it to the lesion that is currently defined. Click the **Add** button begin adding to the lesion.

Note: The new area must be contiguous to the existing area. If the new area is not touching the currently defined lesion, it will not be added.

- **Cut** - To remove an area from the lesion, click the **Cut** button, hold down the **Shift** key, and draw a boundary around the area to be removed.
- **Edit** - Click the **Edit** button to redraw a section of the boundary.

When you have finished modifying the boundary, you must tell the system to recalculate the area and volume of the new lesion. This is done by clicking on **Click here to recalculate**. Once you have clicked, the new measurements are displayed inside the box.

Undo Edit

If you are not satisfied with the changes you have made to the boundary, you can undo the edit. To undo, click the undo icon ( ) in the top toolbar, and the measurement values will be restored to their previous values. If measurements are being tracked, the same measurement in the Findings Viewer will also change back. If you are using a Measurement Protocol, that measurement will also be restored. If you decide to redo that edit, click the redo icon ( ), and the measurement values will be recalculated to what they were after the edit.

Note: You can also use CTRL-Z to undo, and CTRL-Y to redo an edit. **Also note:** You can not remove the measurement itself using Undo. To remove a measurement, right-click on it and select Delete.

Manual Edit on All Planes

In addition to the axial plane, you can edit lesions directly on the coronal and sagittal planes.

1. If you have not already done so, click on **Click here to recalculate** before switching to another plane. Editing will be disabled in any other plane if edits have not been recalculated.

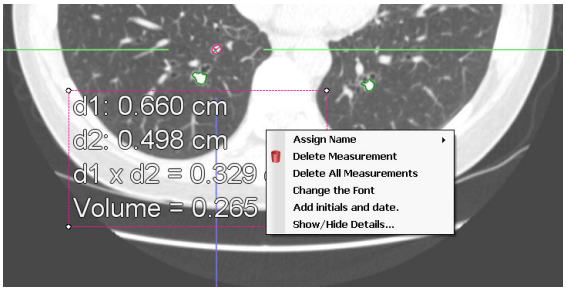
2. Select a 2x2 or other layout that gives you access to the coronal and sagittal images. The lesion that was selected in the axial plane is also selected in the other two views.

3. Perform edits in one of the other planes.

4. Before switching to another plane, recalculate the measurements.

Measurement Options

When you right-click on a measurement annotation, the following menu is displayed:



These options allow you some flexibility in the naming and manipulation of the annotation, and are described below:

- **Assign Name**

  Allows you to insert a name in the annotation text.

- **Delete Measurement**

  Deletes the measurement that you right-clicked on.

- **Delete All Measurements**

  Deletes all measurements from the series. The corresponding markers, if Advanced Processing was performed on the series, are also removed.

- **Change the Font**

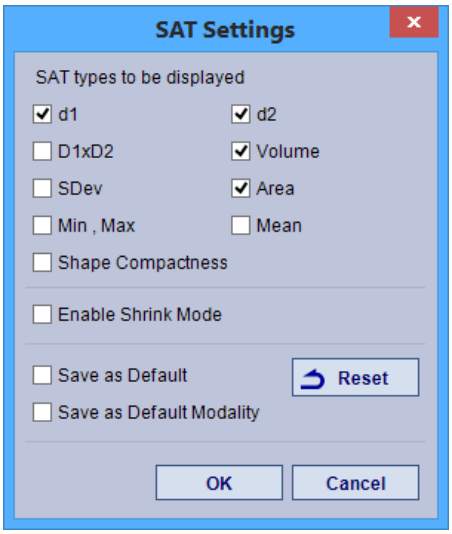
  Allows you to change the font and size of the annotation text.

- **Add initials and date**

  Opens a text-input box where you can enter a set of initials or a name. The initials and the current date are then added to the annotation.

- **Show/Hide Details**

  Opens the SAT Settings dialog box, where you can configure the contents of the measurement display. Check the box for each type of measurement value to be displayed.



Other Settings

- **Enable Shrink Mode** - This setting causes the minimum number of values to be displayed in a measurement, regardless of how many measurements are configured for the display. If you want to see all the values selected in this dialog, make sure **Enable Shrink Mode** is *not* checked.

- **Save as Default** - The current configuration of measurements to be displayed is saved as the default configuration.

- **Save as Default Modality** - The current configuration of measurements to be displayed is saved as the default configuration, only for the modality of the image currently being measured. (This will not change the default displays for other modalities.)

- **Reset** - Sets the values back to the original default.

The Findings Window

The **Findings** window displays a list of all potential lesions found during the examination, with the linear dimensions, area, and status (Confirmed, Pending, or Rejected) of each.

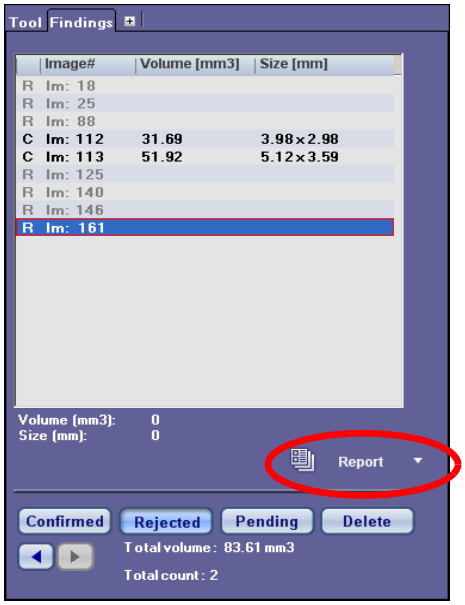


Figure 8-6: The Findings Window

Generating Reports

Images and measurement data are automatically captured for display in the SAT report, so you do not need to capture any images specifically for a report. To begin a report, press the **Report** button located in the lower-right corner of the Findings Window (circled in Figure 8-6).

If this button does not say “Report”, click the down-arrow to the right to display the menu. Select “Report” and then click the button to open the report file.

To save all findings, right-click and select **Save Scene**. You will need to return to the Patient List and send the entire series back to PACS to keep the volume calculations for follow up.

Doubling Time

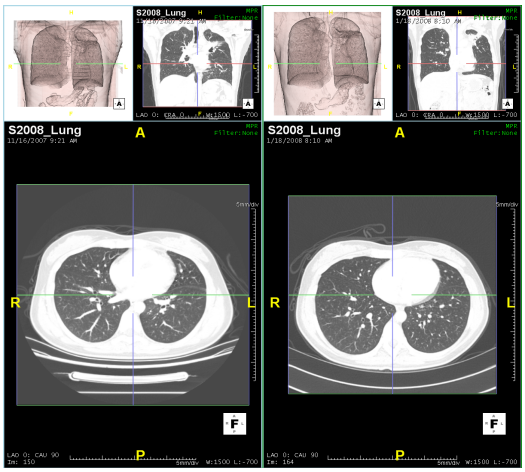
"Doubling Time" refers to the time required for a quantity to double, based on the observed quantity at two given time points, and assuming the growth rate is constant.

Note: In reporting the "doubling time," the software assumes a constant growth rate. However, the software does not verify that the growth rate is in fact constant, or that the measured quantity at the two given time points is accurately representative of any specific physical quantity. This calculated value is for reference only. It is your responsibility to use this information in an appropriate manner.

The formula applied is Td = log(2) / log (1+r/100), where r is the growth rate between the two observed time points, and Td is the reported "doubling time." To find the doubling time of a finding, you must compare it with another study of the same area on the same patient. The SAT module calculates the doubling time only by comparing two studies. Select two studies performed at different times. The purpose of the study is to track the change in volume as time progresses.

To calculate the doubling time, perform the following:

1. From the Series List, select the two studies to be compared and open SAT (if you need instructions, see "Starting the SAT Study" on page 8-1). You can view side-by-side images of the two studies:



2. If either or both of the studies has had Advanced Processing, show the findings in applicable studies by clicking the **Candidate** button in the APS section of the Top Toolbar. Examine each finding to confirm or reject it (see "Performing SAT with Advanced Processing" on page 8-3).

   If either of the studies has not had Advanced Processing, you must find the lesions manually in those studies. See "Performing Manual SAT" on page 8-9 for instructions.

When lesions have been identified and confirmed in both studies, you are ready to compare matching lesions for possible changes.

1. Click the **Findings** tab in the Tool Panel to show the findings list.

2. Click the **Match** button, located in the lower left section of the **Findings** window. The application displays a comparison of the two studies, along with the doubling time, as shown in the images below:

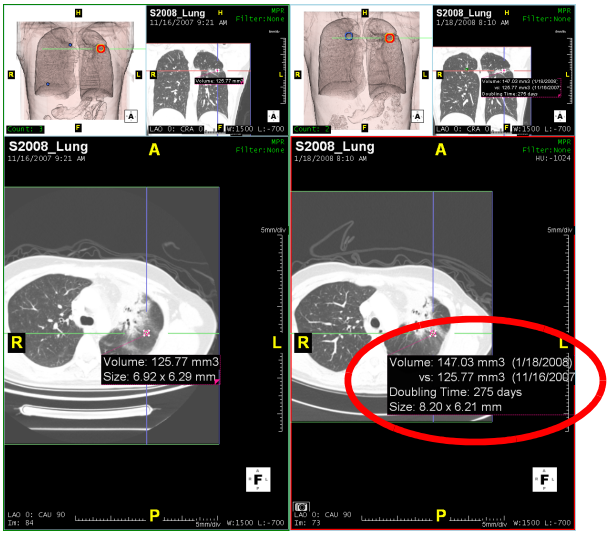
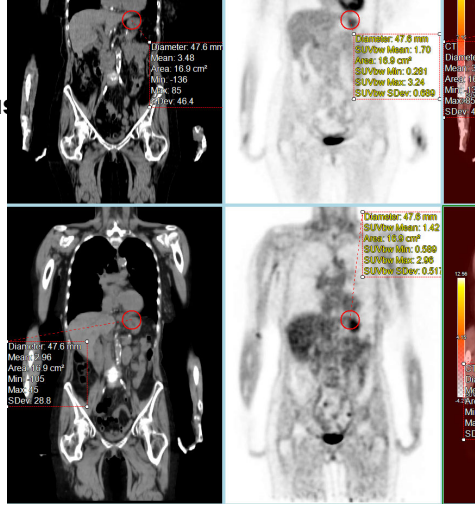


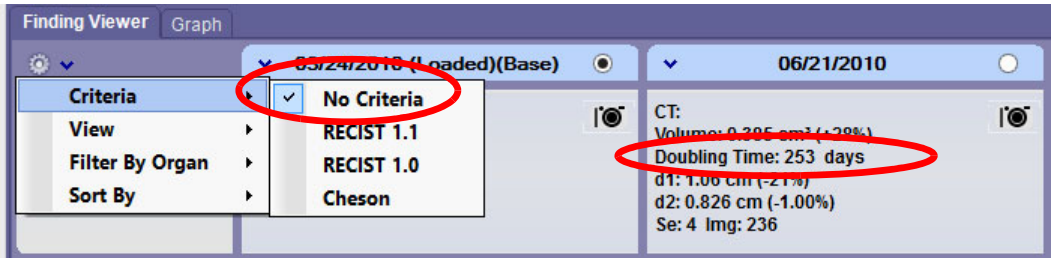
Figure 8-7: Match Displayed in Findings List (right)



Doubling Time in Measurement Tracking

If measurement tracking is enabled, measurements taken in the SAT module are saved in the Finding Viewer. When base and followup exams are both tracked, the doubling time will be displayed on the followup measurements if:

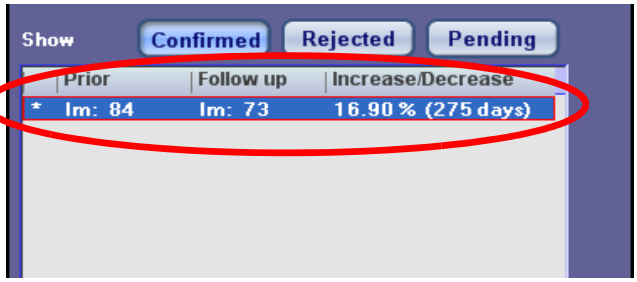
- The volume of a lesion in the followup is larger than the volume of the corresponding lesion in the base exam.
- The criteria is set to **No Criteria**.
- The **Doubling Time** item is checked in the list of measurement items to be displayed.



For information about the Finding Viewer, see "The Findings Workflow" on page 16-1.

Doubling Time in Reports

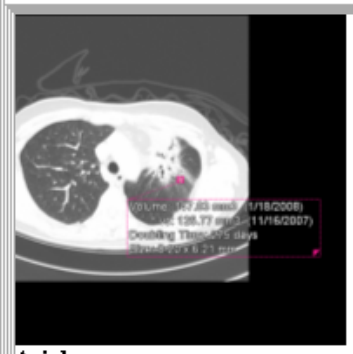
Confirmed finding in AQi:



This information can be included in a report:

Findings

Lesion #1

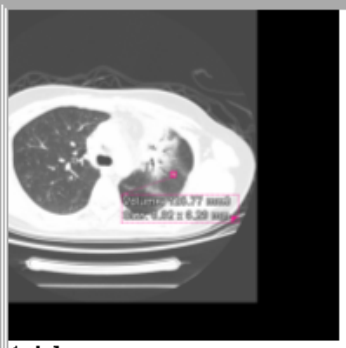


Finding Status:	Confirmed
Central slice:	# 73
Slices spanned:	7 slices
Volume:	147.03 mm^3
Size A:	8.20 mm
Size B:	6.21 mm
Mean pixel value:	811.00 HU
Std Dev pixel value:	696.87 HU
Minimum pixel value:	-593.00 HU
Maximum pixel value:	2013.00 HU

Axial

Comment:

Previous study date:	11/16/2007
Days since study:	62 days
Volume increase since study:	16.90 %
Doubling time:	275.23 days



Finding Status:	Confirmed
Central slice:	# 84
Slices spanned:	6 slices
Volume:	125.77 mm^3
Size A:	6.92 mm
Size B:	6.29 mm
Mean pixel value:	784.00 HU
Std Dev pixel value:	683.80 HU
Minimum pixel value:	-417.00 HU
Maximum pixel value:	2054.00 HU

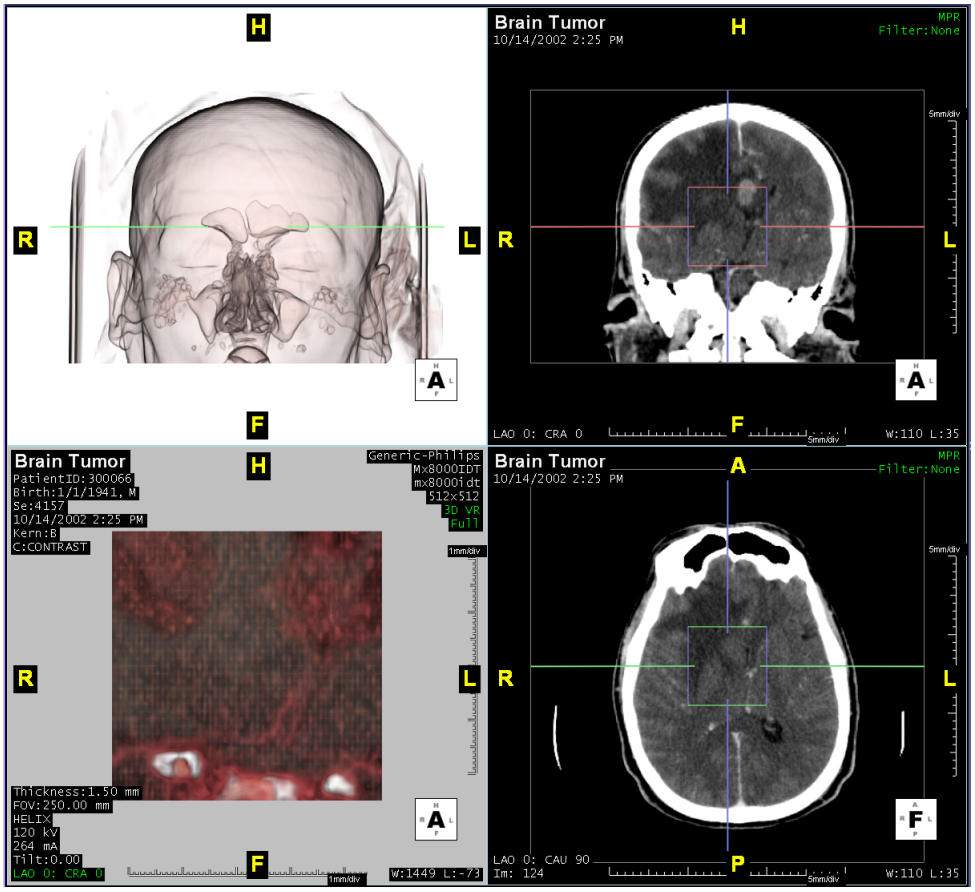
Axial

Comment:

Figure 8-8: Doubling Time in Report

SAT For Non-Lung Studies

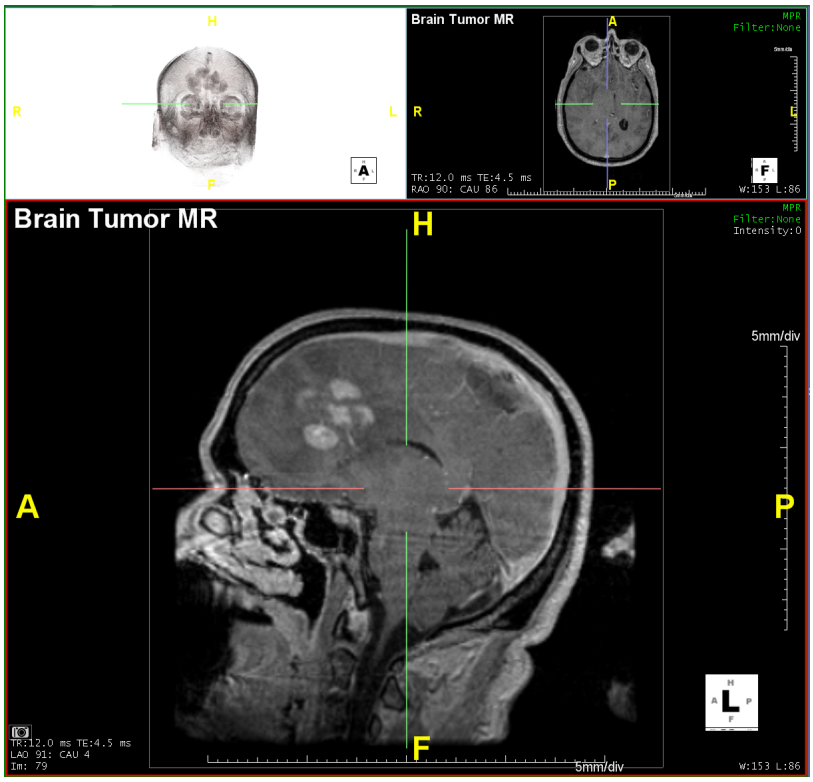
SAT can also be performed on other body parts such as the brain, liver and colon. To open the SAT module on a non-lung study, select the study, click the **Load** button in the Data Management Tools (see "Starting the SAT Study" on page 8-1), and in the Workflow menu, click **SAT (Other)**.



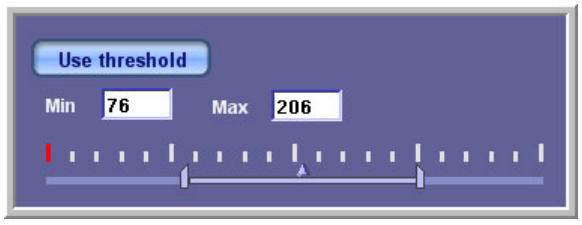
SAT is performed on other body parts in the same way it is done for lung studies. The functions, procedures, and tools are all exactly the same. The difference between the two is that for lung studies, the Window/Level in the main axial window is set to a high level of brightness so that lesions can easily be seen, whereas the Window/Level is set to a more standard default value for non-lung studies.

SAT on MR Studies

To open an MR study for SAT, select the study and then click the **Load** button. Click **SAT** in the Workflow button menu. The study is loaded in the Viewer using the SAT Workflow.

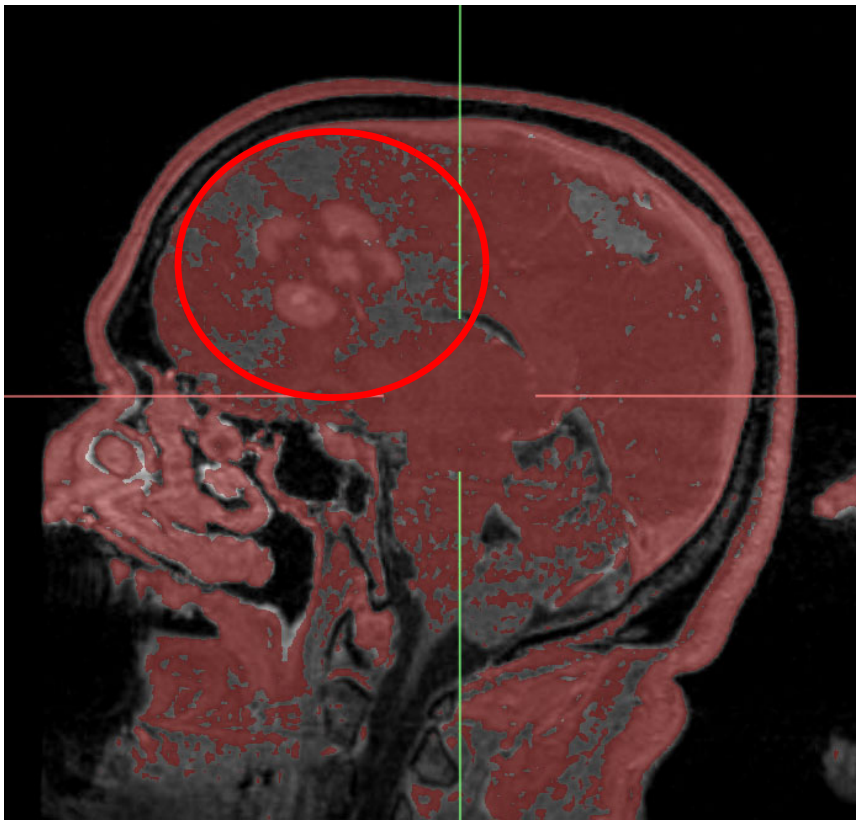


Using Threshold Values



Threshold values make it possible to highlight areas in an MR or non-lung study. To access the threshold menu, click the **Use threshold** button located in the middle of the SAT Tool Panel. The threshold menu is displayed. You can then move the slider to change the overlay threshold:

The new threshold values result in highlighted areas on the image, making it easier to see abnormal tissue:



Chapter 9 Time Dependent Analysis

Topics in this chapter:

IMPORTANT: The calculation for Time to Peak (TTP) in AQi version is different from prior versions. In 4.4.13P3 or older, the software uses the Takeoff time as a parameter to calculate TTP. In 4.4.13P4, the software uses instead the beginning of the scan as a parameter to calculate TTP.

Time Dependent Analysis (TDA)

The **Time Dependent Analysis** (TDA) optional workflow studies blood flow through a structure after the patient is injected with a contrast dye. The study provides a time-dependent curve, for the CT number of an arbitrary region-of-interest (ROI). The study also creates several kinds of functional maps - Blood Volume (BV), Blood Flow (BF), Mean Transit Time (MTT), Time-To-Peak, Temporal Maximum Intensity Projection (MIP) and error maps.

Note: You are obligated to define the parameter ranges that are used in this procedure. When first accessed, the user interface for setting these parameters contains generic default values having no significance. The default values are listed under "Brain TDA - Functional Map (CT)" on page A-27. You must acknowledge this by dismissing a warning message to this effect.

To start Time Dependent Analysis:

1. Select a relevant a study from the Patient List.
2. Select multiple series from the series list.

Note: Each series that you select should have the same number of images. *The minimum number of phases must be set to a value of at least 6.*

3. Either RMB-click on the list and select **TDA (Head)** from the menu or select the **Load** button in the **Data Management Tools** bar, and then select the **TDA (Head)** button in the Workflow Menu.

4. The software calculates the TDA, applies motion correction, and displays the result. (Figure 9-1)

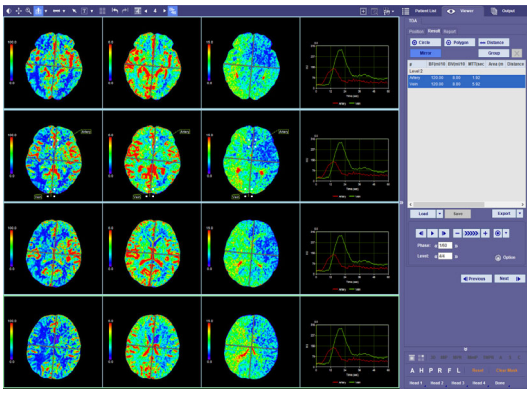


Figure 9-1: Automatic TDA Results

The TDA measurements for absolute values are only meaningful when comparing the left and right hemispheres. The value for each hemisphere can be compared to the corresponding value in the other hemisphere, to view possible abnormalities. Each software vendor utilizes a different algorithm. Therefore, absolute values are not comparable across vendors.

Maps and Graphs

The TDA calculation generates a set of image maps. (Figure 9-1) Only four maps can be displayed for each level at any one time. The default images displayed are a profile graph, the blood volume image (BV), the mean time transit image (MTT) and the MPR image.

However, there are several other displays that contain valuable information. To access these, click the green text in the upper-right corner of any image in the main window. A context menu is displays. (Figure 9-2).

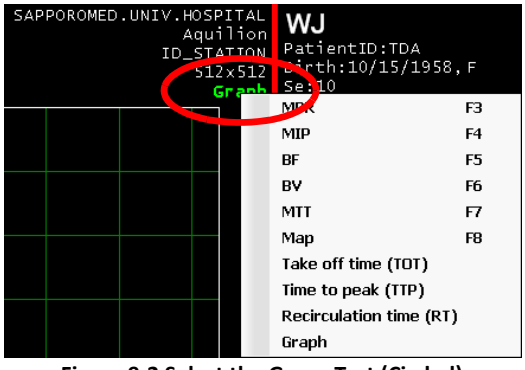


Figure 9-2 Select the Green Text (Circled)

Any image can be displayed in both MPR and MIP rendering modes. In addition, Table 9.1 describes the additional displayable maps and graphs.

Table 9.1: Additional Maps and Graphs

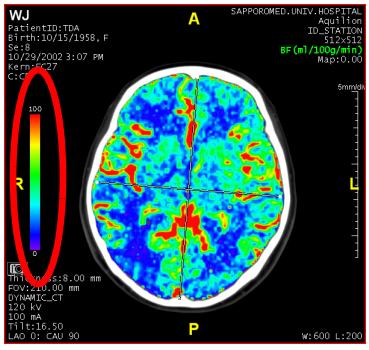
Function	Definition
Blood Flow (BF)	The volume of blood flowing through the specified ROI per unit time.
Blood Volume (BV)	The amount or fraction of blood in a given volume of the structure under analysis.
Mean Transit Time (MTT)	The average time taken by the contrast to reside in a volume of the ROI.
Map	Classification Map. The image is determined by the settings in the Classification Map Preference screen.
Take off Time (TOT)	The time at which the contrast begins to flow into the system.
Time to peak (TTP)	The time taken for the intensity to peak. See IMPORTANT note on page 9-1.
Recirculation time (RT)	The time taken by the contrast to recirculate to the structure.
Graph	• Profile graph of HU values over time. • The red line depicts the pixel at the center of ROI of artery. • The yellow line removes the effect of recirculation. • The blue line is the fitting curve. • The green line depicts the pixel at the center of ROI of vein. • Hover the mouse over a dot on any curve to see the exact HU value.

Single-Level Layouts

You can view a single level in a different layout by double-clicking on any image in the multi-level layout. The layout changes to either 2x2 or 3x3, depending on which has been configured in the preferences (see "TDA" on page A-26).

Configuring the Color Map

Each map is displayed with a color scheme that can be configured. The color map is accessed through the vertical color bar on the left side of each map image.

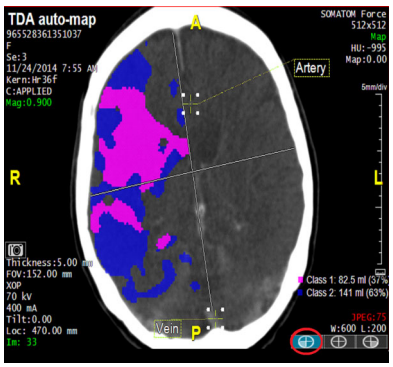


Classification Map Hemisphere Option

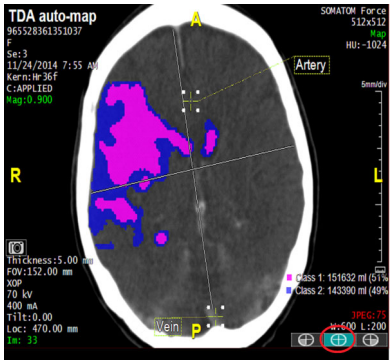
You can view the classification map image for the left or right hemispheres only, or both. Hover the mouse over the image to display icons in the lower-right corner of the image window. Each of these views will also display a ratio in percentage of the classifications.

Select the preferred side using the icons: 

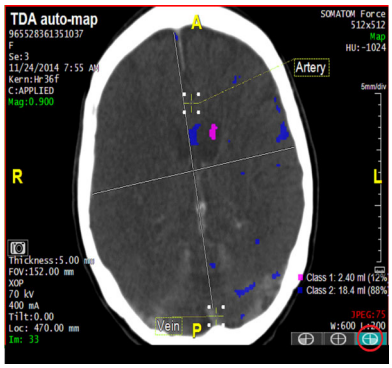
- Left icon - Displays the calculation for the left hemisphere
- Middle icon - Displays both hemispheres
- Right icon - Displays the calculation for the right hemisphere.



Left Hemisphere Icon



Both Hemispheres Icon



Right Hemisphere Icon

Figure 9-3: Classification Map (Icons Circled)

Display Range

The display range refers to the range of calculated functional values that are currently displayed in the map. This range is capped by the upper and lower values shown just above and below the vertical color bar. You can edit these upper and lower limits to show a greater or lesser range of colors.

There are two ways to edit the display range:

- Right-click the vertical color bar and select **Edit**.

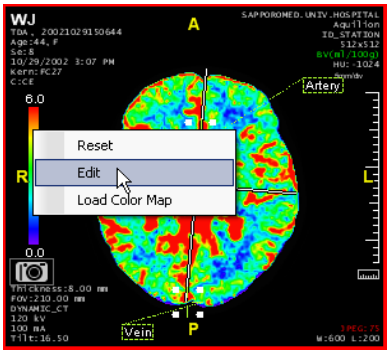


Figure 9-4 Context Menu

The **Display Range** dialog is opened. Enter new **Min** or **Max** values and click **OK** when finished.

- You can also edit the display range by dragging the mouse up or down along the vertical color bar. The numbers shown at the top and bottom change as you move the mouse, and the colors displayed on the map change accordingly.

Changing Color Maps

The color map template currently in use determines which colors represent functional values in each function map. You can select a different color template or create a new one.

To access the color maps, right-click the color bar and select **Load Color Map**. The Color Map Template Editor is displayed. (Figure 9-5)

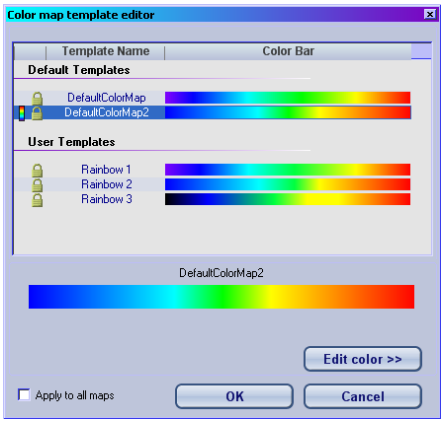


Figure 9-5 Color Map Template Editor

In this window, you can select a different template:

1. RMB-click on the desired template.
2. Select **Set as default** from the context menu.

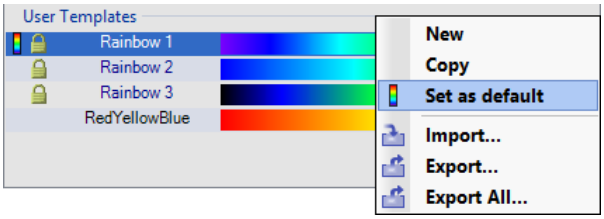


Figure 9-6 Selecting a Different Template

Select **OK** to close the template editor. The map displays with the new template.

Creating Color Map Templates

To create a new color map template:

1. Click the **Edit color** button. The edit panel is displayed in the template editor.

2. At the top of the edit panel, click New.

3. Enter a name for the new template in the dialog that is displayed, and click OK.

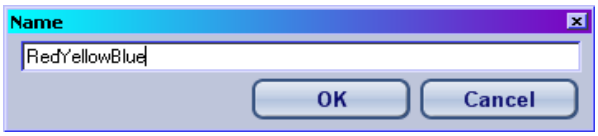


Figure 9-7 New Template Name

A new template is created, and can be viewed and edited in the bottom half of the template editor:

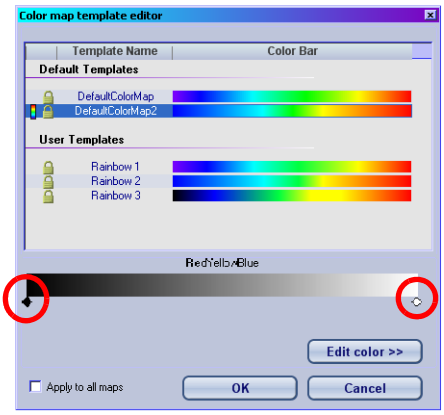


Figure 9-8 Diamond-shaped Markers

You can now add colors to the template. Just under the color bar, there are small diamond-shaped markers. Each of these markers points to the new color threshold.

In this example, a three-color template is being created. Three diamond markers are needed. The template is created automatically with two markers, one at each end.

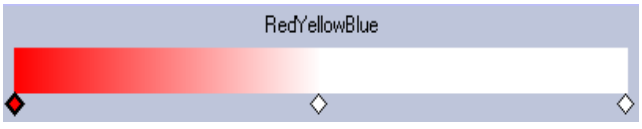
To add the third marker halfway between the first two

1. Click the **Add** button.

Figure 9-9 Adding the Third Marker

To create the new template:

1. Click on the leftmost marker and then click the **Color** button. The Windows color palette opens. Select the desired color and click **OK**. That color is now added to the left end of the bar:



2. Click the middle marker and when the Windows color palette is displayed, select another color. Do the same for the rightmost marker. The new template is now complete.

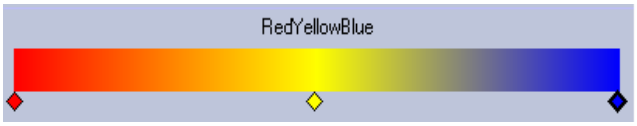


Figure 9-10 Completed Template

3. Click **OK** to exit the template editor.

The function map uses the new color template. (Figure 9-11)

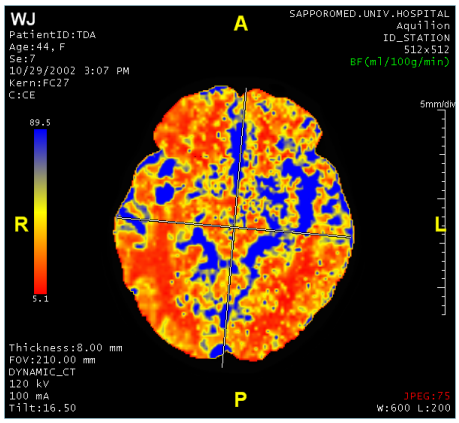


Figure 9-11 Map with New Template

Other features

You can use the color map template to:

- **Copy a template** - You can create a new template by copying an existing template and then renaming the copy. The new file can then be edited.
- **Delete** - Deletes the selected template.
- **Rename** - Renames the selected template.
- **Import** - If you have a TDA color template on your local hard disk (or other storage medium accessible to the Windows file system), you can import it to the AQi TDA module.
- **Export** - Save the selected template on your local hard drive. You can navigate to any folder first.
- **Apply to all maps** (checkbox in the lower left corner) - Anything you select, create or change will be applied to all maps in the module.

ROI Templates

You can load, modify, save, and create ROI templates to designate the examination ROIs on each image. This determines the output values shown on the Result panel.

Loading ROI Templates

On the bottom of the Result Tab, the buttons **Load** and **Save** apply to ROI templates.

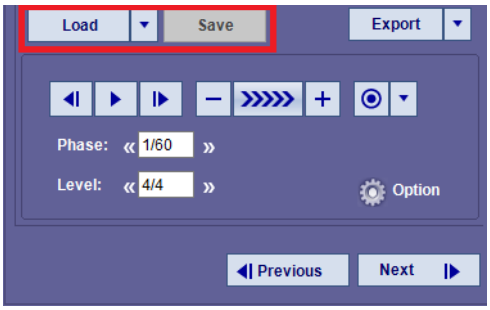


Figure 9-12 Template Load and Save Buttons

To load a default template:

4. Select the **Load** button at the bottom of the Result panel. The template window opens.

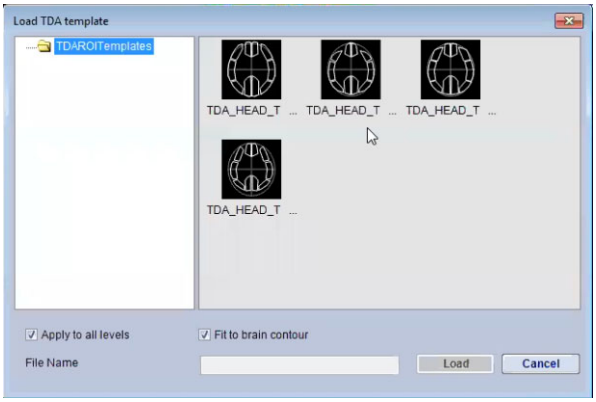


Figure 9-13 Loading TDA Templates

5. Select a template and click **Load** button in the window. The value results for each ROI display automatically in the Result panel.

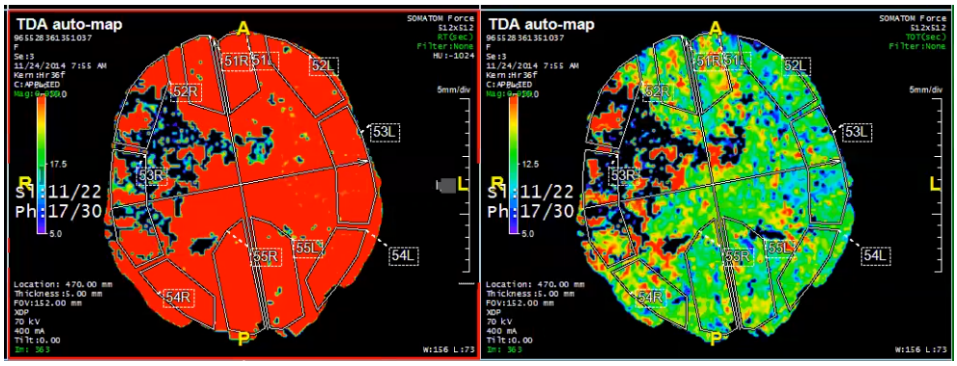


Figure 9-14 TDA Templates

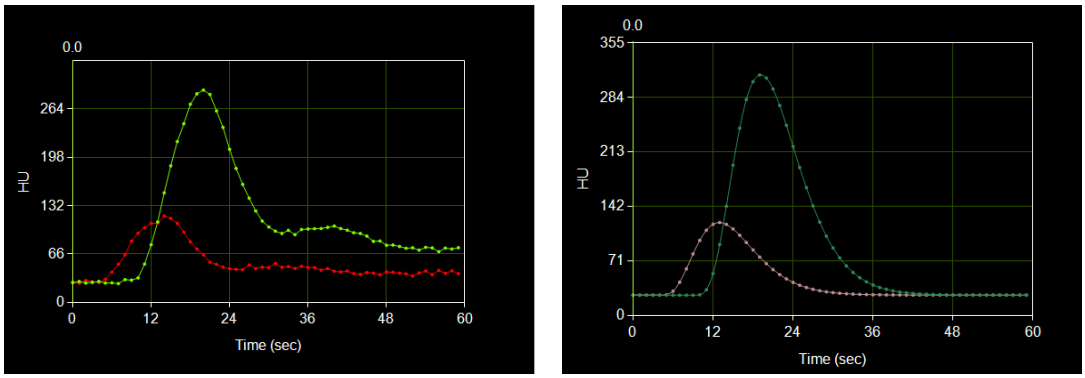
Creating ROI Templates

To create a new ROI template, you first must perform a manual TDA on the study (see "Manual TDA" on page 9-11 for instructions). When the manual process finishes and opens to the Result panel, the results display. You can save this template by clicking the **Save** button at the bottom of the panel. The **Save TDA Templates** window opens, and you can enter a name for the template.

Viewing Graph Curves

The TDA graph shows the changing HU value of a selected point (either the artery or vein) over time, as blood circulates in the brain. Two curves are plotted, one for the artery (red) and one for the vein (green). Together the two curves are referred to as the *profile*.

The graph contains two different kinds of profiles, the raw profile and the fitted profile. The raw profile shows the actual HU values, which may be affected by artifact or other noise. The fitted profile is calculated by the TDA module to reflect the expected values based on the data. The two profiles should have similar contours. If they are noticeably different, this might indicate an incorrectly selected artery or vein point.



Raw Profile **Fitted Profile**

Figure 9-15: Graph Profiles

You can choose to hide either profile to see the one profile clearly. To do this, right-click in the window where the graph is displayed and select either **Hide Raw Profile** or **Hide Fitted Profile** from the pull-down menu, as desired.

Drawing an ROI

You can draw Regions Of Interest (ROI) in a symmetrical structure to calculate various parameters pertaining to the time-dependent behavior of the underlying tissue. The TDA workflow provides several tools for defining and comparing ROIs.

The Result Panel

If you have calculated Time Dependent Analysis on the loaded data, the **Result** tab opens in the Tool Panel.

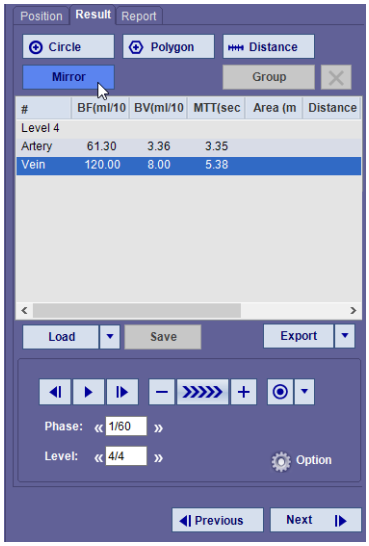
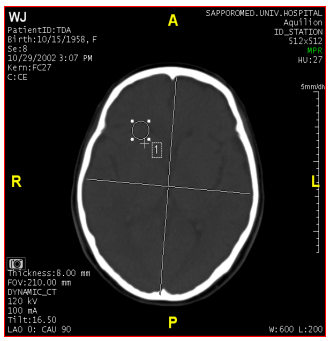


Figure 9-16 Options in the Result Tab

To draw a ROI:

1. Select either **Circle** or **Polygon** from the top toolbar.

2. Click and drag the left mouse button across the area, until the desired size of ROI has been reached (shown at right).



3. Click the **Mirror** button to have the ROI copied automatically to the other half of the symmetrical structure under analysis (see image below).

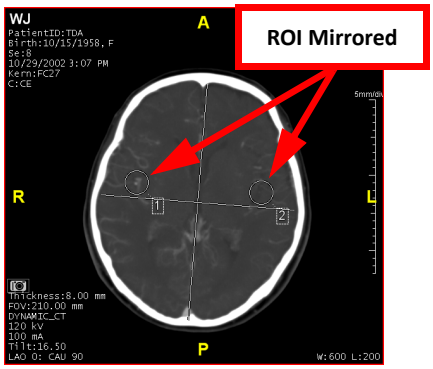
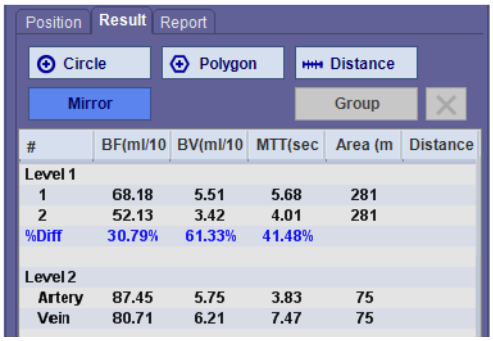


Figure 9-17: ROI Mirrored

This analysis is also reflected in the Results window.



#	BF(ml/10	BV(ml/10	MTT(sec	Area (m	Distance
Level 1					
1	68.18	5.51	5.68	281	
2	52.13	3.42	4.01	281	
%Diff	30.79%	61.33%	41.48%		
Level 2					
Artery	87.45	5.75	3.83	75	
Vein	80.71	6.21	7.47	75	

Figure 9-18 Analysis Results Displayed

Under Level 1, listed in the figure at right, the two ROIs numbered 1 and 2 correspond to the numbered circles in Figure 9-17. The differences between each ROI are calculated and displayed for each pair of ROIs you add to the image.

Note: This analysis is not automatically propagated to the other levels. You must perform it for each level separately.

Distance Measurements

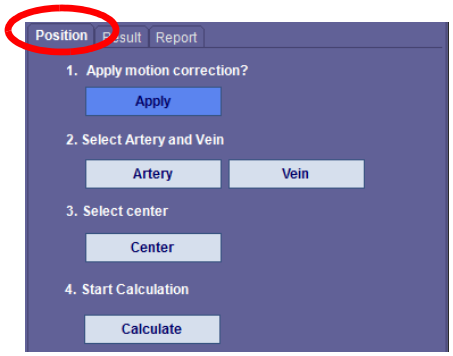
To calculate a distance between two points on the image, select the **Distance** button in the Tool Panel, and then left-click and drag the mouse from the initial point to the final point. The distance is subsequently displayed in the result list in the Tool Panel, in the **Distance** column.

Manual TDA

The software initially selects the artery and vein, first by identifying the long axis of the brain, and then calculating the maximum standard deviation around the axis. This determines the approximate location of the artery and vein. A curve fitting method is applied to the pixels to select the artery and vein that best fits and has the maximum dynamic range.

CAUTION! You are obligated to verify that the automatic artery and vein selection meets your need. If not, proceed to calculate the TDA manually.

To calculate the TDA manually, you can begin the process by clicking the **Position** tab, located at the top of the tool panel. The positioning tool panel is displayed, as shown below:



Step 1 - Apply Motion Correction

To apply motion correction, simply click the **Apply** button located under **1. Apply motion correction?** in the tool panel.

Step 2 - Select Artery and Vein

To select an artery, do the following:

4. Select the **Artery** button under **2. Select Artery and Vein** in the tool panel.

5. Left-click on the center of the region of interest (ROI) For brain perfusion studies, the anterior cerebral artery or ACA is recommended. The ACA is located at the position shown in Figure 9-19. Repeat this step for each phase in the series.

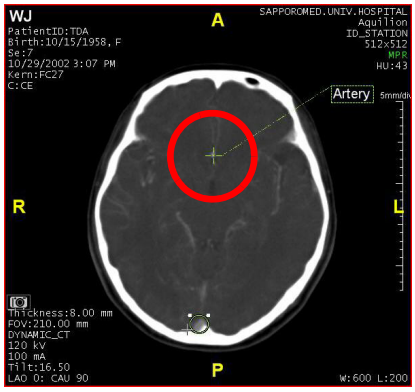


Figure 9-19 Location of the ACA in the brain.

6. Drag the mouse to draw a circle around the artery of interest.

Note: iNtuition automatically selects an ROI that has the maximum change throughout the acquired images.

To select a vein:

1. Select the **Vein** button under **2. Select Artery and Vein** in the tool panel.

2. To select an ROI for a vein, click and draw around the center of an appropriate vein. For example, if you are performing a brain perfusion study, the superior sagittal venus sinus or SSVS is a good selection. Repeat this step for each phase in the series.

Figure 9-20 shows the location of SSVS in the brain.

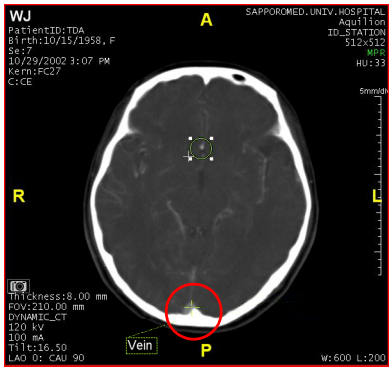


Figure 9-20 Location of the SVSS

Step 3 - Select Center

Select the **Center** button to redraw the crosshair lines.

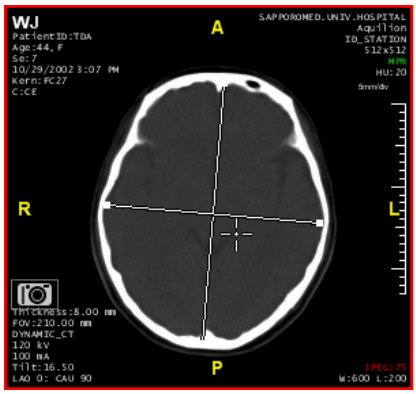


Figure 9-21 Redraw Crosshairs

Step 4 - Start Calculation

Select the **Calculate** button under **4. Start Calculation** in the tool panel**.**

As calculation progresses, functional maps are updated. The application displays a progress bar for the duration of the calculation. Figure 9-22 shows the viewer screen after the calculation is complete.

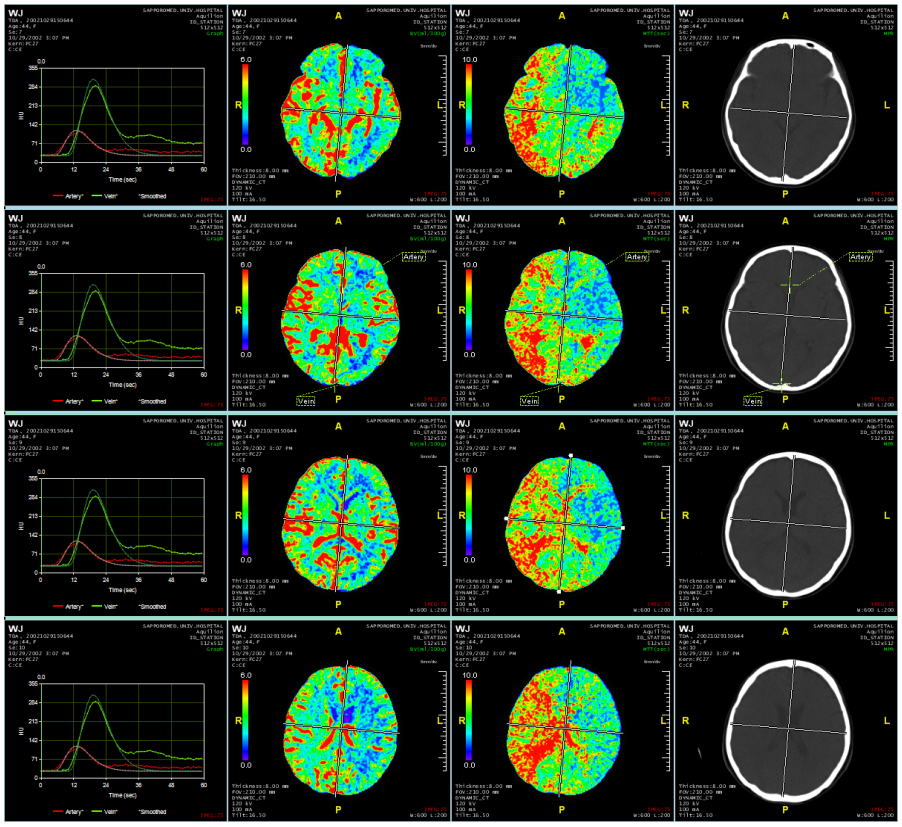


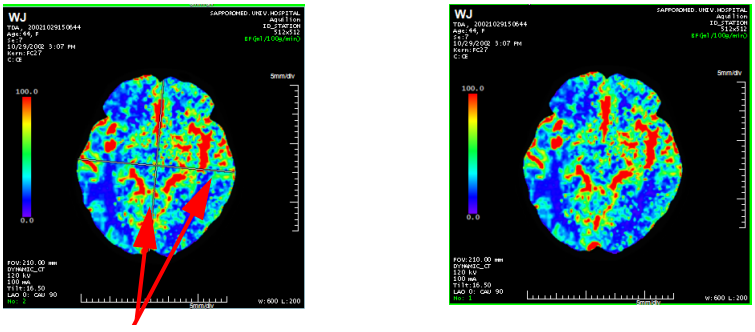
Figure 9-22 Calculation and Update

Capturing Images

You can capture images in any of the following ways:

- **Capture with or without Brain Center Lines**

  Right-click on the view and select **Show/Hide brain Center** before beginning captures (see image at right). This item toggles whether the center lines are shown (see below).



Left - Center Lines (Crosshair) Showing **Right - Center Lines Hidden**

Figure 9-23: Center Lines

- **Capture all levels**

  If all levels are visible in the main window, click the **Capture** button.

  If all levels are not visible in the main window, click the down-arrow next to the **Capture** button, and then select **Capture All Levels** from the pull-down menu.

  The result is a capture of all visible maps, in all levels.

- **Capture a single map for all levels**

  Click the down-arrow next to the **Capture** button, select **Capture Map for All Levels** from the pull-down menu, and then select the desired map (for example, BV, BF, MTT) from the sub-menu.

  The result is a capture of the same map throughout all levels.

- **Capture preset maps**

  This option captures maps that have been preset in the TDA Capture Preferences screen. Only the selected (preset) maps are captured, but are captured in all levels. (To set options in the TDA Capture preferences screen, see "Brain TDA - Capture Settings" on page A-30.)

- **Capture All in One for All Levels**

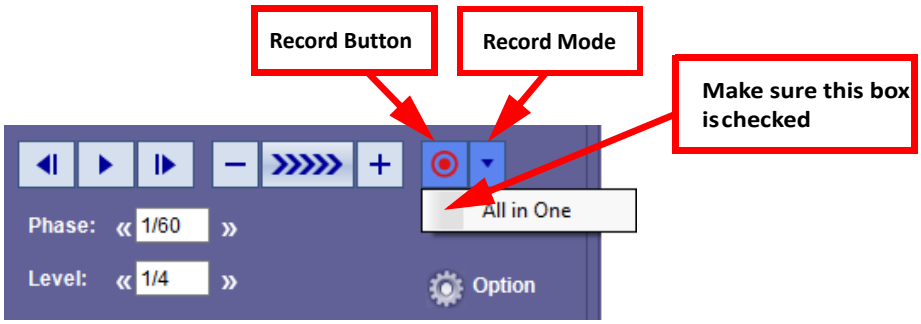
  This is the same as the **Capture All in One** option (see "Capture All in One" on page 3-4), but for all levels. These are displayed in either 2x2 or 3x3 layout, depending on your preference selection (see "TDA" on page A-26).

  When a capture is initiated, a dialog is displayed, asking whether you want to save the capture as a DICOM series. If you want to save the capture as a series, enter a name and series number in the dialog and click **OK**. If not, click **Cancel**. The capture proceeds either way.

- **Capture Phase Cine into AVI File**

  This feature allows you to save a playing cine as a video file. All views that are visible on the screen when the cine is playing are captured to the video.

  1. Click the record button in the cine control panel (see the figure below). When it is ready to record, the button is highlighted.



  2. Click the down-arrow next to the record button to select the record mode (see the previous figure). Although there is only one record mode (**All in One**), it must be selected to activate recording.

3. Start the cine.

4. While the cine is playing, each frame is captured and kept in the Output Panel. Once recording is completed, the Output Panel is reset to its previous state.

Note: The cine plays slowly during recording.

5. When you are done recording, stop the cine. A dialog box appears to ask where to save the AVI file.

Note: The MPR map must be included in the saved video. If the MPR map is not visible when you start to record the cine, AQi will show it temporarily, while the cine is being recorded. When recording is complete, the view is restored to its previous state.

- **Capture using Save a Scene**

  To save a scene, select the scene button at the right end of the top toolbar. Whatever is displayed on the screen is saved to a DICOM file and sent to the Patient List.

Note: The current settings in the user preferences are saved along with the data. If the scene is loaded later and other preferences are in effect, a warning is posted to alert you that the saved settings in the scene do not match the new settings. You are given the option of using either the new (in-effect) settings or the settings that were saved with the scene.

You can also set Capture functions in the Preference window for different types of maps.

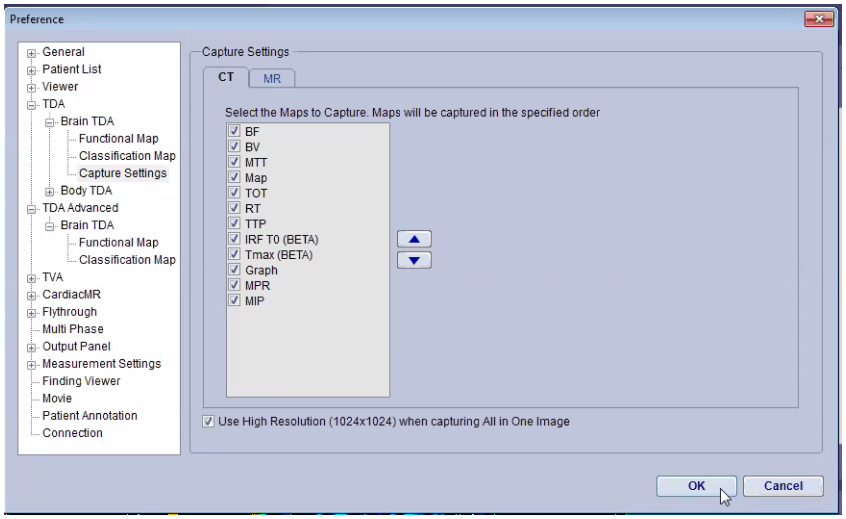


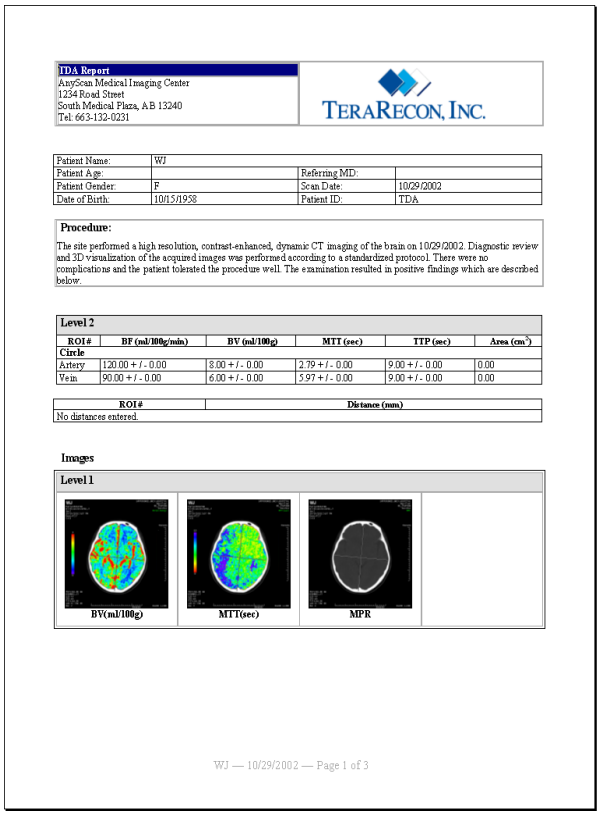
Figure 9-24 Preference Window Capture Settings

Using the arrows beside the CT list changes the order or preference of the maps.

Generating a Report

Once all necessary analysis is performed and images have been captured, you can generate a report. To generate a report, do the following:

1. Click **Generate Report** to create a report.
2. In the following window, select your name and click **Proceed** to sign electronically.
3. The system generates a MS Word report. The sample report shows the values from each measurement, as well as captured images in the 4x4 mode.
4. You can save the report in your computer and attach it to emails to send it to other physicians.



TDA Report
AnyScan Medical Imaging Center
1234 Road Street
South Medical Plaza, AB 13240
Tel: 663-132-0231

TERARECON, INC.

Patient Name:	WJ		
Patient Age:		Referring MD:	
Patient Gender:	F	Scan Date:	10/29/2002
Date of Birth:	10/15/1958	Patient ID:	TDA

Procedure:

The site performed a high resolution, contrast-enhanced, dynamic CT imaging of the brain on 10/29/2002. Diagnostic review and 3D visualization of the acquired images was performed according to a standardized protocol. There were no complications and the patient tolerated the procedure well. The examination resulted in positive findings which are described below.

Level 2

ROI #	BF (ml/100g/min)	BV (ml/100g)	MTT (sec)	TTP (sec)	Area (cm²)
Circle					
Artery	120.00 +/- 0.00	8.00 +/- 0.00	2.79 +/- 0.00	9.00 +/- 0.00	0.00
Vein	90.00 +/- 0.00	6.00 +/- 0.00	5.97 +/- 0.00	9.00 +/- 0.00	0.00

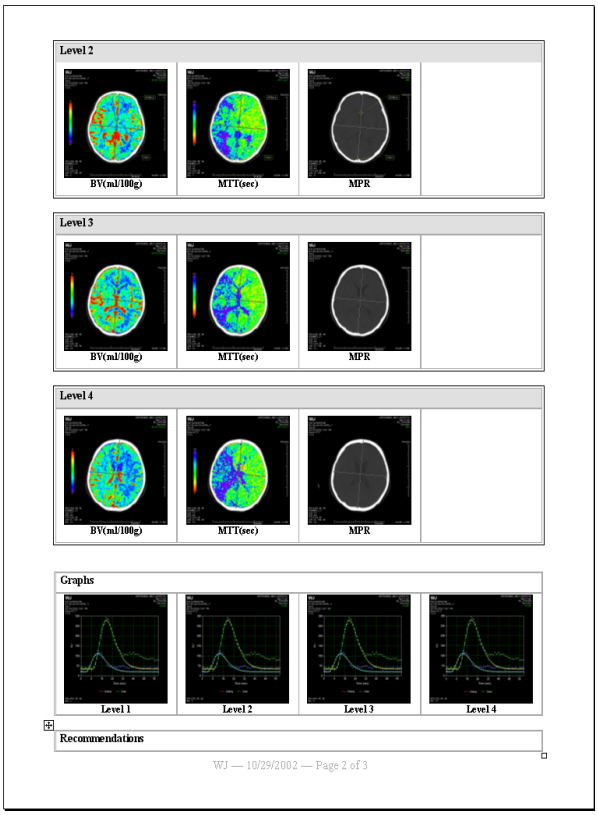
ROI #	Distance (mm)
No distances entered.	

Images

Level 1

BV(ml/100g) MTT(sec) MPR

WJ — 10/29/2002 — Page 1 of 3



Level 2

BV(ml/100g) MTT(sec) MPR

Level 3

BV(ml/100g) MTT(sec) MPR

Level 4

BV(ml/100g) MTT(sec) MPR

Graphs

Level 1 Level 2 Level 3 Level 4

Recommendations

WJ — 10/29/2002 — Page 2 of 3

Advanced Time Dependent Analysis

IMPORTANT: The calculation for Time to Peak (TTP) in 4.4.13P4 is different from prior versions. In 4.4.13P3 or older, the software uses the Takeoff time as a parameter to calculate TTP. In 4.4.13P4, the software uses instead the beginning of the scan as a parameter to calculate TTP.

Similar to the TDA Workflow, the **Advanced Time Dependent Analysis** (TDA) optional workflow studies blood flow through a structure after the patient is injected with a contrast dye. The study provides a time-dependent curve, for the CT number of an arbitrary region-of-interest (ROI). The study also creates

several kinds of functional maps - Blood Volume (BV), Blood Flow (BF), Mean Transit Time (MTT), Time-To-Peak, Temporal Maximum Intensity Projection (MIP) and error maps.

Note: You are obligated to define the parameter ranges that are used in this procedure. When first accessed, the user interface for setting these parameters contains generic default values having no significance. The default values are listed under "Brain TDA - Functional Map (CT)" on page A-27. You must acknowledge this by dismissing a warning message to this effect.

To start an Advanced Time Dependent Analysis:

1. Select an appropriate study from the Patient list.
2. Select multiple series from the Series list.

Note: Each series that you select should have the same number of images. *The minimum number of phases must be set to a value of at least 6.*

3. Either RMB-click on the study and select **Advanced TDA (Head)** from the menu or select the **Load** button in the **Data Management Tools** section and then select the **Advanced TDA (Head)** icon in the Workflow Menu.
4. The software automatically calculates the TDA, applies motion correction, and displays the results.
5. In the viewer, a TDA message window opens. (Figure 9-25)

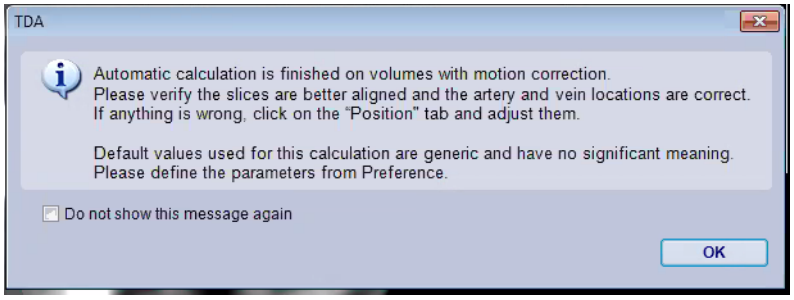


Figure 9-25 TDA Accuracy Message

Note: You are obligated to define the parameter ranges that are used in this procedure. When first accessed, the user interface for setting these parameters contains generic default values having no significance. The default values are listed under "Brain TDA - Functional Map (CT)" on page A-27. You must acknowledge this by dismissing a warning message to this effect, Figure 9-25.

6. Select **OK** in the message window.

In the viewer, the layout is 2x2 with the top viewboxes showing the images with parametric maps and the bottom viewboxes containing the result graph and the displayed measurements in the Results window. (Figure 9-30)

Open the **Preference** window to select and set additional Advanced TDA options.

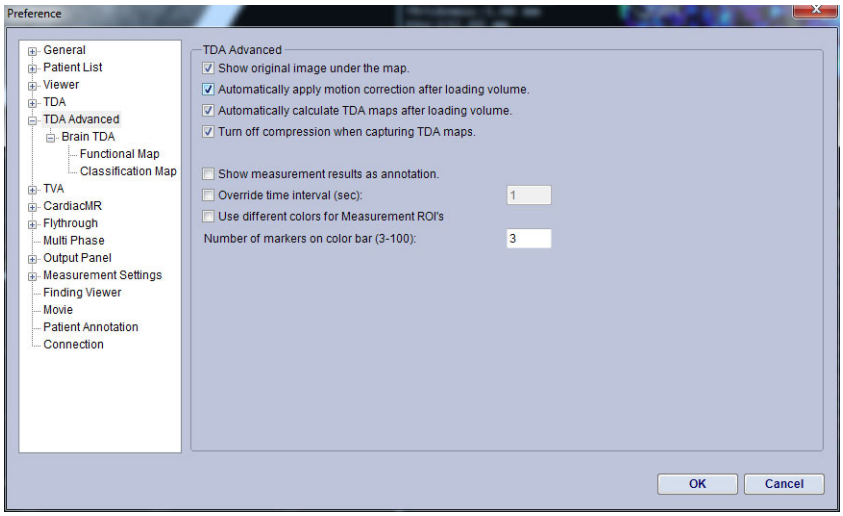


Figure 9-26 TDA Advanced Settings

The additional Preference pages under TDA Advanced are Brain TDA, Functional Map, and Classification Map.

7. The software calculates the TDA, applies motion correction, and displays the result. (Figure 9-27)

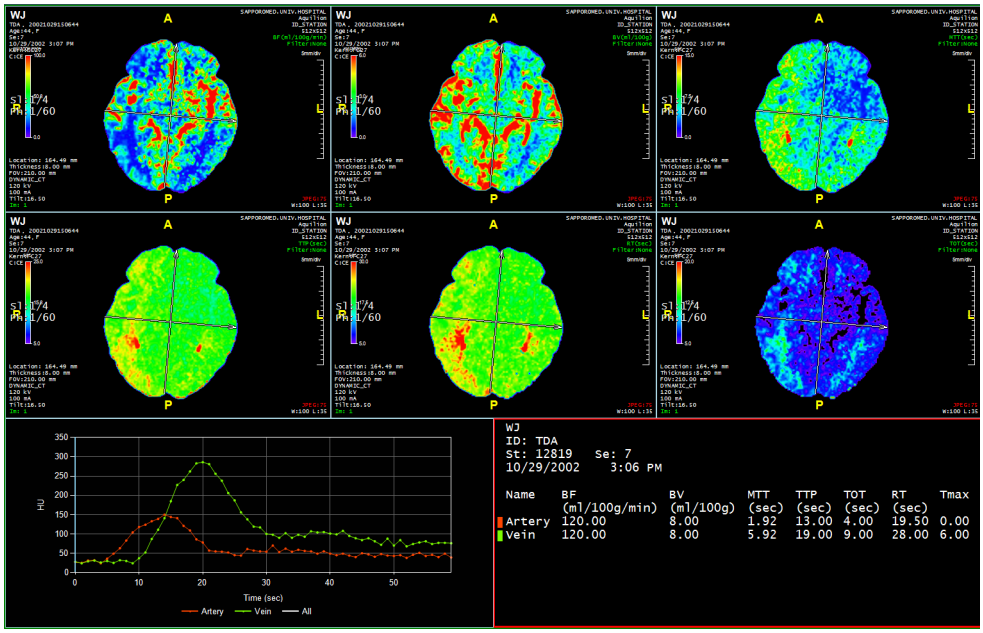


Figure 9-27: Automatic Advanced TDA Results

The TDA measurements for absolute values are only meaningful when comparing the left and right hemispheres. The value for each hemisphere can be compared to the corresponding value in the other

hemisphere, to view possible abnormalities. Each software vendor utilizes a different algorithm. Therefore, absolute values are not comparable across vendors.

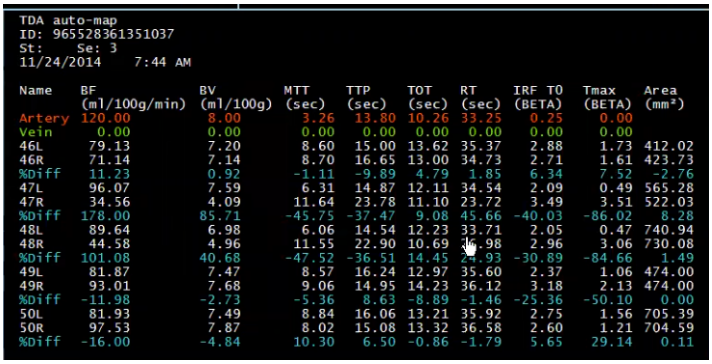
Results Tab

When the automatic calculations are done, the TDA Advanced tool panel opens to the **Result** tab.

Figure 9-28 Result Tab

Result Window

The maps you selected in the Preference window, display results in the Result Window which is to the right of the Result Graph in the viewer..



TDA auto-map
ID: 965528361351037
St: Se: 3
11/24/2014 7:44 AM

Name	BF (ml/100g/min)	BV (ml/100g)	MTT (sec)	TTP (sec)	TOT (sec)	RT (sec)	IRF TO (BETA)	Tmax (BETA)	Area (mm²)
Artery	120.00	8.00	3.26	13.80	10.26	33.25	0.25	0.00	
Vein	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
46L	79.13	7.20	8.60	15.00	13.62	35.37	2.88	1.73	412.02
46R	71.14	7.14	8.70	16.65	13.00	34.73	2.71	1.61	423.73
%Diff	11.23	0.92	-1.11	-9.89	4.79	1.85	6.34	7.52	-2.76
47L	96.07	7.59	6.31	14.87	12.11	34.54	2.09	0.49	565.28
47R	34.56	4.09	11.64	23.78	11.10	23.72	3.49	3.51	522.03
%Diff	178.00	85.71	-45.75	-37.47	9.08	45.66	-40.03	-86.02	8.28
48L	89.64	6.98	6.06	14.54	12.23	33.71	2.05	0.47	740.94
48R	44.58	4.96	11.55	22.90	10.69	24.98	2.96	3.06	730.08
%Diff	101.08	40.68	-47.52	-36.51	14.45	24.93	-30.89	-84.66	1.49
49L	81.87	7.47	8.57	16.24	12.97	35.60	2.37	1.06	474.00
49R	93.01	7.68	9.06	14.95	14.23	36.12	3.18	2.13	474.00
%Diff	-11.98	-2.73	-5.36	8.63	-8.89	-1.46	-25.36	-50.10	0.00
50L	81.93	7.49	8.84	16.06	13.21	35.92	2.75	1.56	705.39
50R	97.53	7.87	8.02	15.08	13.32	36.58	2.60	1.21	704.59
%Diff	-16.00	-4.84	10.30	6.50	-0.86	-1.79	5.65	29.14	0.11

Figure 9-29 Viewer Numerical Results Window

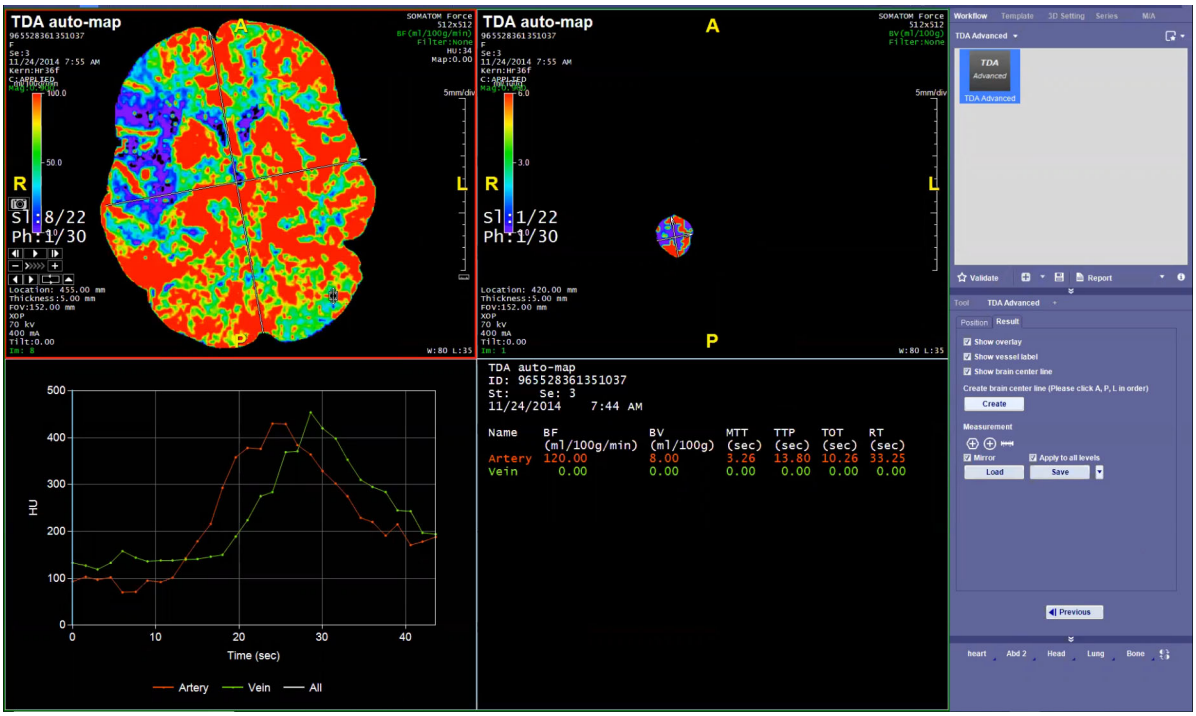


Figure 9-30 Advanced TDA Results Displayed 2x2 in the Viewer

To view other maps and images, RMB-click on the green text in the top right corner of the image and select another map from the context menu.

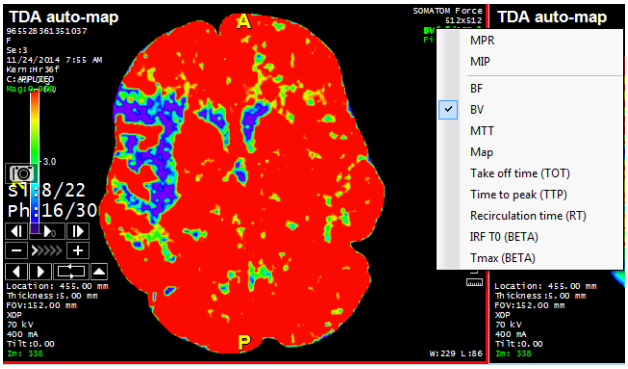


Figure 9-31 Selecting Maps

Workflow Calculations

The Advanced TDA workflow is different from the TDA workflow in that it uses different measurement points.

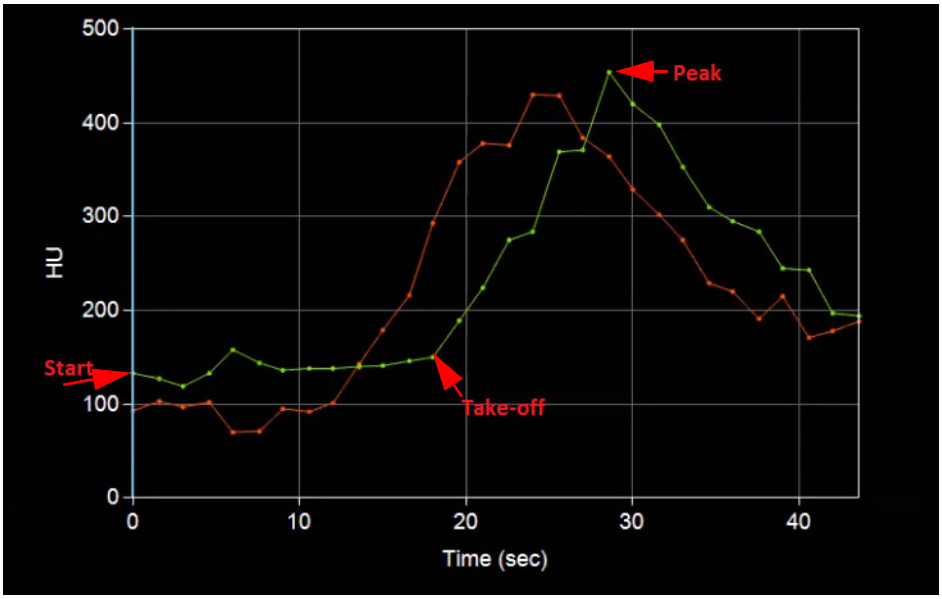


Figure 9-32 Results Graph

The measurements are taken at these points:

- **Start** - the starting time for the calculation.
- **Take-off time** - the time when the contrast is injected.
- **Peak** - the highest point and ending time measurement for the calculation.

Note: If you choose to, you can set the Advanced TDA Workflow to calculate only from Take-off to Time to Peak (TTP).

Advanced TDA Options

The Result tab provides advanced options including **Show overlay**, **Show vessel label**, and **Show brain center line**.

If you scroll through the slices, with the **Show vessel label** checked, you can find the slice with the vessel labels and check the position of the artery and vein.

Reposition the Artery and Vein

If the artery and vein auto placements are incorrect, go back to the **Position** tab to reset their placement. (See "Manual TDA" on page 9-11 for more instruction.) The viewer opens with the **Position** tab open. (Figure 9-33)

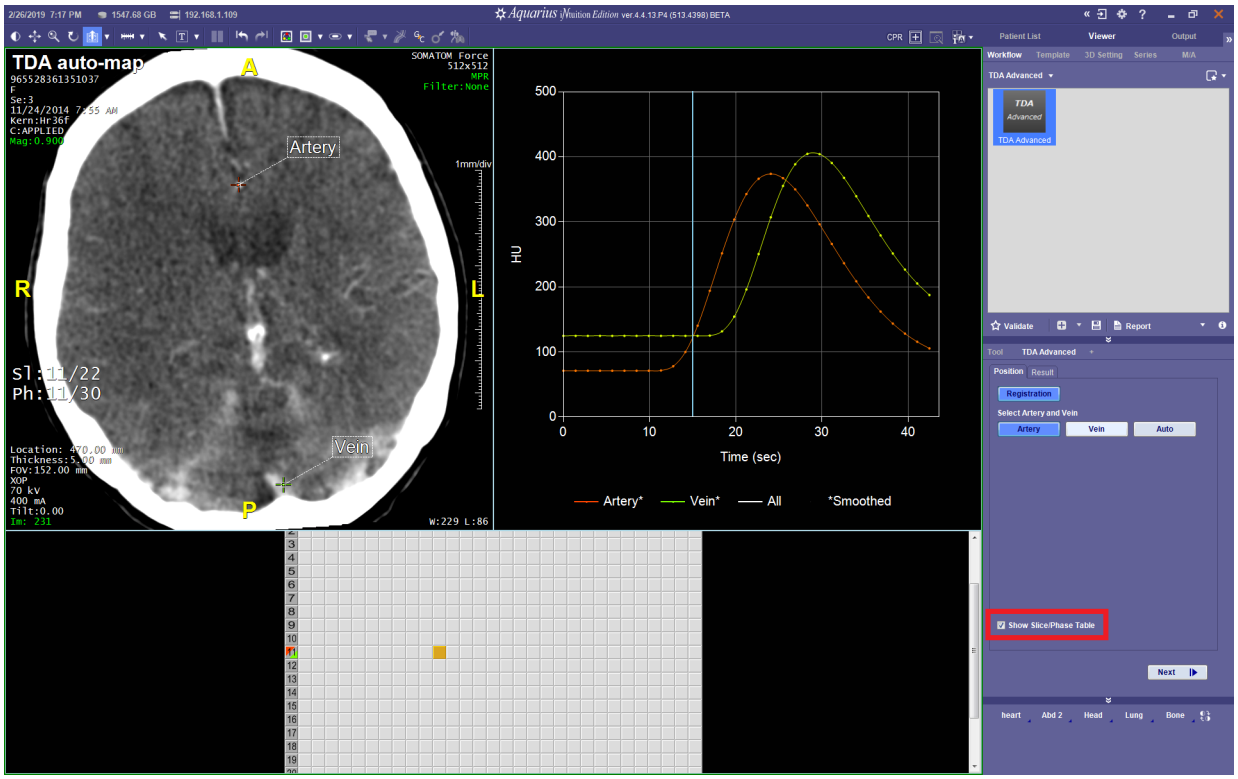


Figure 9-33 Position Tab in the Advanced TDA Workflow

The layout has two viewboxes over a **Slice/Phase** table. You can toggle the table on or off using the checkbox. You can use the **Slice/Phase** table to change the view either by slice or phase, if needed.

To move through slices and phases on the image:

1. Hold down the LMB and drag you mouse up or down to change the slice.

2. Hold down the LMB and drag you mouse left or right to change the phase.

To place the artery, select the **Artery** button and then left-click once on the image. If you need to reposition it, LMB-hold and drag it to another location. If you need to delete the selection, RMB-click on the artery and select Delete.

After manually placing the artery or the vein, if there is no signal at either point you are prompted to do the selection again. Follow the Manual TDA instructions (see page 9-11) to select the artery and vein positions. Then select **Next** and the maps are automatically calculated and the Result tab opens.

Reposition the Center Line

You also need to confirm the placement of the center line. If the center line is not accurate, you can reset the center line by selecting the **Create** button on the panel. You are prompted to select new center lines.

ROI Measurements

You can use the ROI measurement tools to measure and locate additional regions of interest and measure a distance. Since it is important to compare the brain's left and right hemisphere, you can check **Mirror** and then select a ROI. This ROI is exactly mirrored on the opposite side of the brain. If you move or change the size of an ROI, the matching opposite ROI automatically repositions to mirror that location or resizes to match the new size. If you delete one ROI, then the other one is deleted automatically.

You can select **Apply to all levels** to apply measurements and ROI to all series levels. The **Load** and **Save** buttons apply to using a TDA templates.

The process for creating and saving a new template is the same as it is for the TDA workflow, see "Creating ROI Templates" on page 9-9. The process for changing color settings on maps is also the same, see "Changing Color Maps" on page 9-5.

The Advanced TDA settings differ from the TDA workflow settings.

Layout Options

To change the layout, RMB-click on the image and open the context menu. The default layout is 2x2. You can also change to 3x3 layout.

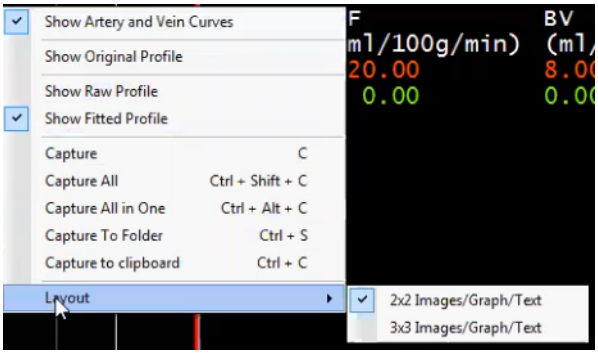


Figure 9-34 Advanced TDA Context Menu

Note: From the context menu, you can select Show/Hide options as well as Capture options.

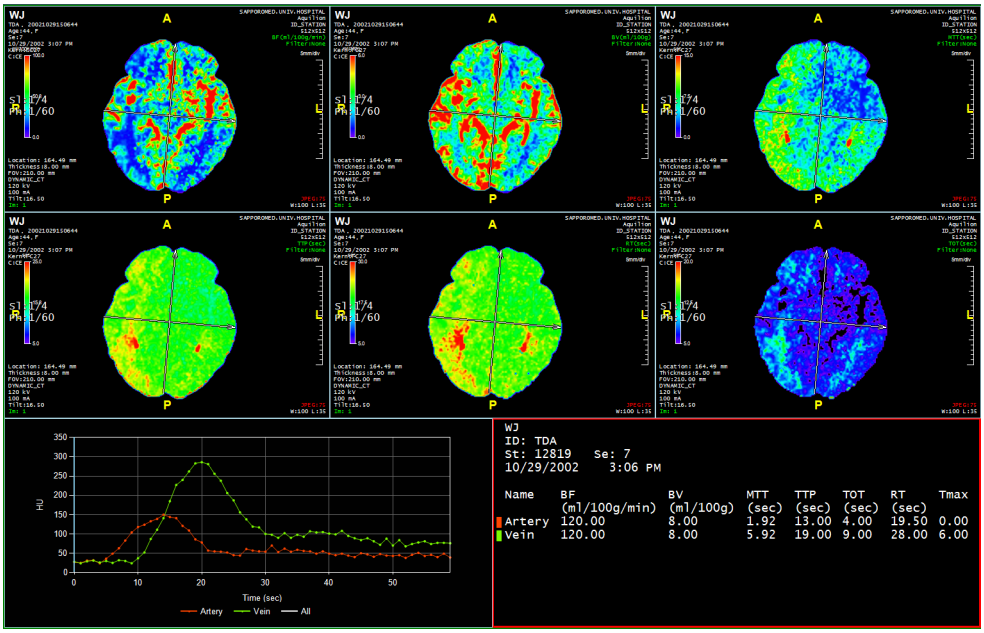


Figure 9-35 The 3x3 Layout showing Advanced TDA Results

Graph Profile Options

You can change graph profiles in the TDA workflow, but the Advanced TDA workflow provides more options. You can change the graph profile by RMB-clicking on the image and selecting **Show Artery and Vein Curves**, **Show Original Profile**, **Show Raw Profile**, and **Show Fitted Profile**. (Figure 9-34)

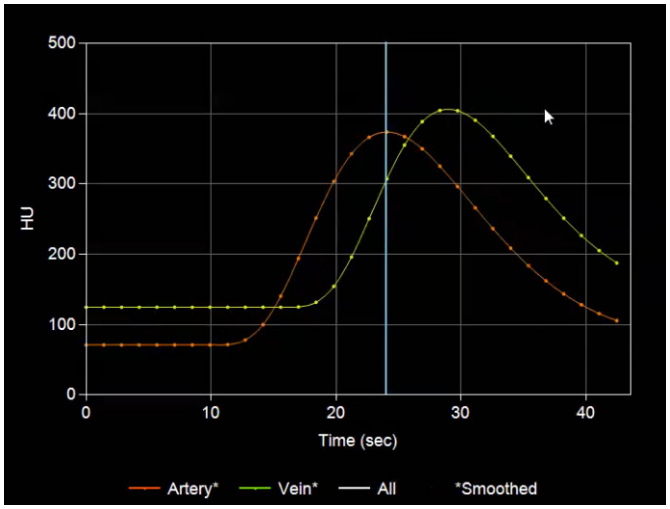


Figure 9-36 Fitted Profile

Additional graph profiles are shown in Figure 9-15 on page 9-9

Chapter 10 Time Dependent Analysis For MR

Topics in this chapter:

The **Time Dependent Analysis For MR** (TDA MR) optional module studies blood flow through a structure after the patient is injected with a contrast dye.

Note: You are obligated to define the parameter ranges that are used in this procedure. When first accessed, the user interface for setting these parameters contains generic default values having no particular significance. The default values are listed under "Brain TDA - Functional Map (MR)" on page A-28. You must acknowledge this by dismissing a warning message to this effect.

The MR signal itself is not used for processing directly, due to the nonlinear relationship between the contrast concentration and the MR signal. However, the logarithm of the MR signal reflects the approximately linear relationship between changes in the magnetic resonance relaxation rate constant (T2*) and the concentration of contrast. This relationship is expressed by the function shown at right.

$$\triangle R2 = \frac{-\ln S/S_0}{TE}$$

The function variables are defined as follows:

- S_0 denotes the average background pixel intensity. It is used as a baseline.
- **S** is the pixel intensity.
- **TE** refers to the echo time of the MR acquisition. This value is a constant for a given series.
- $\triangle$**R2** is used as the contrast concentration, and is applied to subsequent processing.

The study also creates several kinds of functional maps. See "Maps and Graphs" on page 10-2 for descriptions.

Note: To perform TDA, select only dynamic studies from the Study List.

Starting TDA MR

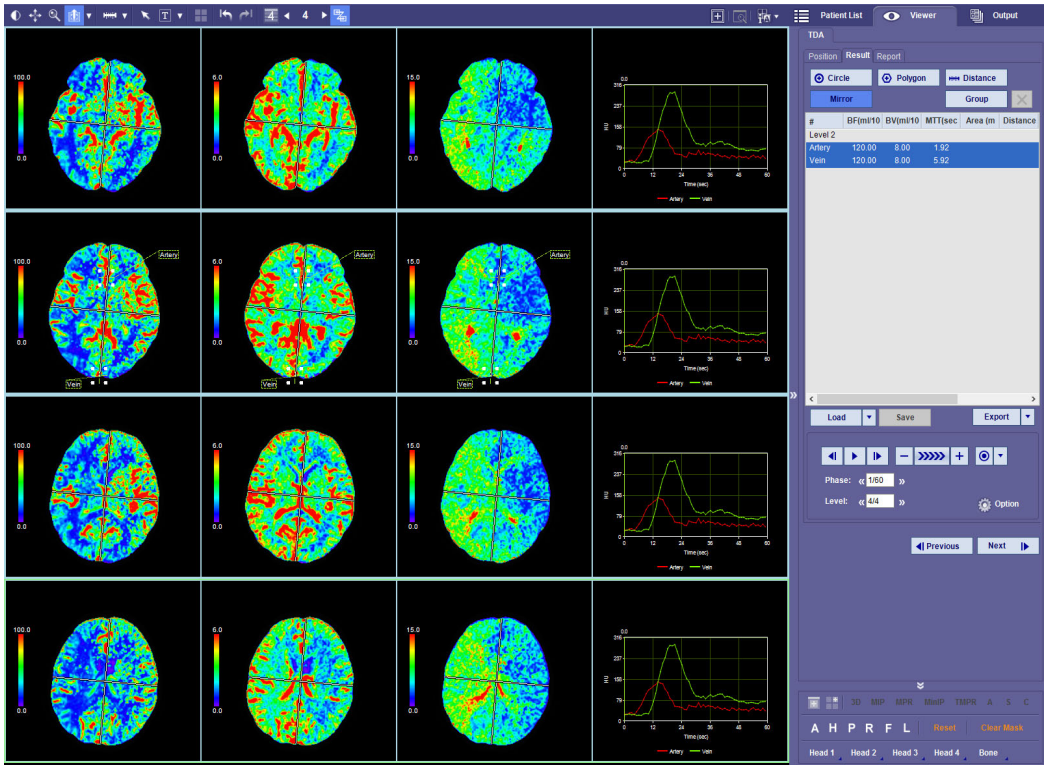
To start Time Dependent Analysis:

1. Right-click on a multi-phase perfusion study and select **TDA (T2*)** from the menu or select the **Load** button in the **Data Management Tools** bar, and then click the **TDA (T2*)** button in the Workflow Menu.

Note: To view temporal resolution MRI datasets, a minimum of 6 acquisition phases is required.

---

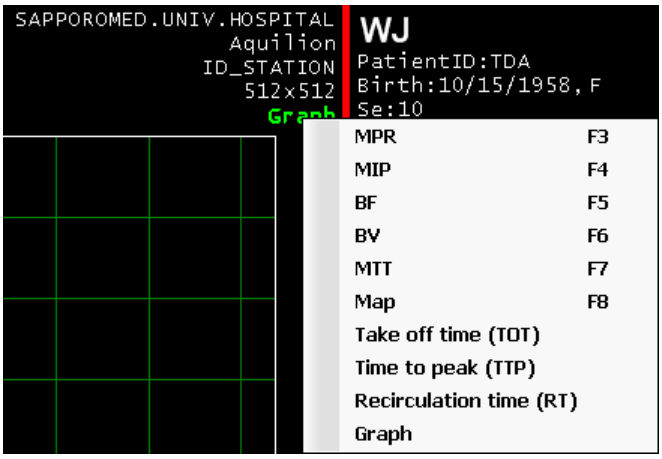
2. The software applies motion correction, calculates the TDA, and displays the results:



Maps and Graphs

The TDA calculation generates a set of image maps, as shown in the previous figure. Only four maps can be displayed for each level at any one time. The default images displayed are a profile graph, the negative enhancement integral image, the mean time to enhance image and the MPR image.

However, there are several other displays that contain valuable information. To access these, click the green text in the upper-right corner of any image in the main window. A menu is displayed, as shown in the following image:



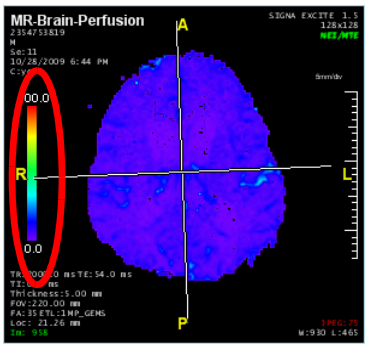
Any image can be displayed in either MPR and MIP rendering modes. In addition, Table 10.1 describes other maps and graphs that can be displayed.

Table 10.1: Displayable Maps and Graphs

Function	Definition
Negative Enhancement Integral (NEI)	Similar to the BV (Blood Volume) map in CT TDA.
NEI/MTE	Similar to the BF (Blood Flow) map in CT TDA.
Mean Time to Enhance (MTE)	Similar to the MTT (Mean Transit Time) map in CT TDA.
Mean Transit Time (MTT)	The average time taken by the contrast to reside in a volume of the ROI.
Maximum slope of increase (MSI)	Similar to the TOT (Take-off Time) map in CT TDA.
Maximum slope of decrease (MSD)	Similar to the RT (Recirculation time) map in CT TDA.
Time to minimum (TM)	Similar to the TTP (Time to Peak) map in CT TDA.
Profile graph	The graph on the left shows the concentration of contrast profile. It shows the original curve (red) and the fitted curve (pale color). The graph on the right shows the pixel intensity profile. Toggle between the two profiles by right-clicking on the graph image and selecting **Concentration Profiles** or **Intensity Profiles**.

Editing the Color Map

Each map is displayed with a color scheme that can be configured. The color map is accessed through the vertical color bar on the left side of each map image.



Display Range

The display range refers to the range of calculated functional values that are currently displayed in the map. This range is capped by the upper and lower values shown just above and below the vertical color bar. You can edit these upper and lower limits to show a greater or lesser range of colors.

There are two ways to edit the display range:

- Right-click the vertical color bar and select **Edit**.

  The **Display Range** dialog is displayed. Enter new **Min** or **Max** values and click **OK** when finished.

- You can also edit the display range by dragging the mouse up or down along the vertical color bar. The numbers shown at the top and bottom change as you move the mouse, and the colors displayed on the map change accordingly.

Color Maps

The following sections are described in full in Chapter 9: "Time Dependent Analysis" for CT studies. They are performed in the same way for both CT and MR data. For instructions or more information about these features, please see the pages indicated.

- **To change color maps** - See "Changing Color Maps" on page 9-5.
- **To create color map templates** - See "Creating Color Map Templates" on page 9-5.
- **For other features** - See "Other features" on page 9-7.
- **To load ROI templates** - See "Loading ROI Templates" on page 9-8.

Creating ROI Templates

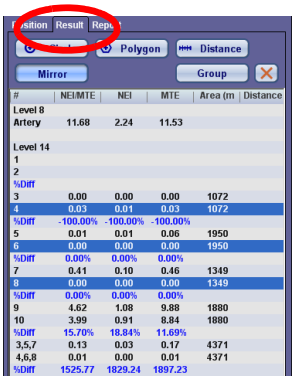
To create a new ROI template, you first must perform a manual TDA on the study (see "Manual TDA" on page 10-6 for instructions). When you reach the Result panel, the results based on the ROIs you placed manually are displayed. You can save this template by clicking the **Save** button at the bottom of the panel. The **Save TDA Templates** window is opened, where you can name the file and also add folders if desired.

Drawing ROI

You can draw Regions Of Interest (ROI) in a symmetrical structure to calculate various parameters pertaining to the time-dependent behavior of the underlying tissue. The Aquarius iNtuition TDA module provide several tools for defining Regions of Interest and comparing them.

The Result Panel

If you have calculated Time Dependent Analysis on the loaded data, the **Result** tab is currently displayed in the Tool Panel:

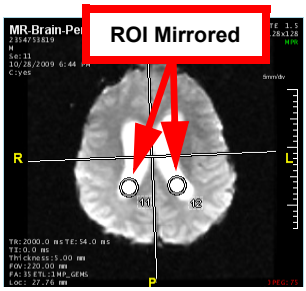


The top of the panel contains tool buttons which allow you to define ROI on data images (using either a circle or a polygon shape), measure distances on the data image, and automatically mirror the ROI on the opposite hemisphere, symmetrical to the center. To draw a ROI, perform the following:

1. Select either **Circle** or **Polygon** from the top toolbar.

2. Click the **Mirror** button so that the ROI is copied automatically to the other half of the symmetrical structure under analysis.

This analysis is also reflected in the results list in the Tool Panel (see image below, right). Under Level 1, listed in the figure above, the two ROIs numbered 1 and 2 correspond to the numbered circles shown in the figure below, on the left. The differences between each ROI are calculated and displayed for each pair of ROIs you add to the image.



Level 15				
11	1.79	0.55	19.99	175
12	2.42	0.63	16.68	175
%Diff	-26.10%	-11.99%	19.85%	

Figure 10-1: ROI Mirrored

Note: If you want the analysis to be propagated to the other levels automatically, enable the "Copy measurements to all levels" setting in the TDA Preferences screen. If this preference is not enabled, you must perform the measurements for each level manually.

Distance Measurements

To calculate a distance between two points in the image, click the **Distance** button in the Tool Panel, and then left-click and drag the mouse from the initial point to the final point. The distance is subsequently displayed in the result list in the Tool Panel, in the **Distance** column.

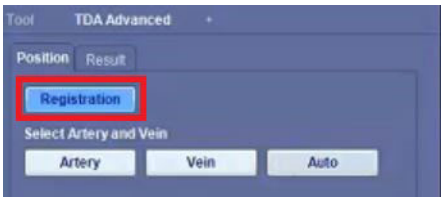
Manual TDA

The software initially selects the artery and vein, first by identifying the long axis of the brain, and then calculating the maximum standard deviation around the axis. This determines the approximate location of the artery and vein. A curve fitting method is applied to the pixels to select the artery and vein that best fits and has the maximum dynamic range.

Verify that the automatic artery and vein selection meets your need. If not, proceed to calculate the TDA manually. To calculate the TDA manually, you can begin the process by clicking the **Position** tab, located at the top of the tool panel (see image at right).

Step 1 - Apply Motion Correction

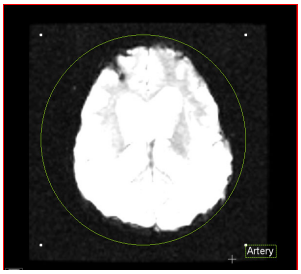
To apply motion correction, click the **Registration** button in the Tool panel:



Step 2 - Select Artery

To select an artery, perform the following:

1. Click the **Artery** button in the tool panel.
2. Drag the mouse to draw a circle around the entire brain. The software automatically selects an artery candidate.



Note: The only way to be sure the artery candidate is valid is to examine the profile graph after TDA completes its calculations. If the graph does not show a plausible profile, try the calculations again, using a different level.

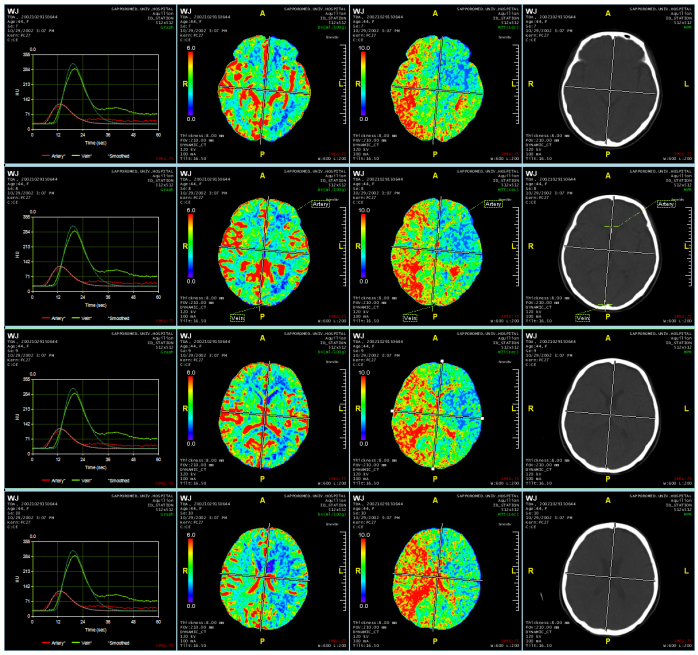
Step 3 - Select Center

Click the **Center** button to redraw the crosshair lines.

Step 4 - Start Calculation

Click the **Calculate** button in the tool panel**.**

As calculation progresses, functional maps are updated. The application displays a progress bar for the duration of the calculation. When the calculation is complete, the screen is displayed:



Generating a Report

Once all necessary analysis is performed, you can generate a report. To generate a report, do the following:

1. Click the **Report** tab in the tool panel.
2. Capture images in one of the following ways:
    - **Capture all levels**

If all levels are visible in the main window, click the **Capture** button. If all levels are not visible in the main window, click the down-arrow next to the **Capture** button, and then select **Capture All Levels** from the pull-down menu. The result is a capture of all visible maps, in all levels.

- **Capture a single map for all levels**

  Click the down-arrow next to the **Capture** button, select **Capture Map for All Levels** from the pull-down menu, and then select the desired map (for example, BV, BF, MTT) from the sub-menu. The result is a capture of the same map throughout all levels.

- **Capture preset maps**

  This option captures maps that have been preset in the TDA Capture Preferences screen. Only the selected (preset) maps are captured, but are captured in all levels. (To set options in the TDA Capture preferences screen, see "Brain TDA - Capture Settings" on page A-30.)

Note: All images are also captured in the Output Panel.

---

3. A dialog is displayed, asking whether you want to save the capture as a DICOM series:

   If you want to save the capture as a series, enter a name and series number in the dialog and click **OK**. If not, click **Cancel**. The capture will proceed either way.

4. Click **Generate Report** to create a report.

5. In the next window, select your name and click **Proceed** to sign electronically.

The system generates a MS Word report. A sample report, beginning with the following figure, shows captured images from the TDA calculation. You can save the report on your computer and attach it to emails sent to other physicians.

Chapter 11 Calcium Scoring

The Calcium Scoring optional module is used to calculate the Agatston score, the volume, and the mass of calcium deposits in coronary arteries.

The AQi Calcium Module

Starting Calcium Scoring

To launch the Calcium Scoring module:

1. Select a coronary study from the Patient List.
2. Open the study in the **Cardiac Workflow:3**
   - Right-click on the study, and select **Cardiac** from the context menu.
   - Select the study, click the **Load** button in the Data Management Tool Bar, and then select the **Cardiac** button in the Workflow menu.

The viewer opens.

To begin Calcium Scoring:

1. Select the **Ca (Calcium Score)** element in the Cardiac Workflow Tool panel or the **Ca Calcium** button in the 3D viewer Tool Panel.

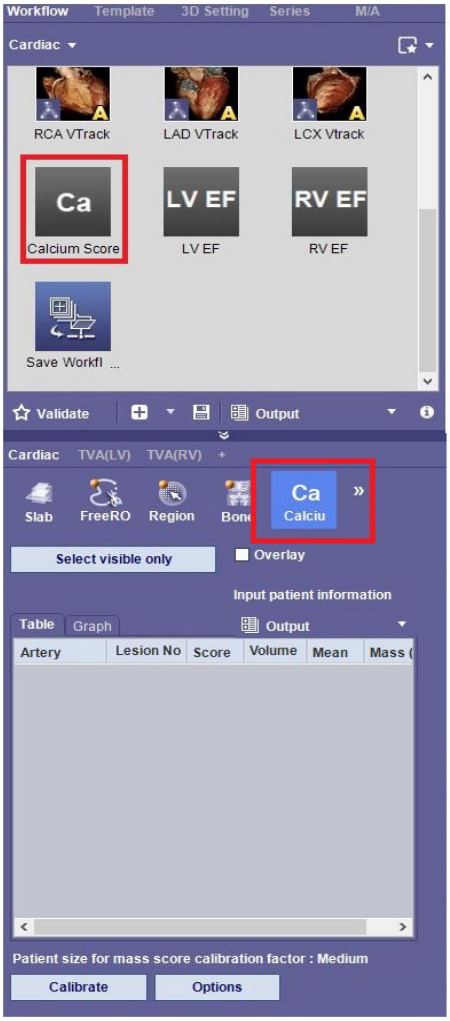
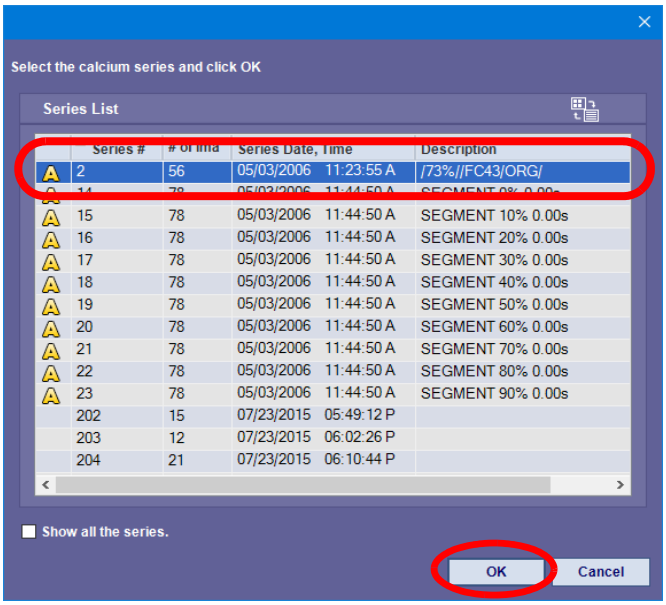


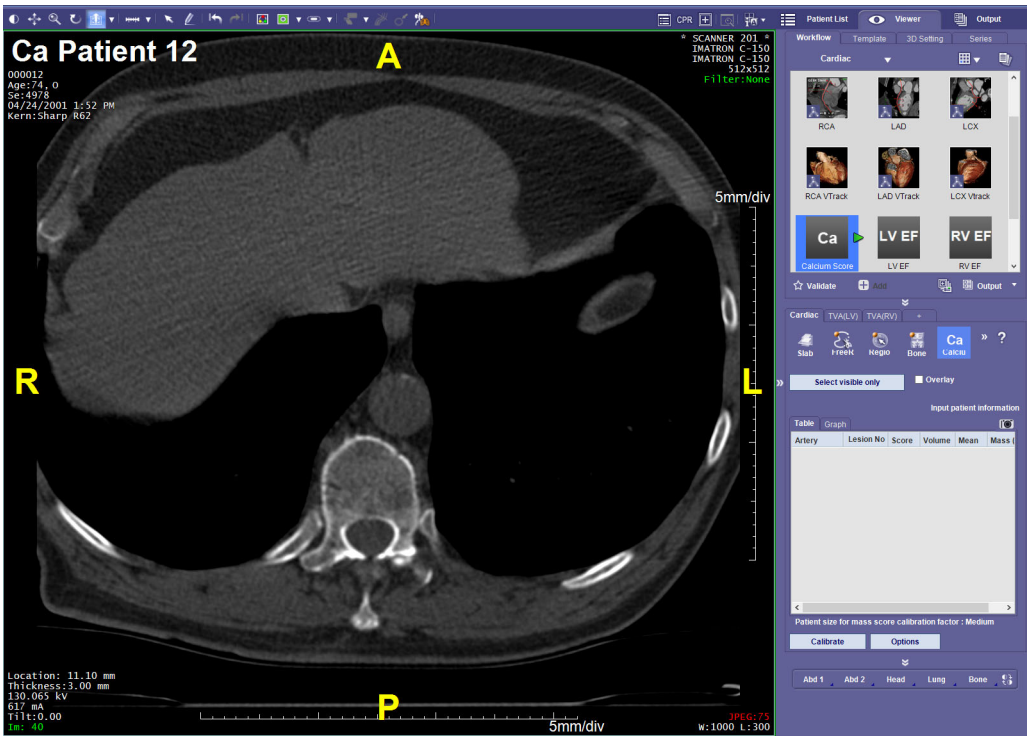
Figure 11-1Using the CA Scoring Tool

2. A popup window asks it you want to load another series for calcium scoring, select **Yes**.

   The **Series List** window opens.



3. Select the appropriate series and click **OK** to start the Calcium Scoring workflow.



According to the Consortium, the patient size is divided into 3 categories:

- Small: < 32.0 cm lateral thickness
- Medium: 32.0 – 38.0 cm lateral thickness
- Large: > 38.0 cm lateral thickness

The lateral thickness is measured from skin-to-skin, at the level of the proximal ascending aorta, from an A/P localizer image. The image may be from Scout, Topogram, Pilot, Scanogram, Surview, Preview, etc.

Because it is not possible to define the thickness of the patient always at the time of scanning, the iNtuition software allows the user to select small, medium or large from the software at any time. Be advised, once the calibration factor is changed, the scoring information will be reset as the initial results will be considered obsolete. It is for this reason, since version 4.4.12 P4, the software will prompt user for calibration information when the workflow is first launched.

Figure 11-2 Patient Size Categories

Viewing Slices

You can page through the slices of the data by using the configured slice/scrolling setting of the mouse or by using the up or down arrow keys on the keyboard.

Overlay

In the Tool Panel, check the **Overlay** box to highlight the parts of the image that have been interpreted as containing calcium.

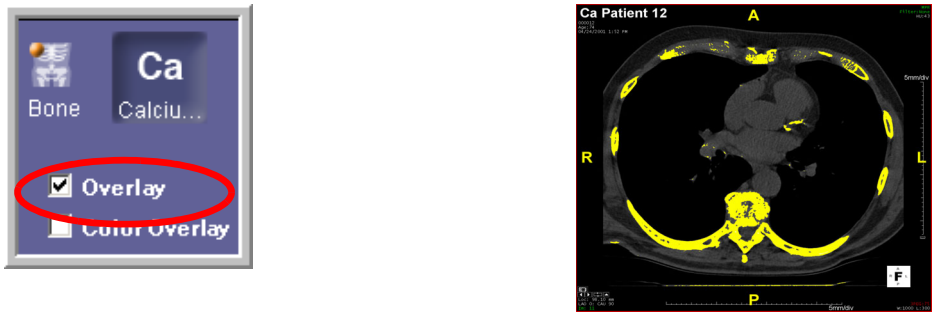


Figure 11-3: Pixels Identified as Calcium Highlighted

Color Overlay

The color overlay enables the display of a color mapping of the Agatston scoring staircase. When enabled, it allows you to investigate the interior density profile of lesions (see Figure 11-5 on page 11-5).

Note: In **Preferences > Viewer > Calcium settings**, enable **Use fast drawing mode for overlay images** to speed up mask and color overlay.

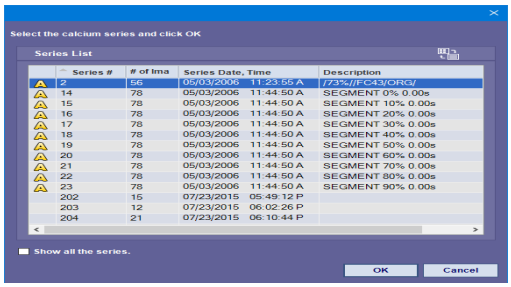


Figure 11-4 Option Off (30 fps) vs. Option On (60 fps)

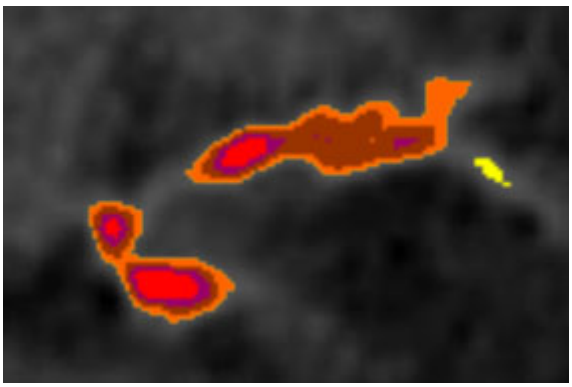


Figure 11-5: Color Overlay of Selected Lesions

Selecting Lesions

The Calcium function provides tools for selecting and labeling lesions. There are two ways to select a lesion, automatically and manually.

To select a lesion:

1. Press the **Shift** key and click on the lesion; or,
2. Left-click on the **Ca Score** button in the viewer. This does not require the **Shift** key.

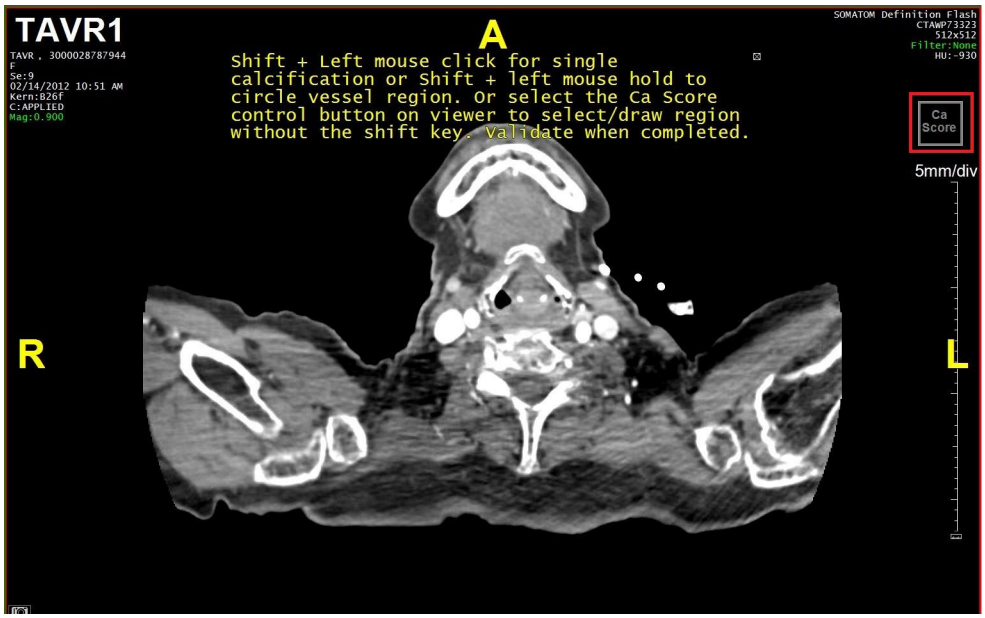


Figure 11-6 CA Score Button Highlighted

Instructions for scoring are shown above in yellow text. This can be turned off in **Preference > Calcium**. With the **CA Score** button on, you can left-click to select lesions.

CA Score Button in Off Position

CA Score Button in On Position

Figure 11-7 Difference in Ca Score button Appearance in Off/On

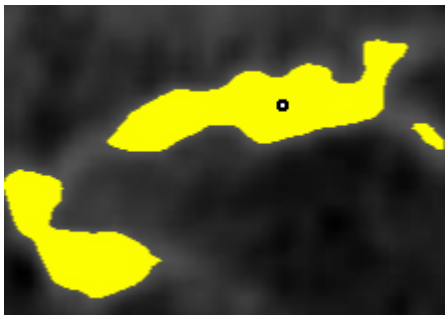


Figure 11-8: Shift+Left-click on Lesion

Once the lesion area is defined, a dialog window opens, where you can select the appropriate artery (see Figure 11-9).

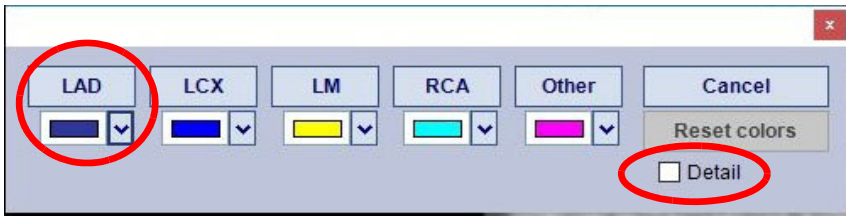


Figure 11-9: Select Region Dialog

Note: None of the selections in the "Other" category are reflected in the total score for the coronary arteries.

3. Select the name of the artery that contains the lesion. In this example, the lesion is in the LAD.

4. If you need to include more detail, check the **Detail** box (circled in Figure 11-9). The dialog is expanded to show greater detail about the main vessels (see Figure 11-15).

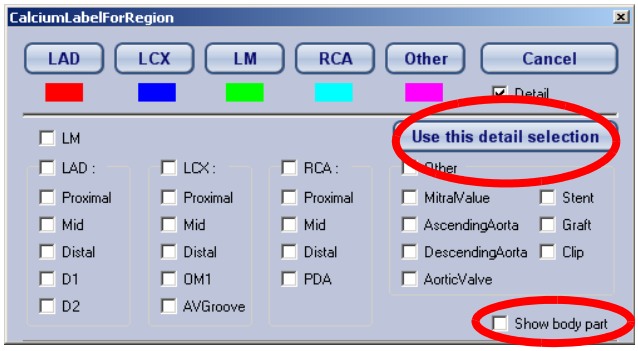


Figure 11-10: Calcium Label For Region

You can now score by vessel instead of by slice. After selecting the first lesion, the dialog box will appear and remain on the screen until the "Complete" box has been selected (pictured above in Figure 11-10). This allows for the option of detailed scoring.

Changing the Overlay Color of the Calcium Score

You can change the overlay color or create an unique color for one or all region overlays.

To change overlay colors:

1. In the CA Scoring workflow, RMB-click on a calcium area on the image and open the Select Region Dialog. (Figure 11-9)

2. Select the drop-down menu under one region (LAD for this example).

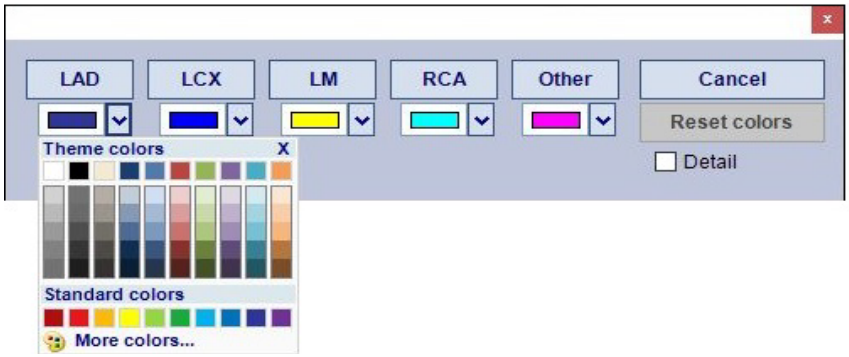


Figure 11-11 Drop-down Color Selection

3. Select a new color or select **More colors...**. the **Color** window opens.

4. You can select from the available basic colors or select the **Define Custom Colors>>** button.

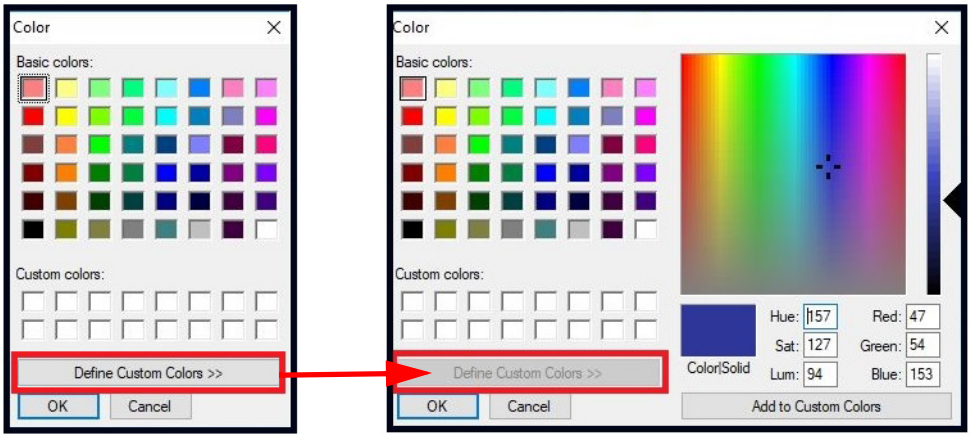


Figure 11-12 Basic or Custom Color Selection

5. Select **Ok** to exit each window.

Color Settings in the Preference Window

The above steps can be repeated using the **Preference Window**. You can the change Mask Color, Export Color, Import Color or Reset colors to the default in this window:

1. Open the **Preference Window** navigate to the **Calcium>Calcium Mask** settings.

2. Save the changed color settings by selecting the **Export Colors** button. This opens the **/bin** directory.

3. Select **Import Colors** to import other colors. This opens the **/bin** directory as well.

4. Any changes can be undone by selecting the **Reset colors to default**.

5. Select **Ok** to exit the **Preference Windows** and save the color settings.

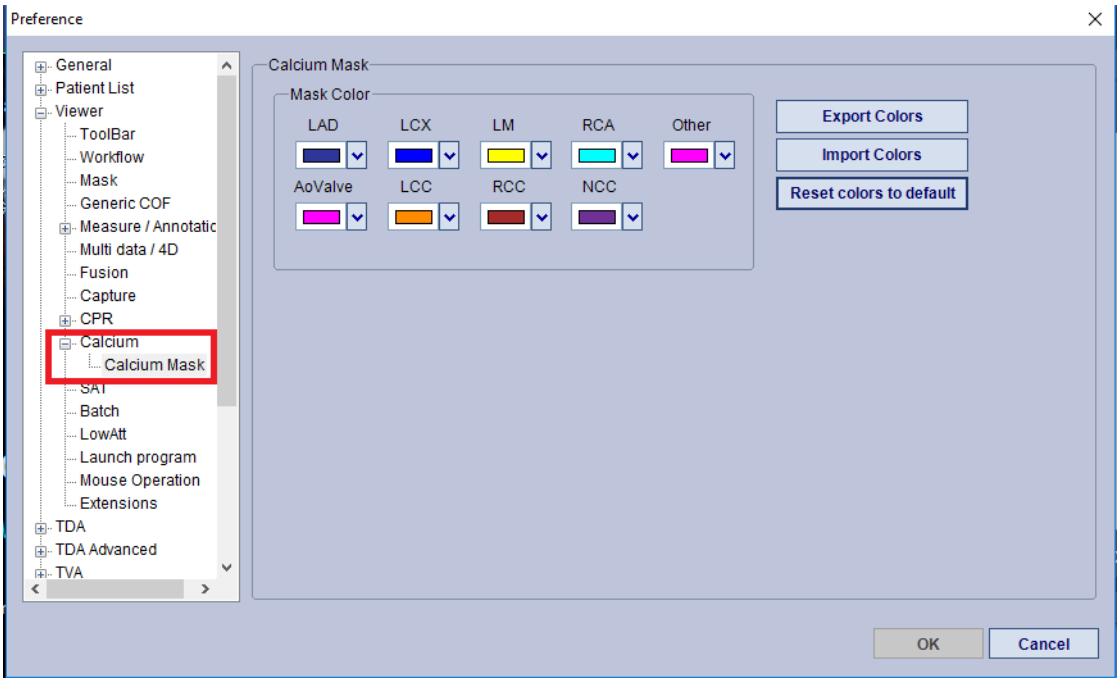


Figure 11-13 Preference>Calcium>Calcium Mask

Editing Lesion Labels

During scoring, you might want to give a new name when “other” is selected in this case select “New Label” and type in a custom name. If the user wants to edit the label after it is submitted they can click edit on the GUI.

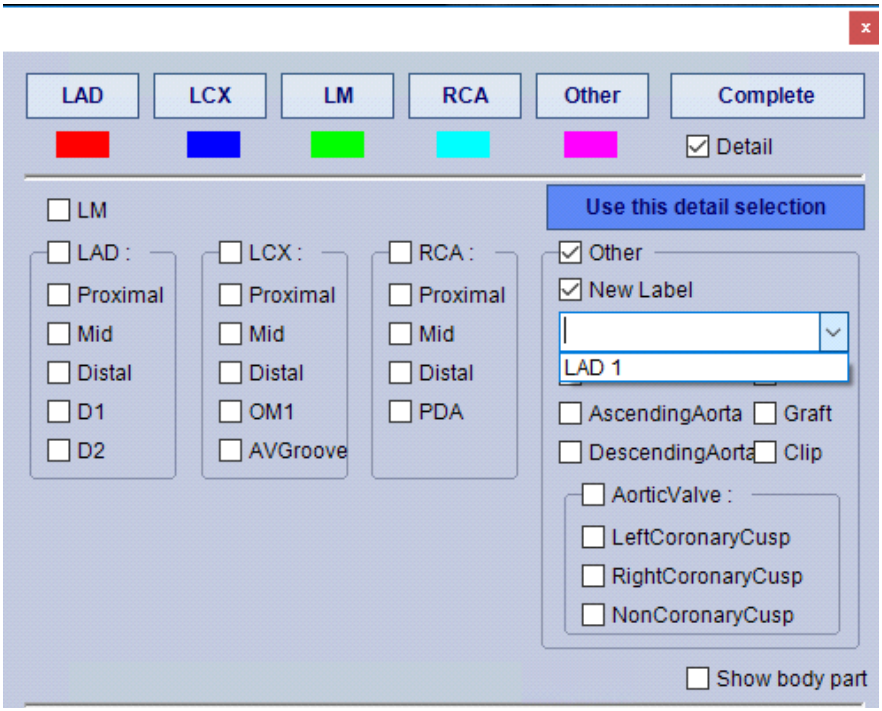


Figure 11-14 Editing Lesion Labels

Note: To access detailed scoring, go to **Settings > Viewer > Calcium** and enable **Serially Classify Calcium By Vessels**.

If the lesion is not in a coronary artery, you can specify the location of the body part. Check the **Show body part** box in the lower-right corner of the dialog (circled in Figure 11-10). A third section is shown beneath the detail section, where you can check which part of the body contains the artery (see Figure 11-15).

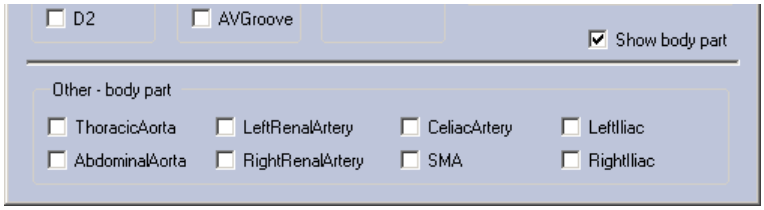


Figure 11-15: Artery Detail Dialog

If you have included details, click the **Use this detail selection** button (circled in dark blue, in Figure 11-10) to complete the segmentation. Otherwise, click the name of the artery in the upper portion of the dialog. The lesion is highlighted to show segmentation.

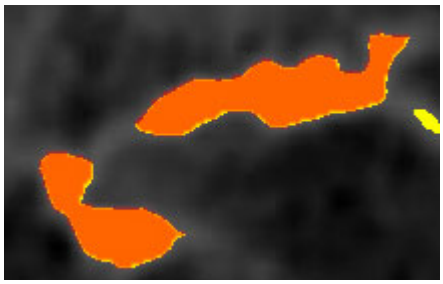


Figure 11-16 Highlighted Lesion Selection

By default, the Calcium tool selects the entire lesion, including all slices the lesion encompasses. If you select only the section (Figure 11-17, middle image), the entire lesion is selected. If you scroll through nearby slices, you see the other lesion portions included in the selection.

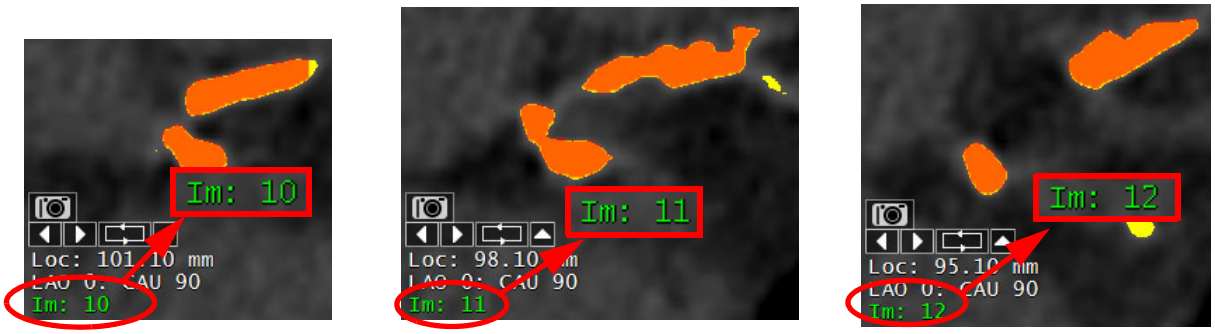


Figure 11-17: The Entire Selected Lesion on different Slices

Selecting and Dividing Lesions

Occasionally, you may want to divide a lesion which spreads across two arteries, or to select two or more visible but disconnected lesions in the same artery. The manual selection tool is useful for both of these cases.

Select a lesion using **Shift** + click. The entire lesion is selected and highlighted. If you want to select only part of a lesion, you can press the **Shift** key and manually drag the mouse around the desired area (shown in the following figure). When the area is encircled, release the mouse. The dialog (shown in Figure 11-9 on page 11-7) is opened. Follow instructions 1 - 4, explained above, to use the dialog.

Note: Subdividing a lesion results in different peak densities for the two partial lesions and may modify the total Agatston score for the patient slightly.

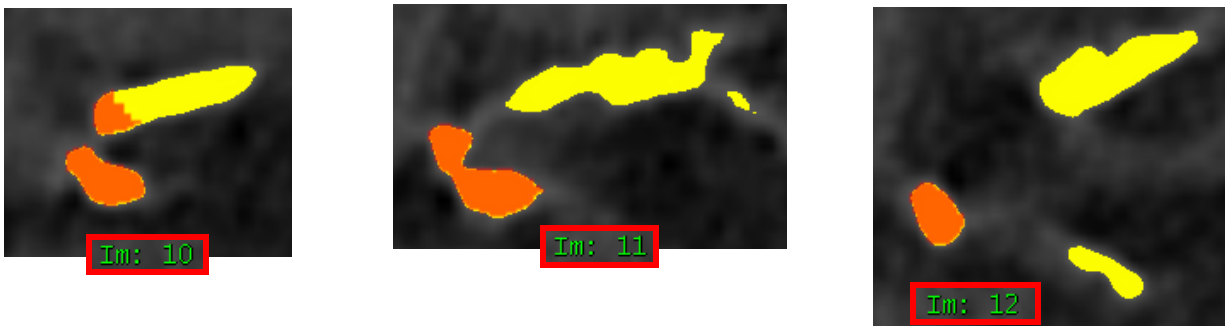
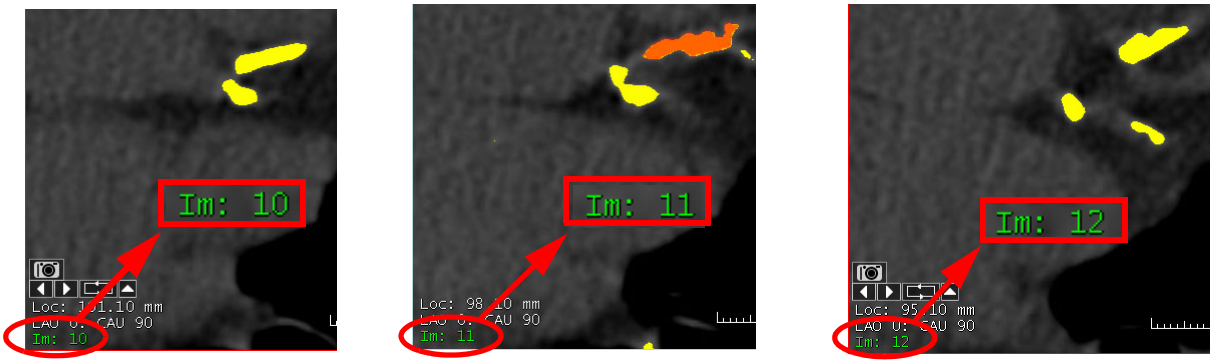


Figure 11-18: Middle: Manually Selected Section of Lesion;
Left: Selection as it Appears in Previous Slice; Right: The Following Selection as it Appears in Following Slice

Select Visible Only

To select only the visible (on-screen) portions of a lesion, click the **Select visible only** button first.

The following image shows the same three slices as they would appear when using the **Select visible only** feature. Again, image 11 (the middle image) is where the lesion was selected. But the parts of the lesion appearing in images 10 and 12 are not selected.



Deleting Lesions

Delete a lesion in one of two ways:

- Shift-click on the selected lesion in the image. Click **OK** in the dialog to delete.
- From within the table, right mouse click on the lesion you wish to delete.
  - Select **Delete**
  - Select **Delete All** to remove all lesions from the table.

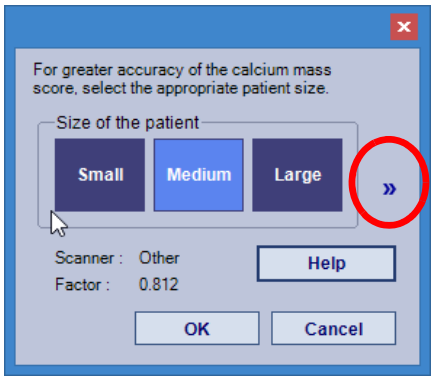
Mass Score Calibration

Calibration factors are derived from the size of the patient and the scanner type. There are three patient sizes: Small, Medium and Large. The physician must identify the appropriate size of the patient, based on standard criteria. The scanner type is part of the dataset's DICOM header. However, you can change these values if needed.

Note: If you would like to show the Calcium calibration dialog every time a series is loaded in Calcium, you can change this in **Settings > Viewer > Calcium** by enabling "Show calcium calibration dialog on loading series. Also note, if you would like to customize your preference to calibrate, then you must disable the DICOM scanner using default patient size in the **Viewer > Calcium** settings by disabling the "Use DICOM scanner type and default patient size for calibration" option.

---

1. Click the **Calibrate** button near the bottom of the Calcium tool panel. The following dialog is opened:



2. If all you need to change is the patient size, click the button for the correct value and then click **OK**.

3. If you also need to change the scanner type, click the double right-arrow on the right side of the **Calibrate** dialog. The dialog expands to display calibration factors for each patient size, depending on the scanner type.

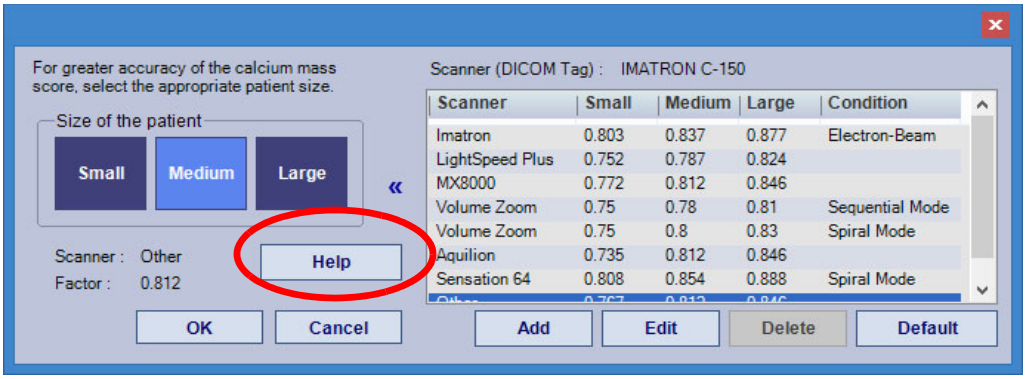
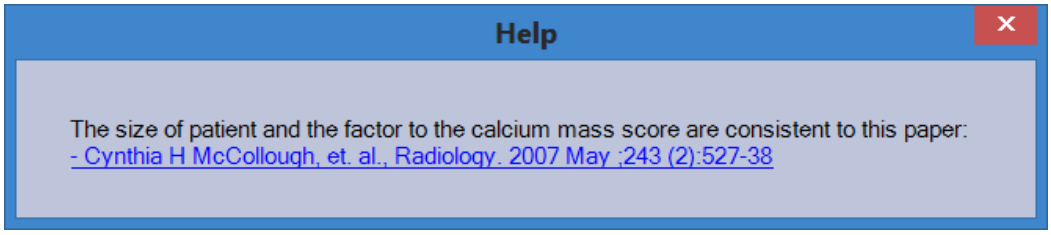


Figure 11-19: Calibration Dialog with Scanner Types

Patient Size and Mass Scoring

To read more about patient size as a factor of the calcium mass score, click the **Help** button in the calibration dialog, as shown in Figure 11-19. The following message is posted:



Click on the link in this message to view the paper.

According to the Consortium, the patient size is divided into 3 categories:

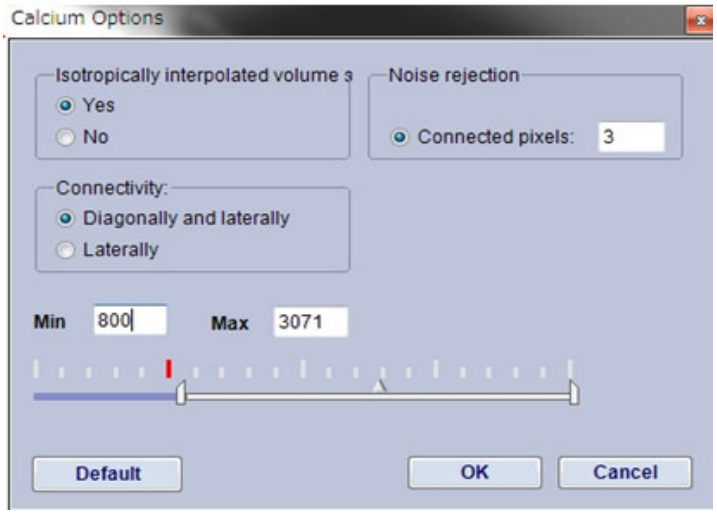
- Small: < 32.0 cm lateral thickness
- Medium: 32.0 – 38.0 cm lateral thickness
- Large: > 38.0 cm lateral thickness

The lateral thickness is measured from skin-to-skin, at the level of the proximal ascending aorta, from an A/P localizer image. The image may be from Scout, Topogram, Pilot, Scanogram, Surview, Preview, etc.

Because it is not possible to define the thickness of the patient always at the time of scanning, the iNtuition software allows the user to select small, medium or large from the software at any time. Be advised, once the calibration factor is changed, the scoring information will be reset as the initial results will be considered obsolete. It is for this reason, since version 4.4.12 P4, the software will prompt user for calibration information when the workflow is first launched.

Options

The **Calcium Options** panel allows you to configure various settings used during the calculation of the calcium score.



The settings are defined as follows:

- **Isotropically interpolated volume score**

  Enable or disable isotropic interpolation when calculating the volume score. The default setting is **Yes**. If you disable the feature by selecting **No**, you can perform the volume score without performing any isotropic interpolation.

- **Connectivity**

  When deciding whether voxels are connected or not, the software needs to know if diagonally adjacent voxels should be considered to be connected. The default setting is **diagonally and laterally** and we recommend using it.

- **Noise Rejection**

  In order to minimize the contribution that comes from small areas of noise that may peak above the threshold, the software requires that a certain number of pixels be connected before the collection is considered a lesion. The default setting takes account of the actual area of pixels in a slice, so that only collections with a combined area of one square mm or more are considered lesions. You can change this pixel value by selecting the option **Connected Pixels**, and entering the number of pixels in the box.

- **Threshold**

  This option allows you to specify the threshold range in which a pixel is considered to be calcium, for the current exam. Use the slider to set the minimum and maximum values of the range, or enter the values into the text boxes.

- **Automatic Validation (Figure 11-20, #1)**

  This option allows you to automatically validate when scoring is complete.

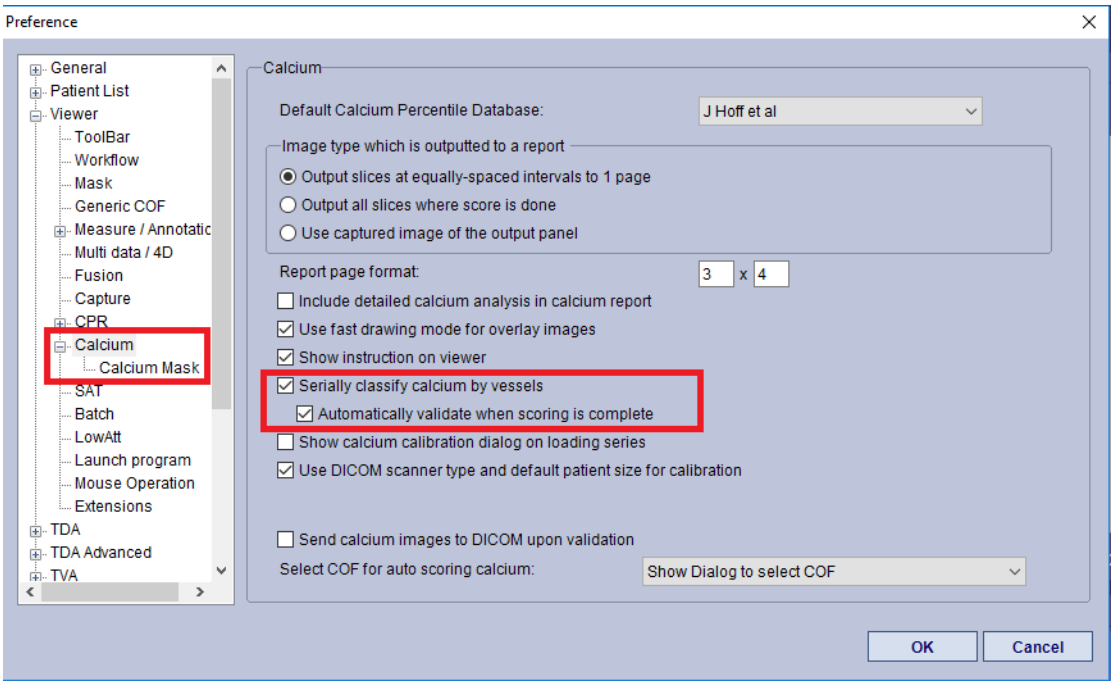


Figure 11-20 Preference>Calcium Settings

After selecting “complete” on scoring GUI, the calcium scoring workflow is automatically validated.

Note: You can also edit these settings by right-clicking on the Viewer and going to **Calcium Score > Settings.**

- **Select COF for auto scoring calcium**

This setting allows you to use multiple company COFs (masks) or the latest COF for automatic calcium scoring. If any COF is available, you are prompted to use it.

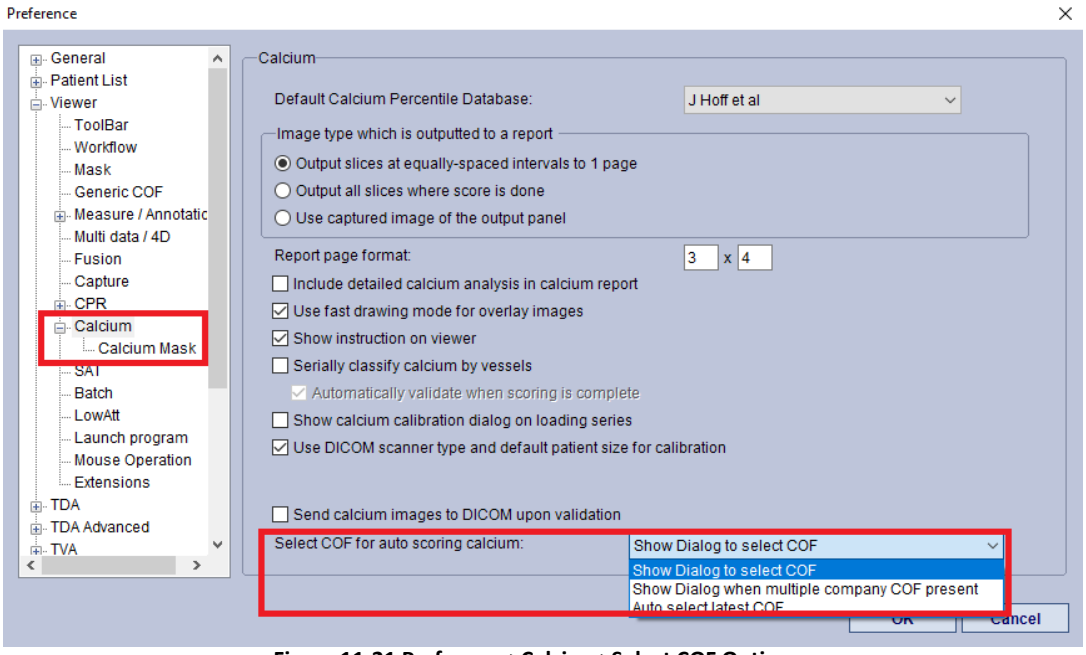


Figure 11-21 Preference>Calcium>Select COF Options

Note: This feature is not available in the current release.

Capturing the Result Table and Percentile Graphs

You can open the result table (from the tool panel) in a separate window, which can then be captured. Right-click on the result table and select **Preview**. The result table opens. To see the graph, select the

graph tab in the tool panel and graph information replaces the table window. You can also right-click on the table window and select **Graph**. You can right-click on the window and select **Table** as well.

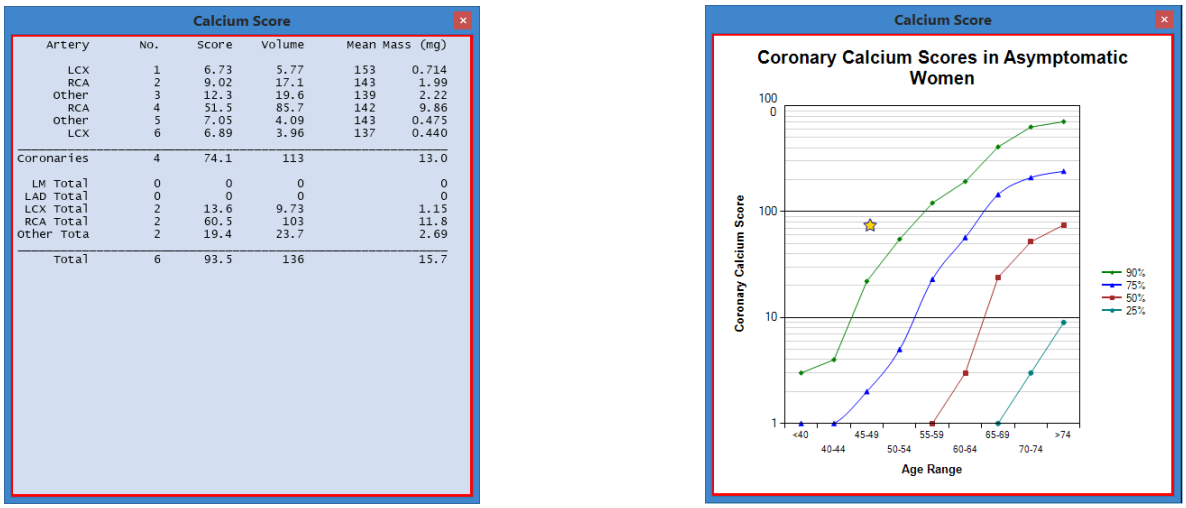
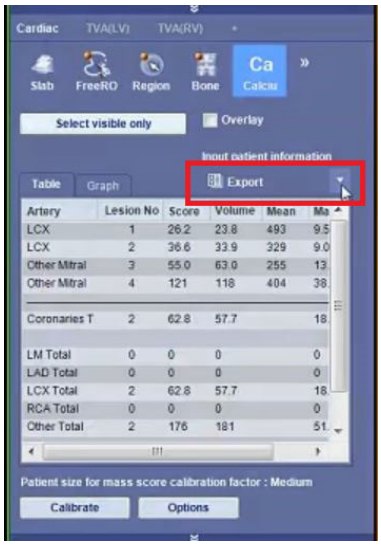


Figure 11-22: Table and Graph Previews

If **Send calcium images to DICOM upon validation** is checked in the preferences window, the result table and percentile graph is included.

Exporting Results Table and Graph

Next to the Table and Graph tabs is the Export menu.



This menu defaults to **Export** until you select a results output type from the menu.

The drop-down menu options for exporting the Table result are:

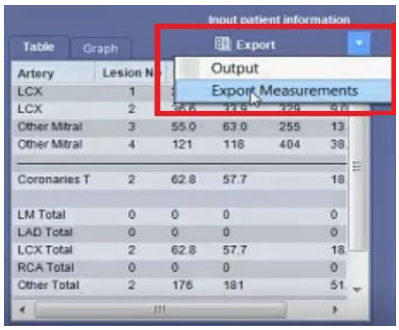


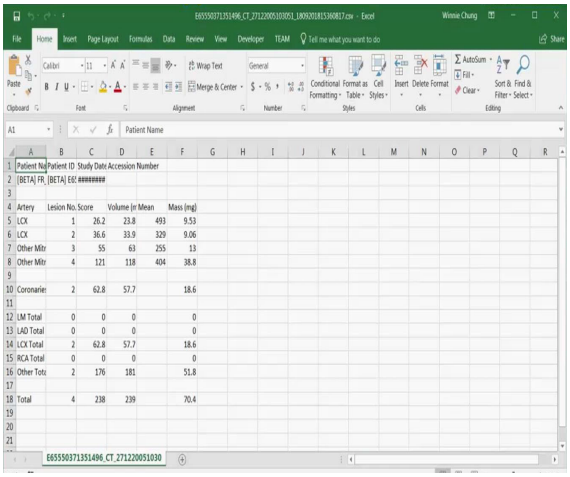
Figure 11-23 Drop-down Exportation Menu

- Output
- Export Measurements

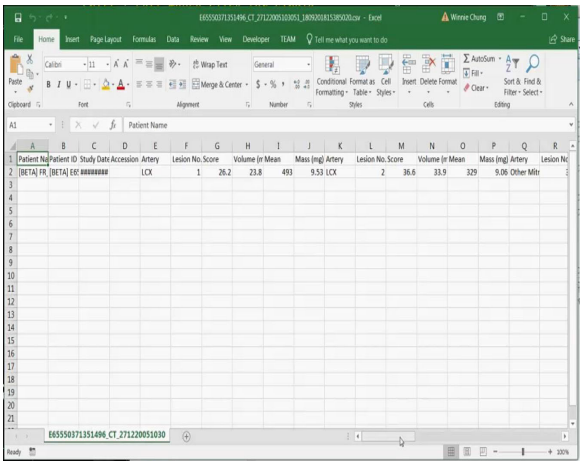
When you select Export Measurements you are asked to save the output file. The window defaults to the Username > Documents folder until you change the path. The changed path is retained for all future output files.

You can save the file in the following formats:

- As a text file,
- As a CSV file in Tabular Format,
- As a CSV file in a Single Row Format, and;
- As an XML file.



Tabular Format

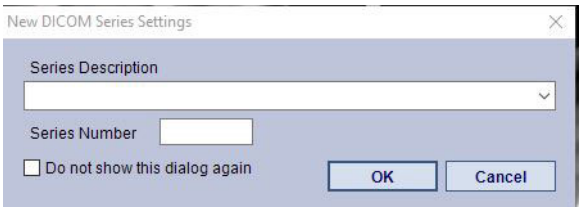


Single Row Format

Figure 11-24 Example of Tabular and Single Row Output Formats

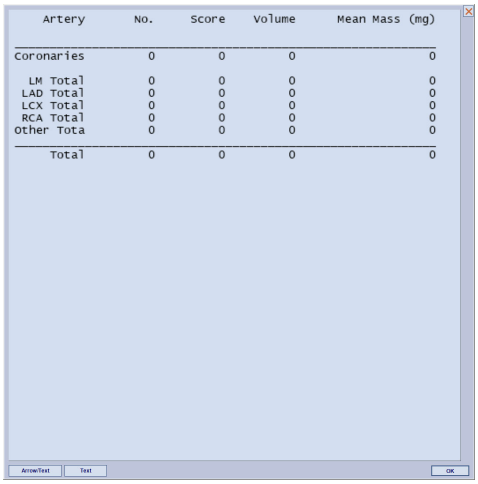
To output a graph:

1. Select the **Graph** Tab
2. The only item on the Export drop-down menu for **Graph** is **Output**.
3. You are prompted to Description and Number a DICOM Series:

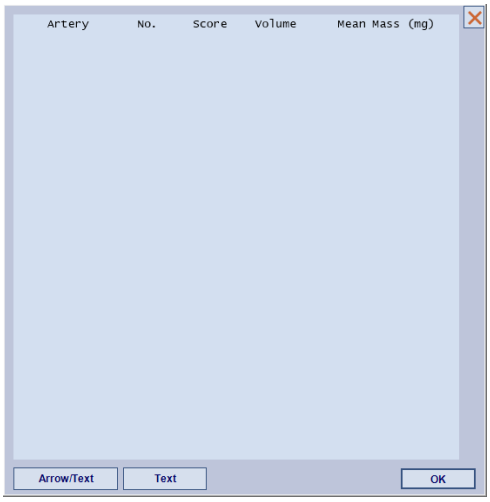


Capturing a Zero Calcium Score

If you try to capture a zero result from calcium score, AQi posts a dialog asking whether you want to capture the Zero Calcium Score text. Click Yes to capture the results. If you click No, a blank table is captured instead (see Figure 11-25).



Results Captured



Blank Screen Captured

Figure 11-25: Zero Calcium Score Capture

Saving Screen Captures Separate from Reports

If “Send calcium images to DICOM upon validation” is checked it will send calcium score screen shots to the location selected for general captures.

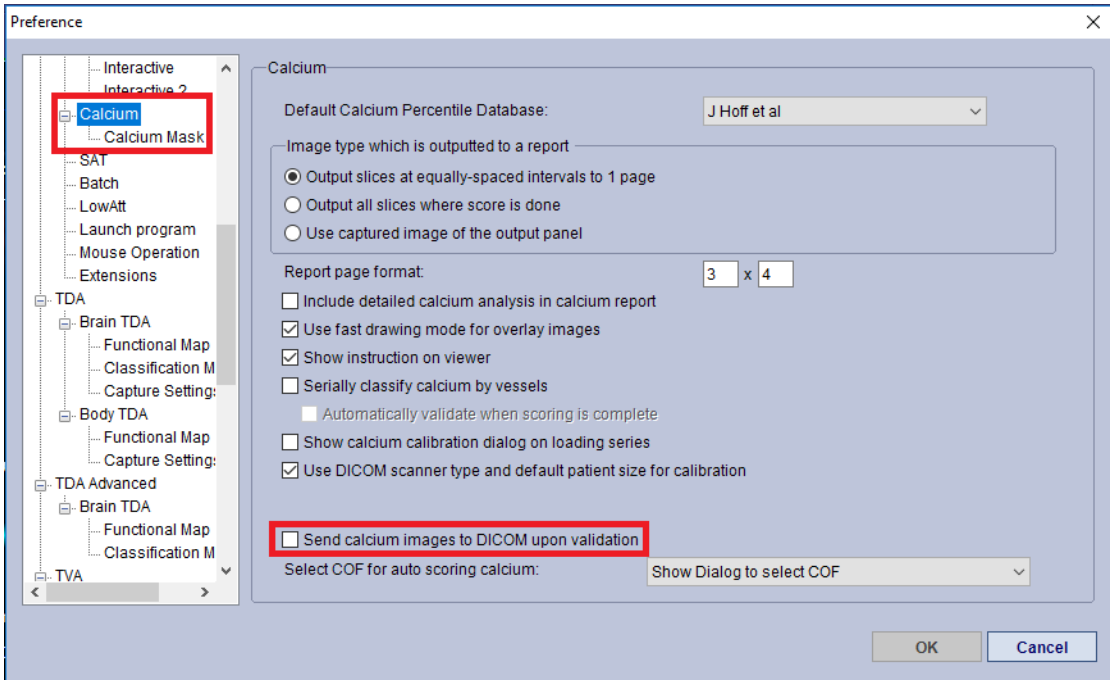


Figure 11-26 Preference>Calcium Options>Send to DICOM

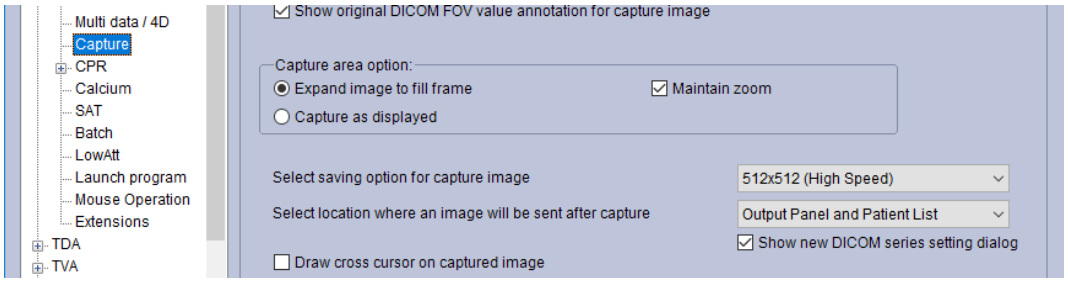


Figure 11-27 Preference>Capture Options

Generating a Report

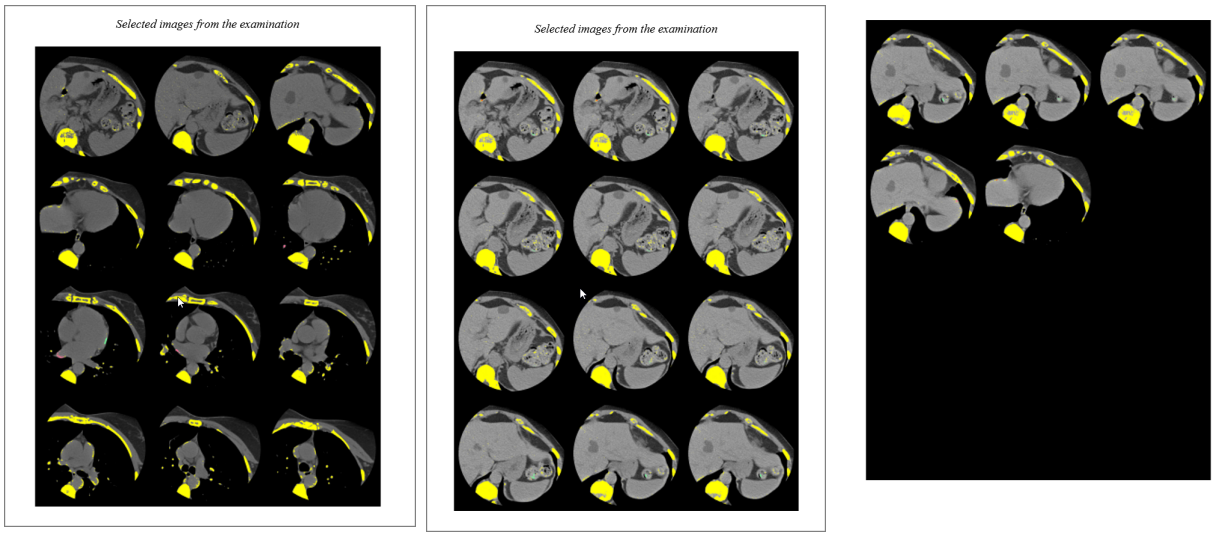
Including Images in the Report

There are three options for including images in a report. To select an option, open preferences and go to the **Viewer**->**Calcium** screen.

- Output slices to one page - Report images are auto-selected to fit on one page.
- Output all slices where calcium scoring has been performed - Report images include all axial images where calcium score has been done with a color overlay.

- Use a captured image of the output panel - Report images include captured images from the Output Panel.

Note: To include captured images in the report, make sure to capture the images to the Output Panel before validation.



All Slices on One Page **Slices Where Score Is Done** **Capture of Output Panel**

Figure 11-28: Images Included in Report

You can include lesion-specific details by vessel in the report. To include this information, a setting in the user preferences must be enabled. See "Calcium" on page A-20 for more information. Figure 11-30 on page 11-24 shows the difference between including and not including lesion-specific details.

If “include detailed calcium analysis in Calcium Report” is selected the report shall display the detailed lesion locations from the check boxes so the report accurately reflects the details selected.

You can generate a calcium report by doing the following:

1. Locate the button in the lower-right corner of the Workflow area (see figure below). It says either **Output**, **Output All**, **Report**, **Send to DICOM** or **Export Measurements**.

2. If it does not say **Report**, click the down arrow located to the right of this button (circled). This opens a pull-down menu.

3. Select **Report** from this menu. The button changes to **Report**.

4. Click the **Report** button. The **Report Templates** dialog is displayed.

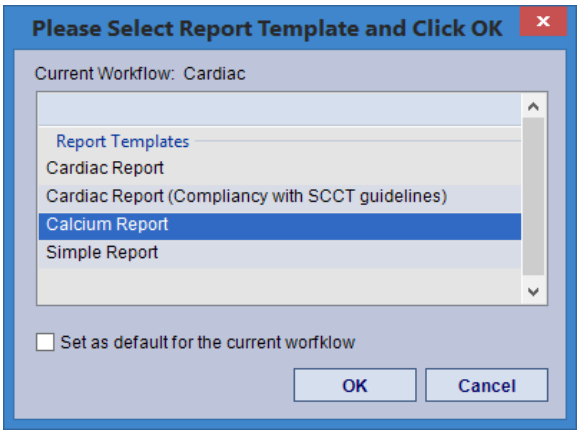
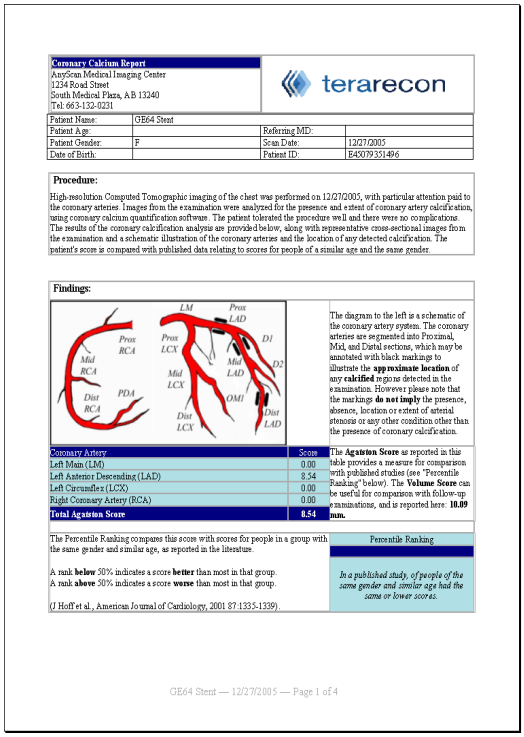


Figure 11-29 Report Templates Dialog

5. Select the desired type of report and click **OK**.

The report is opened in MS Word:



Coronary Calcium Report
AnyScan Medical Imaging Center
1234 Road Street
South Medical Plaza, AB 13240
Tel: 663-132-0231

terarecon

Patient Name:	GE64 Stent		
Patient Age:		Referring MD:	
Patient Gender:	F	Scan Date:	12/27/2005
Date of Birth:		Patient ID:	E4507935149 6

Procedure:

High-resolution Computed Tomographic imaging of the chest was performed on 12/27/2005, with particular attention paid to the coronary arteries. Images from the examination were analyzed for the presence and extent of coronary artery calcification, using coronary calcium quantification software. The patient tolerated the procedure well and there were no complications. The results of the coronary calcification analysis are provided below, along with representative cross-sectional images from the examination and a schematic illustration of the coronary arteries and the location of any detected calcification. The patient's score is compared with published data relating to scores for people of a similar age and the same gender.

Findings:

The diagram to the left is a schematic of the coronary artery system. The coronary arteries are segmented into Proximal, Mid, and Distal sections, which may be annotated with black markings to illustrate the **approximate location** of any **calcified** regions detected in the examination. However please note that the markings **do not imply** the presence, absence, location or extent of arterial stenosis or any other condition other than the presence of coronary calcification.

Coronary Artery	Score
Left Main (LM)	0.00
Left Anterior Descending (LAD)	8.54
Left Circumflex (LCX)	0.00
Right Coronary Artery (RCA)	0.00
Total Agatston Score	**8.54**

The **Agatston Score** as reported in this table provides a measure for comparison with published studies (see "Percentile Ranking" below). The **Volume Score** can be useful for comparison with follow-up examinations, and is reported here: **10.09 mm.**

The Percentile Ranking compares this score with scores for people in a group with the same gender and similar age, as reported in the literature.

A rank **below** 50% indicates a score **better** than most in that group.
A rank **above** 50% indicates a score **worse** than most in that group.

(J Hoff et al., American Journal of Cardiology, 2001 87:1335-1339).

Percentile Ranking
In a published study, of people of the same gender and similar age had the same or lower scores.

GE64 Stent — 12/27/2005 — Page 1 of 4

Coronary Calcium Scoring:

It has been established that calcification of the coronary arteries, which can be detected by the scanner used in this examination, is a marker for the presence of Atherosclerosis (hardening of the arteries)[1]. If calcification of a coronary artery is detected by the scanner, this indicates the presence of atherosclerotic plaque in the blood vessel. Such calcifications often appear many years before symptomatic heart disease develops, and as such they can represent an early indication of the presence of developing coronary artery disease.

If calcification is detected in the coronary artery system by the scanner, the Calcium Score[2], is computed for each of the coronary arteries based upon the size and density of the regions identified to contain calcium. While this Calcium Score does not correspond directly to narrowing in the artery due to atherosclerosis, it does have correlation with the severity of coronary atherosclerosis present. The Calcium Score is used to compare the patient's result with results from people of the same gender and a similar age, from published tables of Calcium Scores[3]. This process is referred to as "Percentile Ranking". A second score, the Volume Score[4] is also calculated and recorded in this report. The Volume Score is sensitive to the size of the lesion and helpful when performing comparison with a follow-up examination.

The scores and percentile ranking reported here are intended to enable your physician to better evaluate your risk of developing symptomatic coronary artery disease. They can also be helpful to track the progression or regression of disease and effectiveness of treatment administered.

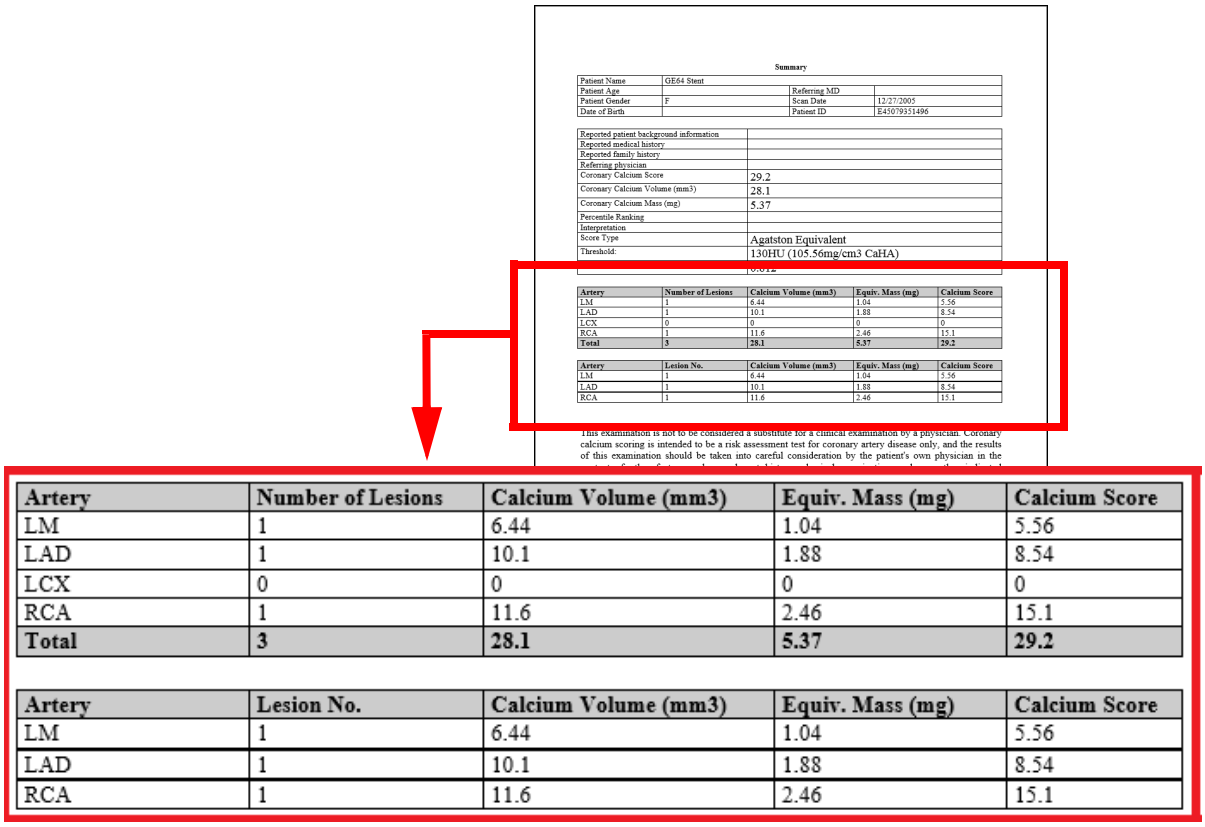
A full evaluation of cardiac risk should include an assessment of all conventional risk factors, and the scores and percentile rankings reported herein should be evaluated in this context. The following table provides guidelines for the interpretation of the results[4].

Calcium Score	Interpretation
0	No identifiable atherosclerotic plaque. Very low cardiovascular disease risk. Less than 5% chance of presence of coronary artery disease. A Negative Examination
1-10	Minimal plaque burden. Significant coronary artery disease very unlikely.
11-100	Mild plaque burden. Likely mild or minimal coronary stenosis.
101-400	Moderate plaque burden. Moderate non-obstructive coronary artery disease highly likely.
Over 400	Extensive plaque burden. High likelihood of at least one significant coronary stenosis (>50% diameter).

Recommendations

Adoption and maintenance of a healthy lifestyle is recommended for all people. This should include regular, appropriate exercise and observance of a proper diet, to ensure balanced nutrition and weight control. Tobacco use should be avoided. Cholesterol has been linked to coronary atherosclerosis, and we strongly encourage adhering to the recommendations of the National Cholesterol Education Panel (NCEP) in this regard. For primary prevention, these include a target goal for total cholesterol of less than 200 mg/dl, HDL cholesterol of greater than 40 mg/dl, triglycerides of less than 200 mg/dl, and LDL cholesterol of less than 100 mg/dl. Secondary prevention involves more stringent goals. However note that these are general recommendations only, and as with all such matters, the personal physician should be consulted regarding recommendations appropriate for the individual.

GE64 Stent — 12/27/2005 — Page 2 of 4



Summary

Patient Name	GE64 Stent		
Patient Age		Referring MD	
Patient Gender	F	Scan Date	12/27/2005
Date of Birth		Patient ID	E45079351496

Reported patient background information	
Reported medical history	
Reported family history	
Referring physician	
Coronary Calcium Score	29.2
Coronary Calcium Volume (mm3)	28.1
Coronary Calcium Mass (mg)	5.37
Percentile Ranking	
Interpretation	
Score Type	Agatston Equivalent
Threshold:	130HU (105.56mg/cm3 CaHA)

Artery	Number of Lesions	Calcium Volume (mm3)	Equiv. Mass (mg)	Calcium Score
LM	1	6.44	1.04	5.56
LAD	1	10.1	1.88	8.54
LCX	0	0	0	0
RCA	1	11.6	2.46	15.1
Total	**3**	**28.1**	**5.37**	**29.2**

Artery	Lesion No.	Calcium Volume (mm3)	Equiv. Mass (mg)	Calcium Score
LM	1	6.44	1.04	5.56
LAD	1	10.1	1.88	8.54
RCA	1	11.6	2.46	15.1

This examination is not to be considered a substitute for a clinical examination by a physician. Coronary calcium scoring is intended to be a risk assessment test for coronary artery disease only, and the results of this examination should be taken into careful consideration by the patient's own physician in the

Artery	Number of Lesions	Calcium Volume (mm3)	Equiv. Mass (mg)	Calcium Score
LM	1	6.44	1.04	5.56
LAD	1	10.1	1.88	8.54
LCX	0	0	0	0
RCA	1	11.6	2.46	15.1
Total	**3**	**28.1**	**5.37**	**29.2**

Artery	Lesion No.	Calcium Volume (mm3)	Equiv. Mass (mg)	Calcium Score
LM	1	6.44	1.04	5.56
LAD	1	10.1	1.88	8.54
RCA	1	11.6	2.46	15.1

Figure 11-30: Lesion-Specific Details

Chapter 12 Flythrough Workflow

Topics in this chapter:

The Flythrough optional workflow lets you investigate the interior of organs like the colon. The Flythrough camera captures the entire internal structure. This workflow assists in investigating polyps or cancerous growths on the structure's walls.

In the Flythrough workflow, you can review a single series or up to three series simultaneously. This chapter focuses mainly on reviews of the supine and prone series loaded together.

Supine and Prone Scans

In order to perform a comprehensive study, many physicians scan the patient in a supine position (lying on the back) and then in prone position (lying on the stomach). This allows a more complete view of the structure. Fluid and stool that may obstruct pathology in one of the scans lie differently in the other scan. Using this imaging technique allows simultaneous review to resolve any visual uncertainties.

You can use the Flythrough Workflow for either one or both types of scans.

Launching the Flythrough Workflow

To open a Flythrough Workflow:

1. From the Study list on the Patient list page, use the CTRL key and left-click to select multiple studies.
2. From the Series list, select both a prone and a supine scan.
3. Load the series. Select the **Load** button in the **Data Management Tool Bar** and select the **Flythrough** workflow, or right-click on the selected series and then select **Flythrough** from the context menu.

Keyboard Shortcuts

Table 12.1 contains a list of all the keyboard/mouse shortcuts that are used in the Flythrough workflow. These can be used in place of many of the tool panel controls and menu items.

Table 12.1 Keyboard/Mouse Shortcuts

Perspective		
Left	Click and Drag	Rotate
	Alt + Click	Pick location
	Ctrl + Click and Drag	Orbit
Middle	Click	Pick location
	Click and Drag	Go straight forward/backward
Right	Click	Context menu
	Click and Drag	Pan
Wheel		Go straight forward/backward
Flat View		
Left	Click	Pick location
	Click and Drag	Pan left and right
	Alt + Click	Pick location
Middle	Click	Pick location
Right	Click	Context menu
	Click and Drag	Pan left and right
2D (MPR)		
Left	Click and Drag	Slicing
	Alt + Click	Pick location
Middle	Click	Pick location
	Click and Drag	Zoom
Right	Click	Context menu
	Click and Drag	Pan
Wheel		Slicing

Context Menu

A context menu is also available for additional editing options. RMB-click on the image or the path to open the Context menu options.

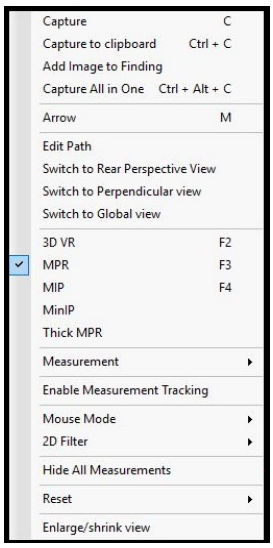


Figure 12-1 Context Menu

This workflow has several context menu with options dependent on where you are in the workflow. They are indicated when there is a different context menu available.

Background Color

If a different background color would make the details in the image easier to see, you can change it by right-clicking on the image panel, selecting **Background Color**, and then selecting a new color from the Windows color palette window.

Segmentation and Flight Path Creation

Segmentation

The colon is segmented automatically displayed with a green overlay as shown in the Figure 12-2.

If a segment of the colon is not selected (indicated by the lack of a green overlay), click on that segment to include it in the segmentation. Non-colon segments appear in a lighter color. If anything non-colon has the green overlay, toggle the section to deactivate the segment.

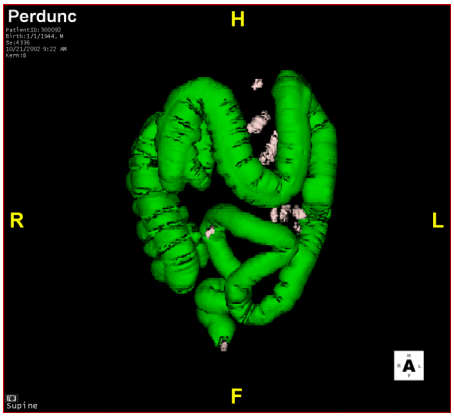


Figure 12-2 Segmented Colon

Workflow Tabs

The Flythrough workflow provides tools via the Lumen, Edit, and Landmark tabs in the tool panel.

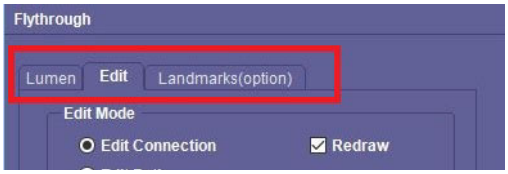


Figure 12-3 The Workflow Tabs

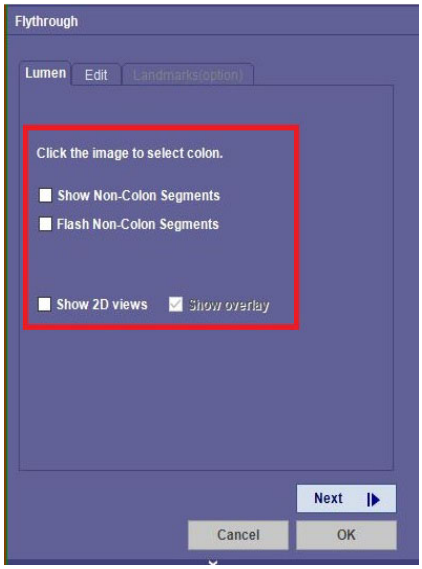
Table 12.2 Flythrough Workflow Tabs

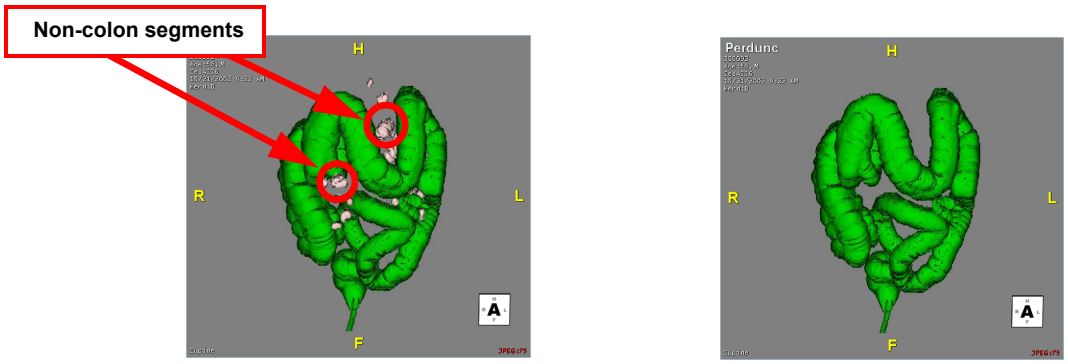
Luman	Edit	Landmarks (Option)
Show or Hide segments and non-colon areas of the image.	Edit connections or paths and to set the **Display** mode.	Add or delete landmarks.

The Lumen Tab

The **Lumen** tab allows you to view or hide non-colon elements and aids in using the 2D views to add or subtract colon segments. The settings are described in Table 12.3. See the **Edit** tab section for more information.

Table 12.3 Description of Lumen Settings

	Setting	Description
	**Show Non-Colon Segments**	Show segments in the image that are not designated by the software as part of the colon. Any of these segments can be added to the colon manually. (See .)
	Flash Non-Colon Segments	When the colon is selected, flash the non-colon segments once.
	Show 2D views	Show the three 2D views (axial, coronal, sagittal) in addition to the 3D. (See Figure 12-5.)
	Show overlay	Show a green overlay where the colon appears in the 2D images.



Non-Colon Segments Shown **Segments Not Shown**

Figure 12-4 Non-colon and Colon Segments

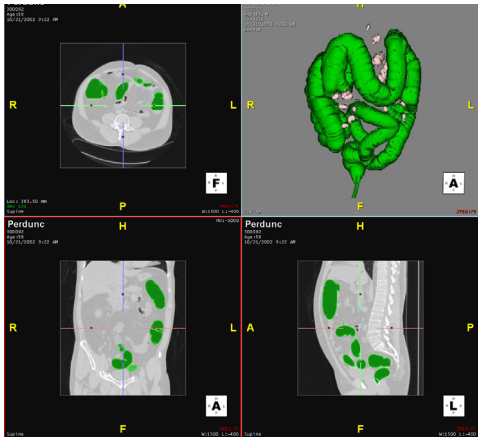
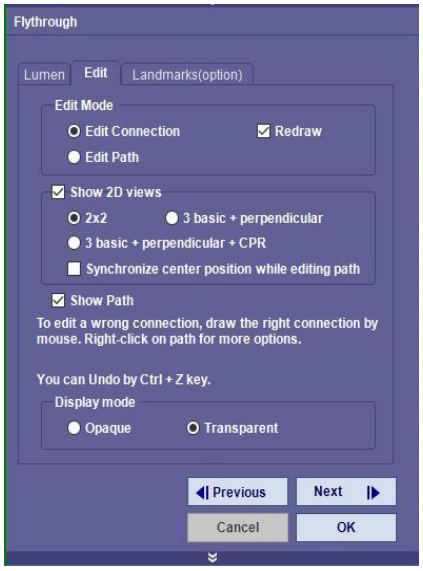


Figure 12-5 Show 2D Views with Overlay

The Edit Tab

When you are satisfied with the segmentation, click **Next** to proceed to the **Edit** tab. This panel allows you to edit connections or paths and to set the views and **Display** mode.

Table 12.4 Edit Tab Settings

	Setting	Description	
	**Edit Mode**	Under **Edit Mode**, you can **Edit Connection**, **Edit Path**, and choose **Redraw** for automatic redrawing after edits. You can RMB-click to select **Edit Path** from the context menu.	
	Show 2D views	You can select **Show 2D** views and then select **2x2** or **3 basic + perpendicular** (for the perpendicular view of the path) or **3 basic + Perpendicular + CPR**. Also, see "Reading Styles" on page 12-14 for more information on these views.	
		Show Path	Select **Show Path** to display the Flythrough path. The flight path is then reconstructed and displayed.
		Synchronize	Select **Synchronize center position while editing path**.
	Undo by CTRL +Z	Keyboard shortcut for undoing any edits. RMB-click on the path	
	Display mode	Allows you to display images as **Opaque** or **Transparent**.	

Edit Mode

Editing the Connection

A small part of the colon can collapsed or appear diminished. The Flythrough software attempts to connect disconnected sections together into a single, unbroken path. In Figure 12-6, the sigmoid colon is missing.

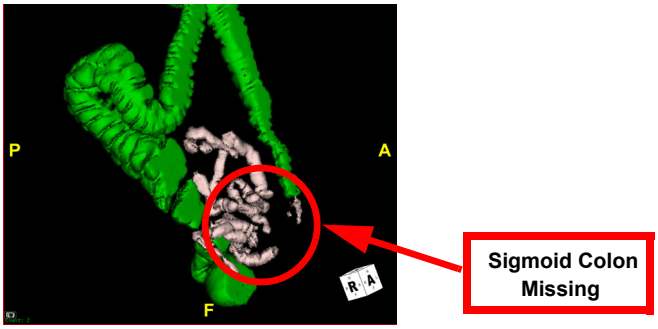


Figure 12-6 Colon with Sigmoid Missing

When you select the **Next** button to generate the flight path, you might see sections drawn in red. The red sections indicate areas automatically configured as connections where the flight path is missing sections. You must check these configured sections and make sure they are correct. If they are not, the tool panel provides tools for adjusting the estimated connections.

In the example below, AQi attempted to connect the rectum to the cecum:

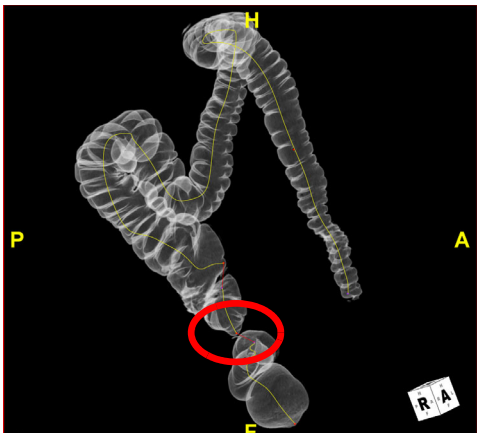


Figure 12-7 Configured Connection

To correct the path, click **Edit Connection** in the **Edit** tab panel. You also RMB-click on the image and select **Edit Path** from the context menu.

There are two ways to edit the connection. One is to draw a line from the incorrect endpoint to the correct one. Flythrough then connects the original start point to the new, corrected endpoint. To use this method, uncheck the **Redraw** box. (Figure 12-8)

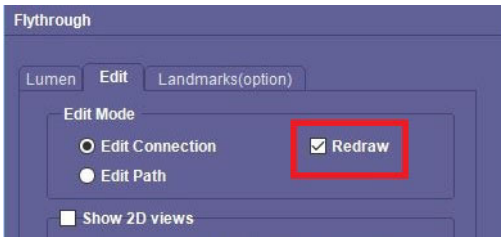
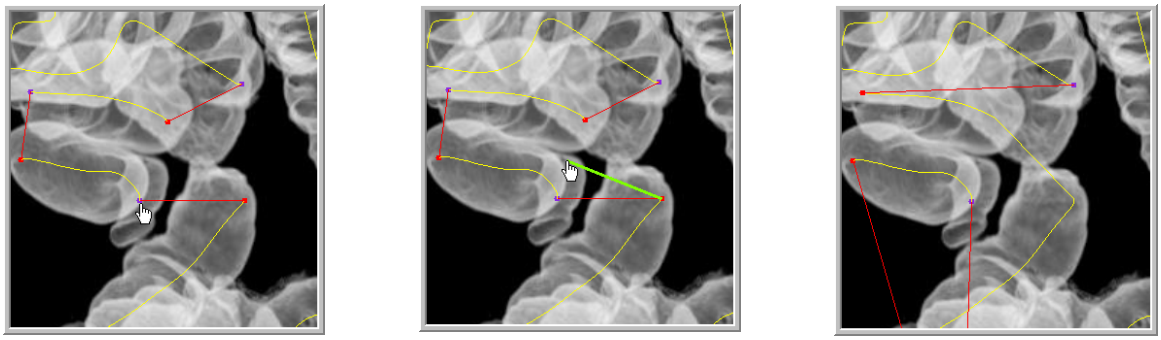


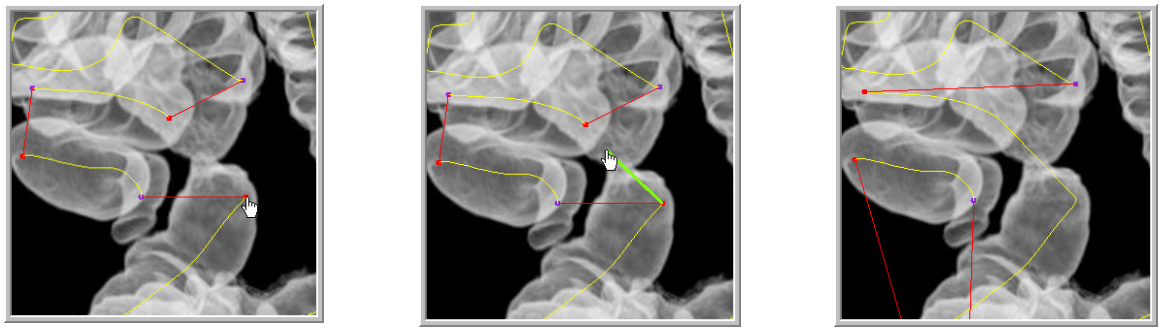
Figure 12-8 The Redraw Box



Click on incorrect endpoint **Move endpoint** **End result**

Figure 12-9 With Redraw Disabled

The other way is to draw a line from the start-point to the correct endpoint. The correction line is displayed as you draw it. Check the **Redraw** box to use this method.



Click on start-point **Draw line to the correct endpoint** **End result**

Figure 12-10 With Redraw Enabled

Note: The end result is the same regardless of how the connection is corrected.

Your line might go through a section of colon that is not distended. (Figure 12-11)

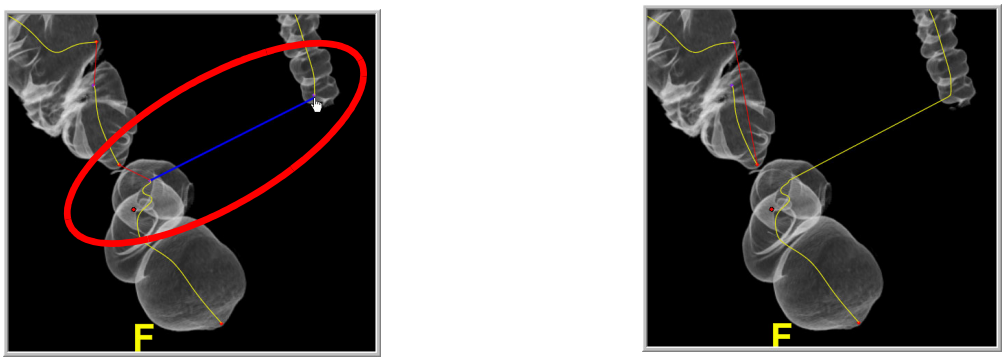


Figure 12-11 Non-Distended Section of Colon

Correct any other connections, using the same tools. (Figure 12-12)

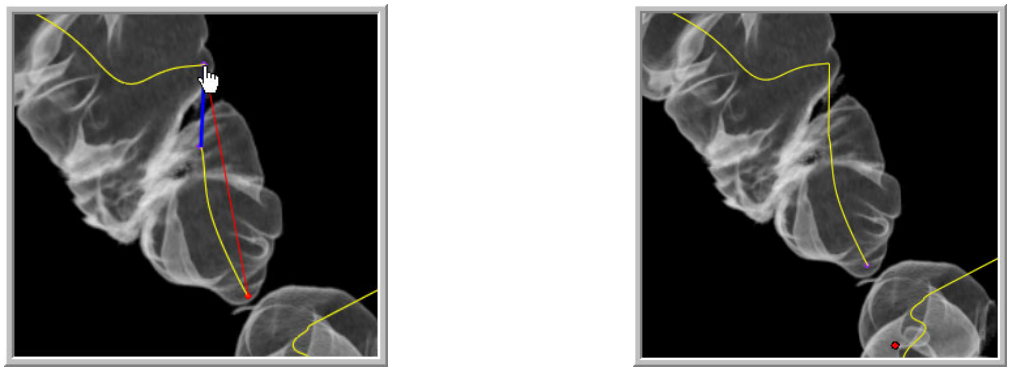


Figure 12-12 Correcting Connections

When you are satisfied that the path connections are correct, you have the option of editing the flight path for smoothness. See the following section, Editing the Flight Path, for instructions. Otherwise, click the **OK** button. (Instructions continue in the section titled "Reading Styles" on page 12-14.)

Editing the Flight Path

The flight path that has been automatically generated by the software might contain some errors. Check the path carefully to make sure it is smooth. If you detect any errors, you can edit the area to correct it.

To edit the flight path:

1. Select the **Edit Path** radio button in the Edit tab tool panel. You can also select the **Edit Path** workflow element or RMB-click to select it from the context menu.

   The flight path in the main window switches to edit mode, containing control points that allow you to smooth sections of the curve or correct problems (Figure 12-13).

2. On the flight path, select the active control points to drag them to another area inside the segmented colon, or to move them further up or down along the flight path.

Error in Path **Fixing Path**

Figure 12-13 Dragging Control Points

3. Create a new control point by clicking on the flight path where you would like to add it. The mouse cursor changes to indicate a new control point is being added. (Figure 12-14)

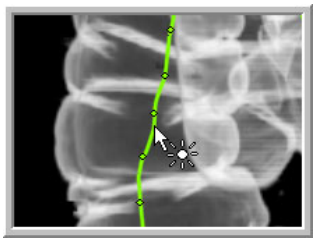


Figure 12-14 Creating New Control Points

Editing the Path on 2D Images

If, after editing, the path on the 3D view is not satisfactory, you can also edit the path using one of the 2D views. To edit the path in a 2D view:

1. Enable the **Show 2D views** checkbox in the Edit tab.

   The three MPR views are displayed along with the 3D image. See Figure 12-5. Make sure that the **Show Path** checkbox is also enabled.

2. Click on any section of the path that has not been rendered smoothly. A dot appears on the path at that location, indicating that it can be moved. Continue to move sections of the path until it has a smooth contour. You can add as many points onto the path, as close together as you need to, to smooth out the path.

3. When you are satisfied that the flight path is correct, select **OK**.

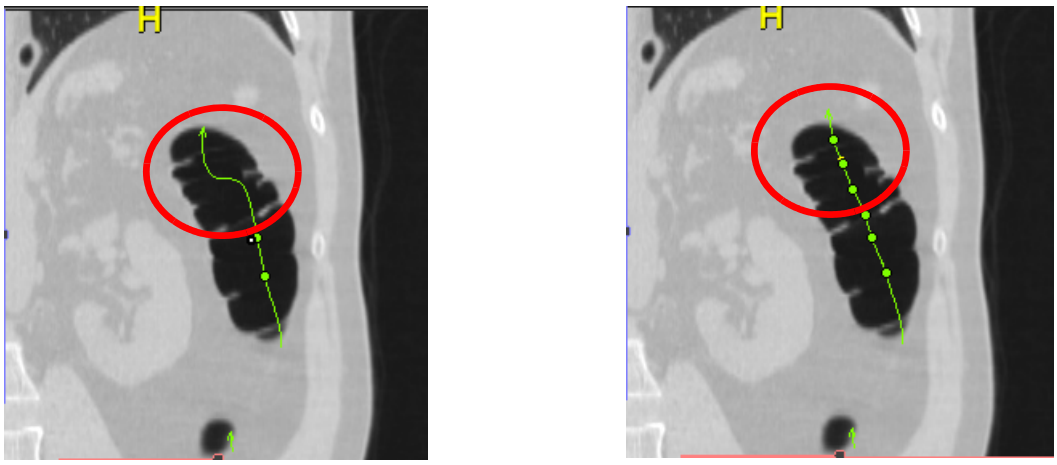
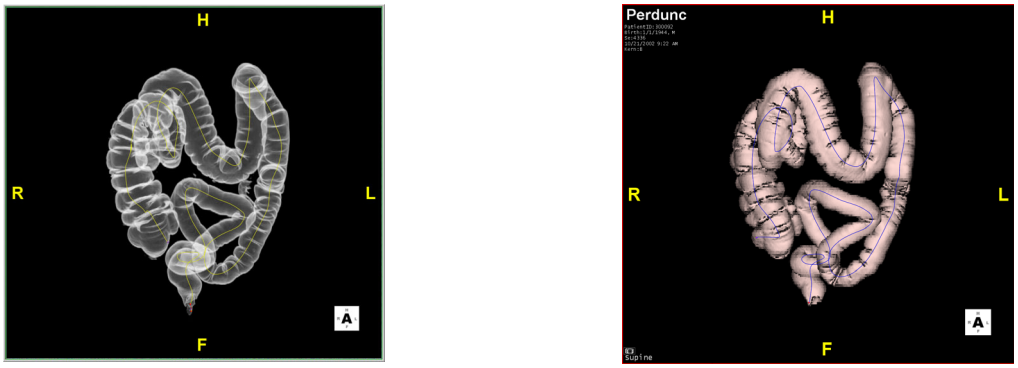


Figure 12-15 Corrected Flight Path

Display Mode

Transparent vs. Opaque Colon Display

The flight path is displayed with a transparent colon by default. If you would prefer to view the flight path in an opaque colon, click the **Opaque** button under **Display mode** (Figure 12-16)on the **Edit** tab.



Default Transparent View **Opaque View**

Figure 12-16 Views

Landmarks (option) Tab

When multiple series are loaded, this tab is active. When only one series is loaded, this tab is disabled. Each point and, in the order they are placed, are labeled sequentially with alphabet letters. The max number of landmarks is 26 (A-Z).

Figure 12-17 Landmarks (option) Tab

To add a Landmark:

1. Select the **Add** button in the tab panel.
2. LMB-click anywhere on the centerline, the first point is always A.
3. Each point is labeled sequentially through the alphabet, A through Z.
4. When done, select the **OK** button.

Synchronization

When a landmark is placed on one series, a related landmark is added to the other series automatically. You can drag a landmark to another position. When a landmark is deleted on one series, the corresponding landmark is deleted on the other series.

To delete any or all landmarks:

1. RMB-click on the path to open the context menu and select either **Delete landmark** or **Delete all landmarks**.

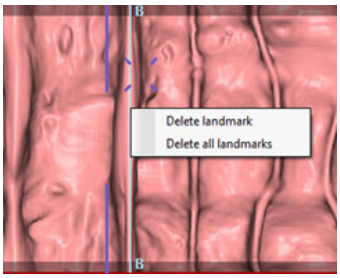


Figure 12-18 Landmark Context Menu

2. You can remove one landmark at a time, by selecting the landmark and then selecting the **Remove** button.

After placing landmarks, select the **OK** button. (You can add additional landmarks in the Flat View, see Figure 12-19.) This opens the Tool and Option tabs. Depending on which workflow you select, (Flat View 4 shown as example), the viewer show both MPR, CPR, Global and Flat views. See Figure 12-19.

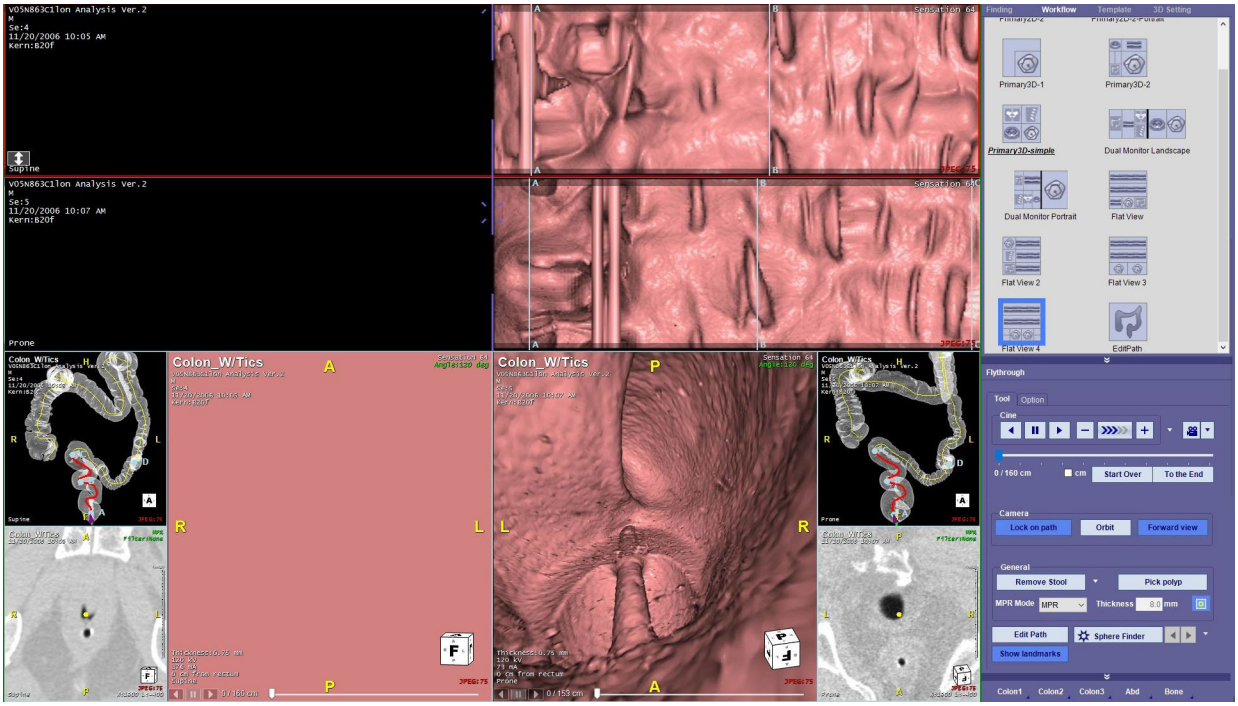


Figure 12-19 The Flat View 4 Workflow

As you run the Cine, the landmarks synchronize. You can still edit the flight path at this point by either selecting the **EditPath** element (does not work on Flat View layouts) in the workflow panel or selecting the **Edit Path** button on the Tool panel. You can also RMB-click and select **Edit Path** in the context menu. In the two flat views, landmarks cannot be moved. In the 3D view window, the amount of movement per one frame is changed according to the landmarks. You can also synchronize the Perspective views (camera angle).

Select the **Show landmarks** button to either hide or show landmarks. Landmarks appear on both the Global view and Flat views. Landmarks can also be selected and dragged in either view. When an finding arrow is added to an image, it is used as a landmark.

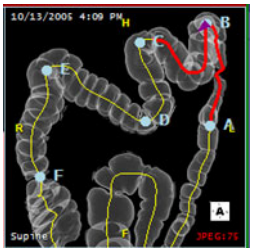


Figure 12-20 Global View with Labeled Landmarks

The Global view also has a RMB-click context menu that allows you to set this view to Show or Hide the Path, Camera position, finding position and the Perpendicular line.

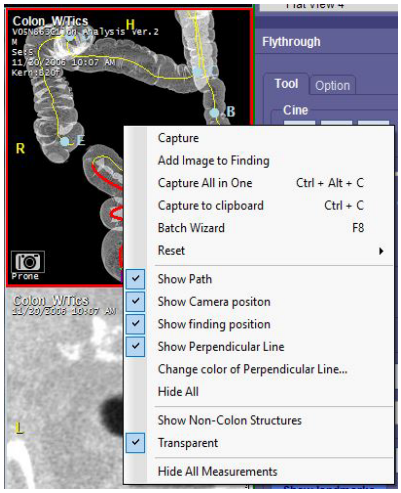


Figure 12-21 Global View Context Menu

You can switch replace the Perspective Views with the Global by double-LMB-clicking. To return the views to their original place, double-LMB-click on the Global view. The Global view window can also be resized. To resize the view, LMB-click-hold on a corner and drag to the desired size.

Reading Styles

The *reading style* determines the way the Flythrough data is presented in the viewer. For example, some practitioners might prefer to read series data primarily in 2D mode, while others prefer 3D images. You can choose your primary reading style according to your preference and the data is loaded into that layout.

Each type of image displayed in Flythrough (2D, 3D, Flat View, Inset, MPR, and CPR) is called a view. A layout refers to the display of views in the Flythrough viewer. It refers to *where* each view is displayed and to the actual views included in the layout. Each reading style uses preassigned layouts.

Table 12.5 Flythrough Viewer

Label	View	Description
A	Perspective view	This is where you can view the flight in 3D.
B	MPR views	The MPR windows show the current position of the flight in 2D. In some reading styles, all three MPR windows are displayed, while in others, only the axial view is shown initially. However, you can use the right-click menu to select the sagittal and coronal views.
C	Flat view	View of the colon as if it were sliced open lengthwise and laid out flat. This window can be used as an alternate view of the colon. You can also use it as a navigation tool.
D	Inset or Global view	A small image of the transparent colon and flight path, which shows the progress of the Flythrough with a moving marker. You can chose to hide or show findings positions, camera position, or the path by RMB-clicking in the image and selecting show/hide from the context menu. This smaller view can be resized using the LMB-click on the inset corner.
E	CPR view	This view shows a sagittal scan view. The 2D 3 Basics + Perpendicular + CPR style does not work in the Flat View. If you do select this layout when in a Flat view, you are prompted to change the layout.
F	Perpendicular view	This view shows the flight path vertically and from the patient's front (coronal).

The following figures show each of the reading style layouts. The views included in each layout are labeled for easy reference to Table 12.5.

2D Layouts

- **Primary2D-2**

  This layout allows you to view the prone and supine scans side-by-side (A), while focusing the examination on the 2D MPR views (B).

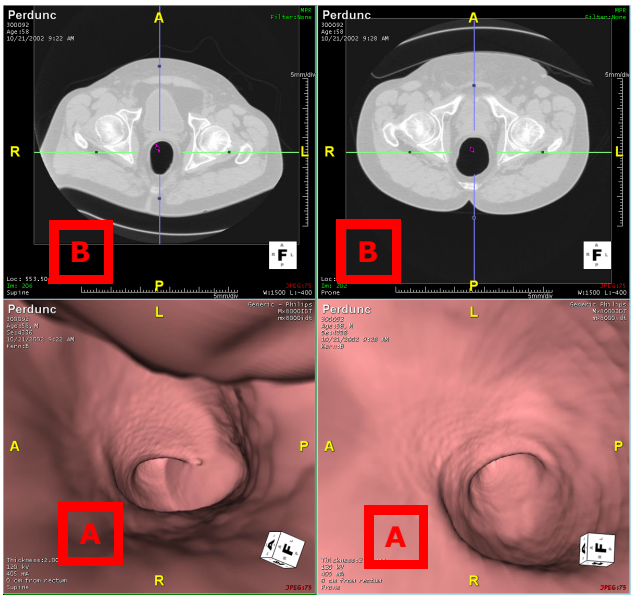


Figure 12-22 Primary2D-2 Layout

- **Primary2D-2-Portrait**

This view functions like the Primary2D-2 view, except that the axial views are on the left rather than on the top (B), and the 3D perspective views are on the right (A), rather than on the bottom.

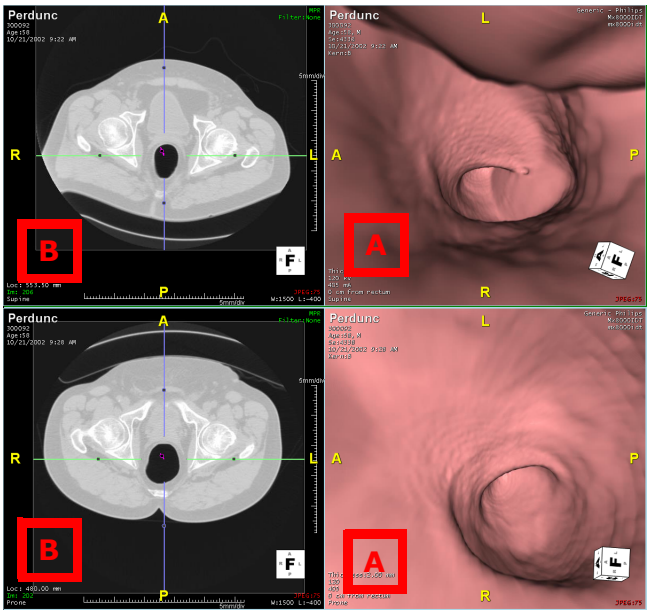


Figure 12-23 Primary2D-2-Portrait Layout

Layouts for 3 Series

Both the **Primary2D-2** and **Primary2D-2-Portrait** layouts can be used to perform a Flythrough on three series loaded simultaneously.

- **Primary2D-2 With 3 Series**

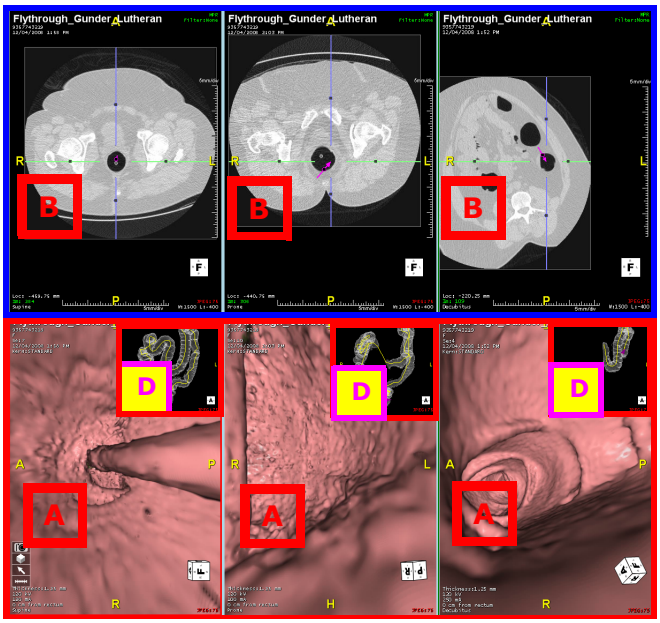


Figure 12-24 Primary2D-2 With 3 Series Layout

Note: The **Global** (D) view can be resized by LMB-clicking on the outer corner and dragging to the desired size. Or, you can double-LMB-click on the inset to enlarge it to full view.

- **Primary2D-2-Portrait With 3 Series**

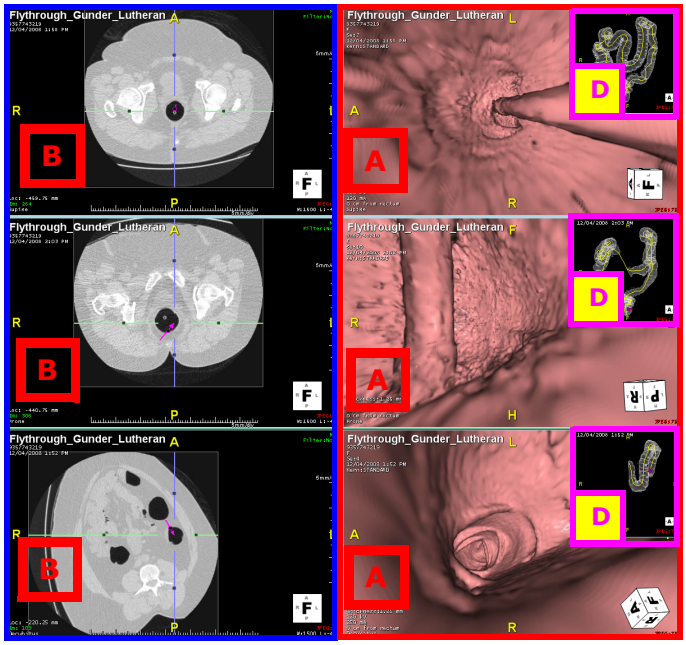


Figure 12-25 Primary2D-2-Portrait with 3 Series Layout

- **2D - 3 Basic + Perpendicular**

This view displays 3 Basic (B) views with 2 Perpendicular views (F).

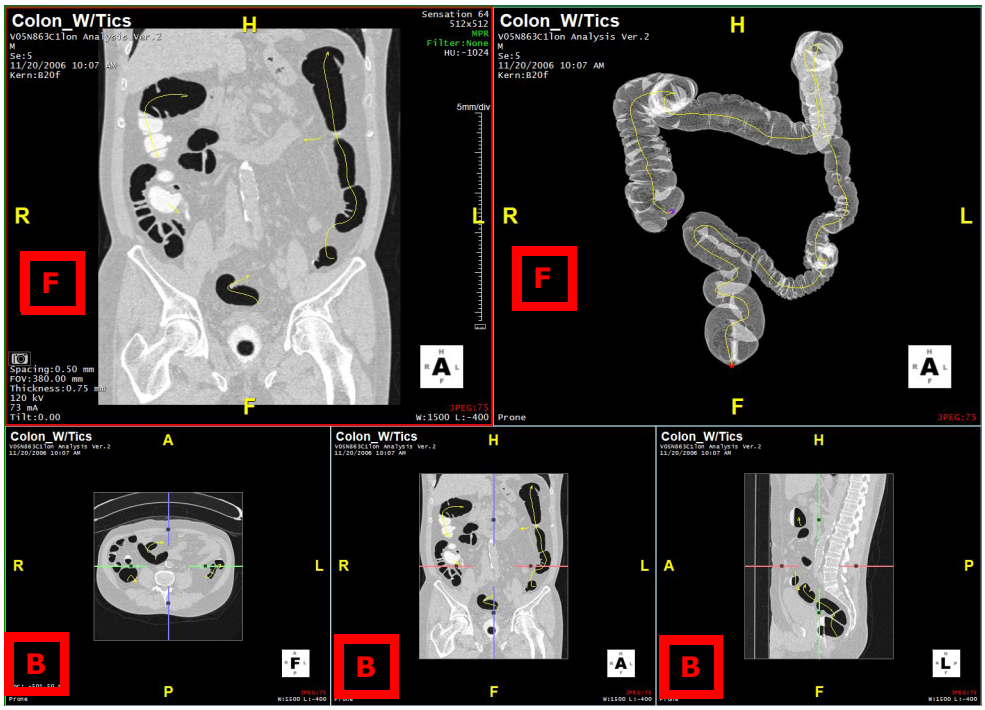
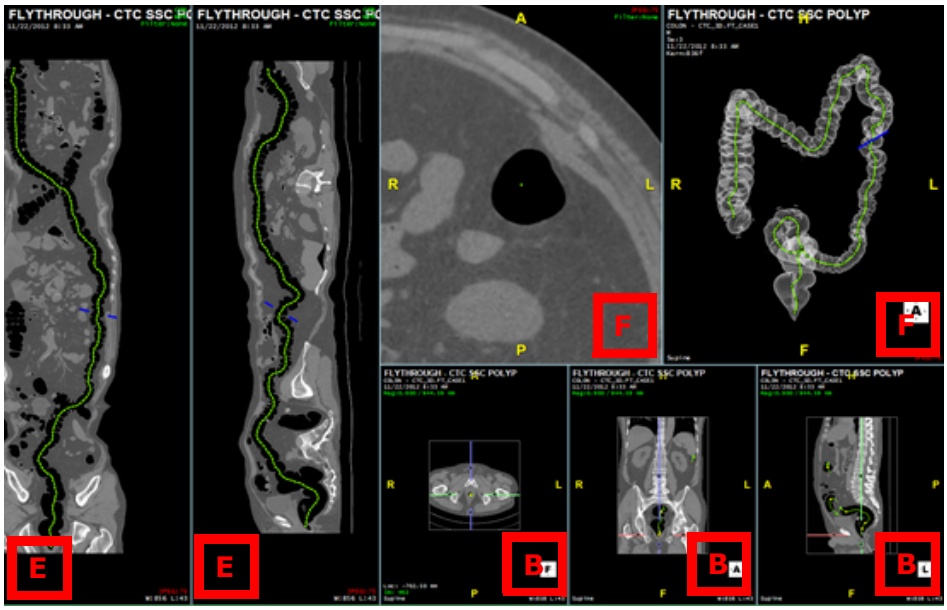


Figure 12-26 2D 3 Basic + Perpendicular Layout

- **2D - 3 Basic + Perpendicular + CPR**

  This view adds CPR views (E) to the 3 Basic (B) + Perpendicular views (F).



Note: The 2D 3 Basics + Perpendicular + CPR style does not work in the Flat View. If you do select this layout when in a Flat view, you are prompted to change the layout.

3D Layouts

- **Primary3D-Simple**

  This layout contains a Perspective view (A) in 3D and three MPR windows showing the coronal, sagittal and axial views.

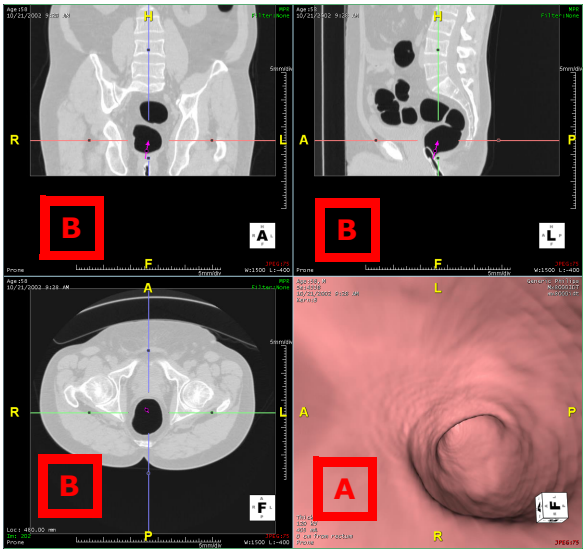


Figure 12-27 Primary3D-Simple Layout

- **Primary3D-1**

  This layout is similar to **Primary3D-Simple**, but contains two extra elements: the flat (or Unfolded) view of the colon (C), and the Inset view (D).

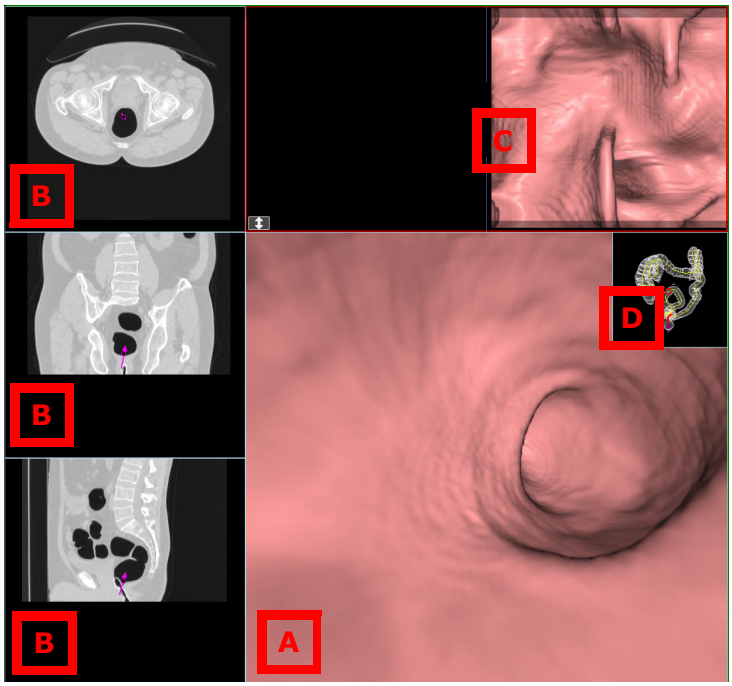


Figure 12-28 Primary3D-1 Layout

- **Primary3D-2**

  This layout contains a Perspective view (A) in 3D, three MPR windows showing the coronal, sagittal and axial views (B), the flat view of the colon (C), and an enlarged global view (D).

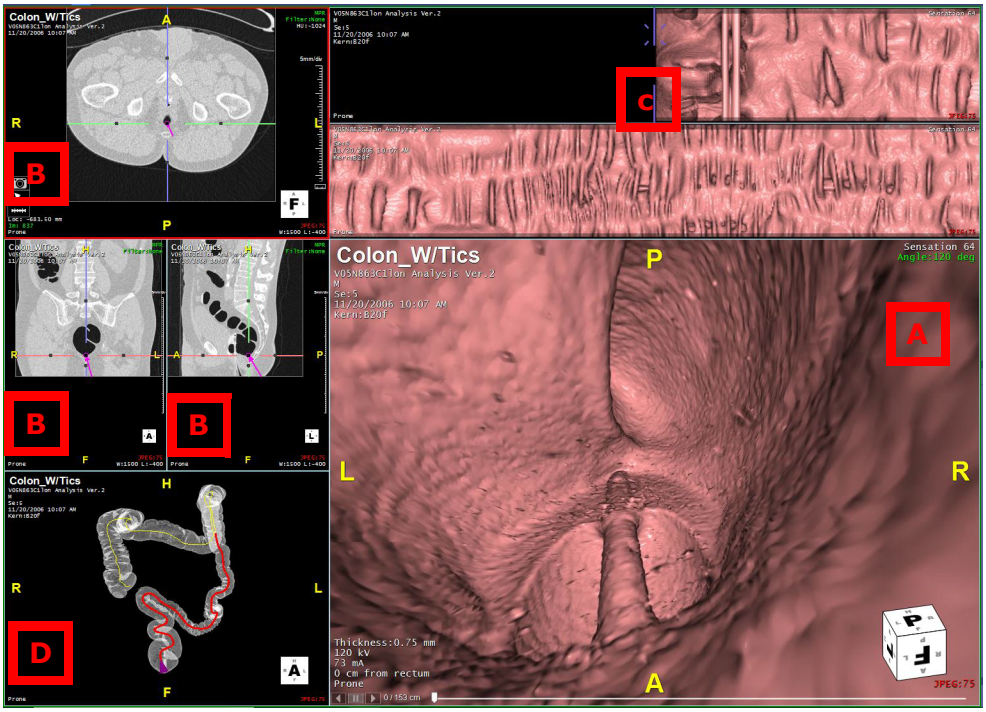


Figure 12-29 Primary 3D-2 Layout

Dual Monitor Layouts

These layouts can be used only when two monitors are available on the client system.

- **Landscape Dual**

  This layout contains a Global view (D), Flat View (C), three MPR windows showing the coronal, sagittal and axial views (B) and the Flythrough perspective view in 3D (A).

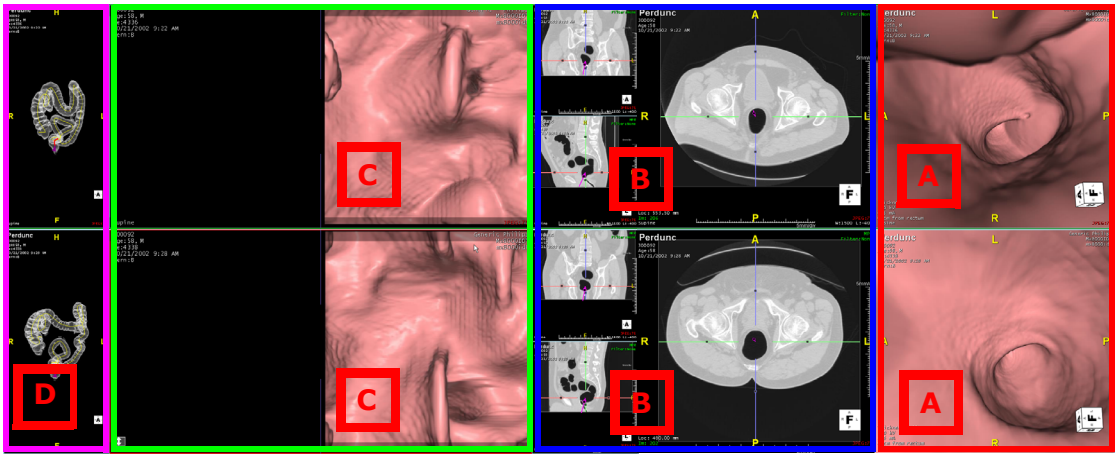


Figure 12-30 Landscape Dual View

- **Portrait Dual**

  This layout contains a Global view (D), Flat View (C), three MPR windows (B) showing the coronal, sagittal and axial views and the Flythrough Perspective view in 3D (A).

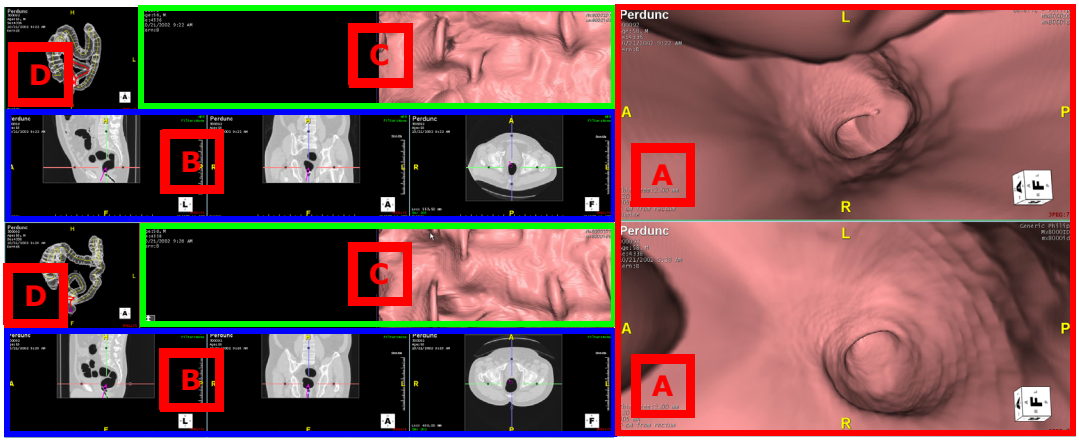


Figure 12-31 Portrait Dual View

Flat-View Layouts

- **Flat View**

  This layout contains the 3D Flat View (C) in three sub-windows, the Perspective view (A) in 3D, and Global (inset) view (D).

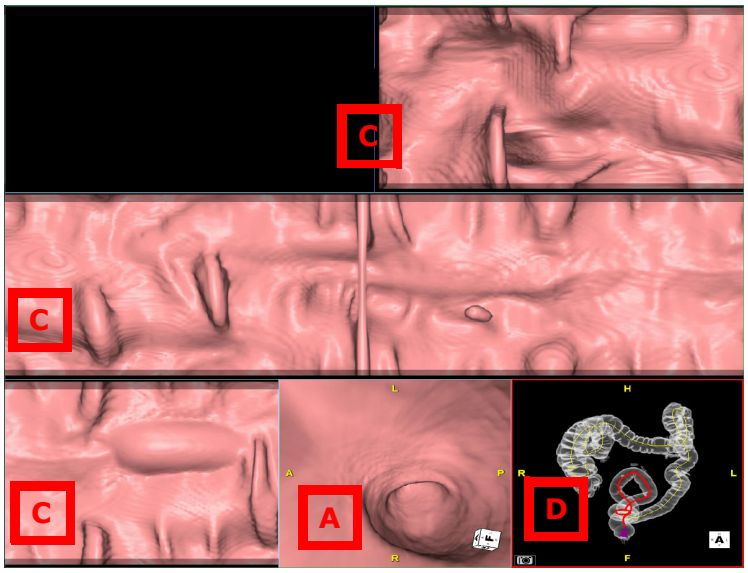


Figure 12-32 Flat View

- **Flat View 2**

  This layout contains the Flythrough Perspective view in 3D (A), an MPR window showing the axial plane (B), the Global (inset) view (D) and the Flat View (C) in three sub-windows.

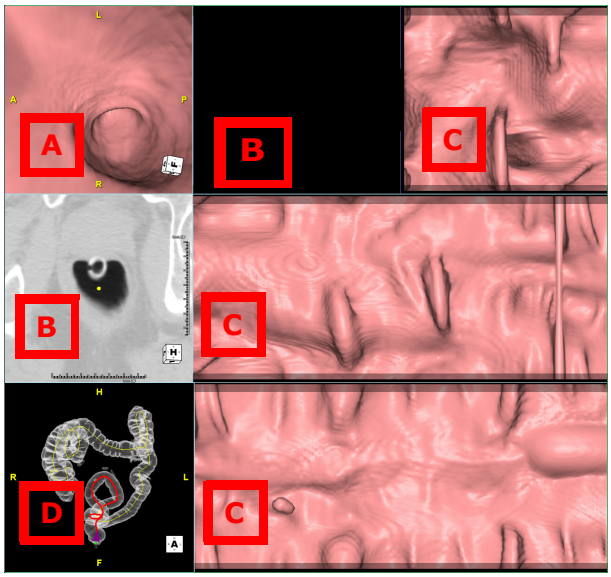


Figure 12-33 Flat View 2

- **Flat View 3**

  This layout requires two series. It contains the Flat View (C) in two sub-windows (one for each series) and two Perspective view (A) windows with corresponding Global views (D).

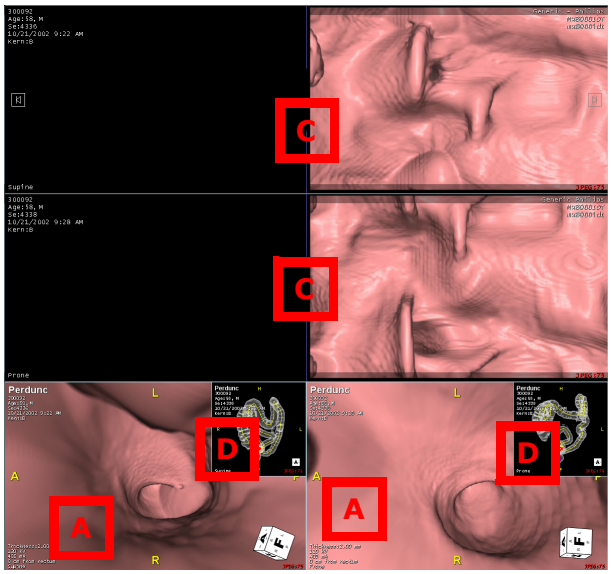


Figure 12-34 Flat View 3

- **Flat View 4**

  This layout requires two series. It contains the Flat View (C) one for each series, two Perspective view (A) windows with corresponding Global views (D) and two MPR views (B).

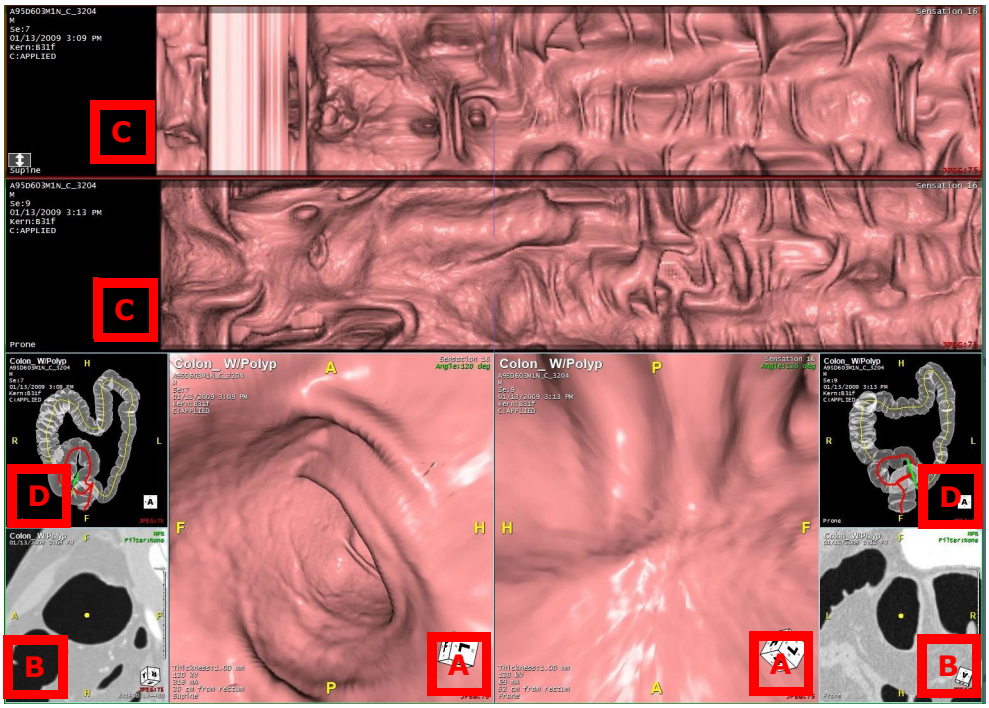


Figure 12-35 Flat View 4

Portrait Monitor

Flythrough supports the portrait display mode. If your monitor is configured to display images on the screen in portrait mode, multi-data studies are displayed one atop another, rather than side-by-side.

Synchronization

Synchronization means that operations performed in one of the MPR windows are automatically performed in the other. For example, as you page through the slice images in the prone scan, the corresponding slices are displayed in the MPR window of the supine scan. When you zoom in on one of the images, the other is automatically zoomed to the same magnification.

To enable synchronization, click the synchronize button in the top bar. (Figure 12-36)

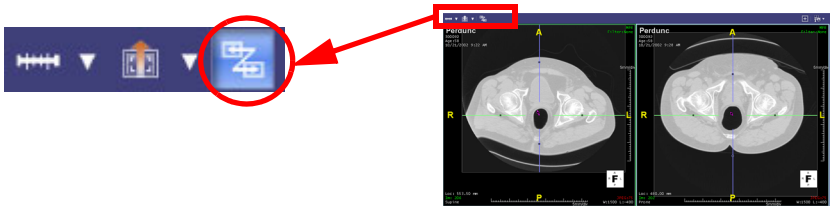


Figure 12-36 Enabling Synchronization

When the synchronize button is on, both Flythrough windows are active and the Flythrough of each is performed simultaneously. When the button is off, only the selected Flythrough window is active.

Re-synchronization of 2D Images

If you disable synchronization to work on one of the 2D images, and want them to re-synchronize later, you must enable the **Re-synchronize on 2D** setting to **Automatic** in the GUI configuration. The setting is found in the **Flythrough Details** screen. See "Flythrough Tools and Option Tabs" on page 12-31 for more information.

Make one of the following selections:

- **Automatic** – The other 2D window automatically re-synchronizes.
- **Manual** – The other 2D window does not re-synchronize. To synchronize the images, you need to scroll manually to the corresponding slice.

Synchronization while Editing

While editing the path you can synchronize the images as you edit:

1. In the **Edit** tab, select the **Show 2D views**. All 2D options are enabled.
2. Select the **Synchronize center position while editing path** option.
3. The flight path will synchronize as you edit.

You can also synchronize the path angle when you are in the Perspective view.

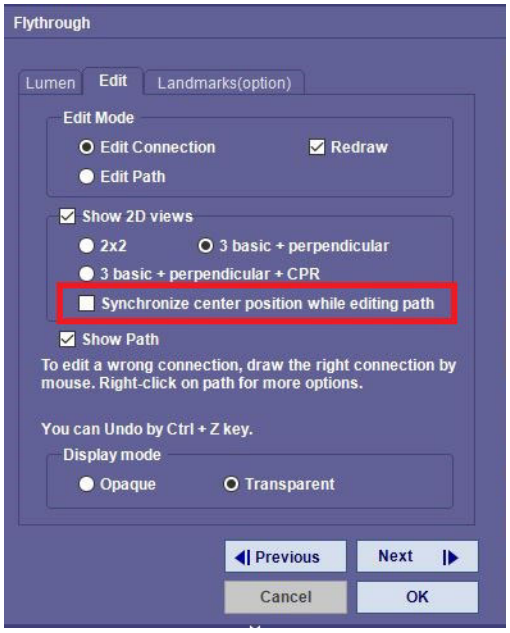


Figure 12-37 Synchronize on Edit Tab

MPR-Only View

If you would prefer to view only the MPR images, you can do so by double-clicking on any MPR image. You can hide the control panel by clicking on the double right-arrow located on the left edge of the control panel. (Figure 12-38)

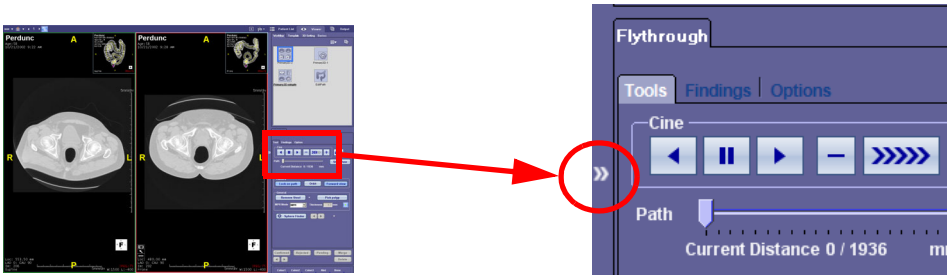


Figure 12-38 MPR-Only View

The resulting display allows for a large view of the areas of interest.

2D/3D Correlation and Orbit

When you have discovered a potential finding in one of the MPR views, and would like to examine it in the corresponding 3D (perspective) window, click on the potential finding in the MPR window using the middle mouse button. The same area will be displayed in the center of the corresponding 3D view. (Figure 12-39).

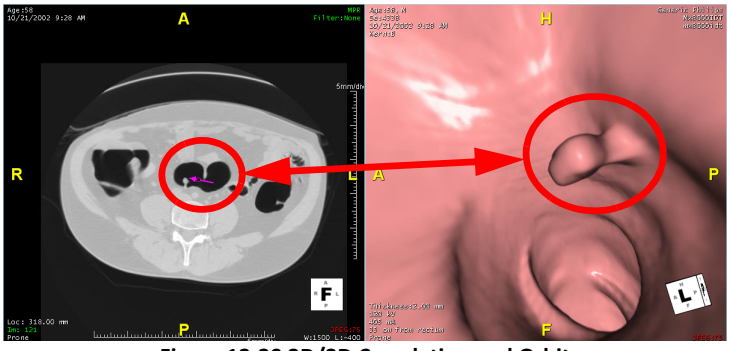


Figure 12-39 2D/3D Correlation and Orbit

You can then use the Orbit function to look at all sides of the object under examination. To do this, click the **Orbit** button in the Tool Panel, or hold down the **CTRL** key. At the same time, hold down the left mouse button and move the mouse around to show different sides of the object. (Figure 12-40)

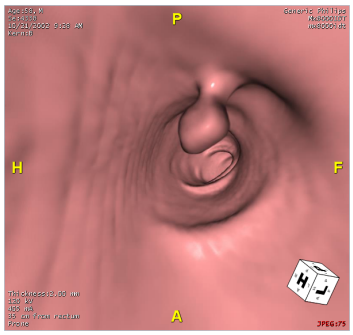


Figure 12-40 Moving Around the Different Sides of an Object

Options for Paging Through Slices

There are two modes available for paging through the slices of an image in a 2D window.

- **Normal** - Scrolling up or down the 2D image while holding down the left mouse button ("slice mode") causes the slice images to advance rapidly.
- **Control** - Scrolling on the 2D image causes the slice images to advance slowly, giving you more control over the viewing of each slice.

To toggle the paging mode between Normal and Control, click the down arrow to the right of the slice icon in the top tool bar. See the following figure:

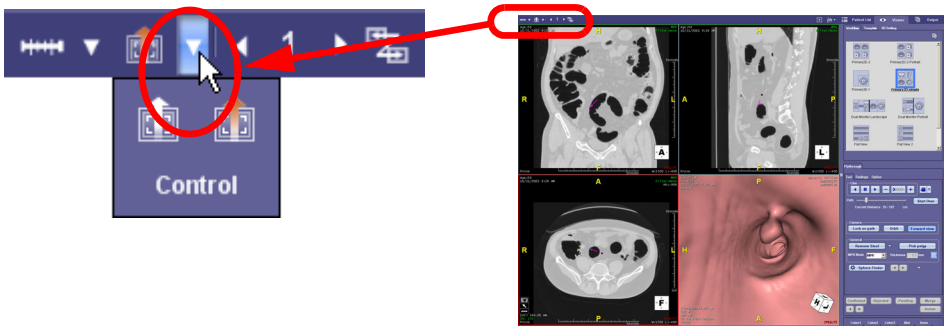


Figure 12-41 Paging between Normal and Control

Select OK Button

At any point in your workflow you can select **OK** to open the Flythrough Work Tools and Option panel.

The Flythrough Workflow Elements

The Flythrough Workflow provides shortcuts (elements) for switching among primary reading styles and for returning to Edit Path mode. (Figure 12-42)

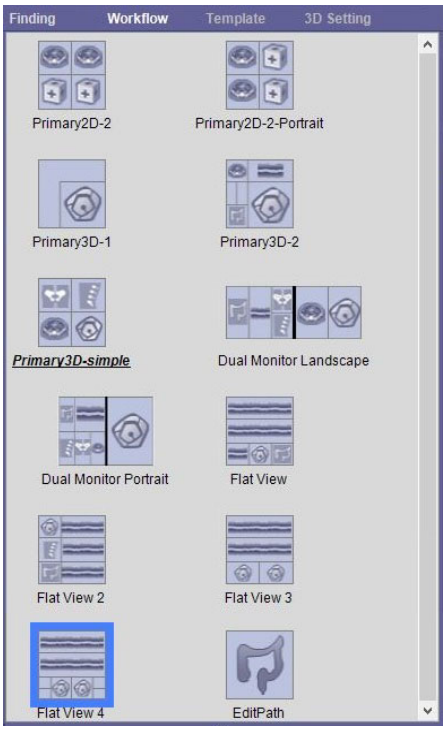


Figure 12-42 Workflow Elements with Flat View 4 Highlighted

To view data in the desired reading style, click the corresponding element in the Workflow. Click the **Edit Path** element to redo colon segmentation, connection editing, and path editing.

Starting and Stopping the Flight

There are several ways to start or stop the flight, or to resume a stopped flight.

- **Cine tools in the tool panel**

  The cine tools are part of the Tool Panel. These allow you start and stop the Flythrough. See "Cine Tools" on page 12-34 for a more detailed description of these tools.

- **Directional arrows on the perspective image**

  You can also start or resume a Flythrough using directional arrows in the perspective window. The arrows are not normally visible. To see them, hover the mouse over the perspective window while the Flythrough is stopped. Two arrow images appear on the left side of the image. To begin (or resume) the Flythrough in the forward direction, click in the center of the right-facing arrow. To go backward, click the left-facing arrow:

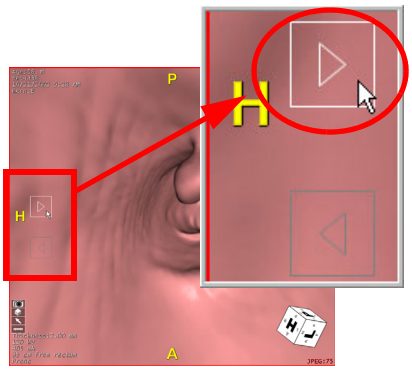


Figure 12-43 Right-Facing Arrow: Select to Go Forward

- **The space bar**

  Press once on the space bar to toggle the flight on and off.

- **Mouse click on the flight window**

  As with the space bar, click once on the perspective view to start (or resume) the flight, and click again to stop it.

  While using the Perspective view, you can adjust your mouse operations in the Interactive or in the Preference window.

  To adjust your mouse operations for focus, stop/start, or speed while in Cine mode,

  1. Under the **Options** tab select **Interactive...** button.

  2. The **Interactive** window opens. Adjust the mouse operations in this window.

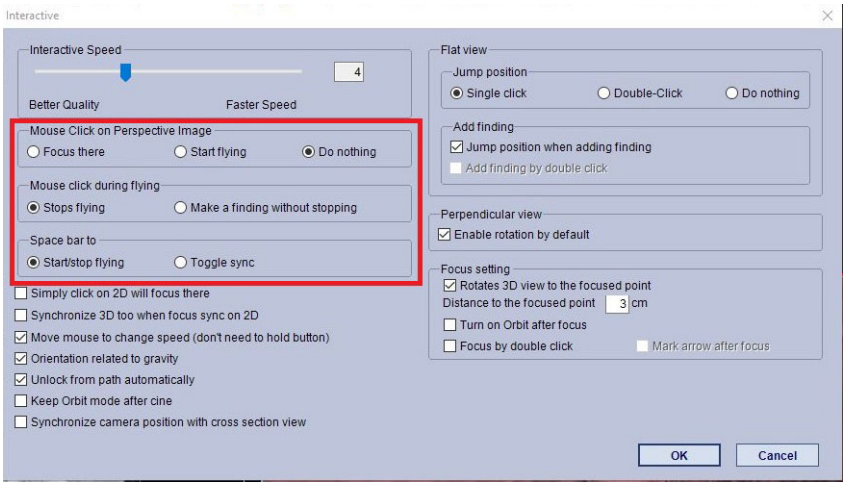


Figure 12-44 Mouse Operations in the Interactive Window

  3. Select **OK** to close the window.

You can also adjust focus, adjust the speed, and change settings for the mouse button including mapping options. To adjust mouse operations in the **Preference** window.

1. Open the **Preference** window.

2. In the navigation bar, go to **Viewer>Mouse Operations**. Select your adjustments.

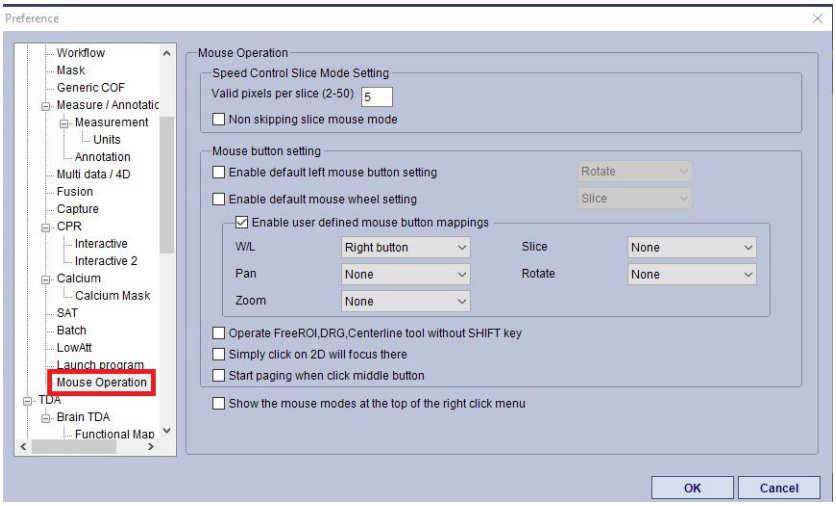


Figure 12-45 Preference Window>Viewer>Mouse Operation

3. Select **OK** to close the window.

Note: For additional options and Interactive options, see "Other Viewing Options" on page 12-50.

Flythrough Tools and Option Tabs

When you select the **OK** button in the Flythrough tool panel, the tool tabs open. The Tool tabs contain the functions necessary for viewing and evaluating a colon Flythrough.

The tools available in the Flythrough workflow allow you to:

- Start and stop the flight when desired.
- Survey the wall of the colon along the entire path.
- Select objects for measurements and further study.
- Examine and confirm potential findings.
- Capture images for output.

- Generate reports and AVI recordings of the Flythrough.

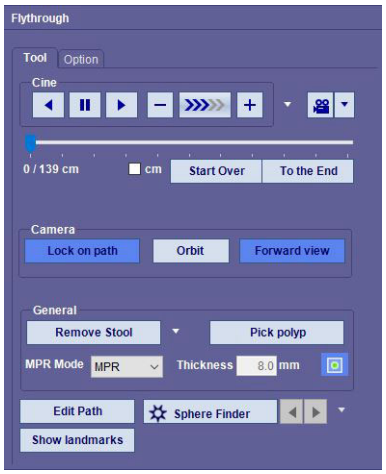


Figure 12-46 Tool Tabs

Editing the Flight Path in the Tool Tab

You can edit the flight path without returning to the start of the Flythrough Workflow. First, stop the flight. To edit the path in the Tools Tab:

1. Select the **Edit Path** button.
2. The buttons change at this point to **Finish** and **Cancel**.
3. Edit the path as described in the section, "Edit Mode" on page 12-7.
4. When done, select **Cancel** to undo any of your changes or **Finish** to save changes.
5. The **Finish** and **Cancel** buttons change back to the original button selection.

Alternatively you can RMB-click on any of the 2D images and a context menu opens with the follow options:

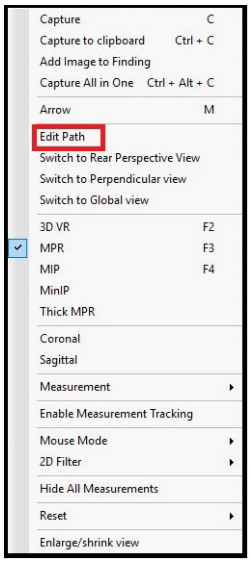


Figure 12-47 Context Menu available while in the Tool Tab

The flight path is displayed on that 2D image. (Figure 12-48)

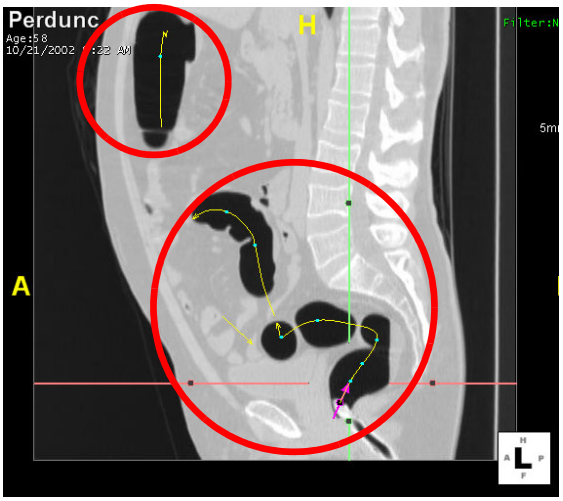


Figure 12-48 Editing the Flight Path without Restarting Workflow

You can then edit the path by LMB-clicking at any location in the path and dragging that section to the desired location.

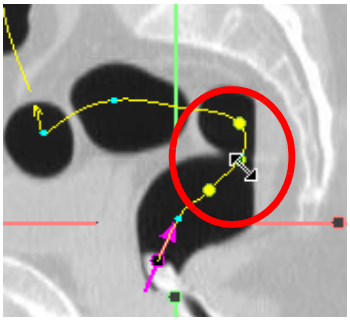


Figure 12-49 Click and Drag Path

When finished, RMB-click again and select **Finish**. You can resume the flight from the last stopping point.

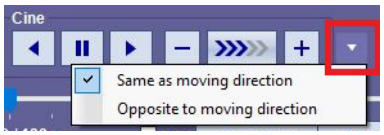
Cine Tools

At the top of the Tool tab are the cine tools. The cine tools allow you to set the speed and direction of the Flythrough. This tool uses control buttons similar to any recording device. You can set the cine tool by speed or by distance. You can select the distance by centimeters. Select the **cm** check box and the cine arrows change to - or + centimeters.

Operating the Cine by Speed **Operating the Cine by Distance**

Figure 12-50 Operating the Cine Tool

Camera Direction



Click the down-arrow to the right of the Cine tools to select the camera direction from the drop-down menu

Figure 12-51 Context Menu

- **Same as moving direction** - Camera faces the same direction as the cine, so that you see what is in front of the camera.
- **Opposite to moving direction** - Camera faces the opposite direction from the cine, so that you see what is behind the camera.

Record Flythrough

You can record all or a partial segment of the Flythrough and save the result as a video file. The record button is a video camera image located to the right of the Cine tools.

Aquarius iNtuition supports two output formats, AVI and DICOM. To select or change the output format, click on the down-arrow to the right of the record button. Then click the record button to begin recording.

A Windows **Save As** window is displayed to prompt you for the location, file name, and file type of the video.

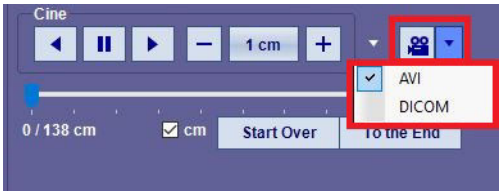


Figure 12-52 Selecting Output Format

Create a file to save on your hard drive:

1. Navigate to the folder where you want to save the video file.
2. Type in a file name, if you prefer not to use the default.
3. Select the video file type from the pull-down menu.

Path Slider

You can use the path slider to move through the flight path quickly, in order to focus in on a particular section. The **Start Over** button returns the camera to the beginning point of the Flythrough. The **To the End** button moves the camera to the end point of the Flythrough.

Figure 12-53 Starting Over or Moving to End

Flythrough Slider in Perspective View

Another way to move through the colon in the Perspective view is to use the slider at the bottom of the view. You can LMB-click and drag this slider to a new location or LMB anywhere on the slider for a random selection. The MPR views also synchronize to this location.

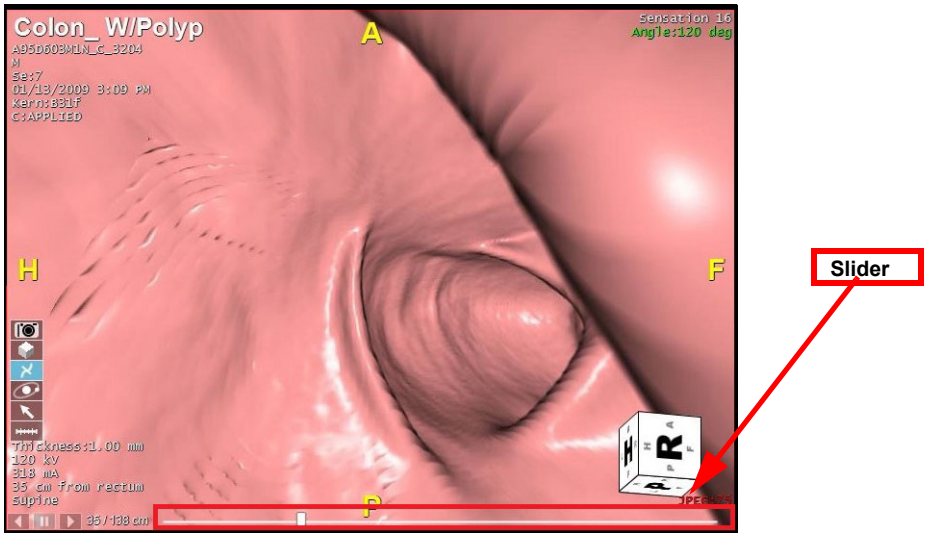


Figure 12-54 Using the Slider

Option Tab

You can use the Option tab to adjust settings for the Flythrough.

These settings include:

- **View Angle**
- **Cine replay settings**
- **MPR Update settings**
- **Interactive**

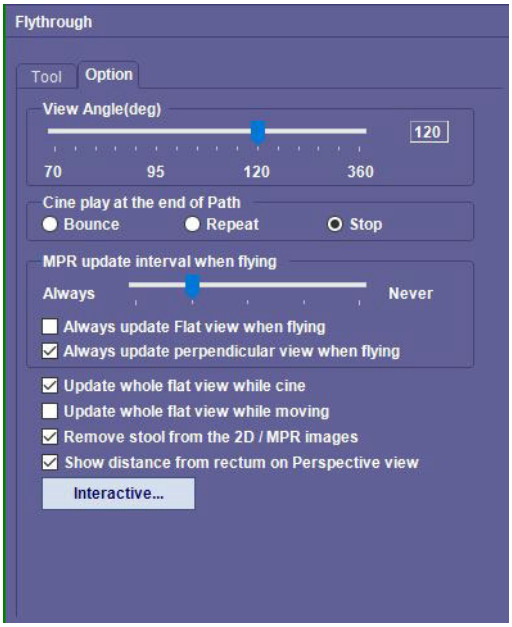


Figure 12-55 Options Tab

Interactive Button

Select the Interactive button and a window opens for setting up interactive parameters.

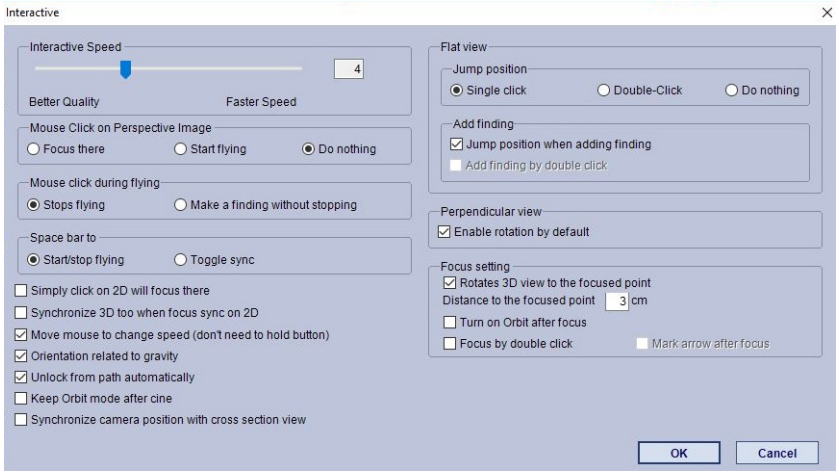


Figure 12-56 Interactive Settings

Showing Colon Coverage

These tools allow you to see which parts of the colon have already been viewed. By default, these tools are not visible in the tool panel. To display the tools, enable the **Show colon coverage in tool panel** setting in the **Flythrough** preferences screen. (See Appendix A: "Flythrough" on page A-40 for more information.)

The colon coverage tools are now displayed in the tool panel, and are as follows:

Overlay Viewed

Check this box to display a green overlay on the areas that have been viewed in the Flythrough module.

Percentage Viewed

This displays the percentage of the entire colon that has been viewed.

Unviewed list

Select this button to display a list of the areas of the colon that have not yet been viewed. You can click on any of the areas listed and the image screens will display those regions. You can also view them consecutively by using the left and right arrows below the list, on the left. (Figure 12-57)

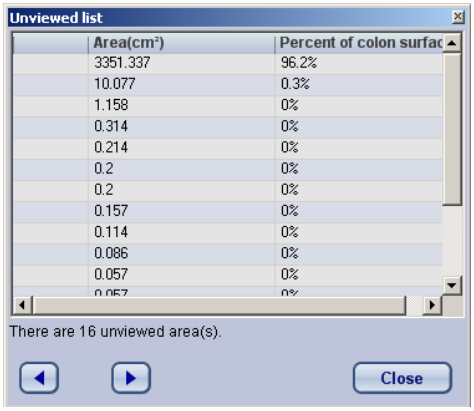


Figure 12-57 Navigating the Unviewed List

Camera Tools

The “camera” refers to the point-of-view in the main Flythrough window. In a straight Flythrough, the camera is always pointing forward along the flight path. These tools allow you to move the camera around so that you can examine the walls of the colon directly. These tools work only when the Flythrough is paused. There are three camera tools.

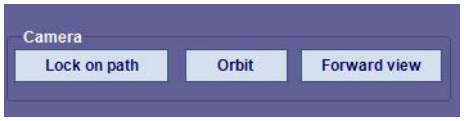


Figure 12-58 Camera Tools

- **Lock on path** - This indicates that the camera is locked onto the flight path. By default, the auto-unlock feature is enabled so that the camera can be automatically unlocked whenever the image is rotated. You can disable auto-unlock using the Interactive Options (see "Interactive Options" on page 12-53).

- **Orbit** - This allows you to revolve the camera around an object so that you can see the object from different sides. Before using this feature, make sure the object is in the center of the Perspective view.

- **Forward view** - This brings the camera back to point forward along the flight path. It is useful when you want to resume the Flythrough with a forward view. However, you can also fly while the camera is pointing at the intestinal wall. To do this, turn the **Forward view** off by clicking the button so that it is not highlighted (see the following image).

You can then rotate the perspective view so that the camera points at whichever part of the wall you want to view, and then resume the Flythrough (see the following figure).

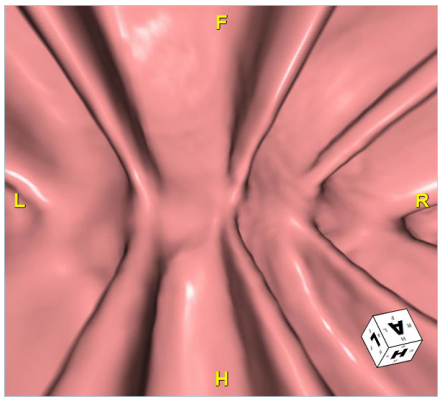


Figure 12-59 Rotating the Perspective View

General Tools

These tools are found in the **General** section of the Tool Panel.

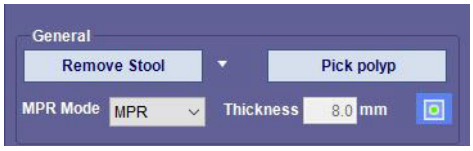


Figure 12-60 General Section of Tool Tab

- **Remove Stool** - Allows you to remove obstructing stool or fluids from the colon path. Select the **Remove Stool** button to perform this operation automatically.

  You can set the HU threshold and transition layer thickness by clicking the down arrow to the right of the **Remove Stool** button. This opens a dialog that allows you to set these parameters.

- **Pick polyp** - You can choose a suspected polyp to isolate, take measurements and capture for a report. To select a polyp for further examination, do the following:

  1. Bring the suspected polyp into view in the main window.
  2. Select the **Pick polyp** button in the General section of the Tool panel.
  3. LMB-click on the polyp in the Flythrough window.

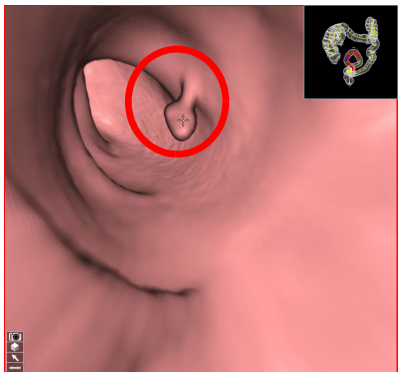


Figure 12-61 Pick Polyp

The polyp is displayed with a dark gray overlay to indicate which part of the image has been included in the volume calculation. The volume is displayed over the image:

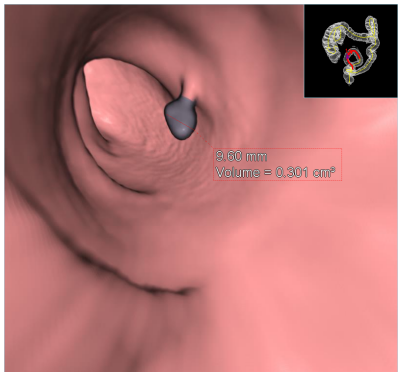


Figure 12-62 Polyp with Dark Gray Overlay

Note: The overlay and measurement are calculated automatically, and must be verified by a qualified person. If it is incorrect, delete it by right-clicking on the measurement and selecting Delete from the menu. You can then measure the finding manually, using the distance tool in the Viewer's top bar (see "Distance" on page 3-147). Also note, You can also pick polyps in Cube View, Flat View and on any of the MPR images. Using Cube View may make it easier to see the object under investigation. (See "Cube View" on page 12-41 for more information.)

- **MPR Mode** - Changes the rendering mode of the 2D images along the left side of the main window. Change to another rendering mode (including 3D) by selecting another view from the pull-down menu.

  Enter a number in the **Thickness** box at the right to set the thickness of the images (2D only).

Measurement Options

When you RMB-click on a measurement annotation, a popup menu is displayed. The options listed in the menu allow you some flexibility in the naming and manipulation of the annotation.

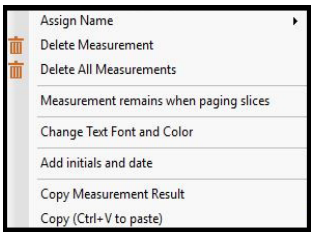


Figure 12-63 Context Menu for Measurement Options

Delete

- **Delete Measurement** - Deletes the measurement that you right-clicked on.
- **Delete All Measurements** - Deletes all measurements from the series.

Changing The Font and Color

You can change both the font and the size of the annotations on any of the measurements described in this section.

To change the font:

1. Right-click on the annotation you want to change.
2. From the right-click menu, select **Change Text Font and Color**. A dialog box is opened.
3. From the font menu, select the desired font. From the color menu, choose a color.
4. Click **OK** when finished.

Add Initials and Date

Opens a text-input box where you can enter a set of initials or a name. The initials and the current date are then added to the annotation.

Window/Level Presets

The Flythrough module has special preset window/level buttons for viewing colon structures. They are located at the bottom of the tool panel. Each preset button sets the levels in the MPR windows slightly differently. You can change any of these presets by right-clicking on them.

Cube View

Cube View allows you to obtain a 3D/cutplane image of a segment of the anatomy. This is very useful for 3D examination of pathology, such as a polyp in the colon.

To see the Flythrough image in Cube View, right-click on the image and select **Cube View** from the menu.

You can also click on the cube icon that appears in the lower-left area of the 3D image whenever you hover the mouse over the image:

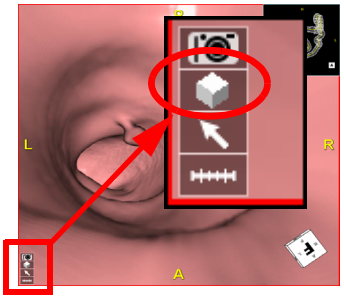


Figure 12-64 Select the Cube

The area of interest is displayed in Cube View:

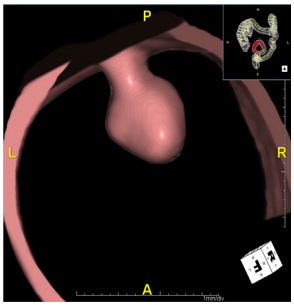


Figure 12-65 Cube View

Mouse Controls in Cube View.

Mouse controls are the same in Cube View as they are in the 3D Viewer:

- **Left Mouse** - Rotates the image
- **Right Mouse** - Pans the image
- **Middle Wheel** - Zooms in (when moved upward) and out (when moved downward)

Use the left mouse to rotate the image so that you can see the area of interest clearly.

Restoring Perspective View

To return to the 3D Flythrough (Perspective) view, right-click again on the cube image, and select **Perspective View**.

Continue the Flythrough by clicking on the image, or by using the Cine buttons described under "Cine Tools" on page 12-34.

360 Degree Fisheye View

The 360 degree Fisheye View offers an alternative way to view the path and walls of the colon. To display the flight in Fisheye View, right-click on the image and select **Fisheye View** from the menu. This toggles the Fisheye View on. (Figure 12-66)

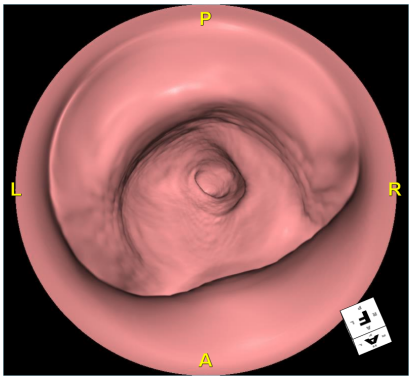


Figure 12-66 Fisheye View

To go back to Perspective view, select **Fisheye View** from the menu again to toggle it off.

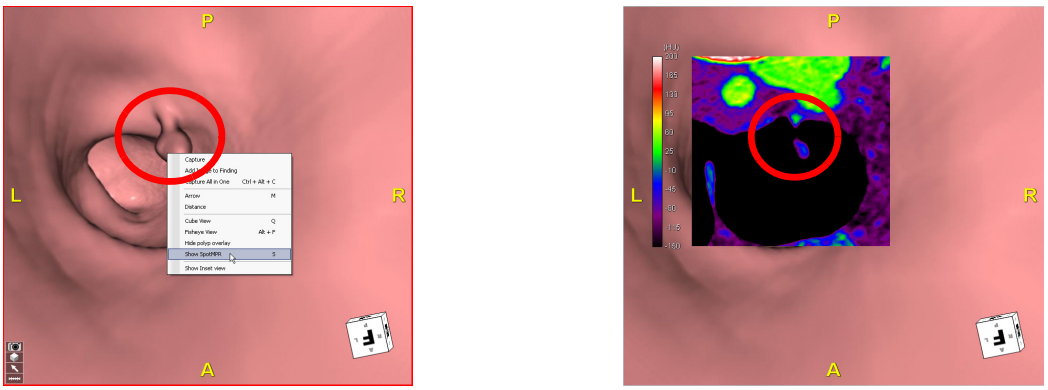
SpotMPR

The SpotMPR feature superimposes a two-dimensional color map on the 3D main window, showing the MPR slice where the flight is currently stopped. The slice is color-coded to show HU values, and is parallel to the screen.

Note: The color settings can be changed in the Preference window and are assigned in the finding description. See "Findings" on page 12-54.

To display SpotMPR, RMB-click on the perspective window and select **Show SpotMPR**.

When you RMB-click on the image, the SpotMPR image is overlaid on the 3D image so that the center of the overlay is where you RMB-clicked.



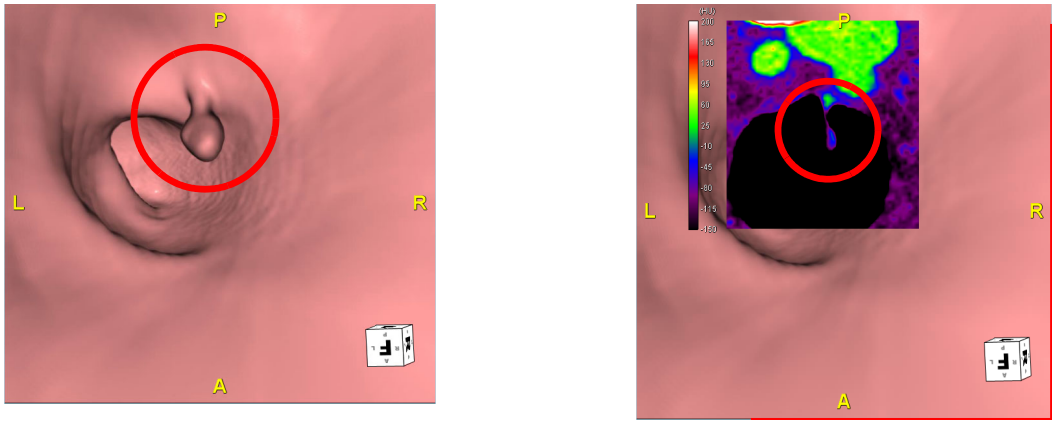
Left: Right-Click Point on Image **Center of SpotMPR Lies on the Same Point**

Figure 12-67 Centering the SpotMPR

Paging Through Slices on SpotMPR

You can page through the slices on the SpotMPR, because it is a 2D slice image. The SpotMPR slice is a cross-section of the colon at the current position in the flight. As you page through the slices, the

SpotMPR advances along the flight path. However, the 3D image (and the Flat View, if that is visible) do not advance. Changes in SpotMPR are not linked to the flight.



Stopped Flight in Main Window **Color Map of the HU Values**

Figure 12-68 Changes in SpotMPR not Linked to Flight

Panning SpotMPR

You can also pan the SpotMPR area around the Flythrough window. To do so, right-click and drag to a new area.

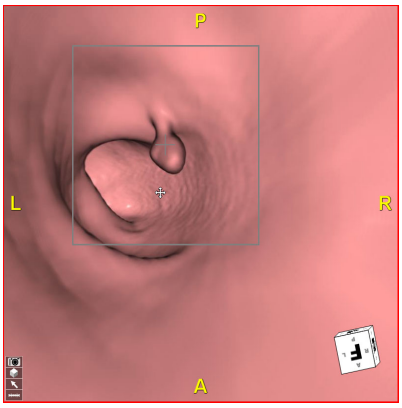


Figure 12-69 Panning the SpotMPR

SpotMPR in Grayscale

SpotMPR can be viewed in Grayscale. To do this, right-click on the SpotMPR area and select **Show Color Map** to toggle the color map off. (Figure 12-70)

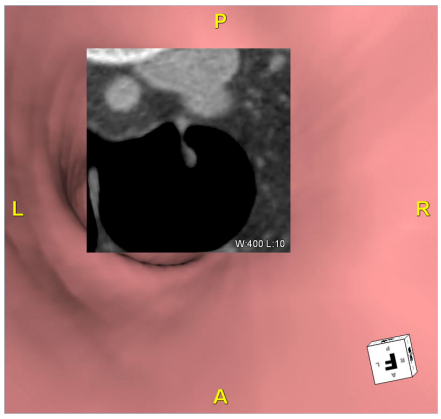


Figure 12-70 SpotMPR in Grayscale

Changing the Color Scale

To adjust the colors in the SpotMPR:

1. RMB-click on the SpotMPR and the Change Min/Max window opens.

2. Adjust colors as needed and then select **OK**.

This setting must be adjusted in the Preference window for this to change the coloring of the SpotMPR.

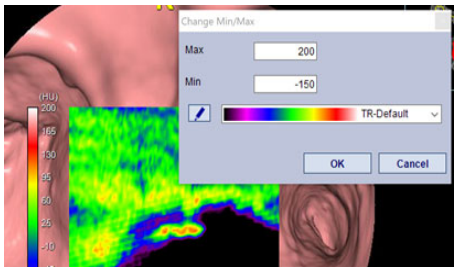


Figure 12-71 Changing Min/Max Settings in SpotMPR

Changing WW/WL

On the Grayscale SpotMPR, you can change the window width/window level in the same way it is changed in any 2D image. Hold down the left and right mouse buttons, and then drag the mouse across the image to change the brightness and contrast.

Setting the Default WW/WL

You can set the default window width/window level specifically for the SpotMPR area. RMB-click on the SpotMPR and select **Change default WW/WL**. A dialog is opened where you can enter new values.

Enter new defaults and click **OK** to save them. These defaults do not affect the defaults of any other 2D image. Please note that you will not see the effects of the change until you turn off the color map to view the SpotMPR in Grayscale.

Flat View

The **Flat View** is the view showing colon as if it were sliced open and stretched out flat. This view is very useful because it gives another view of the objects in the colon walls not available in the forward view.

Note: The 2D 3 Basics + Perpendicular + CPR style does not work in Flat View. If you do select this layout when in a Flat view, you are prompted to change the layout.

There are two ways to scroll through the Flat view image. One is to use the left or right arrows, located next to the left or right edge of the Flat view window, respectively. These buttons advance the Flat View one full window length.

For example, if you are viewing the Flat view in multiple windows, the image appearing in second window will be moved to the top window after you click the right-pointing arrow. The objects in the top window will be located in the same positions, with respect to the start of that window, as they did in their previous location. (Figure 12-72)

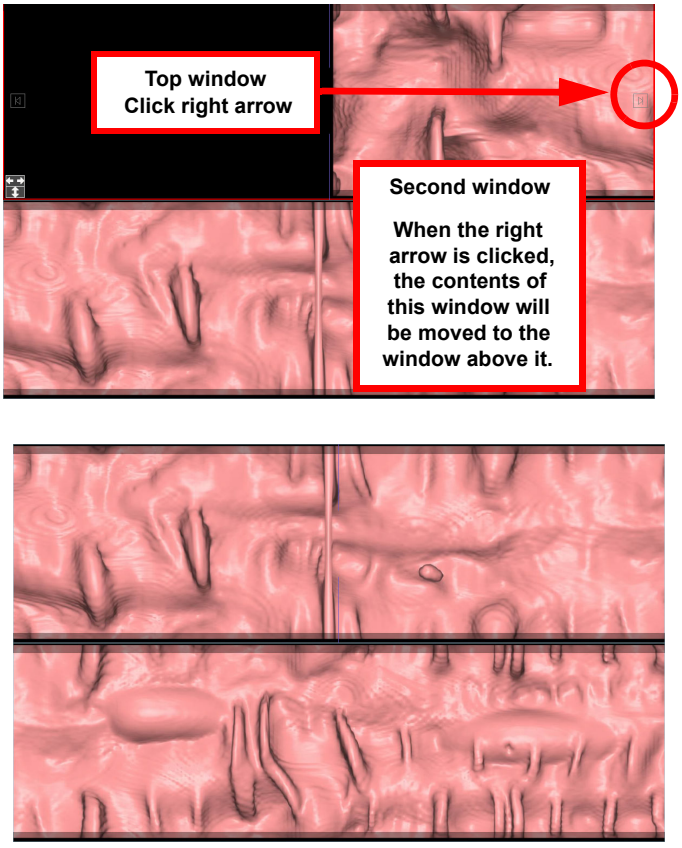


Figure 12-72 : Moving within the Flat View: Top and Second Windows

To scroll in smaller increments, you can also click on the Flat View itself. The vertical blue line in the middle of the image determines which direction the image will be scrolled. If you click on the left side of the blue line, the image scrolls to the left. Clicking on the right of the blue line scrolls the image rightward.

You can scroll a small distance by clicking on the image close to the blue line. The further from the blue line, the larger the scrolling distance.

You can also use the Flat View to bring the camera to a specific spot in the Flythrough window by clicking on it. Every spot on the Flat View corresponds to a spot in the Flythrough window. For example, if you see an object in the Flat View that is potentially pathological, you can click on the object to bring the camera to that spot in the Flythrough window. (Figure 12-73)

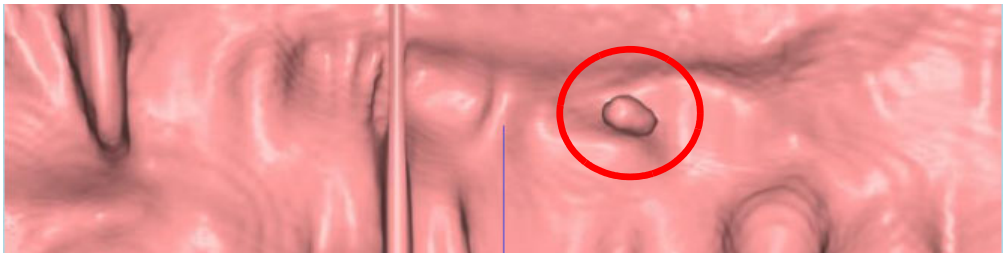


Figure 12-73 Focus View on a Potentially Pathological Spot

For example, if you click on the object circled in the previous figure, the Flythrough window displays the image shown in Figure 12-74.

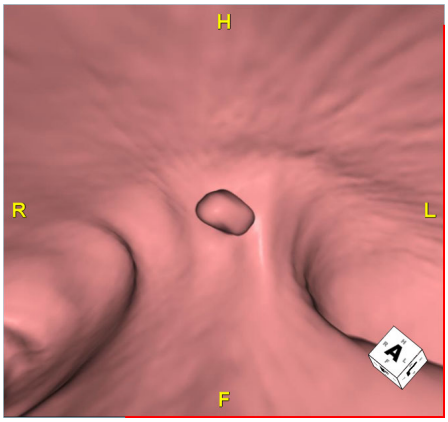


Figure 12-74 Displaying Spot

Note: Because the Flat View image is distorted, it is often hard to tell whether the structures viewed in the Flat View are meaningful. The object must be viewed in the 3D or MPR window to determine whether it is significant.

Auto Capture Whole Flat View

You can capture the Flat View for the entire colon into the Output Panel.

1. Right-click on the Flat View image and select **Auto capture whole flat view**.

   The image is captured, and a dialog is opened so that you can specify the layout of the images in the Output Panel.

2. Select the page format from the pull-down menu. The page format determines how captured images are displayed in the Output Panel.

Note: These are the same as the standard Output Panel formats, which you can also control in the Output Panel itself.

For example, the figure below shows 2x2 format. This means that the images are arranged in four cells (two columns, with two rows in each column) per page. Therefore, each page in the Output Panel contains four image cells. If fewer than four images are captured, some of the cells will be empty. If more than four images are captured, pages are added as needed, each one containing four image cells in the same configuration. (Figure 12-75)

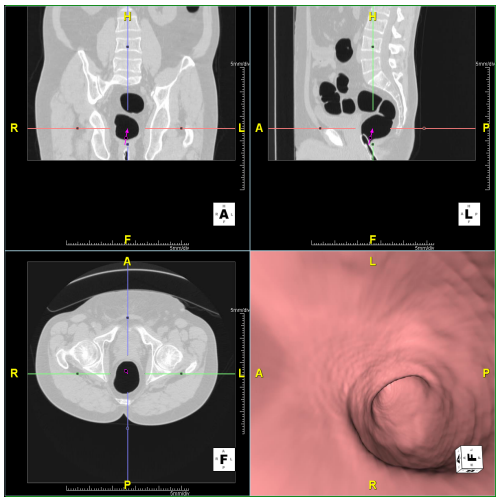


Figure 12-75 2x2 Layout Format

3. Select a sub layout from the left column of the Auto Capture dialog. This selection determines how each individual *cell* will be divided into a sub layout.

   For example, if you select a 1x2 sub layout, each cell is divided by two (one column, two rows), resulting in eight images per page.

In the Auto **capture whole flat view** dialog, the **# of Images** column shows, for each corresponding sub layout, how many whole image cells will be required to hold all the images. These numbers are determined by the total number of captured images.

Floating Tabs in the Workflow Panel

The tabs in the Workflow Panel (Finding, Workflow, Template and 3D Setting) can each be detached from the AQi viewer so that you can use them simultaneously, without needing to switch tabs.

1. Click and drag the desired tab to any other location on the monitor.

2. Release the mouse. The tab is now displayed separately from the rest of Workflow Panel.

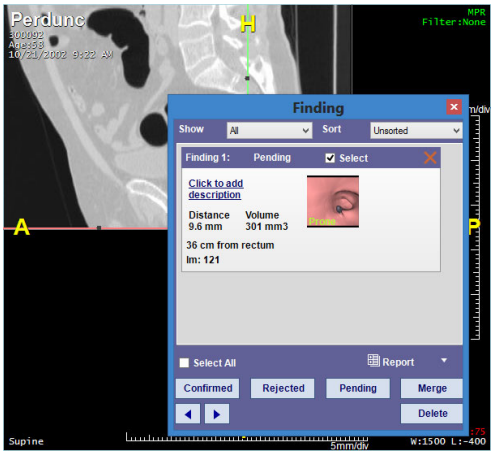


Figure 12-76 Floating Tabs in the Workflow Window

You can detach any or all of the Workflow Panel's tabs. To place a tab back in the Workflow Panel, click the X in the upper-right corner of the tab to close it.

Anchoring the Tabs on the Top Bar

You can anchor the tabs on the top bar so that they can be closed momentarily, without being placed back in the Workflow Panel.

1. Open the Preferences and expand the **Flythrough** link in the navigation panel.

   Click **Details**.
   Check the box for **Put Workflow, Template and 3D Setting on the top bar**.
   Click **OK** to save.

The tabs have been moved to the top bar and are now displayed as icons. From left to right, the icons (Figure 12-76) open the Workflow, Template and 3D Setting tabs. The Finding tab is still located in the Workflow Panel.

Figure 12-77 Anchoring Tabs

Placing Reading Style Layouts on the Top Bar

If the Workflow tab is not visible because you are currently using another tab in the Workflow Panel, you can place layout icons on the top bar so that it is more convenient to switch layouts.

1. Right-click on a layout in the Workflow tab.

2. Select Register on top bar.

Note: This does not remove the layout icon from the Workflow tab.

To switch from one layout to another, click the desired icon on the top bar.

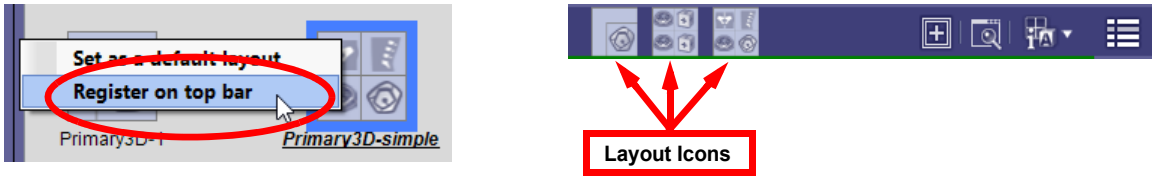


Figure 12-78 Layout Icons

To remove layout icons from the top bar, right-click on them and select **Delete**.

Other Viewing Options

These options give you control over image viewing and Flythrough direction.

Rear Perspective View

To view the Flythrough looking toward the rear (as well as looking forward), right-click in any of the 2D windows and select **Switch to rear perspective view**. To return to the 2D image, right-click and select **Back to 2D view**.

Perpendicular View

The perpendicular view shows the perpendicular slice that the Flythrough centerline is crossing at each point along the centerline. Because the flight changes directions as it progresses (in all 3 dimensions), the orientation of the perpendicular slice also changes. To show the perpendicular view, select **Switch to Perpendicular view** from the right-click menu on any 2D image. To return to the 2D image, right-click and select **Back to 2D view**.

Global View

The Global view refers to the image shown in the inset. It allows you to track the Flythrough in progress from a global perspective on the colon.(Figure 12-79) To enlarge the global view, select **Switch to Global view** from the RMB-click menu on any 2D image. To return to the 2D image, RMB-click and select **Back to 2D view**.

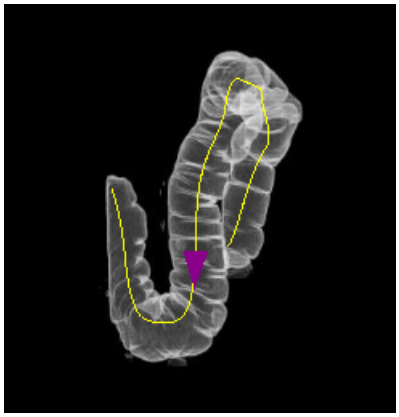


Figure 12-79 Global View

Other options for the Global view are available when you LMB-click on the inset itself. You can chose to **Hide all** or **Show all** Finding markers in this view, in addition to other menu options. (Figure 12-80)

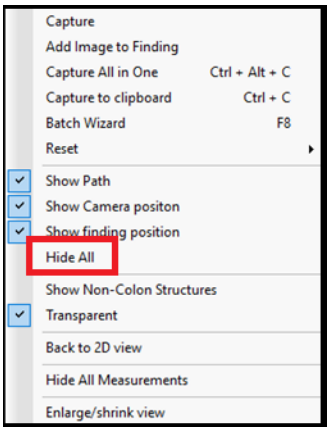


Figure 12-80 Hide All or Show All

The Global view inset can be resized by LMB-clicking on one corner and dragging it to the desire size. You can also double-LMB-click on the Global view to exchange places with the main perspective image. To return the Global view to the inset, double-LMB-click on the inset box again.

Modifying Views in the Options Tab

Click the **Options** tab to access the following viewing options:

- **View Angle**

  The View Angle allows you to narrow the camera lens in order to have a more detailed view of the Flythrough path, or to widen the lens to include more of the wall in the viewing window. Valid range is from 70 to 360 degrees, with 120 degrees as the default. (Figure 12-81).

Narrow Angle **Wide Angle**

Figure 12-81 View Angle Setting

Use the slider to change the view angle.

You can also change the view angle by RMB-clicking on the Angle annotation on the image.

- **Cine Play at the End of Path**

  When the Flythrough reaches the end of the path, the default is for it to begin the Flythrough again at the start. You can change this so that the action at the end of the path suits the needs of your examination.

  - **Bounce** - Automatically plays the Flythrough from end to beginning.
  - **Repeat** - Starts the Flythrough over at the beginning (default)
  - **Stop** - Stops Flythrough at the end.

- **MPR Update Interval When Flying**

  MPR and other 2D images have two options:

  - Always update Flat View when flying - The Flat View is updated during Flythrough so that it reflects the current position of the camera.
  - Always update perpendicular view when flying - MPR images are updated during Flythrough so that they reflect the current position of the camera.

- **Update whole flat view while cine** - When enabled, Flat View is updated during cine, when Perspective view goes out of the currently viewed flat view range.

- **Remove stool from the 2D/MPR images** - Stool is removed from 2D images as well as 3D when the **Remove Stool** button is clicked.

Note: When stool has already been removed from an image, an annotation appears on the image.

- **Show distance from rectum on Perspective view** - When the flight is stopped, the distance is displayed in the lower-left annotations of the Perspective view.
- **Interactive** (button) - Open a second Options window for mouse operations. These are described in the following section.
- Synchronize angles

Interactive Options

When you click the **Interactive...** button, a dialog is opened which allows you to set several parameters:

- **Interactive Speed**

  This controls the speed of the Flythrough. To obtain a faster speed, some image quality is lost. A better image quality results in a slower Flythrough speed.

- **Mouse Click on Perspective Image**

  This section allows you to choose which action will result when you click on the Perspective image:

  - **Focus there** - places the point clicked on in the center of the image
  - **Start flying** - resumes the Flythrough
  - **Do nothing** - has no effect

- **Mouse click during flying** - Either stops the Flythrough or captures a finding (at the spot clicked on) without stopping the Flythrough.
- **Space bar to**
  - **Start/stop flying** - When this is selected, press the space bar to start and stop flying.
  - **Toggle sync** - When this is select, press the space bar to sync/unsync the 2D views from the perspective view.
- **Focus setting**
  - **Rotates 3D view to the focused point** - Focus point placed in the center of the perspective window, and the view is rotated when necessary.
  - **Distance to the focused point** - Enter this amount in the text box. Default is 3cm.
  - **Turn on Orbit after focus** - Orbit mode is automatically turned on after the clicked point is in focus on the perspective view.

  - **Focus by double click** - Double-click to stop flight and focus. (When this is unchecked, use **Alt+Click** to focus.)

  - **Mark arrow after focus** - A finding arrow is displayed to point to the focus point.

- **Simply click on 2D will focus there** - Single click on a 2D image, while not flying, to focus the all 2D images on the corresponding spots.

- **Synchronize 3D too when focus sync on 2D** - Focus the 3D image on the corresponding spot when focusing on a 2D image.

- **Move mouse to change speed**

  When this is checked, moving the mouse over the Perspective window during Flythrough changes the speed. To increase the speed, move the mouse up. To decrease, move down.

- **Orientation related to gravity**

  The orientation of the camera is turned so that any residual fluid in the colon appears on the bottom.

- **Unlock from path automatically**

  When checked, you can use the zoom and orbit functions without explicitly unlocking from the flight path.

- **Keep Orbit mode after Cine**

  When checked, orbit mode remains on when flying. When not checked, orbit mode turns off automatically when flight is started.

- **Synchronize camera position with cross section view**

Gravity Settings

The gravity menu is located on the left side of the top toolbar. The selections are as follows:

- **All data following gravity** - The Perspective view is rotated so that the gravity direction is downward.

- **Fit to Supine** - The Perspective view is rotated to follow the gravity direction of supine data. Therefore, the “P” orientation is at the bottom.

- **Fit to Prone** - The Perspective view is rotated to follow the gravity direction of Prone data. Therefore, the “P” orientation is at the top.

Findings

Capturing Findings for the Report

To capture findings for a report, right-click on the image to be captured, and then select **Capture** or **Capture All in One** from the pull-down menu.

You can also capture findings using the shortcut key, C (not case-sensitive). This allows you to capture findings without interrupting the Flythrough. The finding is stored on the **Finding** tab in the Workflow panel, in the upper-right corner of the AQi viewer.

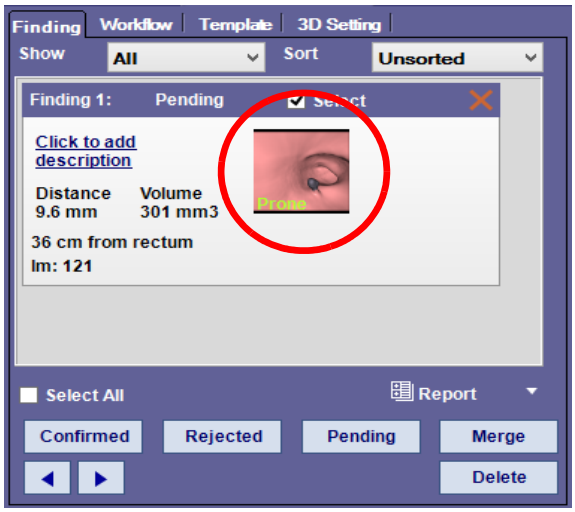


Figure 12-82 Capturing the Findings

If you need to re-examine the finding, you can click on the icon (Figure 12-82) to display the image in the main window.

Automatic Capture of Findings

Flythrough also allows you to set preferences for automatic captures of findings. Any of the following actions can create a finding:

- When an arrow is added to the image
- When a distance is measured
- When a polyp is picked
- When the CAD marker is turned on

To set any of these preferences, click the Preference icon ( ) in the top toolbar and then click Flythrough in the navigation panel on the left of the Preference screen. For details, see "Appendix A", Flythrough, on page A-40.

When a finding has already been captured, and a new finding is located close to the first one, you can add the second image to the first finding. This feature is useful when both the prone and supine scans are loaded, and you are capturing the same finding from each scan. When the second finding is captured, a dialog is opened asking whether you want to add the image to the current finding or create a new finding.

Click **Add** to add the new capture to the current finding.

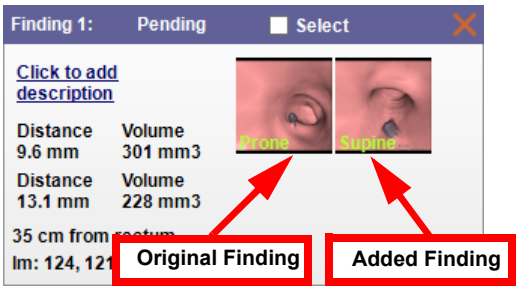


Figure 12-83 Adding Captures to Findings

Add Image to Finding

You can add an image to the current finding even if the new image is not itself a finding. To do so, right-click on the image in the perspective or perpendicular view and select **Add Image to Finding**.

If the location of the image to be added is within 10cm (along the flight path) of the finding it is being added to, the image is added. If the new location is greater than 10cm from the current finding, a dialog is opened with the message, “New finding is more than 10 cm away from current findings. Are you sure to add to current finding?” Click **Yes** if you intended to add this image to the finding, and **No** to cancel.

Assigning Colors to Findings

In the Preference window, you can edit color settings for findings.

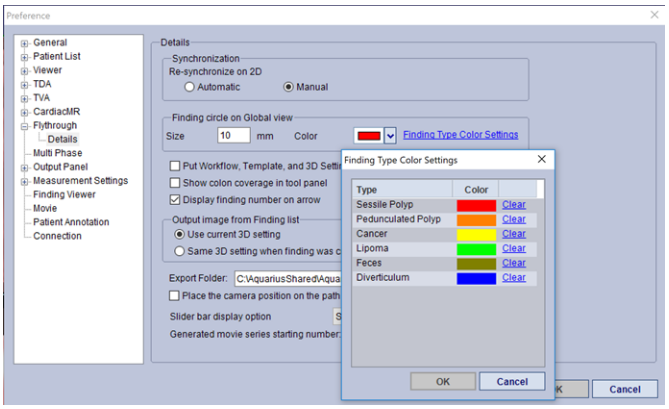


Figure 12-84 Color Settings in the Preference Window

In the finding window, when you select Click to add description, you will see the colors in the Type drop-down menu.

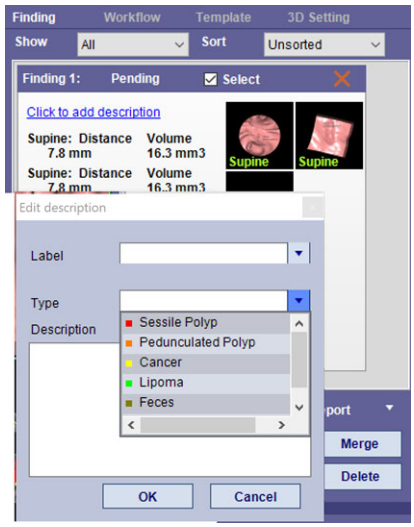


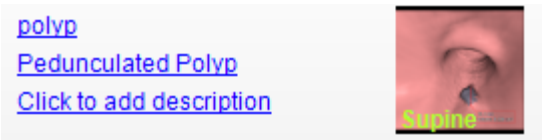
Figure 12-85 Selecting the Finding Type

Adding Label and Description to Finding

You can add specific, descriptive information to a finding:

1. Click the **Click to add description** link. The **Edit Description** dialog is opened.
2. Select a **Label** from the pull-down menu. You can also type in any label name, if you prefer.
3. Select a **Type**, or enter your own type manually.
4. Add a description (optional).

The label is added to the finding:



Confirmation

The finding cannot be included in the report until it is confirmed. To confirm a finding, do the following:

1. Check the **Select** checkbox in the Finding.

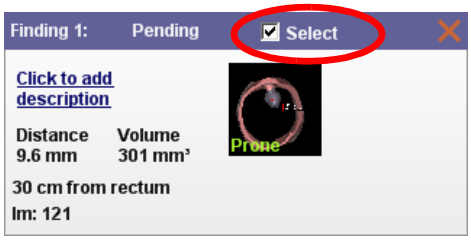


Figure 12-86 Confirming the Finding

2. Click the **Confirmed** button, located at the bottom of the Tools tab:

   The status of the finding is changed to **Confirmed**:

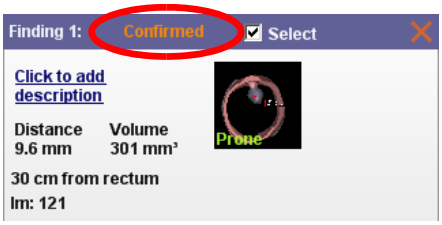


Figure 12-87 Confirmation Indicated

If you determine that the finding is not a pathology, click the **Rejected** button to change the status to Rejected. A rejected finding will not be included in the report.

You can change the status at any time; for example, if you decide to have a colleague examine a finding, you can change the status back to pending just by clicking the **Pending** button on that finding.

Dividing Findings

If findings have been merged by mistake, you can divide them so that they are separate again.

1. Right-click on the finding.

2. Select **Divide Finding**.

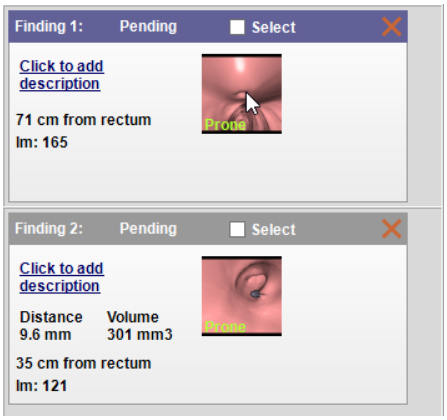


Figure 12-88 Divided Findings

Generating a Report

After you have completed the Flythrough study, you can generate a report of your findings.

1. Select a report option from the pull-down menu in the lower-right area of the **Findings** window (Figure 12-89).

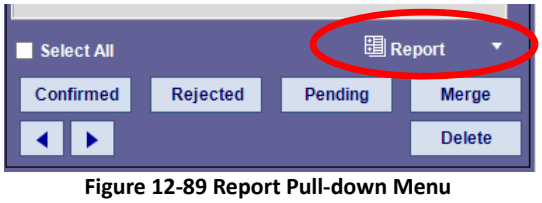


Figure 12-89 Report Pull-down Menu

   The options are as follows:

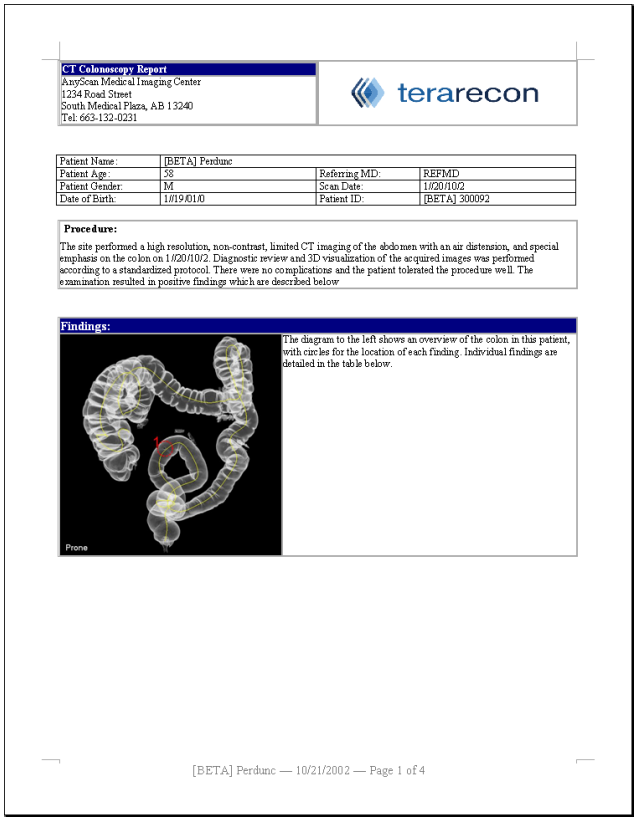
- **Report** - Generate a standard report.
- **Output** - Batch all Confirmed findings to the Output Panel.
- **Text** - Save a text file containing the results on your local PC. A Windows navigation dialog opens so that you can choose the folder where the findings will be saved.
- **XML** - Save an XML file on your local PC.

Note: Only confirmed findings are included in a report, sent to the Output Panel or included in a text file.

---

2. Click the button for the output function you have selected (**Report**, **Output**, or **Text**).
3. Sign electronically and the report is generated in MS Word.

Figures 12-90 and 12-91 on the next pages display a Flythrough Report.



CT Colonoscopy Report
AnyScan Medical Imaging Center
1234 Road Street
South Medical Plaza, AB 13240
Tel: 663-132-0231

terarecon

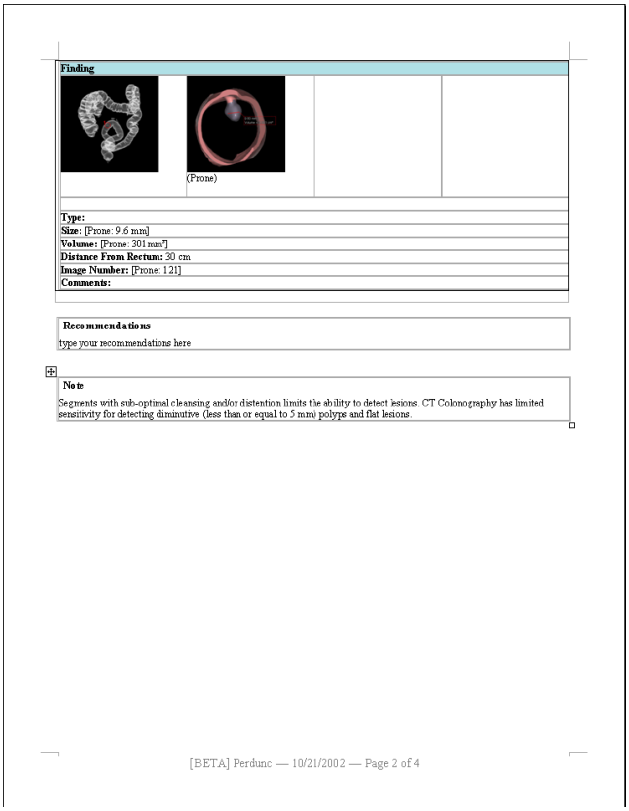
Patient Name:	[BETA] Perdunc		
Patient Age:	58	Referring MD:	REFMD
Patient Gender:	M	Scan Date:	1/20/10/2
Date of Birth:	1/19/01/0	Patient ID:	[BETA] 300092

Procedure:

The site performed a high resolution, non-contrast, limited CT imaging of the abdomen with an air distension, and special emphasis on the colon on 1/20/10/2. Diagnostic review and 3D visualization of the acquired images was performed according to a standardized protocol. There were no complications and the patient tolerated the procedure well. The examination resulted in positive findings which are described below

Findings:

The diagram to the left shows an overview of the colon in this patient, with circles for the location of each finding. Individual findings are detailed in the table below.



Finding

(Prone)

Type:
Size: [Prone: 9.6 mm]
Volume: [Prone: 301 mm³]
Distance From Rectum: 30 cm
Image Number: [Prone: 121]
Comments:

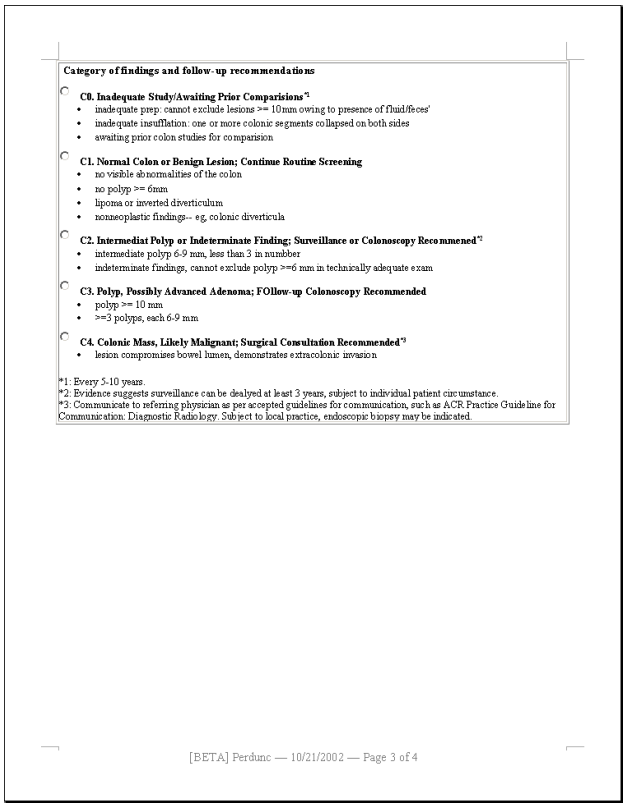
Recommendations

type your recommendations here

Note

Segments with sub-optimal cleansing and/or distention limits the ability to detect lesions. CT Colonography has limited sensitivity for detecting diminutive (less than or equal to 5 mm) polyps and flat lesions.

Figure 12-90 Flythrough Report - Pages 1 and 2



Category of findings and follow-up recommendations

C0. Inadequate Study/Awaiting Prior Comparisions*2
- inadequate prep: cannot exclude lesions >= 10mm owing to presence of fluid/feces'
- inadequate insufflation: one or more colonic segments collapsed on both sides
- awaiting prior colon studies for comparision

C1. Normal Colon or Benign Lesion; Continue Routine Screening
- no visible abnormalities of the colon
- no polyp >= 6mm
- lipoma or inverted diverticulum
- nonneoplastic findings-- e.g, colonic diverticula

C2. Intermediat Polyp or Indeterminate Finding; Surveillance or Colonoscopy Recommened*2
- intermediate polyp 6-9 mm, less than 3 in number
- indeterminate findings, cannot exclude polyp >=6 mm in technically adequate exam

C3. Polyp, Possibly Advanced Adenoma; FOllow-up Colonoscopy Recommended
- polyp >= 10 mm
- >=3 polyps, each 6-9 mm

C4. Colonic Mass, Likely Malignant; Surgical Consultation Recommended*3
- lesion compromises bowel lumen, demonstrates extracolonic invasion

*1: Every 5-10 years.
*2: Evidence suggests surveillance can be dealyed at least 3 years, subject to individual patient circumstance.
*3: Communicate to referring physician as per accepted guidelines for communication, such as ACR Practice Guideline for Communication: Diagnostic Radiology. Subject to local practice, endoscopic biopsy may be indicated.

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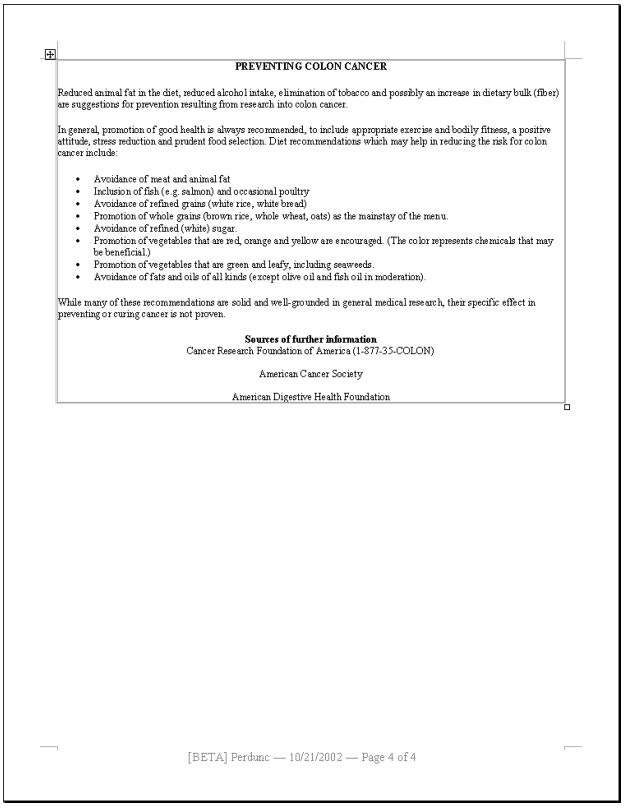


PREVENTING COLON CANCER

Reduced animal fat in the diet, reduced alcohol intake, elimination of tobacco and possibly an increase in dietary bulk (fiber) are suggestions for prevention resulting from research into colon cancer.

In general, promotion of good health is always recommended, to include appropriate exercise and bodily fitness, a positive attitude, stress reduction and prudent food selection. Diet recommendations which may help in reducing the risk for colon cancer include:

- Avoidance of meat and animal fat
- Inclusion of fish (e.g. salmon) and occasional poultry
- Avoidance of refined grains (white rice, white bread)
- Promotion of whole grains (brown rice, whole wheat, oats) as the mainstay of the menu.
- Avoidance of refined (white) sugar.
- Promotion of vegetables that are red, orange and yellow are encouraged. (The color represents chemicals that may be beneficial.)
- Promotion of vegetables that are green and leafy, including seaweeds.
- Avoidance of fats and oils of all kinds (except olive oil and fish oil in moderation).

While many of these recommendations are solid and well-grounded in general medical research, their specific effect in preventing or curing cancer is not proven.

Sources of further information
Cancer Research Foundation of America (1-877-35-COLON)

American Cancer Society

American Digestive Health Foundation

[BETA] Perdunc — 10/21/2002 — Page 4 of 4

Figure 12-91 Flythrough Report - Pages 3 and 4

Chapter 13 Measurement Protocols

Topics in this chapter:

Measurement Protocols allow you to define standard procedures for obtaining measurements on study data. Each protocol can be defined as a precise sequence of individual measurements. In the same manner, each measurement can be defined precisely, using a standard procedure.

Naming Measurements

An important concept is the consistent naming of measurements. It is strongly recommended that you give the exact same name to the same measurement, taken on the same body part, throughout all measurement protocols in your system. This will ensure that the Measurement Protocols tool can identify the measurements appropriately. For example, if you follow one measurement protocol to take measurements on an image, and then load a second protocol that happens to have one or more of the same measurements as part of its procedure, those measurements will be automatically filled in, because you have already performed them. This can save a lot of time and effort.

Integration

Measurement protocols are customizable and can be constructed so that the measurements can be easily integrated into other software such as RIS or Excel.

Using Measurement Protocols

This section describes how to use measurement protocols that have already been defined.

Opening the Measurement Protocols Tool Panel 

To display the Measurement Protocols tool, click the Measurement icon in the 3D Viewer Tool Panel.

Click the Measurement icon. The Measurement Protocols tool is displayed in the Tool Panel, as shown in Figure 13-1.

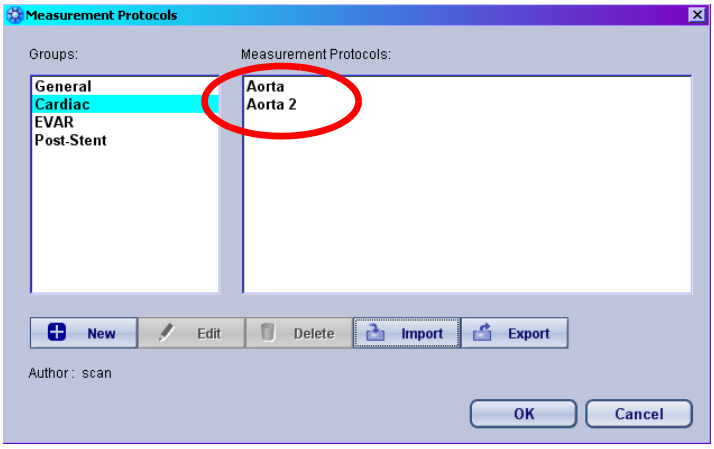
Note: The measurement protocols tool panel is empty at first, because a measurement protocol has not been opened.

Opening a Protocol

Click the down-arrow located in the upper-right corner of the Tool Panel (circled in Figure 13-1). This opens the Measurement Protocols dialog.

The Measurement Protocols Dialog

1. Select the appropriate group from the **Groups** column on the left. A list of the protocols in that group is displayed on the right.



2. Select the required protocol from the list in the right panel (circled, at right).

3. Click **OK.**

   The selected protocol is displayed in the Tool Panel, as shown in Figure 13-1.

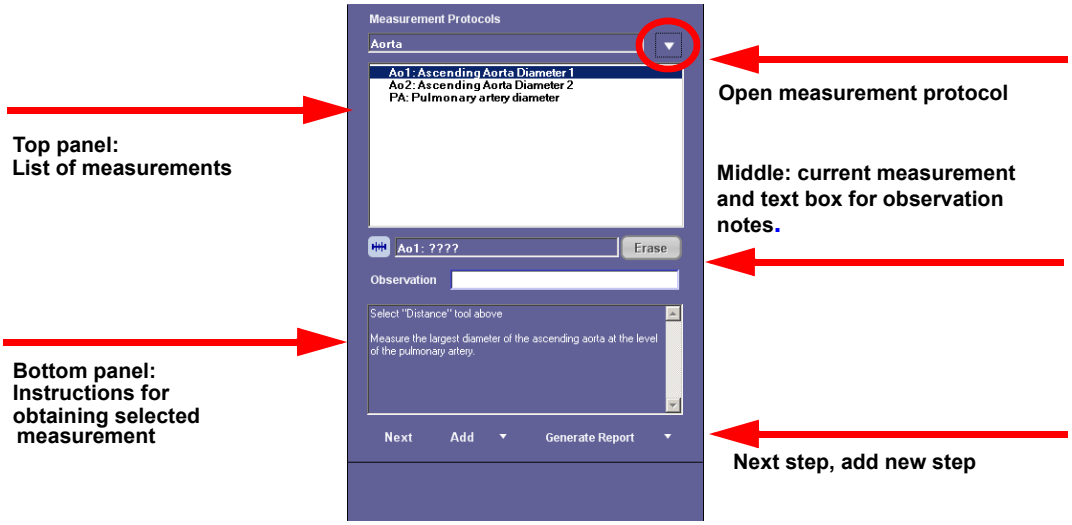


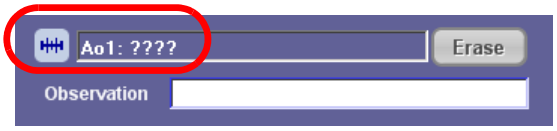
Figure 13-1: The Measurement Protocols Tool Panel

The top (white) panel contains the list of measurements you need to obtain. Each separate measurement is listed on a separate line.When a measurement is selected in the top panel, the instructions for obtaining that measurement appear in the bottom (blue) panel.

Obtaining Measurements

1. Click on the first item, **Ascending Aorta Diameter 1**. The instructions for obtaining this measurement are displayed in the bottom panel, as shown in Figure 13-1).

The measurement value (circled in the figure below), has not been filled in yet. This is indicated by the four question marks in the value field. When you complete this measurement, the value will be displayed in this field.



Instructions

1. Select the Distance tool in the Measurement Protocols tool panel.

2. On the axial view, draw a line across the ascending aorta, at the level of the pulmonary artery (see the following figure). The distance is displayed on the image.

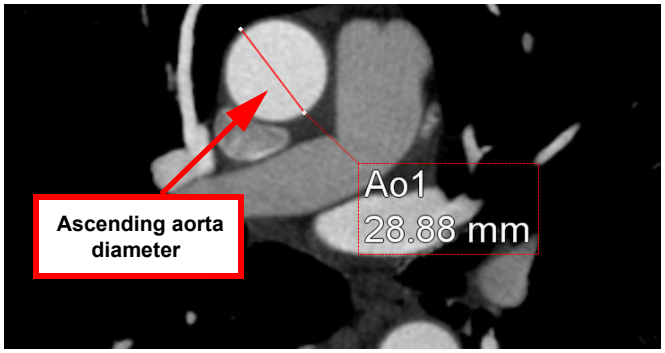
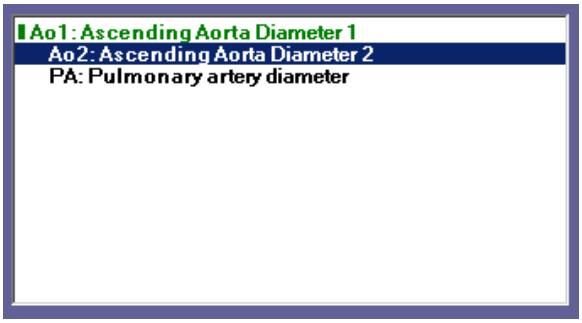


Figure 13-2: Diameter of Ascending Aorta

3. Confirm that the diameter value is displayed here:

4. Add a comment about this measurement in the Observation text box if desired (optional).

When you have completed the instructions for this measurement, click the following item on the list, or click the **Next** button (located at the bottom of the tool panel). The completed measurement is displayed in green text:



Measurement Undo

To undo a measurement, click the undo button in the top toolbar (see "Top Toolbar Buttons" on page 3-143 for information).The most recently completed measurement is erased.

If you continue to click the undo button, previously completed measurements will be erased, in reverse order. The redo button (to the right of the undo button) restores the measurement that was erased by the last undo.

Generating a Report

When all required measurements in the protocol have been completed, you can generate a report. It is not necessary to complete every measurement in the protocol in order to create the report; however, you must complete all *required* measurements. Measurements can be tagged as required when the measurement protocol is created. See "The Measurement Definition Dialog" on page 13-8 for more information.

To generate a report, click the **Generate Report** button, located in the bottom-right corner of the Tool Panel.

The report, containing all the required measurements for this protocol, is created and opened in Microsoft Word.

Exporting Measurement Data

You can export measurement data obtained from specific studies, which can then be incorporated into third-party software such as RIS. To export the current set of measurements, do the following:

1. Click the down-arrow located to the right of the **Generate Report** button. A pull-down menu is opened.

2. Select one of the output file types to contain the data. The choices are as follows:

   - XML
   - AIM XML
   - Plain text
   - CSV (comma-separated values) - useful for Excel or similar software
   - Copy measurements to clipboard

   Your selection should depend on what kinds of software are used at your institution for presenting measurement data.

Creating Your Own Measurement Protocols

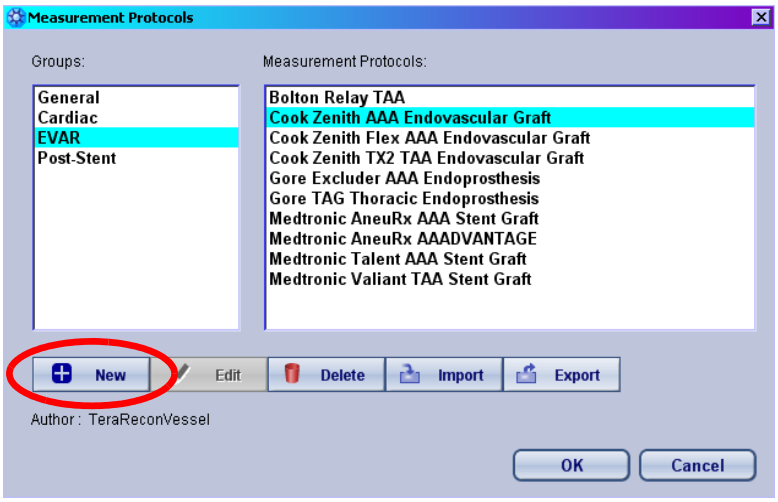
This section describes how to create new measurement protocols.

Opening the Measurement Protocols Dialog

1. Display the Measurement Protocols tool panel. If you do not know how to do this, see instructions under "Opening the Measurement Protocols Tool Panel" on page 13-1.

2. Click the down-arrow located in the upper-right corner of the Tool Panel (circled in Figure 13-1 on page 13-2). This opens the Measurement Protocols dialog.

Elements of the Measurement Protocols Dialog



- Groups List - Measurement Protocol groups, for related kinds of studies.

- Measurement Protocols List - The list of protocols in the currently selected group.

- Function Buttons:

  - New - Create a new protocol.
  - Edit - Edit the currently selected protocol.
  - Delete - Delete the currently selected protocol.
  - Import - Import a protocol from your hard drive.
  - Export - Save the currently loaded protocol to your hard drive.

To create a new protocol, click the **New** button (circled in the previous figure). The **New Measurement Protocol** dialog is displayed (see figure at right).

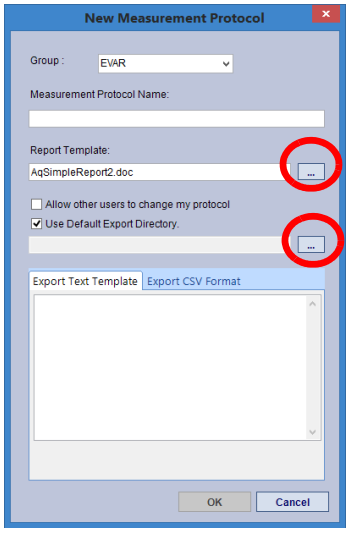


Figure 13-3: New Measurement Protocol Dialog

The New Measurement Protocol Dialog

The New Measurement Protocol dialog is used to create a new measurement protocol.

Description of Input Fields

- Group - Before you can create a measurement protocol, you first must select a group from the menu for the protocol. This will depend on which kind of study you are measuring.

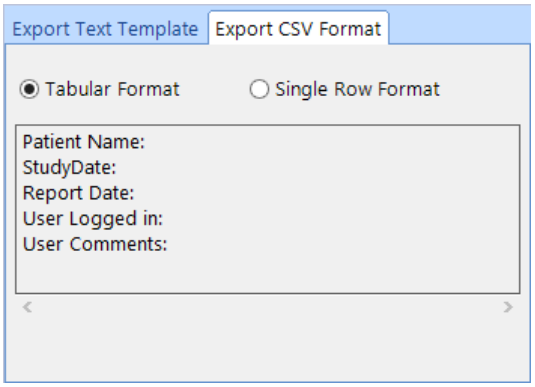
- Measurement Protocol Name - This is the name of the measurement protocol that will show in the Measurement Protocols list.

- Report Template - Use the default report template that is provided, **AqSimpleReport2.doc**.

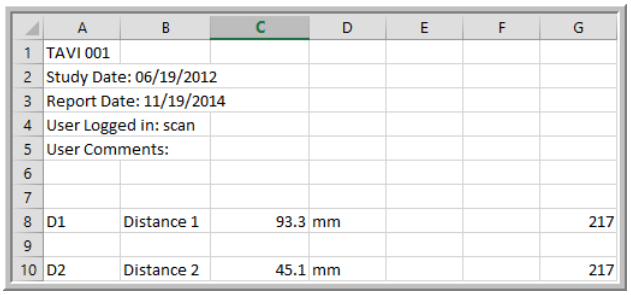
- Allow other users to change my protocol - You can export the protocol for others to use. If you check this box, others will be able to modify it. If you want the protocol to be used exactly as you have created it, leave this box unchecked.

- Use Default Export Directory - The Aquarius iNtuition Viewer has a default folder for storing exported protocols on the local hard drive. You can use this folder, or change it to a preferred folder by clicking the "**...**" button on the right (circled in light blue in Figure 13-3). You can also change the default itself in the Preferences menu. Please see "Measurement Settings" on page A-45 for details.

- Export Text Template - The Measurement Protocols tool allows you to export measurement data obtained on specific studies, so that the information can be integrated into third-party software, such as RIS. The template allows you to present the measurement data within a description intended for physicians.



- Export CSV Format - The **Export CSV Format** tab allows you to configure the output format of exported data. **Tabular** format outputs the data in table form. **Single Row** format places all the data on one row (see Figure 13-4 on page 13-7).



	A	B	C	D	E	F	G
1	TAVI 001						
2	Study Date: 06/19/2012						
3	Report Date: 11/19/2014						
4	User Logged in: scan						
5	User Comments:						
6							
7							
8	D1	Distance 1	93.3	mm			217
9							
10	D2	Distance 2	45.1	mm			217

	A	B	C	D	E	F
1	Patient First Name	Patient Last Name	Accession Number	Exam Date	Distance 1	Distance 2
2		TAVI 001		6/19/2012	93.3	45.1
3						

Figure 13-4: CSV Output
Top: Tabular Format; Bottom: Single Row Format

Entering Data into the Input Fields

1. Click the down-arrow for the **Group** menu, located at the top of the dialog. This displays a pull-down menu of group choices:

2. Select the desired group from the pull-down menu. (For the example used in this chapter, the protocol should be created in the Cardiac group.)

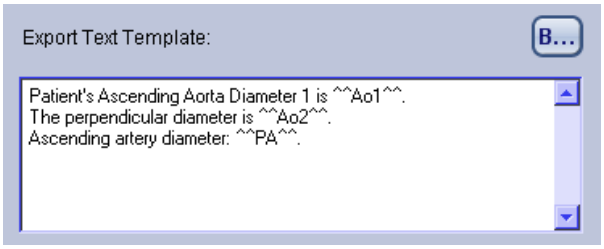
3. Type in the name of the new protocol in the **Measurement Protocol Name** text box.

4. Use the default report template displayed in the input field (**AqSimpleReport2.doc**).

5. If you want to allow others to modify the protocol, check this checkbox.

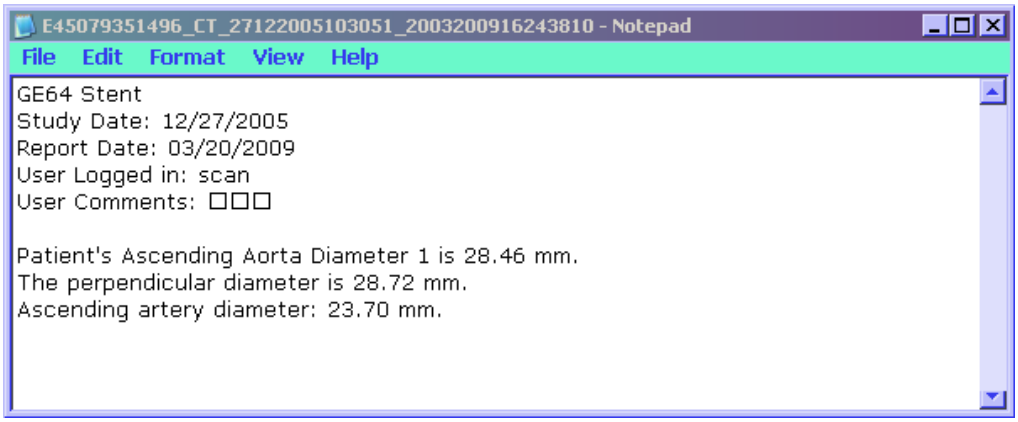
6. If you want to export measurements to the default export directory (folder), check this checkbox. Otherwise, click the **Browse** button to navigate to a folder of your choice on the iNtuition Server.

7. Enter the text to be used in exported measurement data. The following figure is an example of a template.

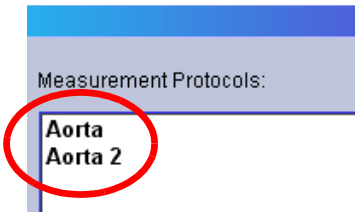


The text you add to the template will be included in the output file created when measurement data are exported. Text enclosed in the carat symbols (“^^”) are *measurement short names*, which will be discussed in the section entitled "The Measurement Definition Dialog" on page 13-8.

The template above produces the following output when the completed measurements are exported to a text file:



8. Click **OK** to create the protocol. The new protocol is now listed in the selected group (see figure at right).



Adding Measurements to a Protocol

To add a measurement to a measurement protocol, do the following:

1. Open the **Measurement Protocols** dialog.
2. Select the group from the left-hand list. The list of protocols in this group is displayed in the right panel.
3. Select the name of the protocol from the right-hand list.
4. Click **OK**. This loads the selected protocol into the Tool Panel (as shown at right).

   The protocol is currently empty because it has just been created.
5. Click the **Add** button at the bottom of the Tool Panel. This opens the Measurement Definition dialog (see figure below).

The Measurement Definition Dialog

Description of Input Fields

The following is a description of each field in this dialog:

- Long Name - This name is the ID for the measurement. *The name should be standard throughout all measurement protocols*, for the body part and measurement being named. Whenever this particular

measurement is needed in any protocol, it should always have the same name so that any software that accesses measurement data will recognize and accept this measurement.

- Short Name - The short name is used for easier labeling on the image. It is an alias for the long name and has an identical value.

- Measurement Type and Property List - This is where you define the actual measurements. When you click in the field, a drop-down menu is displayed where you can select the type of measurement you need (distance, angle, area, etc.). (See figure at right.)

- Swappable With - This is used for EVAR measurements only. See Chapter 14: "Endovascular Aortic Repair" for more information.

- Mandatory for Report - Check this box if you want to define this measurement as required for the report. If this is checked, you will not be able to generate a report for this protocol until this measurement is completed.

- Description - The description allows you to provide exact instructions for obtaining the measurement, so that everyone who uses this tool will follow the same standardized procedure.

- Auto Complete

  This is used only for the **Centerline Length** property of **Path Length**. When this is enabled, you can click on the centerline (at any point), draw a straight line toward the end point, and release the mouse on the end point, and the length along the centerline between the start and end points will automatically be calculated.

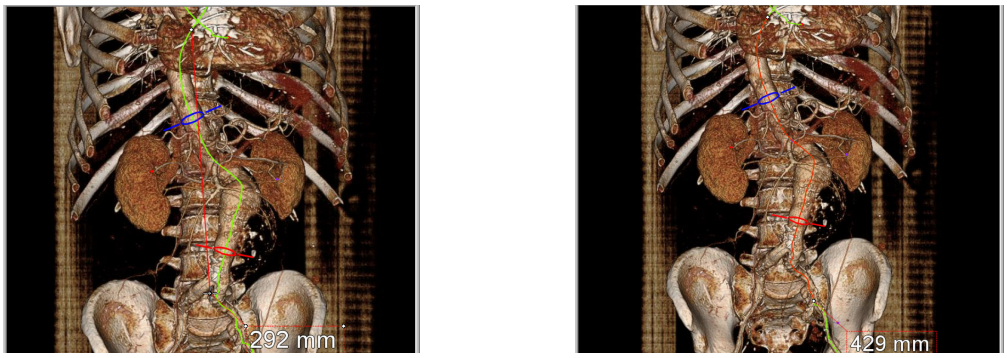


Figure 13-5: Left: Drawing Path; Right: Path Fitted to Centerline

- Begin Point and End Point

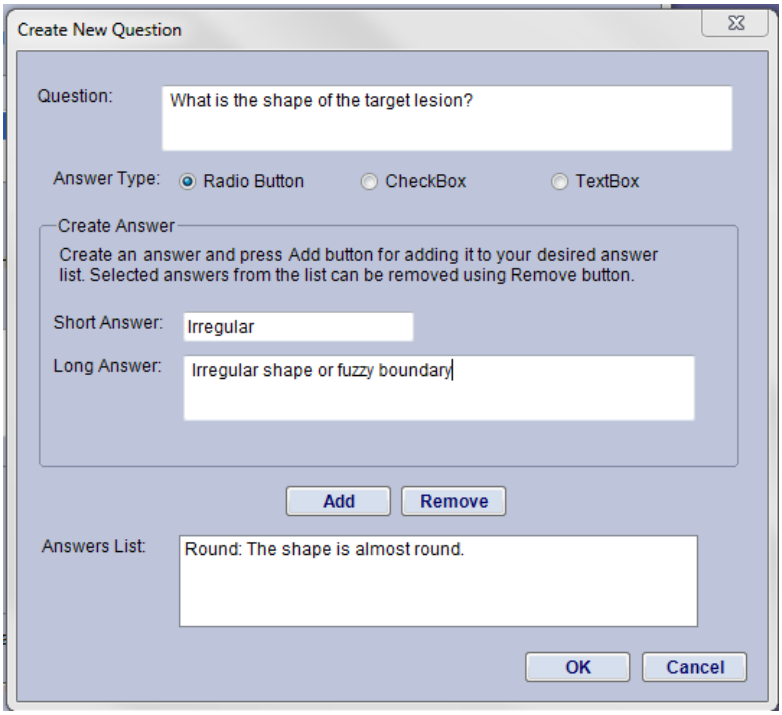
  The beginning and end points of the length being measured along the centerline.

Question-Answer Selections

This is a special kind of instruction that allows you to add a question-and-answer step to the measurement protocol. This format allows you to specify one question and then create a list of possible answers. When the measurement protocol is performed, one of the answers will be selected.

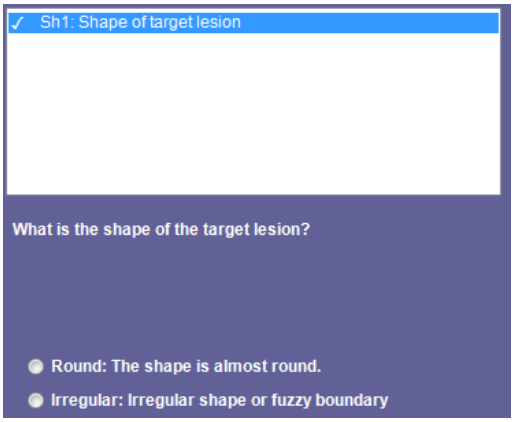
To create a question-answer instruction, do the following:

1. In the **Type** section, select **Question-Answer** from the menu. The **Create New Question** dialog is opened.



2. Enter the question in the **Question** input box.
3. In the **Create Answer** section, enter the first possible answer, in both short and long-answer forms.
4. Click **Add** to add the answer to the **Answers** List.
5. Repeat steps 3 and 4 until all potential answers have been added.
6. Click **OK** when done.

The question and answers appear in the measurement protocol as shown below:



Measurement Specifications

In this field, you can select the measurement type from a drop-down menu. To do so, click the phrase "(click to add)" located below the **Type** column header in the **Measurement Type and Property List** section (see image at right).

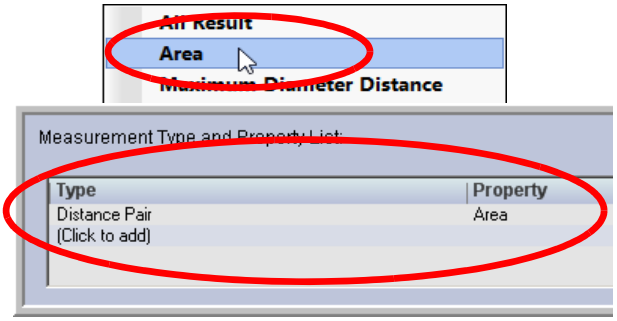
Selected Components

Some of the measurement types have sub-menus containing a list of properties associated with that measurement. For example, the **Distance Pair** measurement item in the menu has the sub-menu shown at right, which lists the measurement's properties.

The property menu allows you to do several things:

- Add a measurement to the protocol that will show just one of the values from the property list.

  To add one property to the protocol, select the desired property from the sub-menu:



  The measurement type and property is assigned to this measurement.

- Add a measurement that contains all of the values from the property list.

  To add all properties from the property list, select **All Result** from the property list sub-menu.

- Add any number of values from the property list.

  To select any number of measurement components from the property list, first choose **Selected Components** from the sub-menu. A dialog box is opened

- Export measurements separately.

  This feature allows you to export the selected components separately or as one measurement. The **Select Measurement Components** dialog is opened.

  For example, suppose you created two new measurements, "Distance Pair - Export Separately" (Short name L1) and "Distance Pair - Export As One Measurement" (L2). In the dialog pictured above, all five components would be selected in each measurement, but in L1, the **Export the measurements separately** box is checked, and in L2, it is unchecked.

  After obtaining the measurements and then exporting the protocol to a CSV file, you can open the file in Microsoft Excel to see the results.

In the following figure, the L1 measurement lists five separate measurements, whereas the L2 measurement contains all five measurements in one field.

AAA1			
Study Date: 04/26/2005			
Report Date: 04/26/2012			
User Logged in: scan			
User Comments:			
L1_Area	Distance Pair - Export Separately_Area	5.5	cm
L1_D1	Distance Pair - Export Separately_Maximum Diameter D	29	mm
L1_D2	Distance Pair - Export Separately_Minimum Diameter D	24.4	mm
L1_AvgD	Distance Pair - Export Separately_Avg.Diameter	26.5	mm
L1_Per	Distance Pair - Export Separately_Perimeter	86.5	mm
L2	Distance Pair - Export As One Measurement	Area: 5.50 cm D1: 29.0 mm D2: 24.4 mm AvgD: 26.5 mm Per: 86.5 mm	

Description

Write standard instructions on how to obtain the measurement in the **Description** text box. These instructions will appear in the Tool Panel during use, such as for EVAR measurements.

Editing Standard Measurement Protocols

TeraRecon standard measurement protocols are read-only. If you try to make a change to a non-editable measurement protocol, a dialog is posted where you can save your changes to a new measurement protocol and group. The new group can be edited.

Exporting Measurement Protocols

To export a protocol, do the following:

1. Open the Measurement Protocols dialog.
2. Select the group from the list on the left.
3. Select the protocol from the list that is displayed on the right.
4. Click the **Export** button. A Windows **Save As** dialog is displayed.
5. Enter the file name in the **Save As** dialog.

Chapter 14 Endovascular Aortic Repair

Topics in this chapter:

The Endovascular Aortic Repair (EVAR) Workflow provides tools for taking the required measurements for a stent.

Opening a Study for EVAR

To load a study for EVAR, do the following:

1. From the Patient List, select a study or series appropriate for the analysis, such as a CTA examination exhibiting an aortic aneurysm.
2. Load the study or series into the EVAR Workflow by doing one of the following:
   - Right-click on the study or series, and select EVAR from the pulldown menu.
   - Select the study or series, click **Load** in the Data Management Tool Buttons (located in the middle-left of the screen), and then click **EVAR** from the workflow buttons.

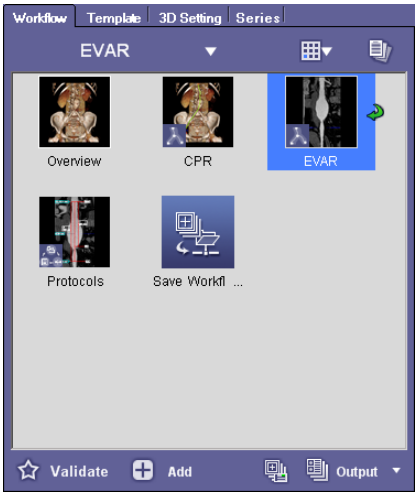
The study is opened in the 3D Viewer, using the EVAR Workflow.

The EVAR Workflow

The EVAR Workflow guides you through the steps of preparing for and then performing stent planning.

Elements of the EVAR Workflow

- **Overview:** Displays the study in the standard 2x2 layout, allowing you to view the image in 3D and MPR modes.
- **CPR:** Displays the study in 3D mode and allows you to draw and edit centerlines through the vessels where the stent will be placed.
- **EVAR:** Displays the data in 3D, sMPR and cross-section images.
- **Protocols**: Opens the Measurement Protocol tool, which allows you to select the appropriate measurement protocol from a list. The measurement protocol contains detailed instructions for obtaining the measurements required by the stent vendor and type of stent.



The CPR Element

The CPR element of the Workflow is used for adding and editing the centerlines needed for the stent. When you click on the CPR element, the 3D image is displayed in 1x1 layout, ready for adding centerlines. Centerlines can be copied between series in the same study.

Studies containing Advanced Processing

If you have loaded a study that has had centerlines added by Advanced Processing (APS), the data already contains a centerline through each vessel. In addition, the centerline button in the APS Functions, located in the Top Toolbar, is displayed in color.

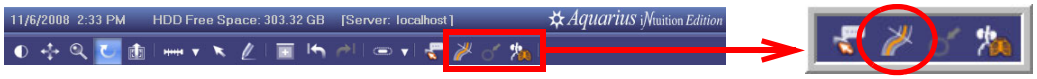
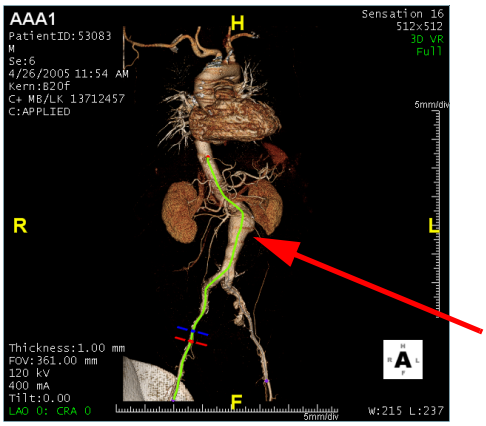


Figure 14-1: APS Centerline Function

To see the centerlines in the image, click the centerline button (circled in Figure 14-1). The centerline of each vessel is highlighted in green when you pass the mouse over that vessel:



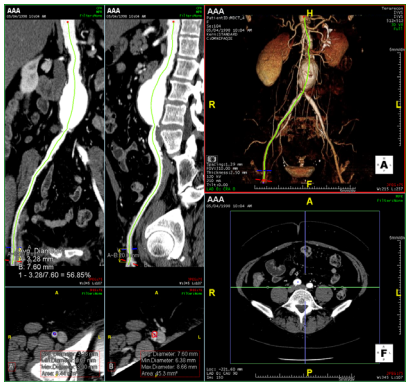
To display the vessel in CPR view, click on the vessel.

Studies With No Advanced Processing

If the study you have loaded has not had centerlines added by Advanced Processing, centerlines must be added manually. To add a centerline, do the following:

1. Position the mouse over the first vessel where you want to add a centerline.

2. Shift-click to add the centerline. This automatically opens the CPR view for that vessel, as shown in the following figure:



3. Repeat steps 1 and 2 to draw a centerline on another vessel, if needed.

Editing Centerlines

You can edit a centerline, whether it was created manually or by Advanced Processing. To edit a centerline, do the following:

1. Press the Shift key and pass the mouse over the centerline to be edited. A set of dots, which are editing control points, are displayed on the centerline.

Note: You can perform the editing on the 3D image or on one of the CPR or MPR windows.

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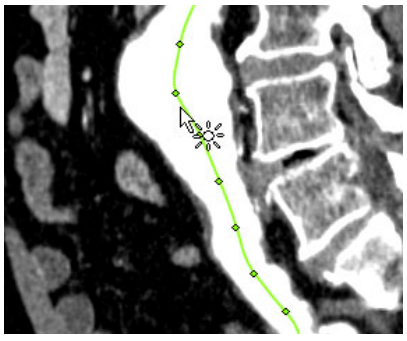
2. To make the centerline smoother or to place it in a more appropriate position, drag a portion of the centerline by clicking on a control point and then moving the mouse.



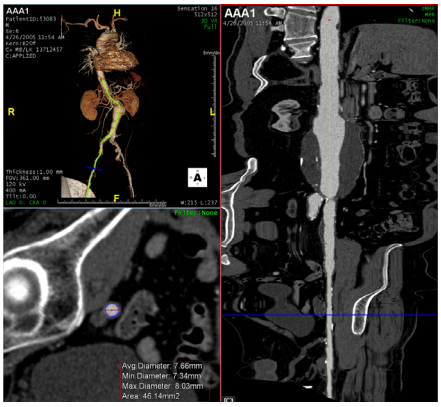
3. Click on any point along the centerline to add new control points.

4. If the centerline looks too rough or bumpy, you can use a CPR tool to smooth it out.

See "Smooth" on page 3-36 for more information and instructions.

When you are satisfied with the centerline in the vessel or vessels required for the stent, click the EVAR Workflow element to begin taking measurements.

The EVAR Element



When you click the EVAR workflow element, the study is displayed in 3D VR view, straightened MPR (sMPR) view, and cross-section view. These are the images you will use to take measurements.

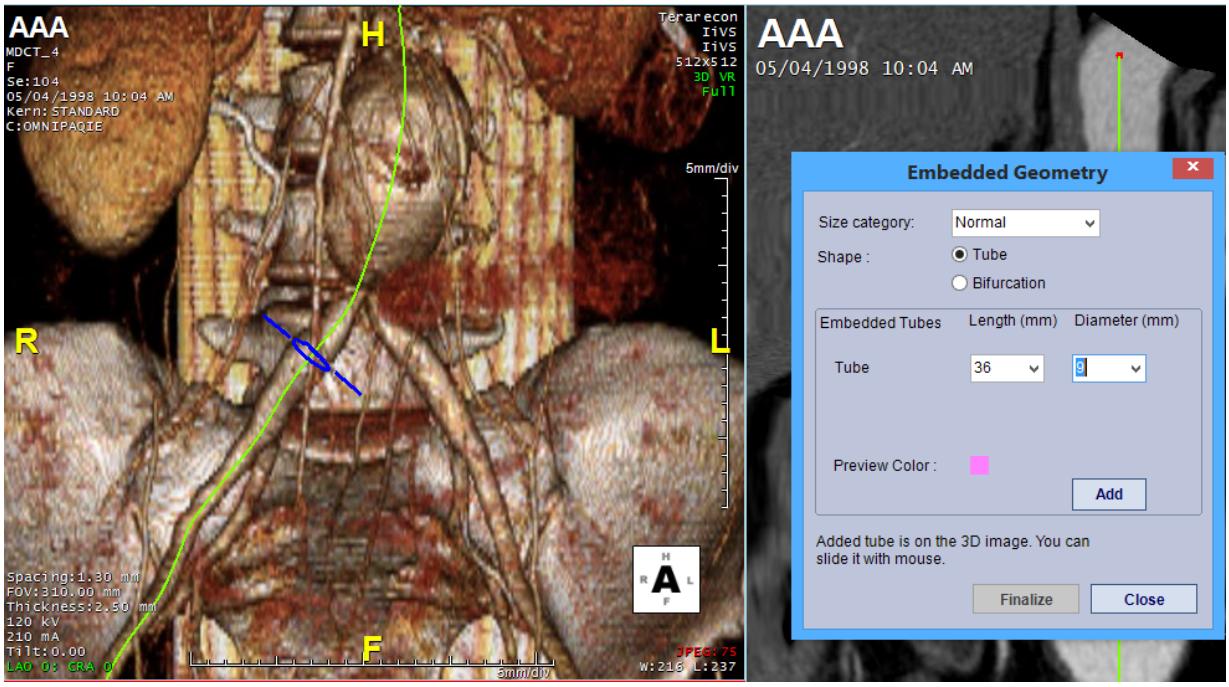
Embedded Geometry

This feature allows you to model and plan out the manufacturing of a medical implant device.

To embed geometry, do the following:

1. Create a centerline using the EVAR workflow element.
2. Right-click and select **Embedded Geometry** from the drop-down menu. The **Embedded Geometry** dialog is opened (see figure below).
3. Select a **Size** category from the menu (**Normal** or **Small**).
4. If the device being planned for contains a bifurcation, select **Bifurcation** as the shape. Otherwise, select **Tube**.
5. Specify the measurements for the embedded tubes to ensure that they fit properly within the vessel.

You can use the preset values for the **Length** and **Diameter** of the tubes (listed in each menu, respectively), but you can also customize them if you know the values already.



Once you have determined the customized embedded tube measurements, select **Add** to embed the geometry into the vessel(s). This will display as shown in Figure 14-2.

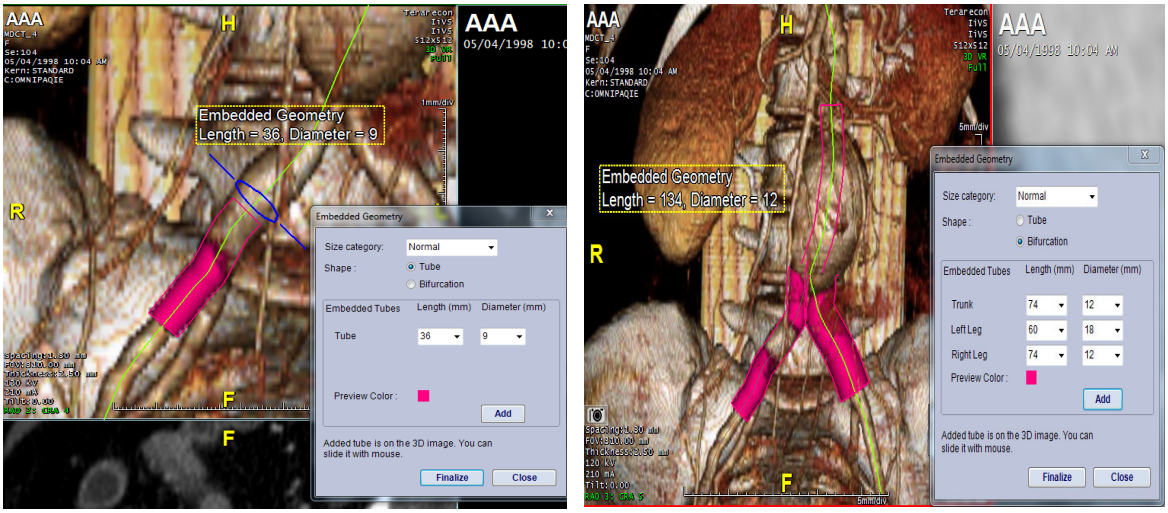
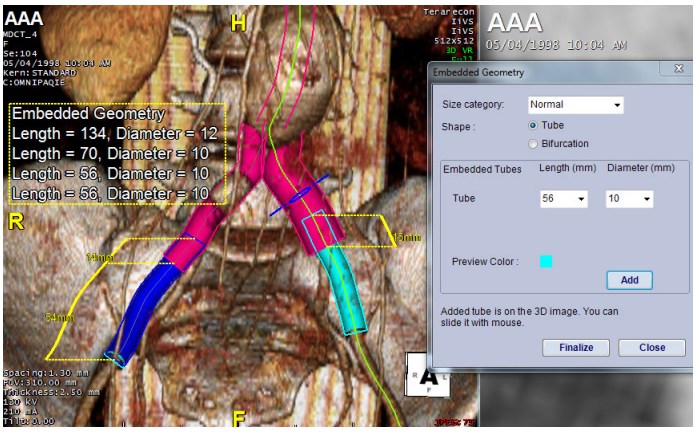


Figure 14-2: Left - Tube Geometry; Right - Bifurcation

You can also add additional parts to the existing model. After you are satisfied with the displayed measurement values for the additional part, select **Add**. You can add an unlimited number of new parts before clicking the **Finalize** button. Once you have clicked **Finalize**, you can no longer edit any parts.

When new parts are added, any overlap occurring between parts will be identified clearly on the image. A measurement showing the length of the overlap is also shown.



After all geometry has been embedded, you must finalize the measurements to save them as a series. Once you are satisfied with the positioning and measurements of the parts, select **Finalize**.

Note: You will no longer be able to edit the parts once they are finalized.

CAUTION! The embedded geometry is a mathematical model with limited capability. It is not intended to predict the implantation device's shape or location, and is not intended to be used as a decision-making tool for the procedure.

The Protocols Element

The EVAR workflow element opens the Measurement Protocol tool in the Tool Panel, which allows you to select a stent vendor and type. Each measurement protocol contains detailed instructions for taking the required measurements.

Note: Supported templates may vary depending on your software versions.

For a full description of the Measurement Protocols, see Chapter 14: "Endovascular Aortic Repair".

Opening an EVAR Measurement Protocol

Click the down-arrow in the upper-right corner of the tool panel. A dialog is opened that allows you to select which type of measurement protocol to load.

1. Select **EVAR** from the **Groups** column on the left. A list is displayed on the right.
2. Select the protocol required from the list in the right panel, and click **OK**.

   The selected protocol is displayed in the Tool Panel, as shown in Figure 14-1 on page 14-2.

The top (white) panel contains the list of measurements you need to obtain. Each separate measurement is listed on a separate line.

When a measurement is selected in the top panel, the instructions for obtaining that measurement appear in the bottom (blue) panel.

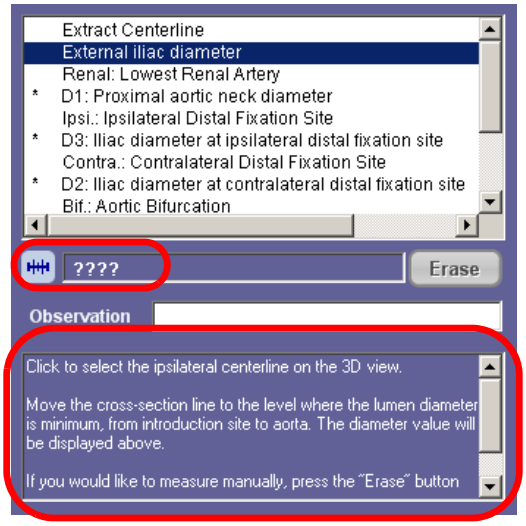
General EVAR Measurement Protocols

The General EVAR protocols allow you to obtain measurements first, before deciding which vendor to use. Two general EVAR protocols are available, Renal Donor and Thoracic Aortic Aneurysm (see the following image).

Obtaining Measurements

1. The very first item in the top panel, provided by the vendor, is **Extract Centerline**. If you have not done so yet, you can click on the **CPR** workflow element to extract centerlines on the vessels you are measuring.

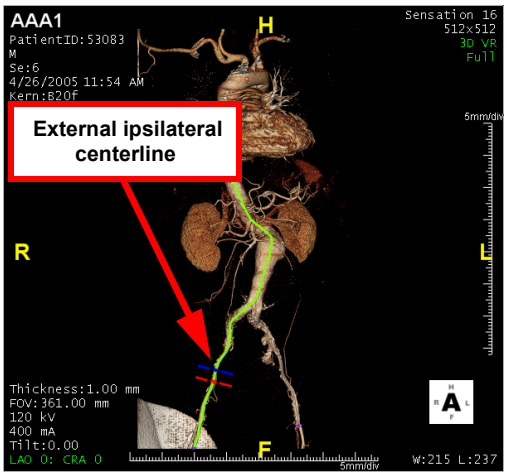
2. The second item, **External iliac diameter** is the first actual measurement you will obtain. Click on this item to display the instructions in the bottom panel, as shown in the following figure:



The measurement value, circled in light blue in the above image, has not been filled in yet. This is indicated by the four question marks in the value field. When you complete this measurement, the value will be displayed in this field.

Instructions

1. On the 3D view, click the ipsilateral centerline to select it. The cross-section line is displayed on the centerline:



2. Move the cross-section line to the position between the introduction site and the aorta, where the lumen diameter is smallest. The diameter of the cross-section is displayed in the lower-right corner of the cross-section view.

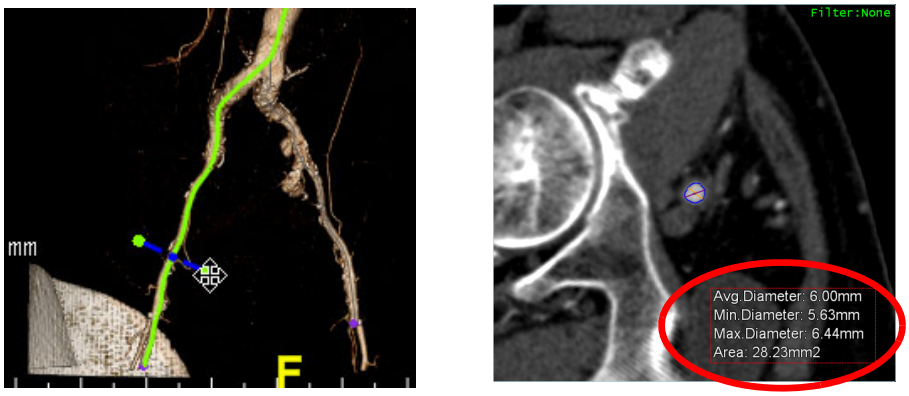


Figure 14-3: Left - Moving the Cross-section line; Right - The Cross-section View

3. Confirm that the diameter value is displayed here.

Capturing the Measurement

You can capture measurements, along with the image that contains the measurement result, to be stored within the measurement protocol. The image can then be exported with the measurement results at a later time. (See "Exporting Measurement Data" on page 14-25 for details.)

To capture a measurement, do the following:

1. Click the camera icon (circled in the previous image). The **Capture Preview** window is displayed (see Figure 14-4 on page 14-9).

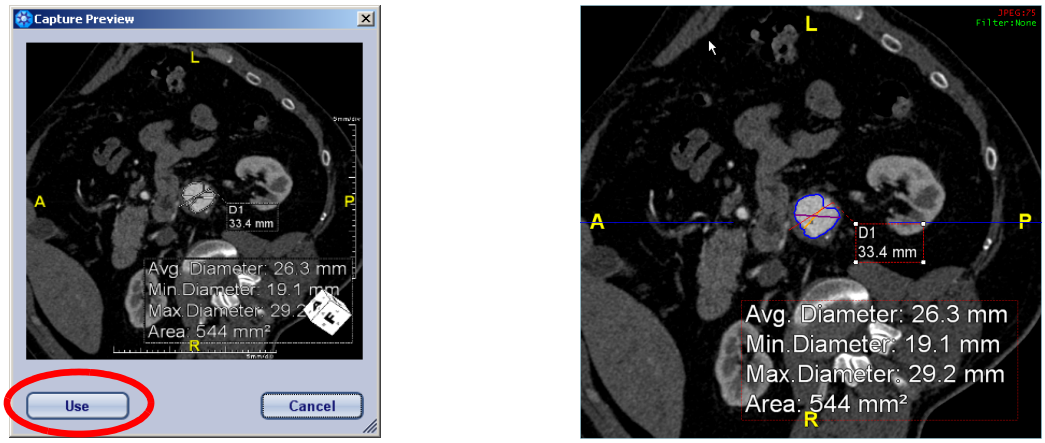
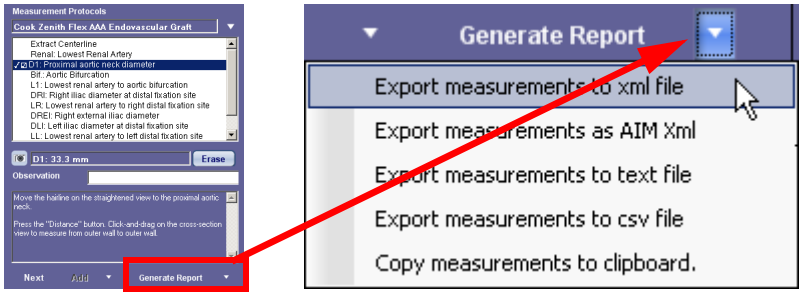


Figure 14-4: Left - Capture Preview Window; Right - Measurement on Cross-Section View

2. To save the preview image, click the **Use** button (circled in Figure 14-4).

3. To export the image along with measurement data, click the down-arrow to the right of the **Generate Report** button, in the lower-right corner of the Measurement Protocols tool panel.

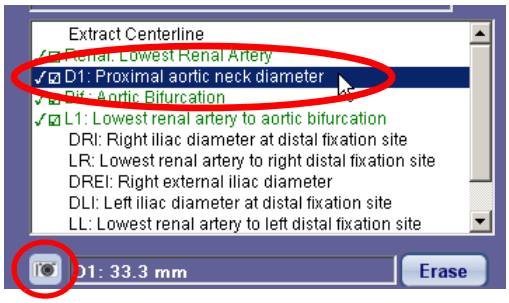


An XML file containing all the measurement data is exported to the pre-configured export folder (see "Measurement Settings" on page A-45 for more information). In addition, captured images of each measurement are exported to the same folder.

If a measurement that has already been captured is later discovered to be incorrect, you can go back to the image in the main window and perform the appropriate changes to the measurement. You can also zoom or pan the image, or change the window level. All of these edits can be recaptured.

To recapture the measurement, do the following:

1. Click on the measurement in the Measurement Protocol. Then click the camera icon.



The Capture Preview window is displayed, containing the edits.

2. Click **Use** if you want to capture the updated measurement. When the measurements are exported to an XML file, the updated measurement will be exported instead of the original capture.

When you have completed the instructions for this measurement, click the following item on the list, or click the **Next** button (in the lower-left corner of Figure 13-1 on page 13-2). The completed measurement is displayed in green text.

sMPR Centerline Tools

Right-click on the sMPR view centerline to access some useful commands and features for obtaining measurements. The menu items are as follows:

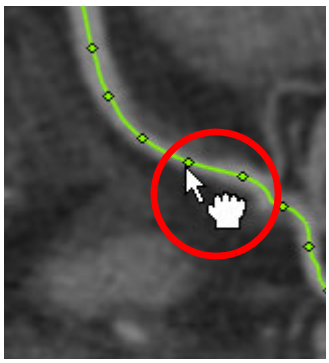
- Mark Here - Place a mark at this location along the sMPR centerline. This function places a red horizontal line at this location, but you will need to enter a name for the mark, if desired. To do so, right-click on the mark and select **Assign Name**. A text-input box is displayed where you can type in the name.

- Delete to the Red Dot - Remove everything in the selected branch above the selection point (from the selection point to the red dot).

- Delete to the Purple Dot - Remove everything in the selected branch below the selection point (from the selction point to the purple dot).

- Delete Branch - Remove the entire branch.

- Edit - When this item is selected, control points are added to the centerline in the CPR windows so you can edit the centerline. When you place the cursor close to one of the control points on the centerline, the curser turns to a “hand” sign (see figure below), indicating that you can move and stretch the centerline from its current position.



  When you have repositioned that section of the centerline, release the left mouse button and position the cursor on another section you want to change.

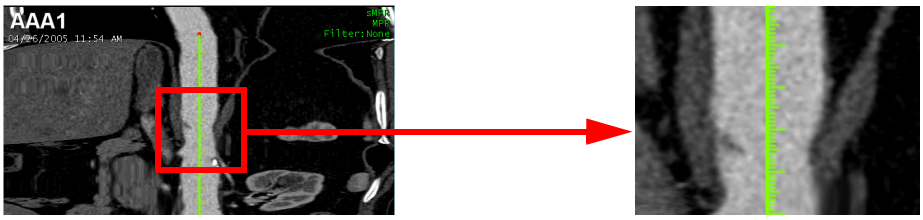
- Change Root - The start point of the vessel is indicated by a red dot. There is a blue dot at the terminating point of the vessel. This feature switches the start and end points. You can also see that the start and ending points on the vessel in the 3D window have been switched.

- Change Global Threshold From Here - If you are not satisfied with the outline drawn on the vessel, this feature allows you to change the HU threshold levels along the entire centerline, so that the boundaries of the vessel will be recalculated.

- Show Measurement Summary

  When all measurements are hidden, select this items to redisplay them. This item appears in the menu only after at least one measurement has been completed.

- Show Grid Marks - Displays grid marks along the sMPR centerline. These marks provide guidance for obtaining accurate measurements (see the following figure).



- Change Grid Marks Interval - Change the distance between each tick mark on the centerline (in mm). This item appears in the menu only when **Show Grid Marks** is selected.

- Export Grid Marks Data - Output the centerline's grid mark information into a comma separated values file on local storage.

Note: This item will not appear in the menu unless the Enable Centerline Export preference is enabled. To enable the option, open Preferences, navigate to the CPR screen, and check the box for Enable Centerline Export. See Appendix A: "CPR" on page A-16 for more information.

- Reset Grid Marks - Align the grid marks with the position of the most recent measurement. This item appears only when **Show Grid Marks** is selected, and whenever a measurement has been completed, since the previous time the grid marks were reset.

Show/Hide Measurements

Right-click on a measurement to display a pulldown menu. Menu items are:

- Show/Hide Text - Show or hide the text of a measurement. The line that connects the measurement to the centerline continues to be displayed, so that if you want to redisplay the text, you can right-click on the connecting line.

Figure 14-5: Left: Right-click on connecting line; Right: Text Redisplayed

- Show/Hide All Text - Show or hide the text of all measurements. To redisplay the text, right-click on the connecting line of any measurement, and select either **Show Text** to show the text of that measurement, or **Show All Text** to show the text of all measurements.

- Hide - Hide the entire measurement, including the connecting line. To redisplay the measurment, right-click on any other measurement and select **Show All**. If there are no other measurements showing, right-click on the sMPR centerline and select **Show Measurement Summary**. (See "sMPR Centerline Tools" on page 14-10.)

- Hide All - Hide all measurements. To redisplay the measurements, right-click on the sMPR centerline and select **Show Measurement Summary**. (See "sMPR Centerline Tools" on page 14-10.)

- Show All - Redisplay all measurements.

Common EVAR Measurements

This section explains how to do some commonly required measurements.

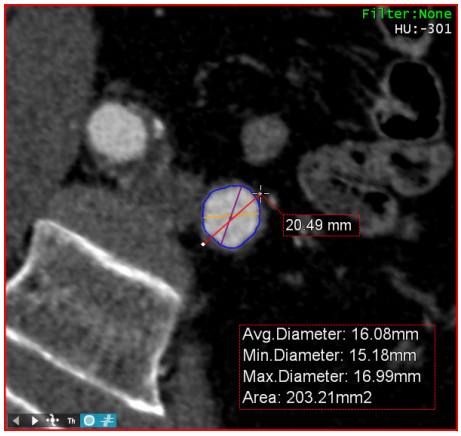
Outer Wall To Outer Wall

Some measurements call for the diameter of a vessel from outer wall to outer wall. To do this, follow these steps:

1. Move the cross-section line along the vessel on either the 3D image or the sMPR image, to find the most appropriate position.

2. Click the measurement tool in the tool panel.

3. Draw a line across the vessel, measuring the distance from the outer wall to the outer wall:



The measurement is displayed in the tool panel.

If you have obtained an incorrect measurement, click the **Erase** button to delete the value. Then redraw the measurement line.

Marking a Location

Some measurement protocols require you to mark and label certain locations on vessels. These locations may be used in a later step, for example as end points in a distance measurement.

1. Find the location to be marked.

You can use the 3D, sMPR or CPR image to find the location needed. To see the CPR image, right-click on the sMPR image and select **CPR** from the menu. After positioning the cross-section line, you can return to the sMPR by right-clicking on the CPR image and selecting **Straightened MPR**. Whenever you move the cross-section line in one of these windows, it is moved to the same position in all other views.

2. Click the Marker Tool symbol (circled in the image at right) in the Measurement Protocols Tool.

3. Click the horizontal blue line (which indicates the position to be marked) on the sMPR view.

   The label for this location is automatically added, as shown in the following figure:

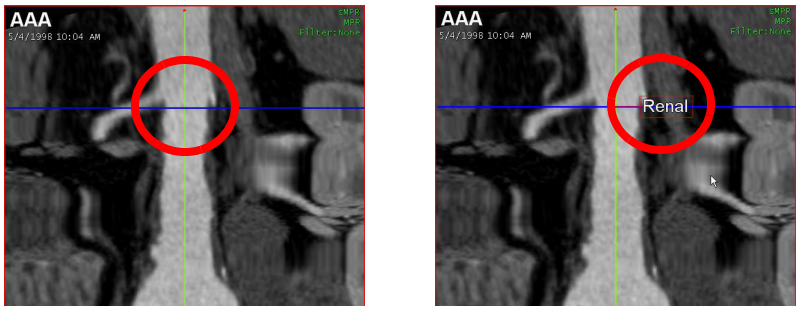


Figure 14-6: Left: Marker Tool; Right: Label

Path Lengths

Several important measurements involve distances from one point on a vessel to another, called the *path length*. Prior to measuring a path length, you will have been required to mark locations on the vessel, which will now serve as end points for the measurement.

Measuring the Path Length

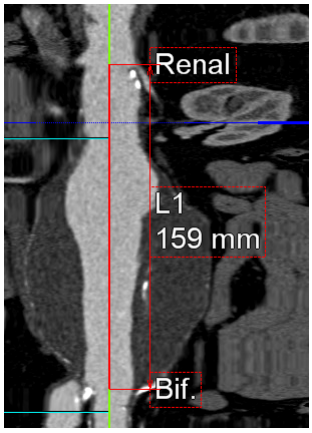
Note: Path Length measurements can be tracked in the Finding Viewer (see "The Findings Workflow" on page 16-1 for information about the Finding Viewer).

First, click the **Distance** tool (circled in the image at right).

If there is already a marker or other measurement on the image defining the end point, do the following:

1. On the sMRP image, click on the starting location, and hold down the mouse.

2. Drag the mouse toward the end point, as shown in the example at right.



If you are not sure where to end the measurement at the time you have determined the start point, do this instead:

1. Single-click on the start point.
2. Rotate the SMPR image to find the end point.
3. Single-click again to define the end point.

Snap to Other Measurement

You can enable a user preference so that when you click on a start point with the mouse, the end point is automatically snapped to a nearby marker or measurement. This assures that you will obtain an accurate length measurement.

1. Click the **Preference** button.
2. Navigate to the **CPR Interactive** screen.
3. Enable the **Snap to Other Measurement** option and click **OK**.

See "CPR Interactive" on page A-18 for more information.

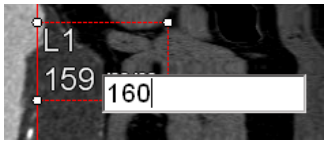
Note: To temporarily disable this “magnetic” effect for a particular measurement, hold down the *Alt* key before beginning to do the measurement.

Entering a Path Length Manually

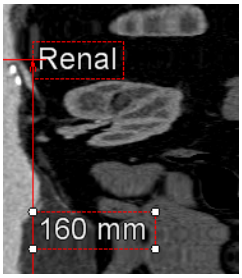
If the path length between two markers does not match the required length for the product you need, you can change the length manually.

1. Right-click on the measurement.

2. Select **Type Length Value**. An input box is opened for you to enter the correct length.



3. Press **Enter** when done. The length of the path is adjusted to reflect the new value, and the new value is displayed in the measurement.



Sac Volume

Note: The Sac Volume measurement can be tracked in the Finding Viewer (see Chapter 16: "The Findings Workflow" for information about the Finding Viewer).

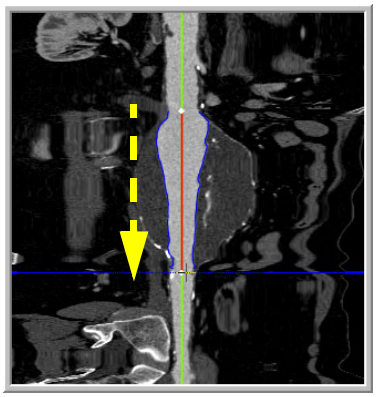
To find the volume of an aneurism sac, follow these steps:

1. Right-click on the sMPR image to display a popup menu.

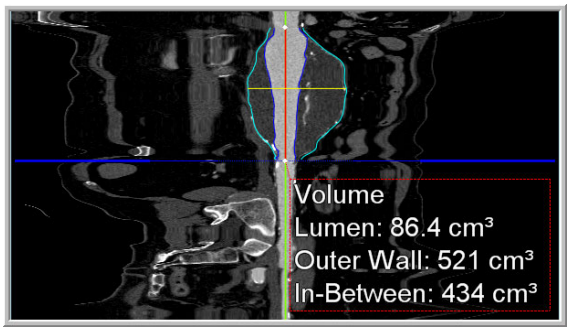
Note: Do not place the mouse directly over the sMPR centerline. Right-clicking on the centerline opens a different menu.

2. Select **Volume**.

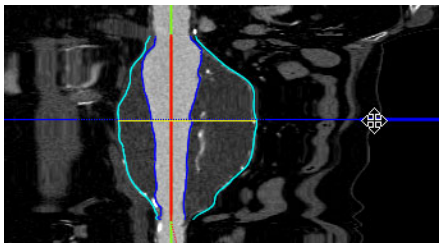
3. Drag the mouse along the centerline, from the top to the bottom of the aneurism. Release the mouse when you have reached the bottom:



The aneurysm is segmented, after which the volumes of the lumen, outer wall and in-between areas of the vessel are displayed on the sMPR image.



4. Drag the horizontal blue crosshair on the sMPR to the horizontal yellow line, which crosses the vessel at the widest point. The cross-section view shows the outlines around the lumen and the outer wall.



Sac Volume Editing Tools

If needed, you can edit the outer wall, using any of the following tools:

- Drawing a new circle around the wall
- Redrawing in freehand
- Using the nudge tool
- Edit on sMPR

These tools are described below.

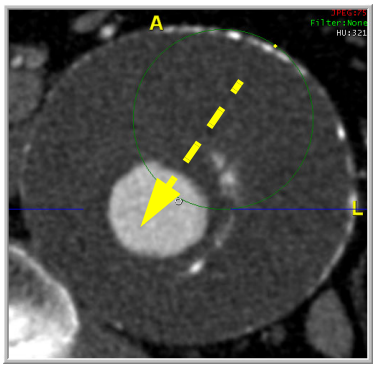
- **Draw Circle**

  Use this tool when you need to redraw the outer wall completely. The tool draws a perfect circle that may need to be adjusted using one of the other tools.

  a. Press and hold the **Ctrl** key.

  2. Click the edge of the outer wall and drag across the cross section image. A new circle is drawn on the image, which increases in diameter as you drag the mouse.

  3. When the circle matches the outer wall, release the mouse.



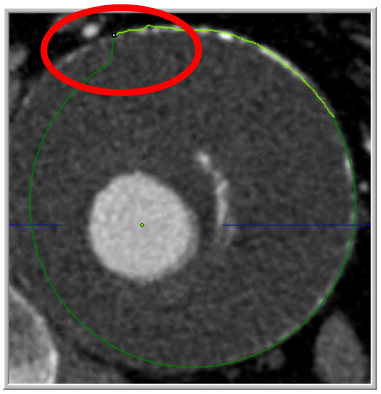
- **Redraw**

  Use this tool to redraw the outer wall freehand.

  a. Press and hold the **Shift** key.

  2. Click on the edge of the outer wall, in an area that needs to be redrawn.

  3. Drag the mouse along the correct circumference of the outer wall.

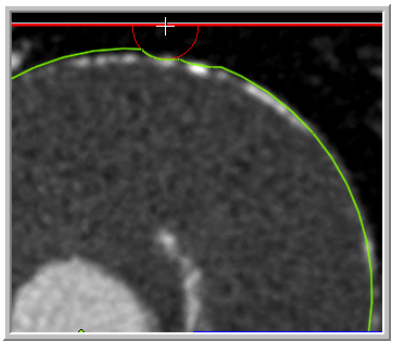


- **Nudge Outer Wall**

  Use this tool to adjust small areas of the outer wall.

  a. Press and hold the **Alt** and **Ctrl** keys together. The nudge tool (a circle) appears.

  2. Click and hold down the mouse.

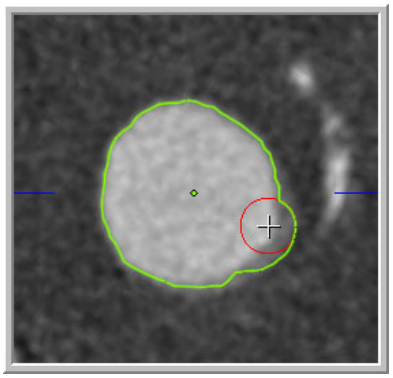


Note: When you click on a spot close to the outer wall, the nudge tool circle is small and therefore affects a small section of the outer wall boundary. Clicking further away from the wall results in a larger circle that can move larger sections of the wall.

  3. Move the mouse along the outer wall to push the outline into the correct place.

- **Nudge Inner Wall**

  This is the same as the outer wall nudge tool, except that it is used to push the wall *out* from inside the wall. To open the tool, press the **Alt** key before clicking on the image.



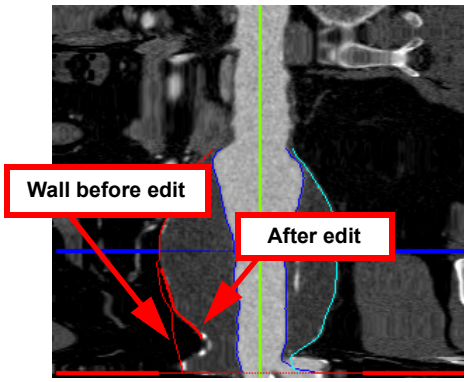
- **Edit on sMPR**

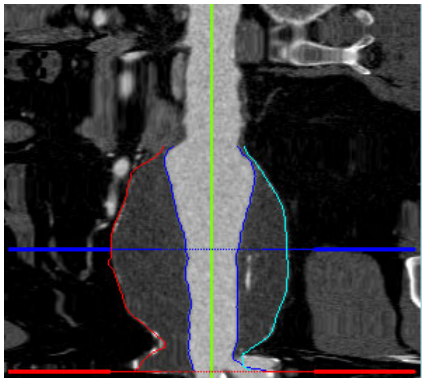
  After a volume measurement on a vessel sac has been obtained, it is possible to edit the outline around the sac using the sMPR view.

  a. Obtain the sac volume.

  2. Select edit mode in the bottom toolbar (see Figure 3-24 on page 3-32).

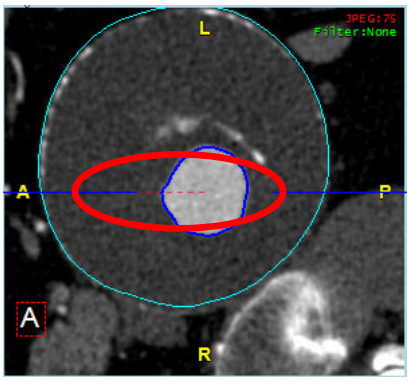
  3. To redraw part of the outline, hold down the **Shift** key and drag the mouse to draw a freehand curve along the outer wall (left). The contour is redrawn (right):



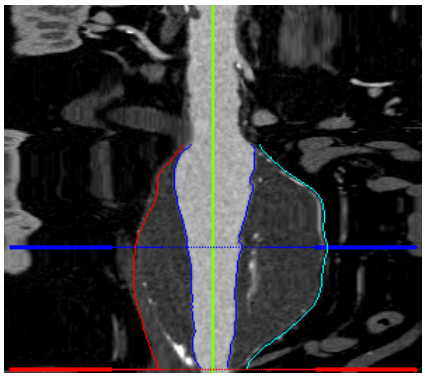


Alternatively you can draw using multi-clicks. In this case, double-click to finish drawing.

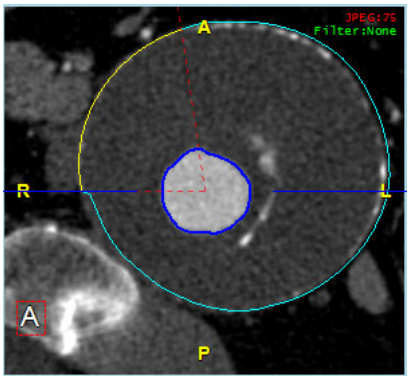
A dotted red line is shown on the cross-section view where the edit was done on the sMPR.



4. Rotate the sMPR view to show another section of the sac outline. If editing is needed, repeat Step 3.



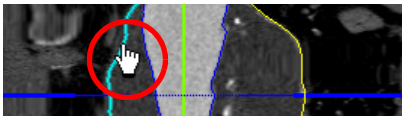
The outline contour is interpolated between the two sections:



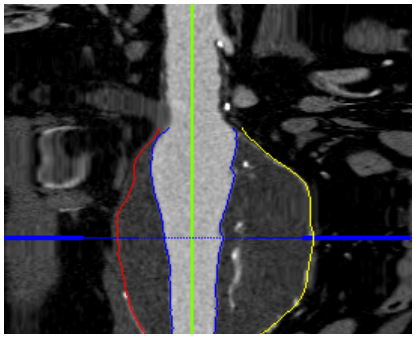
Further Interpolations

If there are sections of the outline that have already been drawn correctly, you can mark those sections as valid so they will be used as anchor points for further interpolations.

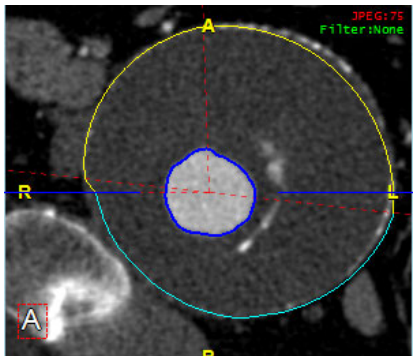
To do so, hover the mouse over the outline on the sMPR. When the cursor changes to a hand image, double-click on the outline.



The line changes to a red color to indicated that it has been edited:



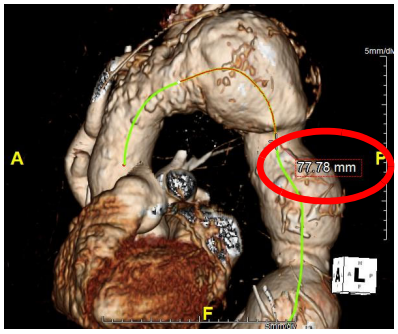
The contour between the previous edit and the current one is interpolated. The interpolated part of the contour is changed to a yellow color:



Min/Max Curved Length

Curved lengths can be measured only on 3D images. The value is obtained by first finding a distance along the centerline that has been drawn on a vessel in the 3D image.

To do this, hold down the Shift key, click on a starting point on the centerline, and then drag the mouse to the end point, which must be on the same centerline. When the mouse is released, the distance is displayed:

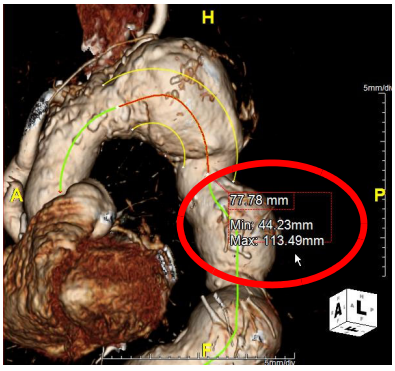


You can then show the curved length values by right-clicking on the measurement and selecting the appropriate item. There are two types of curved lengths.

Min/Max Arc

The Min/Max arc lies on an arc defined by 3 points: the start, middle and end points. This would be a good measurement for a regular aortic arc.

To display this length, select **Show Min/Max Arc** from the pull-down menu. The curved length is displayed:

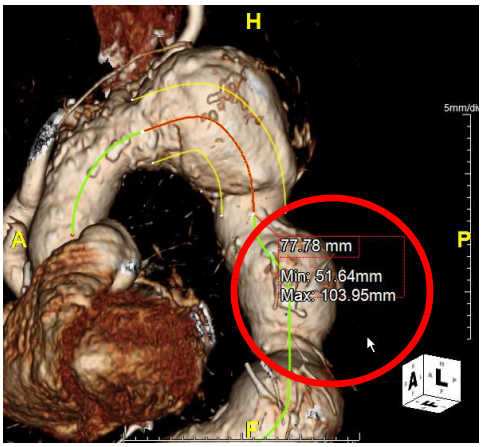


Min/Max Tube Path

The Min/Max tube path runs along beside the centerline, at a calculated distance from the centerline. The distance is the linear interpolated radius between the start and the end points. This is best used for following a tortuous vessel.

To display this length, select **Show Min/Max Tube Path** from the pull-down menu.

The curved length is displayed:



Get Greater/Lesser Curve

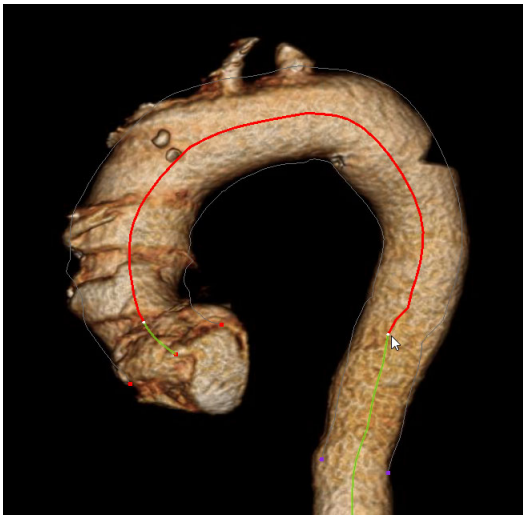
This tool is used to measure the length of the greater (outer) and lesser (inner) curves of the thoracic aorta at the site of an aneurysm, for the purpose of stent graft planning.

To identify and measure the greater and lesser curves, do the following:

1. On the 3D image, right-click on the centerline and select **Get Greater/Lesser Curve** from the menu.

   The cursor is displayed as a plus (‘+’) sign, indicating that you can draw a line along the centerline.

2. Click and drag along the centerline, covering the desired range.



When you release the mouse, the greater and lesser curve lines are calculated. To see the greater curve, hover the mouse over the outside edge of the curve. To see the lesser curve, hover over the inside edge:

Figure 14-7: Left - Greater Curve; Right - Lesser Curve

Editing the Greater and Lesser Curves

If the initial curve is not quite in the right place, you can move it with the **Edit** tool. To edit the greater curve:

1. Right-click on the greater curve and select **Edit**. Control points are displayed along the curve. These allow you to move small sections of the curve.

2. Change the position or contour of the curve in the same way that you would edit a centerline (see "Edit Centerline" on page 3-32 for complete instructions).

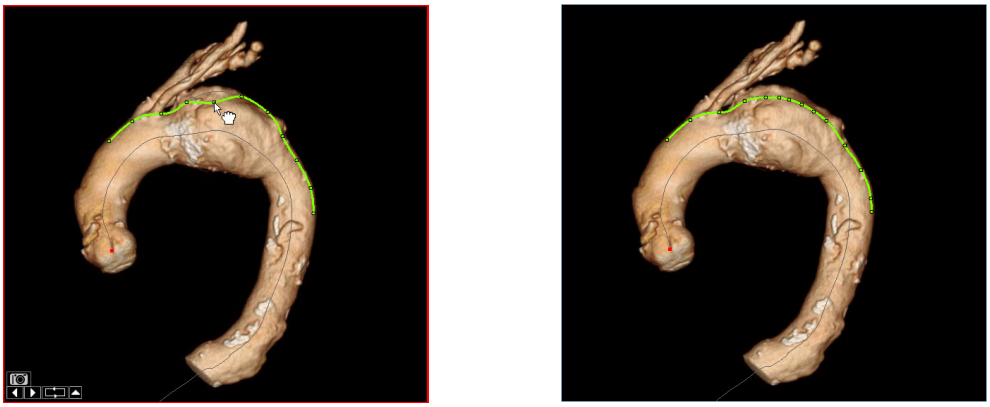


Figure 14-8: Edit Greater Curve
Left: Adjusting Control Points; Right: Curve Corrected

The lesser curve is edited in the same way.

Measuring the Greater and Lesser Curves

1. Determine the start and end points of the section to be measured.

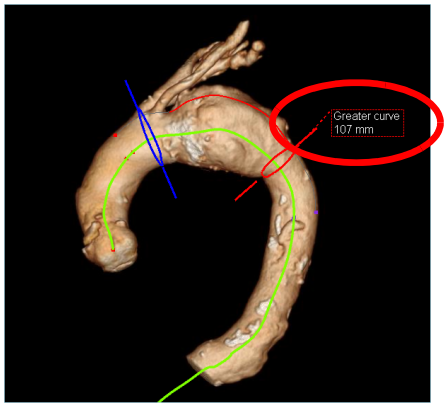
2. Click the distance measurement icon from the top toolbar.

3. Drag the mouse along the section of the greater or lesser curve from the start point to the end. When you release the mouse, the measurement is displayed on the screen (circled in the following figure).

To name the measurement, do the following:

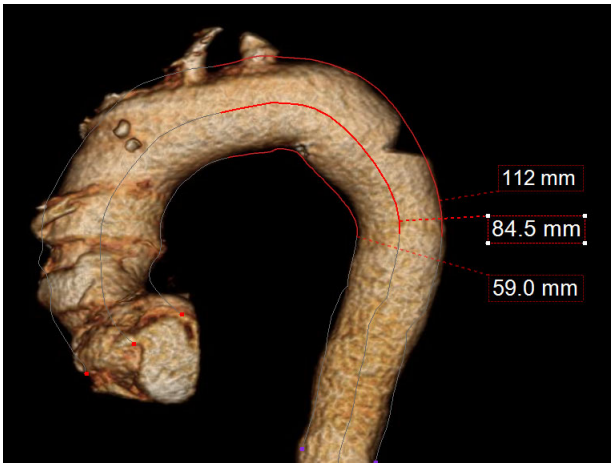
1. Right-click on the measurement and select **Assign Name** ->**Type Name**. A text input box is opened for you to type in the name.

2. Press **Enter** when done. The name ("Greater curve" in the example shown below) is then included in the measurement text.



Other Measurements

1. Measure the length of the centerline or the lesser curve that falls within the range that is being measured. These are measured in the same way as with the greater curve.



2. You can also measure the diameter of the aorta at the start and end points of the same section.

   a. Position the red cross-section line at the start point of the section.

Note: The cross-section plane is always perpendicular to the centerline, not to the Greater Curve.

---

b. Measure the diameter of the corresponding cross-section of the vessel (outer wall to outer wall). See the left-hand image in Figure 14-9.

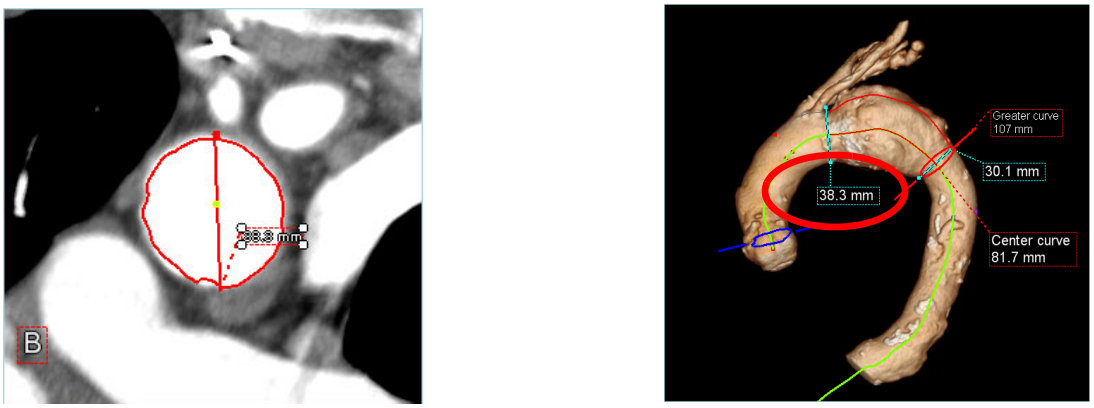


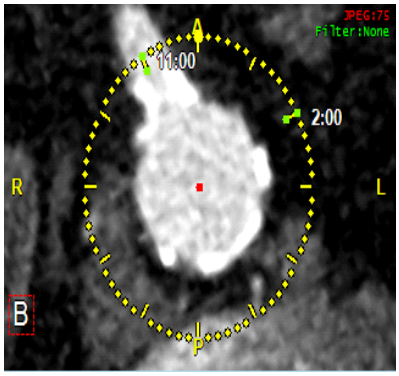
Figure 14-9: Left: Diameter of Vessel Cross-section
Right: Diameter shown on 3D Image

This measurement is also displayed on the 3D image (circled in Figure 14-9, right).

c. Repeat steps **a** and **b** for the end point of the range.

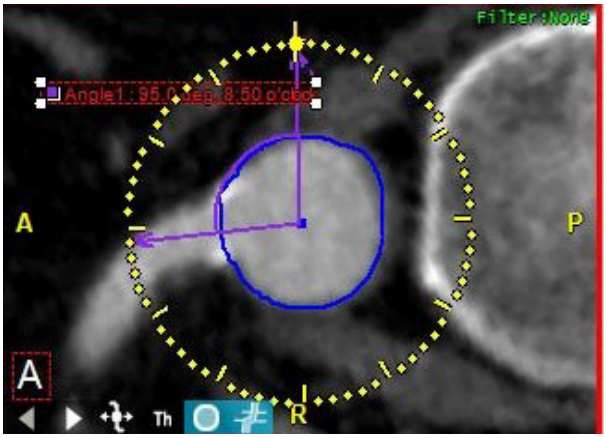
Clock Face

The 12:00 position on the clock face is can be rotated to match the rotation of the patient. To show the clock face on the cross-section view, right-click on the image and select **Show Clockface** from the menu. You can click on the clock face to derive the clock time.

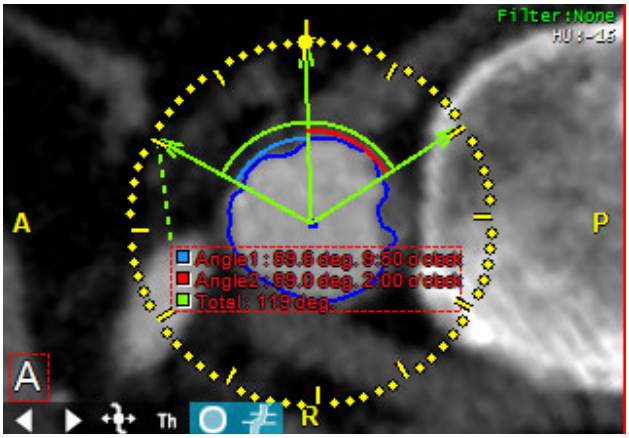


Clock Face and Angle Measurements

The **Clockface Angle** feature provides 1 or 2 angle measurements. To get an angle on a vessel, select **Show Clock Face** from the right-click menu. On the clock face, right-click and select either **Single angle clock** or **Two angle clock**. The clock measures from the click on the vessel to the 12 o'clock position. If measuring with a Two angle clock, the clock measures from both vessel clicks to the 12 o'clock position. These measures appear on the image. The measurement results and clock face can be capture for output.



Single Angle Clock



Two Angle Clock

Exporting Measurement Data

You can export measurement data obtained from specific studies, which can then be incorporated into third-party software such as RIS. To export the current set of measurements, do the following:

1. Click the down-arrow located to the right of the **Generate Report** button. A pull-down menu is displayed.

2. Select one of the output file types to contain the data. The choices are as follows:

    - XML
    - AIM XML
    - Plain text
    - CSV (comma-separated values) - useful for Excel or similar software
    - Copy measurements to clipboard

Generating a Report

When you have completed the measurement protocol, all the items in the protocol are displayed in green text.

At this time, you can generate the report that will be used to order the stent. Click the **Generate Report** button, located at the bottom of the Measurement Protocols tool panel.

Measurement fields in the report are automatically filled in with the values obtained in the measurement protocol.

Worksheet for Zenith®
AAA Endovascular Graft

terarecon

Date:	May 04, 1998	Patient ID:	MDCT_4
Hospital:	AnyScan Medical Imaging Center		
Physician Name:			
Physician Signature:			
Physician Phone #:			
Physician email:			

STEP 1
Main Body Introduction and Fixation Sites

○ Right Iliac ○ Left Iliac

External iliac (EI) measurement: 6.34 mm

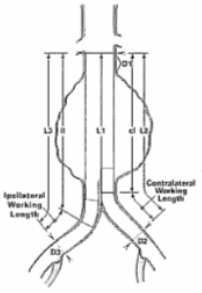
(Minimum diameter, inner wall to inner wall, from introduction site to aorta.)

STEP 2
Anatomical Measurements

(These measurements should be given in mm rounded to the nearest mm. The following CT diameters are outer wall to outer wall.)

CT table position at:

- lowest renal artery
- ≥15 mm below lowest renal artery
- aortic bifurcation
- origin cl internal iliac
- origin il internal iliac



Diameters:	D1	29.69	D2	12.67	D3	13.70
Lengths:	L1	71.24	L2	94.36	L3	89.59

D1: Proximal aortic neck diameter
D2: Iliac diameter at contralateral distal fixation site
D3: Iliac diameter at ipsilateral distal fixation site

L1: Lowest renal artery to aortic bifurcation
L2: Lowest renal artery to contralateral distal fixation site
L3: Lowest artery to ipsilateral distal fixation site

STEP 3
Main Body

- From D1, select graft diameter.
- If the choice of graft diameter is affected by other considerations, adjust accordingly.
- From L1, select the graft lengths.

Main Body (TFE) Graft Lengths		
L1	*cl Length **	*cl Length ***
○ 80-95	74	104
○ 96-110	88	118
○ 111-125	103	133
○ 126-140	117	147
○ 141-155	132	162

* main body length on contralateral side
** main body length on ipsilateral side

- Using graft diameter and cl length, complete the Main Body Order Number.

Main Body Order Number =

TFB	-		-	
		(Graft diameter)		(cl Length)

Main Body (TFE) Graft Diameters	
D1 (mm)	*Graft Diameter (mm)*
○ 18-19	22
○ 20-21	24
○ 22-23	26
○ 24	28
○ 25-26	30
○ 27-28	32

STEP 4
Contralateral Iliac Leg

- From D2, select graft diameter.
- If the choice is affected by other considerations, adjust accordingly.
- From L2 and cl length, complete the following equation.

94.36	-		=	94.36
(L2)		(cl Length)		(CWL)

- From contralateral working length, select graft length.

Contralateral Leg (TFLE) Graft Lengths (mm)		
Contralateral Working Length (mm)	*Graft Length (mm)***	*Recommended Overlap (cents)*
○ 25-41	37	1-1.5
○ 42-58	54	1-1.5
○ 59-75	71	1-1.5
○ 76-92	88	1-1.5
◉ 93-109	105*	1-1.5
○ 110-122	122*	1-1.5

* Graft length 105 and 122 mm are available in 8-12 mm diameters only
** Other considerations may affect the choice of graft lengths

- Complete the Contralateral Leg Order Number below:

Contralateral Leg Order Number =

TFLE	-	14	-	105
		(Graft diameter)		(Graft Length)

Contralateral Leg (TFLE) Graft Diameters	
D2 (mm)	*Graft Diameter (mm)*
○ < 8	8
○ 8-9	10
○ 10-11	12
◉ 12-13	14
○ 14-15	16
○ 16-17	18
○ 18	20
○ 19	22
○ 20	24

STEP 5
Ipsilateral Iliac Leg

- From D3, select graft diameter.
- If the choice is affected by other considerations, adjust accordingly.
- From L3 and il length, complete the following equation.

89.59	-		=	89.59
(L3)		(il Length)		(IWL)

- From ipsilateral working length, select graft length.

Ipsilateral Leg (TFLE) Graft Lengths (mm)		
Ipsilateral Working Length (mm)	*Graft Length (mm)***	*Recommended Overlap (cents)*
○ 25-41	37	1-1.5
○ 42-58	54	1-1.5
○ 59-75	71	1-1.5
◉ 76-92	88	1-1.5
○ 93-109	105*	1-1.5
○ 110-122	122*	1-1.5

* Graft length 105 and 122 mm are available in 8-12 mm diameters only
** Other considerations may affect the choice of graft lengths

- Complete the Ipsilateral Leg Order Number below:

Ipsilateral Leg Order Number =

TFLE	-	14	-	88
		(Graft diameter)		(Graft Length)

Ipsilateral Leg (TFLE) Graft Diameters	
D2 (mm)	*Graft Diameter (mm)*
○ < 8	8
○ 8-9	10
○ 10-11	12
◉ 12-13	14
○ 14-15	16
○ 16-17	18
○ 18	20
○ 19	22
○ 20	24

Chapter 15 The TAVR Workflow

The TAVR Workflow provides tools for taking measurements to assist with Transcatheter Aortic Valve Replacement procedure planning.

CAUTION! The embedded geometry is a mathematical model with limited capability. It is not intended to predict the implantation device's shape or location, and is not intended to be used as a decision-making tool for the procedure.

The TAVR Workflow

Opening the Best Data for TAVR

A typical TAVR study consists of two series, one of the chest, gated for the heart, and the other of the abdomen/pelvis. Both body parts can also be part of the same series.

The best phase for measuring is the systolic phase, when the diameter of the aortic valvular annulus is at its largest. Choose the best systolic phase and load it to the TAVR workflow.

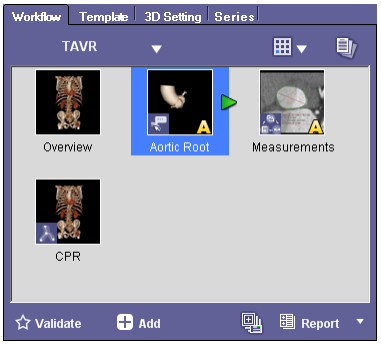


Figure 15-1 The TAVR Workflow

The TAVR Workflow guides you through the process of obtaining the image orientations, angles and measurements required for aortic valve replacement.

The Aortic Root Workflow Element

If your data includes APS results, selecting the **Aortic Root** workflow element applies the mask automatically. The image moves to a position that makes the approximate position and orientation of the aortic valve visible:

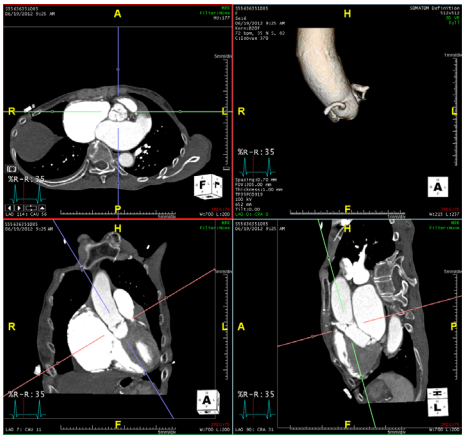


Figure 15-2 Visible Aortic Value

If you do not have APS results available, AQi performs the segmentation. You are prompted to shift-left-click on the aortic valve to provide input for the segmentation process.

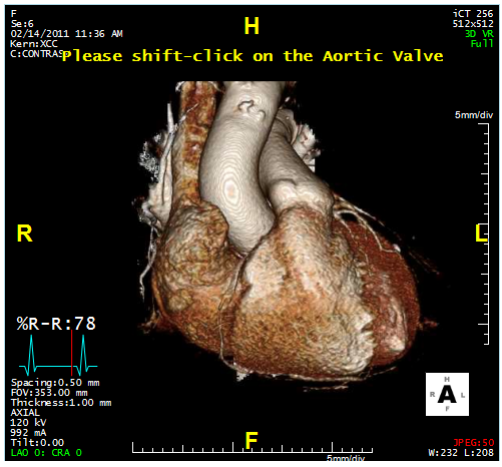


Figure 15-3 Shift-left-click on Aortic Value Overlay

Short and Long Axis Views

An easy way to access the short and long axis views is to use the **Anatomy Label** tool panel's **Orientation** feature to select a cardiac rotation. You can also show oblique images using the **Oblique** rotation selection. See "Anatomy Label Type" on page 3-80, in the Anatomy Label section for instructions.

In the short axis view, you can grab the crosshair handle to adjust the orientation for the best view of the valvular annulus. If you are in the long axis view and you wish to switch over to short axis view, simply click directly on the line and it will switch from long axis to short.

The Measurements Workflow Element

This workflow element opens the TAVR Measurement Protocol that is configured in the workflow for TAVR. The protocol is displayed in the tool panel.

Note: You can reconfigure a different TAVR Measurement Protocol to be opened when this Workflow element is selected. For more information, see "Measurement Protocols" on page 4-17 in Chapter 4.

Measurements Commonly Used for TAVR

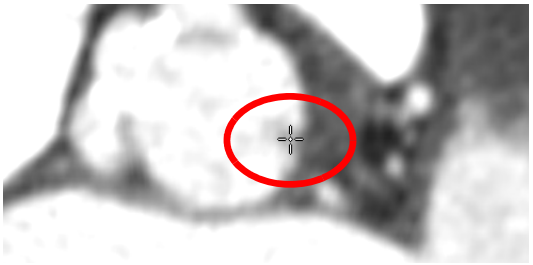
Follow the steps of the Measurement Protocol below. Instructions are included in the lower section of the tool panel. For general information about Measurement Protocols, see Chapter 13: "Measurement Protocols".

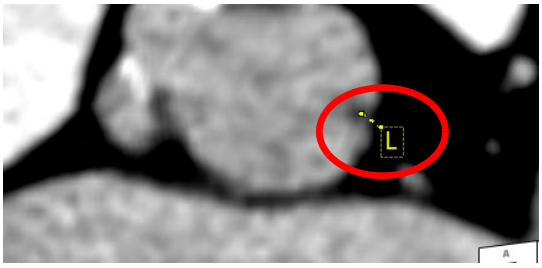
Three Landmarks of the Aortic Valve.

Mark three landmarks (on the left, right and non-coronary cusps) to define the plane that is perpendicular to the aortic root.

1. Click the triangle tool (on the left side of the tool panel, about halfway down) to activate it.

2. Scroll the mouse wheel on the axial image until the left cusp begins to disappear. At the point where it is almost invisible (see image below, left), click on it. The cusp is then labeled (right).



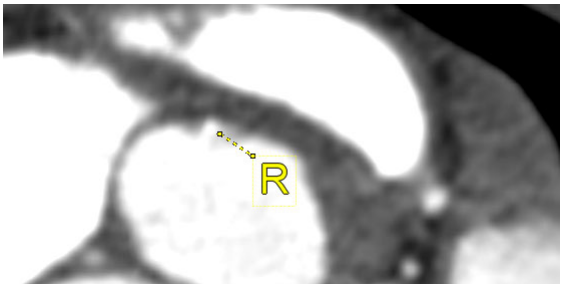


3. Scroll until the right cusp has almost disappeared, and click on that.

4. Do the same for the non-coronary cusp.

   You have now marked three points, which define a plane (see Figure 15-4).

   The three points should lie along a straight line in the 3D image.



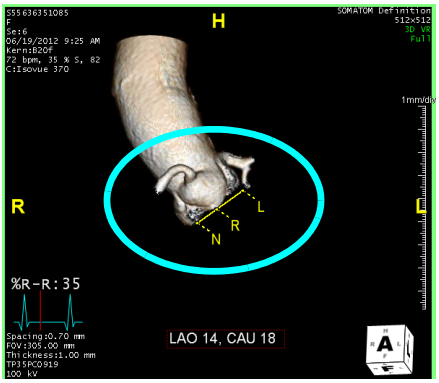


Figure 15-4 Three Cusps Marked

Note: The plane must be perpendicular to the aortic root. This is essential for a proper fit.

The Base Plane

After the three cusps have been marked, the triangle that results defines a plane called the *base plane*. This plane is indicated on the long-axis views with a dotted line, shown below. This line is always displayed, even when the axial image is scrolled.

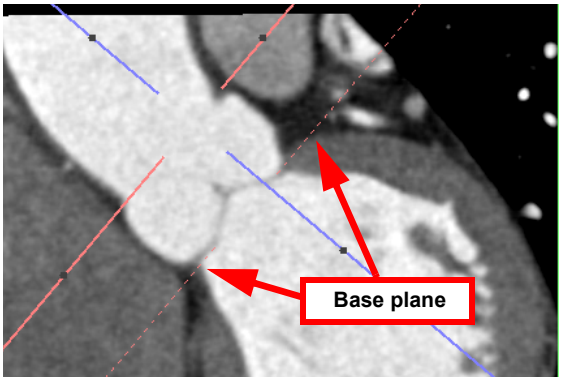


Figure 15-5 The Base Plane

Mark the Esophagus

This procedural is for predicting the approximate location of the transesophageal echocardiogram (TEE) probe during the procedure.

Note: This step is necessary only if a TEE probe will be used during the procedure.

---

1. Click the arrow tool to activate it. 
2. Draw an arrow to mark it:

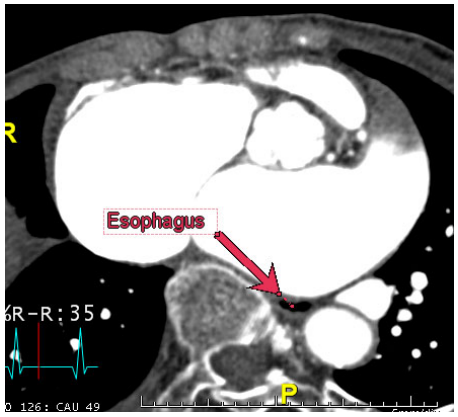


Figure 15-6 Marking the Esophagus

Setting the Angle of the C-arm.

The following three measurements are recommended to assist in determining the optimal angle for the C-arm.

- 3-cusp View

  In the 3-cusp view, the right cusp is halfway between the left and non-coronary cusp in the 3D view (see below).

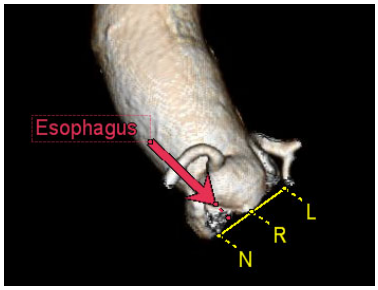


Figure 15-7 3-cusp View

  Click the C-arm tool button (see image below) to capture the angles. 

  The result is saved as follows: 

- Anterior View - Capture the RAO and LAO values:

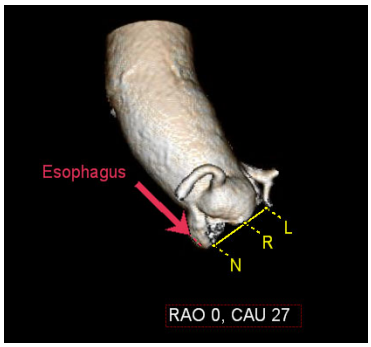


Figure 15-8The RAO and LAO values

- No-CRA-CAU view (see image below)

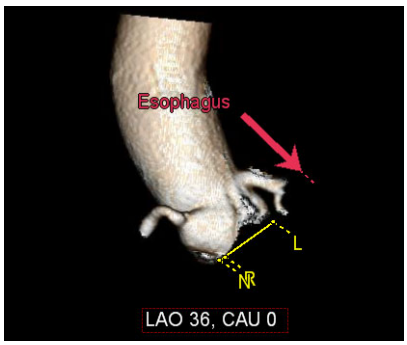


Figure 15-9The No-CRA-CAU View

The three measurements should appear in green text in the Measurement Protocol tool panel, to indicate that they are completed.

Measure Annulus Size

To obtain the distance pair measurement, the average diameter, the area and the perimeter length of the annulus:

Note: If you prefer, you can use oblique ellipse measurement tool. See "Oblique Ellipse" on page 3-148 in Chapter 3 for instructions. **Also note:** The *average diameter* is defined as the diameter of the circle that has the same area as the contour.

---

1. Scroll down until all 3 cusps disappear.

2. Activate the measurement tool, and click on the image.

The contour of the valvular annulus is drawn on the image, along with the major and minor diameters.

The perimeter length of the contour is calculated in such a way that ragged edges are smoothed out, within a configured scale. The default scale is 2mm, which means that if a feature (indentation) of the contour is smaller than 2mm, it will be smoothed out. The contour area will remain the same after smoothing.

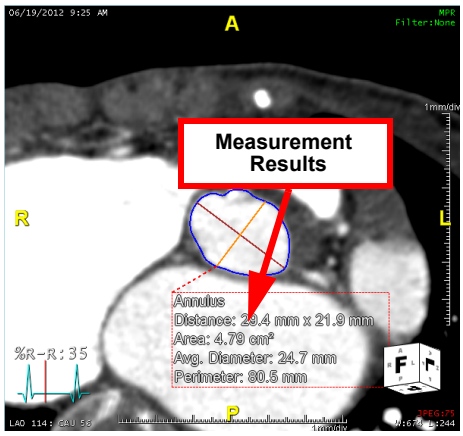
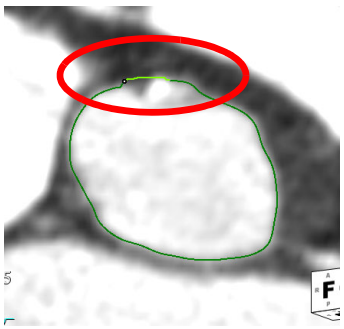


Figure 15-10 Measurement Results

You can modify the contour if desired. To edit the contour:

1. Click the measurement results.
2. The contour is displayed in green to indicate that it is selected.
3. Zoom in on the image if needed.
4. Hold down the **Shift** key and redraw the desired sections of the contour:



Smoothing and other settings for distance pair measurements can be configured using the **Distance pair options** dialog. After the measurement is obtained, right-click and select **Option**.

For a full description of the distance pair options, see "Distance Pair Options" on page 3-159 in Chapter 3.

Embedded Geometry

This feature allows you to model and plan out the manufacturing of a medical implant device. To embed geometry:

1. Follow the TAVR elements to just before **Measurements**.
2. Click the **Measurements** workflow element. The **General TAVR** measurement protocol is loaded into the tool panel.
3. In the measurement protocol, complete the **3 Landmarks - L, R, N** measurement to get an accurate valvular annulus plane.

4. Continue through each step of the measurement protocol to the **Annulus: Annulus** step.

5. On the short-axis view, perform a distance pair measurement on the valvular annulus.

6. Go to the next step, **Embedded Geometry**, to display the **Embedded Geometry (Stent Template)** dialog (shown at right).

This dialog allows you to select a part from preset measurement values, listed under **Parts Available**. Click the right-arrow between that list and the **Parts Being Used** list to move it.

If none of the preset values is appropriate for your needs, you can also create a customized part:

1. Right-click in the blank space in the **Parts Available** section.

2. Select **Create New** from the menu. This opens the **Create New Part** dialog.

   You can change the location and diameter values in the **Control Points** list.

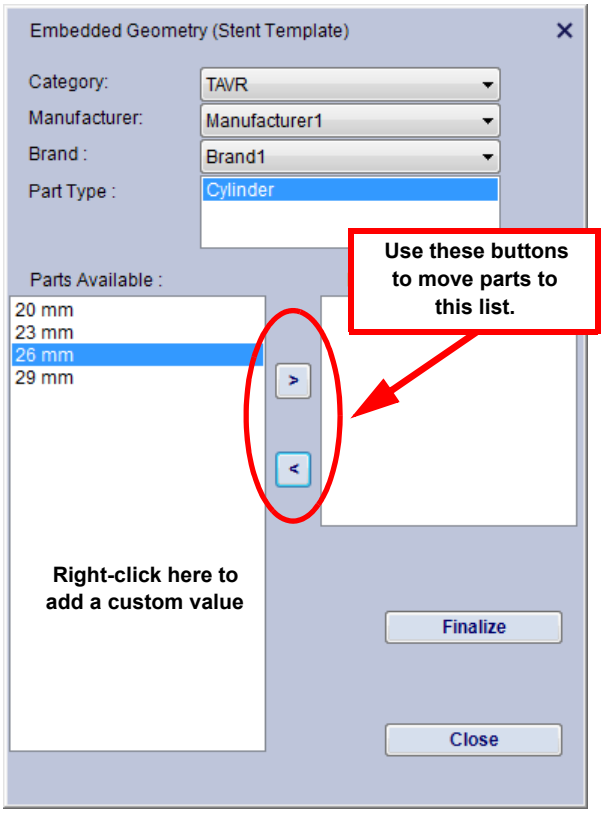
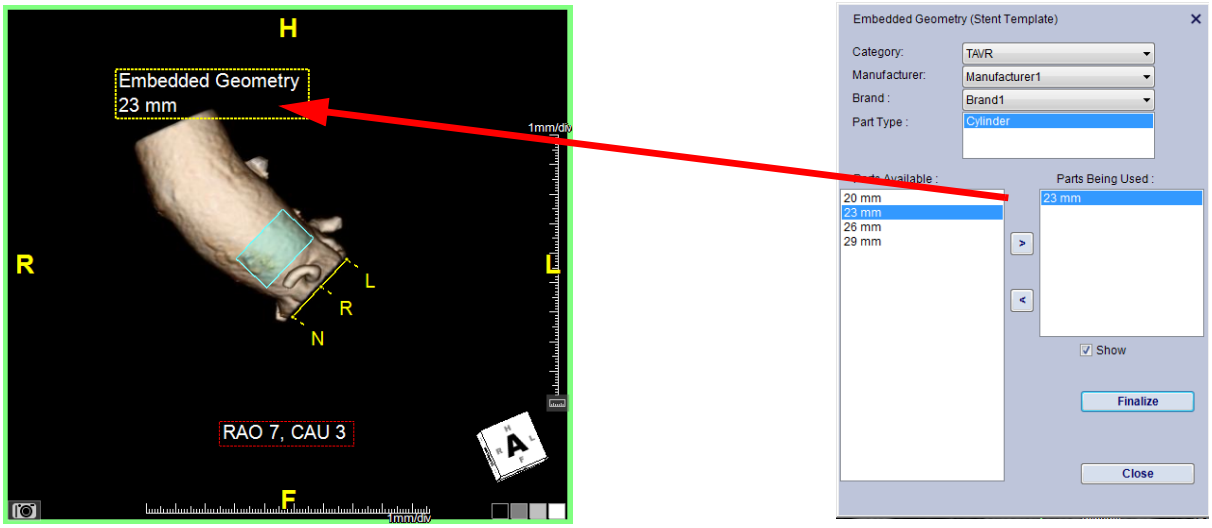


Figure 15-11Embedded Geometry (Stent Template)

Note: You must change the Part Code value to a number that is not already listed in the *Parts Available* list. It is recommended that you name the part code to reflect the diameter of the new part.

3. Click **OK** when finished. The fields in the **Embedded Geometry (Stent Template)** dialog will auto-populate, based on the part selected or created.

Once values are chosen, the geometry will embed into the anatomy. You then can move it around and edit the size to fit the anatomy.



To change any of the measurements, use the arrows in the **Embedded Geometry (Stent Template)** dialog. Once you are satisfied with the geometry, click **Finalize**.

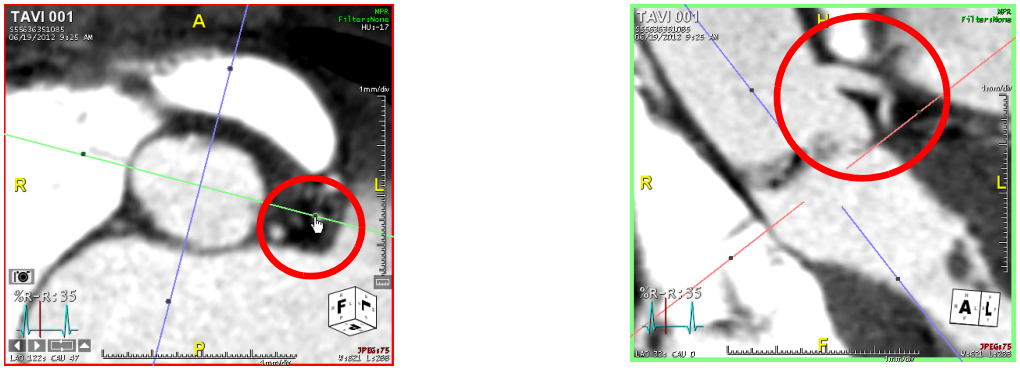
Note: From this point forward you *cannot* edit the embedded geometry. If you would like to go back and edit, you must first select Unfinalize.

CAUTION! The embedded geometry is a mathematical model with limited capability. It is not intended to predict the implantation device's shape or location, and is not intended to be used as a decision-making tool for the procedure.

Coronary Height

This measurement is essential. Its purpose is to make sure the implant does not block the ostiums.

1. Scroll the short axis view to where only the hinges of the cusps are visible.
2. Rotate the cross-hair on the short axis view so that the ostium of the left main is visible on the long axis view.



Rotating Crosshair on Short Axis View **Ostium Visible**

Figure 15-12 Displaying Left Main Ostium

3. Click the Distance tool and measure the distance from the plane perpendicular to the aortic root and the point just below the ostium.

4. Rotate the crosshair on the short axis view so that the ostium of the RCA is visible on the long axis view.

5. Click the Distance tool and measure the distance from the perpendicular plane to the point just below the ostium.

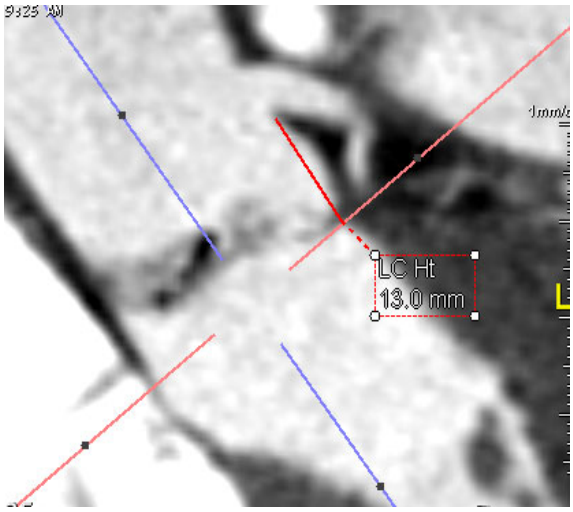


Figure 15-13Perpendicular Plane to Lower Point Measurment

Sinus, Sinotubular Junction and Ascending Aorta

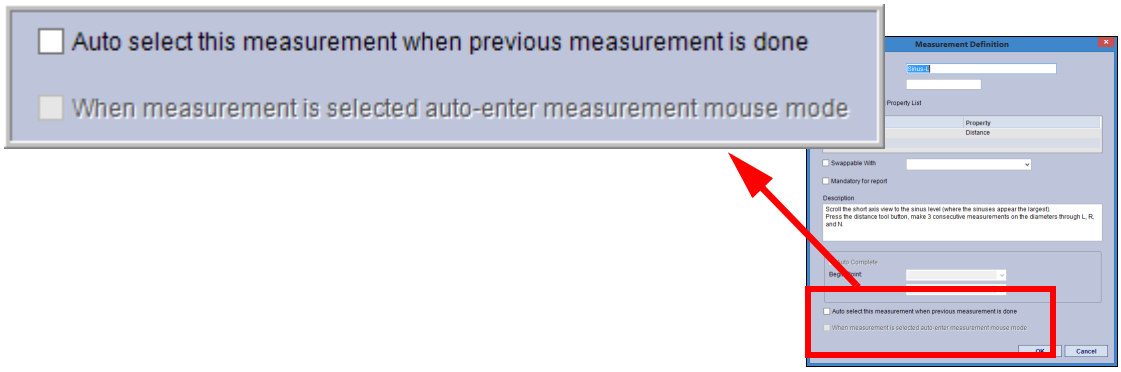
Use the ruler icon in the Measurement Protocol to obtain measurements for the sinus, sinotubular junction (STJ) and ascending aorta.

The sinus measurements can be done for all three diameters (L, R, N) without any need to go back to the Measurement Protocol tool panel to click the distance measurement icon between each measurement. To enable this feature, do the following:

1. Select the first of the three measurements (Sinus-L).

2. Click the down-arrow to the right of the **Add** button, at the bottom of the tool panel, and select **Edit** from the menu. This opens the **Measurement Definition** dialog.

3. Check the box for **Auto select this measurement when previous measurement is done**. This automatically enables the setting right below it (**When measurement is selected auto-enter measurement mouse mode**). This second setting is the one that allows you to continue taking measurements without going back to the measurement Protocols tool panel.



4. Click **OK** to save the change.

5. **Repeat this process for each of the three measurements**.

Once this property has been changed, you will not need to change it again. You will always be able to obtain these three measurements with one selection of the measurement icon.

Note: When you start to measure the STJ, you will see a popup dialog asking whether to unlock the crosshairs. Click Yes. Otherwise, you will not be able to rotate the image properly.

The measurements on the best systolic study are now completed. The remainder of the measurements are obtained from the abdominal series.

The CPR Element

This element is used to obtain measurements in the abdominal series.

Loading the Abdominal Series

To load the second series and also preserve the measurements already taken from the coronary series, use the “mini” Patient List from the 3D Viewer.

1. Click the mini Patient List button in the top toolbar. 

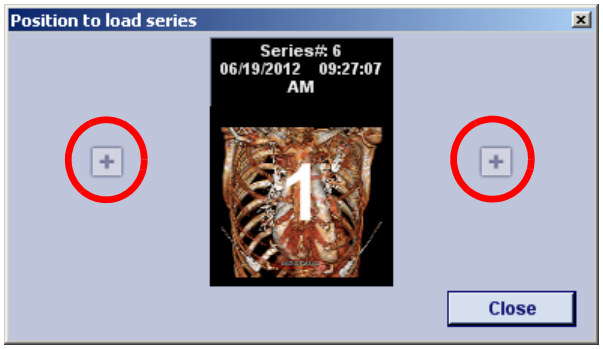
   The mini Patient List is opened. See "Mini Patient List" on page 3-188 for a full description.

2. Click the pin button (shown at right) in the upper-right corner to keep the Patient List visible.

3. Select the abdominal series from the Series List.

4. Click the **Load** button in the bottom-right corner of the Patient List. A dialog is opened asking where you want to place the second series, in relation to the coronary series already loaded.

5. To load the abdominal series to the right of the coronary series, click the plus sign on the right of the dialog. Click the plus sign on the left to load the abdominal series on the left.



Note: Click the pin icon in the upper-right corner of the Patient List to unpin the Patient List and dismiss it.

6. Select **Multi data 1x1** layout.

7. Remove the CT table, and bone if desired.

8. Click the CPR Workflow Element (see image at right).

9. Shift+click on one of the iliac arteries to open the CPR view.

10. Click the Measurements workflow icon again to show the TAVR Measurement Protocol.

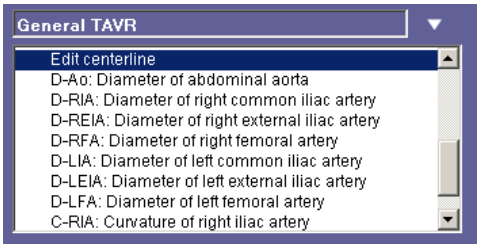


Figure 15-14TAVR Measurement Protocol

Other Features

Jump to It

You might sometimes need to see how an image appeared on the screen at the time you completed a certain measurement. To do this, right-click on the completed measurement and select **Jump to it**. The images are displayed in the same orientation and visible slice level as they were when the measurement was performed. Alternatively, you can simply double-click on the measurement to restore the images to that measurement.

Measuring the Tortuosity and Curvature of a Vessel

The tortuosity index of a vessel is defined the distance between two points along the centerline, divided by the straight-line distance between those points.

1. Right-click on the centerline and choose **Measure Curvature/Tortuosity** from the menu.
2. Draw a line segment along the centerline, of the length to be measured. Release the mouse when done.

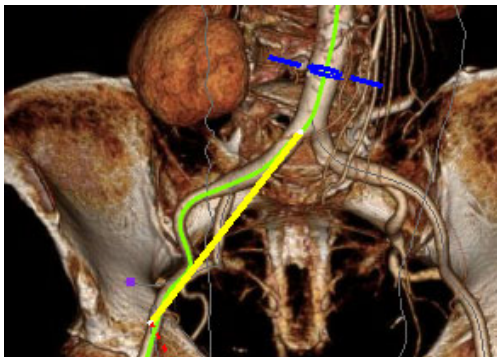


Figure 15-15Average Curvature of the Segment

The software calculates the average curvature of this segment. It also highlights the path segment, draws a straight line between the start and end points and calculate the tortuosity index.

The result is displayed as follows:

- Average curvature
- Path length - length of the path, as traveled along the centerline.
- Distance - Length of the straight line between start and finish.
- Tortuosity Index - Path length divided by Distance

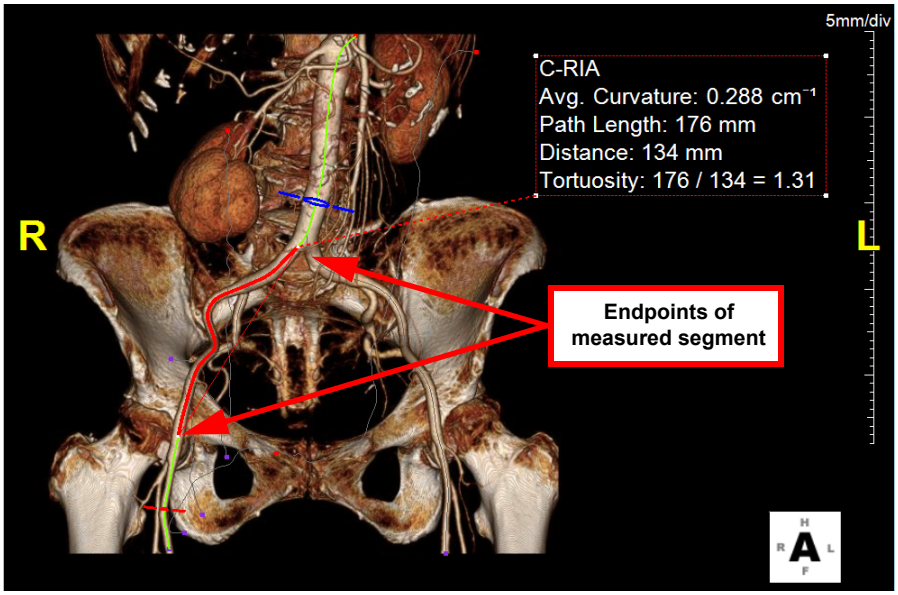
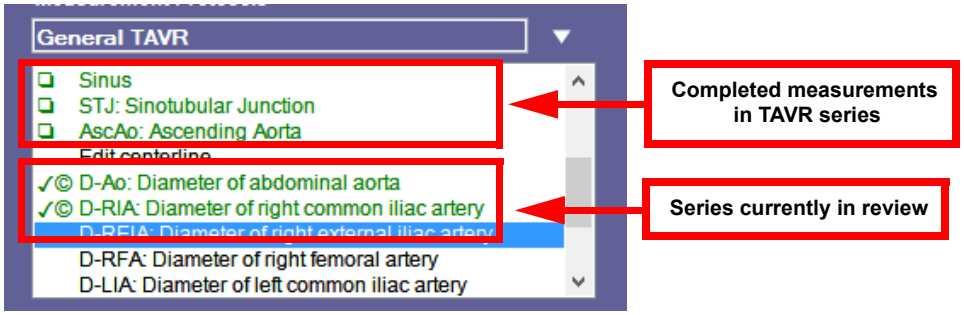


Figure 15-16 Endpoints of the Measured Segment

Other Measurements

The remaining measurements in the TAVR Measurement Protocol are standard measurements, mostly using the Distance tool. To begin, click the **Measurements** workflow element again to redisplay the TAVR measurement protocol.



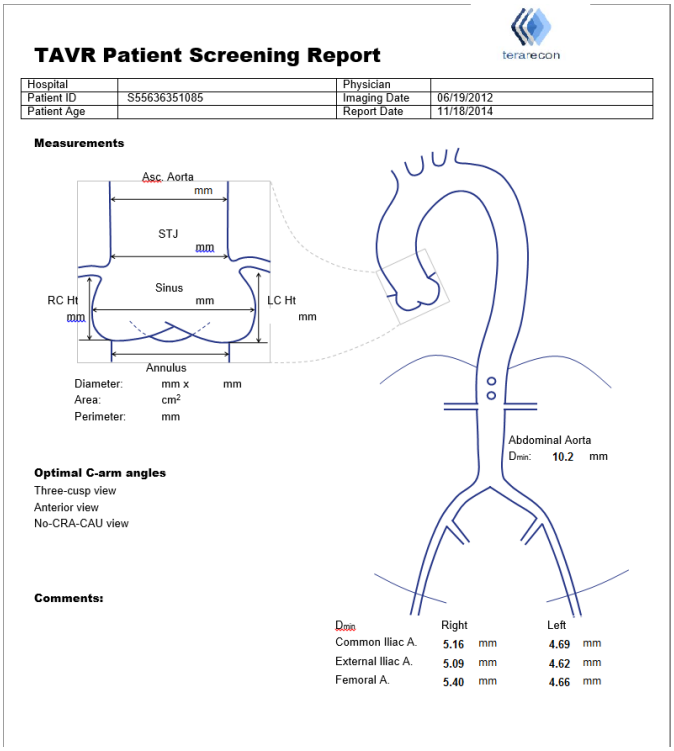
Note that when you are examining the abdominal series, the measurements in green text having a checkmark and circle on the left indicate that those measurements have been completed. The completed measurements in the TAVR series are also displayed in green text, but those show a box on the left. This indicates that those measurements are part of a different series, not currently being examined. When using a measurement protocol on multi-data, these symbols differentiate between the series currently being reviewed and the other series, which is also loaded, but is not currently displayed in the main window.

For more information about Measurement Protocols, see Chapter 13: "Measurement Protocols". These measurements are very similar to the work done for endovascular aortic repair (EVAR). Please see Chapter 14: "Endovascular Aortic Repair" for more information.

Generating a Report

Click the **Generate Report** button in the bottom-right corner of the measurement protocol tool panel.

If you need to show the measurement results from both the abdominal and TAVR studies, make sure that the associated setting, **Include measurements from all loaded studies/series when generating report and exporting XML**, is enabled in the user preferences. The setting is located in the Measurement Settings Options page. See "Measurement Options" on page A-46 for more information.



TAVR Patient Screening Report

teracon

Hospital		Physician	
Patient ID	S55636351085	Imaging Date	06/19/2012
Patient Age		Report Date	11/18/2014

Measurements

Asc. Aorta mm
STJ mm
Sinus mm
RC Ht mm
LC Ht mm
Annulus
Diameter: mm x mm
Area: cm²
Perimeter: mm

Abdominal Aorta
Dmin: 10.2 mm

Optimal C-arm angles
Three-cusp view
Anterior view
No-CRA-CAU view

Comments:

Dmin	Right		Left	
Common Iliac A.	5.16	mm	4.69	mm
External Iliac A.	5.09	mm	4.62	mm
Femoral A.	5.40	mm	4.66	mm

Figure 15-17 Generated Report

Chapter 16 The Findings Workflow

Topics in this chapter:

The Findings Workflow feature provides a framework for tracking findings across serial examinations. A database holds measurements and key images. The database provides support for structured comparisons and tabulated reporting of findings over time, for presenting serial comparisons. The Annotation and Image Markup (AIM) XML schema is supported, and Word-based reports may be derived from the database.

Measurements saved in the Finding Viewer and Scenes

When a scene is loaded, measurement values in the scene, and the corresponding measurement saved in the finding viewer may not match, in certain instances when a study has multiple scenes. Measurements in the Finding Viewer are given precedence.

You are responsible for comparing each measurement in the Finding Viewer to the corresponding measurement saved in a scene, and for validating the results prior to use.

Elements of the Finding Viewer

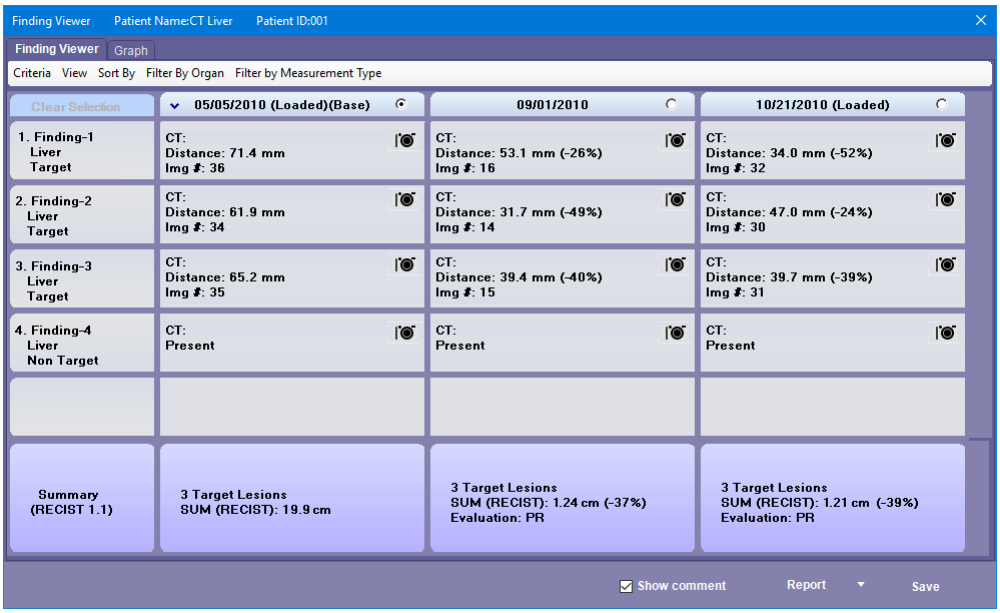
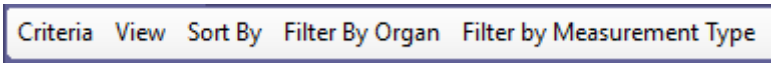


Figure 16-1: The Finding Viewer

Tabs

- **Finding Viewer** - This tab contains the measurement findings, as shown in Figure 16-1.
- **Graph** - This tab contains graphs that represent the changes in measurements from one scan to the next. See "Graphs" on page 16-12 for details.

The Menu Toolbar



- **Criteria** - Criteria for evaluating and categorizing the level of pathology in the tissue under examination. See "Measurement Criteria Evaluation" on page 16-25 for details.
- **View** - **Full** (show all priors and loaded data) or **Compact** (show only base, prior and loaded data).
- **Sort By** - Sort in order of finding date, finding name, or by targeted/untargeted.
- **Filter by Organ** - Show results only in certain organs. The selection depends on the type of data currently loaded.
- **Filter by Measurement Type** - Show only the selected type of measurement (distance, ellipse, and so on).

Measurement Rows

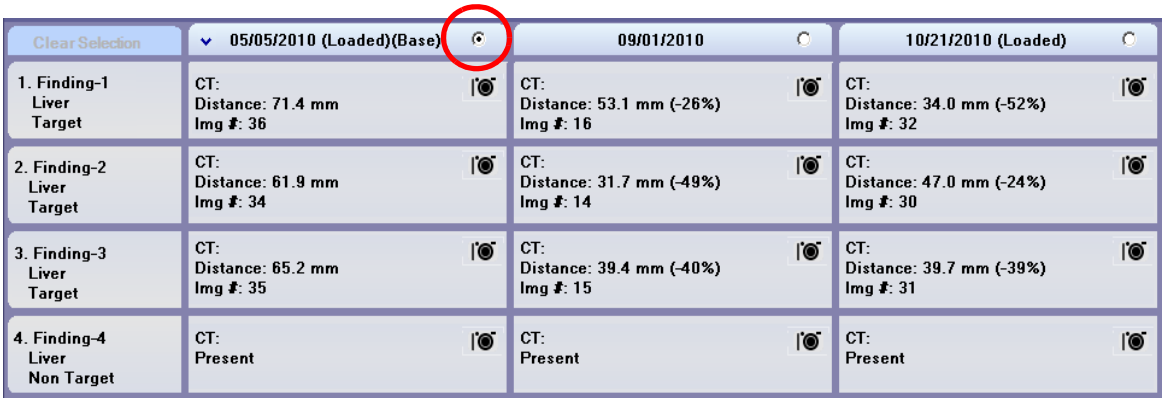
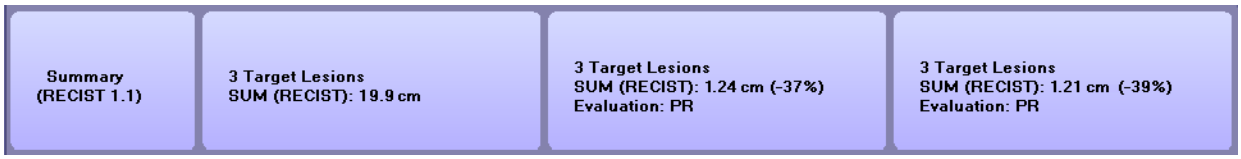


Figure 16-2: Measurement Rows

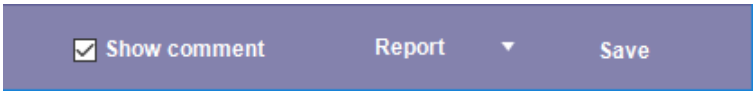
- **Scan Date Columns** - At the top of each column is a header containing the date of the scan. Each row in that column can contain a finding (a measurement performed on that scan data).

- **Select Base Scan** - To designate a scan as the base, click the radio button at the right end of the header (circled in Figure 16-2).

Summary Row



Bottom Tools



- Show comment - Check the box to show any comments that were entered when the measurements were performed. The comments are shown in with the corresponding measurements in the Finding Viewer.

- Report - Click to generate a report. See "Generating Reports" on page 16-24 for details.

- Export - Click the down-arrow next to the **Report** button to access a drop-down menu, where you can select a format in which to export the findings. XML, AIM XML, CSV and text outputs are supported.

- Save - Save measurements in the database.

Enabling Measurement Tracking

There are several ways to enable measurement tracking:

- **Enable tracking all the time**

  This is configured in the user preferences:

  a. Open the Preferences dialog and click the **Finding Viewer** navigation link to the page.

  2. In the menu labeled **Enable Measurement Tracking**, select **Always**.

  See "Finding Viewer" on page A-46 for more information.

- **Select from Right-click Menu**

  Right-click on an image in the Viewer and select **Enable Measurement Tracking**.

- **Load data using the MT (Lung) workflow**

  Please see "The MT (Lung) Workflow" on page 16-14 for information about this feature.

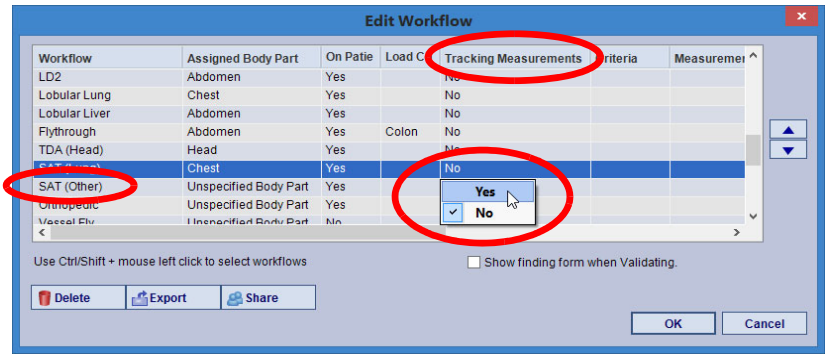
- **Track Measurements Based on Workflow**

  You can link measurement tracking to a specific workflow, and enable tracking only when a study is opened in that workflow. Do the following:

  a. Open the **Finding Viewer** Preference screen and select **Based on Workflow** from the **Enable Measurement Tracking** menu.

  2. Open a study in any workflow. Click the down-arrow beside the workflow name and select **Edit Workflow** from the menu.

  The **Edit Workflow** dialog is opened (see the following figure).



In the row that contains the desired workflow, go to the **Tracking Measurements** column. If the value in that cell is **No**, click the cell to open the drop-down menu, and then select **Yes**. See "Editing Workflow Settings" on page 4-16 for more information about editing workflows.

Measurements Supported in the Findings Workflow

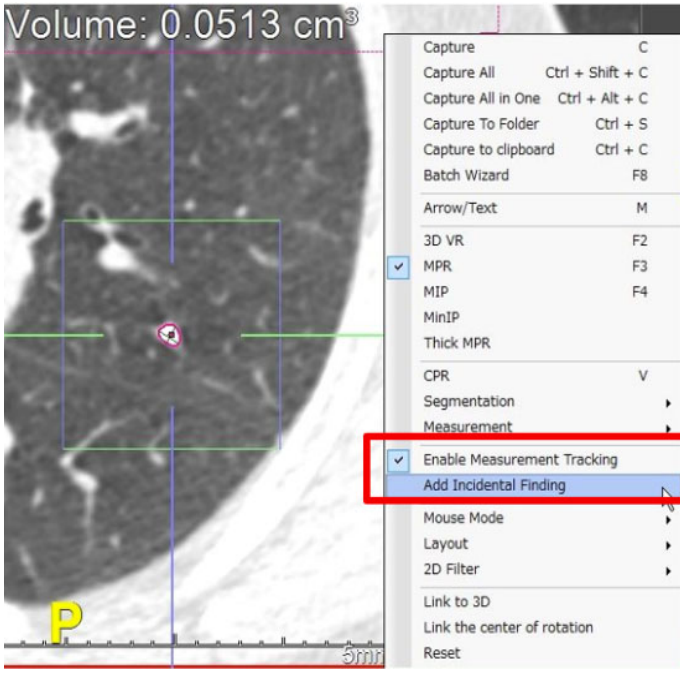
The following measurements can be tracked in the Findings Workflow:

- Assisted distance pair
- CircleROI
- Distance pair
- Ellipse
- Polygon
- Distance
- Line Segment
- Path Length (CPR)
- SAT
- Calcium Scoring
- Profile
- Plaque Analysis
- Fat Analysis
- Fat Analysis 3D
- Sphere
- Volume
- Volume histogram
- Sac Volume (EVAR)
- Low Attentuation

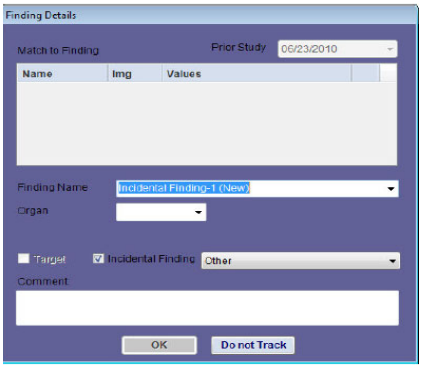
Incidental Findings

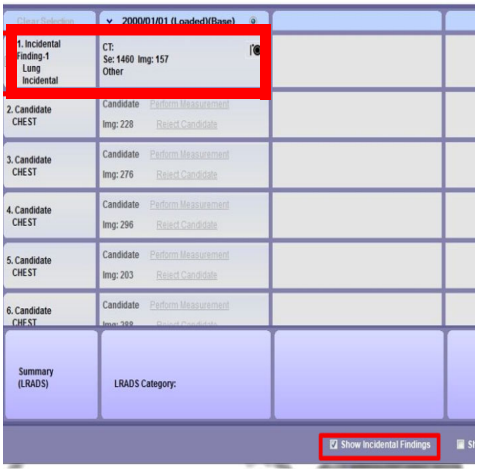
This setting allows you to mark any incidental findings when no measurement is needed. In Viewer, right mouse click to display the menu, and locate “Add Incidental Finding”. Once clicked, you can customize the name of the finding.

Note: Must add a comment before clicking OK

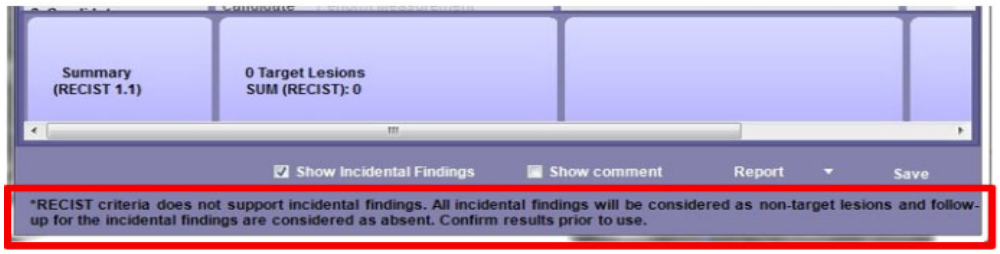


The Finding Details dialog opens and you can see the Finding Name is automatically set to Incidental Finding -1 and the next finding would be named Incidental Finding-2, and so on. These findings can be seen in the Findings Viewer, however, make sure the “Incidental Findings” box is checked.





If the criteria is RECIST, then a warning message will appear at the bottom.



Performing and Tracking Measurements

Select the study that contains baseline data and click the **Load** button. Select **MT (Lung)** or **MT (Other)** from the workflow menu.

The data is loaded into a 1X2 layout, with the axial image on top and the coronal image on the bottom.

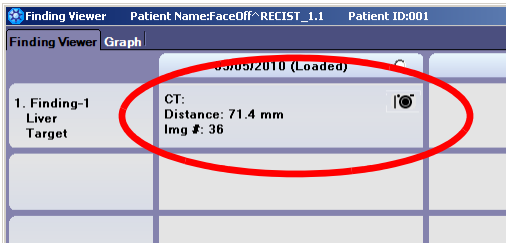
1. Page through the slices to find the lesion.
2. Measure the lesion using the Distance measuring tool. The **Finding Details** window is opened (see image at right).
3. If this is a target measurement (intended for inclusion in the sum), check the **Target** box.
4. Enter or select the following:
   - A name for the finding in the **Finding Name** box.
   - The organ from the pulldown menu (optional).
   - A comment in the text input box (optional).
5. If you choose not to track this measurement, click the **Do not Track** button on the Finding Details form. Otherwise, click **OK** to add the finding to the Finding Viewer.

Note: If at a later time you want to track the measurement, right-click on the measurement and select *Add to Finding Viewer*. The Finding Details form is reopened for you to enter the relevant information.

Open the Finding Viewer

1. Click the Finding Viewer icon, shown at right, in the Top Toolbar (see "Top Toolbar Buttons" on page 3-143) to open the Finding Viewer.

   The finding you have just created is shown in the Finding Viewer:



Further measurements on this data will be displayed in other cells in the Finding Viewer.

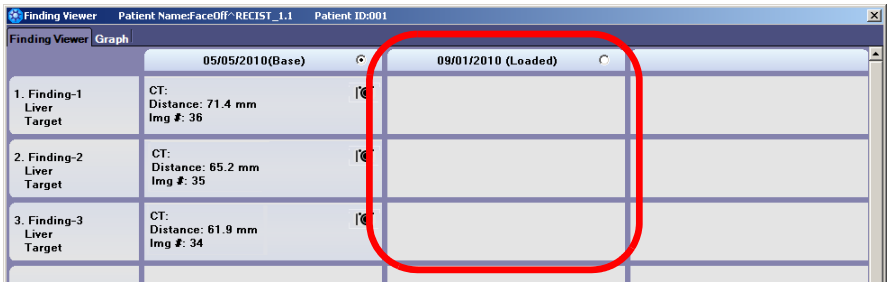
2. Click **Save** to save the measurement in the database. The **Save Scene** dialog is opened so you can enter a name.

Note: Do not load another study without saving the measurements, or those measurements will be lost.

Followup

When a followup study becomes available, load it into the viewer, and then open the Finding Viewer. By default, the Finding Viewer populates previous findings for the same Patient ID and Patient Name. A new column is added for the new study. The cells beneath the new date are blank because no measurement have been performed yet.

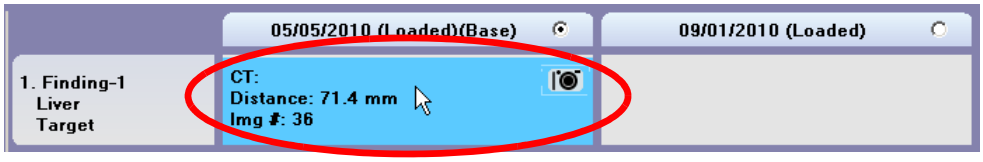
Note: If the prior and followup measurements have the same patient ID but different patient names, this means that an option was set to allow data to be grouped together by patient ID only. This option cannot be changed by users. If you would like to have it changed, contact your system administrator.



Obtain a measurement in the followup study that corresponds to the first finding in the base study. To access the first finding in the base study, you can do one of two things:

- Hover the mouse over the corresponding cell in the followup study column. Two links are displayed in the blank cell: **Perform Measurement** and **Mark as Absent**. The key image is also displayed for reference. Click on the **Perform Measurement** Link.
- Double-click on the first finding in the base study.

Note: Available only when the base study is loaded together with the followup.



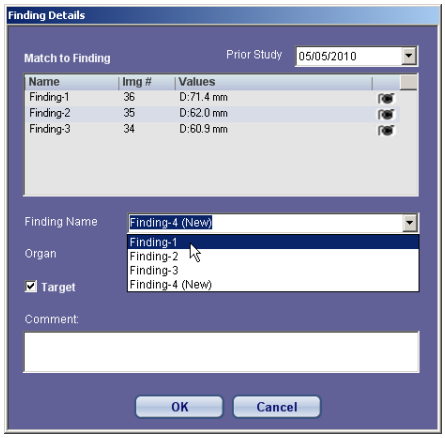
The axial image jumps to the slice that contains the finding stored on the same row. The new image jumps to the corresponding slice.

Note: Corresponding slices in different scans might not have the same image number.

3. Perform a measurement on the lesion in the followup study.

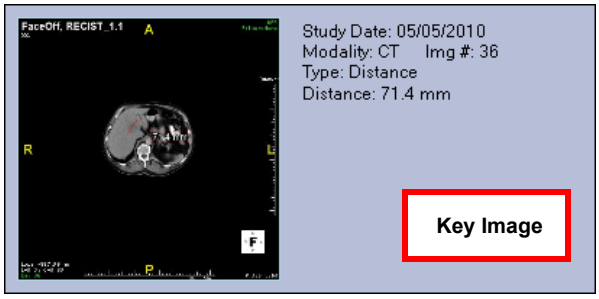
   If you used the **Perform Measurement** link in the Finding Viewer, the measurement is automatically matched to the first finding in the base study. It is then added to the corresponding cell in the follow-up study column.

   If you double-clicked on the finding in the base study, the **Finding Details** dialog is opened so that you can match the current finding with the corresponding finding in the base study:



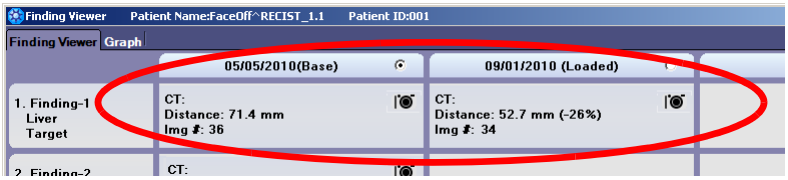
   The new finding is added to the cell in the follow-up study that corresponds with the selected finding from the base study.

   If you are not certain which image to perform the measurement on, hover the mouse over the camera icon in any of the prior findings. The *key image* is displayed in a separate window (see image below). You can then compare the key image with the current study.

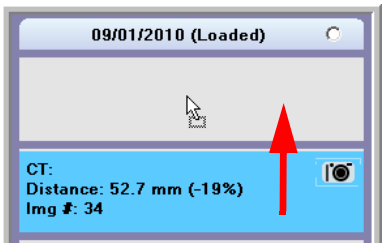


You can open the key image by clicking on the camera icon. This image can be zoomed and panned; however, those changes cannot be saved.

4. Open the Finding Viewer. The new measurement is matched to the corresponding measurement in the baseline study.



If the measurement is incorrectly matched, you can drag and drop it into the correct cell (see the following figure).



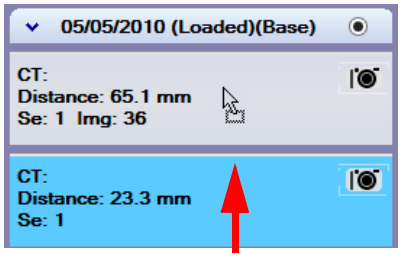
5. Continue performing measurements for other findings.

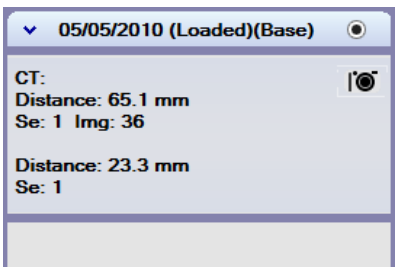
6. Click **Save** to save the measurements as a scene.

Grouping Measurements Together

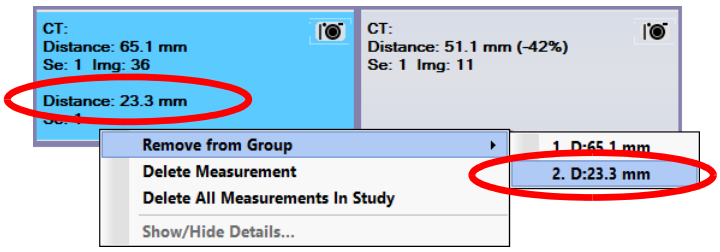
Each time you obtain a measurement and track it in the Finding Viewer, the new measurement is saved as a new finding. However, you can group two or more measurements together in the same finding.

To group a measurement with another finding, click on the measurement and drag it to the desired finding.





Grouped measurements can also be separated. Right-click on the finding and select **Remove from Group**. Then select which measurement to remove.

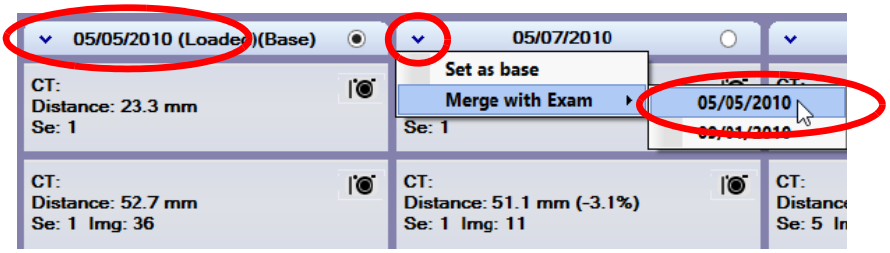


When the measurement is removed from the group, a new finding is automatically created for that measurement.

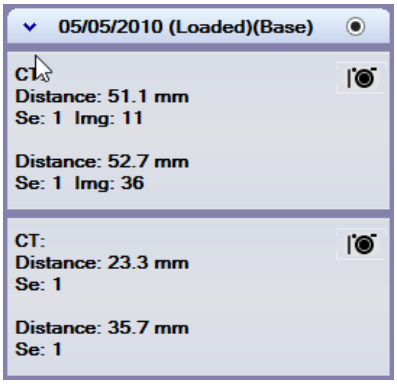
Merging Scans

Whenever two scans have different study dates, they are automatically placed in separate columns in the Finding Viewer. The later scan is considered to be a follow-up. This is true even when the two scans are very close together, time-wise, such as one day apart. In this case, you might prefer to record them in the Finding Viewer as a single scan. You can do this using the **Merge with Exam** feature.

1. Right-click the down-arrow at the top of the column (circled, below) for the date you want to merge.
2. Select **Merge with Exam**.
3. If there is more than one other scan date recorded, Merge with Exam opens a sub-menu where you can choose the date to merge *into*.



When the merge is complete, the measurements appear as shown below:



Graphs

To view the graphs associated with the measurements, click the **Graph** tab in the Finding Viewer (see the following figure).

The graphs in this tab show the Total Burden (the sum distance of all measured target lesions for each scan date) and the percentage change in each followup, relative to the base:

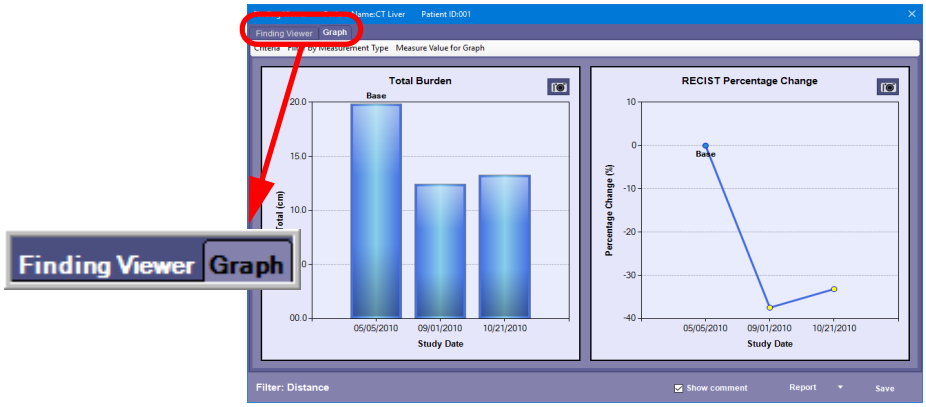


Figure 16-3: Finding Viewer Graph

The graph cannot be produced unless one or both of the following conditions is met:

- A set of criteria has been applied. (See "Measurement Criteria Evaluation" on page 16-25 for a complete description.)
- A measurement type has been selected in the Filter by Measurement Type menu. (See "No-Criteria Studies" on page 16-21 for details.)

Capturing Graphs

To capture the graph to the Output Panel, do either of the following:

- Right-click on one of the graphs and select **Capture** (to capture only the graph that the cursor is on) or **Capture All** (to capture both graphs).
- Click the camera icon in the upper-right corner of the graph (see Figure 16-3). This captures only the graph that the cursor is on.

Calcium Scoring

Calcium scoring studies can be tracked in the Finding Viewer over time. Follow-up results are tracked in separate columns by study date.

1. Set the user preference to use the AQi calcium module (see "Calcium" on page A-20).
2. Select a CT cardiac study that has a follow-up study available.
3. Load the Cardiac study and open the Calcium module.

4. Right-click on any view and select **Enable measurement tracking**.

5. Perform calcium score and validate activity. The measurement results are tracked in the Finding Viewer.

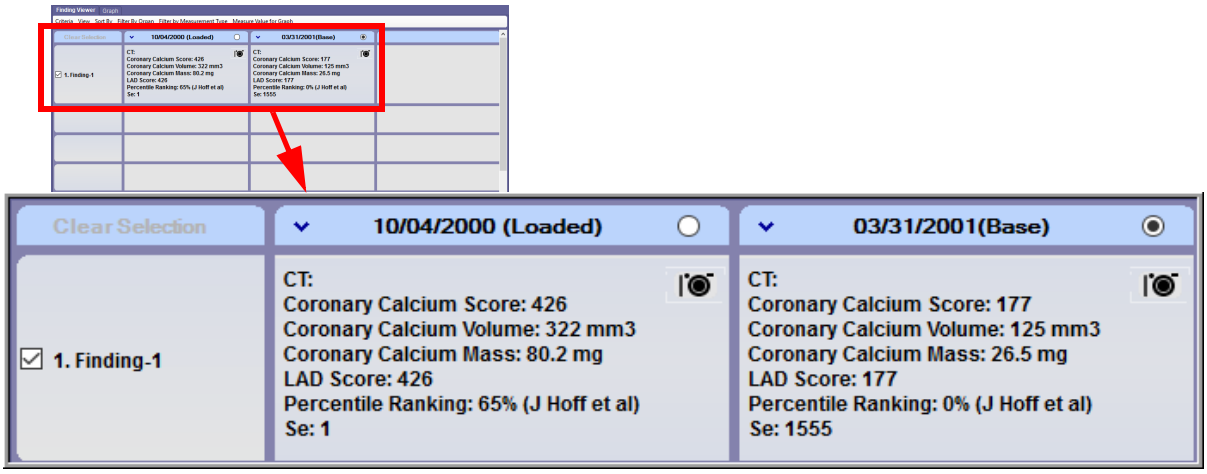
6. In the Finding Viewer, change the criteria to **No Criteria**.

7. Perform any other calcium measurements on the current data, and re-validate each one.

   The measurement is updated in the Finding Viewer. It does not track new scores as new measurements. Instead, new scores are added into the finding that is already being tracked.

8. Do the same for follow-up studies.

All calcium measurements are shown in the Finding Viewer. The follow-up measurement values are compared, vessel to vessel.



You can also right-click on the calcium result in the Finding Viewer and select **Show/Hide** details. This allows you to choose which measurements to display in the Viewer.

Calcium Score Selections

When using the Calcium Scoring workflow, you have several options for selection:

1. Shift + Left-click for a single calcification.

2. Shift + Left-click and hold to circle a vessel region.

3. Select the CA Score control button on the viewer to select or draw the region without using the shift key.

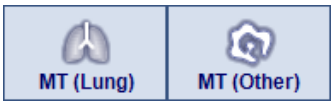
It is recommended that you validate your scoring. When selected the CA Scoring control button changes to a green background.

CA Score is Off

CA Score is On.

The MT (Lung) Workflow

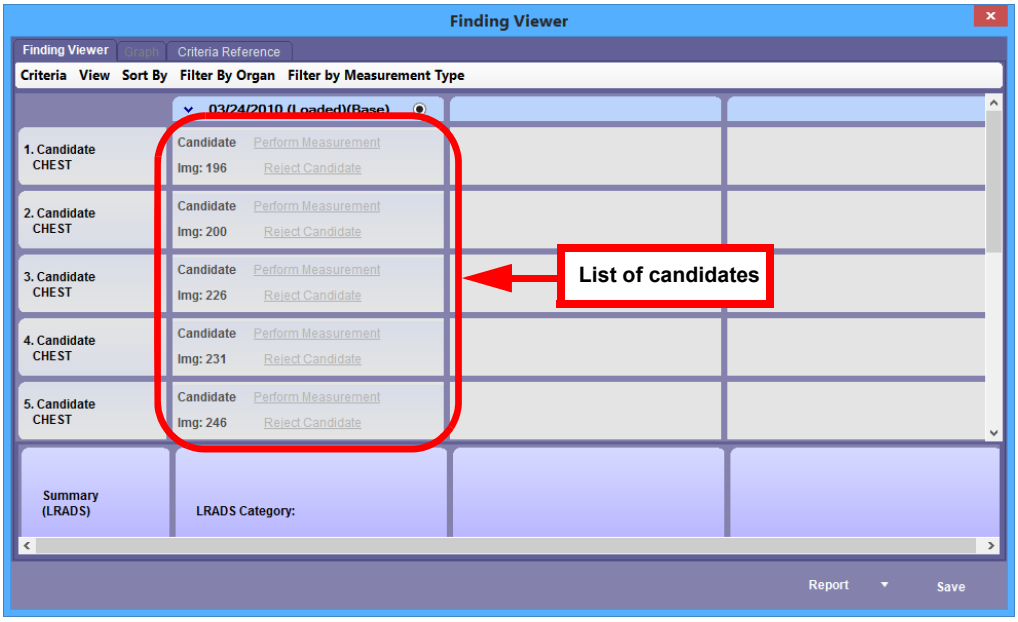
Use **MT (Lung)** for lung studies, or **MT (Other)** for all others (see figure below).



This workflow is designed to facilitate the efficient navigation through nodule candidates.

Note: APS SpherefinderL results are required to use this workflow.

When data is loaded into this workflow, measurement tracking is automatically enabled, and the Finding Viewer is opened. If measurements have not been previously performed on any of the images in the study, there are no measurements saved in the Finding Viewer. However, candidates that have been found by Sphere Finder are listed in the Viewer, in the order of the image slices where candidates were found.



When a study loaded into the **MT (Lung)** workflow does have one or more scenes with confirmed SAT findings, these findings are automatically added to the **Finding Viewer**. You can review them and either click them to save them to the Findings Database or delete them.

Navigating the Candidates

You can step easily from one candidate to the next using a set of control icons located at the bottom of the main (axial) image. To see the icons, hover the mouse at the bottom of the image:

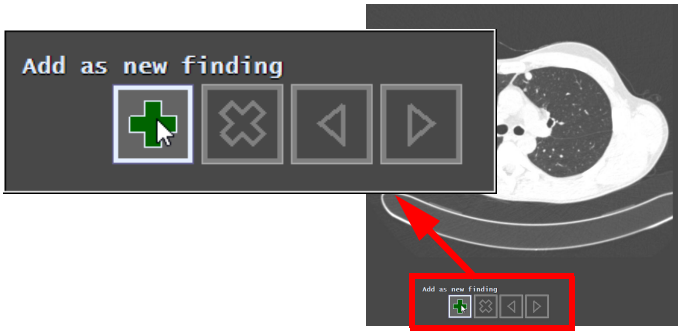
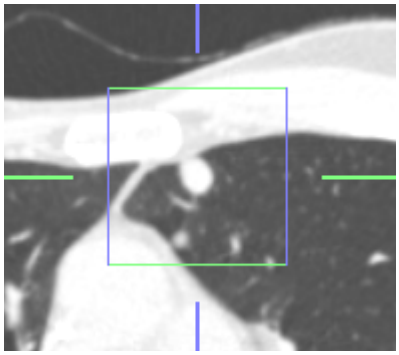


Figure 16-4: Navigation Control Icons

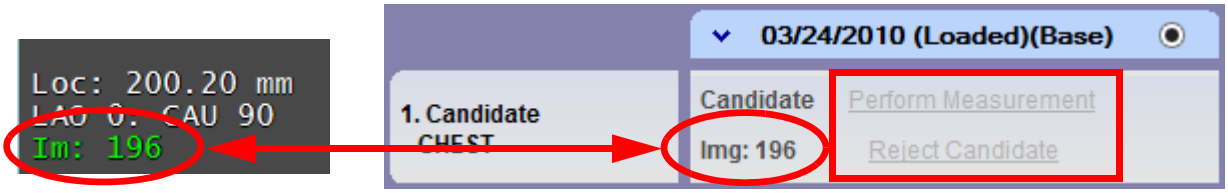
Initially, only the two right-most icons (left- and right-arrows) are displayed. To select the first candidate, click the right-arrow. The image is then focused on the first candidate, surrounded by a box and cross-cursors pointing toward it:



All of the icons are now displayed when the mouse is hovered over the region. You can also hover the mouse over each icon to see what its function is (see Figure 16-3 on page 16-12).

Confirm or Reject Candidate

The image number in first candidate in the list matches the image number that appears in the lower-left annotation on the data (see figure below).



To confirm the candidate, you can do one of two things:

- Click the **Perform Measurement** link (bounded in dark blue in the figure above).
- Click the '**+**' icon in the navigation controls.

The measurement is performed automatically and the results are displayed on the image. The Finding Details dialog is opened so that you can track this measurement (see "Incidental Findings" on page 16-5).

If you chose to reject the candidate at this time, click the **Do Not Track** button in the Findings Details dialog. You can also delete the measurement by clicking the '**X**' icon in the navigation controls (see "Navigating the Candidates" on page 16-15).

Click the right-arrow icon to view the next candidate.

IMPORTANT: When you are finished reading this study, make sure to click the Save button in the lower-right corner of the Finding Viewer. This saves all your findings in a scene, so that they will be there the next time this study is loaded. The findings are also saved to the Findings database in the Finding Viewer. If you exit the Finding Viewer without saving, your measurements will be lost.

Follow-Up Data

Use the Mini Patient List to load a follow-up scan. (For information about the Mini Patient List, see "Mini Patient List" on page 3-188). The Finding Viewer shows the follow-up candidate list in the second column, beneath the date of the scan. See Figure 16-5 on page 16-17.

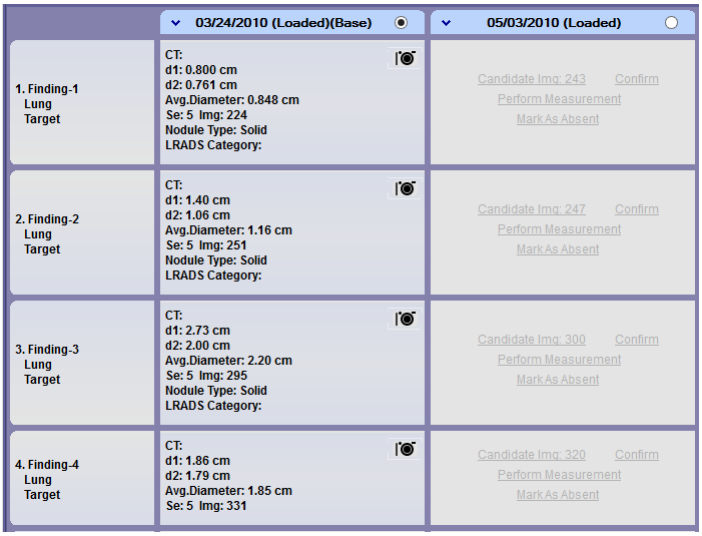
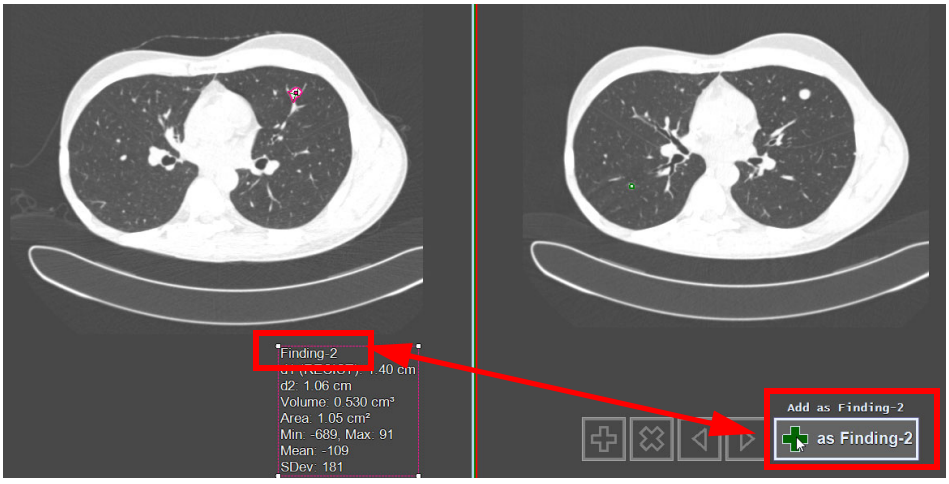


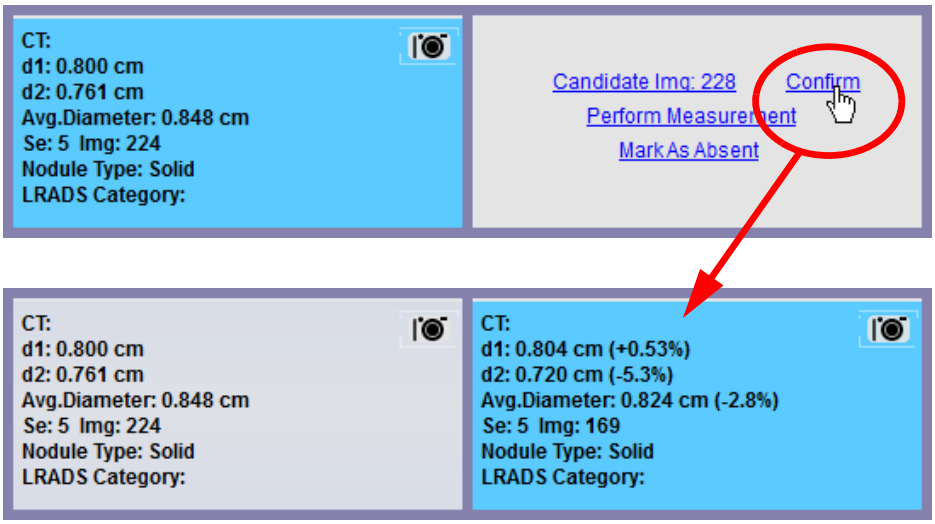
Figure 16-5: Follow-up study Loaded

Note: When possible, the candidates are matched with confirmed findings in the base study. However, be aware that the image numbers usually do not match, depending on a number of factors.

If you choose to confirm a matching candidate in the follow-up, select **Add as `<finding-name>`**, where “finding-name” is the name of the matching candidate in the previous study.



Another way to confirm a finding is to click the Confirm text in the corresponding cell of the current finding in the Findings Viewer. The matching measurement is displayed in that cell.

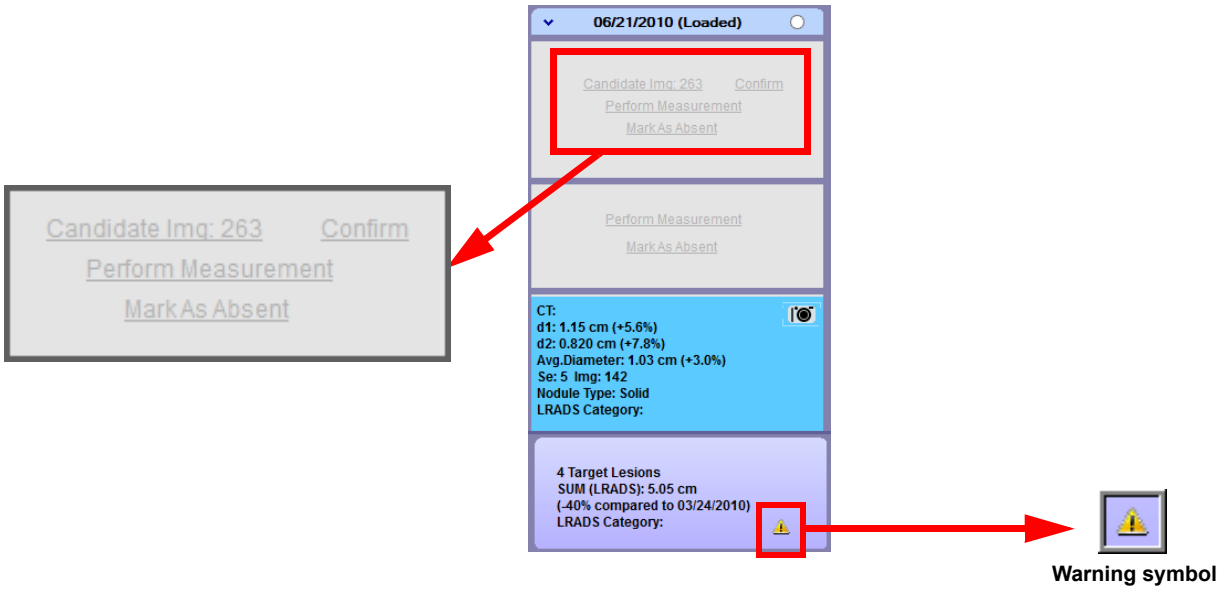


If you select **Add New** (the '**+**' icon), the follow-up finding is placed in a new row by itself and is not associated with any finding in the previous study.

When candidates do not match because a confirmed finding in the previous study does not have a matching candidate in the follow-up, click the **Mark as Absent** link in the follow-up. If there is a new candidate that has no match in the previous study, this must be added as a new finding (see figure at right).

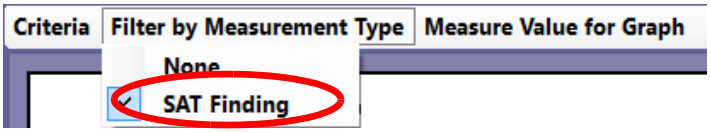
Incomplete Follow-up Measurements

If there are measurements still pending for any candidates in the Finding Viewer, a small warning symbol is displayed in the Summary row at the bottom (see the following figure). If you hover the mouse over the symbol, you will see a message that describes the issue.

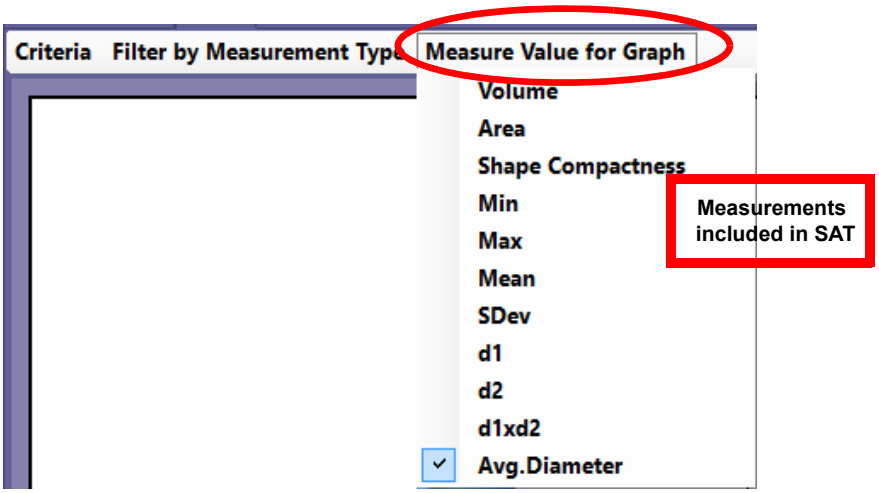


Graph for the MT Lung Workflow

The following two figures illustrate how to show a graph for the different measurements included in an SAT finding:



After selecting the measurement type, select the property to display as a graph from the **Measure Value for Graph** menu:



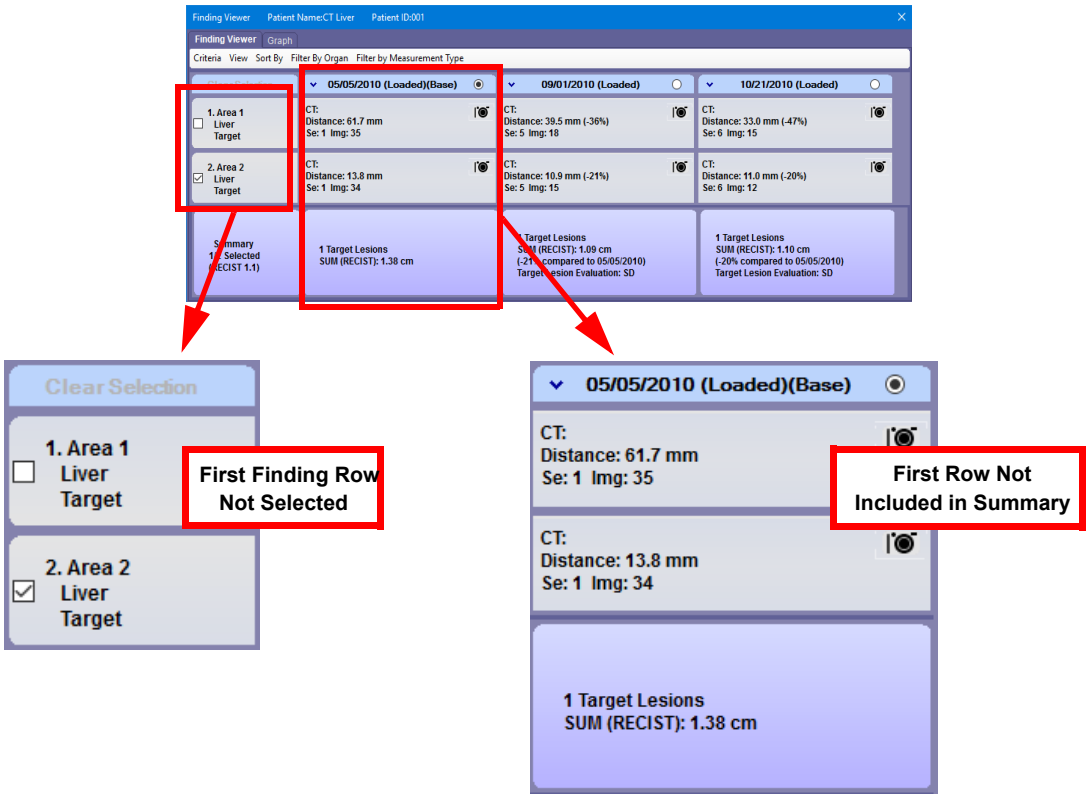
Other Tools

Selection of Findings

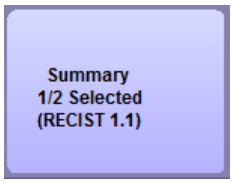
Findings selection allows you to choose specific measurement rows to be included in summaries, graphs, reports, and measurement exports.

Note: By default, all measurement rows are included in the summaries at the bottom of each column. The checkboxes are also *unchecked* by default. Therefore, if either all boxes are checked, or all boxes are unchecked, the result is the same: all rows are included. It is only when some of the boxes are checked that the summaries will be partial.

To select a row for inclusion in summaries and graphs, check the checkbox in the leftmost column.

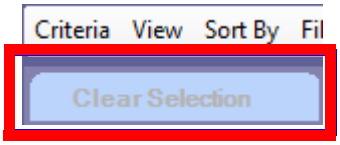


Partial selection/partial summary



If any row is not included (checked), the bottom-left cell of the viewer indicates that the summary contains only some of the measurement rows (see figure at right).

Clear Selection link (at the top of left column)



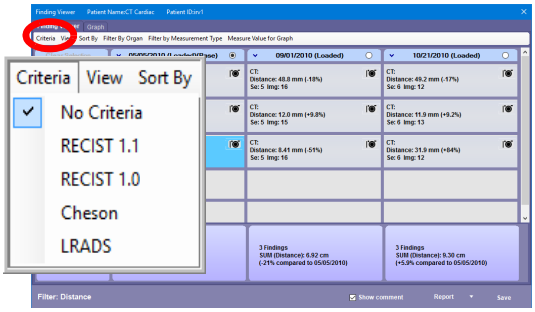
The Clear Selection link is in the upper-left cell of the measurement rows (located just under the menu toolbar). Click this to remove all checkmarks from the measurement rows.

Reports and Exports

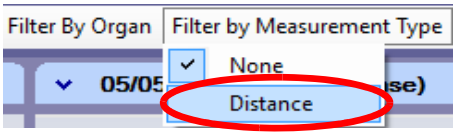
If you have some measurement rows checked, then only the measurements being tracked in those rows are included in reports generated from the Findings Viewer. Only those measurements are included when you export measurements to a file.

No-Criteria Studies

If your workflow does not require you to specify oncology criteria or target and non-target measurements, you can select **No Criteria** from the **Criteria** menu:



To view the graph of a measurement that has no criteria, you must select a measurement type as a filter. If **None** is selected, the Finding Viewer cannot produce a graph.



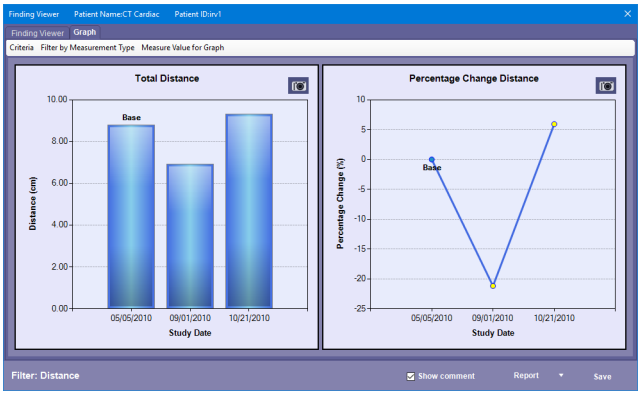


Figure 16-6: Graph For No-Criteria Measurement

Right-Click on Measurement Menu

Right-click on a measurement in the Finding Viewer. The menu items offer additional options for the Finding Viewer.

- **Lesion/Lymph** - Mark this finding as either a lesion or a lymph node.
- **Mark as Target/Non-Target Lesion** - Mark this finding as a target or non-target lesion.
- **Organ** - Identify the organ where this finding is located.
- **Delete Measurement** - Delete the measurement in this cell.

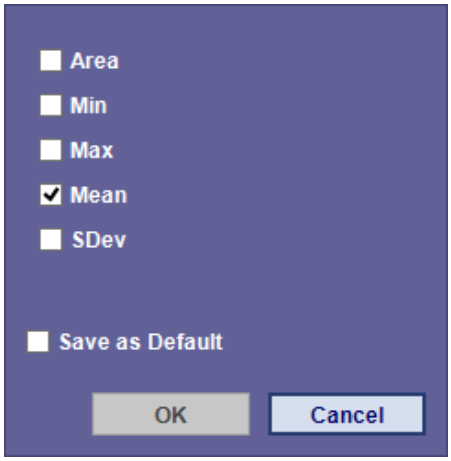
Note: You can undo **Delete Measurement** by clicking the **Undo** button in the AQi Viewer top tool bar.

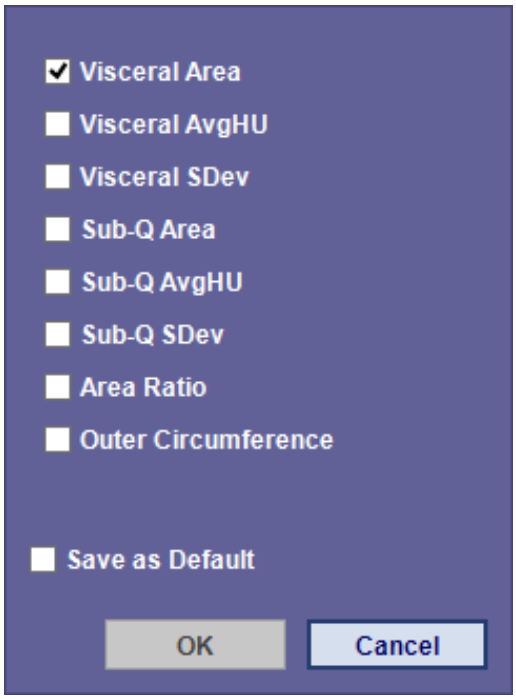
- **Delete All Measurements** - Delete all measurements in the Finding Viewer.

- **Show/Hide Details**

When this item is selected, the **Show/Hide Details** dialog is opened. If a measurement contains more than one value, you can choose which of these values are shown in the Finding Viewer.

Depending on the type of measurement, the optional values listed here will vary. For example, an ellipse measurement (figure below, left), contains the area, mean, min, max and standard deviation values. Body fat analysis contains a different list of values, as shown in the image on the right.



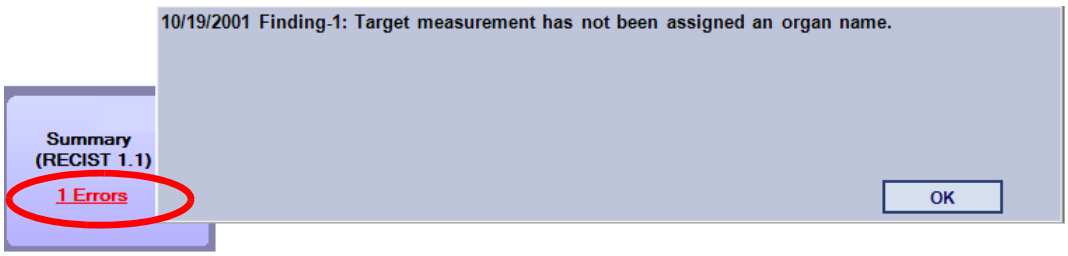


By default, one value is shown in the Finding Viewer. You can add any number of measurement values by checking the box for those values. Check **Save as Default** if you want your selections to show in the Finding Viewer by default for this measurement.

Note: If a measurement has only one value (for example, a distance measurement), this menu item is inactive (grayed out).

Errors

When measurement conditions for the selected criterion are not met, an error notice is shown in the **Summary** cell, in the bottom-left of the Finding Viewer.



Changing the Finding Name

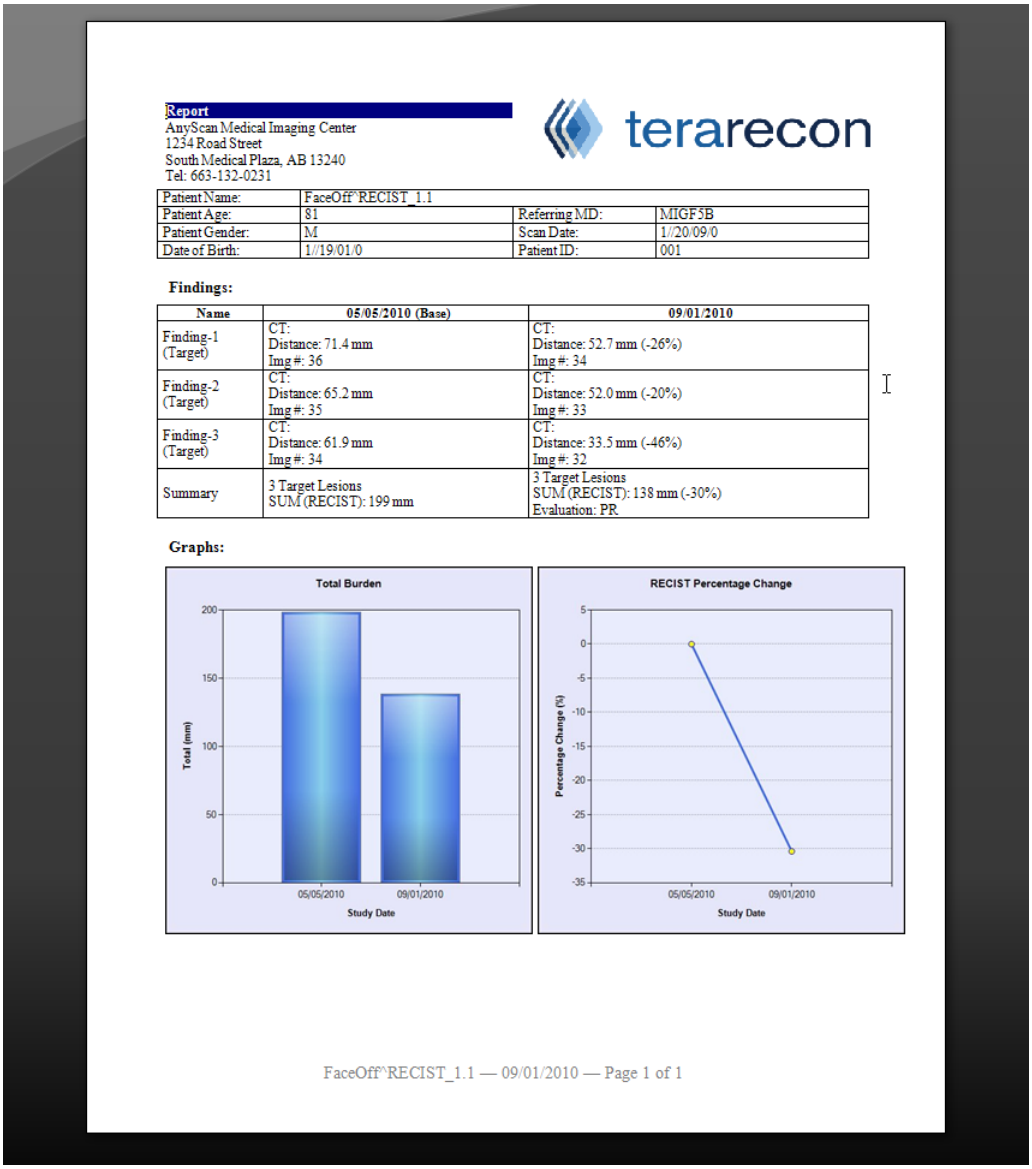
If you want to change the finding name, first select the cell containing the name to be changed. The background color changes to blue. Then double-click anywhere inside the cell. The name becomes editable (see the image on left in the image below). You can then add or remove characters in the name. When done, click anywhere outside that cell to deselect it. The name is changed (below, right).

Generating Reports

Click **Report** to open a report (see Figure 16-1 on page 16-2). A Findings report is generated and opened in Microsoft Word (see figure at right).

Reporting Findings Using LRADS Criteria

Reports of findings using the LRADS criteria are currently available as web reports only, and web reports must be enabled. If web reports are not enabled in your system, you will receive an error message if you attempt to generate a report. Please contact TeraRecon customer support to enable web reports.



Report
AnyScan Medical Imaging Center
1234 Road Street
South Medical Plaza, AB 13240
Tel: 663-132-0231

terarecon

Patient Name:	FaceOff^RECIST_1.1		
Patient Age:	81	Referring MD:	MIGF5B
Patient Gender:	M	Scan Date:	1//20/09/0
Date of Birth:	1//19/01/0	Patient ID:	001

Findings:

Name	05/05/2010 (Base)	09/01/2010
Finding-1 (Target)	CT: Distance: 71.4 mm Img #: 36	CT: Distance: 52.7 mm (-26%) Img #: 34
Finding-2 (Target)	CT: Distance: 65.2 mm Img #: 35	CT: Distance: 52.0 mm (-20%) Img #: 33
Finding-3 (Target)	CT: Distance: 61.9 mm Img #: 34	CT: Distance: 33.5 mm (-46%) Img #: 32
Summary	3 Target Lesions SUM (RECIST): 199 mm	3 Target Lesions SUM (RECIST): 138 mm (-30%) Evaluation: PR

Graphs:

FaceOff^RECIST_1.1 — 09/01/2010 — Page 1 of 1

Measurement Criteria Evaluation

The following RECIST criteria information can be provided to assist with target lesion evaluation, if the option is selected. The software assists you by utilizing (user-defined) measurements and correlating it with published RECIST criteria for target lesions, and does NOT provide you with a complete RECIST evaluation. It is your responsibility to evaluate and validate all information in multiple methods prior to proceeding with treatment decisions.

Warning: Information displayed for each time point is shown for user selected lesions. The target lesion evaluation compares findings to the base measurement or nadir as applicable by the RECIST criteria. However, the summary measurements are compared to the baseline measurement. The software does not assist with gathering information on non-target lesions or best overall response, and therefore does not assist with a complete RECIST evaluation.

RECIST 1.1 Criteria

Reference: New response evaluation criteria in solid tumours: Revised RECIST guideline (version 1.1), E.A. Eisenhauer, et al, European Journal of Cancer 45, 2009.

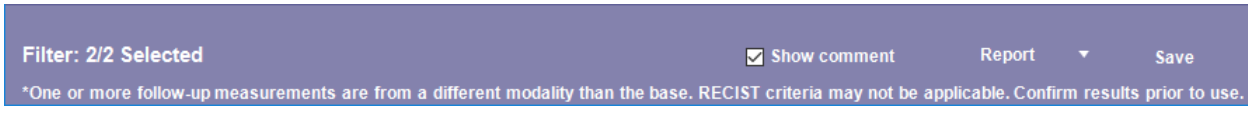
- **Complete Response (CR)**: Disappearance of all target lesions. Any pathological lymph nodes must have reduction in short axis to <10 mm.
- **Partial Response (PR)**: At least a 30% decrease in the sum of diameters of target lesions, taking as reference the baseline sum diameters.
- **Progressive Disease (PD)**: At least a 20% increase in the sum of diameters of target lesions, taking as reference the smallest sum on the study (this includes the baseline sum if that is the smallest on study). In addition to the relative increase of 20%, the sum must also demonstrate an absolute increase of at least 5 mm. (Note: the appearance of one or more new lesions is also considered progression).

Note: When one or more new lesions are added on the follow-up study and marked as a target lesion, the target lesion evaluation will not be provided in the summary row. An error is displayed in the lower left corner of the viewer, indicating that a new target lesion cannot be defined on the follow up study without a base measurement.

- **Stable Disease (SD)**: Neither sufficient shrinkage to qualify for PR nor sufficient increase to qualify for PD, taking as reference the smallest sum diameters while on study.

Followup from a Different Modality

RECIST 1.1 criteria state that the same modality must be used for the baseline and follow-up studies being compared. However, some cases might require a comparison between CT, MR or PT studies. AQi allows such usage, but will also post a warning at the bottom of the Finding Viewer stating that RECIST criteria might not be applicable, and that you must confirm the results prior to use (see figure below).



RECIST 1.0 Criteria

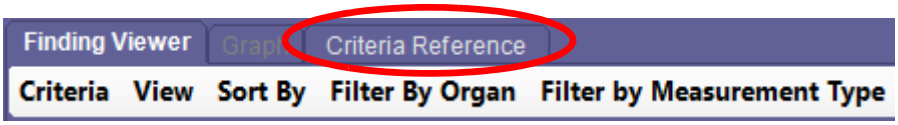
Reference: New Guidelines to Evaluate the Response to Treatment in Solid Tumors, Patrick Therasse, et al, Journal of the National Cancer Institute, Vol 92, No. 3, February, 2000.

- **Complete Response (CR)**: Disappearance of all target lesions. Any pathological lymph nodes must have reduction in short axis to <10 mm.
- **Partial Response (PR)**: At least a 30% decrease in the sum of longest diameters of target lesions, taking as reference the baseline sum longest diameter.
- **Progressive Disease (PD)**: At least a 20% increase in the sum of diameters of target lesions, taking as reference the smallest sum on study (this includes the baseline sum if that is the smallest on study). (Note: the appearance of one or more new lesions is also considered progression).
- **Stable Disease (SD)**: Neither sufficient shrinkage to qualify for PR nor sufficient increase to qualify for PD, taking as reference the smallest sum diameters while on study.

Note: RECIST 1.0 criteria state that the same modality must be used for the baseline and follow-up studies being compared. Please see "Followup from a Different Modality" on page 16-26 for details.

LRADS Criteria

The full description of the LRADS criteria is available in the Finding Viewer. Click the **Criteria Reference** button at the top of the Finding Viewer to see the description.



Chapter 17 T1 Mapping and T2/T2* Mapping

An MRI (magnetic resonance imaging) machine generates an extremely strong magnetic field and pulses of radio-frequency energy, which align hydrogen nuclei in tissues and body water. There are two main MRI sequences:

- T1: Water is dark - better for anatomy (soft tissue structures).
- T2: Water is bright - better for pathology (inflammation, oedema). T2* is data slightly different than T2.

Gadolinium is a metal-based contrast given intravenously (IV) to assist in diagnosis. Edema (oedema) is a condition of abnormally large fluid volume in the circulatory system or in tissues between the body's cells (interstitial spaces).

Data Needed for T1/T2/T2* Workflow

The data needed for the workflow differs slightly between T1 and T2/T2*.

- **T1 Mapping:**
  - Modality = MRI; Series data: T1 Look-Locker, Modified Look-Locker and MOLLI.
  - Number of series: single or two (pre and/or post)
  - Image count each series: greater than 1 (2 or more) in multiple phases
  - Vendors supported: any
- **T2/T2* Mapping:**
  - Modality - MRISeries Data: Single series T2 or T2*
  - Number of series supported: 1
  - Image count each series (2 or more) in multiple phases
  - Vendors supported: any

The T1 Mapping Workflow

The T1 mapping workflow guides you through the process of examining the strength of tissues in a patient's study. This is especially important in studies focused on heart muscle.

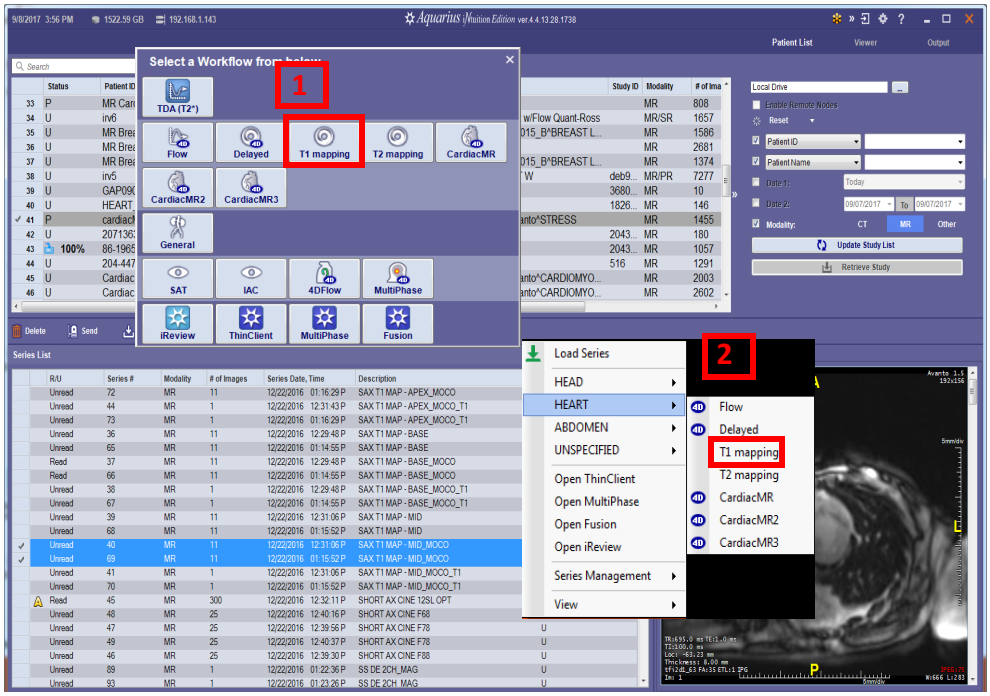
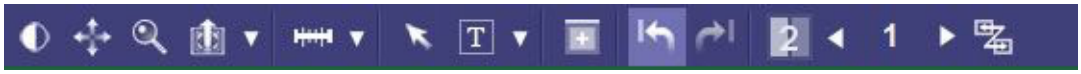


Figure 17-1 Selecting the T1 Workflow Template

Viewing an Image

Users can customize the tools in the top of the Viewer (basic list):



To customize the tools go to **Preferences>Viewer>Toolbar>Tool Button Groups**. Table 17.1 shows a basic list of icons and their corresponding usage. See "Chapter 3Top Toolbar Buttons" on page 3-143 for further details on Toolbar tools.

Table 17.1: Tools and Icons

Tool	Definition	Tool	Definition
Rotate (no icon)	**Rotate**		**Text Annotation.** The Arrow allows the user to choose where the annotation is placed: on the anatomy or on the screen.
	**W/L**		**Tile (Image) Layout**
	**Pan**		**Undo or Redo**
	**Zoom**		**Multi-data Display**
	**Scroll**		**Show Volume.** The arrows show the choice of going to previous volume or to the next volume.
	**Distance Measurement**		**Synchronize Images**
	**Arrow**		

Setting Preferences

Before starting the T1 Mapping Workflow, open the **Preference** window and adjust the T1/T2 mapping settings and then adjust the T1 Mapping settings. The settings in the following images are suggested only

and are used for illustration throughout this workflow. For default settings and options, see Appendix A: "GUI Configuration".

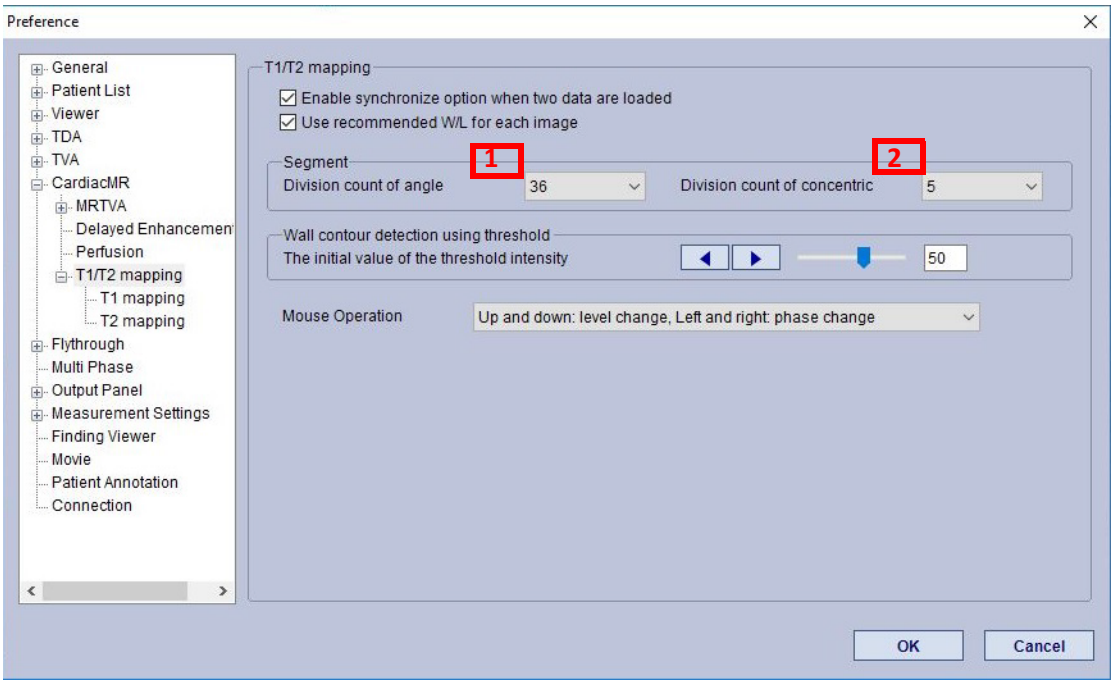


Figure 17-2T1/T2 Mapping Settings in the Preference Window

1. This setting is related to the number of segments in equal degrees around the myocardium. As an example, a clinician may 6 to match the AHA 17-segment model.

2. This setting is related to the number of rings that appear around the myocardium. As an example, a clinician may want only 1 division and to utilize the result areas for inner and outer myocardium.

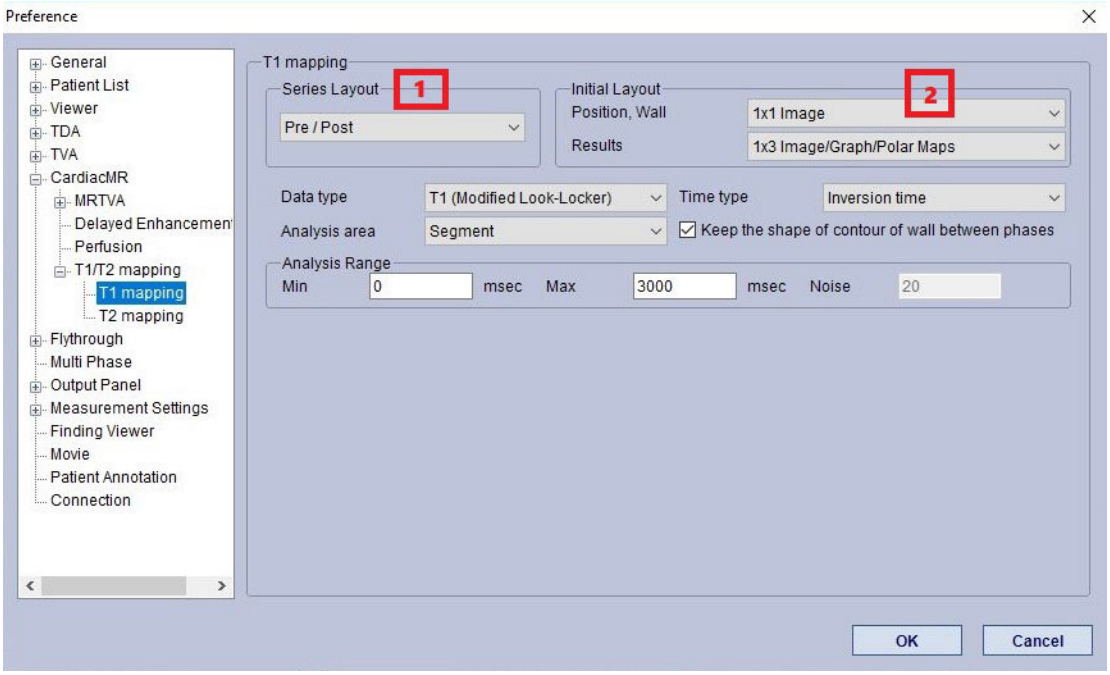


Figure 17-3Specific T1 Mapping Settings in the Preference Window

1. Specifies layouts of perfusion data loaded into the viewer.

2. Allows you select default layout for perfusion data loaded into the viewer.

To see default settings and options, see Appendix A: "GUI Configuration".

T1 Mapping Workflow

To start the T1 Mapping Workflow:

1. Select a study from the **Patient List**.
2. The **Series List** window is populated.
3. From the **Series List**, select a pre- and post- series. (Left-click and then hold the keyboard shift key to select multiple series.)
4. Select the **Load** button and the Workflow menu opens. You can also use the right-click and select a workflow from that menu.
5. Select the **T1 Mapping** workflow template.
6. The Viewer opens.

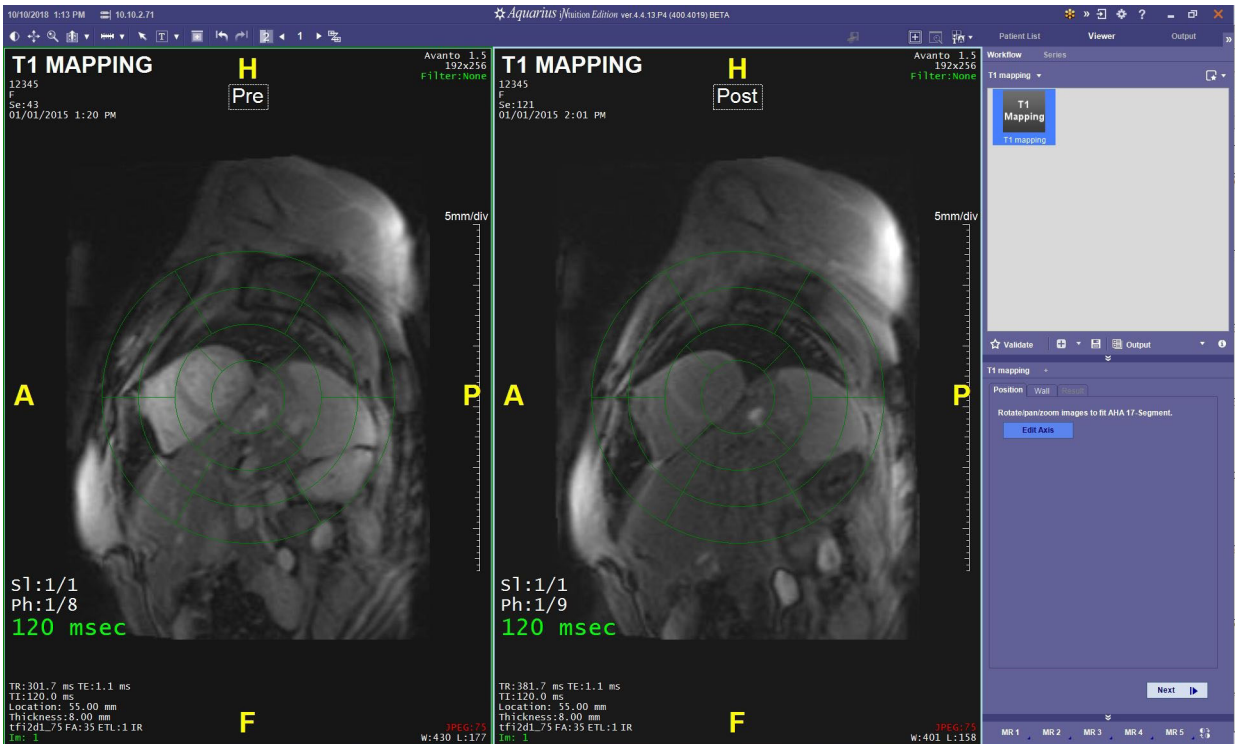
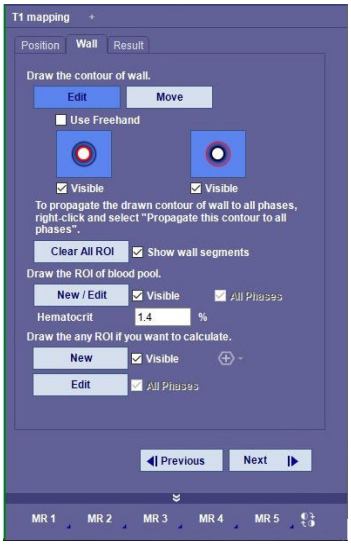
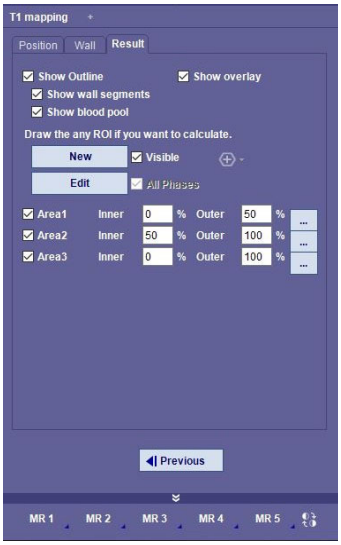


Figure 17-4 Pre- and Post- Images in the Viewer

Workflow Tabs

The mapping workflow steps through all three tabs in the T1 Mapping Tool panel.





Position Tab **Wall Tab** **Result Tab**

The loaded study opens with the **Position** tab open.

After loading, view the same image number for both Pre- and Post- images. Move or rotate the image as needed for viewing. **Rotate** is active after you select the **Edit Axis** button. To deactivate rotation, either click on the **Edit Axis** button, turning the edit off, or select a tool from the top toolbar, see Table 17.1 for information.

You need to center the heart under the 17-segmented circular grid that appears when you select the **Edit Axis** button.

- **Zoom:** Use middle mouse wheel to zoom by pressing down and moving mouse forward and back.
- **Pan:** right mouse click and hold, move mouse forward and back.
- **Rotate:** left mouse click and hold, move mouse forward and back.

To edit the heart axis:

1. Select the **Edit Axis** button and the 17-segmented, round grid appears on both images.
2. Left-click and hold the mouse button to move the grid or move the image so that the innermost circle of the grid is over the heart axis. Use **Zoom** and **Pan** to move the image under the grid until the heart axis is under the middle grid segment. (You may need to select **Edit Axis** and then select it again in order to move the image.)
3. When the center circle is over the heart, select the **Next** button.
4. The **Wall** tab opens.

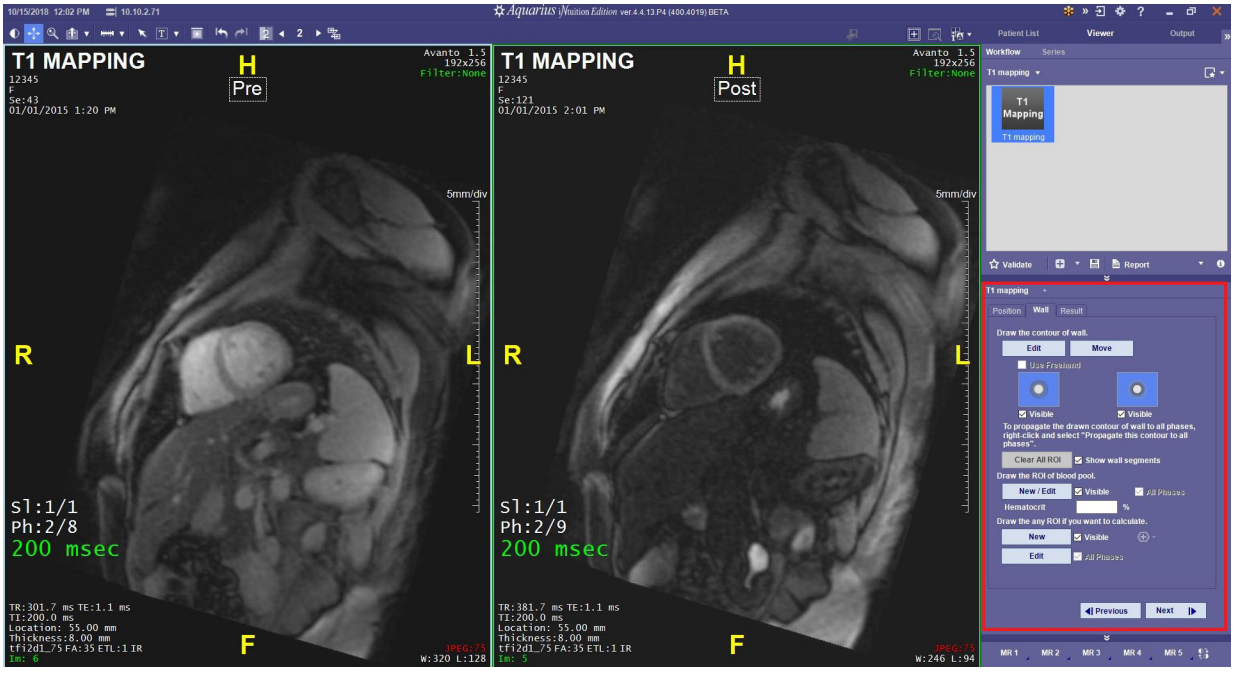


Figure 17-5Wall Tab

The grid does not appear after selecting **Next** on the **Position** tab. An easy practice for the **Wall** tab is to work your way from top to bottom on this tab.

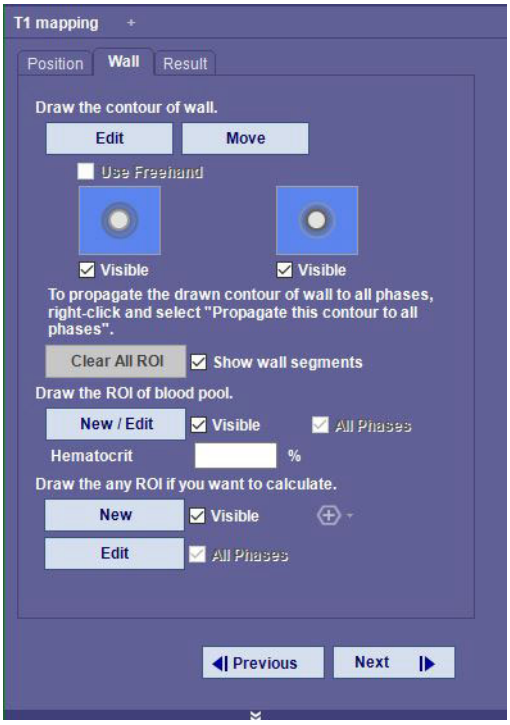
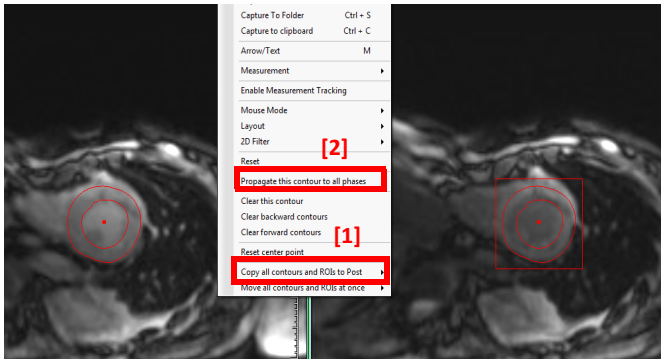


Figure 17-6Wall Tab

To draw the contour in the Post image automatically:

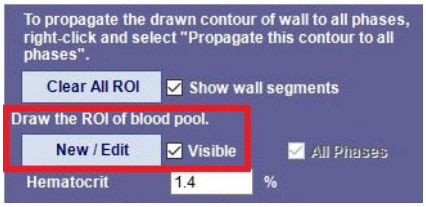
1. Select the **Edit** button.
2. Hold down the shift key and point-and-click along the inner boundary of the heart axis.
3. As you outline the inner contour, an attached outer contour is automatically drawn along the outer contour.
4. To see the segments of the contour, select the box for the **Show wall segments** setting next to the **Clear All ROI** button. These lines are segments areas connecting the two contours.
5. You can adjust the circle if needed by using the Shift key and clicking to adjust the shape.
6. The contour is highlighted in red.
7. After verifying and editing contours, right-click on the image and select **Propagate this contour to all phases** or select **Copy all contours and ROIs to Post** from the context menu.
8. Contours propagated to the series appear highlighted in blue indicating that placement is estimated.
9. Repeat these steps to draw a contour in the Pre- image.

10. When done, right-click on the image and select **Propagate this contour to all phases** or select **Copy all contours and ROIs to Post** from the context menu..



Next, draw the ROI of the blood pool:

1. Select the **New/Edit** button under **Draw the ROI of blood pool**.



2. Draw a small circle inside the heart contour by selecting the shift key and left-clicking to create the circle. This circle appears purple.

3. When complete, right-click in the image and select **Propagate contours to all phases (**or select **Copy all contours and ROIs to Post** from the context menu).

4. The **Blood Pool** now appears on each image slice and throughout the series images.

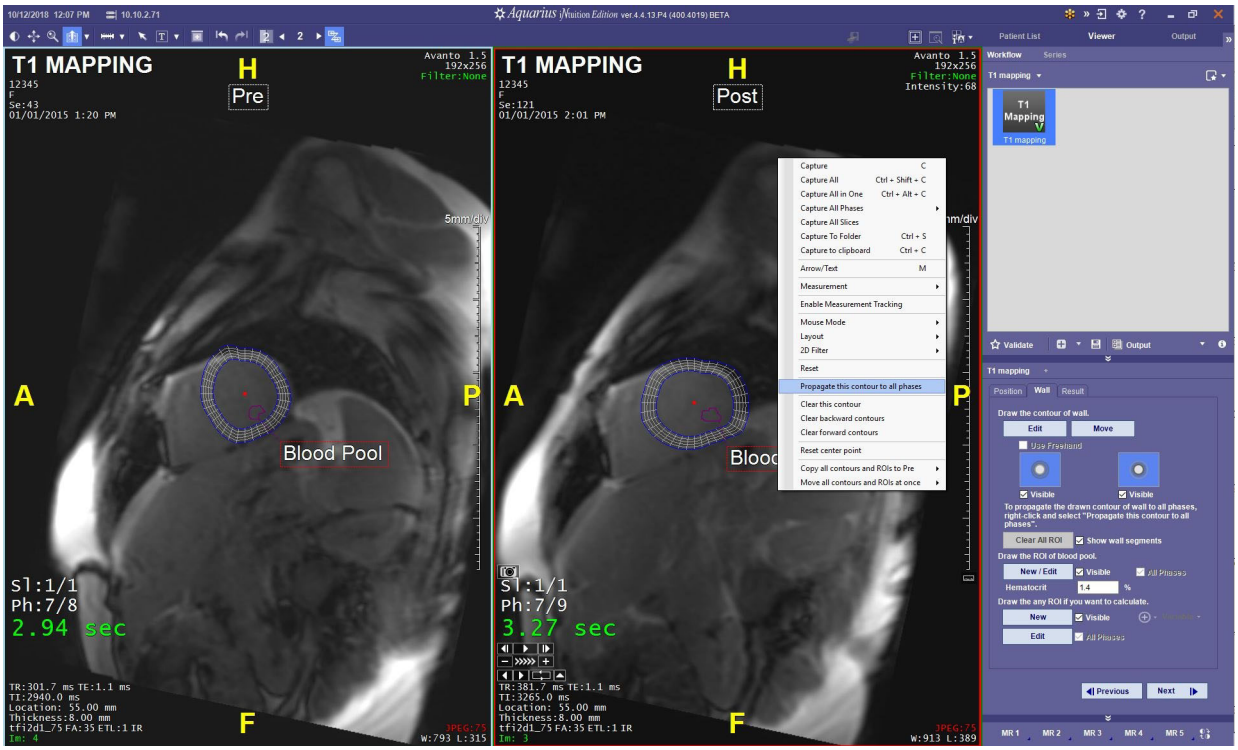
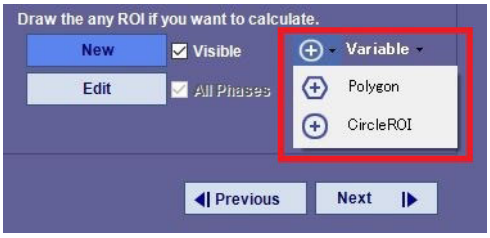


Figure 17-7 Propagating the Blood Pool Contour

5. Under the **New/Edit** button is a setting for **Hematocrit**. If needed, enter an appropriate percentage. For this workflow, 1.4 is entered.

6. You can draw additional ROIs for calculation. Under **Draw any ROI if you want to calculate**, select the **New** button.

7. This activates the drop down menu under **Variable** and you can select either a Polygon or Circle shape.



8. To draw additional ROIs, left-click on the image and the shape appears. You can size the shape by moving the mouse in the shape until you reach the desired size.

9. Select the **Propagate contours to all phases** and **Copy all contours and ROIs to Post** from the context menu as needed.

10. Select the **Next** button to go to the **Results** tab. Calculations begin to run.

The **Preferences** setting determines the layout of the images in the **Result** tab. See the selected setting in Figures 17-2 and 17-3.

Result Tab

Results display per preferences (**Preferences > Cardiac MR > T1/T2 Mapping > T1 Mapping > Initial Layouts**). The **Result** tab allows showing overlay (or raw image), show outline (for contours), and show wall segments for definition for areas. For Additional ROI calculations, use the ROI tool under the Result tab, or right-click to utilize the context menu.

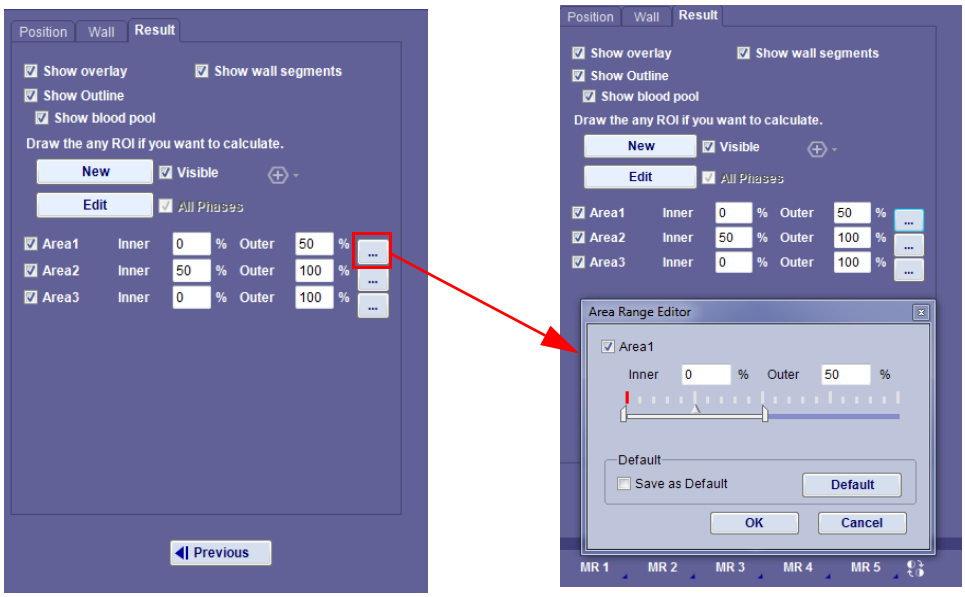
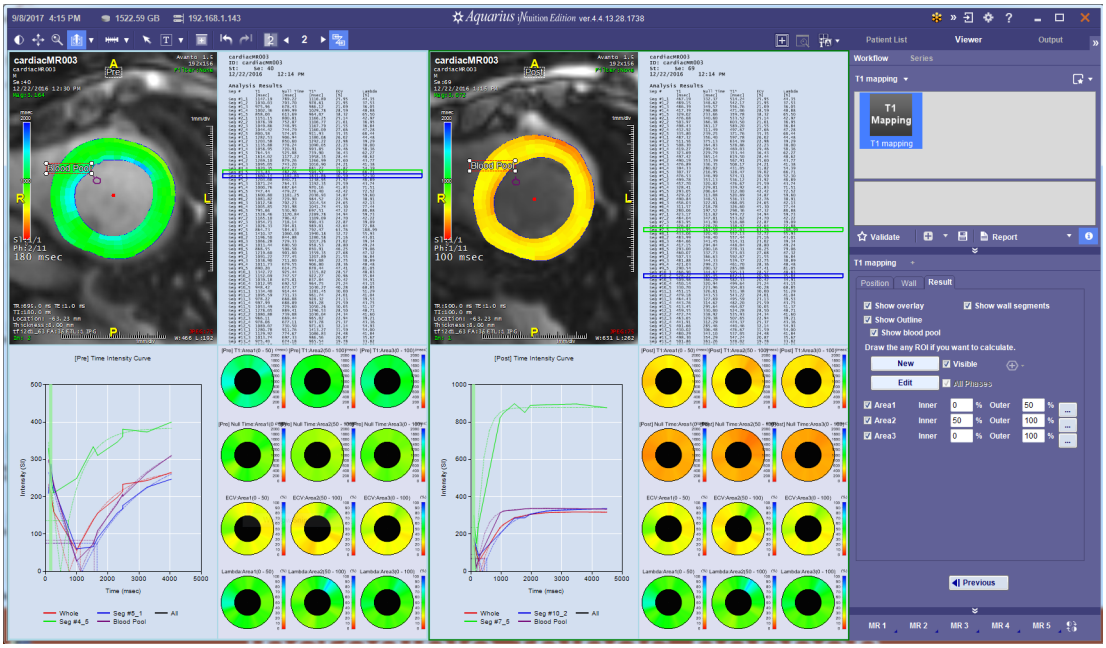


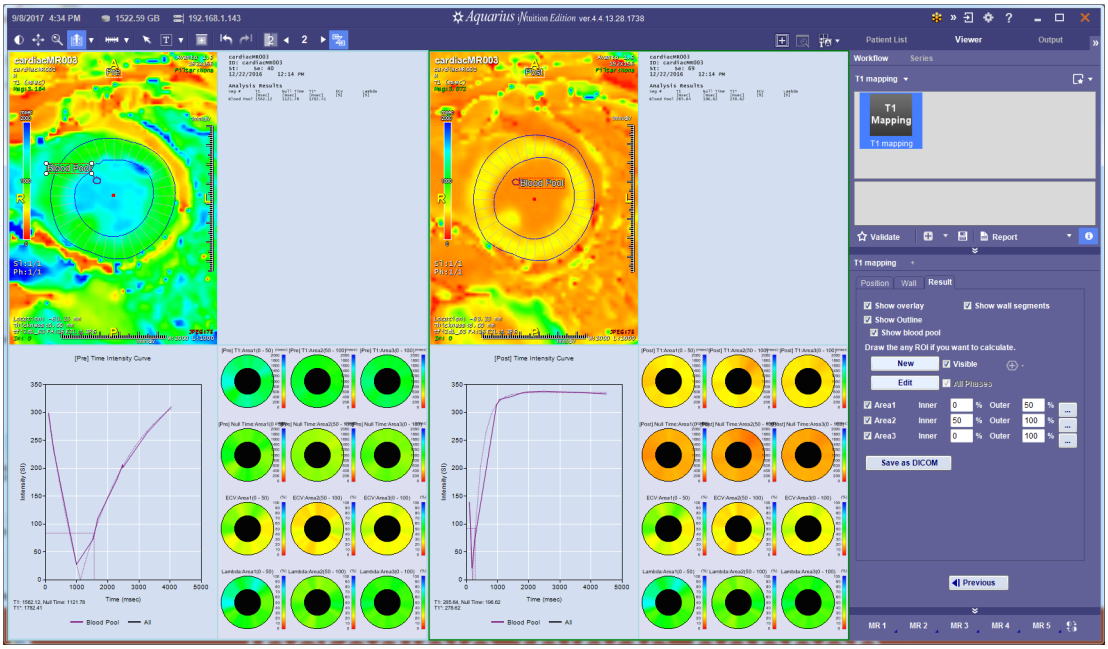
Figure 17-8 Tools on the Result Tab

Sample Result Layouts

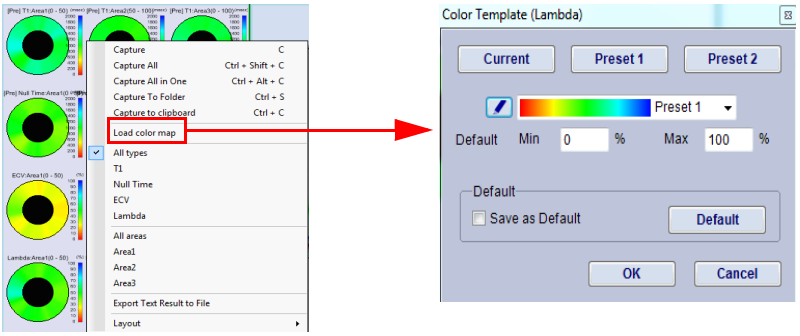
1. Selecting **All**:



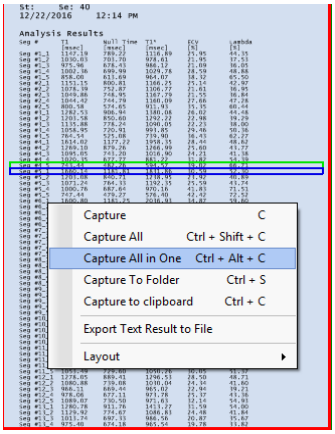
2. **All** (with pixel-wise checked in preferences):



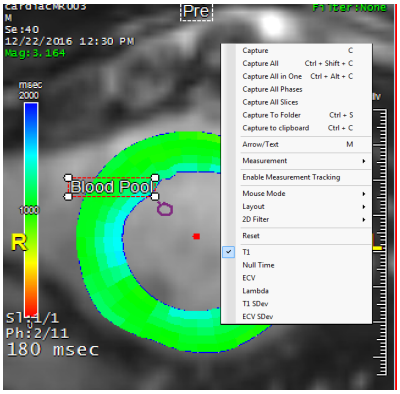
3. **Polar Map Options**: Right-click for context menu while on **Polar Map** viewer. Select All types, T1, Null Time, or Lambda. To change color map, select **Load Color Map** from the menu and edit in the **Color Template (Lambda)** box. Save as default if desired.

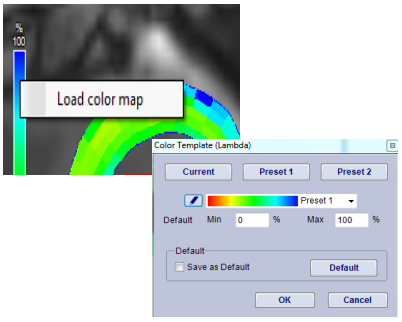


4. **Text Options**: When capturing text, it is recommended to Capture All in One so that the viewer contains all text in a single frame. Additional options include Capture to clipboard and Export Text Result to File.



5. **T1 Overlay Maps**: The overlay map will display T1 result as default. Change map by selecting from the context menu. Adjust the color maps by using the context menu (same as the polar map) or by right mouse clicking on the color bar.





The T2/T2* Mapping Workflow

The T2/T2* Mapping Workflow is very similar to the T1 Mapping Workflow.

Setting T2 Preferences

Before starting the T2 Mapping Workflow, open the **Preference** window and adjust the T1/T2 mapping settings and then adjust the T2 Mapping settings. The settings in the following image is suggested only and are used for illustration.

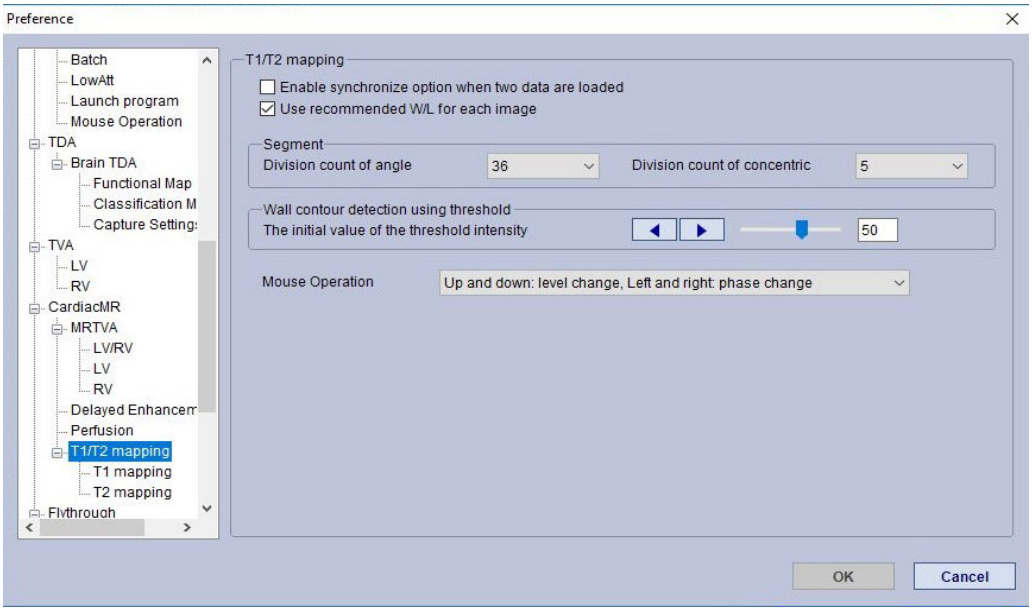


Figure 17-9T 1/T2 Mapping Settings in the Preference Window

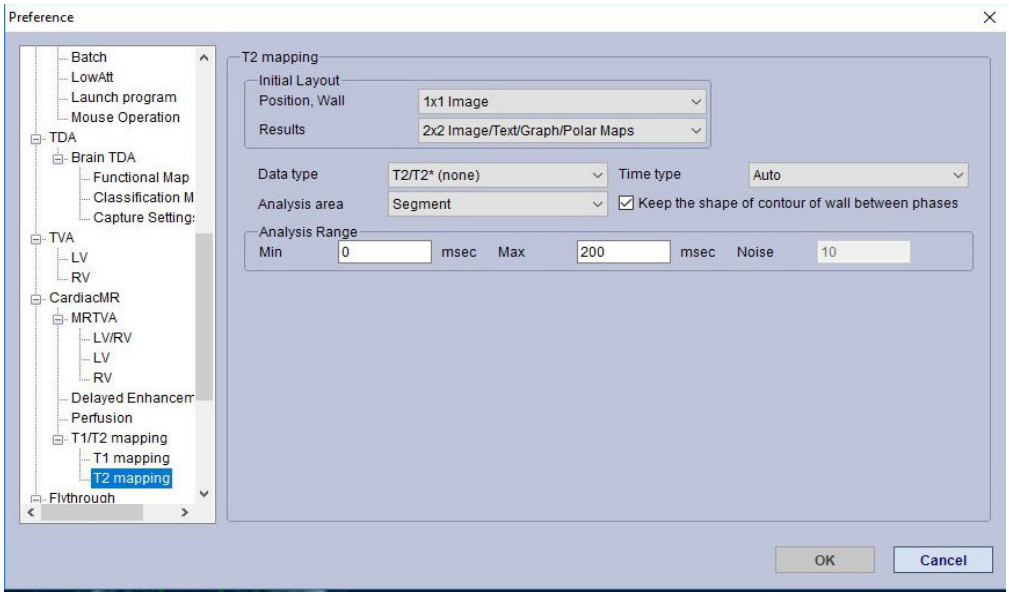


Figure 17-10 Specific T2 Mapping Settings in the Preference Window

To load a T2/T2* study:

1. Select a series from study list and select T2 Workflow.

2. Select **Load**, then choose **T2 mapping** [1] or use right mouse context menu [2].

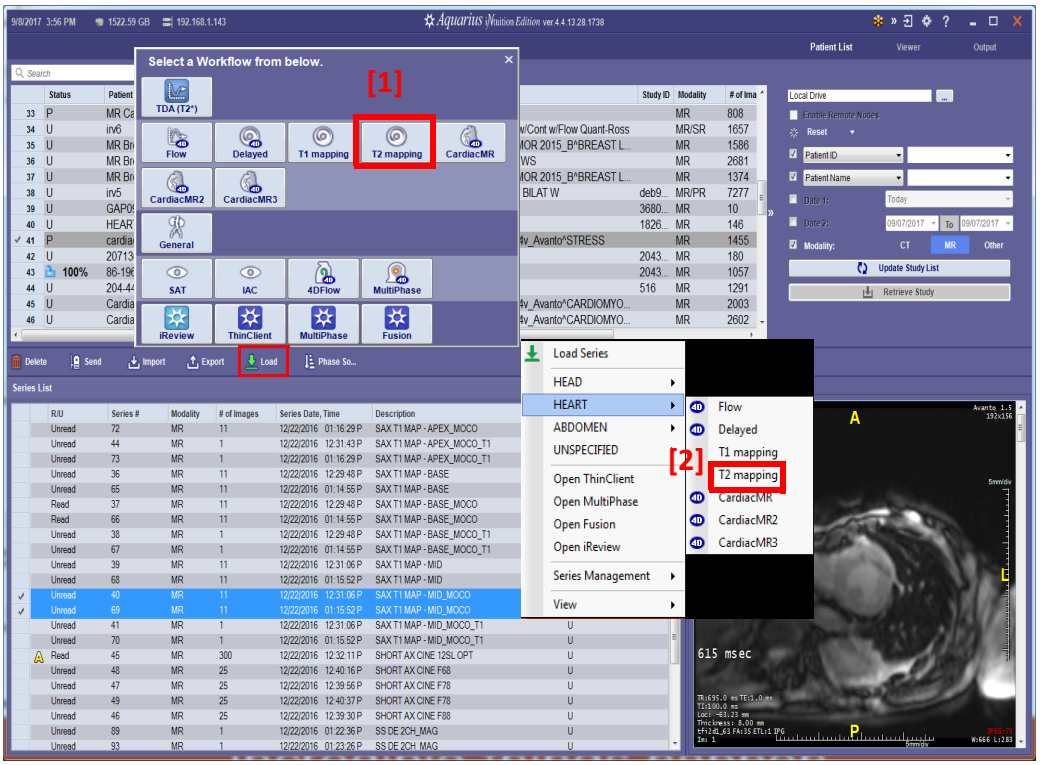


Figure 17-11 Selecting the T2 Workflow

Position Tab

The loaded study opens with the **Position** tab open.

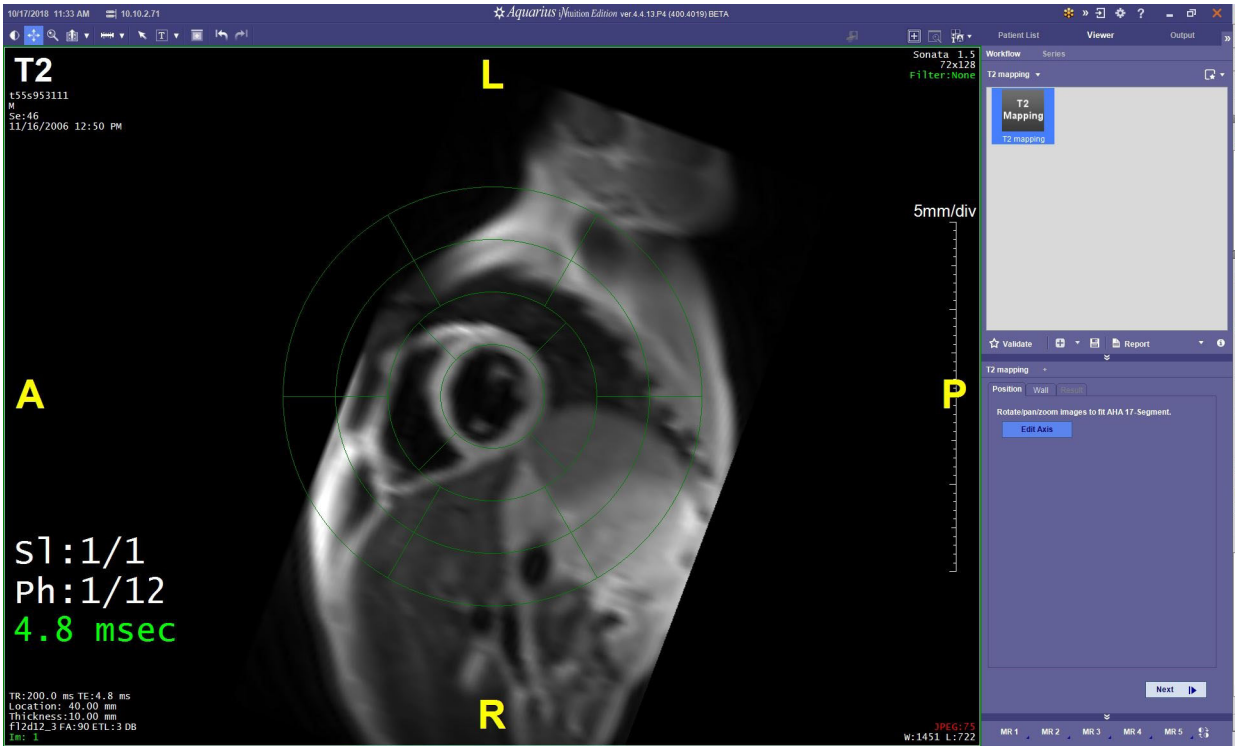


Figure 17-12Loaded Study and Position Tab

To edit the heart axis:

1. Select the **Edit Axis** button and the 17-segmented, round grid appears on both images.
2. Left-click and hold the mouse button to move the grid or move the image so that the innermost circle of the grid is over the heart axis. Use **Zoom** and **Pan** to move the image under the grid until the heart axis is under the middle grid segment. (You may need to toggle the **Edit Axis** button on and off in order to move the image.)
    - **Zoom:** Use middle mouse wheel to zoom by pressing down and moving mouse forward and back.
    - **Pan:** right mouse click and hold, move mouse forward and back.
    - **Rotate:** left mouse click and hold, move mouse forward and back.
3. When the center circle is over the heart, select the **Next** button.
4. The **Wall** tab opens.

The grid does not appear after selecting **Next** on the **Position** tab. An easy practice for the **Wall** tab is to work your way from top to bottom on this tab.

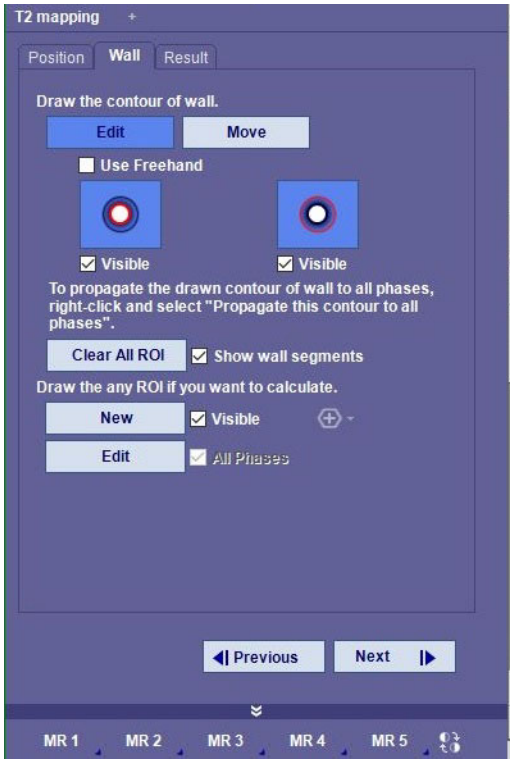


Figure 17-13Wall Tab

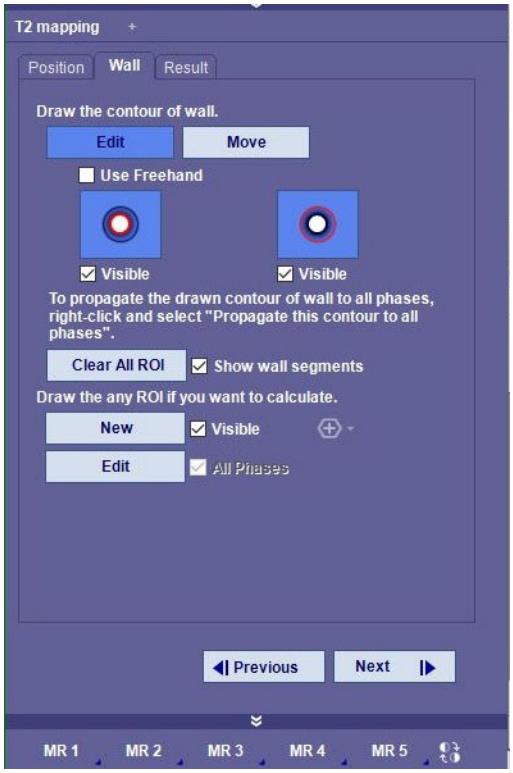
You can check the Use Freehand option to draw the contour by hand or to automatically draw the contour:

1. Select the **Edit** button.
2. Hold down the shift key and point-and-click along the inner boundary of the heart axis.
3. As you outline the inner contour, an attached outer contour is automatically drawn along the outer contour.
4. To see the segments of the contour, select the box for the **Show wall segments** setting next to the **Clear All ROI** button. These lines are segments areas connecting the two contours.
5. You can adjust the circle if needed by using the Shift key and clicking to adjust the shape.
6. The contour is highlighted in red.
7. After verifying and editing contours, right-click on the image and select **Propagate this contour to all phases** or select **Copy all contours and ROIs to Post** from the context menu.
8. Contours propagated to the series appear highlighted in blue indicating that placement is estimated.

Next, draw the ROI of the blood pool:

Wall Tab

1. The **Wall Tab** opens.



2. Select the **Edit** button. To free draw the contour **Use freehand** (with box checked).

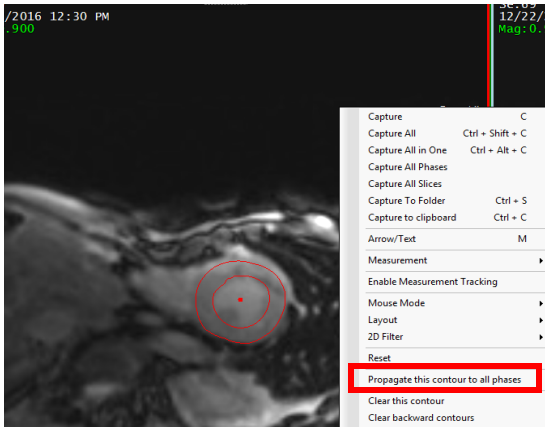
3. To automatically draw both the inner and outer boundaries, do not check the **Use Freehand**.

4. Use the Shift key left-click to outline the inner contour. The outer contour is connect to the inner.

5. Right-click on the image and select **Propagate contours to all phases** from the context menu.

6. Echo time should be automatically determined from DICOM scanner information. If echo time is missing, the software prompts for information.

7. You may also right-click on the green echo time annotation for the edit time information box. This information can be saved as a template.



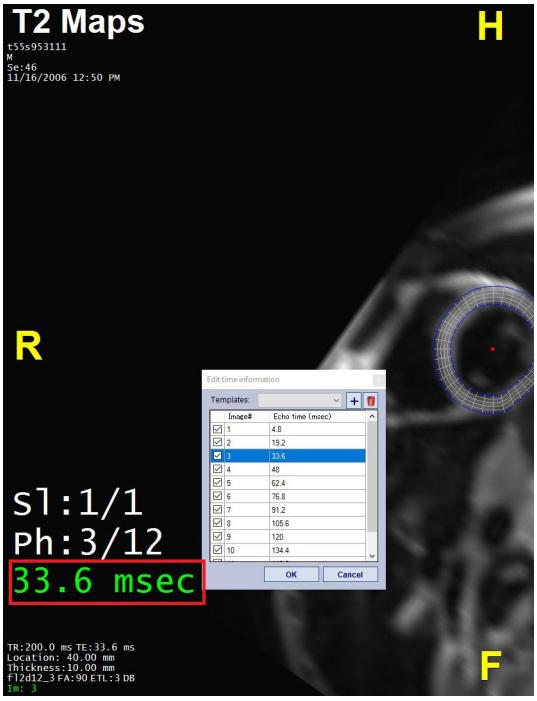
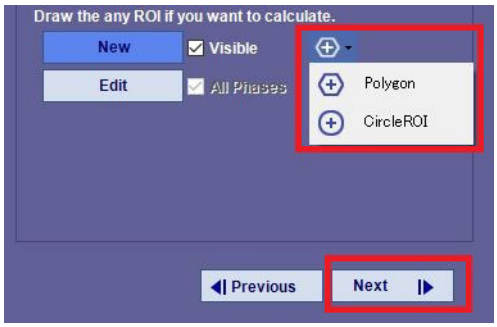


Figure 17-14 Right-click on the Echo Time; the Get Time Information Window Opens.

8. You can add ROI to be calculated on the **Wall Tab** or draw additional ROI on **Results Tab** utilizing the ROI tools.

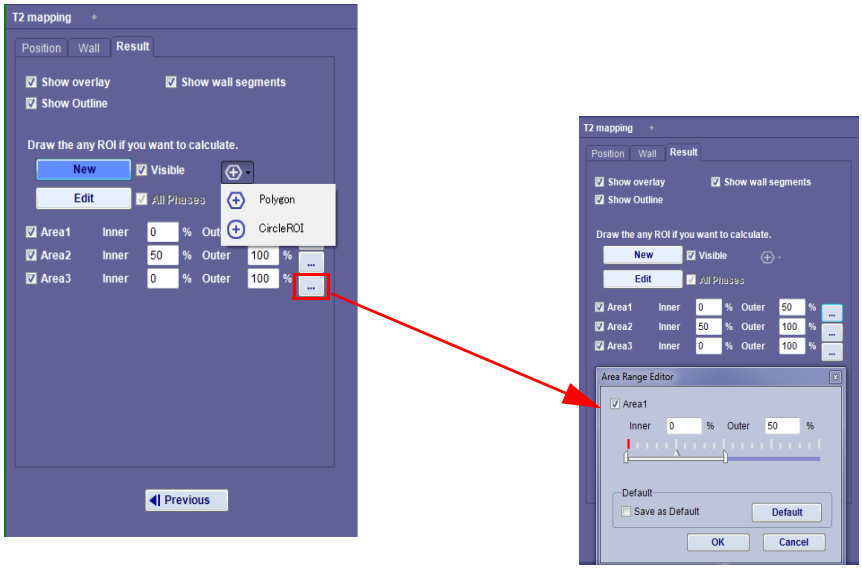


9. Select **Next** to go to **Result** tab.

Result Tab

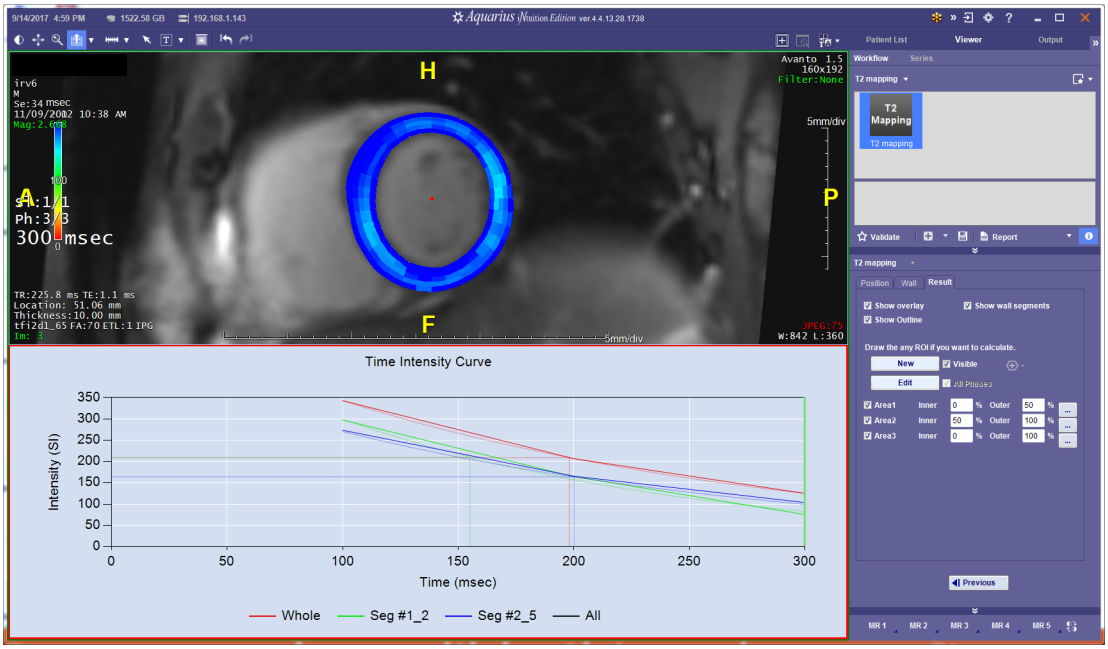
The **Result** tab displays per preference settings (**Preferences > Cardiac MR > T1/T2 Mapping > T2 Mapping > Initial Layouts**). The **Result** tab allows you to show overlay (on raw image), show outline (for contours), and show wall segments and definition for areas.

For **Additional ROI calculations**, use the ROI tool on the **Result** tab, or right mouse click to utilize the context menu:

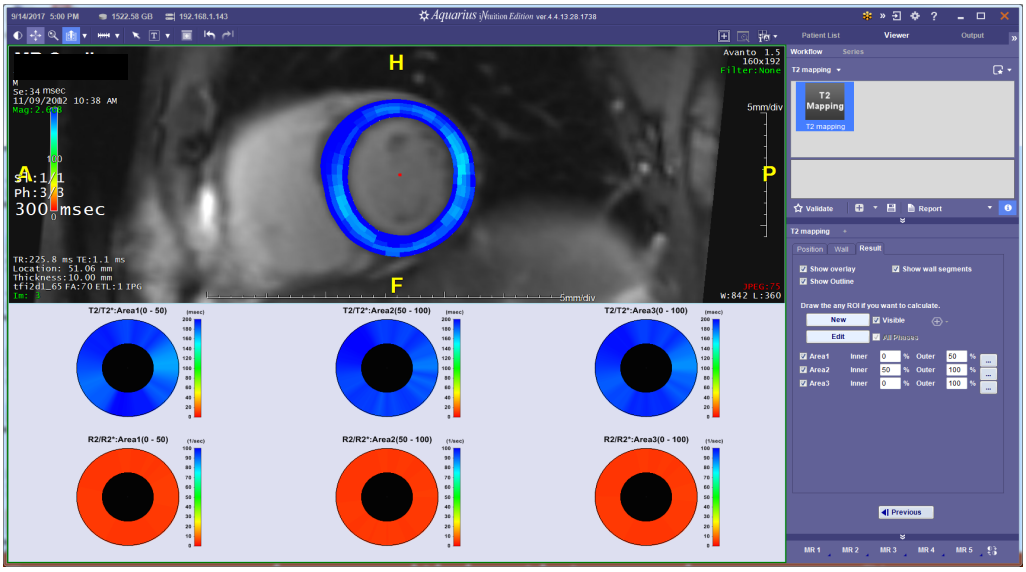


Sample Result Layouts

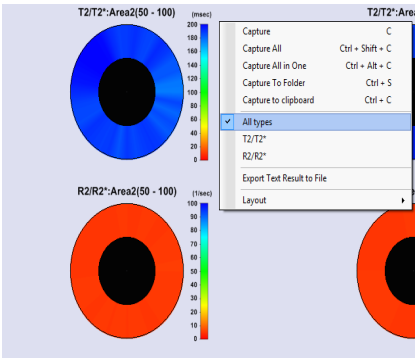
1. 1x2 Image/Graph



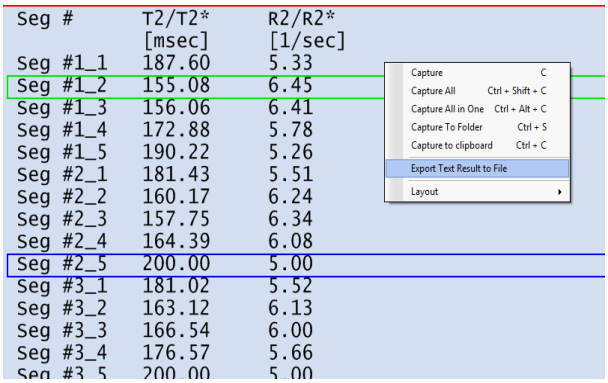
2. 1x2 Image/Polar Map



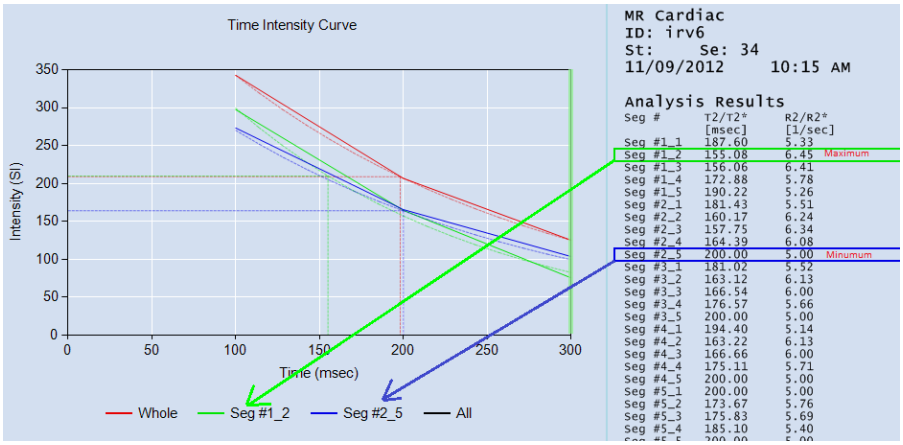
3. Polar Map Options: Right mouse click for context menu while on Polar Map viewer. Select **All** types, T1, Null Time, or Lambda. To change color map, select **Load Color Map** from the menu and edit in the **Color Template (Lambda)** box. Save as default if desired.



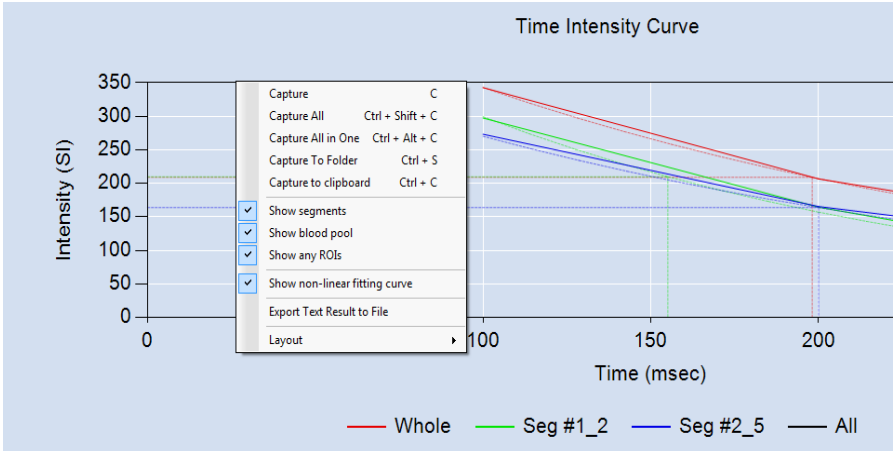
4. Text Options: When capturing text, it is recommended to **Capture All in One** so that the viewer contains all text in a single frame. Additional options include **Capture to clipboard** and **Export Text Result to File.**



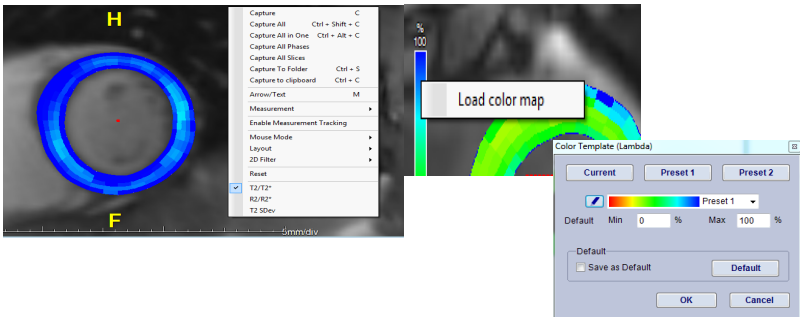
Note: The software automatically detects the maximum and minimum values. These are highlighted on the text results and graphs with blue and green lines, shown above and below.



5. **Graph Options:** Use check boxes to show segments, blood pool or ROI curves or choose between linear or non-linear fitted curves. You may also show/hide curves by left mouse click on the graph labels.



6. **T2 Overlay Maps:** The overlay map will display T2 result as default. Change the map by selecting from the context menu. Adjust color maps by using context menu (same as polar map) or by right-mouse clicking on color bar.



Chapter 18 Dual Energy and MultiKV Applications

Topics in this chapter:

The optional VEn Workflow is developed for Dual Energy CT scan data. It provides blending capability to improve the contrast-to-noise ratio, bone-subtraction for CT angiographic studies, and contrast media removal to improve anatomic definition.

The virtual data without enhancement reconstructed from the VEn module can be used to differentiate between normal and abnormal tissues, and to reduce image noise from metal artifact, maximizing reading efficiency.

These capabilities can improve detection and characterization of lesions in the abdomen and pelvis and for the evaluation of vascular structures.

Note: The instructions in this section of this chapter use a Siemens Dual Energy series (140KV and 80KV) as an example. However, you can use this feature with data from other vendors and/or with different KV values.

Dual Energy

Load a dual energy study into the **VEn** Workflow.

The images are loaded in 4X1 layout, with the 80KV series in the left column and the 140KV series in the right column. Each series shows a 3D image in the top row and three MPR images (axial, coronal and sagittal) in the three lower rows.

The study is reloaded, displaying one image from each series: 80KV (left), 140KV (middle) and the blended series (right). (Figure 18-1)

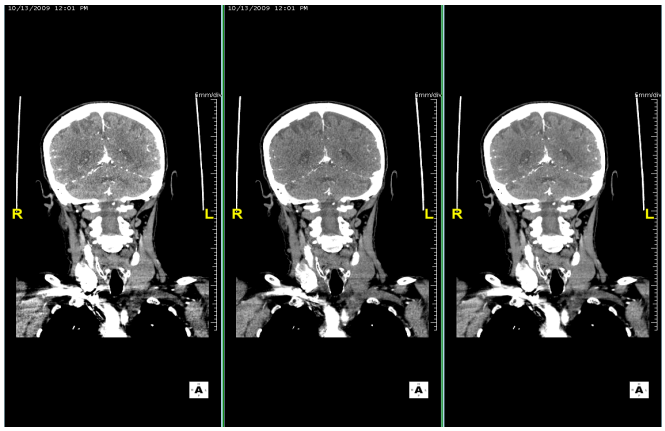
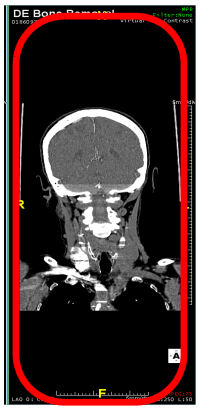


Figure 18-1 Three Series - 80KV, 140KV and Blended

Basic Tools



The **CTA** tab (displayed initially by default) contains the following tools:

- **Remove Bone** — Click **Remove Bone** to create the bone removal volume.
- **Remove Contrast** — Click **Remove Contrast** to create the virtual non-contrast volume. The image below shows the blended image without contrast.
- **Percentage Slider —** Drag the slider bar on the control panel to change the percentage of the third (Figure 18-1) image. This example is set to the monochromatic adjustment. Select the **Use Blender** box to turn this setting off.

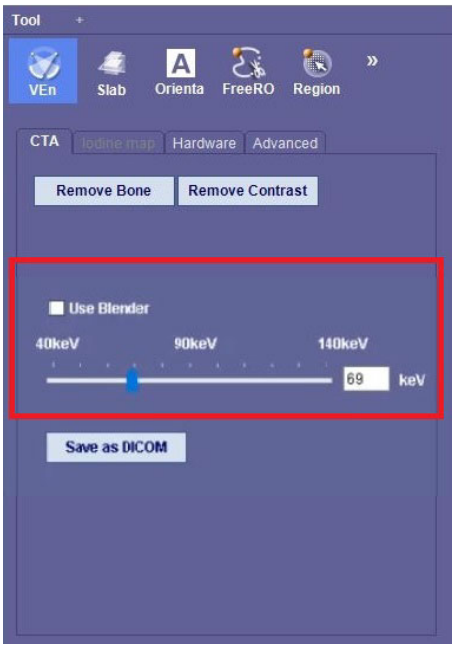


Figure 18-2 Slider set to Monochromatic

The slider setting determines the HU values for the blended image. For each pixel in the blended image, the HU value is set to [slider setting]% of the HU value of the corresponding pixel in the 80KV image, plus (100-[slider setting])% of the HU value of the corresponding pixel in the 140KV image.

This can be written in equation form as follows:

For each pixel in the blended image, where S = the slider setting:

$$HU_{Blended} = S/100 * HU_{80KV} + (100 - S)/100 * HU_{140K}$$

Example

Suppose the HU value of a pixel in the 80KV image is 400, and the HU value of the corresponding pixel in the 140KV image is 300. The slider is set to 75. Then the corresponding pixel in the blended image will be calculated as:

- 75% of 400 = 300
- 25% of 300 = 75

- HU of pixel in blended image = 375

As you move the mouse, the blended image is changed in real time. This is because only the slice that is displayed is being updated. When the mouse is released, the entire volume is calculated to the current blend percentage setting on the slider.

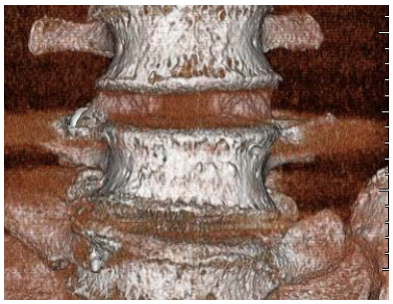
- **Save as DICOM**

Click **Save as DICOM** to save the newly created volume set to the server as a new series. A dialog is opened for you to enter a series number in the bottom text box. (The description is optional.) Refresh the Patient List to show the new series.

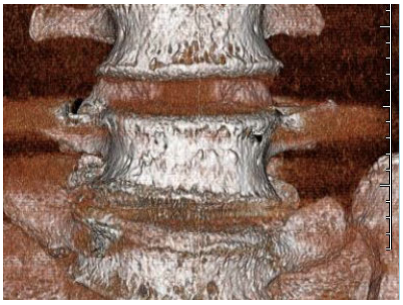
Hardware Removal Tab

Click the **Hardware** tab if the patient has any hardware to remove from the image. You can adjust the threshold that determines what is removed by using the **Threshold** slider under the **Remove Hardware** button. Then click the **Remove Hardware** button.

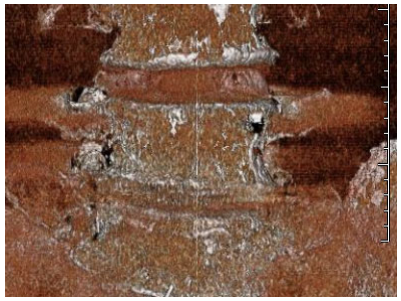
Figure 18-3The Hardware Tab



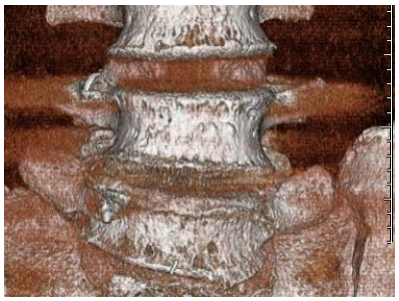
Before removal



Threshold at 45 percent



Threshold at zero percent



Threshold at 100 percent

Figure 18-4: Removing Hardware at Different Threshold Settings

In this case, setting the threshold to 45 percent gave the best results. A setting of a zero percent threshold removed too much, and at 100 percent threshold, nothing was removed.

Advanced Tab

Click the **Advanced** tab to view the advanced features panel for dual energy data.

The main window changes to a 2x2 layout. The top row shows the 80KV (left) and 140KV (right) images. The image in the bottom-left quadrant is called the *reference image*. The bottom-right quadrant contains a graph that corresponds to the reference image. See Figure 18-5.

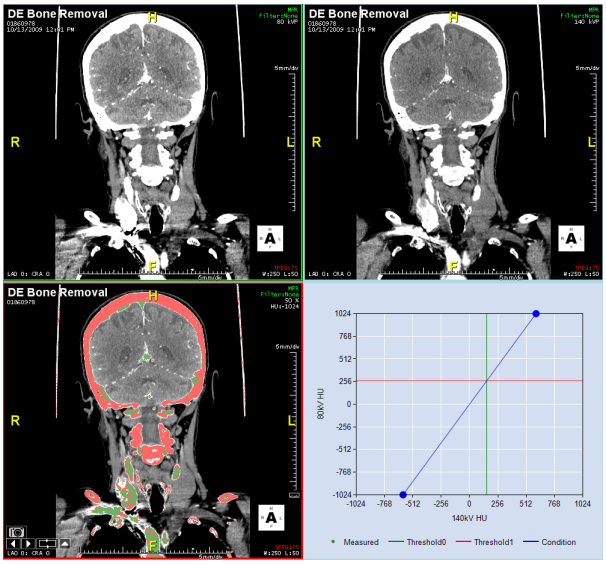


Figure 18-5: Advanced Tab Main Window

The Tissue Separation Graph

The graph shows the portions of the reference image that fall within defined HU values at each energy level.

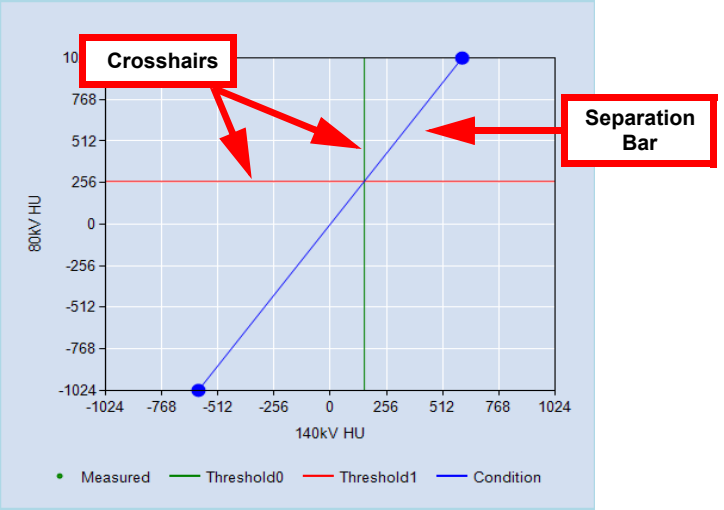


Figure 18-6Crosshairs and Separation Bar

The crosshairs (Figure 18-6) together with the upper bounds of possible HU values, form a bounding box around the area of HU values that are being evaluated. (Figure 18-7) Tissue having these values will show color overlay in the reference image.

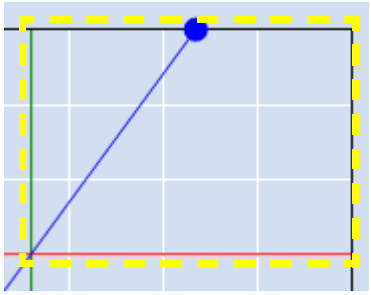


Figure 18-7The Tissue Separation Bar

The tissue separation bar (Figure 18-7)provides a threshold between the two types of tissue, based on the HU values obtained from each scan. Tissue whose HU values fall between the green crosshair (Figure 18-6) and the blue separation bar display a green overlay on the reference image. Tissue whose HU values fall between the separation bar and the red crosshair (Figure 18-7) display a red overlay. HU values falling entirely outside the bounding box do not display an overlay in the reference image.

Adjust the crosshairs to widen or narrow the HU values included in the overlay. (Figure 18-8)

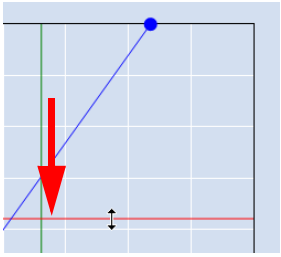


Figure 18-8 Adjust the Crosshair Lines

Adjust the separation bar to change the separation threshold between the two types of tissue.

Analyzing the HU Values in a ROI

Use the **Ellipse (virtual energy)** measurement tool to draw an ROI on any of the images. Measurements are displayed in the corresponding locations on each of the images. A dot is displayed on the graph to represent the tissue within the drawn ROI.

Saving Current Separation as Template

To save the current separation as a template, select the **Add** button. Enter a name for the template in the dialog that opens. To load an existing template, click the **Template** button, and then click the name of the desired template. The reference image and graph are changed accordingly.

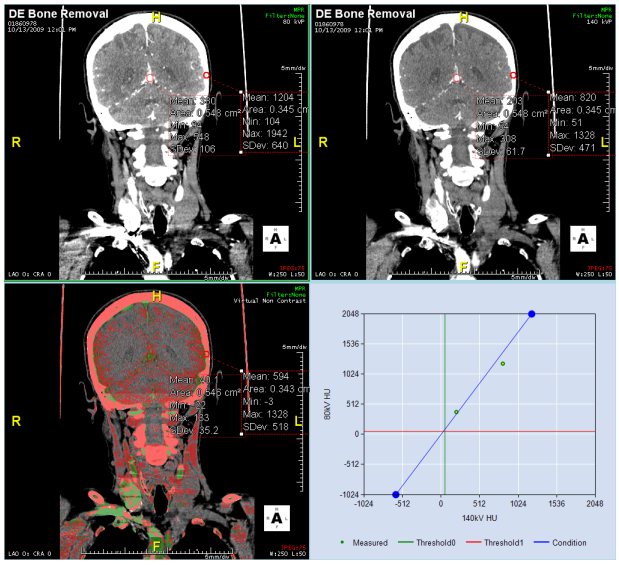


Figure 18-9: Results of New Template

Iodine Mapping

VEn Layout Options

There are four different layouts in the VEn workflow. The first layout (element) confirms and accepts the APS result.

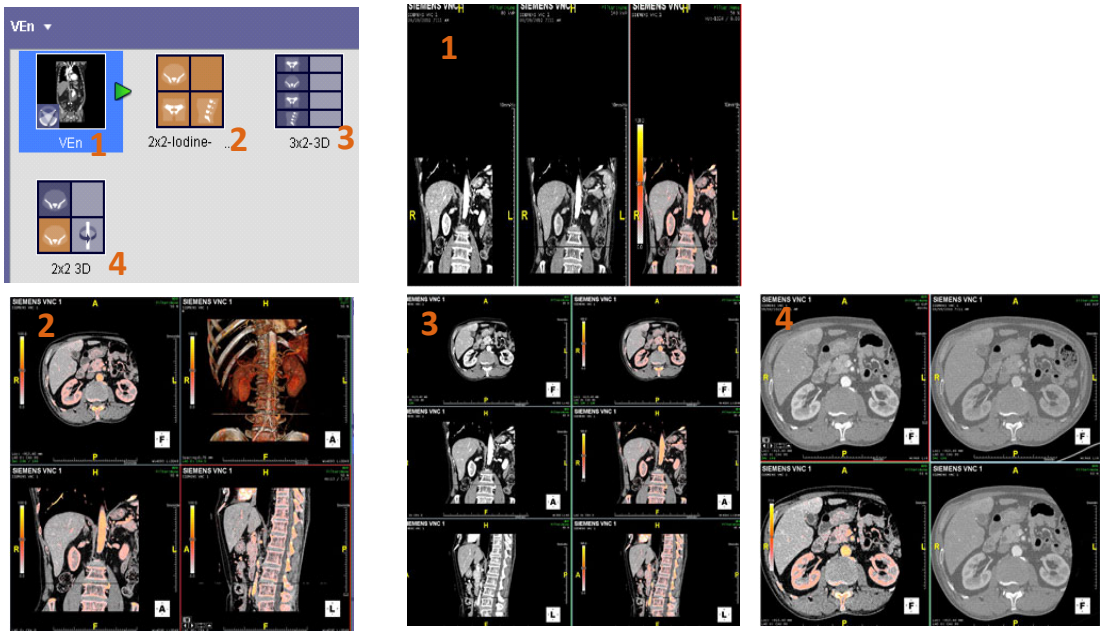


Figure 18-10 Layout Options

APS Processor

R/U	Series #	Modality	# of Images	Series Date, Time	Part	Description
Read	8	CT	392	09/09/2010 07:15:02 A	ABDOMEN	DE DE_Abdomen 0.75 D30f A_140kV
Read	9	CT	392	09/09/2010 07:15:02 A	ABDOMEN	DE DE_Abdomen 0.75 D30f B_80kV
Unread	10	CT	392	09/09/2010 07:16:19 A	ABDOMEN	DE DE_Abdomen 0.75 D30f M_0.3
Read	900	CT	392	08/29/2017 02:06:22 P	ABDOMEN	AqAPS_Iodine_Density_Map

Figure 18-11 APS Processor

The APS Processor will show Iodine Mapping Results with the description AqAPS_Iodine_Density_Map. This enables you to see if the APS processor has processed this study for the given series.

Relative Values verses Absolute Values

Selecting the check box in the VEn element under the Iodine Map tab toggles between displaying absolute pixel values or relative percentages.

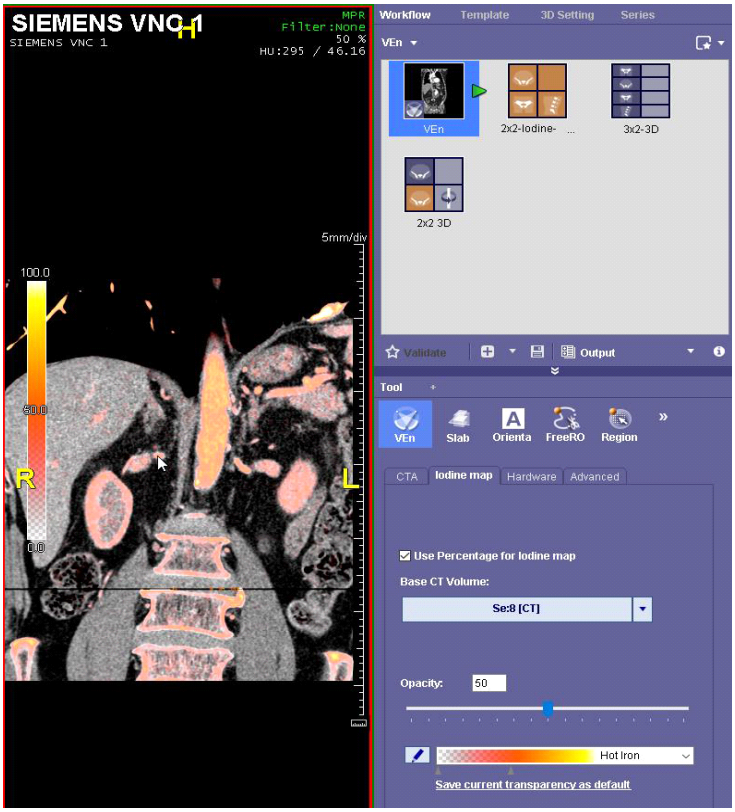


Figure 18-12 Iodine Map Tab

VEn ROIs

Each ROI drawn on the viewer displays values for the low and high energy series.

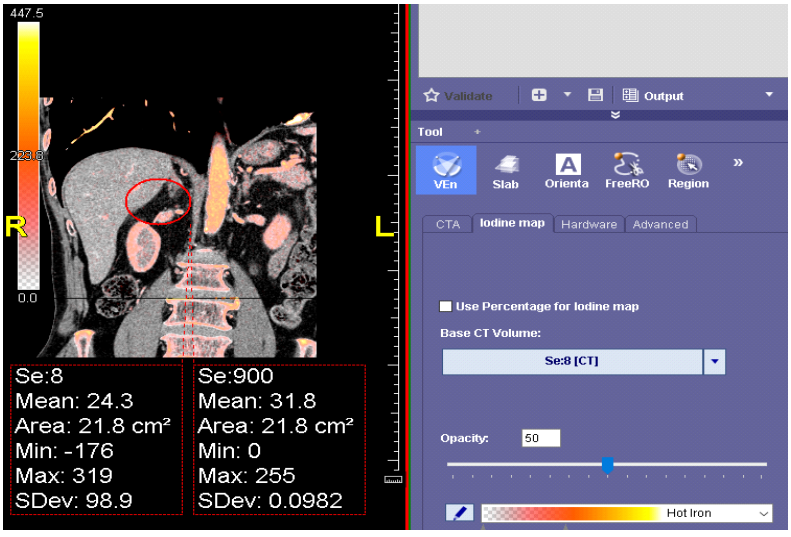


Figure 18-13 Low and High Energy Series

Chapter 19 Dynamic Volume Fusion

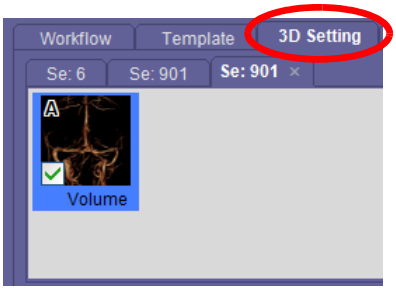
Dynamic Volume Fusion fuses different imaging modalities (up to 4 volumes), to provide a more complete picture of the anatomy for visualization. This module can be applied to compare anatomic information with function, localization and boundary definition of organs and lesions, and planning, biopsy, or surgery. Dynamically fused volumes cannot be saved as DICOM.

Fusing Images for Visualization

In the example used in this chapter, a CT series and two MR sub-series are loaded as three separate head scans. The CT series shows the skull and is used as a base. One of the MR series shows vessels, and the other MR series shows pathology in the brain.

Creating Masks

If you require a volume mask that is not present, you will need to create one. Masks can be viewed in the 3D Setting tab of the Workflow panel.



For more information about creating masks and the 3D settings, see "3D Settings Tab" on page 3-10.

Opening Dynamic Volume Fusion

To open the fusion panel, click the dynamic volume fusion button, which is located on the top toolbar.

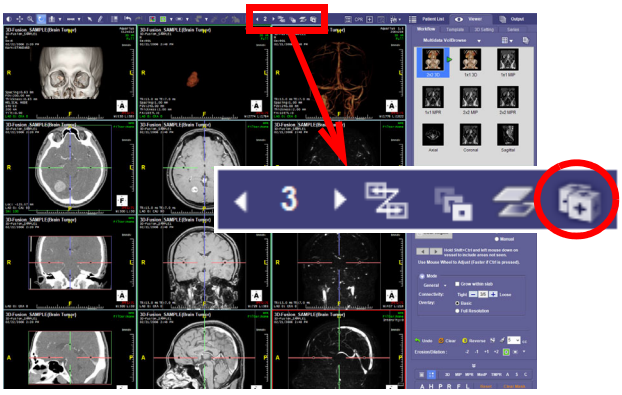


Figure 19-1: Dynamic Volume Fusion Button

The Dynamic Volume Fusion Tool Panel

When dynamic volume fusion is opened, the layout is changed to 3x1, with the volume image in the main view, and MPR images in a column on the left side of the viewer. The Fusion tool panel is located just below the 3D VR image (see Figure 19-2).

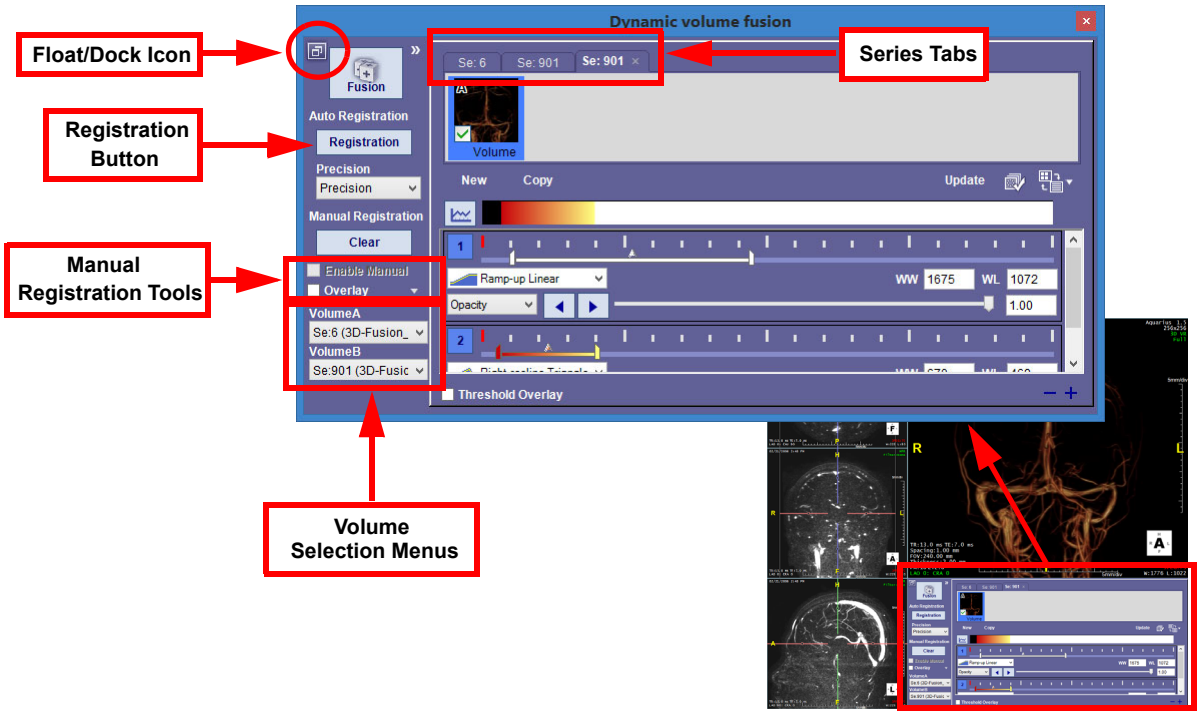


Figure 19-2: Dynamic Volume Fusion Tool Panel

The Fusion tool panel has a multi-mask and multi-object view, similar to the 3D Setting area of the AQi viewer. There is a separate tab for each loaded series, and a volume mask is shown in each tab. The volume fusion enable button (**Fusion**), **Registration**, and associated menus are located on the left panel.

The Fusion tool panel can be floated so that it can be moved independently of the AQi viewer. Click the float/dock icon in the upper-left corner of the Fusion tool panel to pop it out of the viewer. Click the icon again to dock it in the viewer.

Dynamic Volume Fusion Modes

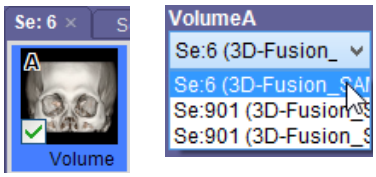
There are two modes of operation in dynamic volume fusion: Edit and Fusion. In Edit mode, you can edit the masks and perform registration. Fusion mode allows you to isolate components of the fusion image, while showing an overlay of the base.

Registration

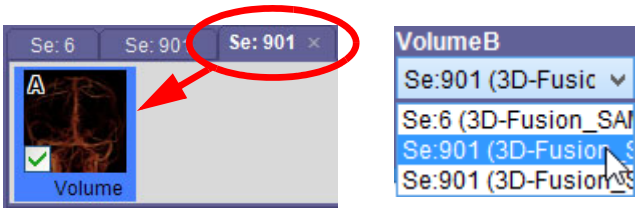
Registration is performed on two volumes at a time, referred to as **VolumeA** and **VolumeB**. Before beginning the registration, select the two volumes to be registered in the volume selection menus (see Figure 19-2).

As stated earlier, the example used here contains two series, a CT scan of the bone (skull), and an MR scan split into two sub-series, one of the vessels of the brain and the other containing the ROI.

The CT scan is the base for registration, and should be selected as VolumeA (see image at right).



Select one of the MR sub-series as VolumeB, to register against VolumeA (see figure below).



When this registration is complete, select the other MR sub-series as VolumeB, to register the second scan against the base.

Auto Registration

Click the **Registration** button in the Fusion tool panel to run auto registration. This will align the volume selected as VolumeB against VolumeA. To run auto registration on another volume, select that series or sub-series as VolumeB, and click **Registration** again.

Note: You must validate automatic registration before assigning any clinical significance. Please check the registration results on the axial, coronal and sagittal views. Please use manual registration if you are not satisfied with the results of auto registration.

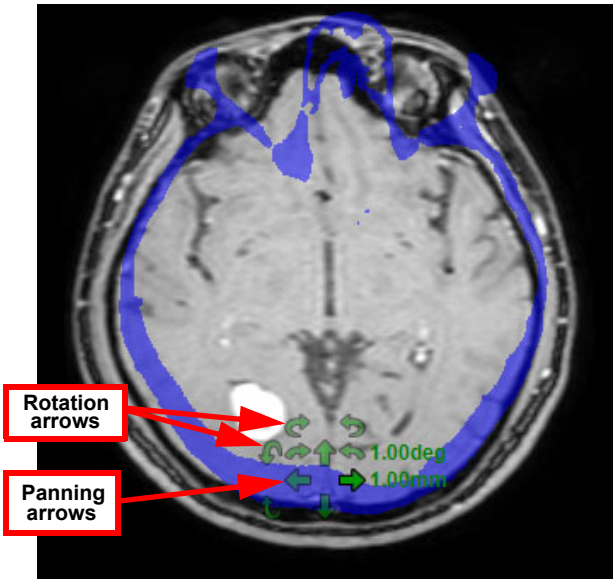
Manual Registration

To perform manual registration, do the following:

1. Click the **Overlay** checkbox (see Figure 19-2 on page 19-2).
2. Click the **Enable Manual** checkbox.
3. Select Volumes A and B from the volume selection menus.
4. Move the overlay to align it with the base (as described in the following instructions).

Tools For Moving the Overlay on MPR Image

Hover the mouse over one of the MPR images, and you will see a set of directional arrows near the bottom of the image:



This tool allows you to make minute changes in the position or orientation of the overlay with respect to the other volume.

The four straight arrows allow you to pan the overlay up, down, left or right.

Note: You cannot pan in a random direction when using arrows.

The three sets of curved arrows allow you to rotate the overlay around one of three axes, each corresponding to the orientation of the MPR images. Each axis of rotation has two directional arrows, one clockwise, and one counterclockwise. The overlay on the 3D VR image rotates with the overlay on the MPR images.

You can configure the distance each arrow click will pan the overlay, and the number of degrees for each click on a rotation arrow. To the right of arrows are two unit values. Right-click on the degree value to change the angle of rotation for each click. Right-click the distance value to change the distance (in millimeters) to pan with each click on a panning arrow. Select **Edit** from the menu to enter a value not provided in the menu.

Note: It is essential to do manual registration on all three MPR images.

You can also pan the overlay on the MPR images in the usual way, by holding down the right mouse button and dragging the overlay across the image. This is useful when you do not need to be very precise, but you need to pan in any direction.

Note: It is your responsibility to verify that the placement of overlays is accurate, on the 3DVR image and on each of the MPR images, so that fusion will be accurate. If you are not satisfied with any of the overlays, you must adjust them manually.

Dynamic Volume Fusion Mode

Fusion mode fuses the volume images together. The fusion image is displayed in the main view, with the three MPR images displayed on the left side of the viewer.

While the data is in fusion mode, you will not be able to perform mask operations. However, you can continue to rotate, pan, zoom or change the W/L on a fused image. To perform a mask or segmentation operation, click the **Fusion** button to toggle fusion mode off.

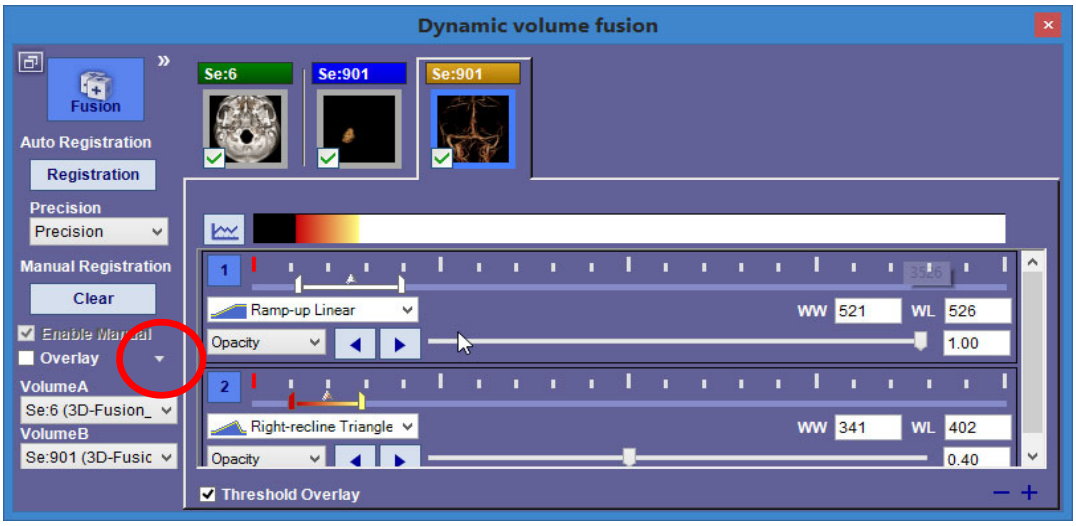


Figure 19-3: Fusion Mode

In fusion mode you can isolate one or more of the volume masks. When a mask icon in the fusion tool panel is checked, the corresponding mask is shown in the main view. In Figure 19-4 below, the fused image on the left is shown with all three masks visible. The mask icons shown below (from the Fusion tool panel) are all checked. On the right, only one of the mask icons is checked, and only the corresponding mask is displayed in the main view.

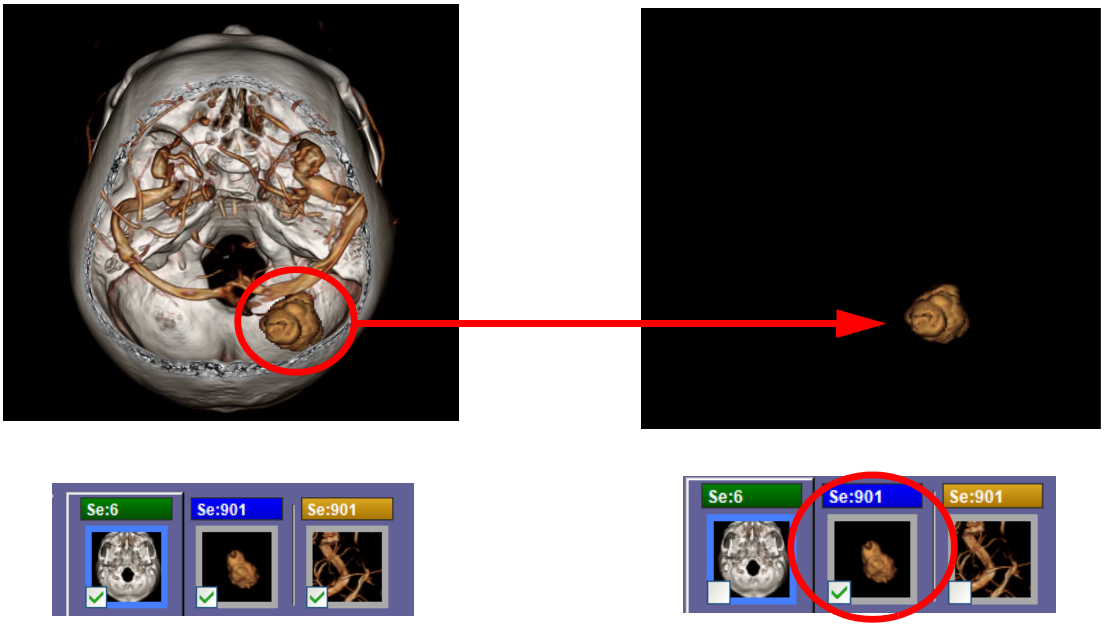
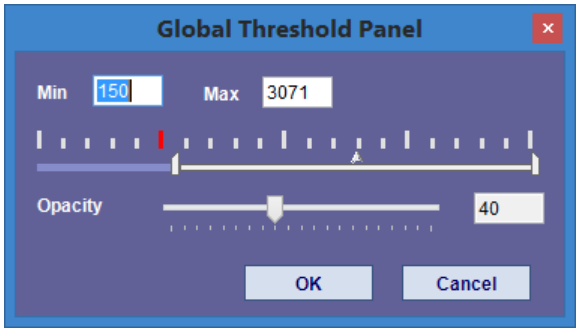


Figure 19-4: Fusion Images (top) and Mask Icons (bottom)

MPR and 3DVR Overlays

In Edit mode (Fusion mode disabled), you can enable overlays on the MPR images as well as the 3DVR displayed in the main view. To enable overlays, click the down-arrow to the right of the **Overlay** checkbox, on the side of the Fusion tool panel (circled in Figure 19-3). A dialog, the **Global Threshold Panel**, is opened (see the following image).



You can use the threshold slider (or the **Min** and **Max** input boxes) to change the overlay threshold on the MPR images. Use the **Opacity** slider (or numerical input box) to change the opacity of the 3DVR image.

Chapter 20 Multi Modality Fusion

Topics in this chapter:

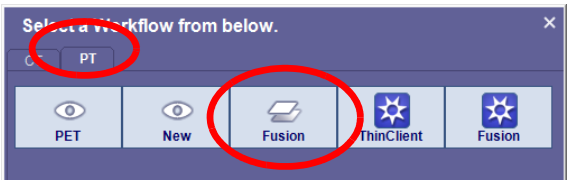
Multi-modality fusion, an optional module, is where two different types of scans are taken and the images from each are fused together. The composite image can provide more precise information about how different parts of the body function and more clearly identify pathology. The software provides an initial registration, but the user is responsible for reviewing, validating and making necessary adjustments as necessary prior to use.

Opening Data for Fusion

An example of this fusion, a CT with a PET study, is provided below. The PET image provides the information about the pathology, while the CT image provides the anatomical reference.

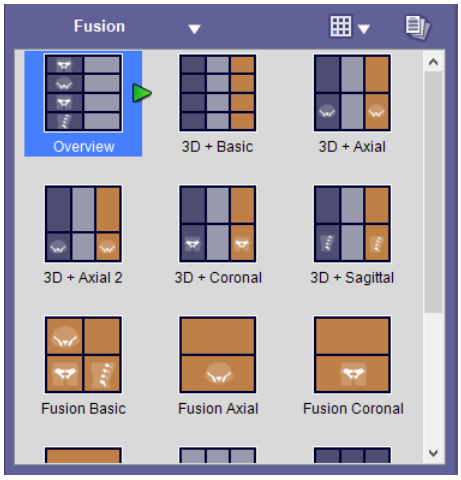
Note: Prone and decubitus datasets are not supported in the Fusion module. To load them into the Fusion module, you must reprocess the data so that it is in the supine position.

Load both types of data into the **Fusion** workflow (circled in the following image):



Fusion Layouts

AQi offers several layout options for displaying CT/PET fusion data. These layouts are for displaying CT/PET data within one or more study on the same patient. They are accessed through the **Fusion** workflow. After loading the data, you can select a layout from the workflow panel:



Fusion Workflow Elements

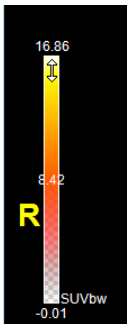
The workflow elements in the **Fusion** and **2 Studies Fusion** workflows are colored to help you identify which type of data is displayed in each view, when that layout is selected:

- Blue - CT data
- Gray - PET data
- Orange - Fused image, axial, coronal and sagittal images, and spinning man.

The Color Bar

The color bar allows you to control the window/level of the color overlay volume. Hover the mouse over either end of the color bar until the cursor turns to a vertical double arrow. Then click and drag the mouse up and down the color bar to change the window/level.

You can still change the window/level on the base volume in the usual way, by holding down the left and right mouse buttons and dragging the mouse on the image.



The Fusion Tool Panel

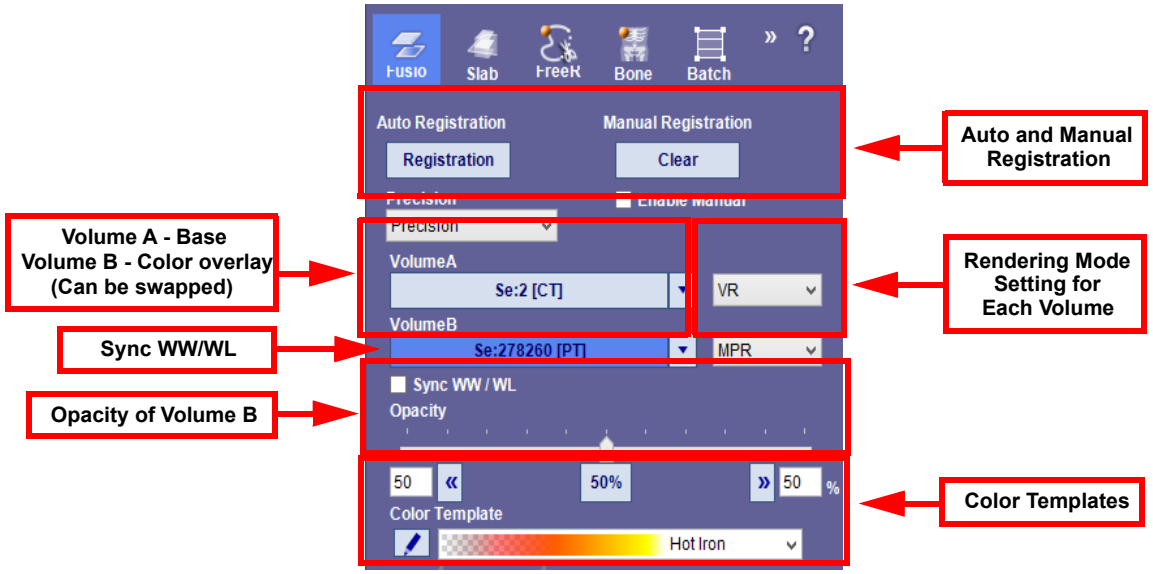


Table 20.1: Elements of the Tool Panel

Button or Menu	Description
Registration	Click this to perform automatic registration.
Clear	Reset the overlay to its original position. **Note:** The overlay position will not appear to have changed until an operation such as zoom, pan, slice, or W/L, is performed on the image.
Enable Manual	Check this to enable manual registration.
VolumeA	Base volume (the CT series, in this example)
VolumeB	The PET series
Rendering setting menu	Rendering mode for VolumeA
Rendering setting menu	Rendering mode for VolumeB
Sync WW/WL	Synchronize changes to W/L between images in the following ways: W/L changes made to the CT image are also made to the fused image. W/L changes made to the fused image are also made to the PET and spinning man images W/L changes made to the spinning man image are also made to the PET and fused images.
Opacity slider	This allows you to set the opacity of the overlay in the fused image.
Color Template	Menu of color maps used for visualizing the overlay data in the fused image. Pull down the menu to see default selections. See "Right-click on the measurement results and select Change Threshold. This opens the Set Threshold dialog." on page 20-11 for more information.

Button or Menu	Description
Save current transparency as default	Save the current setting of the color template as the default.

Multi-Time Point Data

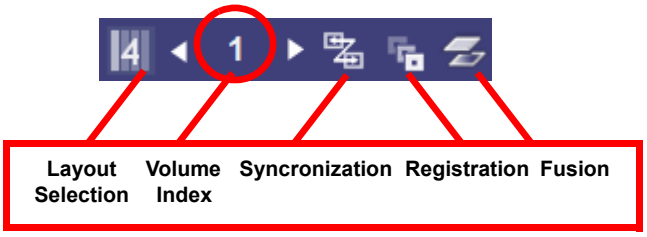
You can load multiple fusion studies from the same patient simultaneously, to compare changes over time. Each study is referred to as a time point, and each scan within a single study is called a volume. When only one time point (study) is loaded, you can select the images of individual volumes (for example, the CT volume, followed by the PET volume, within the study).

When multiple studies are loaded together, you can select and step sequentially through either time points or volumes, using the navigational tools in the top toolbar (described below). As you step through volumes, each volume is selected sequentially. When stepping through time points, the same volume of the following study is selected. For example, if the CT volume of a study is selected, and you click the Next Study arrow, the CT volume of the following study is selected.

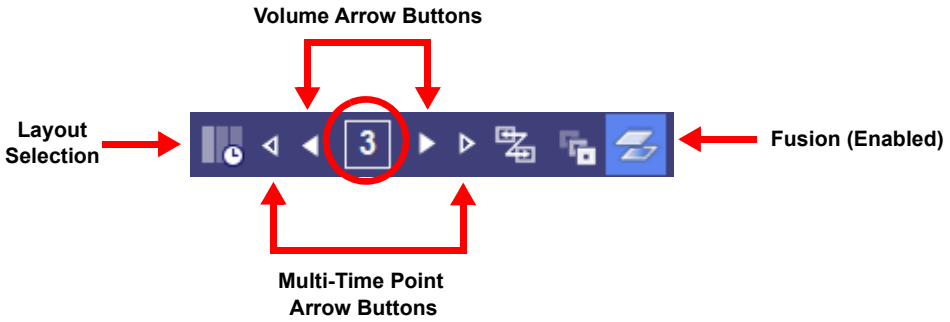
When a set of images in a volume or study is selected, a green box highlights the selected images.

1. Load a CT/PET fusion study, and one or more followup CT/PET studies, into the **Fusion** Workflow, which is on the **PT** tab.

In the Viewer, the top toolbar shows the Volume Index:



2. Click the Fusion button. The Volume Index is changed to the Multi-Time Point Index (circled):



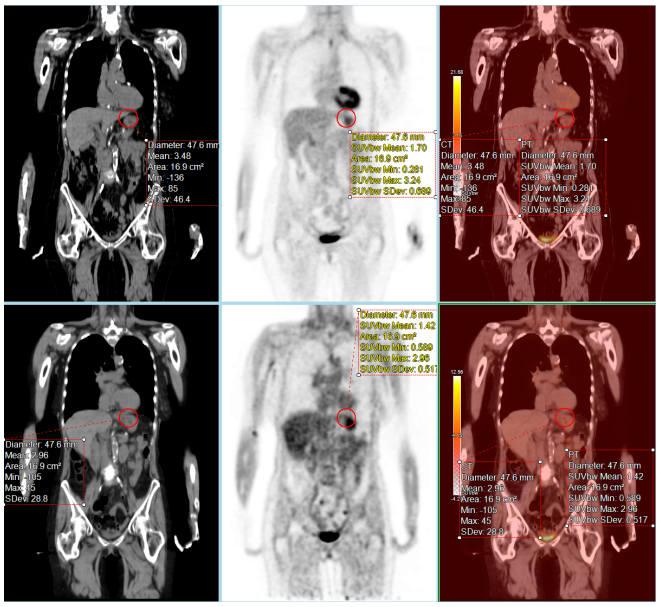
- **Multi-Time Point Index** (circled in figure above) - The currently selected study.
- **Multi-Time Point Arrow Buttons** - The two outer arrows. Use these to step sequentially through studies. Each click of the right arrow selects the following study (or time point). The left arrow selects the previous time point.
- **Volume Arrow Buttons** - The two inner arrows. Use these to step sequentially through each volume of all loaded studies. Each click of the right arrow selects the following volume within a single time point (the left arrow selects the previous volume). When the final volume of a time point is selected, the next volume to be selected is the first volume of the following time point.
- **Layout Selection** - This allows you to select how many studies are displayed on the screen at one time.
  - Single Time Point - Shows one study in the viewer.
  - Two Time Points - Shows two studies.
  - All Times Points - Shows all studies.

The following figure shows the images of three time points in Fusion mode.

Synchronizing Measurements in Multi-Time-Point Data

To synchronize measurements on two or more fusion studies, load a CT/PET study and its followup into the **Fusion** workflow.

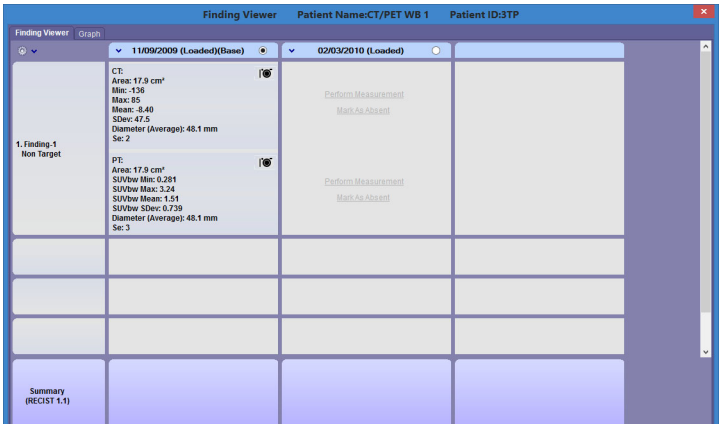
1. Click the synchronization, registration and fusion buttons in the top toolbar.
2. Make sure that all images are displayed in MPR rendering.
3. Obtain a measurement on the fused image of the original study.
4. The measurement is copied to the CT and PET images of the original study and also to the followup studies (see figure below).



Note: AQi does not support re-slicing of fused images. If you need to be able to re-slice fused images, you can open the data in the Thin Client.

Tracking Measurements

Before taking the measurement, right-click on any of the images and select **Enable Measurement Tracking**. Any measurements you choose to save from that point on are recorded in the Findings Workflow. You can also specify this in workflow preferences.

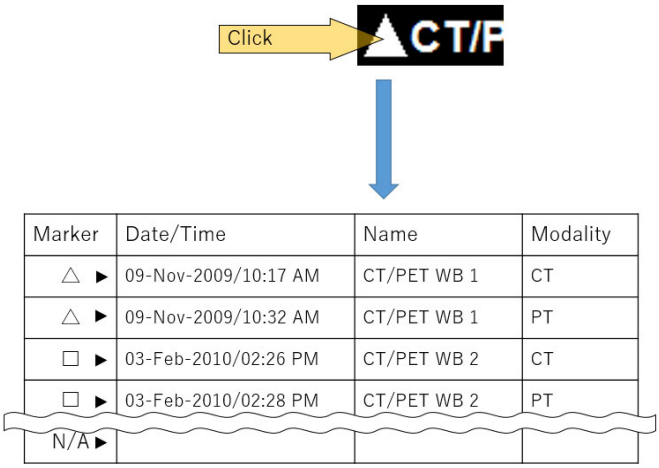


For more information about tracking and the Finding Viewer, see Chapter 16: "The Findings Workflow". For information about SUV measurements, see "SUV Measurements on PET Studies" on page 3-168.

Series Time

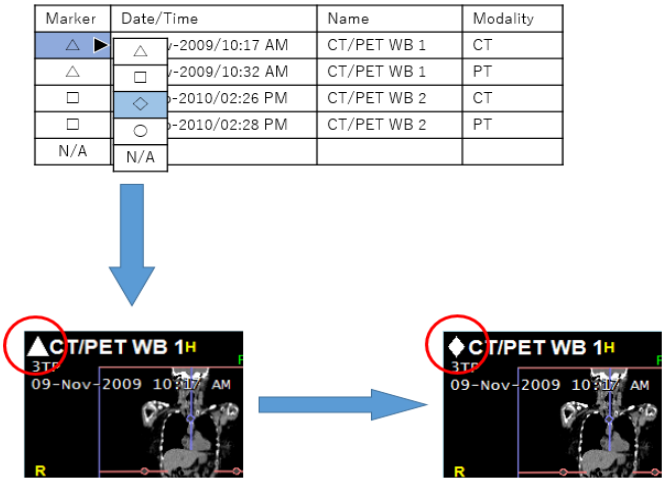
When multi-time point data are loaded, you can view the series time by looking to the marker image at the top left. The study level marker is assigned automatically upon loading the multi-time point data using the current date or date of inspection.

You can customize the assignment of the markers by clicking directly on the marker.



Marker	Date/Time	Name	Modality
△ ▶	09-Nov-2009/10:17 AM	CT/PET WB 1	CT
△ ▶	09-Nov-2009/10:32 AM	CT/PET WB 1	PT
□ ▶	03-Feb-2010/02:26 PM	CT/PET WB 2	CT
□ ▶	03-Feb-2010/02:28 PM	CT/PET WB 2	PT
N/A ▶			

You can change the image of the marker assignment by clocking on the drop down menu and selecting the shape you prefer.



The Spinning Man Image

The spinning man is a 3D PET image that can be animated with cine buttons located in the lower-left corner of the image.

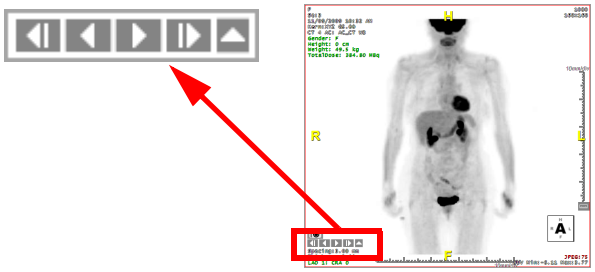


Figure 20-1: Spinning Man

Move clockwise one step

Spin clockwise

Spin counterclockwise

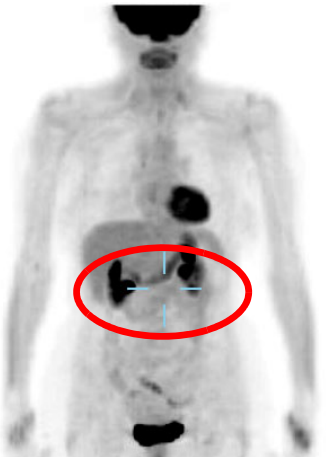
Move counterclockwise one step

Control the speed and turning angle for each step

Output Movie

Creating a movie from the spinning man image is not supported in multi-modality fusion. However, you can create a movie using the Batch3D tool. See "Batch3D" on page 3-75 for a description and instructions.

Triangulation Mark



A cross marker is displayed on the spinning man view (see image at right). It can be moved by holding down the **Alt** key and dragging it with the mouse. When the cross marker is moved on the spinning man, the crosshair on all MPR views is moved in the corresponding direction and distance. Similarly, when a crosshair is moved on an MPR view, the triangulation cross marker is moved.

You can show or hide the cross marker by right-clicking on the spinning man image and selecting **Show/Hide Cross Marker** from the menu.

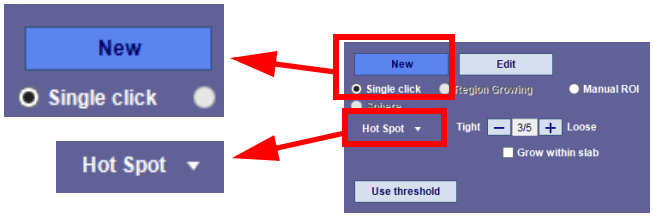
Note: Make sure that synchronization is enabled.

Pick Lesion

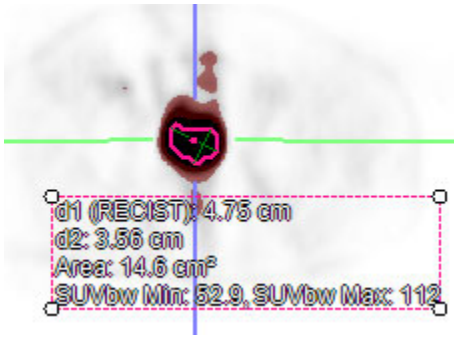
The Pick Lesion tool is used for PET data, to measure a Hot Spot in an image.

Note: The slice thickness, spacing, and voxel size are different in PET and CT. Measurement results might differ in each modality.

1. When the study is loaded, click the SAT tool icon (see figure at right) to open the **SAT** tool panel.
2. Click **New**. The SAT tools are displayed below the **New** button.
3. Select **Single click**. The **Hot Spot** menu will appear underneath. See the following figure:



4. Hold down the **Shift** key and click on an area of interest in any of the PET images. Measurement results are displayed:

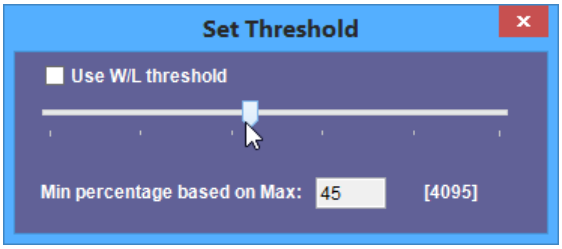


For a full description of the editing tools available in this tool panel, see "Performing Manual SAT" on page 8-9.

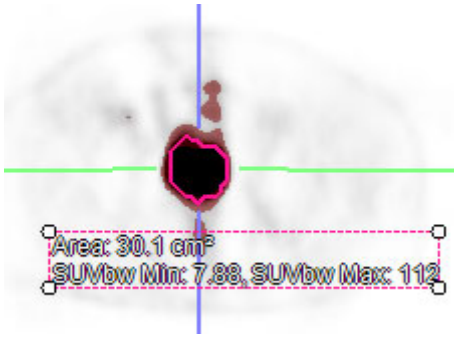
Editing the Lesion by Threshold

You can change the area included in the lesion by changing the threshold.

1. Right-click on the measurement results and select Change Threshold. This opens the Set Threshold dialog.



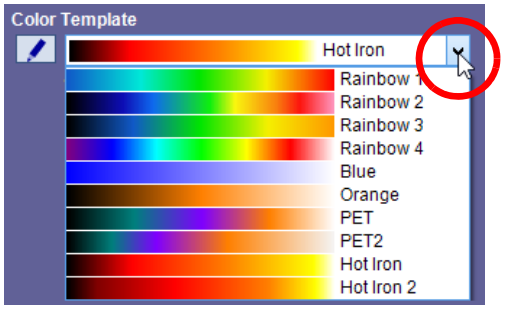
2. Move the slider to change the size of the area to include more or less of the targeted region. The region is automatically recalculated:



Changing the Color Transparency

In the Fusion tool panel (see "The Fusion Tool Panel" on page 20-3), the color transparency template can be used to make it easier to view the fused images, in the following ways:

- Select the best transparency for your needs. Click the down-arrow at the right end of the template bar to see the menu of other templates.



- Change the light-dark range of the selected transparency. Click and hold the up-arrow marker located under the left end of the template bar, and drag it to the right.

Note: The color of this marker is very close to the background color when it is not selected. It changes to white when selected.

This marker changes the upper end of the color range. A second up-arrow marker appears where the first one was shown initially. This marker changes the lower end of the range. You can move both markers back and forth to change the lightness range of the color transparency.

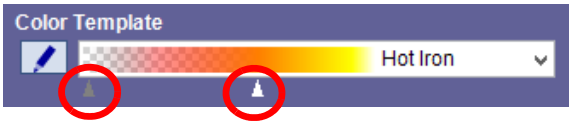


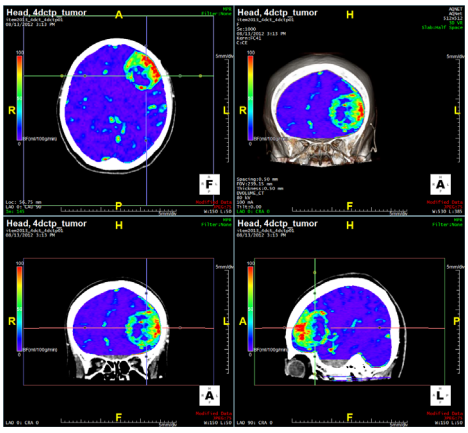
Figure 20-2: Color Range Markers

- **Save current transparency as default**. Click this text (just below the Color Template bar) to save both the template selection and the current lightness range as a default for future Fusion data.

You can also configure new color templates. See "Changing Color Maps" on page 9-5 for instructions.

Example: TDA CT and AquariusAPS Map Fusion

This case combines a 4D CT TDA series in the arterial phase (Volume A) with a BF map AquariusAPS result (Volume B).



1. Select both series and load into the Multidata Volbrowse workflow.
2. Click the **Fusion** button.
3. Adjust for better visualization by doing the following:
   - Display in half-slab view.
   - Move crosshairs in the 2D images so that the area of interest is in the center of the crosshairs in each view.
   - Set the Opacity value of Volume B to 100%.

If desired, you can fuse different maps from the Series List. Open the “Mini Patient List” from the Viewer to load another map. (See "Mini Patient List" on page 3-188 for more information.)

You can output these images to the Output Panel or the Patient List using the Batch tool (see "Batch Tool" on page 3-65). You can also save them as a scene.

CT/SPECT Fusion

The multi-modality fusion workflow calculates time-dependent behavior in multi-phase studies from SPECT. When combined with CT cardiac data, it provides improved visualization and analysis in relation to the coronary arteries.

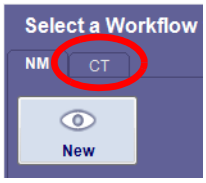
1. Select one CT series and two SPECT series, Stress and Rest, from the Series List.

Series #	Modality	# of Images	Series Date, Time	Part	Description
	NM	1	09/11/2013 01:47:10 P	Heart	STRESS
	NM	1	09/11/2013 01:47:10 P	Heart	REST
	NM	1	09/11/2013 01:47:10 P	Heart	AC-STRESS
	NM	1	09/11/2013 01:47:10 P	Heart	AC-REST
	CT	379	09/11/2013 04:44:01 P		

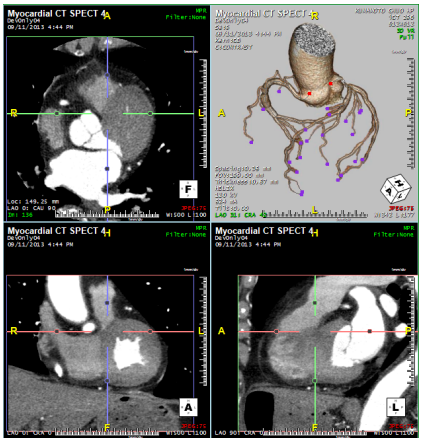
Note: SPECT is referred to as NM (nuclear medicine) as the modality in the Patient List.

2. Load the three series into the MMF (multi-modality fusion) workflow.

Note: The MMF workflow is located on the CT tab in the workflow menu (as shown below).



3. Click the **Coronary** workflow element (see image at right). If there are APS results included with the study data, the aortic root and coronary arteries will already be segmented. If not, you will need to segment them manually. See "Segmenting the Aortic Root and Coronary Arteries" on page 3-38 for instructions. The results are shown as follows:



4. Click the **SPECT** workflow element. This loads the SPECT overlay and opens the tool panel:

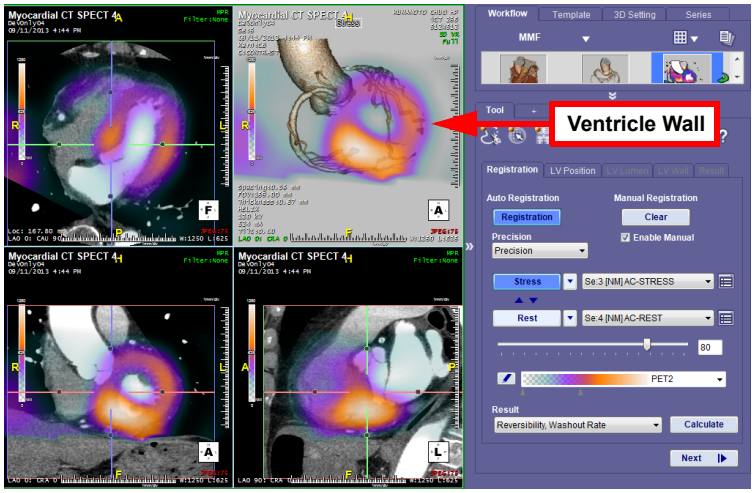


Figure 20-3: CT and SPECT Overlay, Tool Panel (right)

The Tool Panel

The following table describes each element of the tool panel interface:

Table 20.2: Tool Panel Interface Elements

Button or Menu	Description
Registration	Click this to perform automatic registration.
Clear	Reset the overlay to its original position. **Note: The overlay position will not appear to have changed until an operation such as zoom, pan, slice, or W/L is performed on the image.**
Stress	Refers to the stress period SPECT series. It is the period of high cardiac activity.
Rest	Rest is the other SPECT series and is a period of lower cardiac activity.
	Mini Patient List icon. Click this to open the Patient List without leaving the Viewer. You can load additional series from here.

Button or Menu	Description
Slider	This allows you to set the opacity of the SPECT overlay.
Color Template	Menu of color templates used for visualizing the SPECT data. See "Changing Color Maps" on page 9-5 for instructions on configuring color overlays.
Result	Menu of calculation algorithms.
Calculate	Click this button to begin calculation.

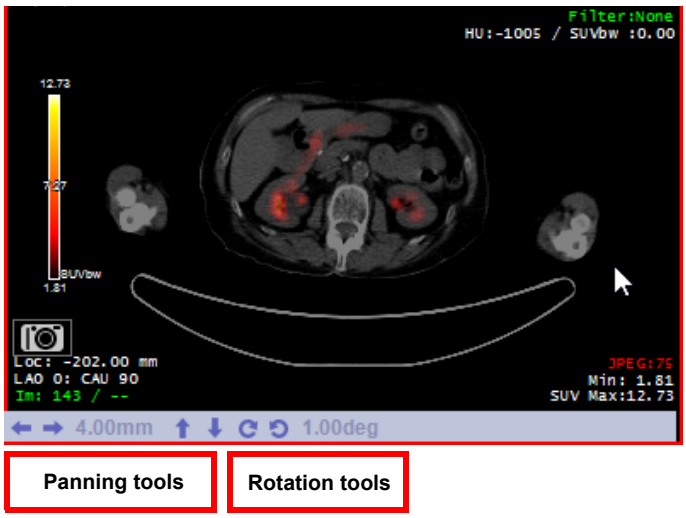
Registration

You can perform automatic or manual registration. To perform automatic registration, click the **Registration** button located under **Auto Registration** in the tool panel.

To perform manual registration, check the **Enable Manual** checkbox under **Manual Registration** in the tool panel.

Manual Registration Tools

Hover the mouse over one of the 2D fusion images, and you will see a set of tools at the bottom of the image:

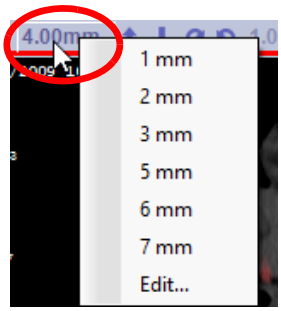


These tools allow you to make minute changes in the position or orientation of the overlay with respect to the base volume.

The four straight arrows allow you to pan the overlay up, down, left or right.

The curved arrows allow you to rotate the overlay around the axis of the 2D image. Each 2D fusion image has two directional arrows, one clockwise, and one counterclockwise.

You can configure the distance each arrow click will pan the overlay, and the number of degrees for each click on a rotation arrow. To the right of left and right arrows is a menu of pan distance values. Right-click the menu to change the distance (in millimeters) the overlay will pan with each click on a panning arrow. To the right of the rotation arrows, there is a menu containing rotation degrees. Right-click on the menu to select the number of degrees the overlay will rotate with each click.



Select **Edit** from either menu to enter a value not provided in the menu.

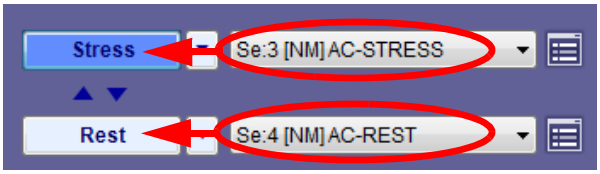
Note: It is essential to do manual registration on all three MPR images.

You can also pan the overlay on the MPR images in the usual way, by holding down the right mouse button and dragging the overlay across the image. This is useful when you do not need to be very precise, but you need to pan in any direction.

Note: You cannot pan in a random direction when using the arrows.

Calculation

When you have completed registration, the next step is calculation.

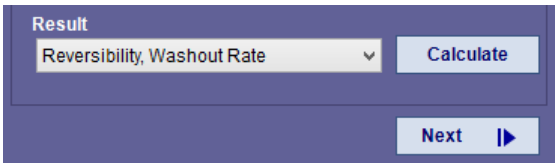


IMPORTANT: Before starting calculation, make sure that the Stress and Rest series are properly selected.

Automatic Calculation

Segmentation of the LV and wall in the CT series is required to create the polar map and wall fusion image. If you prefer to perform this process manually, click **Next**.

To calculate automatically, select **Reversibility, Washout Rate** from the **Result** menu and then click the **Calculate** button. The process calculates counts for the stress and rest series, within each segment of the AHA segmentation map.



Manual Calculation

To begin manual calculation, click **Next** (in the lower-right corner of the tool panel) to go to the next step.

LV Position, LV Lumen and LV Wall

The following three steps, LV Position, LV Lumen and LV Wall, are described in detail under "Performing Manual TVA(LV)" on page 6-2. Please note that although the instructions for each step described in Chapter 6 correspond to the steps you will perform for CT/SPECT, the tabs and step titles are named slightly differently in that chapter:

- **LV Position** - corresponds to the **Position** tab, and is described under "Step 1 - Positioning and Threshold" on page 6-3.
- **LV Lumen** - corresponds to the **Chamber** tab and is described under "Step 2 - Chamber Segmentation" on page 6-5.
- **LV Wall** - corresponds to the **Wall** tab, described under "Step 3 - Wall Correction" on page 6-8.

For viewing the results, use the instructions described below, because these results are specialized for SPECT data.

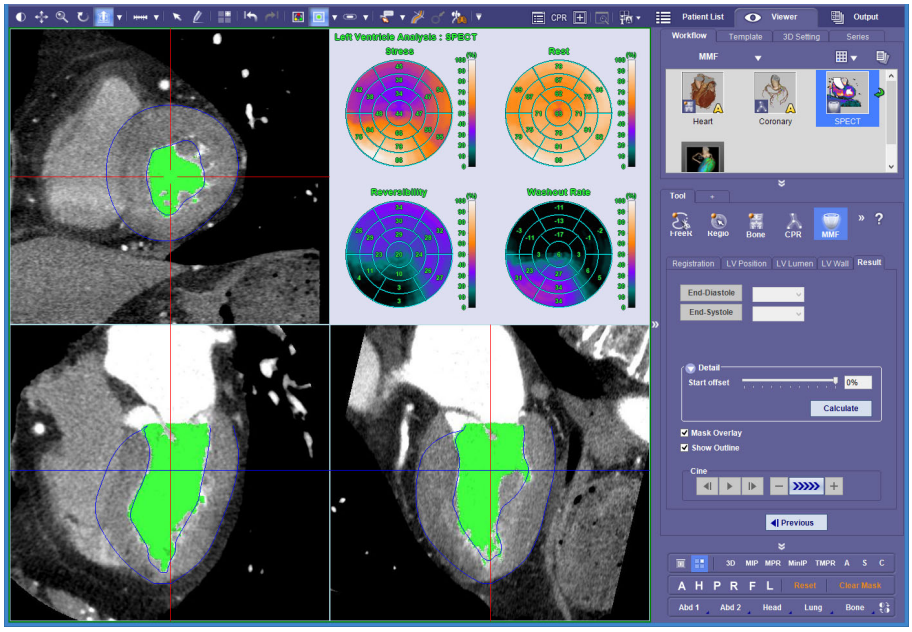
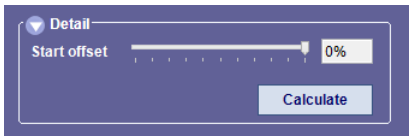


Figure 20-4: Analysis on SPECT Data

The results are displayed in the final step, as shown in Figure 20-4.

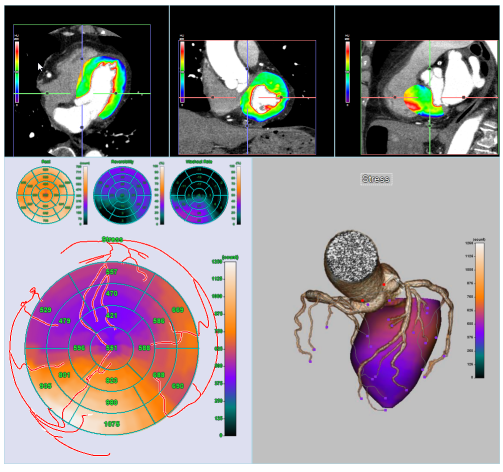
You can view other results by right-clicking on the polar maps in the upper-right window, and selecting other maps, graphs and text results from the menu.

- SPECT Polar maps - The SPECT polar maps show the counts or percentages in the SPECT data, as seen in Figure 20-4.
- CT Polar Maps - The Wall Thickness and Wall Intensity maps are shown, and are similar to the maps shown in "Wall Thickness and Wall Thickening" on page 6-11 and "Segmental Ejection Fraction and Wall Intensity" on page 6-11, respectively.
- Text, Graphs and Time Volume maps - These are described in "Text and Graphs" on page 6-12.
- Show Count - The SPECT polar maps can show either the counts for each segment of the AHA-17 segmented map, or percentages. If counts are shown and you would like to see the percentages, right-click the polar maps and select **Show Count** again to toggle it off.
- Start Offset (tool panel function) - The **Start offset** value is used when the wall boundary lies within a section of the SPECT data that has widely varied count values, which could skew the results. You can configure the start offset in the **Detail** section, locaed in the middle of the tool panel. Using the slider, move the inner wall by an offset percentage, and then click **Calculate** to recalulate.



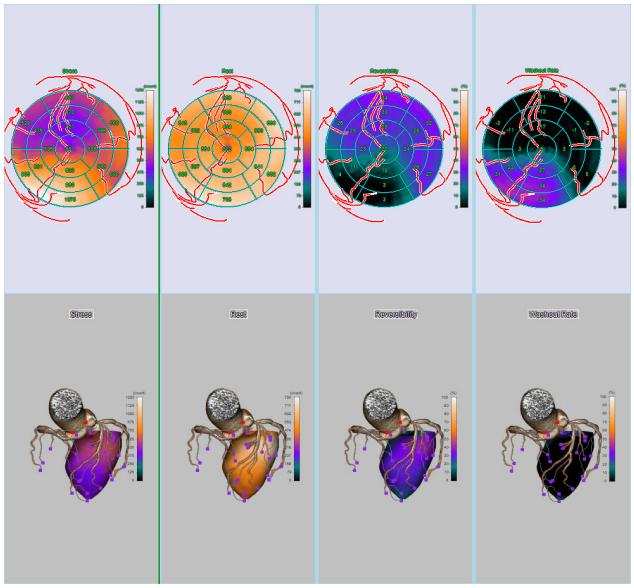
Wall Fusion

Click the **Wall Fusion** workflow element (shown at right). A combined layout, including the volume rendered coronary artery, three MPR views with a color overlay and the polar maps, is displayed (see image below).



Multi-style Layout

To view the data in multi style, right-click on the polar maps display and select **Multi Style**. The maps are displayed in multi style, as shown in the following image:



Multi-Modality Fusion in the Thin Client

Right-click on one of the desired studies and select **Filter by this Patient ID** from the pull-down menu. The Patient List displays all the studies of the corresponding patient ID.

Select series from each of the studies in the Series List and click the **Load** button. The Workflow menu dialog is opened. Because two different modalities are being loaded together, each modality has its own set of Workflows on a separate tab.

The iNtuition Thin Client Viewer is opened, and the series are automatically loaded in Fusion mode.

For a detailed discussion of the tools used in Fusion, please see “Chapter 11 - Using Overlay for Multi-modality Exams” in the *AquariusNet ThinClient iNtuition Edition* user manual.

Chapter 21 The Multiphase Workflow

In a Multiphase workflow, you can view multiphasic data over time. This allows you to visualize both static images or images in motion (cine), to plot contrast “wash in – wash out” curves along time, and to display parametric maps for enhanced image analysis.

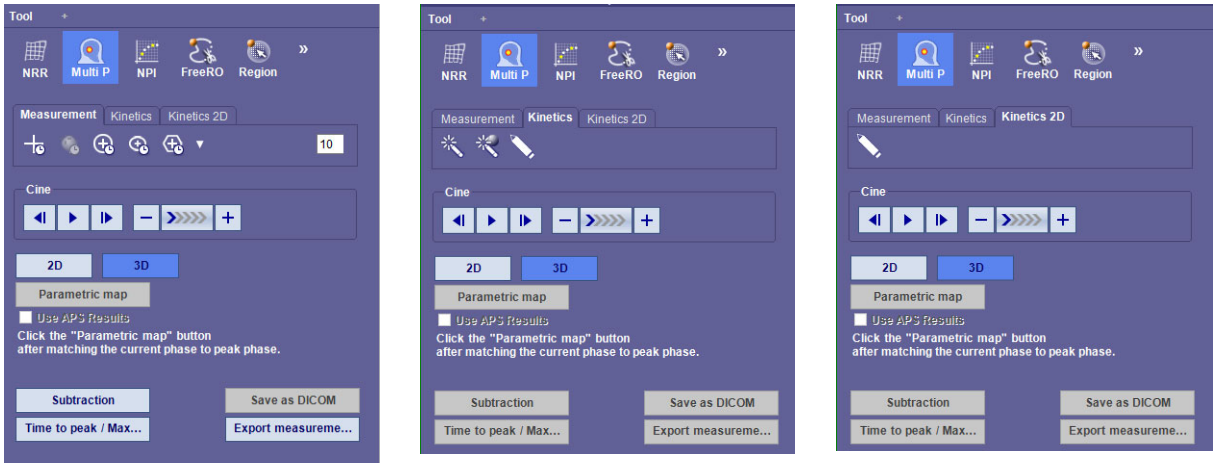
The time-intensity curve tool allows you to visualize the lesions' enhancement behavior by plotting the signal intensity values over time after a contrast material is injected.

Multiphase Workflow Tool Panel

When loading a Multiphase series, the images open in 3D view mode. The 3D layout displays three MPR views on the left side and one MIP viewbox set over a Time Intensity Curve (TIC) graph (default viewer layout). This provides the best visualization of slices. Selecting the 2D button on the Tool panel allows you to view thumbnails of the series data by slice or by phase.

The lower half of the Workflow Tool Panel has three tabs - **Measurements**, **Kinetics**, and **Kinetics 2D**. Each tab same buttons for Cine, 2D or 3D, Parametric map, Subtraction, Time to peak/Max, Export measurements, and Save as DICOM. Each tab has a different set of tools for selecting Regions of Interest (ROI). The ROI tools provide measurements and kinetic results.

Workflow Tabs



Measurement Tab **Kinetics Tab** **Kinetics 2D Tab**

Figure 21-1 Multiphase Workflow Tabs

Measurement Tab

The Measurement tab contains these ROI tools:.

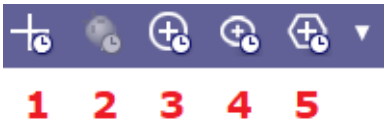


Figure 21-2 Labeled ROI Tools, see Table 21-1 Key

Table 21.1 Key for Figure 21-2

Tool Number	Description
1	LMB-click point
2	High Uptake Position in Sphere
3	Select an ROI with a Circle outline
4	Select an ROI with a Ellipse outline
5	Select an ROI with a Polygon outline

If you want the TIC graph to include Time to Peak/Max, select this button before going to the next tab or action.

Kinetics Tab

The Multiphase tools under this tab provide Kinetic results. The ROI selection tools include a tool for selecting or placing a sphere on an ROI. A freehand draw tool is also available.

Kinetics 2D Tab

This tab provides a freehand drawing tool to select a ROI for kinetic results in a 2D view.

Selecting an ROI

Selecting an ROI assists in analyzing a specific area of data. Depending on the tool selected:

- If you select the + tool, LMB-click on the image (as many times as needed) and view measurement in the graph.
- Select a tool to form a shape around an ROI. LMB-click and hold and drag outward until the shape is the desired size (circle, sphere, polygon, and ellipse shapes).
- Select the Freehand Draw tool (pencil). LMB-click and hold and move the mouse around the ROI to outline and include the area.

Starting a Multiphase Workflow

To start a multiphase workflow:

1. Select a multiphase study from the Patient List.

2. Select at least two multiphase series from the Series List. You can LMB-click on the first multiphase series then hold the Shift key and LMB-click on the last multiphase series. Or you can select several series by checking the box next (left side) to the series' name in the Series List.

3. Load the series by RMB-clicking in the Series List or Patient list and selecting **Multiphase 4D** from the context menu; or select the **Load** button from the Data Management menu then select **Multiphase 4D** from the Workflow Template Window.

Dynamic Subtraction and Parametric Maps

The workflow starts with plotting and graphing the movement of contrast in and out of an ROI. The first step is to subtract the non-contrast studies from the contrast studies. Subtraction localizes lesions.

4. Select the **Subtraction** button from the Tool panel. The remaining images reflect the process of subtraction.

5. After subtraction you can select the option to **Show subtracted image side by side**.

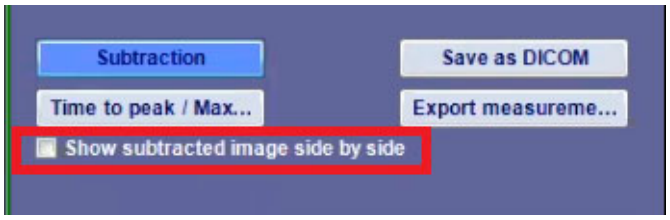


Figure 21-3 Side by side Option

Figure 21-4 shows a comparison of subtracted (top) image and original (bottom) image.

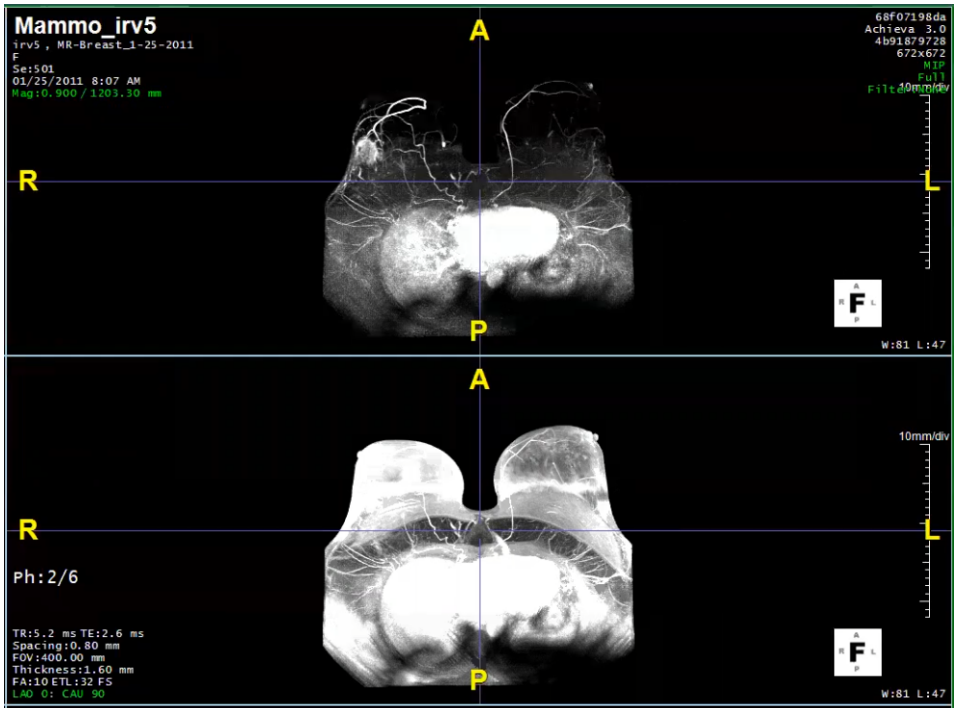


Figure 21-4 Comparison side by side

After using Subtraction, you can select the **Parametric Map** button, see "Parametric Maps" on page 21-9, or continue to the next section for selecting an ROI and seeing those results on the **Time Intensity Curve**, see "Time Intensity Curve" on page 21-6.

Calculating Regions of Interest (ROI)

To plot the movement of contrast over time:

1. The first image must have T zero selected **Time Zero** as the default setting. If this is not already set on the first image, right-click on the image and select T zero (**T0**) from the context menu. Make sure this is set on the correct, first image.

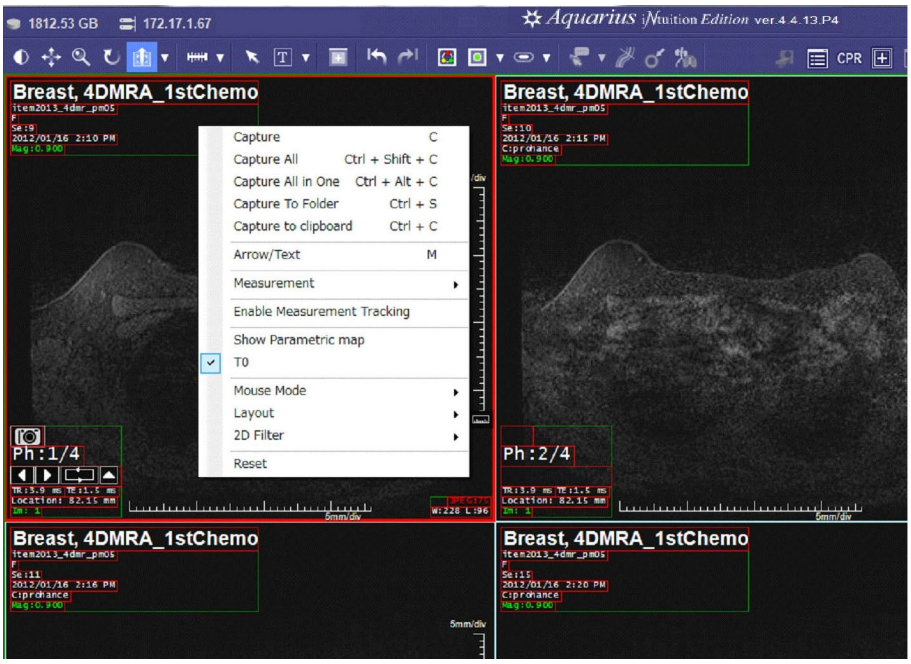


Figure 21-5 Selecting the T0 Setting

2. Select a subtracted series and scroll to find an image with the ROI indicated. If there isn't an image with a ROI indicated you can draw an ROI on the image. See "Selecting an ROI" on page 21-2.

3. Select an ROI using the tools in the Measurement tab or from the top toolbar **Distance** tool. You can also RMB-click on the image and select from the context menu.

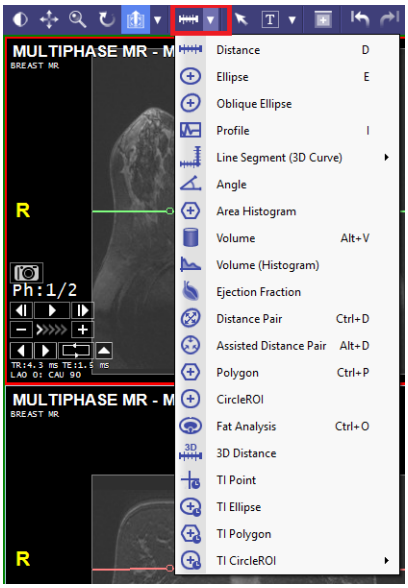


Figure 21-6 Distance Tool Drop-down

4. Place or draw an ROI on the image.

Note: You can use the zoom and pan functions to position and size the image before drawing the ROI. All of the remaining images automatically update to this zoom percentage/pan position.

Time Intensity Curve

The Time Intensity Curve (TIC) graph is populated with the selected ROI information.

The signal intensity of a ROI (lesion) is calculated and plotted against the levels of injected contrast over time. The TIC provides evaluation of tissue areas characterized by rapid contrast wash-in and wash-out.

Using the TIC Graph

1. The Time Intensity Curve (TIC) graph plots any ROI you place. When you hover your mouse over that ROI, it is highlighted in the graph.

2. To display the percentage of enhancement instead of the intensity, select the check box next to **Display Relative Values (%)** under the TIC graph. (Figure 21-7)

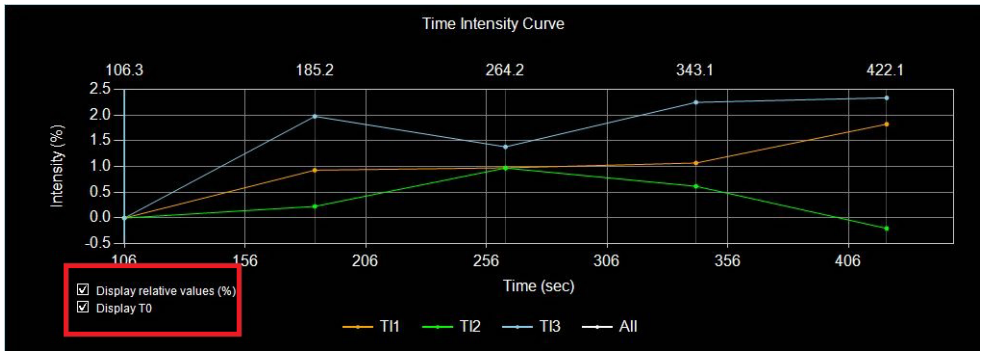


Figure 21-7 Check Boxes for Display Relative Values and T0

Note: You can move the graph box around the viewer by LMB-clicking on it and then dragging it to a new position.

Within the TIC graph, you can modify the graph to view all or individual ROI lines. To modify the graph:

- Single LMB-click on the line reveals values for the corresponding ROI.
- Double LMB-click on the line hides the selected ROI.
- Clicking on a line that was previously hidden from view on the Time Intensity Curve, makes it viewable again. (Figure 21-8)

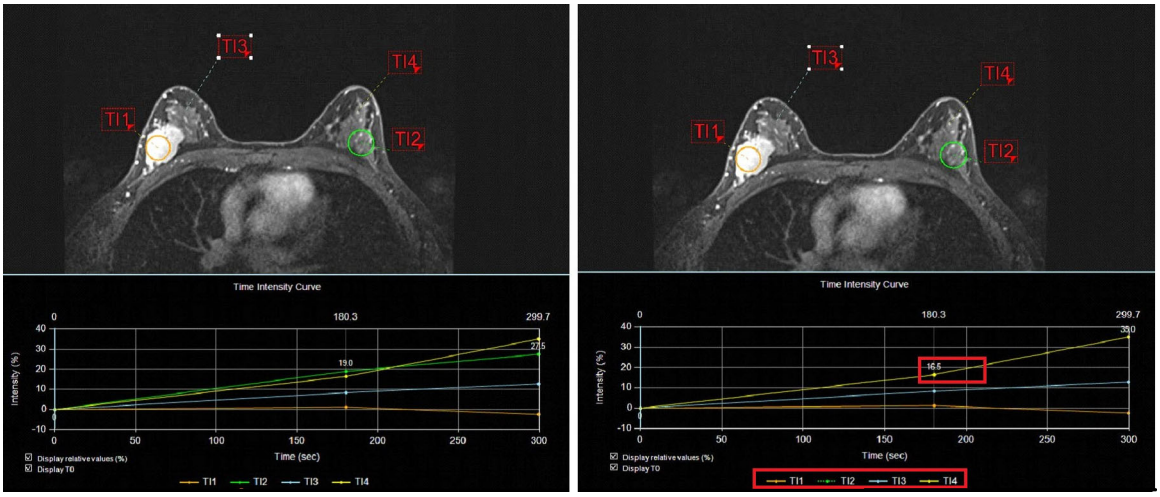


Figure 21-8 Modifying the Time Intensity Curve Graph

You can see this same behavior by RMB-clicking on the different color T lines in the Key under the graph. By modifying the Time Intensity Curve settings you can select values such as time to peak, sloping line, max slope, and analysis results on graph.

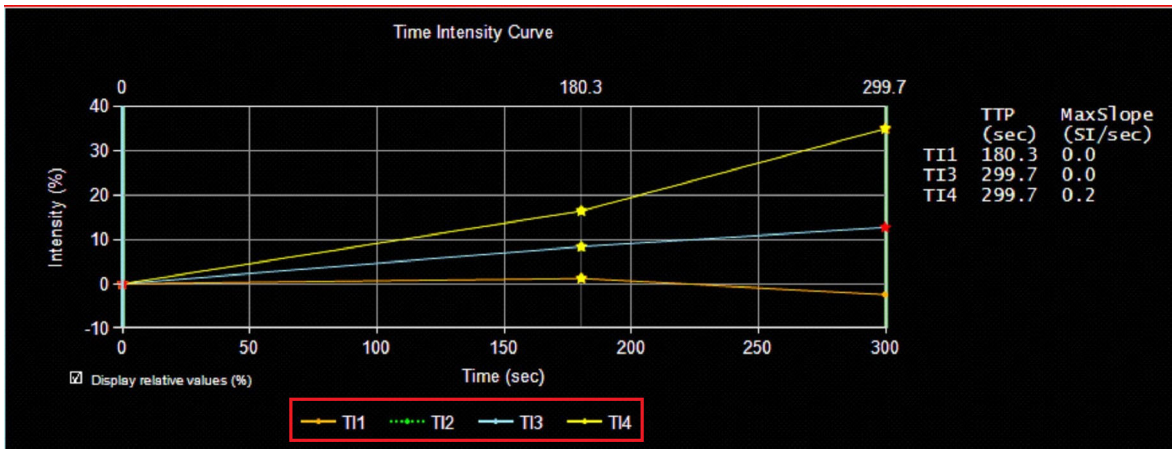


Figure 21-9 Time Intensity Curve Graph Key

To select settings on the TIC:

1. RMB-click on the graph and select **Time to peak / Max slope** from the context menu or select the **Time to peak / Max...** button under the Measurement tab. The TIC Setting window opens.

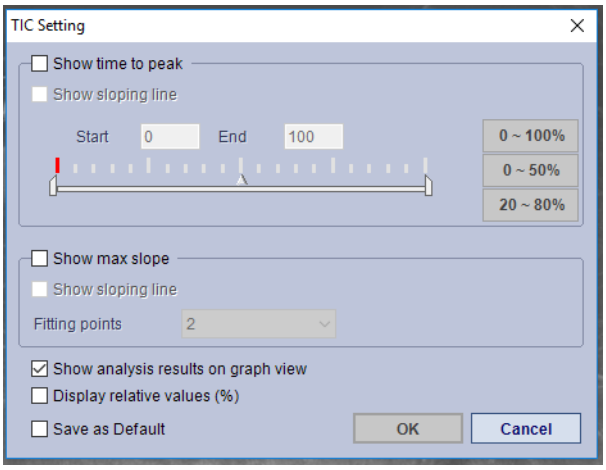


Figure 21-10 TIC Settings

2. RMB-click on the image and from the context menu select **Set injection time**. This window opens.

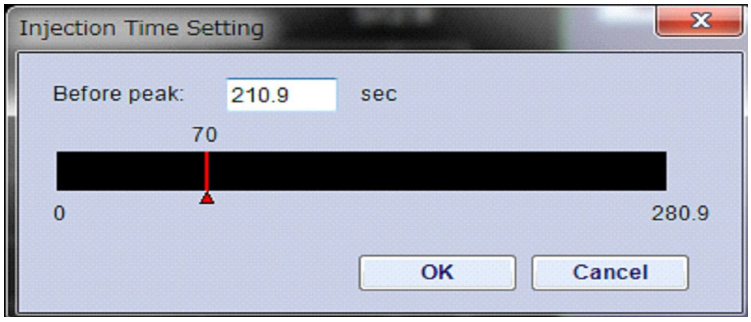


Figure 21-11 Injection Time Setting

3. You can select an injection time by entering a number in the “Before peak” entry field or use your mouse to move the slider right or left in bar below that setting. (Figure 21-12)

4. Selecting **OK** after entering an injection time, the check box next to **Based on injection time** at the bottom of the graph is checked (selected). (Figure 21-12) This is highlighted in red to notify that the first phase time is edited. The phase time is rescaled based on the injection time setting.

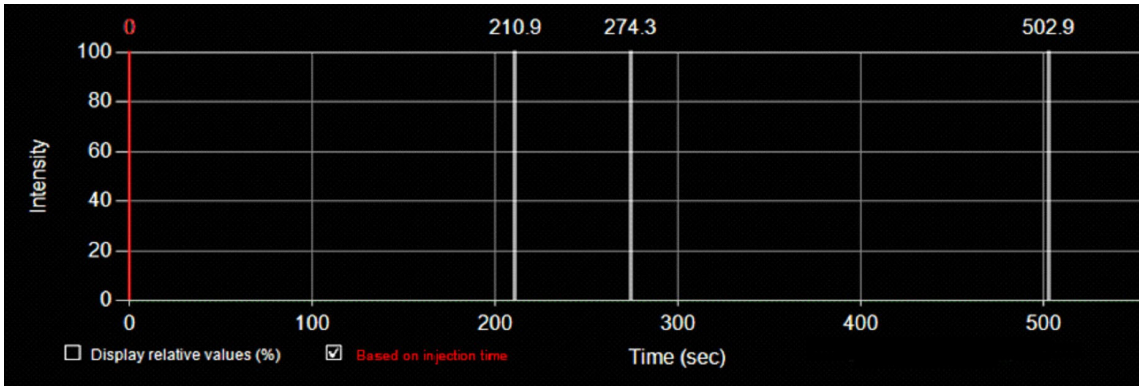


Figure 21-12 Based on Injection Time Option is Selected in this Graph

Parametric Maps

The parametric map, or color map, is defined by calculation parameters of a signal over time threshold and has a definition of a color. If APS results are available, the option is checked in the tool panel. Otherwise, if you want to use APS results check this box.

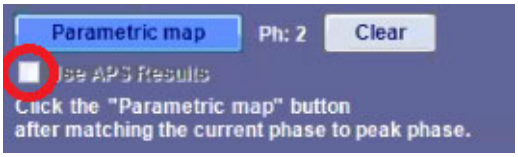


Figure 21-13 APS Option

To activate the parametric map:

1. After **Subtraction**, select the **Parametric Map** button in the tool panel.
2. The software calculates and segments information.
3. The map appears on the images.

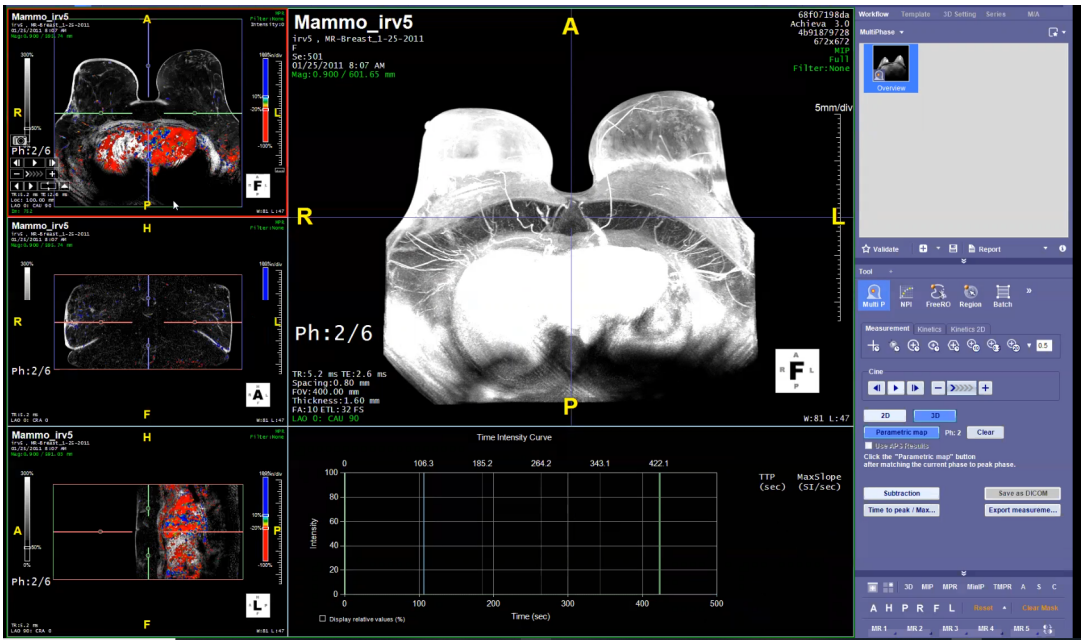


Figure 21-14 Parametric Maps

You can adjust these parameters and colors by right-clicking on the color bar, and if needed, set the new parameters to default. This adjusts both the parametric map colors and the kinetics findings bars in the findings window.

NPI (New Phase Interpolation)

The New Phase Interpolation (NPI) tool allows the user to add data points to the series and then create a new series. NPI tool panel provides additional tools including Set Injection Time, Interpolation Method, Interpolation Interval, Start, and Save as DICOM. The Cine and ROI tools are also available.

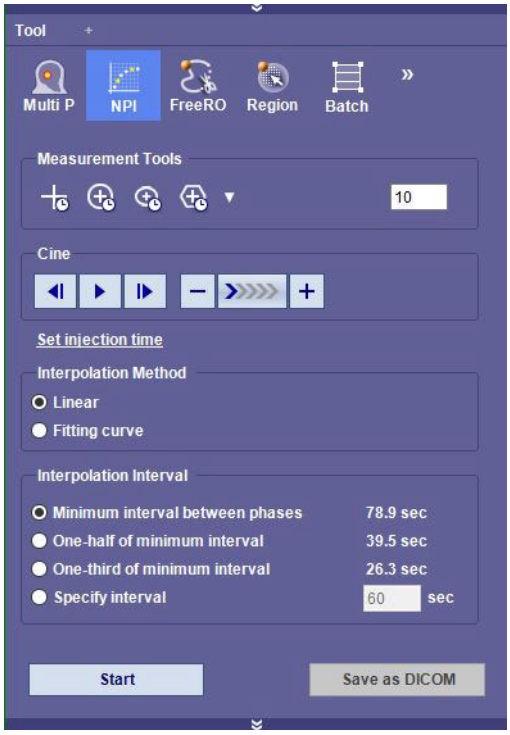


Figure 21-15 NPI Tool Panel

Selecting **Set Injection Time**, opens the **Injection Time Setting** (Figure 21-11 on page 21-8) window. This allows you to set a time before peak in increments of seconds. The TIC graph displays the "*" mark with the intensity value for an interpolated phase.

Pixel Wise

Pixel Wise (T1 point) allows “mousing over” a region to view the signal for each pixel.

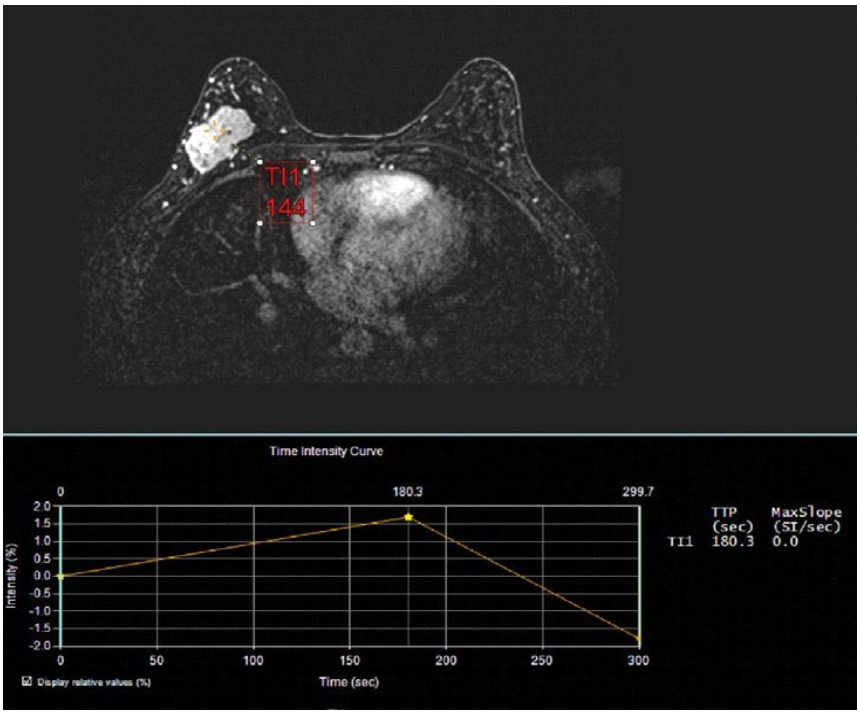


Figure 21-16 Pixel Wise

Kinetics Results

The Kinetics Tab allows you to select and display kinetic curve measurements overtime. To select and display these measurements:

1. Select and process results using the **Parametric Map** button.
2. Select the Kinetics tab in the Tool panel and use the ROI tool to draw an ROI.
3. The Findings measurements are displayed on the image, in the graph, and in the findings viewbox.

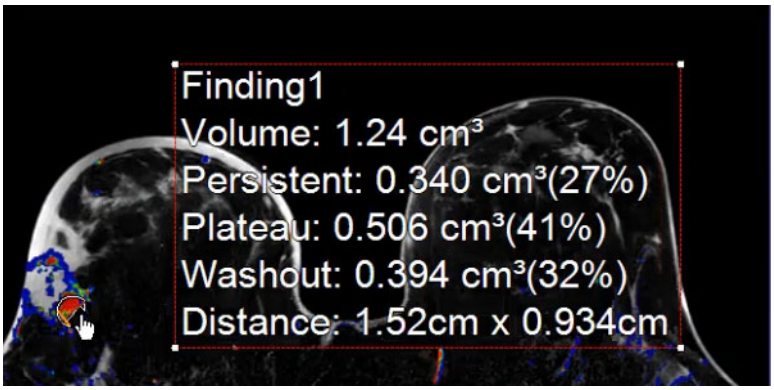


Figure 21-17 Example of Finding1 Results

Figure 21-18 TIC Graph and Findings Window

Each finding shows the measurements for percentage of persistent, plateau, and washout rounded to whole numbers. These are reflected in the Parametric Map results as well. Table 21.2 displays the default colors for these measurements. The colors can be changed by RMB-clicking on the parametric map or in the findings window (above, right, Figure 21-18.

The graph displays the percentage of total pixels of each slope and type.

Table 21.2 Kinetics Measurements Key

Measurement Type	Color (Default)	Change %
Persistent	Blue	>5% change
Plateau	Yellow	Between -5% and +5% change
Washout	Red	-5% change

Kinetic Options

To set additional options for kinetic results:

1. RMB-click on the findings overlay box in the image and select **Options** from the context menu.

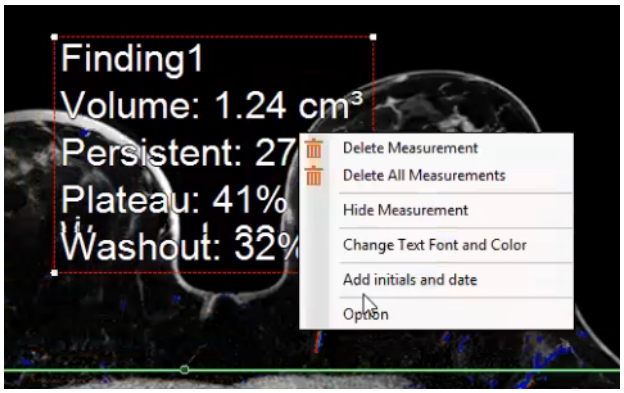


Figure 21-19 Selecting Kinetic Options

2. The **Kinetics Option** window opens.

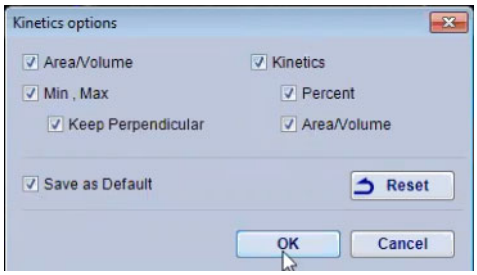


Figure 21-20 Kinetic Options Window

Depending on the options you choose, you can display the finding's area, a Min/Max distance, and add the percentile measurement.

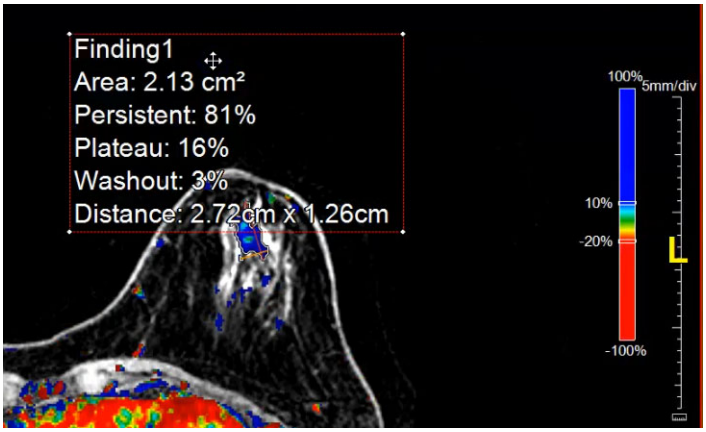


Figure 21-21 Changed Kinetics Options

Figure 21-21 shows that the selected options are Area/Volume, Min, Max and Percent. Any option settings can be Save to Default, if needed.

You can also use the Preference window for additional options.

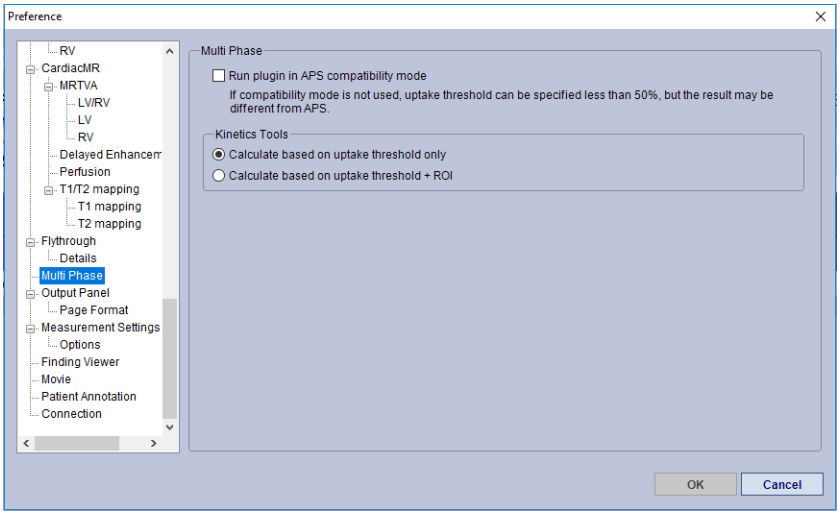


Figure 21-22 Preference Window Multiphase Options.

Chapter 22 AqWEB Viewer and AQiMobile

Topics in this chapter:

The AquariusWEB Viewer feature allows you to view series data even if you do not have access to a TeraRecon Aquarius system. You can view the data in any Web browser.

Accessing Data in AquariusNet ThinClient WEB Viewer

In order for you to have access to the series, someone must send you an email from an Aquarius iNtuition Client or Thin Client, containing a URL to the data on the iNtuition Server. (See "Email Series URL" on page 2-18 for information on how to send the URL.)

Once you have received an email containing the URL, do the following to open the AquariusWEB Viewer:

1. Click on the link. You might see a Windows security alert. If so, click **Yes** to continue.

2. If the sender has required a password, you are asked to enter that password at this time. Type in the password and click the **Login** button.

Note: If you do not know the password, contact the sender to obtain it.

If the sender has required full authentication, you are asked to login to the server in order to access the data. To do this, you must enter your username and password in the login screen.

The AquariusWEB Viewer is displayed, as shown in the figure at right.

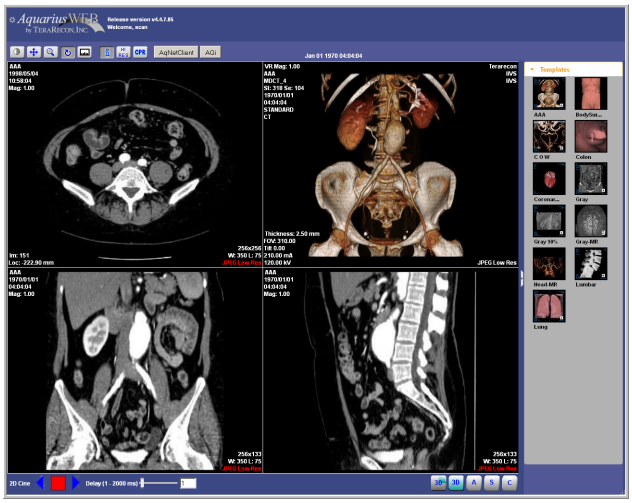


Image Viewing Tools

The AquariusWEB Viewer offers the following tools with which you can view and manipulate the images. The tool buttons are located in the top-left section of the screen.

Mouse Mode 

From left to right, these buttons change the function mode of the *left* mouse button:

- Window/level
- Pan
- Zoom
- Rotate

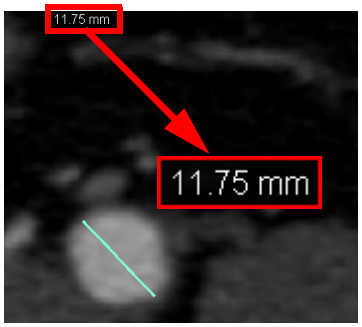
Ruler 

The ruler button allows you to obtain distance measurements on 2D images. To obtain the most accurate measurements, magnify the image first.

Table 22.1: Alternate Ruler Icon

Icon	Function
	Measure the distance between two points by left click and hold; drag the crosshair to the end point and release. For more information see "Distance" on page 3-147.

1. Click the button to toggle the ruler on.
2. Left-click on the 2D image and drag the mouse across the area to draw a measuring line. The line is displayed in light turquoise and the length is displayed at the top of the image.

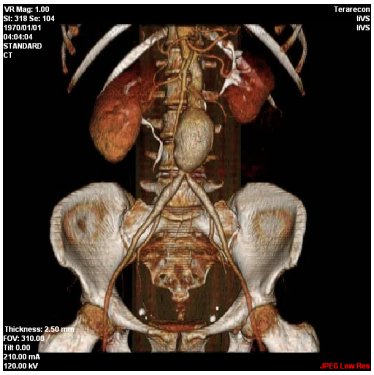


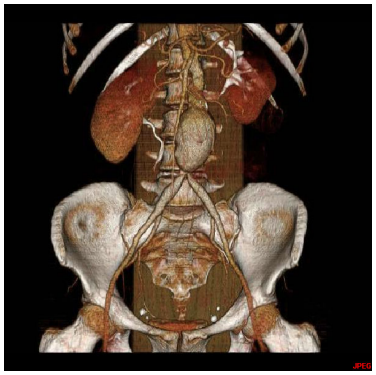
Show/Hide Annotation 

This function allows you to display or hide annotations on the images.

Low/High Resolution 

This function allows you to display the images in high or low resolution.



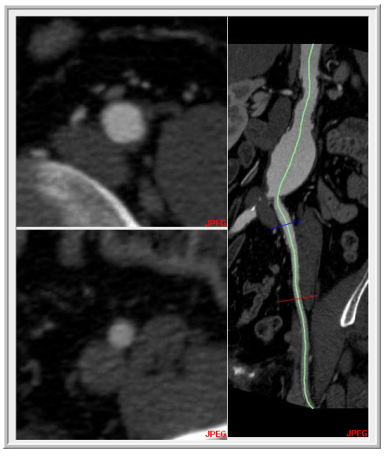


Left - Low Resolution **Right - The Same Image in High Resolution**

Figure 22-1 Comparing Low and High Resolutions

CPR View 

CPR View allows you to see a vessel in cross-section, take measurements, and view a cine of slices.



Note: You can view CPR images only when CPR images are sent to the AquariusWEB Viewer.

Templates

The **Templates** panel is located on the right side of the AquariusWEB Viewer. This feature allows you to view data using some of the standard color and window/level templates available on the AQi Client. (See "Color Template" on page 3-79 for more information.)

Additional Viewing Tools

There are additional viewing tools, located in the bottom-right section of the AquariusWEB Viewer. These allow you to display axial, sagittal, coronal or 3D images in the main window.

Cine Tools

The Cine tools are in the bottom-left corner of the AquariusWEB Viewer. Click the right or left arrows to view a cine (forward or backward) of the 2D slices in the selected window. The red square button stops the cine. The number in the **Delay** text box determines how fast the cine will scroll - 1 is the fastest and 2000 is slowest.

Aquarius iNtuition Mobile (AQMobile)

This product is for medical professionals to view clinical data on mobile devices, including the iPod, iPhone, iPad and iPad Mini.

Warning: Aquarius iNtuition Mobile is not for diagnostic review.

CAUTION! U.S. Federal law restricts use of this device to trained physicians, or other suitably qualified and trained personnel on the order of a physician.

Requirements

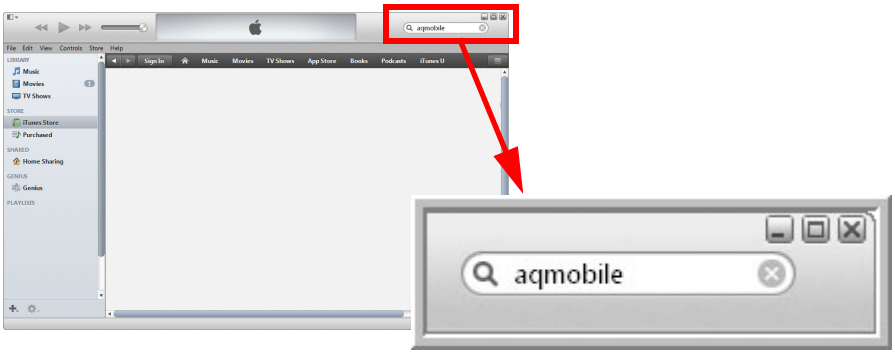
The following is required in order to use Aquarius iNtuition Mobile v2.0 and above:

- A mobile device running iOS 7.1 or above.
- A user account authorizing you to access a TeraRecon AquariusNet ThinClient server, version 4.4.5 or above.
- One of the following:
  - Local access through a wifi connection to the AquariusNet ThinClient server.
  - From an external location, a VPN connection to the AquariusNet ThinClient server.

Downloading and Installing

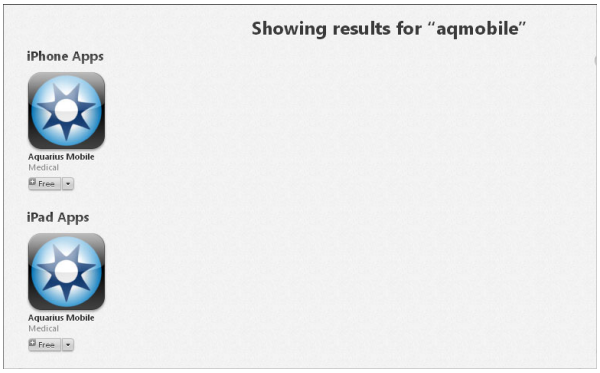
You can download the AQMobile application from the Apple Store using iTunes.

1. Enter “terarecon” or “aqmobile” in the search bar.



The search results are displayed as follows:

2. Click the appropriate link for your device.



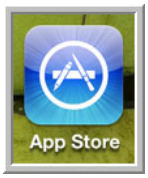
The description page for the application is shown:

3. From the description page, click the **Free** button to begin the download.

Note: If you do not have an Apple Store account, you will need to set up an account before downloading.

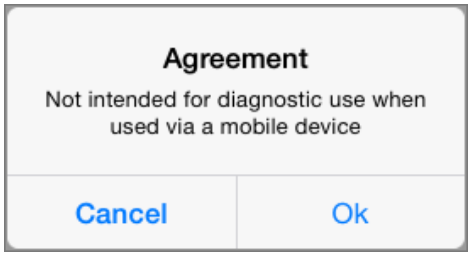
Startup

To start the AQMobile app, first make sure you are connected to the Internet. Then tap the **App Store** icon on the Home screen of your mobile device. If AQMobile is the your only application from the Apple Store, your device will automatically start up AQMobile.



If you have more than one application, touch the **AQMobile** icon to start the application.

When the application starts, the AQMobile splash screen is displayed, immediately followed by a message box describing the agreement.

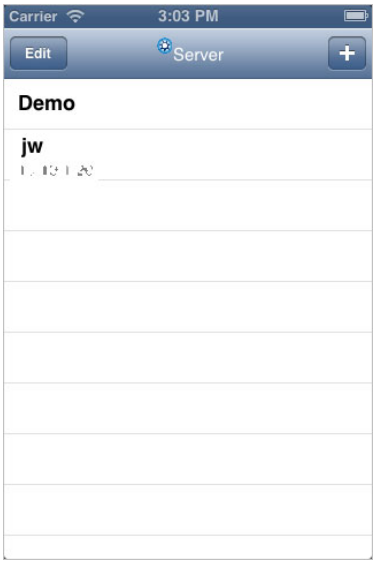


You must touch **OK** to proceed. Once you have touched **OK**, the application can continue.

Note: If there is no activity on AQMobile for ten minutes, you are automatically logged out, and you will need to log in again to continue using it.

The Server List

The server list shows the list of servers available to connect to. Server list information is stored in local memory.



Each server entry contains the server name and its hostname or IP address.

When you select one of the server entries, AQMobile displays the list of patient data available on that server.

Figure 22-2: The Server List

Note: The top bar of the screens shown in this manual might vary in appearance from your device, depending on the product and version of your device. The functionality is the same.

The Demo Server

The Demo server is a special TeraRecon server that is available to anyone who has installed AQMobile 2.0 and above. You do not need to have your own AqNET server or any of your own study data to use the Demo server. It is there so that you can test AQMobile and learn its features. The Demo server provides sample data for this purpose.

Adding a Server to the List

If the server you need to connect to is not in this list, you can add it by doing the following:

1. From the **Server List** screen, touch the "**+**" button, which is located in the upper-right corner (see Figure 22-2 above).

   A server entry form with keyboard is displayed (see figure at right).

2. Enter the following into the form:

   - The Logical Name. Choose a name that will identify this server in a meaningful way to you. This entry is optional. If you do not enter a logical name, only the server's hostname or IP address will appear in the server list.
   - The server's hostname or IP address.
   - The Port. If you do not know the port number, ask the server's system administrator.
   - Username and Password. These will be your credentials for connecting to the server.
   - (Optional) The Group Name. If you can not see the text entry box for Group Name, scroll down. The keyboard hides a portion of the screen.

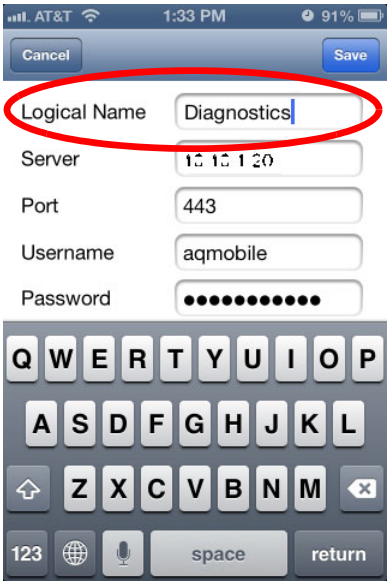
3. When done, touch the **Save** button in the upper-right corner. You can also touch the **Return** button in the lower-right corner to save the server configuration.

   The application attempts to connect to that server, to confirm that the server is alive. If the connection is successful, the server information is saved to local memory and is added to the server list.

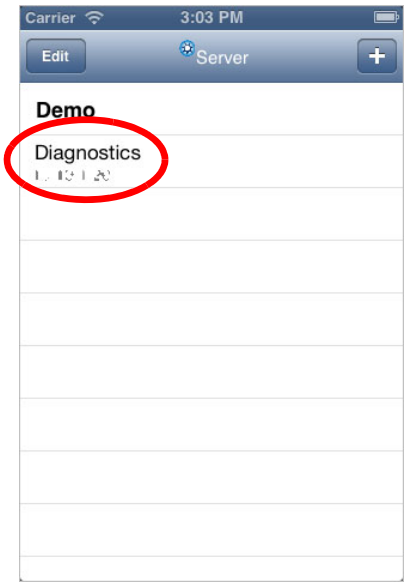
Editing a Server's Configuration

To edit an existing server configuration, do the following:

1. Display the Server List (as shown in Figure 22-2 on page 22-7).
2. Select the server to be edited.
3. Touch the **Edit** button (located in the upper-left corner).
4. The selected server configuration screen is opened (see image at right.
5. Change any of the text entry boxes in the screen. For details, see "Adding a Server to the List" on page 22-7, Step 2. In the example shown at right, the user is changing the Logical Name.
6. When finished, touch **Save**.



The Logical Name change is reflected in the server list, as shown at right.



Deleting a Server From AQMobile

To delete a server from the list, do either of the following:

1. Swipe the server entry from right to left. The **Delete** button is displayed.
2. Touch **Delete** to delete the entry.

- Or -

1. Touch the **Edit** button in the top left corner.
2. Touch the "-" button on the server entry to delete the entry.

The Study List

The Study List displays the patient data available for viewing. Each entry in the list represents a single study.

The URL Link List

If the server you are connected to is running AquariusNet ThinClient server version 4.4.6 or earlier, the Study List is presented as a list of *URL links*. Each link represents one or more series.

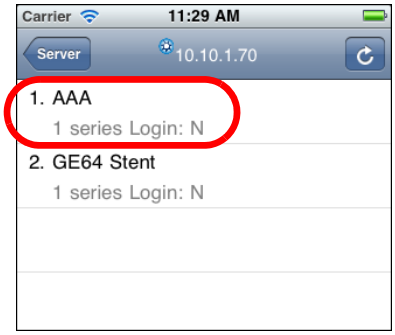


Figure 22-3: URL Link List

A single entry in the URL link list contains the following:

- The name of the data set
- The number of series included
- A field indicating whether an authentication login is required to access the data (Y or N)

The application displays the first 17 entries of data on the server, followed by the **Load Next** button. If you can not see all 17 entries on your device, scroll down to view the rest of the list. To retrieve more data, touch **Load Next**. The application loads the next 17 entries and displays them below the current list.

If you select a URL link entry that does not require a login, the application retrieves the link detail information from the server, and opens one of the following: the series list, the sub-series list, the Workflow scene activity list or the viewer, depending on how many items are in each of the subordinate lists.

When you select a URL link entry that requires authentication (login), a pop-up dialog is displayed with a keyboard to allow you to type in the password. Then the application opens the series list, sub-series list, workflow scene activity list or the viewer.

The Patient List

If the server you are connected to is running AquariusNet ThinClient version 4.4.6 Patch1 or later, the Study List is presented as a Patient List (as shown in the image at right).

A single entry in the Study List contains the following:

- The patient name
- The modality of the study
- The Patient ID
- The number of series included

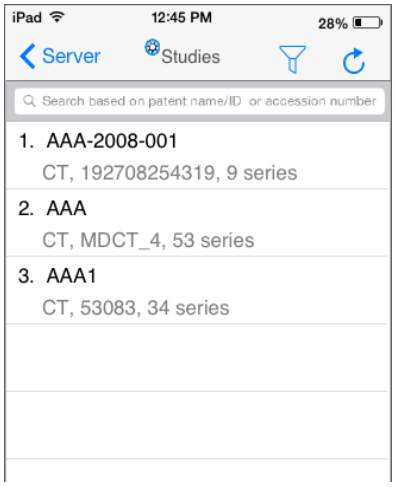
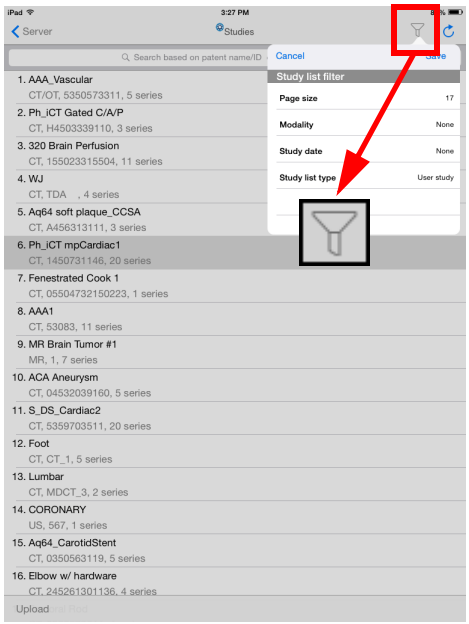


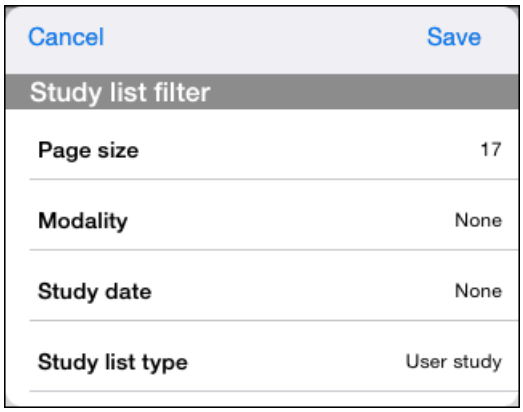
Figure 22-4f: Study List

To avoid confusion, the list of studies, whether in the form of a Patient List or a URL Link List, will be referred to from here on as the **Study List**.

Study List Filtering

In the top bar, on the right side, there is an icon that looks like a funnel. This is the study filtering icon (see image at right). Tap this icon to open the filter menu.





These settings determine which studies are displayed in the Study List.

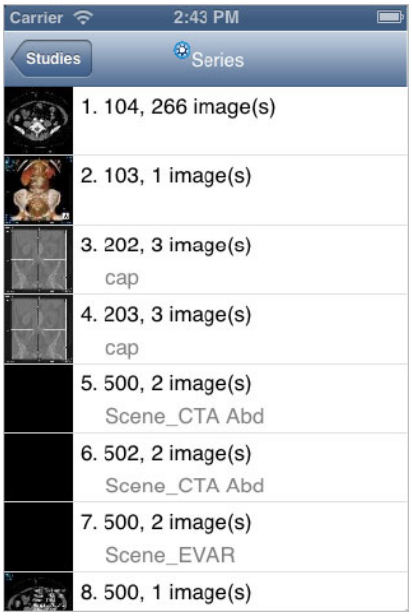
- Page size: Default is **17**.
- Modality: For example, **CT**, **MG**, **MR**, and so on. Default is **None**.
- Study date: For example: **Today**, **Yesterday**, **Last2Days**. Default is **None**.
- Study list types: **User study** or **Published study**. Default is **User study**.
  - User studies are those that have been assigned to you. When you connect and log in to the AquariusNet ThinClient server, you have access to all studies that have been assigned to you.
  - Published studies are those that are accessible to anyone. When a study is published, it becomes publicly accessible. If you choose to view the list of published studies, you will see all studies that have been published by anyone.

The Study List allows you to toggle between the two types. Please see the following section for details.

Other Functions on the Study List Screen

- **Refresh** - To redisplay the Study list, touch the Refresh button ( ) in the top right corner.
- **Close Study list** - To close the Study list, touch the **Options** button in the top left corner. The Study list is closed and the Options list is displayed.

The Series list

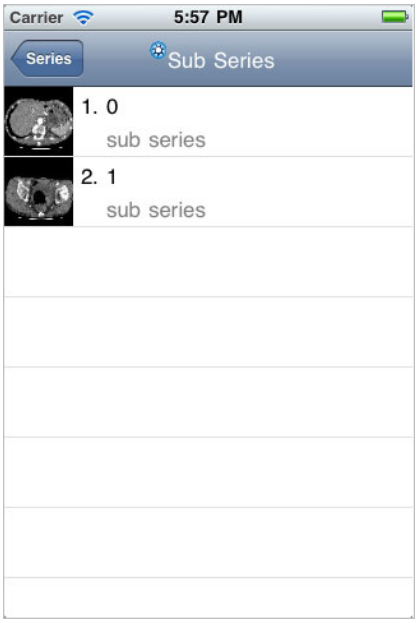


When you select an entry from the Study list that has multiple series, the series list is displayed showing the series included in the study. Each series entry shows a thumbnail icon, the series number, the number of images and series description.

To open a series, touch the desired entry in the list. If there is a sub-series list, that list is displayed. Otherwise, the workflow activity list is displayed.

To close the series list, touch the top left button. The Study list is displayed.

The Sub Series List



When a series is selected that has multiple sub-series, this list is displayed. Each sub series entry shows a thumbnail icon and sub-series number.

When an item in the sub series list is selected, the viewer is opened, displaying the image.

To close the sub series list, touch the **Series** button in the top left corner. The previously displayed list is redisplayed.

Workflow Scene or Sub-series List

When you select a series that is a workflow scene, and if the series has multiple workflow scene activity, the workflow scene activity list is displayed. Each workflow scene activity shows a thumbnail icon and the name of the workflow activity.

To display the image in a workflow scene activity, select the item from the list. The image is opened in the viewer.

To close the workflow scene activity list, touch the **Series** button in the top left corner. The application closes the workflow scene activity list and displays the previous list.

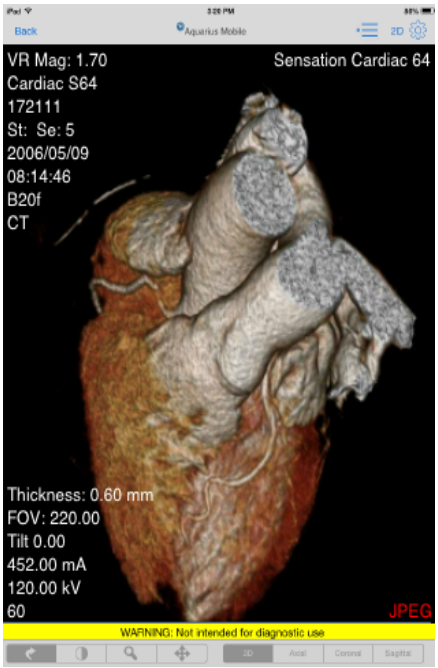
When you select a single image from a list, the Viewer is launched. The data is loaded and the image is rendered and displayed in the Viewer with patient annotation.

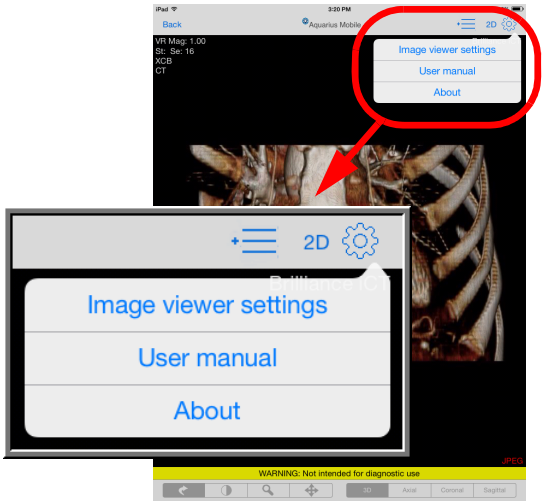
Note: A warning message, reading **WARNING: Not intended for diagnostic use** is displayed at the bottom of the viewer screen, on a strip of yellow background color (see the following figure, at right).

Viewer Settings 

The setting icon is located in the top-right corner of the viewer screen.

The settings allow you to configure viewer settings from within view screen. Tap the setting icon to display a menu of setting options. See the following image.





The menu contains the following image viewer settings:

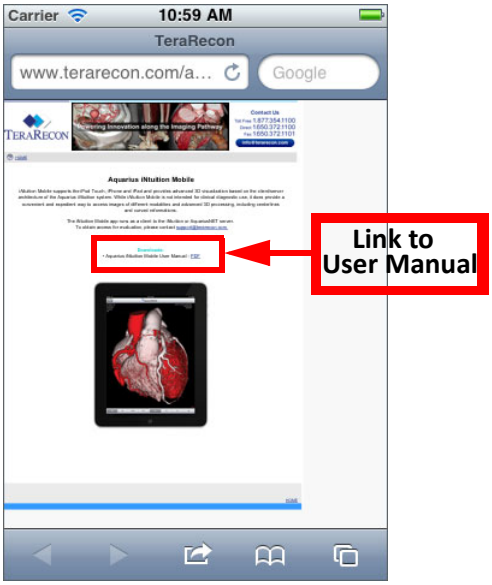
- Image viewer settings

Table 22.2: Image Viewer Settings

Setting	Description
Compression quality	Percentage size of the original image (compression factor). Default is 75%.
Enable image JPEG lossy compression	Enable this to allow image to be compressed according to the quality factor set above. This allows images to load faster. However, be aware that the level of detail will be lower, and some small features of the image could be missed. If you want to see the image at full size, do not enable this setting.
Initial view type	Open all studies in either the 2D or 3D view.
Window step	Size of a single increment or decrement in brightness.
Level step	Size of a single increment or decrement in contrast.
Window/level templates	Preset templates for viewing abdominal organs, or the head, lung or bone. For more information, see "Window/Level Preset Context Menu" on page 22-23.

- User manual

  Open the user manual (this manual) on your device. This menu item opens a screen that contains a link to the manual in PDF format (see image at right).



- About

  Display the product name and version number.

- Cancel (iPod and iPhone)

  On the iPad and iPad Mini, the settings menu disappears automatically when you tap on one of the options, or on any area outside of the dialog. If you are viewing Aquarius iNtuition on an iPod or iPhone, you can also tap the **Cancel** menu item.

Manipulating the Image

The AQMobile Viewer supports some finger gestures for performing operations on the image that change its orientation, scale, position, and window/level.

Gestures

Single-touch gestures use one finger to touch and move around the center or the lower right corner of the image.

Dual-touch gestures use two fingers on the screen simultaneously, in three different configurations:

- **Horizontal** - The two fingers are placed side-by-side horizontally, and the distance between them does not change during movement.

- **Vertical** - The two fingers are placed one above the other, and the distance between them does not change during movement. (It is recommended that you use your index finger and thumb for this gesture.)

- **Pinch** - The two fingers are pulled together or pushed apart.

Operations

The AQMobile Viewer supports the following operations on images: Rotate, W/L, Zoom and Pan. Some gestures are used in conjunction with the four control buttons in the bottom left half of the screen:

Table 22.3: AQMobile Viewer Operations

Operation	Gesture	Description
Rotate	Single touch	When the  button is selected, the image is rotated in the direction of finger movement.
W/L	Single touch	When the  button is selected, finger movement upward causes the W/L to increase; finger movement down causes it to decrease.
	Dual horizontal touch	Movement upward causes the W/L to increase; movement down causes it to decrease.
Zoom	Single touch	When the  button is selected, finger movement upward causes the image to zoom in; finger movement down causes zoom out.
	Pinch	Opening the fingers wider zooms the image out. Closing them together zooms the image in.
Pan	Single touch	When the  button is selected, the image is panned in the direction of the finger movement.
	Single touch and move from the screen edge	This gesture pans the image, regardless of the operation selected with the control buttons. However, when the Viewer is not in pan mode, it is important to touch the *very edge* of the screen before panning. Otherwise, finger gestures are interpreted according to the selected mode.
	Dual vertical touch	Pans the image in the direction of the movement.

Image Rendering

- Normal series or sub-series image

  If the data is from a normal series or sub-series, the image is rendered in 3D VR using the default color template.

- Scene or workflow activity scene

  If the data is a scene or one of the workflow activity scenes, the scene is displayed in the rendering mode that was used to create it.

- Secondary capture image

  If the data is from secondary capture images, the image is displayed in the rendering mode used to create the secondary capture.

Rendering Modes

The image rendering mode is selected using the control buttons in the bottom right corner of the screen. When a normal volume is loaded, the control buttons allow you to choose 3D Volume Rendering (**3D**), or **Axial**, **Coronal** or **Sagittal** MPR.

When a CPR scene is loaded, the control buttons allow you to choose 3D volume rendering (**3D**), **CPR**, **Red** (cross section view on the red line) and **Blue** (cross section view on the blue line). See Figure 22-5 on page 22-16.

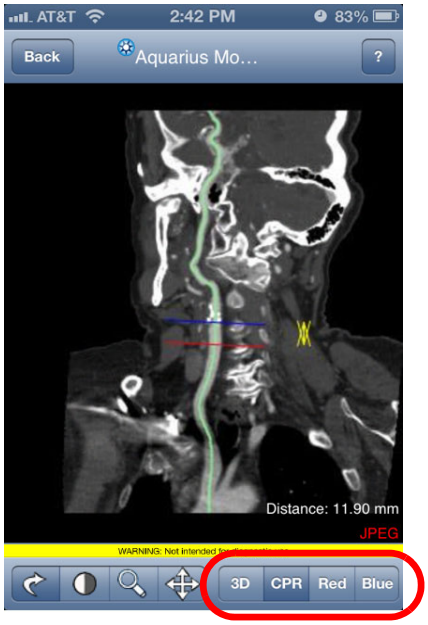


Figure 22-5: CPR View

Image Slice-By-Slice

AQMobile allows you to slice through a series of 2D images one by one.

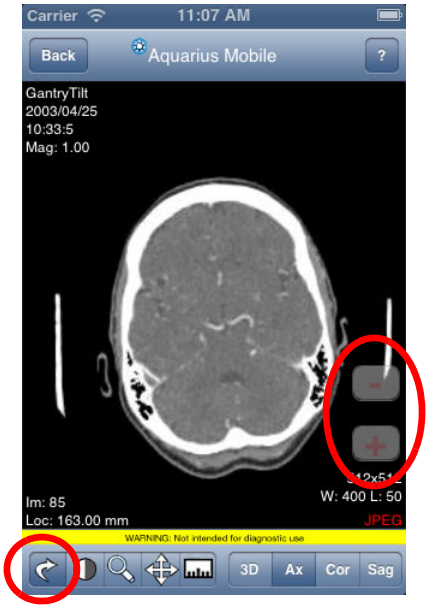
To access slice-by-slice mode:

1. Disable the AQMobile setting, “Enable loading volume in low resolution” on the **Settings** page. See "AQMobile Timeout Settings" on page 22-23 for more instructions.

2. Load a 2D series.

3. Tap the rotate/slice icon (circled in dark blue in the figure at right) to enable rotate/slice mode.

   Buttons for slicing forward (**+**) and backward (**-**) are displayed in the image window (circled in light blue).



2D Measurements

Note: The server must be configured for 2D Measurements. Please contact Customer Support for more information.

This tool allows you to obtain distance measurements on a 2D image. To enter measurement mode, tap the ruler button at the bottom of the Viewer screen (circled in Figure 22-6 on page 22-17).

To obtain the most accurate measurements, we recommend that you first magnify the image. When TeraRecon software distance measurements were tested against a digital phantom, the measurement error was shown to be under 1%. The measurement was tested using the iPad/iPad Mini, enlarging the image to greater than 200 pixels. Please note that this error estimation does not take into account image modality error.

Add New Line

1. Make sure 2D measurement mode is enabled. The ruler icon should be darker than the other icons at the bottom of the screen (see image at right).
2. Touch the image at the start point of the measurement. You can pinpoint the start point with greater precision by moving your finger before lifting it.
3. When you have located the correct start point, lift your finger off the screen.

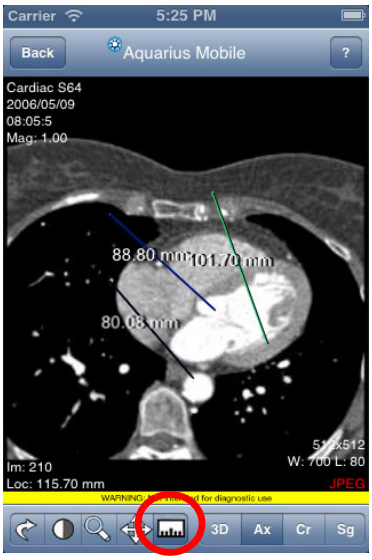


Figure 22-6: Measurement Icon

4. Touch the image at the end point of the measurement. The length of the line is calculated and displayed. If you need to move your finger to find the precise end point, the length is continuously updated.
5. Lift your finger to complete the measurement.

Modify an existing line

To modify an existing measurement, touch the line. The line enters edit mode, indicated by small red circles at the endpoints. You can adjust the distance and position of the line by touching the start or end point and moving your finger. Tap the line a second time to exit edit mode.

Delete an existing line

1. Tap the line that you want to delete. It changes to edit mode.

2. Touch either one of the endpoints.

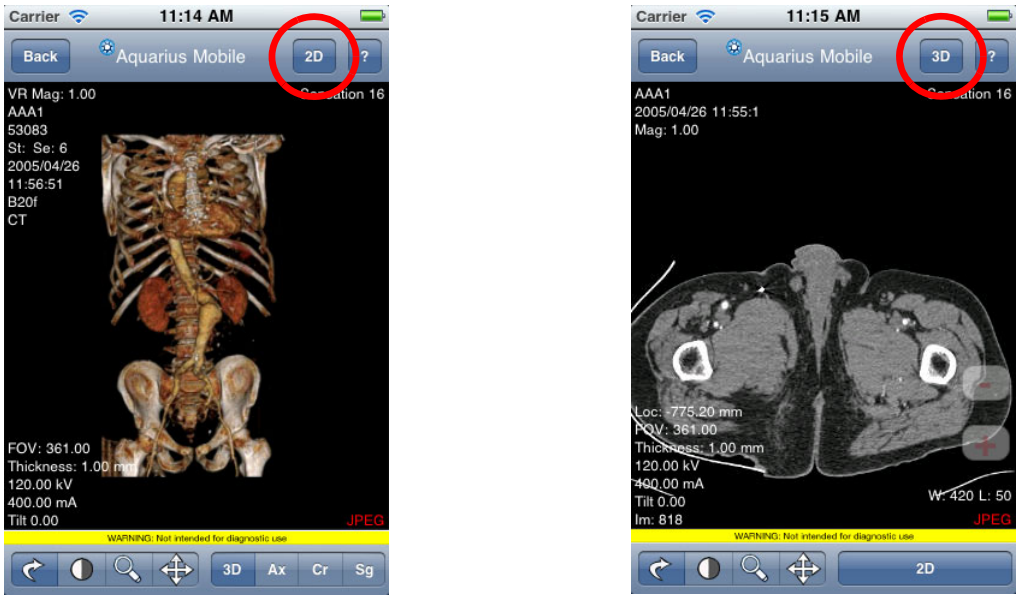
3. Without lifting your finger, move toward the other endpoint.

4. When your finger is as close as possible to the second endpoint, lift your finger. The line is deleted when the distance is very small.

Note: While in 2D measurement mode, you can single-touch the screen and pan the image from the edge of the screen. These operations will not cause AQMobile to exit 2D measurement mode.

Switching Between 2D and 3D Viewers

By default when a study is loaded, the 3D volume rendering viewer is used. To use the 2D image viewer, tap the **2D** button located in the top toolbar on the right. This button toggles between the 2D and 3D viewers. The study is opened in the 2D viewer, as shown in the Figure 22-7 below.



Left - 3D Rendering Viewer **Right - 2D Viewer**

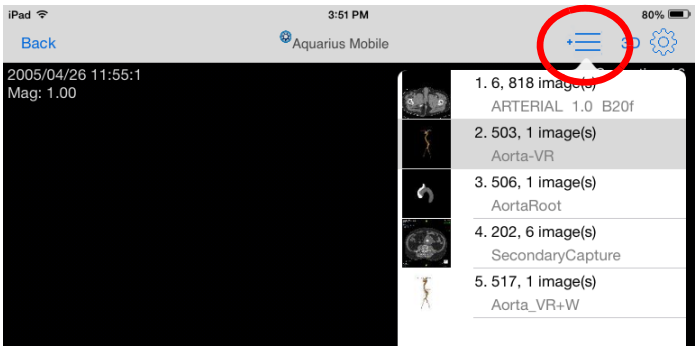
Figure 22-7 Left is the 3D rendering View and right is 2D.

Note that the viewer toggle button now reads 3D (right image). Tap the button to go back to the 3D rendering viewer.

Loading Another Series From the Viewer

In the top bar, on the right side, there is an icon consisting of three horizontal lines (see image at below). This is the load series icon. Tap the icon to show a menu containing all the series in the currently loaded

study. This menu allows you to load another series without leaving the Viewer. Tap the desired series to load it.

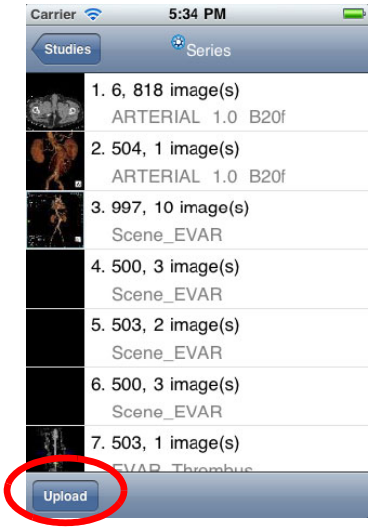


If the series selected has sub-series or workflow scenes, those lists are displayed instead of an image in the viewer, so that you can select a sub-series or workflow scene from that list.

Note: Displaying sub-series or workflow scene lists from the viewer is not supported in earlier versions of the AqNet Server. Instead, the first sub-series or workflow scene is loaded. If you need to load more than one sub-series or workflow scene, you will need to leave the Viewer and go back to the Series list.

Importing Non-DICOM Images

You can upload non-DICOM images to AQMobile.



Note: The server must be configured for non-DICOM file uploading. Please contact Customer Support for more information. Also note, this feature is available only when AQMobile is connected to an AqNET Server version 4.4.11.82 or later.

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1. Tap the **Upload** button. A screen that shows all saved photos in the device is opened (.
2. Tap the desired photo to select it. The selected photo is loaded into the screen.

Note: To go back to the previous screen without selecting a photo, tap the Cancel button.

3. To confirm the selection, tap the **Choose** button.

Once you have confirmed the photo selection by tapping the **Choose** button, a screen is opened that allows you to enter the patient name, patient ID, study description and series description.

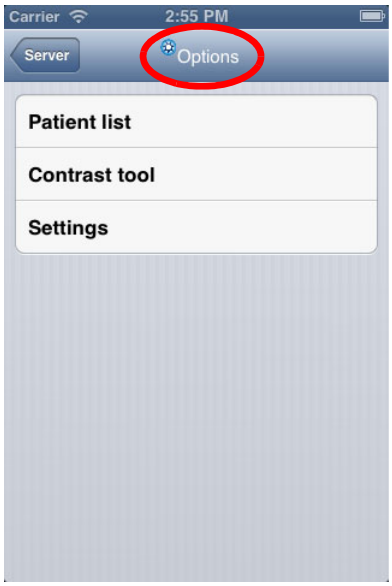
If you had already selected a study before importing the non-DICOM image, the first three items are filled in automatically.

On this screen, you can tap the **Cancel** button to go back to the **Patient List** screen, or tap the **Upload** button to send the photo to the server. The photo will then be converted to a DICOM file and sent to AqNet DICOM server. Eventually, it will be displayed in the Patient List as a DICOM file.

Note: Before uploading the photo to the web server, you must enter the patient name and patient ID in the text input boxes.

AQMobile Options

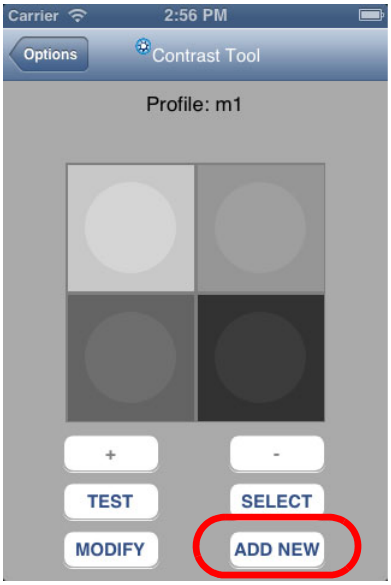
Tap the **Options** button from the Study List (see Figure 22-4 on page 22-9) to open the AQMobile Options screen, as shown at right. There are three options available: **Patient list**, **Contrast tool** and **Settings**.



Patient List

Return to the Study List.

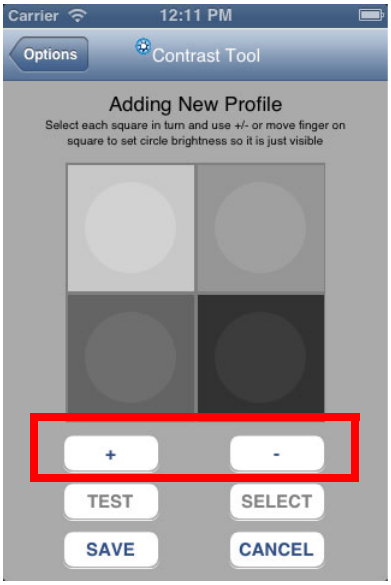
The Contrast Tool



The Contrast Tool allows you to create and save profiles of the lighting conditions in various environments. For example, if you are in a good environment for image viewing, you can create and save a contrast profile of that environment. This profile can later be compared to other environments where the lighting might be different.

A contrast profile contains four color squares. Each square contains a circle that can be adjusted to four levels of color. Using the Contrast Tool, you can add, modify, delete or test the contrast profile.

Add New Profile



In the **Contrast Tool** screen, tap the **ADD NEW** button (circled in the previous image) to open the screen shown at right, **Adding New Profile**.

Adjust the color of each circle as follows:

1. Tap a square to select it.
2. To darken the circle, tap the minus (**-**) button.
3. Continue to tap the minus button, making the circle darker until it is so similar to the color of the square that it is barely visible. If the circle becomes completely invisible, tap the plus (**+**) button to make it slightly lighter.

Note: You can also make the circle lighter or darker by touching the circle and moving in an upward or downward direction on the screen, respectively.

When all four circles have been modified so that they are all just barely visible, save the contrast profile, if desired.

Save Profile

To save a profile, do the following:

1. Tap the **SAVE** button.

A dialog opens, where you can provide the profile name and description.

2. Enter a unique profile name, and optionally, a description.

3. Tap **OK** to save. The profile is stored on the AqNET server.

   To cancel without saving, tap **CANCEL**.

Modify Profile

1. Tap the **MODIFY** button.
2. Adjust the color of the circles in the desired squares, using the plus (**+**) and minus (**-**) buttons.
3. Tap **SAVE** to update the profile on the server.

Delete/Select Profile

1. Tap the **SELECT** button.

2. Tap the desired profile from the list. This selects the profile. The Contrast tool screen for the selected profile is displayed automatically.

3. Touch and move finger from left to right on specific profile row. The **DELETE** button is displayed.

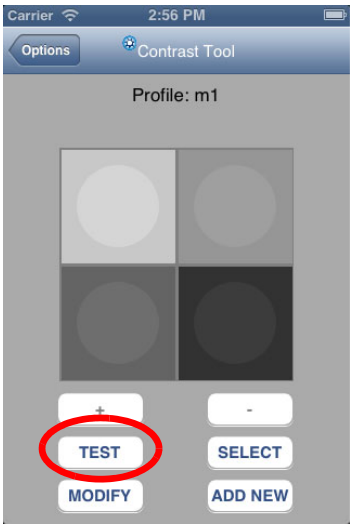
4. Tap the **DELETE** button. The profile is deleted.

Testing a Profile

The purpose of testing is to determine how good the lighting is in your current environment, when compared to a profile previously created in an environment that is optimal for viewing images.

To begin testing, select a profile from the profile list, and then tap the **TEST** button as shown in the following figure:.

During the test, four sets of squares are displayed, one at a time. For each set, tap the square that contains a visible circle.



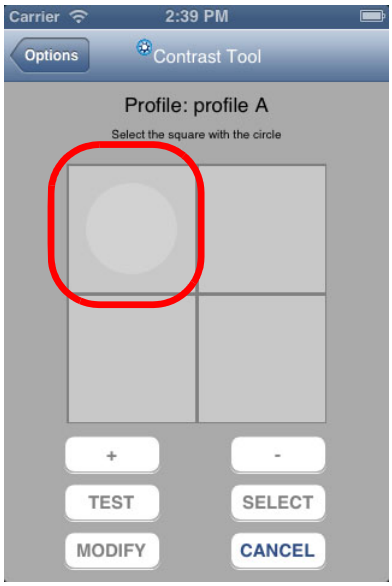
Note: *This test is timed*. For an accurate evaluation, you must tap the visible circle within 5 seconds after the squares are displayed. The circle might be barely visible, so it is also important to look carefully.

The lightest spot is tested first. The circle is placed in one of the four squares at random.

In the image at right, the upper-left square contains the circle, which, although difficult to see, is visible.

If you can not see a circle at all, this indicates to the software that the lighting in your current environment is less than optimal, when compared with this profile.

After you have made a selection, or after 5 seconds have passed, the contrast tool displays the next-darkest set of squares. The circle is shown in one of the other squares, randomly selected, at the gray level stored in the saved profile. This process continues until all four levels of brightness have been tested.

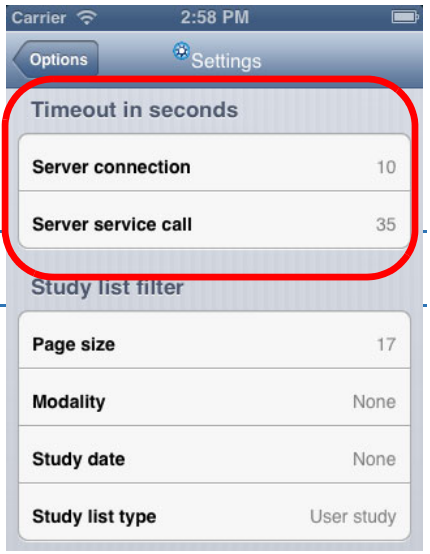


Test Results

When you have finished selecting the circle in each set of squares, the test results are reported. The score represents the percentage of times (out of 4) that you correctly identified the square containing the circle.

AQMobile Timeout Settings

- Server connection timeout. Default is 10 seconds.
- Server service call timeout. Default is 35 seconds.

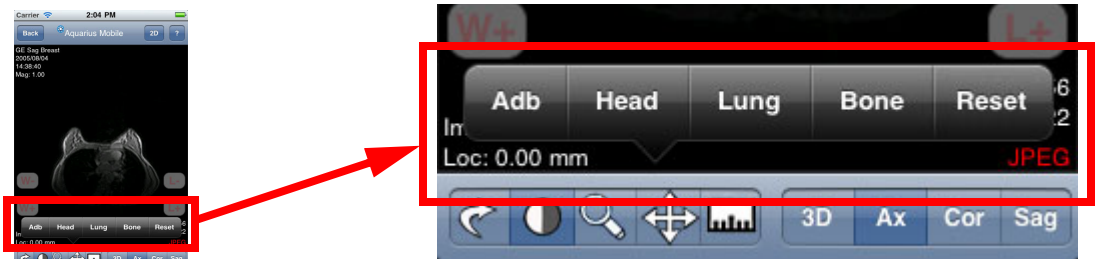


Note: You do not need to exit AQMobile to access these settings.

Window/Level Preset Context Menu

When you tap the W/L icon ( ) in the Viewer, a context menu is displayed on the screen showing each of the four templates, plus a **Reset** button (see image below).

Tap the button for the desired window/level to apply the preset values. To apply the initial recommended window/level for the image, tap the **Reset** button.



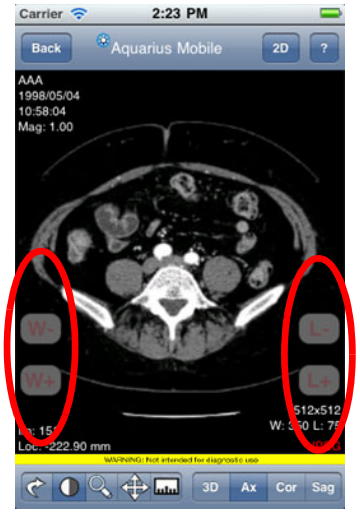
Editing Window/Level Templates

You can change the name, window and level default values by tapping one of the templates (see image at right). This opens the Window/ Level Template screen (shown below).

Enter a new **Name**, **Window** value or **Level** value to change it. To save changes, tap **Save** in the upper-right corner. To cancel, tap the **Cancel** button in the upper-left corner.

W/L Step by Step

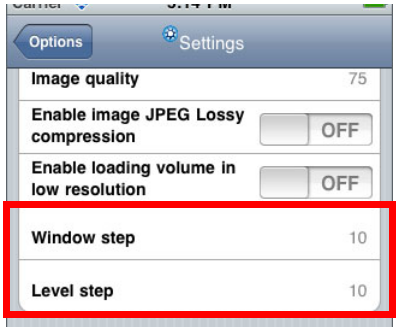
This allows you to increment or decrement the window or level values by steps. Four buttons are displayed on the screen for these functions: W+ and W-, for increasing and decreasing, respectively, the window values, and L+/L-, for the level values. (See image below.)



Each time you tap one of these buttons, the window/level changes by a configurable step value. The default step is 10.

You can also touch the button and hold it down. The value of the window or level is changed continually, step by step, until the button is released.

To change the size of the step for either window or level, open the AQMobile settings screen. The window and level step sizes can be configured independently.



Exiting the Viewer

To close the viewer and display the previous list, touch the **Back** button in the top left corner of the screen.

Note: AQMobile supports both the portrait and landscape orientations of your device. When you rotate the device, the application detects the new orientation and displays the GUI and images accordingly.

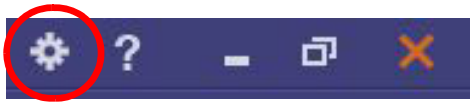
Appendix A: GUI Configuration

Topics in this Appendix

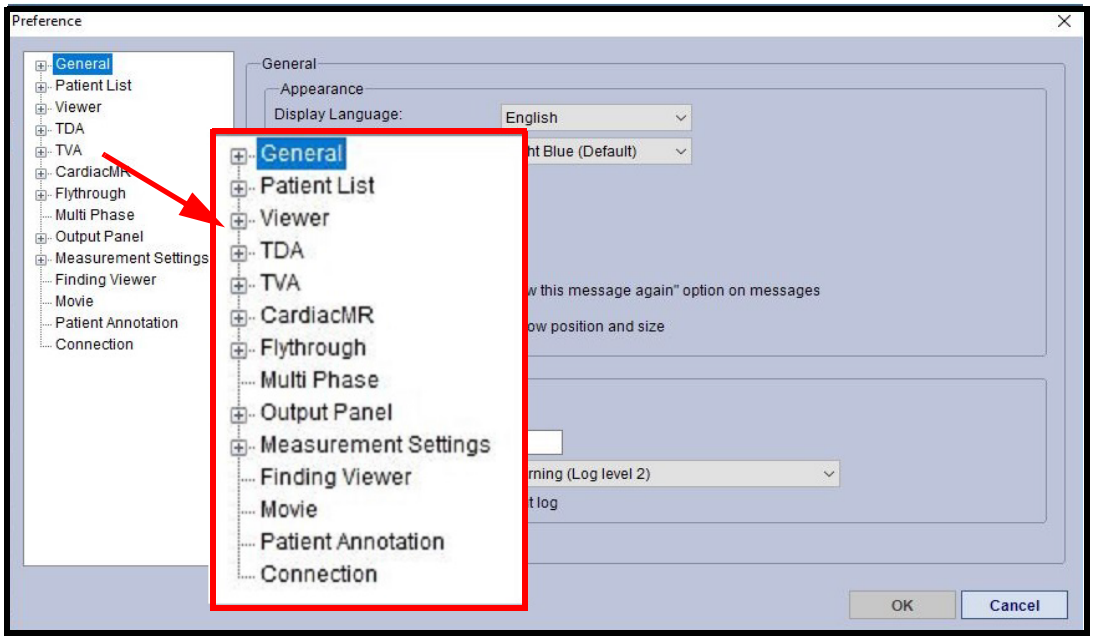
The Preference screens allow you to configure the appearance and function of the Aquarius iNtuition user interface suits your particular needs.

Opening Preferences

To open Preferences, click the **Preferences** button, located in the top-right corner of the Aquarius iNtuition Client screen:



The **Preference** window opens:



Note: Some preferences require the Aquarius iNtuition Client to be closed and then restarted before the change takes place. This is indicated by "(Requires restart)" in the Description column.

General

The **General Preferences** dialog is displayed initially. These settings pertain to the overall look or feel of the Aquarius iNtuition Viewer application.

Table A.1: Viewer Options and Values

Option	Values (Default value bolded)	Description
Enable transparent windows	Enabled/**Disabled**	Allow transparent dialog boxes and progress bars to be displayed on images.
Messages reset to default	Enabled/**Disabled**	Resets all messages so that a dialog box is displayed saying "Do not show this message again".
Display Language	• English • Spanish • French • Japanese • Portuguese • Chinese (PRC) • German	Language used for the Aquarius iNtuition Graphical User Interface (GUI)

Option	Values (Default value bolded)	Description
Color scheme	Bluish Gray, Dark Blue, Dark Brown, Dark Gray, Dark Green, Dark Slate Blue, DarkRoom Mode, DayLight Mode, **Light Blue**, Light Purple, Pastel Blue	Background color of the Aquarius iNtuition Viewer GUI
Use Flat UI	**Enabled**/Disabled	Use flat button icon. Default is Enabled when using Windows 8 or above.
Save current window position and size	N/A	Allows you to save the size you have chosen for your current window (click the **Save** button to enable).
Enable Portrait Monitor Layout	Enabled/**Disabled**	Enables Aquarius iNtuition to be displayed in Portrait mode. **Note: You need to also configure the Windows display options for Portrait mode.**
Enable logging on this machine	Enabled/**Disabled**	When enabled, events occurring on the Aquarius iNtuition Client are logged.
Maximum size of Log file (MB)	Range: 1-100 MB Default: **3 MB**	Maximum file size of log files.
Logging Detail	• Verbose (4) • Information (3) • Warning (2) • Error (1) • Critical (0)	Severity level of information to be logged, from Verbose (all errors, major and minor) to Critical errors only.
Flush immediately when output log	Enabled/**Disabled**	When enabled, log file update as soon as event occurs. You may feel some slowness during the update.
Use DirectX rendering mode	**Enabled**/Disabled	When enabled, the image display speed is improved. **Note: This depends on the graphic card on the client system.**

Application Error

Application Error Preferences allow you to configure which actions to take in the event of a system crash.

Option	Values (Default value bolded)	Description
Log information to be sent to server	• Basic • Detailed	Basic information is fast, but detailed information provides better clues to cause.
Dialog/Restart	• Show Dialog • No Dialog, Auto Restart • No Dialog, No Restart	Choose whether to display a dialog box and/or automatically restart the system after a system crash
Save crash information to the server	**Enabled**/Disabled	Save a copy of the crash log on the iNtuition server.
Scene Autosave Setting	Enabled/**Disabled**	Scene autosaving is disabled by default. Click **Scene** button to enable autosaving. A dialog is opened containing a checkbox to enable autosaving and to configure the frequency (number of times per minute).
Restore User Setting	Click **Restore** button	Restore the most recent valid user settings.
Initialize User Setting	Click **Set to Default** button	When clicked, sets all user settings back to factory default

Command Line

Option	Values (Default value bolded)	Description
For images in the Output Panel on Clean/ClearAll command	• Clear All Images • Show a Warning • Auto Save and Clear All Images	Option how to handle the images in output panel, when clean / clear all command is passed to Aquarius iNtuition,
For images in the Output Panel on StopAll command	• Clear All Images • Show a Warning • Auto Save and Clear All Images	Option how to handle the images in output panel, when stopall command is passed to Aquarius iNtuition,
Send ClearAll to all ThinClient when ClearAll command is passed	Enabled/**Disabled**	Clear images in output panel and logoff ThinClient when clearall command is passed to Aquarius iNtuition.

Remote DICOM Server

Option	Values (Default value bolded)	Description
Enable Remote Nodes	Enabled/**Disabled**	Allow data from remote nodes to be displayed in the Patient List.
Show studies from this server on startup	Enabled/**Disabled**	When enabled, studies from the default remote DICOM server are displayed.
Enable Remote DICOM Server Preset	Enabled/**Disabled**	Enable the remote DICOM presets.
Access Privileges	• **Private** • Group	• Private - The preset button settings apply to your account only. • Group - Allows the preset buttons to be shown among users in the same user group. In this case, the other users in the group must also select the Group option to see the shared presets.
Add preset button	Button (no values)	Select a remote DICOM server to send to, create a button to send to this server, name the button, and then select where to display this button.
Preset buttons setting	Button (no values)	Show the status of the currently defined preset buttons.

Patient List

The Patient List preferences allow you to configure options for the Patient List.

Option	Values (Default value bolded)	Description
Patient List columns	**Status, Patient ID, Patient Name,** Gender, DOB, **Study Time, Accession #, Study ID, Modality, # of Images, Description, Referring Phys Name, AE Name, AE Title, Publish State,** Age, Institution Name, Patient Other ID	Items checked in this list appear as columns in the Patient List.
Display warning when getting Patient List without search filter	**Enabled**/Disabled	Show dialog when Aquarius iNtuition is first started and the Patient List is displayed without any search filter.
Enable color schema for remote server.	**Enabled**/Disabled	Allow options for color display on remote server.

Option	Values (Default value bolded)	Description
Fore color	(Blue)	Select a foreground color for remote server datasets. Click the color square to display the Windows color palette, to select another color.
Update study list after retrieve	**Enabled**/Disabled	Refresh the display of the Study List so that the newly retrieved data is shown.
Automatically update Patient List when external nodes change	Enabled/**Disabled**	Refresh the display of the Study List for external node automatically.
Show hidden patient data	Enabled/**Disabled**	Allows you to display all hidden studies. This allows you to unhide the study, if desired.

Series List

Option	Values (Default value bolded)	Description
Available Series List columns	R/U, Series #, Modality, # of Images, Series Date, Time, Part, Description, Days To Keep, Publish State	Items checked in this list appear as columns in the Series List.
Default Setting of the sub-series Sort	• Image Number • Image Position • Every N Slices	Default mode for sorting sub-series data.
Always use AqNET account authentication (for Web link)	Enabled/**Disabled**	When enabled, a password is automatically generated during Email Series URL. The recipient will be required to enter a username and password. When disabled, the sender can either set a password or not, when sending a link.
Launch email/Copy to Clipboard	• Launch email • Copy to Clipboard	Select whether to copy the series URL to the Microsoft Office clipboard, or send it in an email.
Expiration date	Pulldown menu	Determines how long a Web link is valid.
Series List Options	• Icons • Details	Show Series List as either a detailed list or a set of icons.
Display Series Information	Enabled/**Disabled**	Display the Series information and Sub-series panels by default.
Auto Show/Hide Series Information	Enabled/Disabled	Series information is automatically displayed when the study contains sub-series. Otherwise, the series information is hidden.
Display Preview	**Enabled**/Disabled	Display the Preview Panel in the Patient List, which contains the axial images of the currently selected series. When disabled, this window is not shown. **(Requires restart.)**
Automatically select a series on study selection	**Enabled**/Disabled	When you click on a study, Aquarius iNtuition also selects the main series.
Display Scene list	Enabled/**Disabled**	When enabled, any scenes in the series list are displayed in a separate display box.
Query Level	• Series • Study	If Study is selected, the query searches for studies only. If Series is checked, the query checks for both studies and series.
Text color for Nearline and Offline Series	Pulldown menu containing color palette	Allows you to select a different color for Nearline/Offline series so that they will be easier to distinguish in the series list.

Data Management

Option	Values (Default value bolded)	Description
Available Data Management Functions	• **Delete** • **DVD/CD** • **Send** • **Import** • **Export** • **Load** • Send to Output • Download • Anonymize • Trigger Workflow • Job Status • Info Editor • Stitch Data • Phase Sort Data • Lock • Unlock • Hide/Unhide • Delete All APS Results • Email Series URL • Publish/Unpublish	Items checked in this list will appear in the Data Management Panel located right below the Patient List and above the Series List. Customize to your own liking. Items in bold to the left are considered to be default settings and will appear upon opening the application.
Button Display Option	• Icon only • **Icon and Text**	The “Icon only” option will display the icon referencing the data management function selected to appear on the panel. The “Icon and text” option will have the written text description directly to the right of the icon.

3D Viewer

The Viewer preferences allow you to configure options for the 3D Viewer.

Setting 1 Tab

Option	Values (Default value bolded)	Description
Compression image	• **On** • Auto • Off	When **On** is checked, compress the image (defined by the quality in the Quality Slider).
Quality slider (if compression is on)	75	100 equals no compression, 1 is the lowest quality image. (**Requires restart.**)
Apply slab for MIP/ MinIP/ThickMPR by default	**CT**/MR	Slab is applied by default to 2D images for whichever modality is enabled (either or both).
3DVR default thickness	150mm	Default thickness for the 3D image when the Slab function is applied.
MIP/MinIP/ThickMPR default thickness	8mm	Default thickness for 2D images when the Slab function is applied.

Option	Values (Default value bolded)	Description
Draw slabs with fine mode	Enabled/Disabled	Renders slab images in fine mode. Warning: this may be slow.
Maximum thickness	10 mm	Maximum thickness allowed for slabs.
Snap to slab	Enabled/**Disabled**	Scroll step control on Axial, Coronal Sagittal slab view. When enabled, scroll step becomes N x slab thickness as configured from right click menu on slab setting (green annotation on the view).
Rendering Mode	• Draft • Draft-Fine • Fine	Quality of VR image from Draft (lowest quality/ fastest-loading) to Fine (highest quality, slowest-loading)
Advanced setting	Link	Opens **advanced setting of image quality** dialog. See the following settings.

Setting 2 Tab

Option	Values (Default bolded)	Description
Always display crosshair on main view	Enabled/**Disabled**	When enabled, a crosshair is always displayed on the 3D image.
Do not disable crosshairs in 1x1 view	Enabled/**Disabled**	Crosshairs appear on 1X1 view when enabled.
Use the small type cross hair.	Enabled/**Disabled**	Use small crosshair rather than the standard size.
Show crosshairs and bounding box during cine	**Enabled**/Disabled	When enabled, all crosshairs are visible on the viewer. When disabled, they disappear.
Link the center of rotation	**Enabled**/Disabled	When enabled, all currently loaded images have the same center of rotation.
Always synchronize	Enabled/**Disabled**	When enabled, two studies loaded together are automatically synchronized.
Display tilted data in patient frame of reference	**Enabled**/Disabled	When enabled, data is displayed using patient coordinates. When disabled, data is displayed using scan coordinates.
Show magnification factor on the view	Enabled/**Disabled**	When enabled, the magnification factor is displayed in the main image's annotations. This value changes when the image is zoomed in or out.
Show Magnifier area to context menu	Enabled/**Disabled**	When enabled, option to use Magnifying tool will appear in right-click (context) menu.
Enable Fast Loading Cache	**Enabled**/Disabled	Cache study data for faster loading.
Show Image Comments (0020, 4000) on axial, coronal or sagittal views	Enabled/**Disabled**	Show %RR information from DICOM tag.

Option	Values (Default bolded)	Description
Use Max/Min instead of WW/WL. This setting applies to whichever modalities are checked in the modality list, accessed by the Setting link.	Setting link. Click for modality list. **Default: PT**	In the W/L tool panel, show the text entry fields as Min and Max values rather than Window Width and Window Level. This setting applies to whichever modalities are checked in the modality list, accessed by the Setting link.
Invert WW/WL	Setting link. Click for modality list. **Default: PT**	Invert all pixel values in the modalities checked in the modality list.
Use W/L preset	Setting link. Click for modality list. **Default:** None	Use WL preset configured for each modality that has been select instead of using the W/L from the DICOM header.

Toolbar

Toolbar preferences allow you to configure which buttons appear, and in which order, at the *top* of the 3D Viewer screen. Choose which buttons are to be displayed by checking the box to the left. Position each button on the toolbar by using the Up and Down buttons to the right of the list.

Option	Values (Default value bolded)	Description
Mouse Control	**Enabled**/Disabled	Show W/L, Pan, Zoom and Rotate buttons
Measurement	**Enabled**/Disabled	Show measurement pull-down menu button
Arrow and Text	**Enabled**/Disabled	Show arrow and label buttons
Layout	**Enabled**/Disabled	Show layout mode pull-down menu button
Undo/Redo	**Enabled**/Disabled	Show undo and re-do buttons
Overlay	**Enabled**/Disabled	Show outline of bone mask on an image that has had bone removed.
APS Result	**Enabled**/Disabled	Shows Label, Centerline, Candidate and Mask APS buttons
Enable to apply APS by drag and drop	Enabled/**Disabled**	A set of icons representing each mask applied by APS is displayed when the APS mask icon in the top toolbar is clicked. When one of the mask icons is dragged to the main window, that mask is applied to the image in that window.
Do not use sample icon	Enabled/**Disabled**	Use actual images from the study in the individual mask images, rather than the sample icons.
Display all measurement tools	Enabled/**Disabled**	When enabled, all measurement tools are displayed horizontally along the toolbar. When disabled, the measurement tools can be accessed from a pull-down menu on the toolbar.

Option	Values (Default value bolded)	Description
Continuously use same measurement	Enabled/**Disabled**	Stay in measurement mode (using the same selected tool) after obtaining a measurement. When disabled, the viewer goes back to the currently selected mouse mode.

Workflow

Option	Values (Default value bolded)	Description
Automatically step to next activity after validation	**Enabled**/Disabled	Apply the next Workflow element when a Workflow element is validated.
Enable display of preview by hovering mouse over workflow or color template icon	Enabled/**Disabled**	Show what the image looks like when a Workflow element is applied, by hovering over that element with the mouse.
Use Workflow Template from	• Private • Group	If Private is selected, only workflows (or color templates) from your own user account can be used. If Groups, you can use workflows or color templates that have been saved under your default user group.
Use Color Template from	• Private • Group	
Categorize for body parts in workflow	Enabled/**Disabled**	Display the workflow templates in the workflow menu in categories, determined by body part.
Include validated workflow images in cardiac report	**Enabled**/Disabled	Validated workflow images are included along with captures in cardiac reports.
Automatically name workflow scene	**Enabled**/Disabled	A name is automatically generated for any workflow scene created. When this is disabled, you must provide a scene name.
Send to DICOM after save workflow scene	Enabled/**Disabled**	Upon save, a dialog is automatically displayed asking you to choose a remote DICOM server to send it to.
Automatically input name when image is added by validation mode (scene number)	**Enabled**/Disabled	When this feature is disabled, an input box is displayed when you click **Add**, allowing you to enter a name for the scene. When enabled, a new scene is automatically named “Scene”, with a number appended when needed.
Save only validated workflow scene	**Enabled**/Disabled	When feature is disabled, you can save new workflow scenes whether or not they are validated.
Number of workflow elements to display in a row	• 3 • 4	Option to have 3 or 4 workflow elements in a row in the Viewer.

Mask

Configure the mask functions used in region growing after bone removal (3D Viewer).

Option	Values (Default value bolded)	Description
Dilation	-4, -3, -2, -1, 0, +1, **+2**, +3, +4	Amount added automatically after selecting the **Include** or **Add** options.
Erosion	-4, -3, -2, -1, 0, +1, **+2**, +3, +4	Amount automatically removed after selecting the **Exclude** option.
Enable adjusting growing distance by zoom	**Enabled**/Disabled	Growing distance increases when the image is zoomed.
Show overlay when region is clicked by bone removal tool	Enabled/**Disabled**	Show green highlighting on area that has been removed when clicked.
Show erosion/dilation dialog when applying the region	Enabled/**Disabled**	Display erosion/dilation dialog when applying Region Grow, FreeROI or Threshold mask operations, to obtain level to add or remove.
Apply mask slab MIP/MinIP/ ThickMPR	Enabled/**Disabled**	An option to toggle on/off mask on MIP, MinIP and ThickMPR images. (Masks are not added to images with slab by default.)
Overlay on removed area	**Enabled**/Disabled	Show green highlighting on area that has been removed.
Turn on Mask overlay automatically	Enabled/**Disabled**	If enabled, overlay is displayed to show portions of an image removed by a mask operation. If disabled, the overlay is not displayed.
Enable mask template mode	**Enabled**/Disabled	Allows you to add a mask with a preset name and color, without going to the 3D settings tab.
Same button for Add/Select	Enabled/**Disabled**	When enabled, the Add/Select function replaces both the Include and Select functions. Applies only to Region Grow.
Use main view threshold for region growing	Enabled/**Disabled**	Use the W/L values of the Main View (usually 3D) for Region Grow.
Use new head/neck bone removal	Enabled/**Disabled**	When enabled bone removal includes bone removal from the head/neck.
Enable one-click mode	Enabled/**Disabled**	When enabled, dynamic region growing can be completed with one click.
Fast static growing by click (undo is disabled)	**Enabled**/Disabled	A single-click in Region Grow causes the mask to grow as far as it can, ignoring the mouse button release. Only available when one-click mode is enabled.
Click detection time	Slider - default is on **Fast**	Speed at which Aquarius iNtuition determines whether to grow via click-and-hold (which stops on mouse release) or single-click (which ignores mouse release). Only available when one-click mode is enabled.

Measure/Annotation

Measurement Tab

Option	Values (Default value bolded)	Description
Copy measurement result to clipboard	**Enabled**/Disabled	When enabled, measurement results are automatically copied to the clipboard. They can then be pasted into other documents, such as reports.
By default, measurement remains when paging slices	Enabled/**Disabled**	Measurement annotations remain on 2D image while paging through slices.
Use scan date for initial	Enabled/**Disabled**	When enabled, the date annotated on the measurement is the date of the scan; otherwise it is the date the measurement is taken.
Snap to other measurement	Enabled/**Disabled**	When enabled, the end point of a distance measurement is automatically snapped to a nearby marker or measurement. To release the “magnetic” effect temporarily, hold the Alt key before clicking.
Enable synchronize measurement	Enabled/Disabled	When enabled, measurements are synchronized for synchronized data.
For synched distance measurement show ratio when measurement tracking is enabled	Enabled/Disabled	Show or hide ratio for synched distance measurements.
Measurement annotation default font	Arial Medium. Color: White	Pull-down menus allow you to select a default font, size and color for measurement text
Digit of significant figures for real measurement result	1-5 (default: **3**)	Total number of significant digits in measurement result, including both left and right sides of the decimal point (floating point).
Plaque volume unit	• cm3 • mm3	Allows selection of plaque volume units in either cubic centimeters or cubic millimeters.
Line width	1 or **2**	Width of lines drawn on the image to indicate the line or area measured.
Highlight selected measurement	Enabled/**Disabled**	Highlight only the selected measurement. When disabled, all measurements are highlighted.
Default PET SUV Type	• Body Weight • Lean Body Mass • Body Surface Are	Default SUV measurement type after data loading.

User Annotation Tab

Option	Values (Default value bolded)	Description
Draw simple arrow	Enabled/**Disabled**	Disable ability to change the color and thickness of an annotation arrow.
Input text when arrow is added	**Enabled**/Disabled	When enabled, a text box is automatically opened when arrow is selected from the top tool bar.
Locate text annotation on anatomy	**Enabled**/Disabled	When enabled, text placement is in “On anatomy” mode. Otherwise text is in “On screen” mode.
Delete arrow/text when rotate	**Enabled**/Disabled	When an arrow or text is added to the image, it will be deleted when the image is rotated.
User annotation default font	Arial Medium. Color: White	Pull-down menus allow you to select a default font, size and color for user annotation text

Multidata/4D

Option	Values (Default value bolded)	Description
Enable synchronize option when two datasets are loaded	Enabled/**Disabled**	Setting this option enables synchronization of operations among two or more studies loaded as multidata.
Auto Registration	Enabled/**Disabled**	When enabled, two images from different studies are automatically lined up spatially, so that corresponding places in each study are in the same place on the screen.
Synchronize on after registration	Enabled/**Disabled**	Turn on synchronization automatically after registration.
Registration type	• **Translation only** • Translation and rotation	Correct only for translation (images are in different positions, but have the same orientation), or for both translation and rotation (one image is rotated relative to the other).
Default registration	• **Overlay** • Base	• Select **Overlay** to register the overlay study to the base study, by default. • Select **Base** to register the base to the overlay study. When this option is selected, the fusion view shows the image number and location annotation of the overlay study.
Starting Series number for Multi-data	No default value	You can specify a starting number for multidata series.

Option	Values (Default value bolded)	Description
Synchronize images in 4D cine mode	**Enabled**/Disabled	Allows all four screens in a 2x2 layout to be synchronized in a 4D cine.
Show msec if available	Enabled/**Disabled**	Show milliseconds on the annotations, if information is available.
First phase to display when loading 4D (%RR)	75	Sets which phase to display first when loading a multi-data study.
FOV synchronize option	• **No synchronize** • 1st data • Largest FOV data	1st data - Synchronize all data with the first study loaded. Largest FOV data - Synchronize all data with the study having the greatest zoom factor.
Fusion Default Layout	• Single Data • **Multi data**	Automatically load fusion data into single or multi data layout
Show original image	Enabled/**Disabled**	When enabled, the CT or PET image registers only the position, and not rotation. The axial view always shows original slices. When a PET slice is located between two slices of the CT image, the nearest PET slice is shown. The image number and location annotation is shown on both CT and PET images.

Capture

Set options for image capture in the 3D Viewer, to be sent to the Output Panel.

Option	Values (Default value bolded)	Description
User Capture Path	Default is **C:\Documents and Settings\<*your-account-name*>\My Documents**.	Where to store images that have been captured to the Output Panel. Use the browse button to the right to change folder
Format	• JPG • BMP	Default image format of captured images
Play sound at the time of capture	**Enabled**/Disabled	Play “camera click” sound at the time of capture
Add pixel spacing in DICOM header for Secondary capture	**Enabled**/Disabled	Pixel spacing command (0028, 0030) is added to the DICOM header of the captured image.
Show original DICOM FOV value annotation for capture image	**Enabled**/Disabled	When enabled, the FOV value showing in the annotation of the captured image is the same as what is displayed in the original image.

Option	Values (Default value bolded)	Description
Capture area option	• Expand image to fill frame • Capture as displayed	First option: The dimensions of the captured image (and amount of image captured) fills the entire display box in the Output Panel. When Maintain zoom is enabled, captured image maintains the zoom as seen in the viewer Second option: An image captured to the Output Panel will have the same dimensions it has in the Viewer or module.
Maintain zoom	Enabled/**Disabled**	When enabled, captured image is zoomed to the same level as the original
Select saving option for capture image	• 512x512 • 782x782 • 1024x1024	High speed, high quality, or balanced for performance.
Select location where an image will be sent after capture	• Output Panel • Patient List • Output Panel and Patient List	Send captured images to either the Output Panel, the Patient List (as new files) or to both.
Show new DICOM series setting dialog	**Enabled**/Disabled	When capturing to the Patient List, you can set the series starting number and a description.
Draw cross cursor on captured image	Enabled/**Disabled**	When this is enabled, a cross cursor is added to captures of 2D images.
Capture annotation option	• With full annotations • Annotations as-is	First option: Image is captured with full annotation, whether or not they are showing. Second option: Image is captured with whatever annotations are showing at the time.

CPR

Set defaults for CPR views in the 3D Viewer.

Warning: The orientation annotation on the CPR windows is only an estimation. It should be verified by a qualified professional.

Option	Values (Default value bolded)	Description
CPR initial view setting	Go to CPR when centerline is created: **Enabled**/Disabled	CPR layout is automatically loaded when a centerline is created. (When the setting is not enabled, CPR layout will not load until the centerline is clicked.)
	Show centerline: **Enabled**/Disabled	Automatically show centerline in MPR windows
	Show stenosis result: **Enabled**/Disabled	Show stenosis annotation
	Show cross section lines: **Enabled**/Disabled	Show the cross section lines
	Show cross section result: **Enabled**/Disabled	Show cross-section result
	Show Contour: **Enabled**/Disabled	Show contour of cross-section image
Outline Interpolation (link)	Inner wall: Enabled/**Disabled** Outer wall: **Enabled**/Disabled Interpolatable degrees for edit on sMPR: **110**	The link opens dialog. Select interpolation for inner wall, outer wall, or both.
Enable centerline export	Enabled/**Disabled**	Allow export of centerline data in CPR mode, or grid data from the sMPR in EVAR.
Show CPR based on root	Enabled/**Disabled**	When enabled, CPR display will follow root display option on the CPR tool panel instead of using the Z coordinate.
View setting	Centerline on MPR: Enabled/**Disabled**	MPR window displays the centerline under review.
	Anatomy label on CPR: Enabled/**Disabled**	If there are anatomy labels, the relevant ones are displayed on the CPR windows.
	Annotation of orientation: Enabled/**Disabled**	Displays orientation annotation on CPR windows. (**See warning at end of this table.**)
Show axial view on CPR layout	**Enabled**/Disabled	CPR layout adds window to display the axial view of the study.
Larger cross-section view	Enabled/**Disabled**	Display the cross-section views in a larger window. **(Requires restart.)**
Stenosis algorithm	• Simple • QCA	Use either the Simple or the QCA algorithm to calculate stenosis
Area or diameter stenosis	• Diameter (Average) • Diameter (Min vs Max) • Area • HU/Intensity	Calculate stenosis using either the average diameter, the min and max diameters, the area, the HU value or intensity.

Option	Values (Default value bolded)	Description
Active centerline color and width	Color palette available. Default is green. Valid widths are from 1 to 6. The default is 2.	Set the color and width of the active centerline in the 3D image. The centerlines in the MPR views will automatically change to the same color.
General line color and width	Color palette available. Default is grey. Valid widths are from 1 to 6. The default is 1.	Set the color and width of inactive centerlines in the 3D image.
Cross-section stenosis line color	Default is red.	Color palette available for stenosis line.
Cross-section reference line color	Default is blue.	Color palette available for reference line.
Cross-section outline thickness	1 to 6. Default is **2**.	Thickness of outline shown on the cross-section view.

CPR Interactive

Option	Values (Default value bolded)	Description
Click on sMPR to set cross-section	**Enabled**/Disabled	Click anywhere on the sMPR view to move the red cross-section to that vertical position.
Click on CPR to set cross-section	**Enabled**/Disabled	Click on the centerline in the CPR view to move the red cross-section to that spot.
Click to set red cross-section to a stenosis nearby	Enabled/**Disabled**	Click near a stenosis to move the red cross-section to the nearest stenosis that satisfies the following three parameters.
Snap to stenosis greater than (% simple average diameter)	30	Minimum ratio of stenosis to reference diameter and area (percentage).
Search for stenosis within (mm)	5	Maximum distance between current position of red cross-section and the nearest stenosis.
Search for reference within (mm)	20	Maximum distance between the red and blue cross-section lines.
Also do plaque analysis	Enabled/Disabled (Available only when **Click to set red cross-section to a stenosis nearby** is enabled.)	Whether to run plaque analysis together with "**Click to set red cross-section to a stenosis nearby**".
Update Axial view when cross-section is moved	Enabled/**Disabled**	The axial view displays the slice that corresponds to where the red cross-section is positioned.
Link center of 3D view	**Enabled**/Disabled (available only when previous preference is enabled)	3D view is centered on the red cross-section line when that line is moved on the CPR image.

Option	Values (Default value bolded)	Description
Update cross-section view when measuring path	**Enabled**/Disabled	The red cross-section line follows the cursor while a distance along the centerline is measured. When the mouse is released, the cross-section line remains at the final position of the measurement.
Link CPR windows	Rotate: **Enabled**/Disabled	CPR windows are rotated when main window is rotated
	Pan: **Enabled**/Disabled	CPR windows are panned when main window is panned
	Zoom: **Enabled**/Disabled	CPR windows are zoomed in/out when main window is zoomed in/out
Analyze plaque and stenosis on the same screen	Enabled/**Disabled**	When doing plaque analysis, leave the stenosis results on the screen.

CPR Interactive 2

Option	Values (Default value bolded)	Description
Enable editing centerline by re-creating a path on image	**Enabled**/disabled	Allows you to use the Redraw tool to edit one section of a centerline without affecting the rest of the centerline (see "Chapter 3The Redraw Tool" on page 3-32)
Re-center while editing cross-section	**Enabled**/disabled	Disable this setting if you do not want the cross-section to be re-centered while you are editing the contour.
Display Centerline during rotation	Enabled/**disabled**	This allows you to view the centerline during rotation, when not in edit mode.

Calcium

Option	Values (Default value bolded)	Description
Default Calcium Percentile Database	• **J Hoff et al** • MESA • Raggi • Mayo	Select a default database from which to get percentile rankings.
Image type which is outputted to a report	• Output slices at equally spaced intervals to one page • Output all slices where score is done • Use captured image of the output panel	**Note:** Active only when using Aquarius iNtuition calcium module.
Report page format	Input dimension manually.	3x4 layout is the default.
Note: Active only when using Aquarius iNtuition calcium module.	Include detailed calcium analysis in calcium report	Enabled/**Disabled**
Include lesion-specific details in calcium report and in exports (xml, text, or csv) from a measurement protocol that includes a calcium score. (**Aquarius iNtuition calcium module only**.)	Use fast drawing mode for overlay images	**Enabled/** Disabled
When enabled, drawing time for mask and color overlay is at speed of 60 fps. When disabled, uses previous method at 30 fps.	Serially Classify Calcium By Vessels	Enabled**/ Disabled**
When enabled, allows viewer to score by vessel vs. slice and keeps the scoring GUI on the viewer until finished scoring.	Show Instruction on Viewer	**Enabled/** Disabled
Ability to turn instructions on calcium score viewer on (**Enabled**) or off (Disabled).	Show calcium calibration dialog on loading series	Enabled/Disabled
When Enabled, after starting the Calcium Score element, prompts for patient size and scanner with option to choose from drop-down menu.	When Disabled, choose default.	Use DICOM scanner type and default patient size for calibration
Enabled/Disabled	The scanner is selected automatically from DICOM headers; default Size of the patient is set to Medium.	

SAT

Option	Values (Default value bolded)	Description
Display “WHO” and “RECIST” label into measurement results	**Enabled**/Disabled	Display lesion measurements as follows: d1 (RECIST): xx.xx cm d2: xx.xx cm d1 x d2 (WHO) = xx.xx cm2 Volume = xx.xx cm3
Always update the SAT mask	**Enabled**/Disabled	This must be set when displaying a mask in SAT.
Overlay/current mask	• Overlay • Current mask	Mask of a segmented lesion can be seen in the cube view window (select 2x2 scan window layout to display this window).
Jump to the center point when measurement is created	**Enabled**/Disabled	When a measurement is created, segmentation is performed. When this setting is enabled, the window displays the center of the lesion.
Jump to the center point when measurement is edited	Enabled/**Disabled**	When a measurement is edited, the segmentation is performed again. When this setting is enabled, the window displays the center of the lesion. When disabled, the lesion is displayed from where the edit was done.
Colorize candidate markers by score	Enabled/**Disabled**	Show candidate markers in color to distinguish by score.

Batch

Option	Values (Default value bolded)	Description
Save scout image and results as one series	**Enabled**/Disabled	Save the 3D image containing the batch grid along with the 2D batch images.
Save CPR results and sMPR results as one series	Enabled/**Disabled**	When enabled, CPR batch series includes SMPR images.
Batch Image Quality	• Draft • Fine (Speed) • **Fine (Quality)**	**Draft** is fastest, but of lowest quality. **Fine (Speed)** is of better quality, but is slower. **Fine (Quality)** produces the best quality, but is slowest.
CPR batch - Show centerline/ outline on batch image	Enabled/**Disabled**	This option allows you to capture the centerline and vessel outline on CPR batch (radial or parallel).
CPR batch - Show measurement on batch image	Enabled/**Disabled**	This option allows you to capture stenosis measurements with radial CPR batch.

Option	Values (Default value bolded)	Description
CPR batch - Pan image for perpendicular batch	Enabled/**Disabled**	Enable panning on perpendicular image so it can be moved away from the inset view.
Radial batch - Rotate relative to patient	Enabled/**Disabled**	When this setting is enabled, the image rotates in the selected direction from the patient's perspective, regardless of the image orientation seen on the main view. When disabled, the image rotates toward the left, right, upward or downward edge of the screen, depending on the direction selected.
Parallel batch - Fix the Begin/ End point	**Enabled**/Disabled	When enabled, the beginning and end slices of a parallel batch stay fixed, even when the number of slices or interval size has changed.
Parallel batch - Show batched spacing value annotation	Enabled/**Disabled**	Spacing between slices in batched images. When enabled, this annotation is displayed in the lower-left corner of all batched images.
Parallel batch - Show batched thickness value annotation	Enabled/**Disabled**	Thickness of slices in batched images. When enabled, this annotation is displayed in the lower-left corner of all batched images.
Set same slice location as original series to DICOM tag	Enabled/**Disabled**	Set the DICOM tag for slice location (0020, 1041) in batched images to the same value as the same tag has in the original data.
Generated series starting number	User defined	You can specify a starting number for a generated batch series.
Parallel batch (3 Planes) - Save as one series	Enabled/**Disabled**	Output the three sets of batched images as one series. Otherwise, each set is output in a separate series.
Parallel batch (3 Planes) - Output order	• **Ax-Cor-Sag** • Ax-Sag-Cor • Cor-Sag-Ax • Cor-Ax-Sag • Sag-Ax-Cor • Sag-Cor-Ax	Output batch results as one series. This setting determines the output order.

LowAtt

Option	Values (Default value bolded)	Description
Anti-noise	• 0 (Off) • **1 (Medium)** • 2 (Strong)	0 (Off): No erosion/dilation. Can be used when volume filter is applied with APS. 1 (Medium): Erosion/dilation -1, +2, -1. 2 (Strong): Erosion/dilation -2, +4, -2.
Use threshold for Organ	• Yes • No • **Ask every time**	Option to remove blood vessel from organ based on threshold.
Min	-1024	Minimum threshold for removal

Option	Values (Default value bolded)	Description
Max	-**500**	Maximum threshold for removal
Display the mean organ intensity in measurement result	Enabled/**Disabled**	Display mean intensity for both left and right organ in the measurement result.
Show Parameters (Threshold, Anti-noise)	**Enabled**/Disabled	Show the threshold and anti-noise parameters used in measurement as a reference for followup.

Launch Program

Option	Values (Default value bolded)	Description
Export measurements to text file	Enabled/**Disabled**	When enabled, export measurements to a text file.
Path for text program	C:\WINDOWS\system32\NOTEPAD.EXE	Launch notepad to export measurements to a text file
Export measurements to CSV file	Enabled/**Disabled**	When enabled, export measurements to a CSV file.
Path for Excel program	C:\Program Files\Microsoft Office 15\Root\Office15\EXCEL.EXE	Launch Excel to export measurements to CSV file
Export measurements to XML file	Enabled/**Disabled**	When enabled, export measurements to an XML file.
Path for XML	C:\Program Files\Internet Explorer\iexplore.exe	Launch Internet Explorer to export measurements to an XML file
Export measurements to AIM XML file	Enabled/**Disabled**	Export measurements to a file in the Annotation Imaging Markup format.
Path for AIM XML	C:\Program Files\Internet Explorer\iexplore.exe	Launch Internet Explorer to export measurements to an AIM XML file
Play movie	Enabled/**Disabled**	When enabled, play AVI movie
Path for media player	C:\Program Files\Windows Media Player\wmplayer.exe	Launch Windows Media Player to play movie.
(ThinClient) Show in Workflow dialog	Enabled/**Disabled**	Show ThinClient button as a workflow button in workflow dialog
(ThinClient) Show in Context menu	Enabled/**Disabled**	Show ThinClient as an item in the right-click menu
(iReview) Show in Workflow dialog	Enabled/**Disabled**	Show iReview button as a workflow button in workflow dialog

Option	Values (Default value bolded)	Description
(iReview) Show in Context menu	Enabled/**Disabled**	Show iReview as an item in the right-click menu

Mouse Operation

Option	Values (Default value bolded)	Description
Valid pixels per slice	2-50 (**Default: 5**)	The number of pixels of vertical mouse movement required to advance the 2D image one slice. A higher number means slower slice paging.
Non skipping slice mouse mode	Enabled/**Disabled**	When enabled, slice mode will display every slice without skipping any.
Enable default left mouse button setting. (Pull-down menu.)	**Enabled**/Disabled • Window Level • Pan • Zoom • Slice • Rotate	By default, the left mouse button is set to rotate a 3D image and page through slices on 2D images. You can select any function for the left mouse button by checking the box and choosing another function from the pulldown menu.
Enable default mouse wheel setting. (Pull-down menu.)	• Slice • Zoom	Select a function for the mouse wheel.
Enable user defined mouse button mappings. Select user-defined mouse button setting from pull-down menu.	Enabled/**Disabled** • None • Right • Left+Right • Middle • Middle+Right • Left+Middle (Note: **None** is the default for all functions.)	Allows you to define mouse button settings that map to image manipulation functions. Each mouse button or mouse button combination can be mapped to one of these functions: • W/L • Pan • Zoom • Slice • Rotate Note: the mapping for each button must be unique. **(Requires restart.**
Operate FreeROI, DRG, Centerline tool without **SHIFT** key	Enabled/**Disabled**	Mouse mode to operate listed tools without holding down the **SHIFT** key.
Simply click on 2D will focus there	Enabled/**Disabled**	A single click on a 2D image will move the cross cursor to the clicked location.
Start paging when click middle button	Enabled/**Disabled**	The window will automatically page through slices. Up and down motions with the mouse control the direction and speed of the scroll.

Option	Values (Default value bolded)	Description
Show the mouse modes at the top of the right click menu	Enabled/**Disabled**	List the mouse modes (Rotate, Pan, Zoom, etc) at the top of the right-click menu on the image. When this is disabled, the mouse modes are listed in a sub menu.

TDA

Option	Values (Default value bolded)	Description
Show original image under the map	Enabled/**Disabled**	In a viewing window showing a map, the original image is displayed underneath the map.
Reverse color lookup table for MTT map	Enabled/**Disabled**	Display MTT maps in reverse color scheme.
Automatically apply motion correction after loading volume	**Enabled**/Disabled	Realign images that might not might up if the patient moved during the scan.
Automatically calculate TDA maps after loading volume	**Enabled**/Disabled	Calculate and display maps automatically when volume is loaded.
Change between 2x2 and 4x4 layout when changing stages	Enabled/**Disabled**	When clicking Next to go to the next stage, layout changes from 4x4 to 2x2.
Copy measurements to all levels	Enabled/**Disabled**	When a measurement is done on one level, propagate that measurement to all levels.
Send images to Output Panel / Patient List when capture in TDA	**Enabled**/Disabled	Captured images go to the TDA report. To send them to the Output Panel and/or Patient List in addition, check this item.
Group Captures By:	Level **Maps**	Sort images in a group capture by either the level or by the map type.
Show the same map type for all levels	**Enabled**/Disabled	When loading the data, the map type selected for each window should be the same in all levels.
Adjust ROI template to the current data	**Enabled**/Disabled	The ROI template will be adjusted so that it fits within the skull structure.
Show measurement results as annotation	Enabled/**Disabled**	Show TDA measurements in the view window annotation.
Sync phase on all levels	**Enabled**/disabled	When disabled, it allows you to change phases on the selected level only.
Override Time interval (sec)	Enabled/**Disabled** (1.00)	When enabled, use the value entered in the input box. When disabled, use the value from the DICOM header.
Show selected layout on double click	2x2 3x2	Select one of the layouts from the menu. When you double-click on any image in the viewer, images are shown in the selected layout. They are also captured to the Output Panel in the same layout when **Capture All in One** is used.
Reset to last saved	N/A (button)	Reset all fields in this screen to the values that were most recently saved.
Set to Default	N/A (button)	Reset all fields to the initial default values.

TDA - Brain TDA

Option	Values (Default value bolded)	Description
Plasma ratio	0.85	The values of the map must be divided by the hematocrit to obtain the real CBV. This value can fall between 0.85 and 0.9.
Brain density (g/cc)	1.04	Configure the brain density.
Subtract Ventricle	Enabled/Disabled	When enabled, subtracts ventricles from penumbra map

Brain TDA - Functional Map (CT)

Option	Values (Default value bolded)	Description
BV(ml/100g) : Analysis	Min : 0.00 Max : 8.00	For each map, analyze results that fall within the specified range. When a value is discovered that is outside the range, it is clamped off (values below the range are clamped to the Min value, values above are clamped to the Max).
BF(ml/100g/min) : Analysis	Min : 0.00 Max : 120.00	
MTT(sec) : Analysis	Min : 1.00 Max : 300.00	
BV(ml/100g) : Display	Min : 0.00 Max : 6.00	Set the range that determines which colors are displayed for each value.
BF(ml/100g/min) : Display	Min : 0.00 Max : 100.00	
MTT(sec) : Display	Min : 0.00 Max : 15.00	
TOT(sec) : Display	Min : 5.00 Max : 20.00	
RT(sec) : Display	Min : 5.00 Max : 30.00	
TTP(sec) : Display	Min : 0.00 Max : 25.00	
Default overlay map type in viewers	Available map types are: BV, BF, MTT, TOT, RT, TTP, Map, Graph, MPR and MIP.	Select the map type for each viewing window to be the default type for that window when a study is loaded. These can be configured for a 2x2 or 3x3 layout.
Analysis Resolution	512x512 256x256 128x128	Resolution of data to be analyzed. Higher resolutions result in a finer and more detailed map, but the calculations will take longer.
Default WW/WL	WW : 600 WL : 200	Set default values for window width and window level for TDA.
Reset to last saved	N/A (button)	Reset all fields in this screen to the values that were most recently saved.
Set to Default	N/A (button)	Reset all fields to the initial default values.

Brain TDA - Functional Map (MR)

Option	Values (Default value bolded)	Description
NEI(ml/100g): Analysis	Min: 0.00; Max: 8.00	For each map, analyze results that fall within the specified range. When a value is discovered that is outside the range, it is clamped off (values below the range are clamped to the Min value, values above are clamped to the Max).
NEI/MTE(ml/100g/min): Analysis	Min: 0.00; Max: 120.00	
MTE(sec): Analysis	Min: 1.00; Max: 300.00	
NEI(ml/100g): Display	Min: 0.00; Max: 6.00	Set the range that determines which colors are displayed for each value.
NEI/MTE(ml/100g/min): Display	Min: 0.00; Max: 100.00	
MTE(sec): Display	Min: 0.00; Max: 15.00	
MSI(sec): Display	Min: 5.00; Max: 20.00	
MSD(sec): Display	Min: 5.00; Max: 30.00	
TM(sec): Display	Min: 0.00; Max: 25.00	
Default overlay map type in viewers	Available map types are: NEI, NEI/MTE, MTE, MSI, MSD, TM, Graph, MPR and MinIP.	Select the map type for each viewing window to be the default type for that window when a study is loaded. These can be configured for a 2x2 or 3x3 layout.
Analysis Resolution	• 256x256 • **128x128** • 64x64	Resolution of data to be analyzed. Higher resolutions result in a finer and more detailed map, but the calculations will take longer.
Default MR curve profile	• Intensity • **Concentration**	Different ways to express the vertical axis values in the profile graph. Intensity refers to the pixel intensity in the image over time. Concentration shows the contrast concentration over time.
Reset to last saved	N/A (button)	Reset all fields in this screen to the values that were most recently saved.
Set to Default	N/A (button)	Reset all fields to the initial default values.

Brain TDA - Classification Map (CT)

The classifications are defined as Normal, Class 1 and Class 2. Class 1 and Class 2 can refer to either recoverable or unrecoverable, according to your preference. In this screen you can set the thresholds for each class. The values shown below are defaults and can be changed.

Option		Values and Defaults	Use
Normal Class	BV (ml/100g)	Min: 2.00 Max: 8.00	Disabled
	BF (ml/100g/min)	Min: 25.00 Max: 120.00	Enabled
	MTT (sec)	Min: 1.00 Max: 8.00	Enabled
Class 1	BV (ml/100g)	Min: 0.00 Max: 2.00	Disabled
	BF (ml/100g/min)	Min: 0.00 Max: 10.00	Enabled
	MTT (sec)	Min: 1.00 Max: 300.00	Disabled
Class 2	BV (ml/100g)	Min: 2.00 Max: 8.00	Disabled
	BF (ml/100g/min)	Min: 10.00 Max: 25.00	Enabled
	MTT (sec)	Min: 8.00 Max: 300.00	Enabled
Hemisphere Comparison	MTT	50%	
	BV	2.00	
Use post filtering	Default: **Enabled**/Disabled	Description: Make map images appear smoother.	
Reset to last saved		N/A (button)	Reset all fields in this screen to the values that were most recently saved.
Set to Default		N/A (button)	Reset all fields to the initial default values.

Brain TDA - Capture Settings

Option	Values (Default value bolded)	Description
(**CT modality**) Preset maps to be captured for a TDA report	BF, BV, MTT, Map, TOT, RT, TTP, Graph, MPR, MIP	Items checked in this list are captured when **Capture Preset Maps for All Levels** is selected in the TDA **Report** tab. The graphs can be reordered using the up and down arrow buttons.
(CT) Use high resolution (1024x1024) when capturing All in One image.	**Enabled**/Disabled	
(**MR modality**) Preset maps to be captured for a TDA report	NEI/MTE, NEI, MTE, MSI, MSD, TM, Graph, MPR, MIP	This is the same as above, but the setting is for MR data only.
(MR) Use high resolution (1024x1024) when capturing All in One image.	**Enabled**/Disabled	
Mycardial density	1.05 g/ml	

Advanced TDA

Option	Values (Default value bolded)	Description
Show original image under the map.	Enabled/**Disabled**	In a viewing window showing a map, the original image is displayed underneath the map.
Automatically apply motion correction after loading volume.	**Enabled**/Disabled	Realign images that might not might up if the patient moved during the scan.
Automatically calculate TDA maps after loading volume.	**Enabled**/Disabled	Calculate and display maps automatically when volume is loaded.
Show measurement results as annotation.	**Enabled**/Disabled	Results will be shown as annotation by default.
Override time interval (sec):	**1**	Setting for overriding the default time interval in seconds.
Use different colors for Measurement ROI's.	Enabled/**Disabled**	In placing ROIs ,different colors is disabled by default.
Number of markers on color bar (3-100):	**Enabled**/Disabled (Default: 3)	This is enabled and defaults to 3 markers on the color bar.
Lock color maps from window leveling.	**Enabled**/Disabled	This is enabled and set so that W/L cannot be changed.

Advanced TDA - Brain TDA

Option	Values (Default value bolded)	Description
Plasma Ratio:	**0.85**	This set the ratio of plasma to blood.
Brain density (g/cc):	**1.04**	This set the density of the brain.

Advanced TDA - Brain TDA - Functional MapZ

Option		Values (Default value bolded)	Description
BV(ml/100g): Analysis		Min: 0.00; Max: 8.00	For each map, analyze results that fall within the specified range. When a value is discovered that is outside the range, it is clamped off (values below the range are clamped to the Min value, values above are clamped to the Max).
BF(ml/100g/min): Analysis		Min: 0.00; Max: 120.00	
MTT(sec): Analysis		Min: 1.00; Max: 300.00	
Take off time (TOT) (ml/100g): Display		Min: 0.00; Max: 6.00	Set the range that determines which colors are displayed for each value.

Option		Values (Default value bolded)	Description
Recirculation time (RT): Display		Min: 0.00; Max: 100.00	
Tmax: Display		Min: 0.00; Max: 15.00	
Initial Map Type		**2x2 Image/Graph/Text**	The display is 2x2 showing all results via image, graph, and text.
Map Type			
	Number	1	**BF**
	Type	2	**BV**
Initial Layout			
	Position	**2x1 Image/Graph**	Initial Display
	Result	**2x2 Image/Graph/Text**	The display layout for results.
Analysis Resolution		128	Sets the display resolution.
Edit ROI Color		Select the button to edit the ROI colors and if desired, set them by organ or area.	

Advanced TDA - Brain TDA - Classification Map

Option		Values and Defaults	Use
Normal Class	BV (ml/100g)	Min: 2.00 Max: 8.00	Disabled
	BF (ml/100g/min)	Min: 25.00 Max: 120.00	Enabled
	MTT (sec)	Min: 1.00 Max: 8.00	Enabled
Class 1	BV (ml/100g)	Min: 0.00 Max: 2.00	Disabled
	BF (ml/100g/min)	Min: 0.00 Max: 10.00	Enabled
	MTT (sec)	Min: 1.00 Max: 300.00	Disabled
Class 2	BV (ml/100g)	Min: 2.00 Max: 8.00	Disabled
	BF (ml/100g/min)	Min: 10.00 Max: 25.00	Enabled
	MTT (sec)	Min: 8.00 Max: 300.00	Enabled

Option		Values and Defaults	Use
Hemisphere Comparison	MTT	50%	
	BV	2.00	
Use post filtering	Default: **Enabled**/Disabled	Description: Make map images appear smoother.	
Show total volume	Default: **Enabled**/Disabled	Description: Provides display with the total volume.	

Advanced TDA - Brain TDA - Capture Settings

Option	Values (Default value bolded)
Group Captures By:	**Level**/Map
Map Type	
	BF
	BF
	MTT
	TTP
	TOT
	RT
	Map
	Tmax
	MPR
	MIP
	Graph
	Text

TVA

Option	Values (Default value bolded)	Description
Patient Demographic Unit	• International • lb, ft, in	Metric or imperial units
Number of minimum series to proceed EF	8	If the number of loaded series is lower than the minimum specified here, ask whether user wants to use different data for EF.

TVA(LV)

Option	Values (Default value bolded)	Description
Analysis Method	• **Automatic** • Automatic (all phases) • Manual	Automatic: Calculate left-ventricle ejection fraction automatically. Automatic (all phases): Perform automatic TVA(LV) on all phases. Manual: The user performs each step of the analysis manually.
Perform Wall Analysis	**Enabled**/Disabled	If enabled, wall analysis is performed automatically
Myocardial Density	Numerical (g/ml) **(Default is 1.05 g/ml)**	Set the value of myocardial density.
Show grids on myocardium	Enabled/**Disabled**	Display grids on the myocardium during the Wall step of manual TVA(LV).
Smooth the wall intensity polar map (color only)	**Enabled**/Disabled	Improve the color of the Wall Intensity polar map with smoothing.
Territory volume ignores papillary muscles (fast)	**Enabled**/Disabled	Territory volume calculation ignores papillary muscles, which improves the calculation speed.

TVA(RV)

Option	Values (Default value bolded)	Description
Analysis Method	• **Automatic** • Manual	Automatic: Calculate right-ventricle ejection fraction automatically. Manual: The user performs each step of the analysis manually.

CardiacMR

CardiacMR - MRTVA

Option	Values (Default value bolded)	Description
Patient Demographic Unit	• **International** • lb, ft, in	Metric or imperial units.
Wall - Show Wire Frame	**Enabled**/Disabled	Show or hide wire frame (3D model) in the viewer.
Wall - Quality	• **High** • Medium • Low	Wire frame (3D model) image quality options
Show Wireframe in Capture	**Enabled**/Disabled	
Position, Wall	• 1x1 (tile view) • 3x4 (tile view) • **Horizontal Tile Layout** • Vertical Tiile Layout	
Results	• **Result (Main/Result/ED/ES)** • Tile Layout (Main/Result/ Tile(6x3)) • Tile Layout (Main/Result/ Tile(3x3)/Long-axis • ED/ES/Table Layout	
Initial result type: LV	• Text Result • Time-Volume • Graphs • Polar Maps(Bulls Eye) • Polar Maps(AHA 17 segment : Gradiation) • Polar Maps(AHA 17 Segment : Solid Color) • 3D Color Maps	Option to select and display the initial result type of MRTVA for Left Ventricle analysis.
Initial result type: RV	• Text result • Time-Volume	Option to select and display the initial result type of MRTVA for Right Ventricle Analysis.
Wall contour detection using threshold, initial value	Range: 0 - 80; **Default: 50**	
Myocardial Density	Default: **1.05 g/ml**	
Show grids on myocardium	Enabled/**disabled**	Option to show grid on myocardium
Polar Maps	All are selected by default. Wall Thickening Segmental EF Wall Thickness Wall Intensity Wall Motion	Option to select which polar maps to show as results

Option	Values (Default value bolded)	Description
Wall Motion	Position Inner (0) Center (50) Outer	Option to configure range of wall in percentage to reflect wall motion polar map result.
Units of Measurement: Cardiac Index	• **l/min/m^2** • ml/min/m^2	Express the cardiac index in either liters or milliliters.
Units of Measurement: Cardiac Output	• **l/min** • ml/min	Express the cardiac output in either liters or milliliters.
Units of Measurement: Papillary muscle volume	• cm^3 • ml	Express the papillary muscle volume in centimeters cubed (mass) or milliliters (volume)
Papillary Muscle Volume: Show papillary muscle volumes	• Enabled/**Disabled**	Displays papillary muscle volume in analysis when 'Exclude papillary muscle from LV volume" is enabled
Papillary Muscle Volume: Show as papillary muscle masses	• Enabled/**Disabled**	Displays papillary muscle volume in masses (cm^3)
Papillary Muscle Volume: Include papillary muscle in ED myocardial volume/mass	• Enabled/**Disabled**	Includes the papillary muscle volume with the End-Diastolic myocardial volume/mass

CardiacMR - LV, RV, and LV/RV

Option	Values (Default value bolded)	Description
Wall Computation Method	• Automatic • Manual	Automatic: Calculate left-ventricle ejection fraction automatically. Manual: The user performs each step of the analysis manually. Note: When "Enable RV analysis" is checked on, wall computation includes right ventricle as well.
Enable RV Analysis	**Enabled**/Disabled	Option to run RV analysis together with LV
Perform Wall Analysis for RVP (for myocardial volume and mass)	Enabled/**Disabled**	Option to run wall analysis for RV

Delayed Enhancement (MR)

Option	Values (Default value bolded)	Description
Show Wireframe	**Enabled/**Disabled	Show 3D wire frame in lower-right corner of main window. The wire frame represents each slice in the current phase.
Show Wireframe in Capture	Enabled/Disabled	Include wire frame in captured images.
Quality	• High • Medium • Low	High is best quality; Low is fastest.
Wall contour detection using threshold: The initial vlue of the threshold intensity	42 - 56; Default: 50	Default intensity value when starting threshold editing
Threshold (FWHM)	• **Auto** • Manual • n+	Formula for calculating the threshold between healthy tissue and pathology.

Perfusion

Option	Values (Default value bolded)	Description
Series Layout	• **Stress/Rest - Horizontal or Vertical** • Rest/Stress - Horizontal or Vertical • Single	Specifies layouts of perfusion data loaded into the viewer. “Single” refers solely to the single series view.
Initial Layout	• **1 x 1 image** • 1 x 3 images (multi-slice) • 3 x 1 images (multi-slice) (only available when Series Layout = Single)	Allows you select default layout for perfusion data loaded into the viewer.
Use recommended W/L for each image	Enabled/**Disabled**	Uses the Window/Level values found in the DICOM header.

T1/T2 Mapping

Option	Values (Default value bolded)	Description
Enable synchronize option when two data are load.	**Enabled**/Disabled	Enables data synchronization.
Use recommended W/L to each image.	**Enabled**/Disabled	The image sets the W/L.
Segment		This setting is related to the number of segments in equal degrees around the myocardium.

Option	Values (Default value bolded)	Description
Division count of angle	**36**	
Division count of concentric	**5**	This setting is related to the number of rings that appear around the myocardium.
Wall contour detection using threshold		
The initial valve of the threshold intensity.	**50**	
Mouse Operation	**Up and down level change, Left and right phase change.**	LMB-hold changes level (up and down), both LMB and RMB-held to change phases.

T1 Mapping

Option	Values (Default value bolded)	Description
Series Layout	• **Pre/Post** • Rest/Stress - Horizontal or Vertical • Single	Specifies layouts of perfusion data loaded into the viewer. “Single” refers solely to the single series view.
Initial Layout		
Position Wall	• **1 x 1 image** • 1 x 3 images (multi-slice) • 3 x 1 images (multi-slice) (only available when Series Layout = Single)	Allows you select default layout for perfusion data loaded into the viewer..
Results	**1x3 Image/Graph/Polar Maps**	How the results will display in the viewer.
Data Type	**T1 (Modified Look-Locker)**	
Time Type	**Inversion Time**	
Analysis area	**Segment**	
Keep the shape of contour of wall between phases.	**Enabled**/Disabled	
Analysis Range		
Min (msec)	**0**	
Max (msec)	**3000**	
Noise	**20 (Disabled)**	

T2 Mapping

Option	Values (Default value bolded)	Description
Series Layout	• **Pre/Post** • Rest/Stress - Horizontal or Vertical • Single	Specifies layouts of perfusion data loaded into the viewer. “Single” refers solely to the single series view.
Initial Layout		
Position Wall	• **1 x 1 image** • 1 x 3 images (multi-slice) • 3 x 1 images (multi-slice) (only available when Series Layout = Single)	Allows you select default layout for perfusion data loaded into the viewer..
Results	**2x2 Image/Graph/Polar Maps**	How the results display in the viewer.
Data Type	**T1/T2* (none)**	
Time Type	**Auto**	
Analysis area	**Pixal Wise Fast**	
Keep the shape of contour of wall between phases.	**Enabled**/Disabled	
Analysis Range		
Min (msec)	**0**	
Max (msec)	**200**	
Noise	**10 (Disabled)**	

Flythrough

Option	Values (Default value bolded)	Description
Default WW	1500	Default window width value
Default WL	-400	Default window level value
MPR cutplane VR mode	• Gray scale • Color template	Option to display 3D on MPR cutplane in graycale or color
Synchronize Perpendicular view	**Enabled**/Disabled	When color is selected as MPR cutplane VR mode, perpendicular view will be displayed in color too.

Option	Values (Default value bolded)	Description
Create a new finding when:	An arrow is added. (**Enabled**/Disabled)	When any of these actions are taken, automatically create a new finding and add to the findings list.
	A distance is measured (**Enabled**/Disabled)	
	A polyp is picked (**Enabled**/Disabled)	
	CAD markers are turned on (Enabled/**Disabled**)	
Default perspective view angle	Between 70 - 360 degrees Default: **120** degrees	Default “lens” angle for viewing the flight path
Layout for Primary2D when double-click	• **1x2 Side by Side**	When one of the windows in the Primary2D layout is double-clicked, that window and the corresponding window from the other scan are displayed side-by-side. If you double-click again, it will go back to Primary2D.
	• 1x1	When one of the windows in the Primary2D layout is double-clicked, that window is displayed in the entire main window. If you double-click again, it will go back to Primary2D.
Findings to Report/Output/Text	**Confirmed findings only** Confirmed and pending findings Display findings in the finding list	Select which findings to send to a report, to the Output Panel, or to a text file.
Report method	**Report** Output Text XML	Generate a standard report, output the report information to PACS or generate a text file to contain the report.
Amount of overlapped region for each side of flatview (percentage)	Vertical: **5**, 10, 20 Horizontal: 0, 5, **10**, 20	When the flat view is shown in multiple windows, a small amount of the flat image is displayed at the end of the stretch in one window, and then again at the beginning of the following window. This setting specifies what percentage of each window has duplicated data *at each end*.
Behavior when capture	Create new finding	Add the image to the Findings window, but do not capture it to the Output Panel.
	Capture	Capture to the Output Panel only.
	Create new finding and capture	Add the image to the Findings window and capture to the Output Panel.
Capture SpotMPR	**Enabled**/Disabled	Capture with Spot MPR viewer.

Option	Values (Default value bolded)	Description
Show Reading style preference wizard every time	Enabled/**Disabled**	Display the Reading Style wizard each time the layout is changed. (When disabled, the wizard is displayed only when data is first loaded.)
Skip colon segmentation and path creation when there is APS result	Enabled/**Disabled**	Use the APS result instead of doing these steps manually.
Show stool with color	Enabled/**Disabled**	Display stool in a different color to be easily identified.
Show camera postion on 2D	**Enabled**/Disabled	Display arrow pointing to current camera position on the 2D views during flythrough.
Enable dual monitor	**Enabled**/Disabled	When enabled, Flythrough displays a dual-monitor layout on both monitors.
Load colon by user	**Enabled**/Disabled	

Flythrough Details

Option	Values (Default value bolded)	Description
Re-synchronize on 2D	Automatic/**Manual**	Automatic: If you work on one series while the two series are not synchronized, and then click sync, the other series is automatically synchronized. Manual: The other series is not automatically synchronized.
Re-synchronize on path when switching layout/data	**Enabled**/Disabled	When switching from primary flythrough path to other data or layout, synchronize the new path to the primary path. When returning to the primary path, do not re-synchronize, but go back to where it was.
Finding circle on Global view: Size	30 mm	Change the size of the circle on the Global (or Inset) view, indicating where findings have been saved.
Finding circle on Global view: Color	Windows color palette. Default: **red**	Change the color of the finding circle.
Put Workflow, Template and 3D Setting on the top bar	Enabled/**Disabled**	Place icons on the top toolbar that open/close the Workflow, Template and 3D Setting tabs, respectively, when clicked.
Show colon coverage in tool panel	Enabled/**Disabled**	Display percentage of colon viewed and button to show the unviewed list.
Display finding number on arrow	**Enabled**/Disabled	Display number with finding circle.

Option	Values (Default value bolded)	Description
Output image from Finding list	• Use current 3D setting • Same 3D setting when finding was created	
Place the camera position on the path at cine playing	Enabled/**Disabled**	Option to keep the camera position pointed toward the path so that the camera will not point toward the wall during faster flythrough.

Output Panel

Option	Values (Default value bolded)	Description
Features available for 1x1 output layout	• Film • Save • Report • Print • Email	Images in the output medium are saved and/or displayed in 1x1 layout, regardless of the currently selected layout in the Output Panel.
Select where you want to dock the control panel	**Top** Bottom	Choose where the control panel will appear in the Output Panel (above or below the captured images). **(Requires restart.)**
Automatically open on sending images to Output Panel	Enabled/**Disabled**	When enabled, the Output Panel is automatically displayed whenever an image is captured and sent to the Output Panel.
Automatically close if Output Panel is empty	**Enabled**/Disabled	The Output Panel closes automatically when all captured images are deleted.
Delete images after DICOM transfer is completed	Enabled/**Disabled**	Delete images from Output Panel after **Send to DICOM** transfer is complete.
Save copy of images on AqNET server	Enabled/**Disabled**	If **Delete images after DICOM transfer** is checked, also checking this setting will save a copy of the images on the iNtuition server, in case of lost data or network failure.
Save selected DICOM server as default	Enabled/**Disabled**	Each time you select a DICOM server, that server becomes the default server.
Bit depth (MIN, MPR, etc)	Colored Grayscale (12- or 8-bit) **Show more options**	Set the bit depth for all captures to either grayscale or color. If Grayscale is selected, select whether 8-bit or 12-bit using the pull-down menu at right. If **Show more options** is selected, set bit depth separately according to the rendering mode or view (see next row).

Option	Values (Default value bolded)	Description
Bit depth options (visible only when **Show more options** is checked, above)	Set bit depth for: Preview: Colored Sagittal: Grayscale (12 bit) Coronal: Grayscale (12 bit) Axial: Grayscale (12 bit) Main View: Grayscale (12 bit) CPR: Grayscale (12 bit) sMPR: Grayscale (12 bit) Cross-section MPR: Grayscale (12 bit) MAR: Grayscale (12 bit) 2D Viewer: Grayscale (12 bit) Calcium Score Result: Colored	Allows you to set the bit depth individually for different rendering modes or views.
Capture VR always as colored	**Enabled**/Disabled	When this is enabled, the Capture option does not ask whether you want a VR image to be captured in color or monochrome. It always captures in color.
Capture Image including Color Overlay	• BFA (Body fat analysis) (**On**) • Mask (**On**) • Plaque analysis (**On**) • Volume (Histogram) (**On**) • Colored Motion (**On**)	For any of the types of overlay that are checked, include that overlay in the capture.
Capture annotation in Grayscale	Enabled/**Disabled**	Small annotations may be hard to read when they are not captured in grayscale. The quality of image annotation is easier to read in grayscale..
Generated series starting number	User defined	You can specify a starting number for generated series.

Page Format

Option	Values (Default value bolded)	Description
Display setting	Enabled: 1x1, 1x2, 2x1, 2x2, 2x3, 2x4, 3x3, 3x4, 3x5, 4x4, 4x5, 4x6, 5x5, 5x7, 5x8, 5x9, 6x8, 7x8, 8x9	These describe the number and layout of the images per page in the Output Panel.
New page format	All formats that can be physically displayed (no default)	Create a new page format to add to above list.
Page size setting	Disabled: 8x10 in., 8.5x11 in., 10x12 in., 10x14 in., 11x14 in., 14x14 in., 14x17 in., 24x30 cm, 24x24 cm, A3 (Portrit), A4 (Portrit), 10x8 in., 11x8.5 in., 12x10 in., 14x10 in., 14x11 in., 17x14 in., 30x24cm, A3 (Landscape), A4 (Landscape)	Select all page dimensions to be available in the Page size pull-down menu. These dimensions refer to the size paper the images will be printed on.

Measurement Settings

Option	Values (Default value bolded)	Description
Use Measurement Protocols from	• **Private** • Group	If **Private** is selected, only measurement protocols from your own user account can be used. If Groups, you can use measurement protocols that have been saved under your default user group.
Specify name after a measurement	Enabled/**Disabled**	Automatically pop up text box to manually label measurement.
Export measurement results when opening report for workflow	Enabled/**Disabled**	Export measurement results in xml file when generate report from workflow panel.
Export measurement results when output workflow images	**Enabled**/Disabled	Export measurement results in xml file when output images from workflow panel.
Export folder - choose the location for exporting the images	Your desktop folder	File save path for export measurement results.
Capture to Output Panel when measurement is added or edited	Enabled/**Disabled**	Capture image to output panel when measurement is added or edited for a measurement protocol.
Delete measurement in the viewer when it is erased in the measurement protocol panel	Enabled/**Disabled**	When a measurement is erased in the Measurement Protocol, the annotation is removed from the corresponding measurement in the viewer; however, the measurement itself remains in the viewer.
Erase measurement value from measurement protocol when it is deleted in the viewer.	Enabled/**Disabled**	When a measurement is deleted from the viewer, the corresponding measurement is erased from the Measurement Protocol.
Save images when exporting measurements as XML	**Enabled**/Disabled	When exporting the measurements to xml, export the associated capture too.
Popup the measurement protocol selection dialog automatically	**Enabled**/Disabled	Pop up dialog when measurement protocol tool is selected.
Save the measurement protocol automatically (when measurements are added/ deleted/edited).	**Enabled**/Disabled	Without clicking save button on measurement protocol tool panel, change is saved automatically.
Export Measurement Components only when “All Results” is selected.	**Enabled**/Disabled	If enabled, Measurement Components (all values in the measurement result) are exported only for “All Results”. If Disabled, the Measurement Components are exported for every measurement.

Option	Values (Default value bolded)	Description
Hide prior measurement protocol measurements when switching to another protocol	**Enabled**/Disabled	When switching to a different stent graft while a measurement protocol is in progress, measurement values from the first protocol are automatically incorporated into the corresponding measurements in the second protocol. Enable this setting to hide measurements that are not interchangeable.

Measurement Options

Options for Measurement Protocols.

Option	Values (Default bolded)	Description
Automatically select next measurement	Enabled/**Disabled**	When finished with a measurement during EVAR, automatically step to the next measurement.
Include measurements from all loaded studies/series when generating report and exporting xml.	**Enabled**/Disabled	In TAVR, the chest and abdomen scans are usually two separate series. This setting allows you to load multi-data and use only one measurement protocol.
When exporting to AIM XML output captures for measurements	Enabled/**Disabled**	Output images to AIM XML (DICOM or JPG).
Capture diameter value when cross-section bar is moved.	Enabled/**Disabled**	When cross section line is moved, capture measurement after mouse is released.
Enable Show/Hide Measurements	Enabled/**Disabled**	Hide some or all measurements, or show previously hidden measurements.

Finding Viewer

Option	Values (Default bolded)	Description
Enable Measurement Tracking	• **Based on Workflow** • Disabled	Option to enable/disable measurement tracking.
Default Measurement Criteria	• No Criteria • **RECIST 1.1** • RECIST 1.0 • Cheson	Measurement criteria selection by default.

Option	Values (Default bolded)	Description
Default Finding Viewer view	• **Full (All Prior and Loaded Studies)** • Compact (Base, Prior and Loaded Studies)	Finding viewer type selection by default.
Show Finding Details form after performing a measurement	**Enabled**/Disabled	Pops up dialog after measurement to select finding options.
Prefix for the finding name	User-defined. Default: Finding-	Default prefix for finding name (e.g. Finding-1, Finding-2, ..).
Show prior finding capture as a popup when prior study is not loaded	**Enabled**/Disabled	When only the follow up study is loaded “Perform Measurement” is clicked on the Finding Viewer, then show the prior finding key image as a pop-up.
For Non-Target findings show the values in Finding Viewer	**Enabled**/Disabled	If Disabled then show “Present/Absent” for Non-Target findings. Otherwise display the measurement values for Non-Target findings.
Show Images in Findings Report	• Do Not Show • Show All • **Show Target Only** • Show Non-Target Only	Option to select which images to populate in the report.
Delete measurement in Viewer when it is deleted in Finding Viewer	**Enabled**/Disabled	Deletion of measurement in the viewer will delete the measurement in the finding viewer.
Delete measurement in Finding Viewer when it is deleted in Viewer	**Enabled**/Disabled	Deletion of measurement from finding viewer will delete the measurement in the viewer.
Organs	Body, Brain, Breast, Colon, Heart, Kidney, Liver, Lung, Lymph Node, Muscle, Neck, Ovary, Pancreas, Prostate, Skin, Spleen, Thyroid, Uterus	Labels of organs provided by default.

Movie

Option	Values (Default value bolded)	Description
Resolution	1024	Set the pixel resolution for movie files, for example, 256, 512, and so on.
Square view	Enabled/**Disabled**	Movie capture with square or view size.
Frame rate	8 frame/sec	The number of frames shown per second as the film is playing.

Option	Values (Default value bolded)	Description
Codec (video compression)	Full Frames (uncompressed)	Select compression software from pull-down menu.

Patient Annotation

Option	Values (Default bolded)	Description
Age/Birth patient annotation	• **Age** • Birth	Show either the patient's age or birthdate in patient annotation
Date/Time type	• **Acquisition date/ time** • Study date/time	Show date as time of scan or time the data was received on the iNtuition server.
Date format	• **Month/Day/Year (US)** • Year/Month/Day (JP) • Date-Short Name of Month-Year	Choose date format appropriate for country.
24-hour time format	Enabled/**Disabled**	Either 12-hour (with AM and PM to indicate which part of the day) or 24-hour clock, from 00:00 (midnight) to 23:59 (11:59 PM).

Connection

This screen is made up mostly of user, server and login information, which can not be changed here. See the following table for information about settings that can be configured.

Option	Values (Default value bolded)	Description
Show Last Login info every time after login	Enabled/**Disabled**	Post a dialog immediately after login that contains the last login info shown here.

Appendix B: Keyboard Shortcuts

Group	Function	Keyboard Shortcut
3D Mouse Operation	Rotate	Left button click and drag
	Re-center	Click Middle button
2D Mouse Operation	Paging	Scroll wheel
		Left button click and drag
		Middle and Right buttons click and drag
	Paging with Slow Speed	Left button click and drag, then Shift
		Middle and Right buttons click and drag, then Shift
	Link to 3D ON/OFF	Middle button double click
3D / 2D Mouse Operation	Window Level	Left and Right buttons click and drag
		Move mouse cursor over W/L and Left button click
		Key: 1-9. 0 is for reset.
	Pan	Right button click and drag
	Zoom	Middle button click and drag
	Re-center	Alt + Left button click
	Move Scale Bar	Left button double click on the scale bar. Left button click on it and drag.
Capture	Capture	c
	Capture All	Ctrl + Shift + c
	Capture All in One	Ctrl + Alt + c
	Capture Image and Annotation (Annotation is not able to ON/OFF with	Alt + c
	Capture to Folder	Ctrl + s
Output Panel	Drag and Drop and Image in Format	Left button click + drag and drop
		Ctrl + Left button click and drag
	Open Edit Window	Left button double-click
	Select All	Ctrl + A

Measurement	Distance	d
	Ellipse	e
	Profile	i
	Angle	Shift + comma (,) / Less than (<)
	Distance Pair	Ctrl+d
	Polygon	Ctrl+p
	Fat Analysis	Ctrl+o
	Volume Histogram	Ctrl+Alt+v
	Select Previous Result	Ctrl+Open Brackets ([)
	Select Next Result	Ctrl+Close Brackets (])
	Mouse Escape	Esc
	Delete Measurement	Delete
Measurement Protocol	Export AIM XML file	Shift + e
	Move to Next Step	b
Finding	New Finding	n
	Show Measurement Result	Semicolon (;)
Arrow / Text	Arrow/Text	m
	Landmark Arrow	Ctrl + m
	Text	t
Orientation	Anterior	a
	Posterior	p
	Head	h
	Feet	f
	Right	r
	Left	l
	Rotate to Up	Up (↑)
	Rotate to Down	Down (↓)
	Rotate to Left	Left (←)
	Rotate to Right	Right (→)
	Angle Setting (LAO, RAO)	o

Batch 2D	Wizard	F8
G-Bar	Show G-Bar	g
CPR	Enter CPR Mode	v, F7
	Show / Hide Centerline	Ctrl+t
CPR - Mouse movements are interpreted according to the mode invoked by each of the shortcut keys.	Redraw mode	Shift
	Draw circle around outer wall	Ctrl
	Nudge outer wall	Alt or Alt + Ctrl
CPR - Edit Centerline	Quick Edit Mode	Shift + Move mouse over CPR window
	Add / Delete Point	Shift + Left button click
	Smooth Centerline	Ctrl + Left button click and drag
CPR - Edit Contour	Redraw	Shift + Left button and draw
	Nudge	Alt + Left button and draw
Region Growing	Region Growing	F5
	Select Visible Region	Shift + Left button hold
	Select Visible and Invisible Region	Shift + Ctrl + Left button hold
	Add RG area to existing volume	Shift + Ctrl + Left-click
Free ROI	Free Curve	F6
Free ROI - 3D	Exclude	Shift + Left button drug
	Edit	Shift + Left button click to draw region, then click button from Free ROI tool
	Add Back Previously removed Region	Shift + Right button click and drug
Free ROI - 2D	Edit	Shift + Left button click to draw region, then click button from Free ROI tool
Mask	Smooth Mask	Ctrl + e
Cross Hairs	Re-center MPR Cross Hairs	Alt + x
	Show / Hide Cross Hairs	x
Cutplane	Slab	w
	MPR Map ON/OFF	Alt + w
	Modify Thickness	Ctrl + Middle button click and drag

Cube view	Cube View	q
		Space + Left button click
	Change Cube Size	Middle button click and drag
	Zoom	Ctrl + Middle button click and drag
Render Mode	3D VR	F2
	3D Perspective	Alt + F2
	MPR	F3
	MIP	F4
	Draft/Fine ON/OFF	Ctrl + f
Workflow	Next	Tab
	Previous	Shift + Tab
	Validate	Ctrl + w
4D Cine	Backward	Page Down
	Forward	Page Up
	Play Forward	Period (.)
	Speed Control	Comma (,)
Layout	1x1	Ctrl + F2
	2x2	Ctrl + F3
	2x2 Vessel Track	Ctrl + F4
	2x2 CPR Vertical	Ctrl + F5
	2x2 CPR Horizontal	Ctrl + F6
	Back to Previous Layout	Double click
Other	Undo	Ctrl + z, z
	Redo	Ctrl + y
	Control Panel ON/OFF	Ctrl + r
	Multidata Sync	Space bar
	Full Screen Mode	F11
	AQi Online Help	F1
Mouse Operation	Open Quick View Panel	Left button double click
	Paging with Slow Speed	Shift + Left buttons click and drag

Paging	Move Forward	Up (↑)
	Move Backward	Down (↓)
	Go First Slice	Home
	Go Last Slice	End
	4D Phase Forward	Right (→), Page Up
	4D phase Backward	Left (←), Page Down
	Drag and Drop an Image in Format	Left button click + drag and drop
		Ctrl + Left button click and drag
	Open Edit Window	Left button double click
	Backward	Left (←)
	Forward	Right (→)
	Level Down	Down (↓)
	Level Up	Up (↑)
Autoscroll (2D)	Start/Stop	Back quote (‘)
Rendering Mode	MPR	F3
	MIP	F4
	BF	F5
	BV	F6
	MTT	F7
		F8
	Permeability	F9
Colored Motion	Colored Motion	k
User Annotation	Landmark Arrow	m
Candidate Marker	Candidate Marker On/Off	Pipe (|)
	Previous Maker	Open Bracket ([)
	Next Marker	Close Bracket (])

Flythrough	Forward in Flat View Path	Left button click
	Backward in Flat View Path	Alt + Left button click
	Tilt Flat View Camera Angle between Left and Right	Left button click and drag horizontally
	Change Cube Size in Cube View	Shift + Middle button click and drag
	Orbit in Perspective View	Ctrl + Left button click and drag
	Show SpotMPR	s

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