suiteHEART® Software

cMRI Analysis Software

Instructions for Use

NeoSoft, LLC

NS-03-043-0003-EN Rev. 3

Revision History

Rev	Date	Description of Change	Safety Related Update (Yes/No)
1	22AUGUST2022	Updated for the 5.1.0 product release. This IFU replaces the previous language/revision/part numbers: suiteHEART® Software IFU - NS-03-039-0003, EN-Rev. 6 suiteHEART® Software IFU - NS-03-039-0004, FR-Rev. 5 suiteHEART® Software IFU - NS-03-039-0005, DE-Rev. 5 suiteHEART® Software IFU - NS-03-039-0006, IT-Rev. 5 suiteHEART® Software IFU - NS-03-039-0007, EL-Rev. 5 suiteHEART® Software IFU - NS-03-040-0003, LT-Rev. 4 suiteHEART® Software IFU - NS-03-040-0004, ES-Rev. 4 suiteHEART® Software IFU - NS-03-040-0005, SV-Rev. 4 suiteHEART® Software IFU - NS-03-040-0006, TR-Rev. 4 suiteHEART® Software IFU - NS-03-040-0007, RO-Rev. 4 suiteHEART® Software IFU - NS-03-040-0008, NL-Rev. 4 suiteHEART® Software IFU - NS-03-041-0005, ZH-CN-Rev. 2 suiteHEART® Software IFU - NS-03-040-0030, PT-PT-Rev. 4 suiteHEART® Software IFU - NS-03-041-0007, HU-Rev. 3 suiteHEART® Software IFU - NS-03-042-0006, JA-Rev. 1 suiteHEART® Software IFU - NS-03-042-0007, VI-Rev. 1	No
2	31MAY2023	Updated for the 5.1.1 product release. Estonian added. Moved regulatory information to Regulatory Addendum document.	No
3	30DECEMBER2024	Updated for the 5.1.2 product release. Updated Safety information.	Yes

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To view compliance information (Authorized Representative, Importer, Registration information) after launching the application, click “Help” or “About” from the main screen. Select the “Regulatory Information” option. The document will open in a pdf viewer.

Table of Contents

Safety

Introduction

To assure efficient and safe use it is essential to read this safety section and all associated topics before attempting to use the software. It is important for you to read and understand the contents of this manual before attempting to use this product. You should periodically review the procedures and safety precautions.

The software is intended for use by trained and qualified personnel only.

suiteDXT / suiteHEART® software has an expected useful service life of 7 years from its original release date.

NeoSoft does not provide regular maintenance services for its products. Please contact support for questions and concerns.

CAUTION: Federal Law restricts this device to sale, distribution and use by or on the order of a physician.

The terms danger, warning, and caution are used throughout this manual to point out hazards and to designate a degree or level of seriousness. Hazard is defined as a source of potential injury to a person. Familiarize yourself with the terminology descriptions listed in the following table:

Table 1: Safety Terminology

Graphic	Definition
 **DANGER:**	Danger is used to identify conditions or actions for which a specific hazard is known to exist which will cause severe personal injury, death, or substantial property damage if the instructions are ignored.
 WARNING:	Warning is used to identify conditions or actions for which a specific hazard is known to exist.
 CAUTION:	Caution is used to identify conditions or actions for which a potential hazard is known to exist.

Indications for Use

suiteHEART® Software is an analytical software tool, which provides reproducible tools for the review and reporting of medical images. suiteHEART® Software can import medical images from a MR system and display them in a viewing area on the computer screen. The viewing area allows access to multiple studies and series of multi-slice, multi-phase images. Multi-phase sequences of images can be displayed in cine mode to facilitate visualization.

A report input interface is also available. Measurement tools on the report interface make it possible to quickly and reliably fill out a complete clinical report of an imaging exam. Available tools include: point, distance, area, and volume measurement tools such as ejection fraction, cardiac output, end-diastolic volume, end-systolic volume, and volume flow measurements.

Semi-automatic tools are available for left ventricular contour detection, valve plane detection, vessel contour detection for flow analysis, signal intensity analysis for myocardium and infarct sizing measurement, and T2* analysis.

The results of the measurement tools are interpreted by the physician and can be communicated to referring physicians.

When interpreted by a trained physician these tools may be useful in supporting the determination of a diagnosis.

Intended Use

suiteHEART® Software is intended to assist trained clinical personnel in the qualification and quantification of cardiac function. The software provides the tools to adjust the parameters of the DICOM images and provides presentation states where the user can appreciate various MRI acquired images of the heart and vasculature over time. Additionally, the software provides tools for measuring linear distances, areas, and volumes that can be used to quantify cardiac function. Finally, the software provides the tools for volumetric flow measurements and the ability to calculate flow values.

Supported DICOM Image Formats

suiteHEART® Software supports the following DICOM format; MR and Enhanced MR. Refer to the suiteHEART® Software DICOM Conformance Statement manual for further detail on supported formats.

CAUTION: Data stored as a DICOM image that has been imported by an external PACS may not be compatible viewing for suiteHEART® Software.

Safety Notices

WARNING: The application assists in the analysis of the images only and does not automatically produce a clinical interpretation of the results. The use and placement of quantitative measurements is at the discretion of the user. Misdiagnosis can occur if measurements are inaccurate. Measurements should only be created by a properly trained and qualified user.

WARNING: Artifacts on an image can be misinterpreted, leading to inaccurate results. Do not use images containing artifacts for diagnosis. Analysis should only be performed by a properly trained and qualified user.

WARNING: Diagnosis for the wrong patient could occur if images do not contain patient name or ID. Do not use images that do not contain patient name and ID for diagnosis. Visually confirm the patient information prior to analysis.

CAUTION: Using images upon which an image filter has been applied could result in inaccurate results. The user must exercise discretion before analyzing pixel intensity corrected images. The software will display a warning message if loading images that have been filtered.

Equipment Hazards

CAUTION: Using equipment that is damaged or has been compromised can put the patient at risk by delaying diagnosis. Make sure that equipment is in proper working order.

CAUTION: Applications may run on equipment that includes one or more hard disk drives, which may hold medical data related to patients. In some countries, such equipment may be subject to regulations concerning the processing of personal data and free circulation of such data. Release of personal data may result in legal action depending on the applicable regulatory body. It is strongly recommended that access to patient files be protected. The user is responsible for understanding the laws regulating patient information.

Cybersecurity

NeoSoft takes the following cybersecurity precautions in the design and implementation of its software:

- NeoSoft software administration of certain functions, (user permissions, database rebuild, etc.) may only be performed by trained administrative users.
- NeoSoft software is regularly analyzed for known vulnerabilities listed in the NIST database and patched as needed.
- NeoSoft software uses the DICOM standard to store patient data and to communicate patient data over the network via a user configured port.
- NeoSoft software integrity prior to installation is md5 sum verified to ensure the software has been delivered fully intact.
- NeoSoft software has been verified for use on hardware with encryption enabled.
- NeoSoft mitigates cybersecurity risks by design following the ISO 14971 standard.
- NeoSoft employees receive training in Cybersecurity and Protection of Health Information.
- NeoSoft does not receive or manage protected health information unless specifically granted access by a customer for troubleshooting.
- NeoSoft software has undergone penetration testing.
- Automatic logoff (ALOF) - suiteHEART may be configured to close at a predetermined time of non-use. suiteDXT remains open until closed by a user or system is restarted.
- Audit controls (AUDT) - suiteHEART and suiteDXT produce timestamped logs which include software events and user information
- Authorization (AUTH) - In suiteDXT, an administrator may view and configure access control for other users. Depending on how access is configured, users may only view certain studies in suiteDXT and suiteHEART. For example, User A may only access study information from location A and User B may access study information from location A and B.
- Node authentication (NAUT) - suiteDXT may be configured to communicate with other DICOM devices by configuring the AE title, IP address, and DICOM port. suiteHEART does not utilize networking by default but may be configured to send data to other systems via a configuration change, identifying the other system(s) by AE Title, IP Address, and port. Both products may be used without networking by importing local study data from the filesystem, instead of sending or receiving study data via a network.
- Person authentication (PAUT) - suiteHEART and suiteDXT may be configured to allow user authentication, user password controls, and configuration of available patient data specific to logged in user. User information is logged.
- Connectivity capabilities (CONN) - suiteDXT may connect to other configured DICOM partners in order to transfer data. suiteHEART may be configured to send data to other systems via a configuration change, identifying the other system(s) by AE Title, IP Address, and port.
- Physical locks (PLOK) - N/A. NeoSoft recommends the use of Network security products to protect.
- System and application hardening (SAHD) - N/A. NeoSoft recommends the use of Network security products to protect.
- Health data de-identification (DIDT) - suiteDXT includes a “Anonymize” feature to de-identify patient studies.
- Health data integrity and authenticity (IGAU) - suiteDXT includes status messages for import / transfer of study information resulting in confirmation of successful import or transfer and if errors have occurred. suiteHEART alerts the user via a popup if expected input data is missing or corrupted.
- Data backup and disaster recovery (DTBK) - Data generated by suiteHEART is recommended to be sent to PACS for long term storage / backup. suiteDXT includes a database rebuild tool should local software be corrupted.
- Health data storage confidentiality (STCF) - suiteHEART and suiteDXT are intended to be used by qualified personnel and may be secured by username and password at the discretion of the user.
- Transmission confidentiality (TXCF) - Any transfer of data is in the DICOM format.
- Transmission integrity (TXIG) - Any transfer of data is in the DICOM format.
- Cyber security product upgrades (CSUP) - any installs or upgrades would be in the form of a new software release allowed and applied at the discretion of the customer.
- Software bill of materials (SBoM) - The suiteHEART “About” screen lists third party software. suiteDXT 3rd party software information may be found in the suiteDXT installation directory folder “3pInfo.”
- Roadmap for third-party components in device life cycle (RDMP) - NeoSoft evaluates third party software regularly and may update suiteHEART and / or suiteDXT should the need arise.

- Security guidance (SGUD) - NeoSoft recommends the use of anti-virus software.
- Network Security Feature Configuration (CNFS)- The product's ability to configure network security features based on user needs- Both suiteHEART and suiteDXT may be used without networking. However, if configured for network transfer, only AE Title, IP address, and Port information is needed. No further security is required / recommended.
- Emergency access (EMRG) - N/A. suiteHEART and suiteDXT are not used in emergent situations.
- Remote service (RMOT) - service may be performed remotely via the customer's prescribed remote access method (such as remote desktop). suiteHEART and suiteDXT do not include remote access themselves.
- Malware detection/protection (MLDP) - N/A. suiteHEART and suiteDXT do not include malware detection or protection. NeoSoft recommends the use of Network security products to protect.

Getting Started

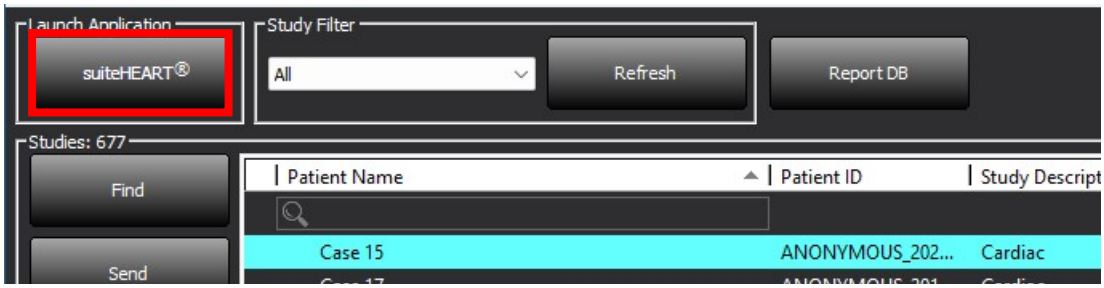
Launching and Exiting the Application

suiteHEART® Software is an application that can be used for analysis, review, and reporting of Cardiac MRI (Magnetic Resonance Imaging) studies. This manual provides a detailed explanation of the suiteHEART® Software user interface and the workflow for performing quantitative analysis on cardiac MR images.

Launching suiteHEART® Software

1. Launch suiteDXT via the desktop shortcut.

FIGURE 1. Launch Application



2. Select a study from the study list and do one of the following:
   - Select suiteHEART®.
   - Double click on the study.
3. Select a group of studies and select suiteHEART®.

   Use File > Switch Study to view other studies.

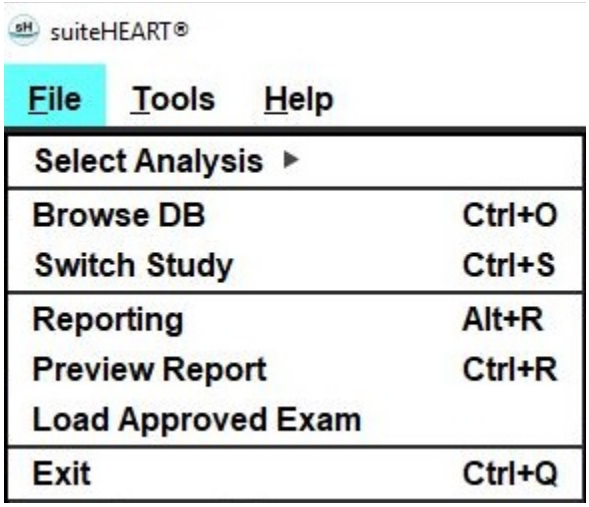
NOTE: The screen resolution must be set to 1920x1080 or higher (Landscape); 2160x3840 or higher (Portrait), otherwise the software will not launch.

WARNING: Using images with pixel intensity filters applied for analysis may cause inaccurate results.

Exiting suiteHEART® Software

To exit the application select **File > Exit** or click on the X in the upper right corner of the interface.

FIGURE 2. Close suiteHEART® Software



An exam is considered “consumed” or “counted” against the Per-Case Pack limit when any of the following actions are performed:

a.) Starting of any analysis mode by placing any ROI on an image.
b.) Creating a custom series.
c.) Report sign off.
d.) Export Cine DICOM.
e.) Export Report.
f.) DICOM series creation.
g.) Preprocessed study.
h.) Virtual Fellow® preprocessing.
i.) Auto Compose series.

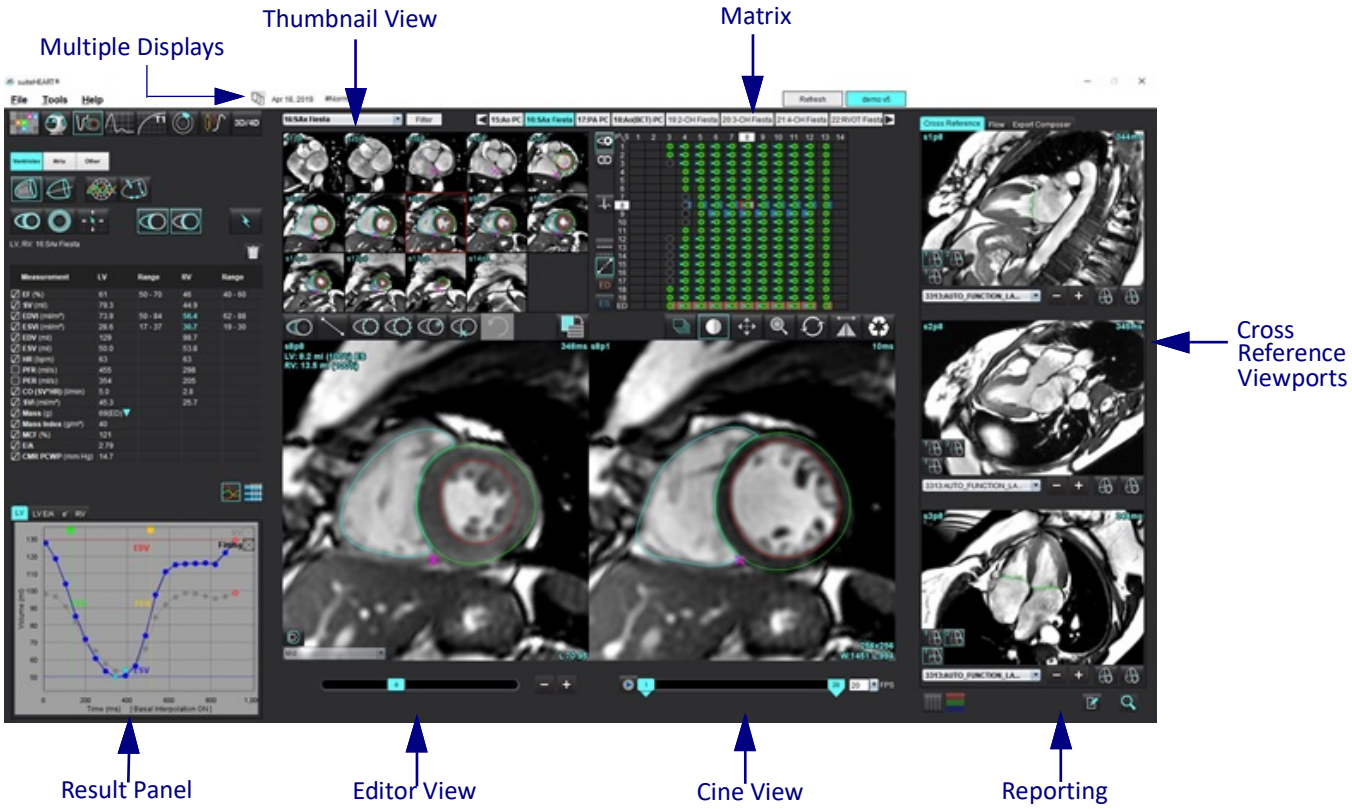
User Interface Overview

Overview

The suiteHEART® Software analysis modes interfaces are organized as follows:

- **Result Panel** - Access analysis tools for each analysis mode and the result table
- **Thumbnail View** - View all slice locations
- **Editor View** - Edit and review segmentation
- **Matrix** - Available for Function and Myocardial Perfusion analysis
- **Cine View** - View the image as a cine
- **Cross Reference** - 3 viewports
- **Reporting** (Alt + R): Access reporting

FIGURE 1. Analysis Mode Interface (Function Analysis Mode is shown.)



Splits the interface into multiple displays.

Restores the single display.

Analysis/Viewer Modes

Table 1: Analysis Modes

						
Function Analysis	Flow Analysis	Myocardial Evaluation	T1 Mapping	T2 Mapping	Myocardial Perfusion Analysis	T2* Analysis

NOTE: Patent Foramen Ovale (PFO) Analysis can be selected from the file pull-down menu or by using Ctrl 5 on the keyboard.

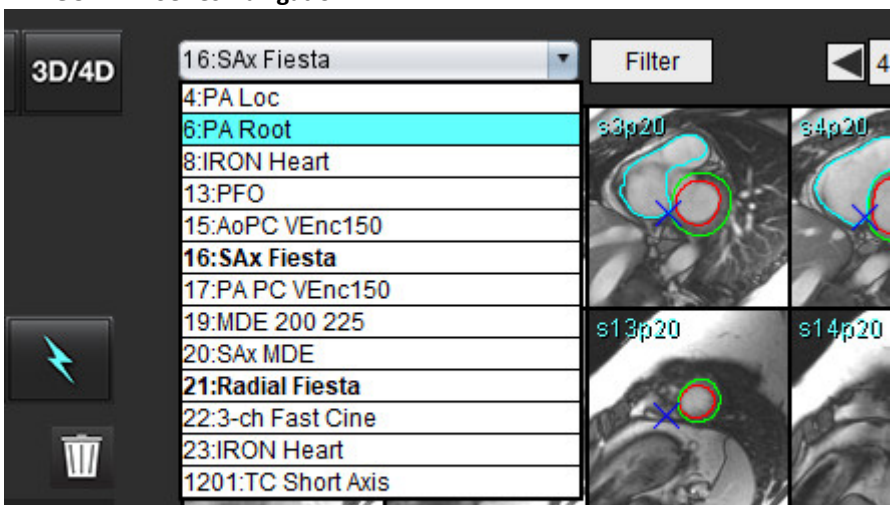
Table 2: Viewer Modes

		
Viewer	Virtual Fellow®	3D/4D Flow Viewer

Series Navigation

To view images or change series within the selected study use the left and right arrow buttons at the top of the Image View. The series file pull-down menu, located to the left of the Filter button, can also be used to select the series. Series which have analysis or regions of interest present will be identified in bold text, as shown in Figure 2.

FIGURE 2. Series Navigation



Editor Window and Mode View

Performing a right mouse click on an image in the Image View will activate image manipulation tools.

Table 3: Image Manipulation Tools

	Window/Level Pan Zoom Rotate Flip Send to Report Export Composer Scan Parameters Reset

File Menu Options

Select Analysis – Selects the analysis mode (Function, Flow, Myocardial Evaluation, Myocardial Perfusion, PFO, T2*, T1 Mapping, T2 Mapping, 3D/4D and DENSE)
BrowseDB – Opens local database
Switch Study – Lists available studies for quick access
Reporting – Opens reporting interface
Preview Report – View the report
Load Approved Exam – Restores a previously opened report
Exit – Closes the application while saving current analysis results to a secondary capture (SCPT) series

Tools Menu Options

Preferences >

Edit – User Level - Grayed out options can only be changed by Admin
Edit System – Admin only
Import – Admin only
Copy – Copy preferences from other users
Export – Exports all user preferences and templates

For the above options, refer to Appendix A: User Level Preferences on page 204.

Export >

Report to Excel – Generates Excel spreadsheet with analysis results
Report to XML – Exports report as an XML file
Data to Matlab – Exports a Mat-file in binary form (Requires a research agreement)
Strain Data to Matlab – Exports a Mat-file in binary form (Strain Analysis requires a research agreement)
Segmentation to NRRD – Stores the segmentation mask for further analysis in 3D Slicer or other in-house tools
Isosurface to STL - Encodes the surface mesh of the vessel for 3D printing or CAD

NOTE: Exporting the report as DICOM or exporting results to a third party reporting system can only be done from the Preview Report (Ctrl + R) screen.

Report Database – Opens database search interface
Toggle Annotation – Toggles the display of the ROI annotation
Toggle Line Thickness – Toggles line thickness of annotations.
Toggle Cross Reference Lines – Toggles cross reference lines on images.
Toggle FOV – Toggles the field of view
Invert Window/Level – Inverts the window/level view

Help Menu Options

Instructions for Use – suiteHEART® Software Instructions for Use
Quick Keys – Keyboard functions
DICOM Conformance Statement – suiteHEART® Software DICOM Conformance Statement
About suiteHEART® – Version information about the application
Regulatory Information – Regulatory compliance information

Editor View Controls

The Phase Slider Bar 

controls the cine phase selection.

Scroll through the phases by simultaneously pressing the Ctrl key and the middle mouse button.

The Image Step Icons 

allow for slice-to-slice navigation when the thumbnail view is in slice or phases. Slice navigation can also be performed using the middle mouse wheel.

On your keyboard, the Left and Right Arrow Keys control navigation between slices and the Up and Down Arrow Keys control navigation between phases, depending on your preference setting.

NOTE: The x (slice) and y (phase) axis can be swapped. Refer to Function Tab on page 44. If swapped the application should be restarted.

Cine View Controls

- Cine Control Bar: Defines the start and end frame of the cine movie.

- Frames Per Second (FPS): Click on the arrow or enter a value in the text box to change the cine speed

 - Play Icon: Located next to the cine control bar

 - Pause Icon: Located next to the cine control bar

Cross Reference Viewports

The three cross reference viewports display the long axis view of an image when the short axis view is currently displayed in the image editor viewport. The long axis view is an orthogonal slice within an angle of the displayed image in the editor viewport. A drop-down menu of all the orthogonal slices available is provided, along with a button to toggle the display of the cross reference slice indicators. Use the minus and plus, or the middle mouse wheel, to navigate between slice locations.

FIGURE 3. Series Drop-down Selector

Image Manipulation Tools

Table 4: Tool Descriptions

	Slice/Phase Review Toggle
	Window/Level – Select and use middle mouse button to make adjustment
	Color Scale - Select and use middle mouse button to make adjustment
	Pan – Select and use middle mouse button to make adjustment
	Zoom – Select and use middle mouse button to make adjustment
	Rotate – Select and use middle mouse button to make adjustment
	Flip Horizontal – Flips the image horizontally
	Scope All – Applies image manipulation to all slices
	Scope Current to End – Applies image manipulations from the current slice to the end slice
	Scope Current Only – Applies image manipulation to the current slice only
	Viewport Layout - Change viewer layout

Table 4: Tool Descriptions

	Compare Mode - Change to compare mode
	Review Mode - Change to review mode
	Show Cross Reference lines - Toggles cross reference lines on/off
	Colormap Overlay - Toggles slice classification colormap on/off
	Reset – Resets the W/L, Pan, Zoom and Rotate back to default, based on the scope setting
	Region of Interest – Provides area and circumference measurements
	Crosshair – Provides sampling of single pixel data
	Linear – Provides measurement of a straight line distance
	Label – Provides the addition of user annotation in the Editor window
	Angle – Provides angle measurement
	Find Feature – Cross reference tool that automatically identifies and displays images that contain the same location
	Undo – Undo functionality available for ROI editing
	Refresh – Click button to update the Image View with newly networked images or to update the analysis modes
	Filter – Sorts series by pulse sequence type according to analysis mode. Can be deselected by selecting ALL. Filters can be set under Preferences. The filter button will be green if a filter is in use.

Quick Keys

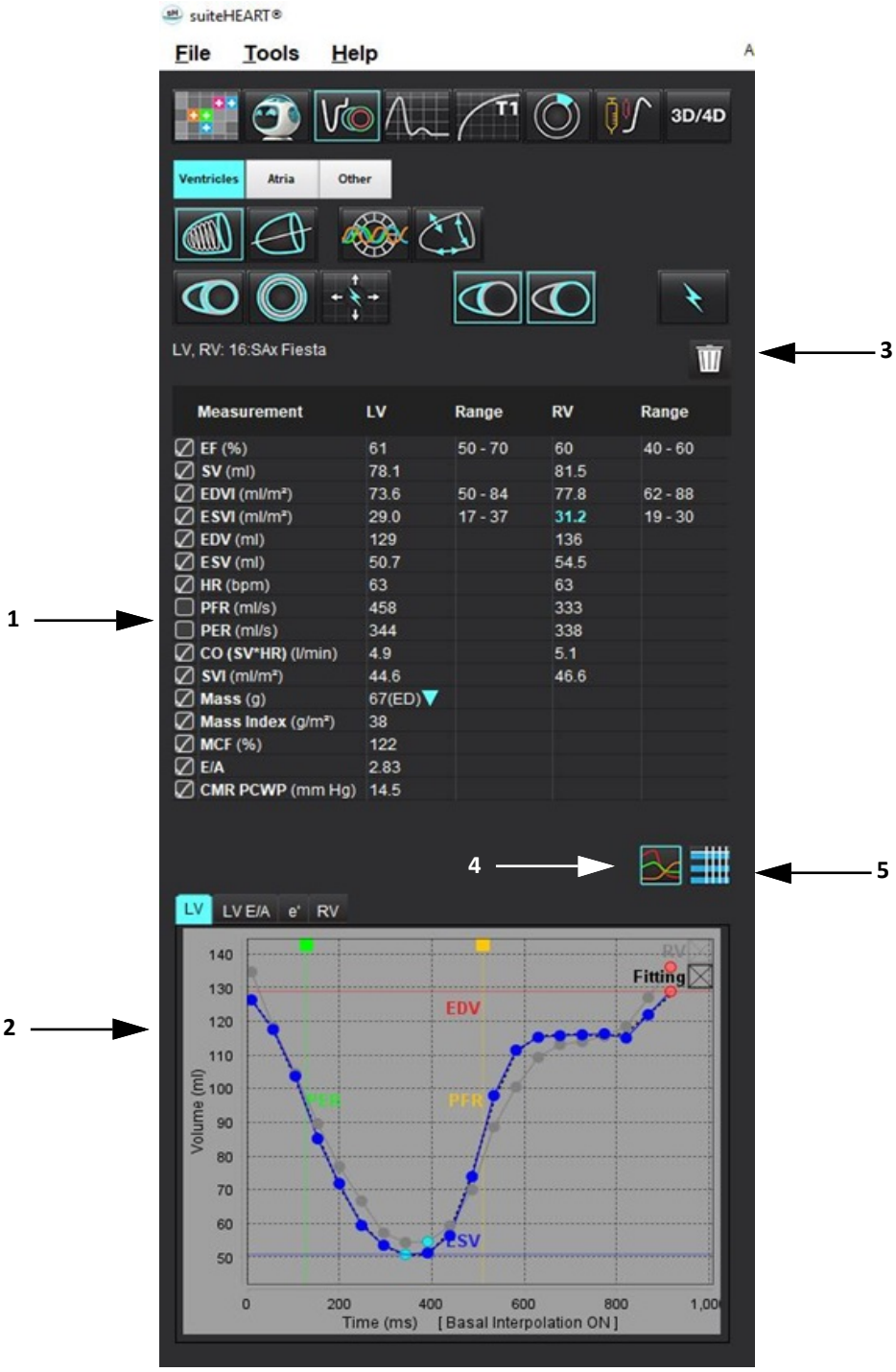
Action	Quick Key	Action	Quick Key
Image Zoom	Ctrl + Middle Mouse Button	**Generic Annotations**	
Rotate Image	Ctrl+Shift+Middle Mouse Button	Linear	Alt+1
Image Pan	Shift + Middle Mouse Button	Crosshair	Alt+2
Window/Level	Alt + Middle Mouse Button	Region of Interest	Alt+3
Cine Play/Pause	Spacebar	Label	Alt+4
Phase Scroll	Ctrl + Middle Mouse Wheel	Angle	Alt+5
Slice Scroll	Middle Mouse Wheel	**ROI Editing Tools**	
Reporting	Alt+R	Copy ROI	Ctrl+C
Reselect all images for viewing	Ctrl+A	Paste ROI	Ctrl+V
Report Database	Ctrl+D	Smooth ROI	Ctrl+S
Edit Preferences	Ctrl+E	Shift ROI horizontally	A & D Keys
Toggle Field of View (FOV)	Ctrl+F	Shift ROI vertically	W & S Keys
Invert Window/Level	Ctrl+I	Generate a point spline corner	Alt + Left Mouse Button
Thick Line Annotation	Ctrl+L	Delete a point (point spline)	DELETE + Cursor on a point
Open Browse DB	Ctrl+O	Threshold Tool	Alt + Left Mouse Button Drag
Quit Application or Exit	Ctrl+Q	**3D/4D Editing Tools**	
Preview Report	Ctrl+R	3D Rotate	Ctrl + Alt + Middle Mouse Button
Switch Study	Ctrl+S	Image Zoom	Ctrl + Middle Mouse Button
Toggle Annotation	Ctrl+T	Window/Level	Alt + Middle Mouse Button
Toggle Cross-Reference Lines	Ctrl+X	Move Crosshair Cursor	Shift
Undo	Ctrl+Z	Brush	Alt+A
DENSE	Ctrl+0	Erase	Alt+E
Function	Ctrl+1	Trace	Alt+T
Flow	Ctrl+2	Cut	Alt+C
Myocardial Evaluation	Ctrl+3	Smooth	Alt+S
Myocardial Perfusion	Ctrl+4	Brush Size	Alt + Mouse Wheel
PFO	Ctrl+5	Quit Editing	Alt+Q
T2*	Ctrl+6	Toggle Display Mode	Alt+D
T1 Mapping	Ctrl+7		
T2 Mapping	Ctrl+8		
3D/4D Flow Viewer	Ctrl+9		
Navigate between Slices*	Left & Right Arrow Keys		
Navigate between Phases*	Up & Down Arrow Keys		
Navigate Virtual Fellow® Slice	Z & A key for next & previous slice		

*The active keys will depend on the preference setting.

Result Panel

The Result Panel is available for each analysis mode.

FIGURE 4. Result Panel



1. Result table, 2. Graph display 3. Delete, 4. Graphs, 5. Tables

Result Table

The measurement results can be reordered and configured in preferences (refer to Print Tab on page 42). The measurement table can be reordered by selecting a row and dragging to a new position. The order of the table will always default to the order in preference for all new studies. Select or deselect a measurement from inclusion on the report by clicking the box next to the measurement.

FIGURE 5. Result Table

Measurement	LV	Range	RV	Range
EF (%)	61	50 - 70	60	40 - 60
SV (ml)	78.1		81.5	
EDVI (ml/m²)	73.6	50 - 84	77.8	62 - 88
ESVI (ml/m²)	29.0	17 - 37	31.2	19 - 30
EDV (ml)	129		136	
ESV (ml)	50.7		54.5	
HR (bpm)	63		63	
PFR (ml/s)	458		333	
PER (ml/s)	344		338	
CO (SV*HR) (l/min)	4.9		5.1	
SVI (ml/m²)	44.6		46.6	
Mass (g)	67(ED)			
Mass Index (g/m²)	38			
MCF (%)	122			
E/A	2.83			
CMR PCWP (mm Hg)	14.5			

NOTE: To edit or enter the heartrate, click directly on the table.

Graph and Table Results

Results can be displayed as a graph or in tabular format by clicking the desired icon located in the lower right hand corner of the Analysis View.

FIGURE 6. Graph (left) and Table (right)


Table 5: Analysis Tools

 Left Ventricular Endocardial ROI	 Long Axis LV Endocardial ROI
 Left Ventricular Epicardial ROI	 Long Axis LV Epicardial ROI
 Right Ventricular Endocardial ROI	 Left Ventricular Septal ROI

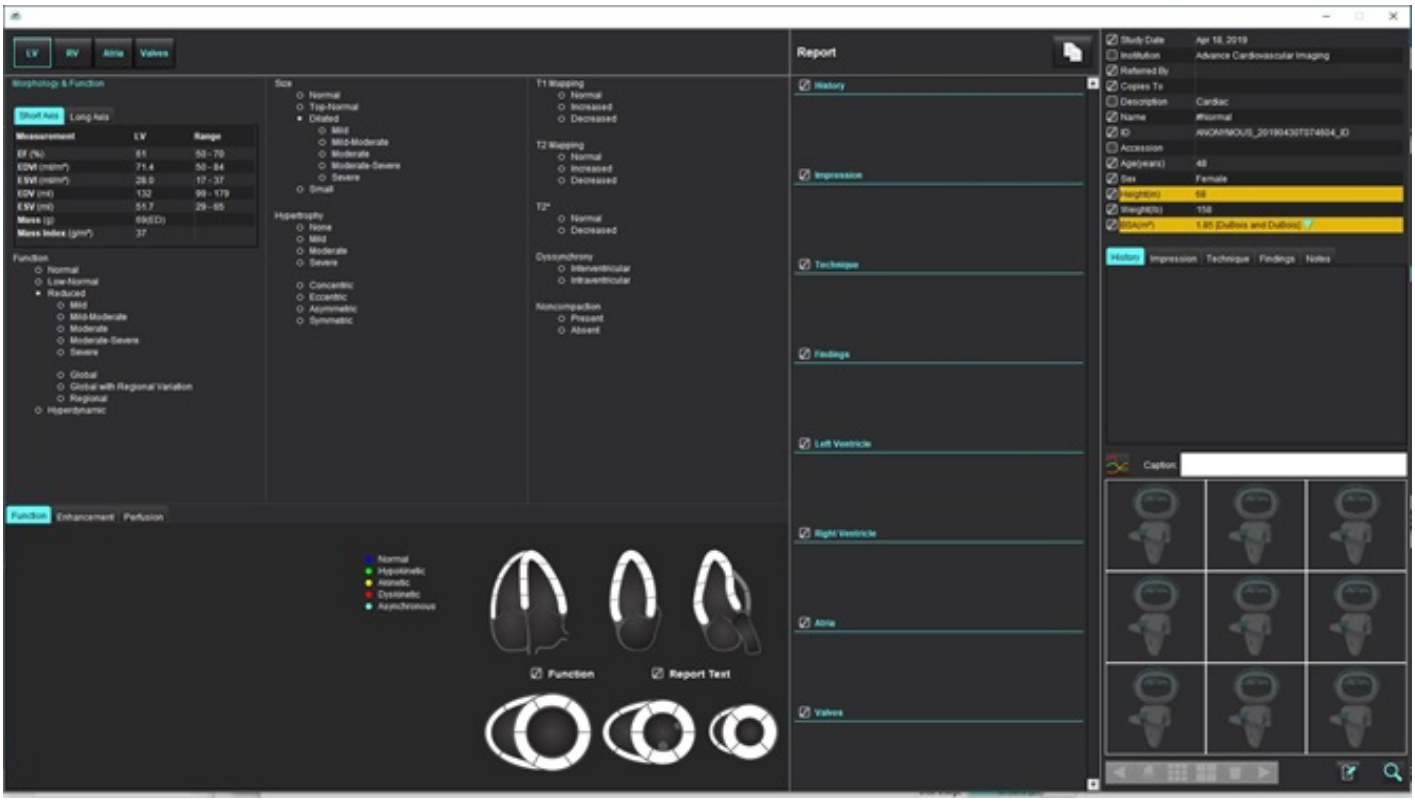
Table 5: Analysis Tools

 Right Ventricular Epicardial ROI	 Left Ventricular Local ROI
 Mitral Valve Annulus	 Left Ventricular Blood Pool ROI
 Tricuspid Valve Annulus	
 Right Ventricular Insertion Point	
 Left Ventricular Papillary Muscle ROI	
 Right Ventricular Papillary Muscle ROI	
 Left Atrial ROI	
 Right Atrial ROI	
 Long Axis RV Endocardial ROI	
 Long Axis RV Epicardial ROI	

Reporting

Simultaneously press Alt + R to open the reporting interface. Refer to Reporting on page 188 for more information.

FIGURE 7. Reporting Interface



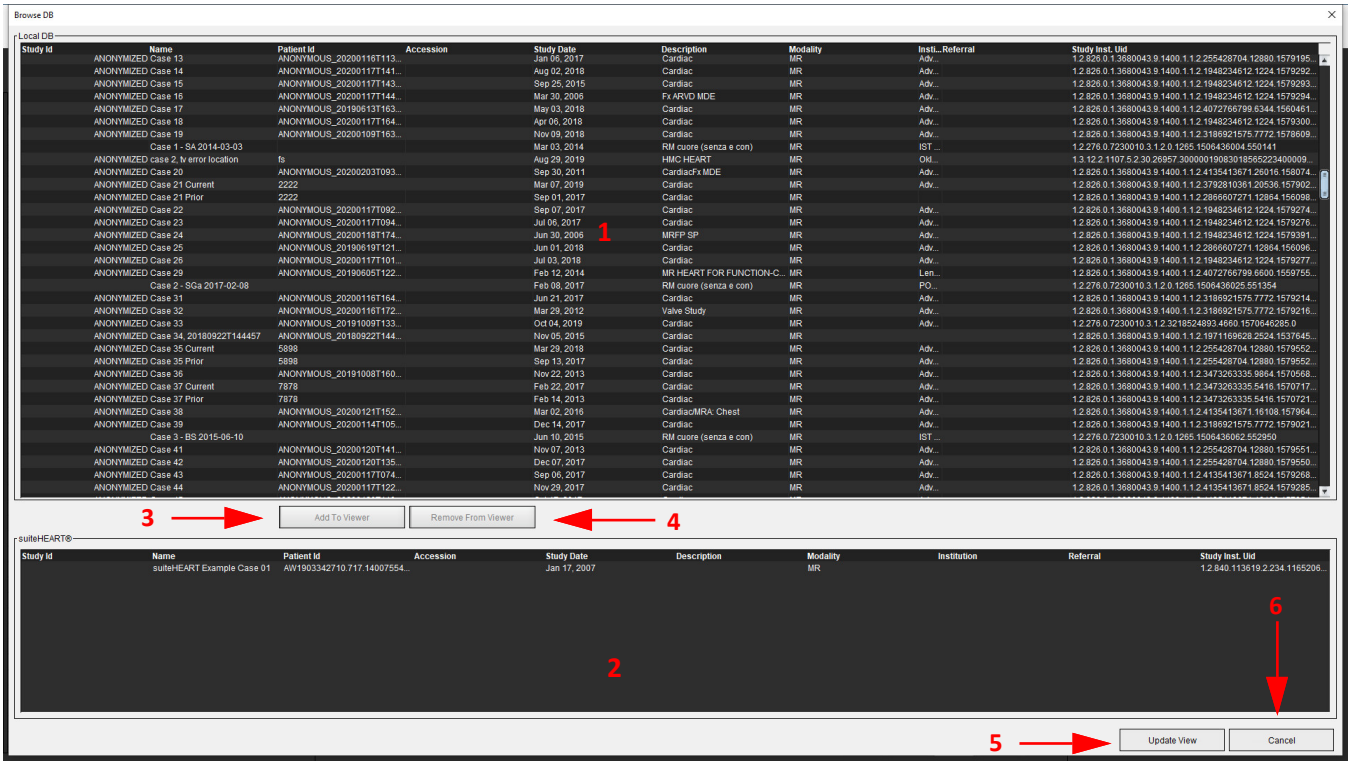
 - Reporting: Used to open the Reporting interface or Analysis Mode

 - Preview Report: Used for previewing a report

Browse DB

The Browse DB window provides a view of the current studies in the local database. There are controls that allow you to choose which studies to view or add to the switch study listing.

FIGURE 8. Browse DB



1. Local database listing, 2. suiteHEART® Software database viewer, 3. Add to Viewer button, 4. Remove from Viewer, 5. Update View, 6. Cancel

Features of the Browse DB

The Browse DB always defaults to the local database.

1. Local database listing – displays the exams that are stored in the local database.
2. suiteHEART® Software database viewer – displays exams that are in the current suiteHEART® Software database.
3. Add to Viewer – Adds the selected exam from local database (shown in the top portion of the window) to the suiteHEART® Software database viewing area.
4. Remove from Viewer – Removes the exam from suiteHEART® Software database viewing area.
5. Update View – Closes the Browse Database window and bring the exams in the viewable listing area to the application viewer. Used to populate the switch studies window.
6. Cancel – Closes Browse Database window with no changes to the list.

Browse DB Procedure

Studies can be viewed by selecting them from the local database, adding them to the suiteHEART® Software database Viewer list and clicking **Update View**.

Add Studies to the suiteHEART® Software Switch Study List

1. Click **File > Browse DB**.
2. Locate the study in the database viewer and click on the exam to highlight it.
3. Click **Add to Viewer**.
4. Click **Update View**.
5. The study now appears in the suiteHEART® Software Switch Study List.

Remove Exams from the suiteHEART® Software Switch Study List

1. Click **File > Browse DB**.
2. Locate the study and then click **Remove from Viewer**.
3. Click **Update Viewer**.

CAUTION: Do not delete the study currently opened in the suiteHEART® Software.

Studies must be loaded into suiteHEART® Software before they can be shown in the Viewer. See Browse DB Procedure on page 20 to learn how to populate the Switch Study List.

Switch Studies within suiteHEART® Software

1. Click **File > Switch Study**.

   The Available Studies window is displayed with a list of all the exams that were previously loaded by the Browse DB procedure.
2. Select the study.

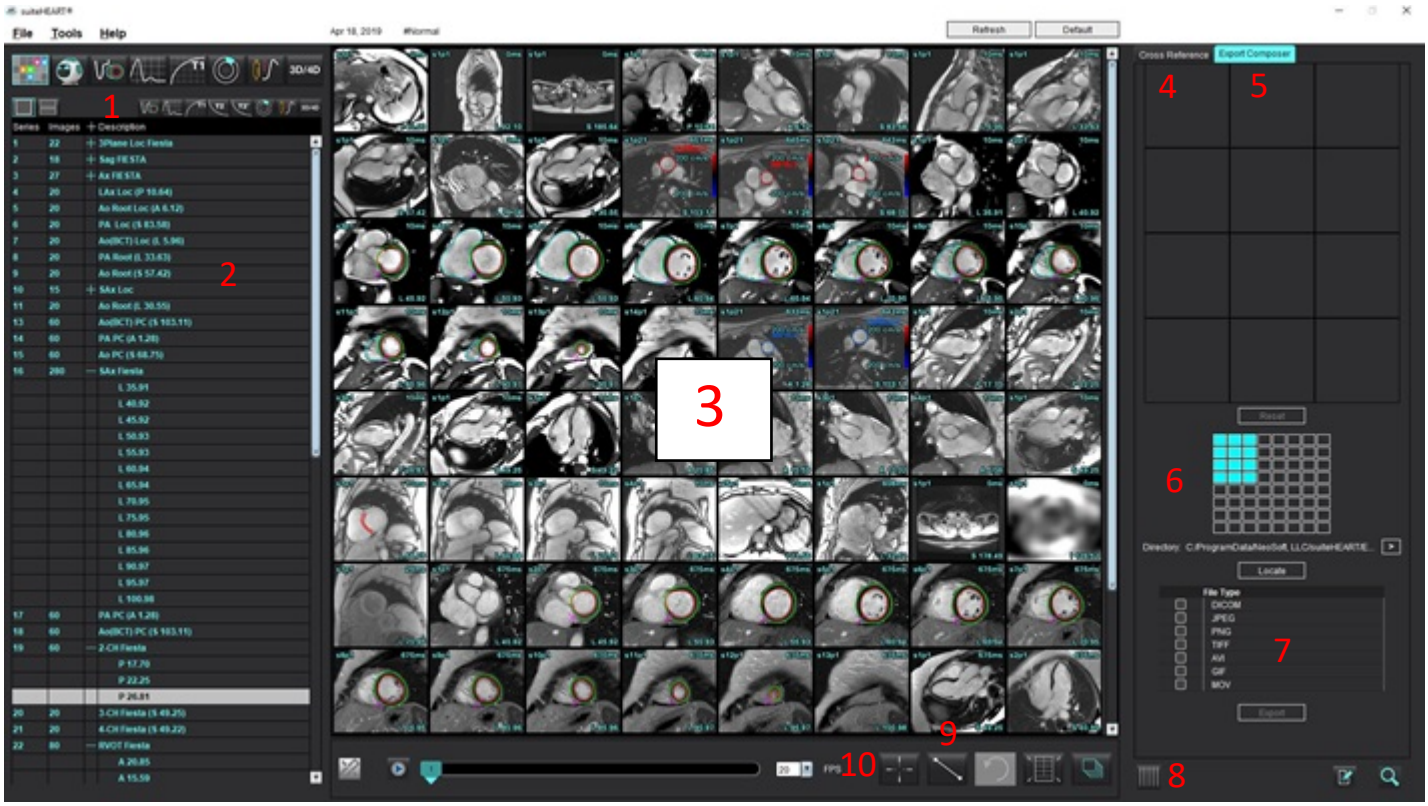
   If you choose not to switch studies after opening the Switch Studies window, click anywhere outside of the window to return to the application.

Image Management Tools

Viewer

The viewer allows for the quick review of the study with cross referencing. The viewer interface displays the listing of the series that have been acquired for the selected study. Each series is displayed in a viewport or in compare mode. New series types can be created for analysis and review within the viewer interface.

FIGURE 1. Viewer



1. Image Filter, 2. Series/Image listing, 3. Image viewports, 4. Cross Reference, 5. Export Composer, 6. Export Matrix, 7. Save series, 8. Cross-Reference, 9. Measurement Tools, 10. Find Feature

Image/Series Navigation

Click on a series and use Page Up or Page Down on the keyboard to navigate through slice locations within the series.

Navigate to the next series by pressing the right arrow key on the keyboard and the left arrow for the previous series.

When navigating to a multi-phase series they are displayed in an auto layout, whereas a single-phase series will be displayed in a 1x1 layout.

Viewport mouse scroll wheel navigation is supported. Double-clicking directly on a viewport in a 1x1 viewport. Double-clicking again will return the viewport to all images.

Find Feature*

1. Select  to use the cross reference tool.

   The purple cursor is the primary cursor that can be positioned on the image.

2. Press the Ctrl key and select the cross reference tool to activate the primary cursor. All close slice locations are automatically displayed.

   The main view will then be populated with only those slices where the secondary green cursor was calculated as close to the primary purple cursor.

NOTE: The green secondary cross annotations appear on viewports containing **non-parallel** images and at points that are calculated to be within 10mm 3D distance of the primary cursor.

NOTE: The green secondary cross annotations appear on viewports containing **parallel** images and at points that are calculated to be within 5mm 3D distance of the primary purple cursor.

*US Provisional Patent Application No. 62/923,061
Title: Method and System for Identifying and Displaying Medical Images
Inventor(s): Wolff et al.

Series Compare Mode

To compare two different series with the study select  . To return to full mode, click  .

Expand/Collapse Series

To expand all series click (+); to collapse click (-).

FIGURE 2. Expand Series

Quick Key

Function	Action
Reselect all images for viewing	Ctrl+A

Viewer Functionality

Create a New Series

The viewer allows for the creation of series types that can be used for Function, Myocardial Evaluation, Myocardial Perfusion, T2*, T1 Mapping, T2 Mapping and for review only (custom). Series that are created will be added to the series listing for that study and are available for viewing and analysis within the suiteHEART® Software application.

NOTE: For a series to be valid for analysis, each slice location must have the same number of phases, same acquisition parameters and scan plane prescription.

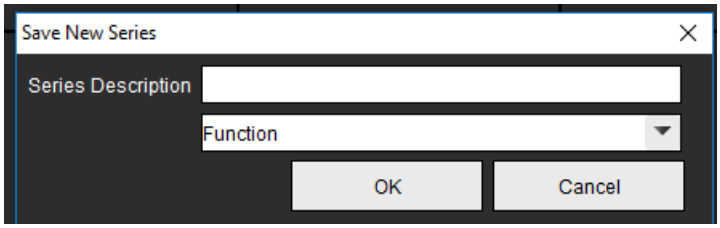
WARNING: The user is responsible for creating new series for analysis that contain the correct images for analysis. Incorrectly formed series may be analyzed but could produce inaccurate results. The user should be properly trained in cardiac analysis and must be aware of the slice locations copied into the new series. Do not delete original images that have been used for DICOM import.

1. Select the desired series or slice locations from the series listing.
2. Select a group of series or slice locations by performing a Shift click or a Ctrl click for adding a single series or slice location.
3. Clicking and dragging allows for the ordering of the images within the viewports.
4. To delete an image from a viewport, select the viewport and press the Delete key on the keyboard.
5. Select  from the Save Series pane Figure 3.

FIGURE 3. Save Series Pane

6. Type in a series name for the application Series description.
7. Select the appropriate series application type from the pull-down menu (Figure 4). If **Custom** is selected, images with different scan planes and sequence types can be saved as a series.

FIGURE 4. Save New Series



Viewing Protocols

Is only available if requested from NeoSoft.

Reporting

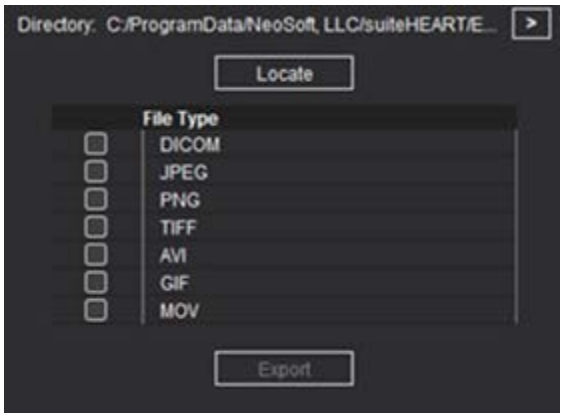
To access the Reporting or return to viewer functionality, click  .

Export Composer

The Export Composer tab allows for the exporting of cine/image file types for images, graphs and polar plots. DICOM files can also be created which can be archived and viewed on PACS.

1. Select the **Export Composer** tab.
2. Select the number viewports in the matrix.
3. Select the file type to be exported. (Figure 5)

FIGURE 5. Export Composer Selections



NOTE: Selecting “DICOM” creates a secondary capture file which is located under the series listing for that study.

4. To save movies or file formats, click > and select the directory. Directory: C:/ProgramData/NeoSoft/suiteHEART >

NOTE: When exporting images to AVI or MOV files, suiteHEART® Software sets the maximum frames-per-second rate to 20 frames-per-second regardless of the settings used for viewing within the application.

IMPORTANT: When exporting cine images, the number of phases must match.

5. To locate the file, select Locate.
6. Select the desired series or slice locations from the series listing.
7. To move a single image to the matrix, from the image viewport left mouse click directly on the image viewport and drag to the matrix or right click and select .
8. To move a group of series or slice locations to the matrix perform a Shift click directly on the image viewport then click and drag the group of images to the matrix or right click and select .
9. To export graphs, polar plots from other analysis modes perform a right mouse click and select .
10. To remove an image, graph or polar plot from the matrix, click on the image viewport and press the Delete key on the keyboard or click **Reset**.
11. To export the images, graphs, or polar plots as they appear in the matrix click Export.

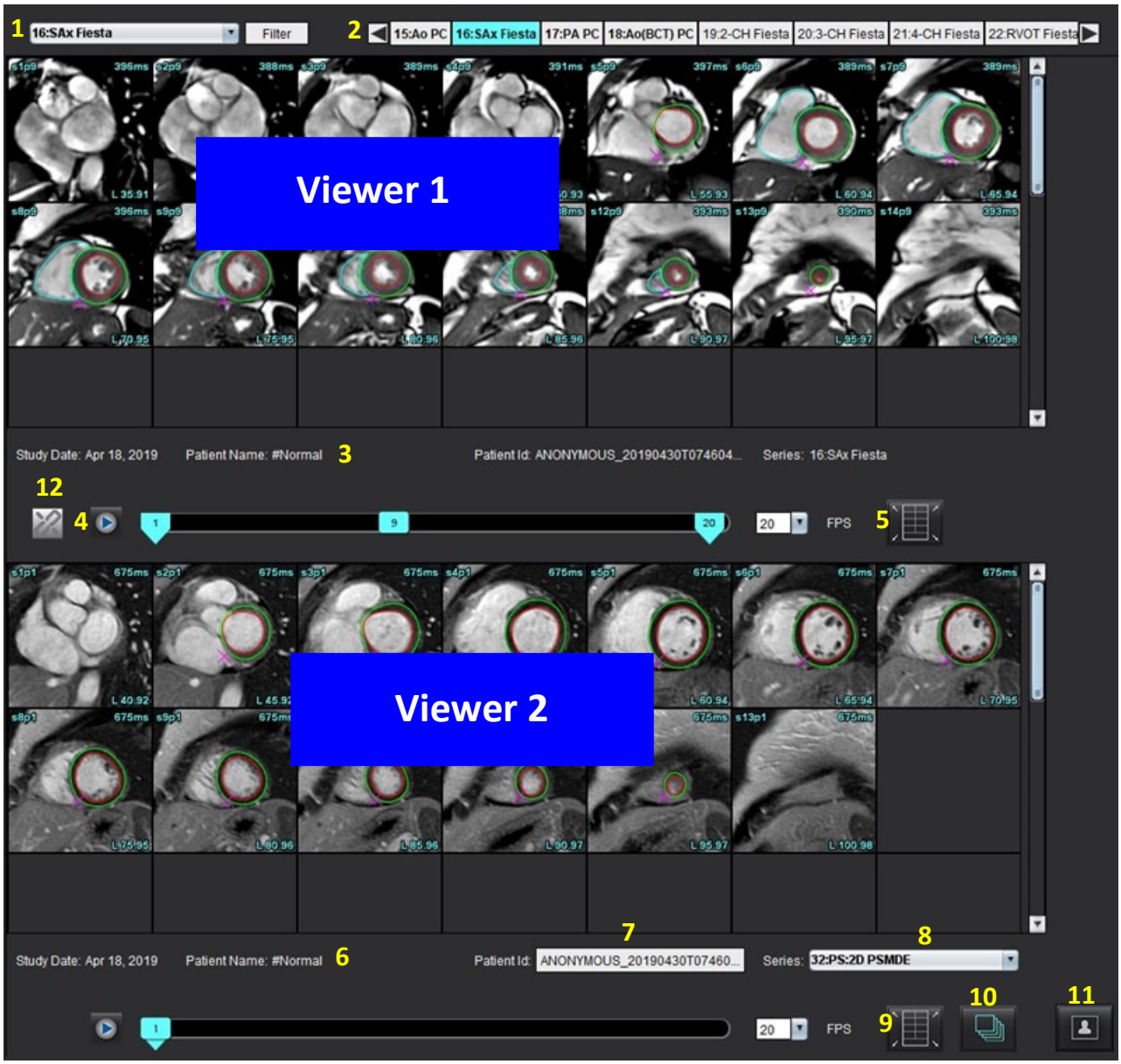
Compare Mode

Compare mode gives you the ability to review images/series from a current exam, or from a prior exam, simultaneously within the same interface.

NOTE: Images sent to a report from the prior exam in compare mode will be in bitmap format. No image manipulations will be possible on these images.

WARNING: Prior to the review or comparison of exams or series within an exam, visually confirm all exam patient indicator information for both viewers.

FIGURE 6. Compare Mode Viewer



Viewer	Callout	Description
Viewer 1	1	Series pull-down
	2	Series selector
	3	Currently viewed patient exam indicator line
	4	Image controls
	5	Viewport layout selections
Viewer 2	6	Currently viewed patient exam indicator line
	7	Exam selector
	8	Series selector
	9	Viewport layout selections
Both Viewers	10	Change scope settings
	11	Toggle for Review Mode
	12	Toggle synchronized cine

Sample Workflow

1. Double click on the editor window on any analysis mode.
2. Select  to split the interface into two viewers, as shown in Figure 6.
3. Change the series in Viewer 1 by using the series selection pull-down menu or right/ left arrows.
   - This upper viewer always displays the current study that has been previously launched.
4. In Viewer 2, use the series pull-down to choose a different series, within the same exam, to compare with that which is shown in Viewer 1.
   - When a viewport is selected in any viewer and if the slice is parallel such as a short axis series, the corresponding slice, based on slice location, will be highlighted.

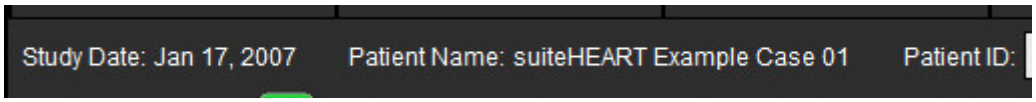
FIGURE 7. Series Pull-down, Viewer 2

5. Use the exam selector, to compare a different exam in Viewer 2 to the current exam shown in Viewer 1.

FIGURE 8. Exam Selector, Viewer 2

6. Confirm proper exam selection by checking the exam indicator information for both viewers.

FIGURE 9. Exam Indicator Information



7. Performing a right mouse click on either viewer will open the image manipulation tools.
   - The scope selection applies to both viewers.

NOTE: Performing image locate from the Images tab will not be valid if the image is from a different study.

NOTE: If a cine series is selected in both viewers and both series have the same number of phases, click the  to sync the cine views.

Defining Preferences

Refer to Appendix A: User Level Preferences on page 204**.**

Selecting **Tools** > **Preferences** from the menu bar on the suiteHEART® Software Interface displays four options:

- Edit
- Edit System (**Admin only**)
- Import (**Admin only**)
- Copy
- Export

IMPORTANT: It is advisable to set up user preferences prior to analyzing the first case to be reported. For changes in preferences to take effect, close the current exam and then close and re-launch suiteDXT.

NOTE: In single user mode, grayed out options can only be changed by the Admin.

Setting Preferences

General Tab - Preferences can be customized for the following features:

- Report
- Viewer
- Virtual Fellow®
- Authorized Report Approvers
- General
- Myocardial Evaluation
- Idle Timer
- Flow
- Series Filter

Template Tab - Create templates for result parameters ranges use for reporting.

Macro Tab - Create predefined text for reporting sections for Impression, Techniques, History and Findings.

Print Tab - Order and selection of result parameters for the report.

Virtual Fellow® Tab - Select viewing preferences.

Function Tab - Select viewing and analysis preferences.

T1/T2/T2* Tab - Select viewing and analysis preferences.

Reporting Tab - Edit menu driven text selections and configure categorical ranges for auto prefill functionality.

Auto Compose Series - T1 and T2 mapping.

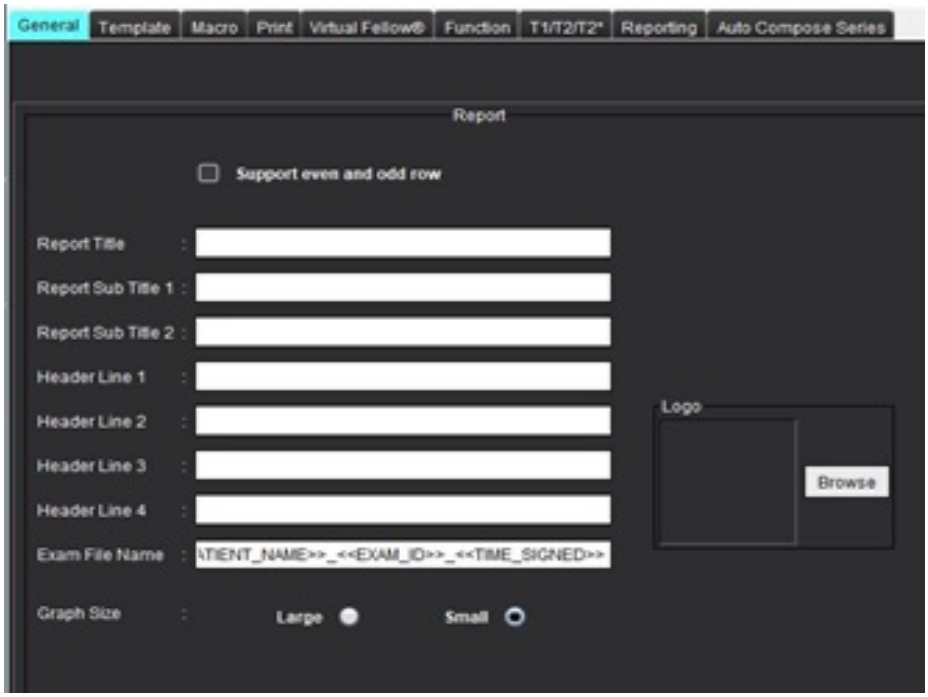
General Tab

Selecting Reset in the upper right corner of the tab will clear all user selections.

Report

Configure report header information.

FIGURE 1. Report Preferences



Selections for Report Preferences

Admin Required for these steps.

1. From the menu bar, select **Tools > Preferences > Edit System**.
2. Select the **General** tab.
3. Place the cursor in the desired field of the **Report** panel and enter information.

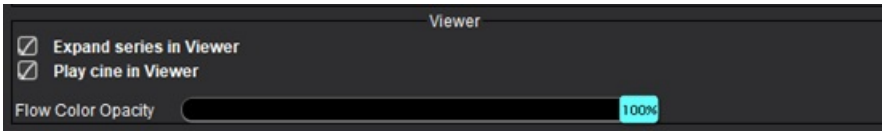
   The titles, headers, and logo will appear on a report with the specified paper size. To omit this information from the report deselect the “Use the field values below in Report” checkbox. This will take effect for all patient reports that are printed.

   Checking “support even and odd row” will highlight the result rows on the interface and on the report.
4. To insert a site logo into the report, prepare the file in a jpeg, png, or gif format and save to hard drive or CD-ROM. Select **Browse** under the Logo section and locate the file from the system browser window. Select the proper logo file and select **Open**.

   The logo should now appear on the report preferences panel.
5. Click on the **Exam File Name** to configure the export report file name.
6. Select **Save and Exit**.

   Select **Cancel** to exit without saving or accepting any changes.

Viewer



1. From the menu bar, select **Tools > Preferences > Edit**.
2. Select the **General** tab.
3. Check to **Expand series in Viewer**.
4. Check to **Play cine in Viewer** upon launch.
5. Use the slider bar to adjust the velocity color overlay on phase contrast images.

   To remove the color overlay set the opacity to 0%.

Virtual Fellow®

FIGURE 2. Virtual Fellow® Preferences

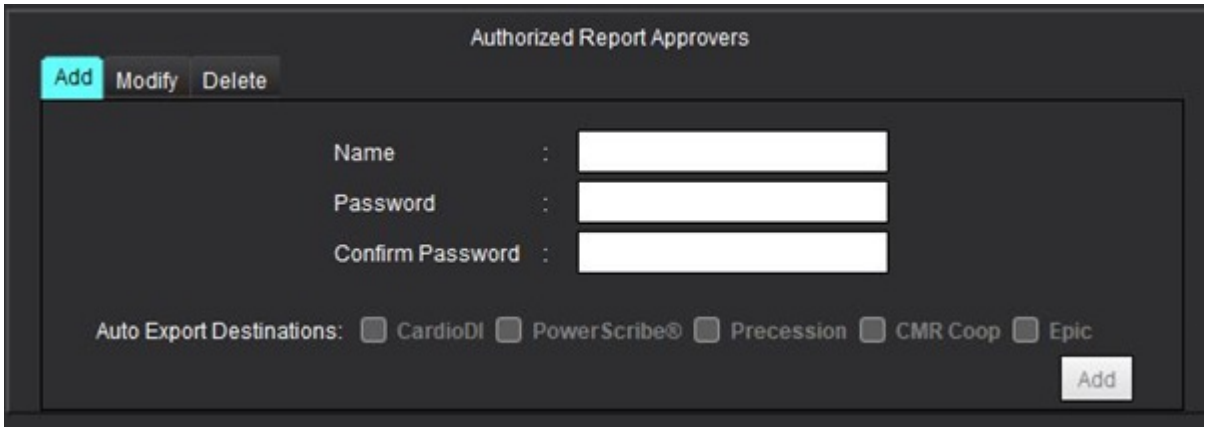
1. From the menu bar, select **Tools > Preferences > Edit**.
2. Select **General** tab.
3. Check **Open study in Virtual Fellow®** to directly open the study with the Virtual Fellow® application.
4. Select **Save and Exit**.

   Select **Cancel** to exit without saving or accepting any changes.

Authorized Report Approvers

The application has a report approval feature that locks the final report. Once approved, the report cannot be modified. Approvers can be added, modified and deleted.

FIGURE 3. Authorized Report Approvers



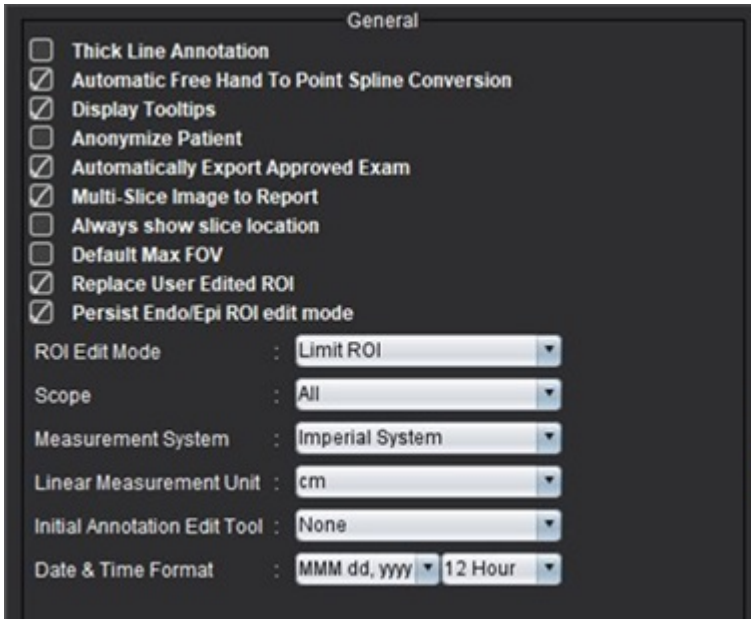
Manage Report Approvers

Admin Required to add or delete approvers.

1. From the menu bar, select **Tools > Preferences > Edit System**.
2. Select the **General** tab and place the cursor in the **Authorized Report Approvers** panel.
3. Select the **Add** tab to add a user name to the authorized approvers list.
    - Enter the user name.
    - Enter the password twice.
    - Select the appropriate Auto Export destinations.
        - The export will be performed automatically when “approved exam” is performed.
    - Select **Add**.
4. Select the **Modify** tab to change the password of a user on the authorized approvers list.
    - Select the user to modify.
    - Enter the old password.
    - Enter the new password twice.
    - Select **Apply**.
5. Select the **Delete** tab to delete a user from the authorized approvers list.
    - Select the user(s) to delete.
    - Select **Delete**.
6. Select **Save and Exit**.
    - Select **Cancel** to exit without saving or accepting any changes.

General

FIGURE 4. General Preferences



Selections for General Preferences

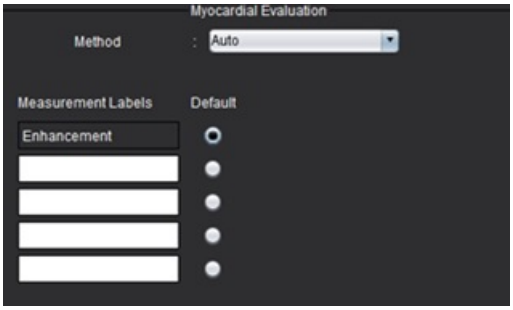
1. From the menu bar, select **Tools > Preferences > Edit**.
2. Select **General** tab.
3. Check the **Thick Line Annotation** check box to show annotation as thick lines.
4. Check **Automatic Free Hand to Point Spline Conversion** to automatically convert a free hand ROI to point spline.
5. Check the **Display Tooltips** to show interface tooltips.
6. Check the **Anonymize Patient** check box to hide the patient name and id from the report.

   All patients' names will be displayed as “anonymous” and the ID will be blank. These changes will apply to the report and Image View.
7. Check **Automatically Export Approved Exam** to export the report as a DICOM file upon approval. (**Admin Only**)
8. Check **Multi-Slice Image to Report** to add a right mouse click option to add a group of multi-frame short axis images.
9. Check **Always show slice location** to display the slice location when annotations are toggled off.
10. Check **Default Max FOV** for default FOV.
11. Check **Replace User Edited ROI**, will replace user edited ROIs if propagation is performed.
12. Check **Persist Endo/Epi ROI edit mode** for performing ROI editing.
13. Set the **ROI Edit Mode**.
14. Set the **Scope** selection for image manipulation from the file pull-down menu.
15. Set the **Measurement System**, either Imperial or Metric from the file pull-down menu.
16. Set the **Linear Measurement Unit** to either cm or mm.
17. Set the **Initial Annotation Editing Mod**e from the file pull-down menu.

    Selections include None, Nudge Tool or Pull Tool.
18. Set the **Date & Time Format** from the file pull-down menu.

Myocardial Evaluation

FIGURE 5. Myocardial Evaluation Preferences



Admin Required for these steps.

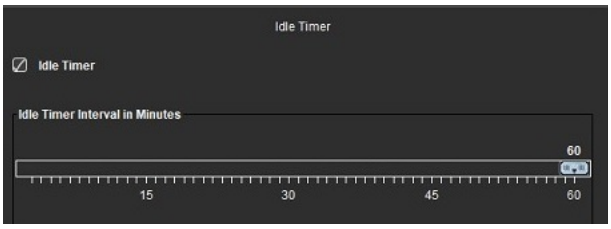
1. From the menu bar, select **Tools > Preferences > Edit System**.
2. Select **General tab**.
3. Select the analysis **Method: Auto, Full Width Half Max, Standard Deviation**.
4. To define measurement labels refer to Define Result Measurement Labels on page 124.
5. Select **Save and Exit**.

   Select **Cancel** to exit without saving or accepting any changes.

Idle Timer

The Idle Timer panel sets the time interval in minutes for the application to close after a set period of inactivity.

FIGURE 6. Idle Timer Settings



Selections for Idle Timer

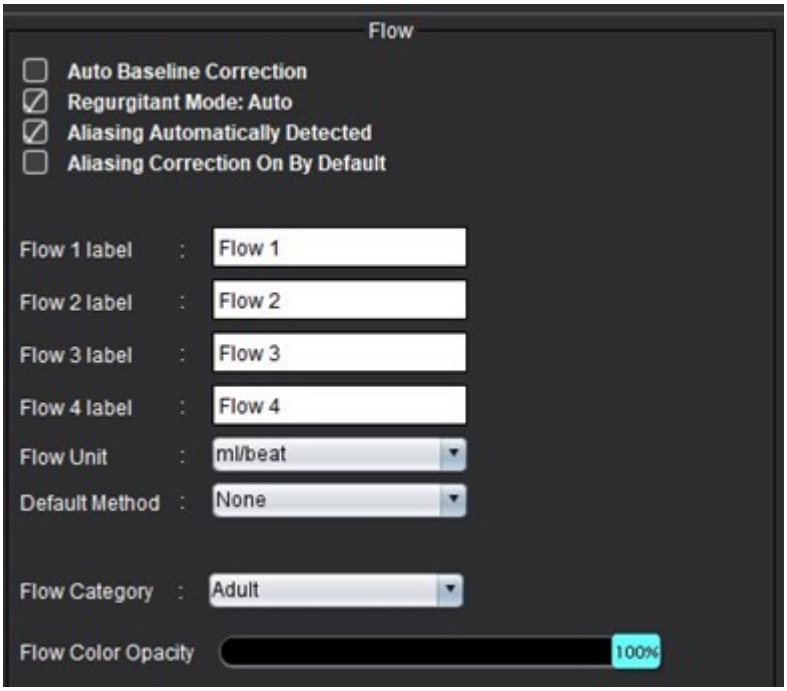
Admin Required for these steps.

1. From the menu bar, select **Tools > Preferences > Edit System**.
2. Select the **General** tab and place the cursor in the **Idle Timer** panel.
3. Select the Idle Timer check box to enable the idle timer feature.
4. Drag the idle timer interval marker to the desired time in minutes.
5. Select **Save and Exit** to store your selections.

   Select **Cancel** to exit without saving or accepting any changes.

Flow

FIGURE 7. Flow Preferences



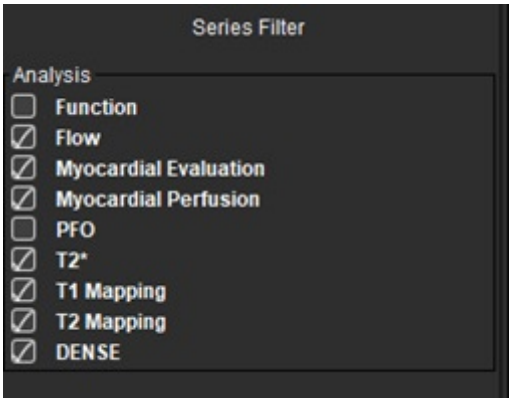
Selections for Flow Preferences

1. From the menu bar, select **Tools > Preferences > Edit**.
2. Select **General** tab.
3. Check the **Auto Baseline Correction** check box to automatically perform auto phase error correction for 2D and 4D phase contrast. (**Admin Only**)
4. Check **Regurgitant Mode: Auto** to automatically calculate the net negative flow (below x axis). (**Admin Only**)
5. Check **Aliasing Correction on By Default** to auto apply correction. (**Admin Only**)
6. Define category labels for **Flow 1**, **Flow 2**, **Flow 3** or **Flow 4** by typing in a new label.
   These labels will appear as tool tips on the flow interface.
7. Select the proper **Flow Unit** of either ml/beat or l/min or none from the file pull-down. (**Admin Only**)
8. Select the **Default Method** for persistence of the calculation method for the Integrated Flow panel. (**Admin Only**)
9. Use the slider bar to adjust the **Flow Color Opacity**.
   To remove the color overlay set the opacity to 0%.
10. Select **Save and Exit**.
    Select **Cancel** to exit without saving or accepting any changes.

Series Filter

Based on analysis modes types, a series filter can be applied to expedite selection of the appropriate series for analysis. The filter preferences can also be selected during analysis by clicking the filter button on the main panel, above the thumbnail view.

FIGURE 8. Filter Preferences



NOTE: If a series filter has been applied and the required series is not present, a message will appear: “There are no series associated with the selected analysis type.” Clicking OK will disable the filter and display all of the series in the study.

Setting Filter Preferences

1. From the menu bar, select **Tools** > **Preferences** > **Edit.**
2. Select **General** tab.
3. Click the appropriate on/off selection for each analysis type.
4. Select **Save and Exit**.
    - Select **Cancel** to exit without saving or accepting any changes.

Template Tab

For additional functionality available to Admin, refer to Appendix A: User Level Preferences on page 204.

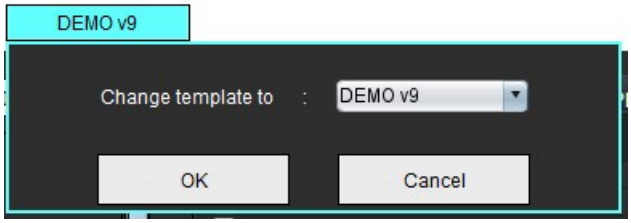
The application provides a tool to create templates based upon user defined normal ranges specified by age and gender. The calculation and reporting of z-scores is supported based on a user defined model. Refer to the recommended references.

FIGURE 9. Template Tab

Considerations

Before starting analysis, the user defined template must be selected from the main interface. Click on **Default** at the upper right and select the template to be used. Changing the template after performing analysis will apply the normal range and/or Z-score defined in the template.

FIGURE 10. Change Template



NOTE: Imported studies with previous suiteHEART analysis may show the name of the template used for that study. That template may not be available for other studies.

It is recommended that if two systems are being used for analysis, create the template preference file on the first system and then import into the second system. Template preference files imported from a different system will overwrite template preferences if they have already been created on that system.

Create a Template

WARNING: The validity of the values entered for normal ranges and Z-scores parameters are the sole responsibility of the user. Confirm all entries prior to analysis. Incorrect values could lead to misdiagnosis.

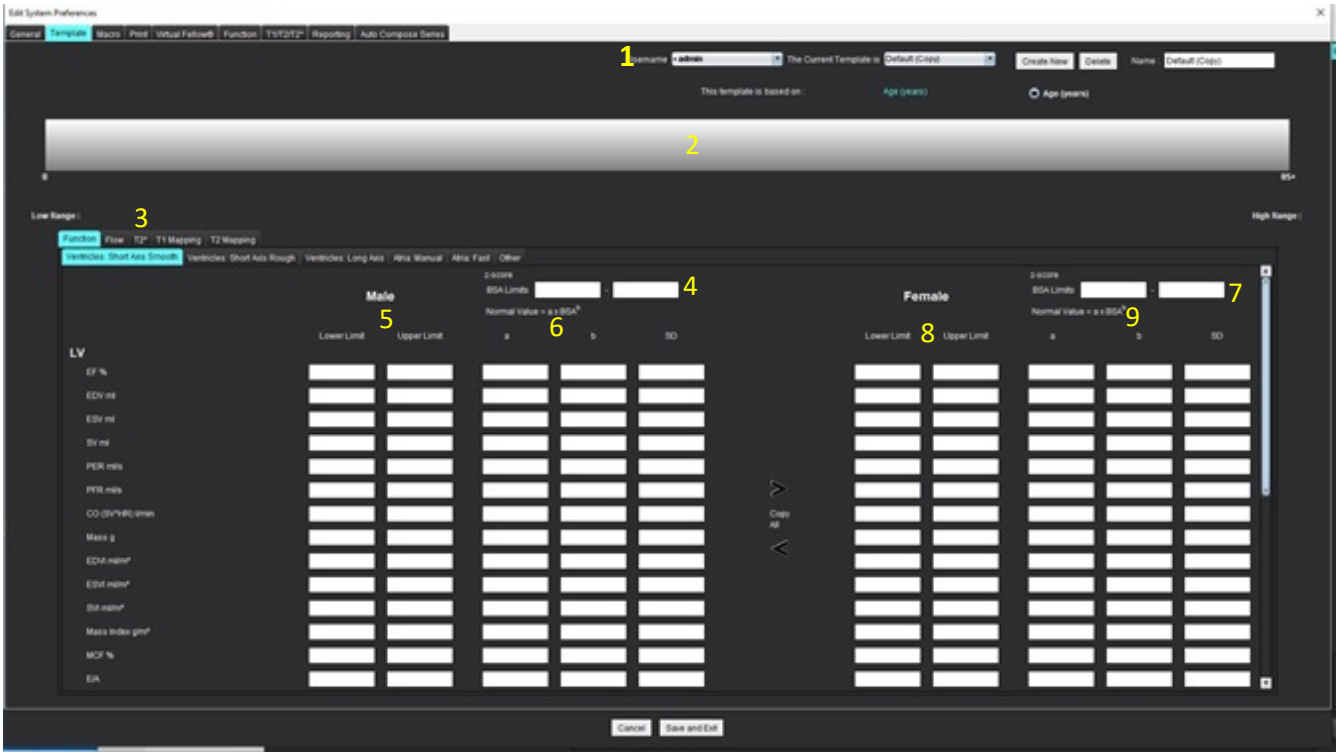
All new templates are created initially by duplicating the default template. The default template is not editable.

1. Select **Tools > Preferences > Edit.**
2. Select the **Template** tab.
3. Click **Create New** to create or duplicate a template.
   Age is the default.

FIGURE 11. Create Template Selections

4. Type in a new name for the template.
   When a new name is entered **The Current Template is**, found in the pull-down menu, will update.

FIGURE 12. Example Template Tab - Short Axis Function is Shown



1. Current template, 2. Age range bar, 3. Result parameters per analysis type, 4. Male Z-score BSA limits, 5. Male upper and lower limits, 6. Male Z-score parameters, 7. Female Z-score BSA limits, 8. Female upper and lower limits, 9. Female Z-score parameters

5. Select the desired application analysis type for which to create a template.
6. If age ranges are to be used, right click on the Age Range Bar to create an age range divider.

   The age range divider bars can be dragged and adjusted for the desired age range.
   Multiple age range divider bars can be created.
   Age Range divider bars can be deleted by placing the cursor close to the bar and selecting **Delete Range** from the right mouse menu.
7. Enter the normal range values for the appropriate analysis mode, as well as both the lower and upper limits.
8. Differentiate between male and female values if necessary. Use the Copy All arrows to copy values between genders. Use the scroll bar to navigate to the complete measurements listing for that analysis type.
9. If z-scores are to be calculated, values for both **a**, **b**, and **SD** as well as the **BSA Limits** must be entered by the user.

The reporting priority is outline in the table below. Depending on the condition either the normal range or the calculated z-score on the measurement result tables will be shown.

Reported/Calculated	Condition
z-score Calculated	If z-score parameters have been entered and the BSA is within limits.
Normal Range Reported	If the z-score and normal range are entered and the BSA is out of limits.
Normal Range Reported	Only if a normal range has been entered.
Neither Normal Range or z-score Calculated	If the z-score parameters are entered. No normal range entered and BSA is out of limits.
Neither Normal Range or z-score Calculated	Nether z-score parameters or a normal range has been entered.

WARNING: The validity of the values entered for normal ranges and Z-scores parameters are the sole responsibility of the user. Confirm all entries prior to analysis. Incorrect values could lead to misdiagnosis.

10. Select **Save and Exit** to save all entries.
    - Select **Cancel** to exit without saving or accepting any changes.

NOTE: For a template to be valid, parameter values must be entered as numerical numbers with both upper and lower values entered. If inconsistencies in the values are found, the following message will appear “Invalid normal range selected. Please correct and save again.” The parameter needing correction will be highlighted in red. Saving a blank template is not allowed and will cause the following message “Unable to Save Template(s)” to display.

NOTE: Normal ranges entered for the Flow tab apply to both 2D and 4D Flow analysis results.

Recommended References

Buechel EV, Kaiser T, Jackson C, Schmitz A, Kellenberger CJ. Normal right- and left ventricular volumes and myocardial mass in children measured by steady state free precession cardiovascular magnetic resonance. J Cardiovasc Magn Reson. 2009 Jun 21;11(1):19. doi: 10.1186/1532-429X-11-19. PMID: 19545393; PMCID: PMC2718870.

Kawel-Boehm, N., Hetzel, S.J., Ambale-Venkatesh, B. et al. Reference ranges (“normal values”) for cardiovascular magnetic resonance (CMR) in adults and children: 2020 update. J Cardiovasc Magn Reson 22, 87 (2020). https://doi.org/10.1186/s12968-020-00683-3

Macro Tab

Customized reporting macros can be created which can automatically populate with calculated values. Macros are independent from templates, as created macros are available to all users.

Macros can be created for the following reporting sections:

- Impression
- Technique
- History
- Findings

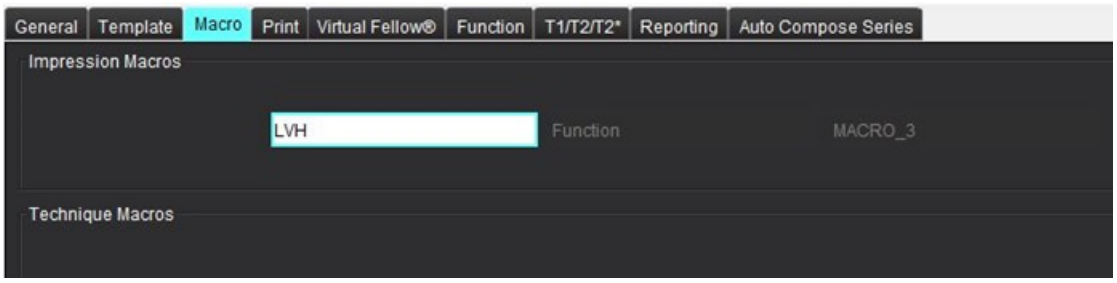
Add an Impressions Macro

NOTE: Creating a History or Technique macro follows the same steps as creating an Impression macro.

1. Select **Tools > Preferences > Edit**.
2. Select the **Macro** tab.
3. Select **Add Impressions Macro**.

   A new text field appears in the Impression Macros panel.

FIGURE 13. Impression Macros Window



4. Place the cursor inside the new text field and edit the name as desired.

NOTE: The macros created can be reordered. Click and drag the desired macro to a new position within the list.

Enter Macro Text

1. Place the cursor in the Macro Information text box and enter relevant text.
2. To enter a parameter result, select any of the analysis tabs below and select the desired parameter button, which will be automatically entered into the macro information. In this example, the LV Ejection Fraction parameter was selected and entered at the end of the text.

FIGURE 14. Macro Information

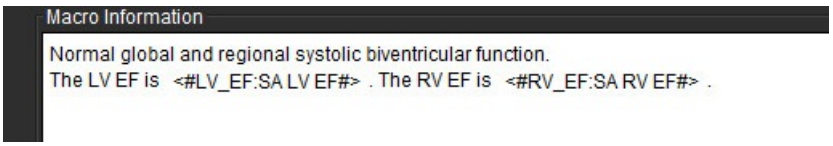


FIGURE 15. Macro Parameter Result Selections

3. Select **Save and Exit**.

   Select **Cancel** to exit without saving or accepting any changes.

Execute a Macro

As a prerequisite to macro execution, analysis results must be generated prior to executing macros that include result parameters. Technique and Impression macros can be created to automate report generation.

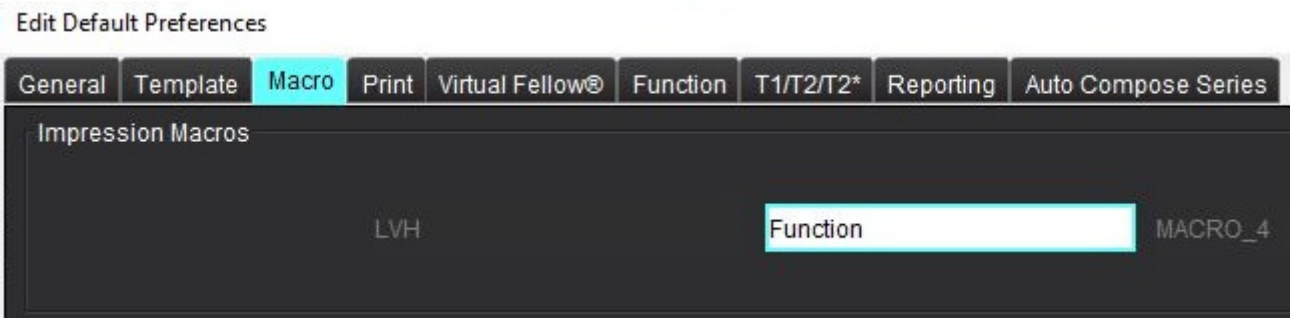
NOTE: If a macro contains a parameter result which has been changed in the analysis mode, the macro must be reselected to reflect the updated result.

Delete a Macro

1. Select **Tools > Preferences > Edit**.
2. Select the **Macro** tab.
3. Select the macro from the list.

   In the example shown, the macro named Function is selected for deletion.

FIGURE 16. Macro Selection List

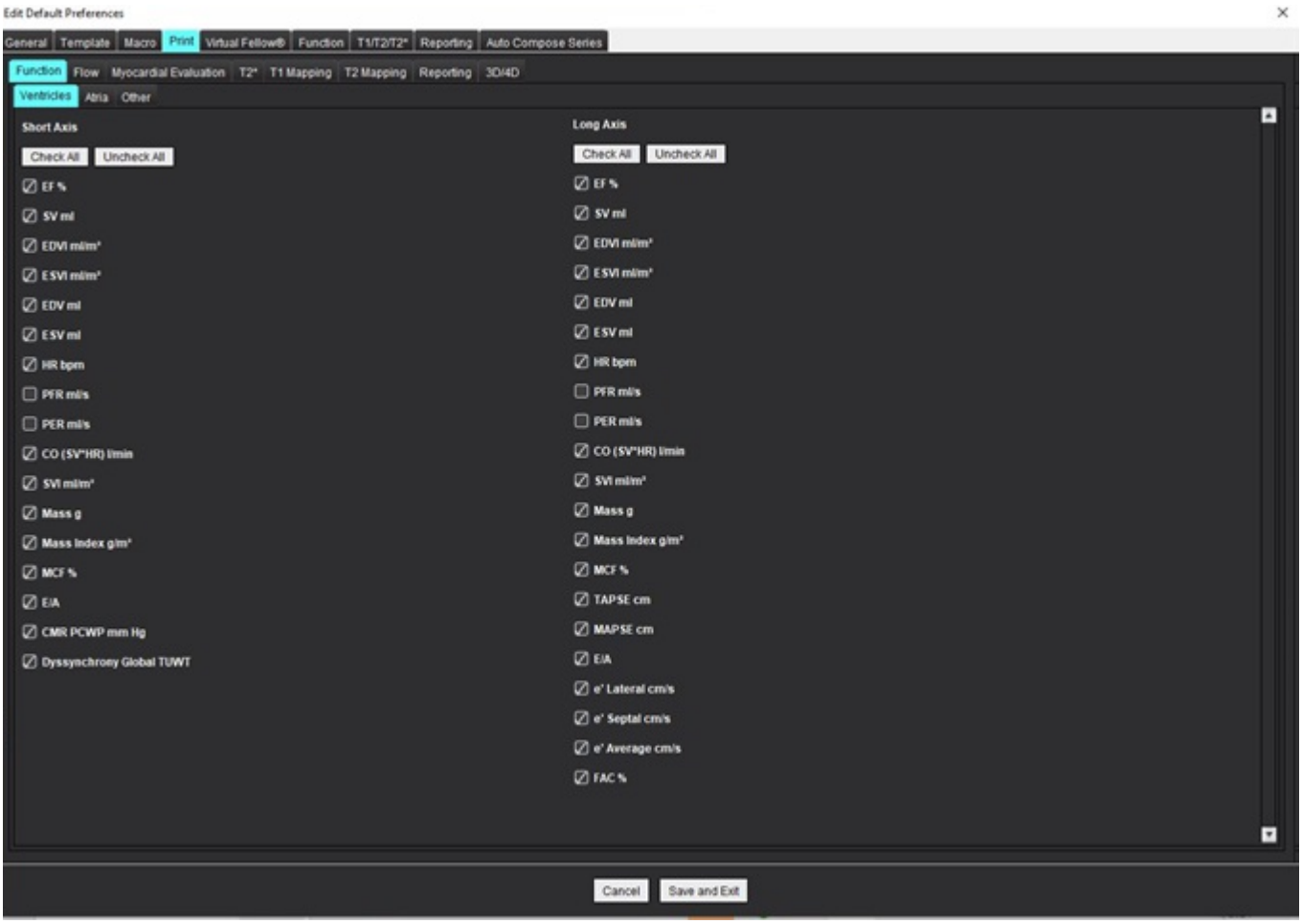


4. Select **Remove Selected Macro(s)**.

Print Tab

Calculated results from each analysis mode can be configured for inclusion and ordered on the report under the **Print** tab.

FIGURE 17. Print Preferences



1. From the menu, select **Tools** > **Preferences** > **Print**.
2. Select the appropriate analysis tab and check the desired result to be included on the report.
3. The order of the results as they are listed on the report can be changed by clicking directly on a result and dragging to a new position on the list.
4. Repeat for each analysis mode tab.
5. Select **Save and Exit**.

   Select **Cancel** to exit without saving or accepting any changes.

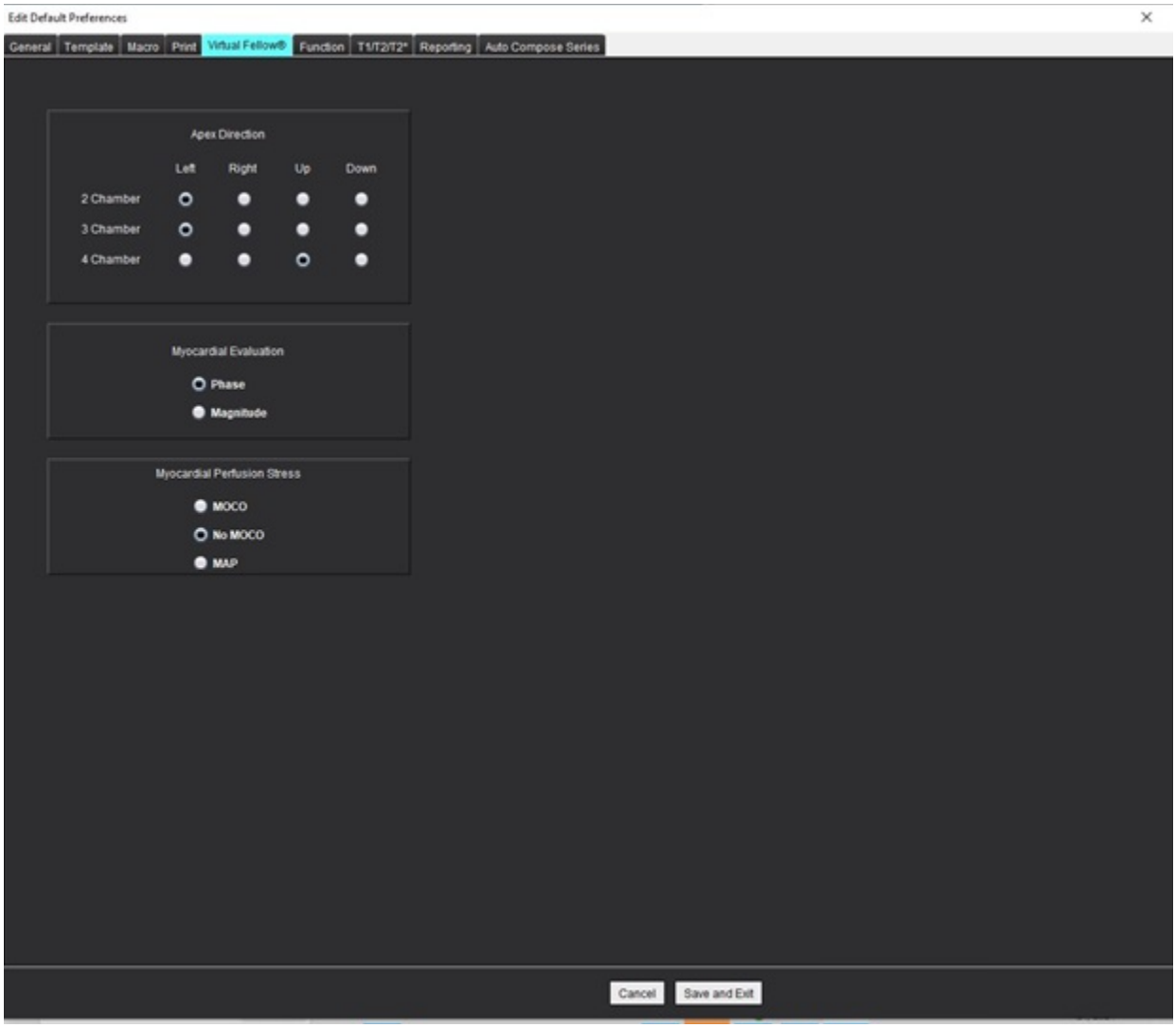
NOTE: If print selections are made directly on the application interface they will not be saved with the template.

NOTE: If the order of the measurements are changed directly on the interface, the change will not be saved with the template.

NOTE: User defined measurements created under Other in Function Analysis will appear in the Print Preference Other tab. These measurements can be re-ordered.

Virtual Fellow® Tab

FIGURE 18. Virtual Fellow® Preferences

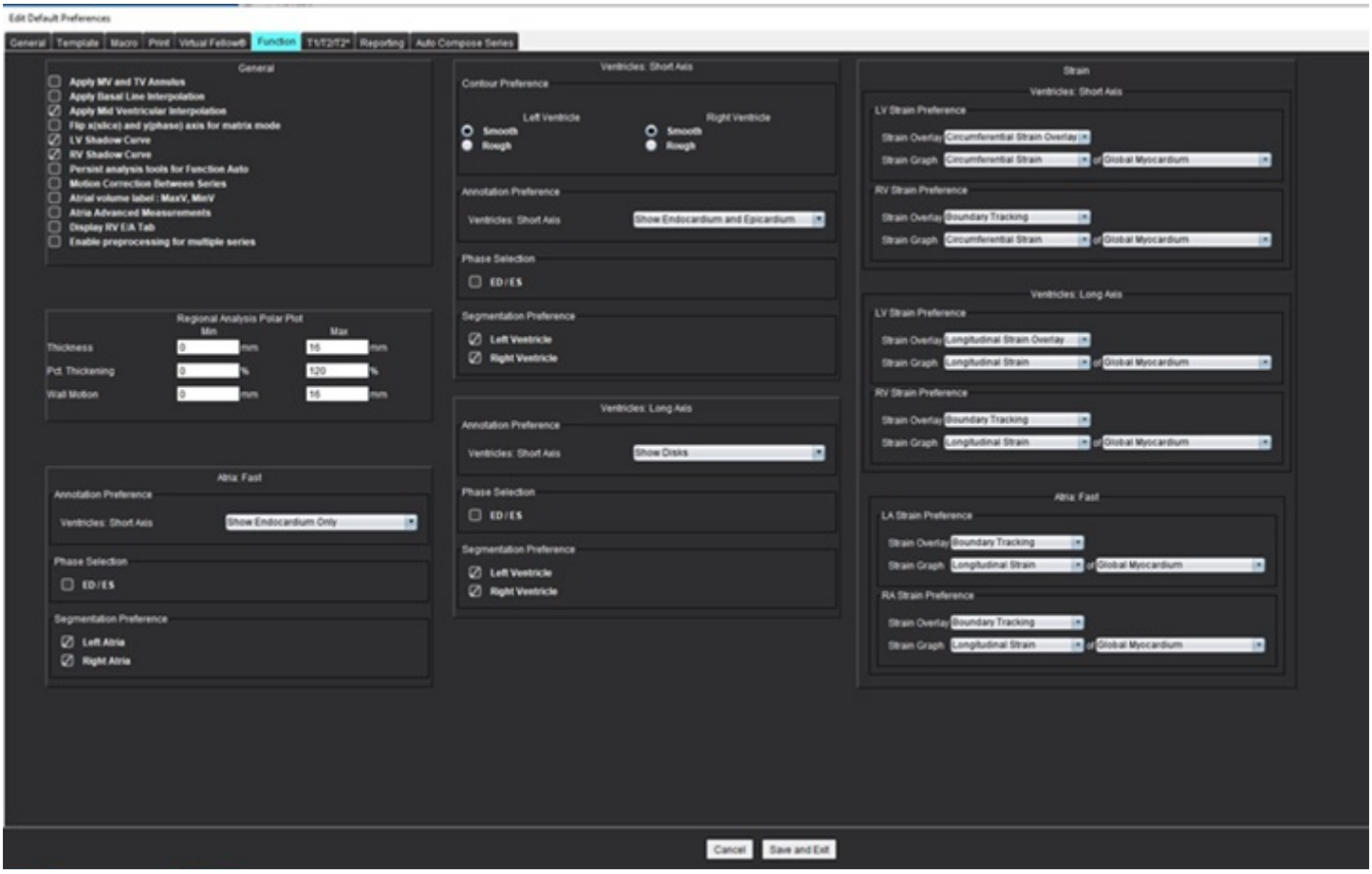


1. Select **Tools > Preferences > Edit**.
2. Select the **Virtual Fellow®** tab.
3. Select the Apical Direction for the long axis views. (**Admin Only**)
4. Select the series for display of either **Phase** or **Magnitude** for Myocardial Evaluation.
5. Select the **MOCO, NO MOCO**, or **MAP** series for display for myocardial perfusion.
6. Select **Save and Exit**.

   Select **Cancel** to exit without saving or accepting any changes.

Function Tab

FIGURE 19. Function Preferences



1. From the Image Viewer menu bar, select **Tools > Preferences > Edit**.
2. Select **Function** tab.
3. For the calculation of MAPSE and TAPSE only, check **Apply MV and TV Annulus**. (**Admin Only**)
4. For automatic annulus insertion for basal interpolation check **Apply MV Annulus and TV Annulus** and **Apply Basal Line Interpolation**. (**Admin Only**)
5. Check **Mid Ventricular Interpolation** for function analysis. (**Admin Only**)
6. Check **Flip x(slice) and y(phase) axis for matrix mode** to swap the axis.
7. Check either **Enable LV** or **RV Shadow Curve** to display both curves.
8. Check **Persist analysis tools for Function Auto** for performing function segmentation.
9. Check **Persist Endo/Epi ROI** edit mode for performing editing.
10. Check **Motion Correction Between Slices** to access this feature in Function Analysis, refer to Motion Correction Between Series on page 74. (**Admin Only**)
11. Check **Atrial Volume label: MaxV, MinV** to change volumetric labels.
12. Check **Atria Advanced Measurements** to show all atrial results.
13. Check **Display RV E/A** tab for Function Analysis.

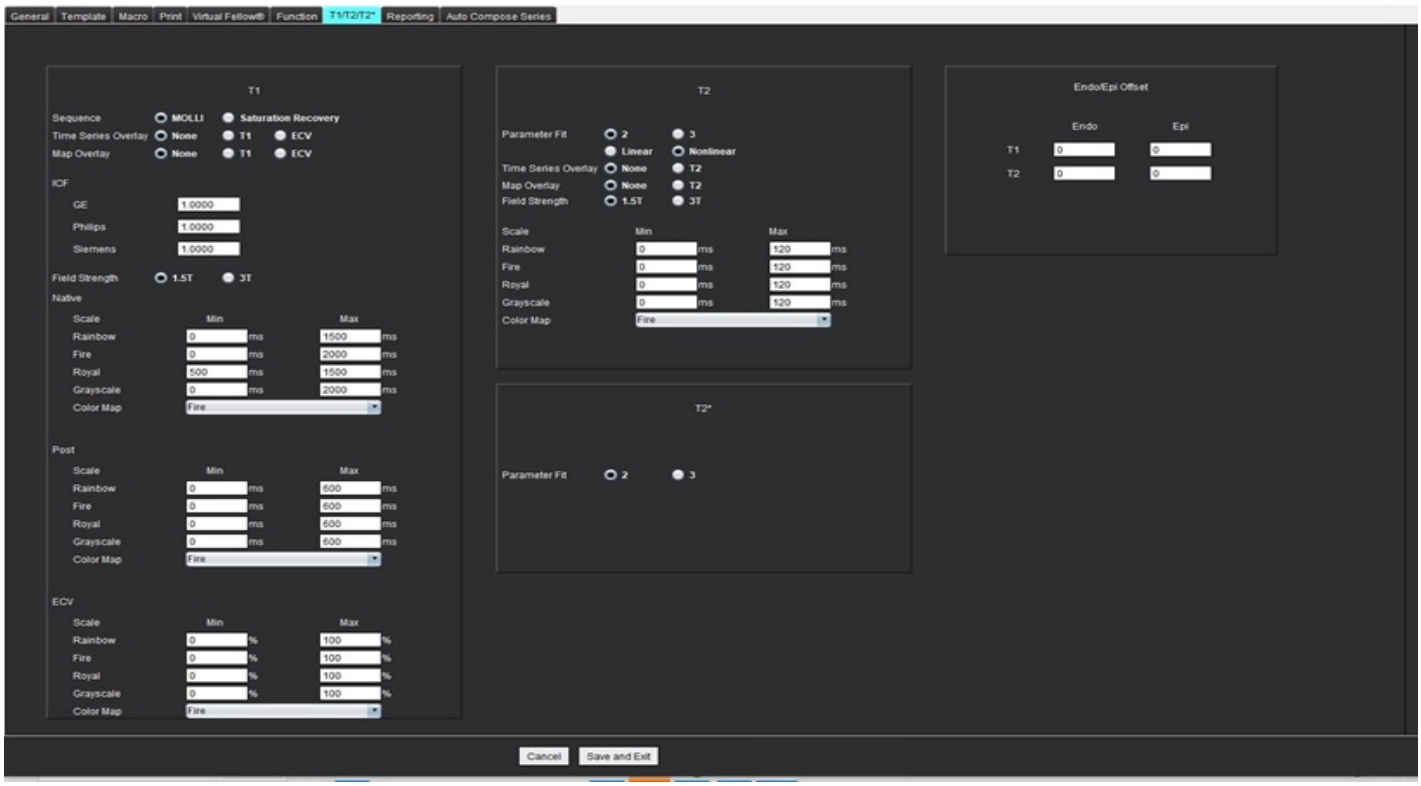
14. Check **Enable preprocessing for multiple series** to preprocess multiple function series. (**Admin Only**)
15. Set upper and lower limits for **Regional Analysis Polar Plots**.
16. Set preferences for **Atria Fast** analysis.
17. Set preference for **Ventricles: Short Axis**.
18. Set preference for **Ventricles: Long Axis**.
19. Select **Save and Exit** to store your selections.

    Select **Cancel** to exit without saving or accepting any changes.

Strain preferences requires a research agreement.

T1/T2/T2* Tab

FIGURE 20. T1/T2 T2* Preferences



1. From the menu bar, select **Tools > Preferences > Edit**.
2. Select the **T1/T2/T2*** tab.
3. To create a valid series for analysis, select the correct option for the vendor type then select the **Auto Compose Series** tab. (**Admin Only**)
4. **Endo/Epi Offset** is set to 1 and -1, with 1 being equal to .25 pixels. (**Admin Only**)
5. Select **Save and Exit**.

    Select **Cancel** to exit without saving or accepting any changes.

T1 Mapping

1. For the analysis of the time series select **MOLLI** or **Saturation Recovery** for the Sequence type for T1 Mapping. (**Admin Only**)
2. To automatically display the color map select either **Time Series Overlay** or **Map Overlay**.
3. Enter the ICF, refer to T1 Mapping Analysis on page 138. (**Admin Only**)
4. Select the **Field Strength** and set the color map type and scale values for either 1.5T or 3T.
5. Select **Save and Exit**.

   Select **Cancel** to exit without saving or accepting any changes.

T2 Mapping

1. For the analysis of the time series select the appropriate **Parameter Fit** calculation. (**Admin Only**)
2. To automatically display the color map select either **Time Series Overlay** or **Map Overlay**.
3. Select the **Field Strength** and set the color map type and scale values for either 1.5T or 3T.
4. Select **Save and Exit**.

   Select **Cancel** to exit without saving or accepting any changes.

T2*

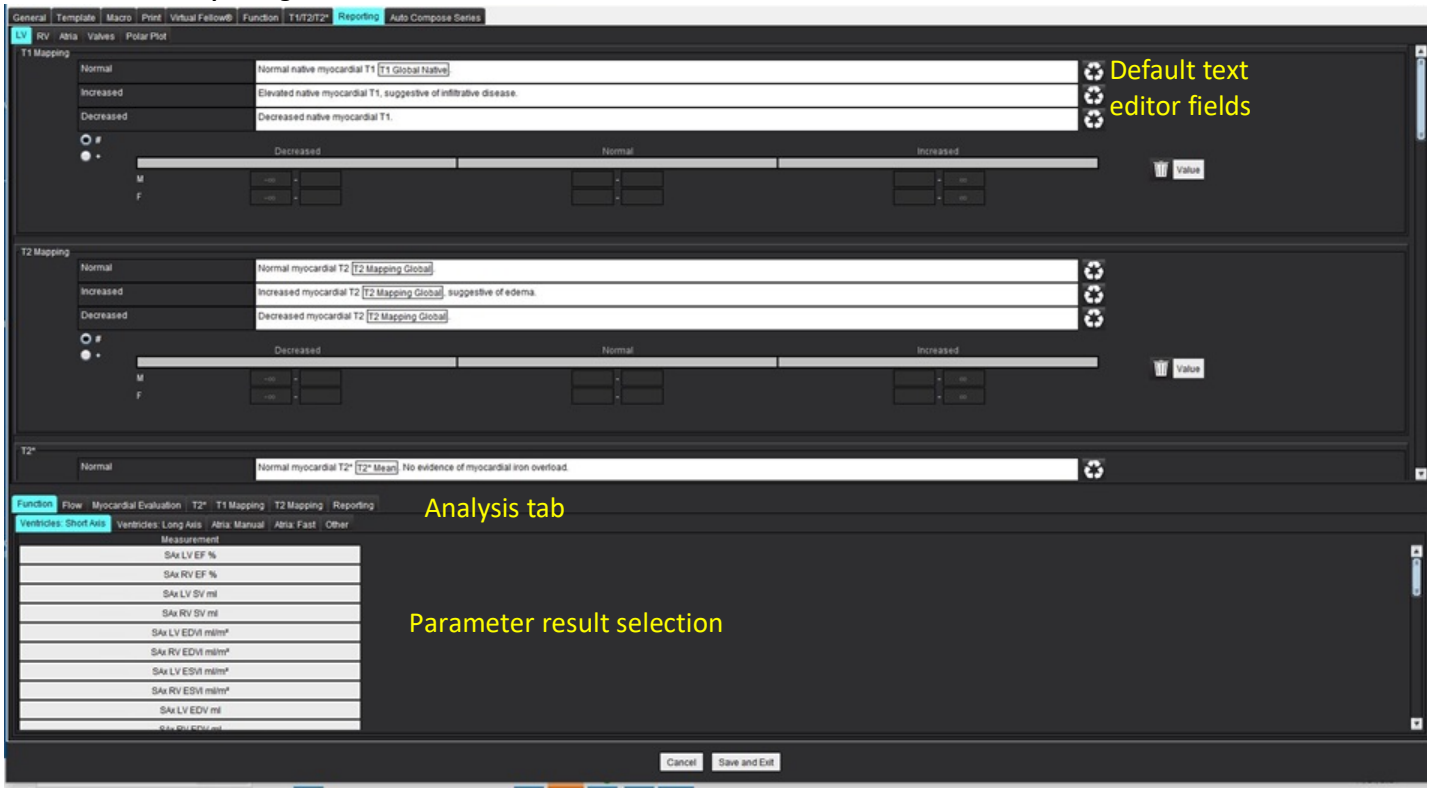
Select the **Parameter Fit**. (**Admin Only**)

Reporting Tab

Admin Required for these steps.

1. Select **Tools > Preferences > Edit System** from the menu bar.
2. Select the **Reporting** tab.
3. Click in the appropriate field to edit the default text for the menu descriptors, as shown in Figure 21.
4. Add a parameter result with the text by selecting the proper analysis tab and clicking the desired parameter, as shown in Figure 21.
5. Remove a parameter result by placing the cursor after the inserted result and pressing the delete key.

FIGURE 21. Reporting Preferences



6. Click  to restore the default text.

7. Define reporting categorical ranges for a parameter result associated with the menu selection by clicking  .

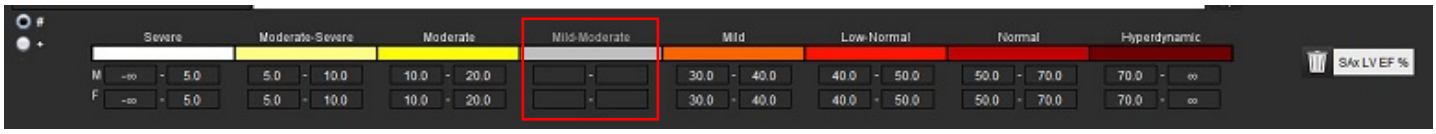
8. Select the appropriate parameter result from the associated analysis tab.

9. Choose either Absolute or Offset  .

Selection	Description
Absolute	Ranges based upon absolute values for gender regardless of age.
Offset	Ranges based upon how much offset there is from the normal range set in a template and age.

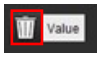
10. Type-in the appropriate values for the category ranges. To eliminate a reporting category, click the color bar, the bar turns grey and the values are removed. Figure 22.

FIGURE 22. Remove a Reporting Category



NOTE: Completing categorical ranges will enable the auto prefill functionality for the report. Text will prefill according to the user defined values. If a selection is made from the menu interface during the reporting process the prefilled functionality is no longer enabled.

NOTE: Prefilled text for the following parameter results requires user completion of the appropriate analysis: Atria Volumes, Hypertrophy: Maximum Wall Thickness, T2*, Valvular Stenosis, Valvular Regurgitation.

11. To reset the reporting categorical ranges and value selected click the 

.

Defining the Hypertrophy Category

Reporting for hypertrophy can be further defined as Concentric or Eccentric. Values must be entered for the categorical ranges and the concentricity values for male and female must be completed. See Figure 23.

FIGURE 23. Hypertrophy Categorical Ranges and Concentricity

Recommended References

Petersen SE, Khanji MY, Plein S, Lancellotti P, Bucciarelli-Ducci C. European Association of Cardiovascular Imaging expert consensus paper: a comprehensive review of cardiovascular magnetic resonance normal values of cardiac chamber size and aortic root in adults and recommendations for grading severity. Eur Heart J Cardiovasc Imaging. 2019 Dec 1;20(12):1321-1331. doi: 10.1093/ehjci/jez232. Erratum in: Eur Heart J Cardiovasc Imaging. 2019 Dec 1;20(12):1331. PMID: 31544926.

Petersen, S.E., Aung, N., Sanghvi, M.M. et al. Reference ranges for cardiac structure and function using cardiovascular magnetic resonance (CMR) in Caucasians from the UK Biobank population cohort. J Cardiovasc Magn Reson 19, 18 (2017). https://doi.org/10.1186/s12968-017-0327-9

Concentricity Reference

Khouri MG, Peshock RM, Ayers CR, de Lemos JA, Drazner MH. A 4-tiered classification of left ventricular hypertrophy based on left ventricular geometry: the Dallas heart study. Circ Cardiovasc Imaging. 2010 Mar;3(2):164-71. doi: 10.1161/CIRCIMAGING.109.883652. Epub 2010 Jan 8. PMID: 20061518.

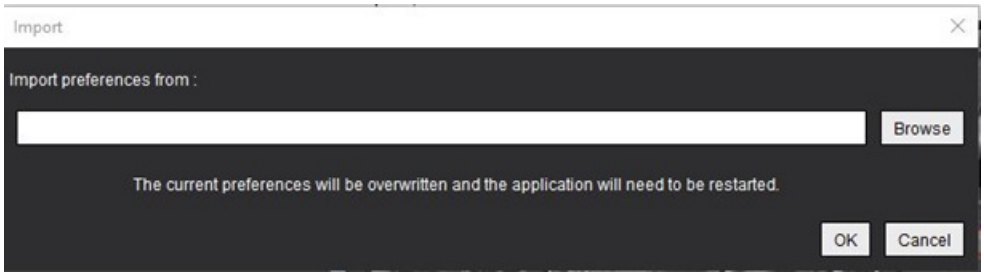
Import Preferences

Admin Required for these steps.

NOTE: Upon import all current preferences will be deleted.

1. Select **Tools > Preferences > Import**.

FIGURE 24. Import Preferences



2. Select the Browse button, select the location of the preference file and then select the Open button.
3. Select **OK** to perform the import procedure as defined.

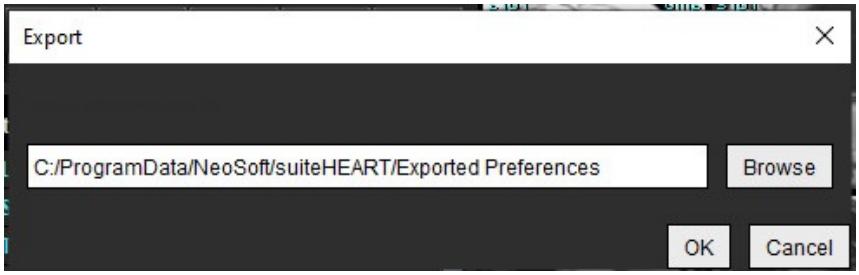
   Select **Cancel** to exit without importing.

NOTE: Importing preferences from prior versions (4.0.4 or below) of suiteHEART® Software is not supported. Contact NeoSoft Support at service@neosoftmedical.com for help with importing preferences from prior versions.

Export Preferences

1. Select **Tools > Preferences > Export**.

FIGURE 25. Export Preferences



2. Select **Browse**, select the folder in which to place the preference file and then select **Save**.
3. Select **OK**.

   Select **Cancel** to exit without exporting.

Virtual Fellow®

Virtual Fellow® is an image viewing standardized feature for cardiac MR studies. The feature improves visualization work-flow making it easier for clinicians to review cardiac MR studies. The feature automatically applies image manipulation tools such as window level, zooming, panning and rotation. Current and prior cardiac MR studies can be easily reviewed with the Virtual Fellow® feature.

NOTE: To enable the Virtual Fellow® feature with preprocessing, refer to the suiteDXT Instructions for Use.

NOTE: The patient ID should match for both the current and prior exam to be viewed in Virtual Fellow®.

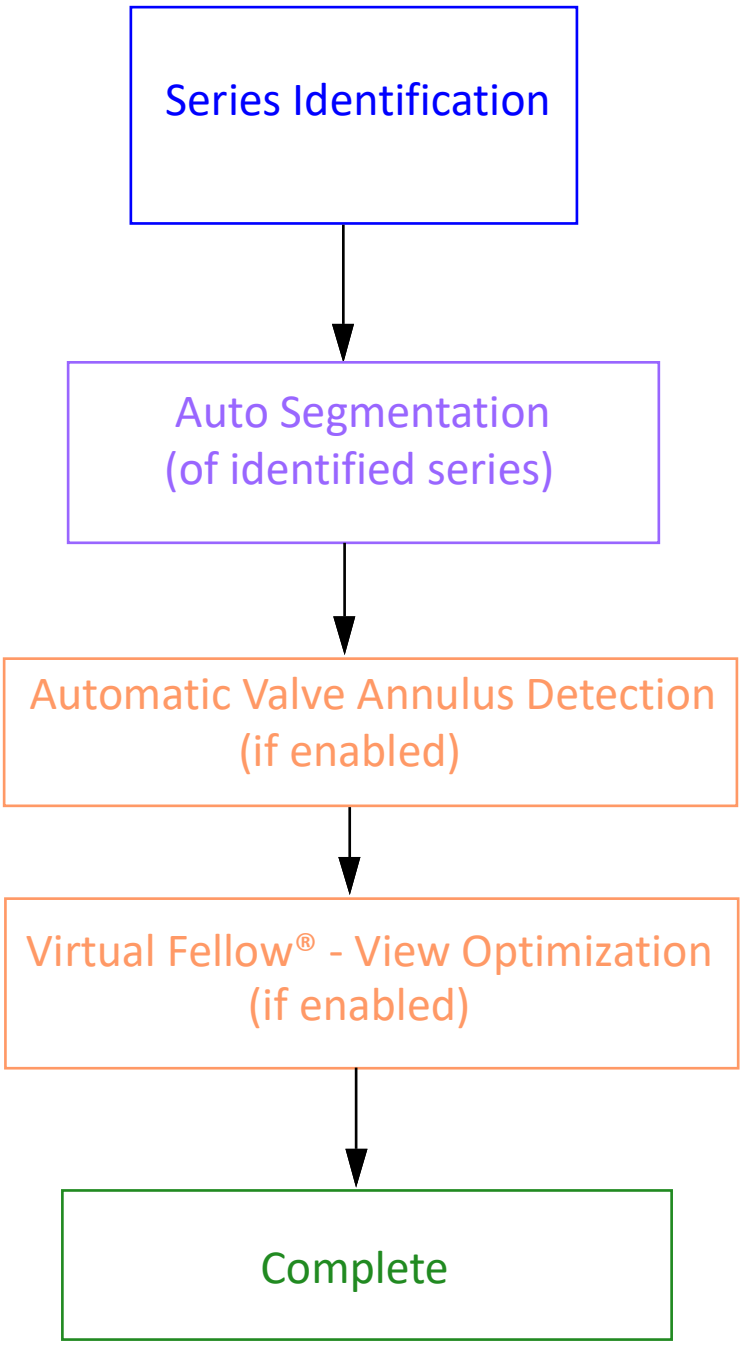
NOTE: Editing of analysis results cannot be performed in Virtual Fellow®, select the appropriate analysis mode to perform editing.

WARNING: The user is responsible for confirming the correct image selection for the viewing protocols created by the Virtual Fellow®. Images identified incorrectly for current/prior viewing protocols can be selected manually. The user should be properly trained in cardiac imaging techniques to ensure that the appropriate images are reviewed. To review all images acquired for the study use the Viewer mode found in Image Management Tools on page 21.

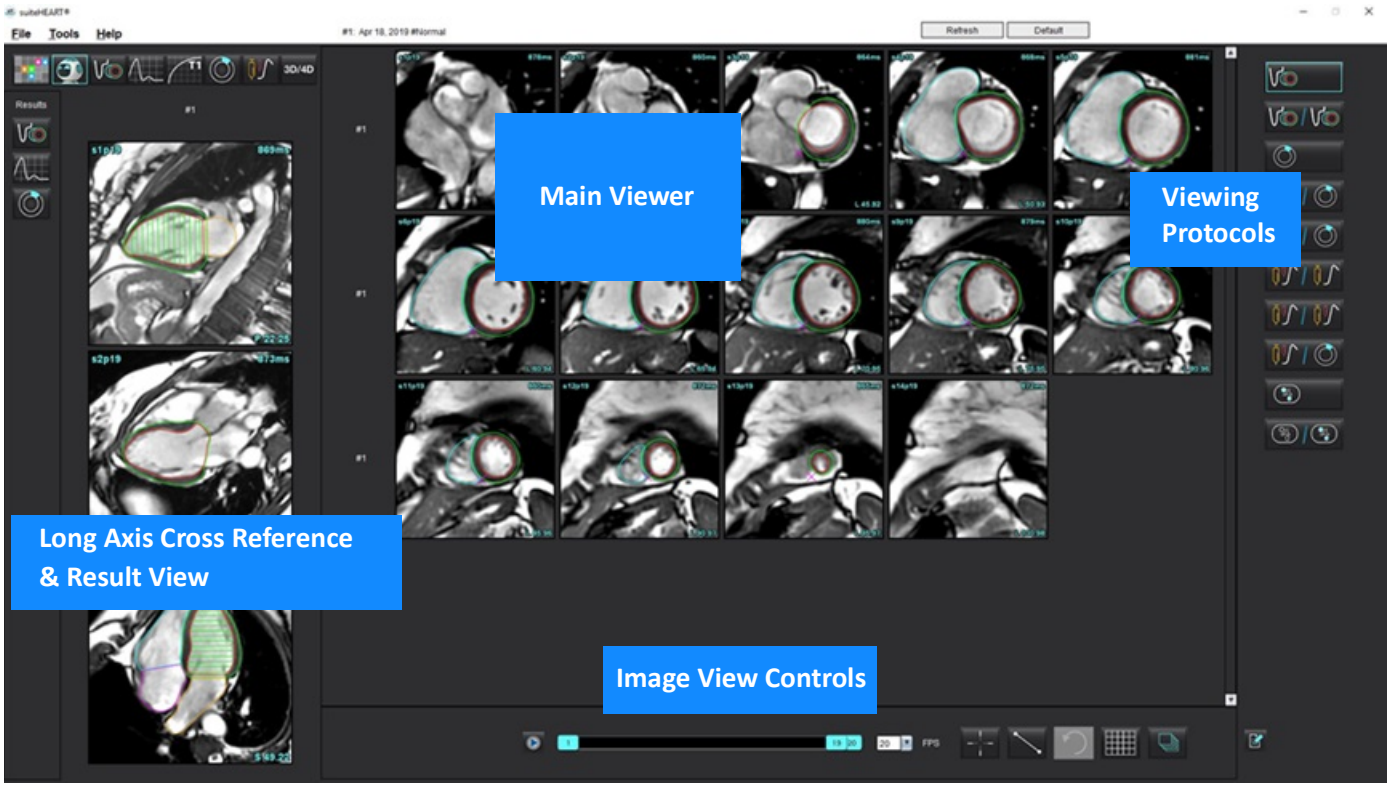
WARNING: Prior to the review or comparison of studies, visually confirm all exam patient indicator information at the top of the interface. #1 indicates the current study, #2 indicates the prior study.

WARNING: Image manipulation such as WW/WL, pan, zoom, rotate, and flip performed by Virtual Fellow® can affect the appearance of different pathologies and the discerning of other anatomical structures. Review each viewing protocol and perform the appropriate adjustments.

Preprocessing with Virtual Fellow®

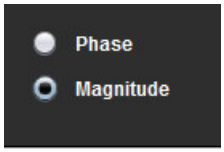
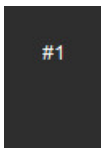
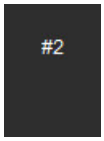
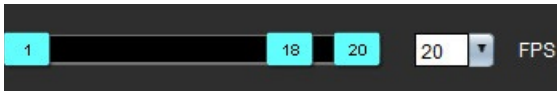


Virtual Fellow® Interface



Virtual Fellow® Selections

Selection	Description
	Virtual Fellow®
	Display Function results
	Display Flow results
	Display Myocardial Evaluation results

Selection	Description
 	Link Toggle used to perform WW/WL, pan, rotate, and flip on both current and the prior series. Unlink Toggle used to perform WW/WL, pan, rotate, and flip on a single series. Note: Zoom is always applied to both current and prior series. To enable, contact NeoSoft Support at service@neosoftmedical.com
	Phase is used to view phase sensitive late enhancement. Magnitude is used to view magnitude late enhancement.
	MOCO: view motion correction Myocardial Perfusion series. NO MOCO: view Myocardial Perfusion series with no motion correction. Map: view third party maps.
	#1 is the indicator for the series displayed for the current study. Left mouse click directly on #1 to change the series.
	#2 is the indicator for the series displayed for the prior study series. Left mouse click directly on #2 to change the series.
	Cine controls are used to play, pause, select the frames per second, and define the start and end frames of the cine movie.
	Cross reference tool that automatically identifies and displays images that contain the same location. For information on using this feature refer to Find Feature* on page 22.
	Measurement tools can be used in the Main Viewer and on long axis views.

Selection	Description
	Undo generic measurement edits.
	Viewport layout options*: 1x1, 1x2, 4x4 and 5x4. *Dependant on selected protocol.
	Scope has the same function as described in Image Manipulation Tools on page 12.
Keyboard Arrow Left	Used to advance the slice location when in a current/prior viewing protocol.
Keyboard Arrow Right	Used to reverse the slice location when in a current/prior viewing protocol.

Viewing Protocols

	Series Type
	Short axis cine function series.
	Current short axis cine function with prior.
	Myocardial Evaluation.
	Current Myocardial Evaluation with prior.
	Short axis cine function with Myocardial Evaluation.
	Myocardial Perfusion Stress/Rest series.
	Current Myocardial Perfusion Stress series with prior.

	Series Type
	Current Myocardial Perfusion Stress with Myocardial Evaluation.
	T1 axial series. (Use left and right arrow keys to navigate to next series.*)
	SSFP with T1 axial series.

*The active keys will depend on preference setting.

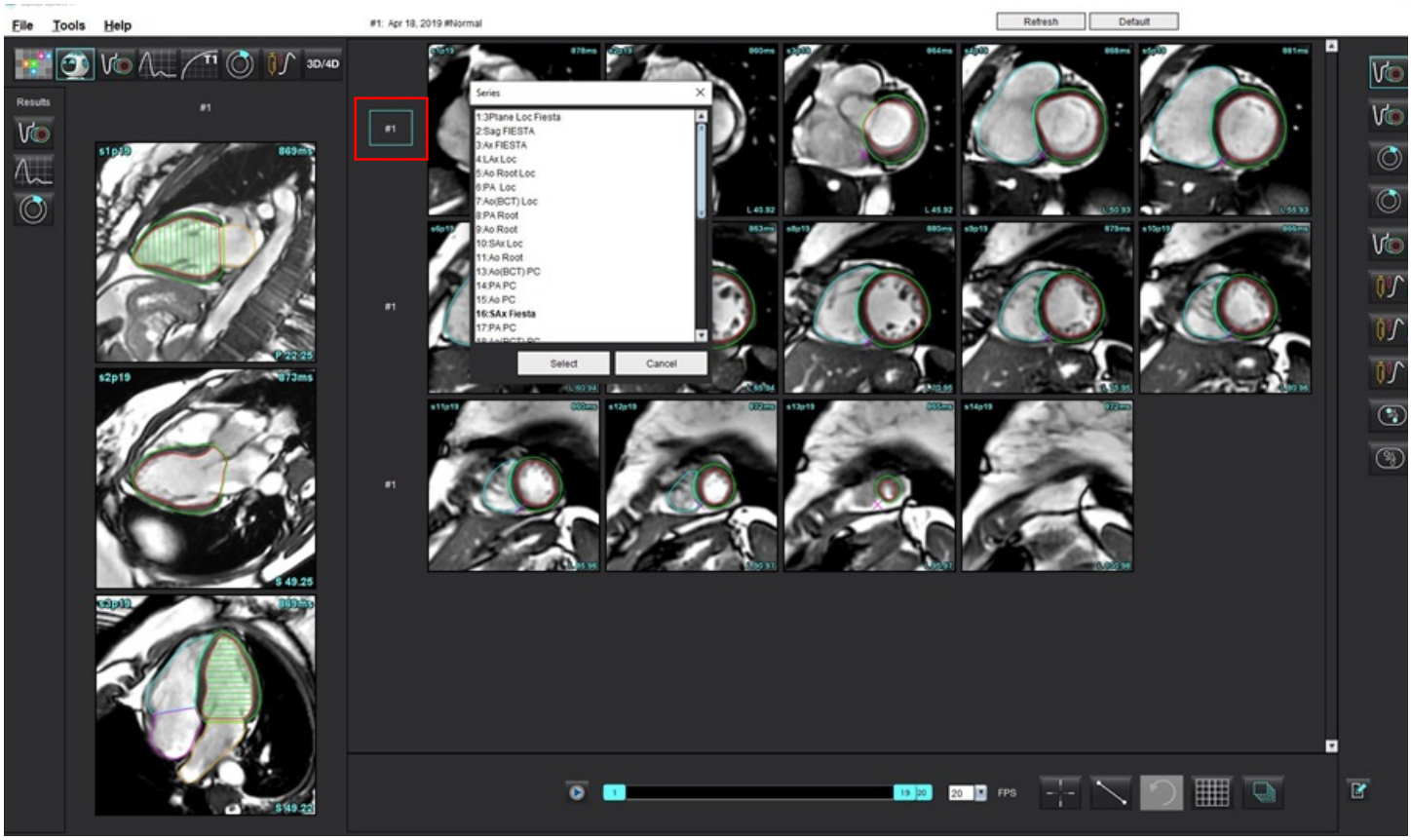
Quick Keys - Long Axis Viewports

Function	Action
Slice navigation forward.	Z
Slice navigation backward.	A
Slice navigation.	Middle Mouse Wheel

User Selection of a Series for Viewing Protocols

Viewing protocols are configured to view images from the current study or from the current and prior study. If the images displayed are not the expected images to be reviewed, reselect the appropriate series by performing a left mouse click directly over the number notation (#1 for current study or #2 for prior study) on the Virtual Fellow® interface as shown in Figure 1. The series listing for the current study (#1) will be displayed, select the appropriate series.

FIGURE 1. Virtual Fellow® Interface



User Selection of a Series for Long Axis Cross Reference Viewports

If images displayed are not the expected views, the appropriate series can be selected by directly clicking on a long axis viewport and then selecting the image from the file pull-down menu, as shown in Figure below.

NOTE: If the keyboard selections of **Z** or **A** are used the user selected image will no longer be present in the viewport.

NOTE: To set the desired apical direction from the Image Viewer menu, select Tools > Preferences > Edit and select the Virtual Fellow® tab.

Auto Update

The Auto Update feature allows for the launching of a study with background processing. If images are being networked when the study has been launched, analysis (and Virtual Fellow® if configured on) will be performed in the background if a valid series type is identified by the algorithm. Supported analysis modes include:

- Function
- Flow
- Myocardial Evaluation (Short Axis Late Enhancement only)
- T1 Mapping
- T2 Mapping
- T2*
- Myocardial Perfusion
- 3D/4D

Refer to the suiteDXT Instructions for Use to configure the Auto Update feature.

WARNING: Following preprocessing, the user is responsible for assessing the accuracy of the entire analysis and making any necessary corrections.

Workflow

1. If a study has been networked or if the study is in process of being performed and networked and a light blue circle indicator is present on the DXT study listing, as shown in Figure 1, the study can be launched.

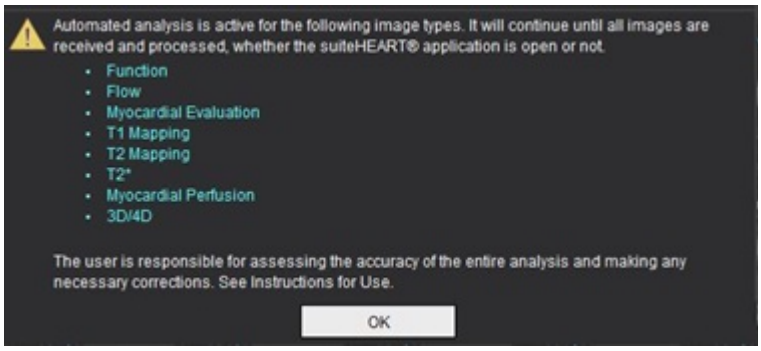
NOTE: If an analysis is performed manually before the auto update the results will not be overwritten.

NOTE: If the study is closed, a green circle indicates completed processing.

FIGURE 1. DXT Study Listing

2. When the study opens the message shown in Figure 2 appears.

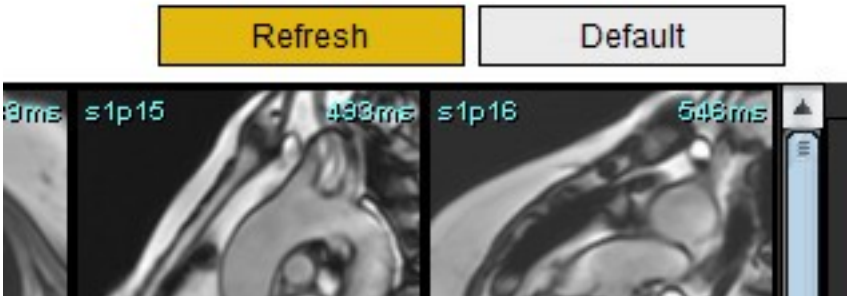
FIGURE 2. Study Launch



3. When analysis has been completed on a series the Refresh indicator will turn yellow, as shown in Figure 3. Click to update the analysis modes.

   Depending on the number of series types for analysis the Refresh may need to be clicked several times.

FIGURE 3. Refresh Indicator



NOTE: If after closing the study additional series types are networked, processing can take place.

Editing Contours

Editing contours, as described in this section, is available in all analysis modes. This feature is available in both the Editor Window and in Review Mode.

ROI Point Spline

1. In the Editor Window, left mouse click on the contour. The contour will turn purple when selected.
2. Left mouse click and drag on the center of the contour to move it, as shown in Figure 1.
    - If the selected contour was created using the point spline method, the points are displayed for editing. Left mouse click and drag any of the points to adjust the contour size and shape as shown in Figure 1.
    - If the selected contour was created using the free-hand trace tool, left mouse click and use free-hand edit to update the contour.

Additional functionality:

- Alt+ Left mouse generates a corner point.
- Clicking the first point closes the contour.
- Clicking on a contour directly generates a point.
- Delete + cursor on point removes a point.
- Dragging a point close to a neighboring point removes the neighboring point.
- If the number of points becomes less than 3, the ROI will be deleted.

FIGURE 1. Conventional Contour Edit

Nudge Tool

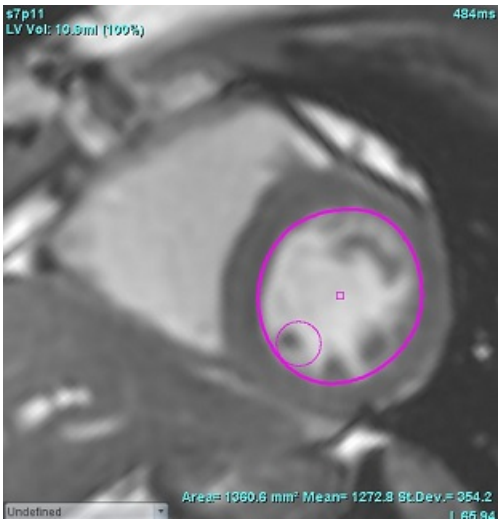
1. To activate the nudge tool, left mouse click on the contour to select it. Then right mouse click and select the nudge tool from the pop-up menu, as shown in Figure 2.
    - When the nudge tool is applied, the selected point spine ROI automatically becomes a free-hand ROI.

FIGURE 2. Nudge Tool Activation

2. The cursor will appear as a square. Position the cursor away from the ROI and press and hold the left mouse button. The nudge tool will appear, as shown in Figure 3.

NOTE: The size of the nudge circle defaults to the size that is an equal distance from the mouse point to the selected ROI. Reposition the cursor to change the size.

FIGURE 3. Nudge Tool



3. To deactivate the nudge tool, left mouse click on the contour, then right mouse click and select the nudge tool from the pop-up menu, as shown in Figure 4.

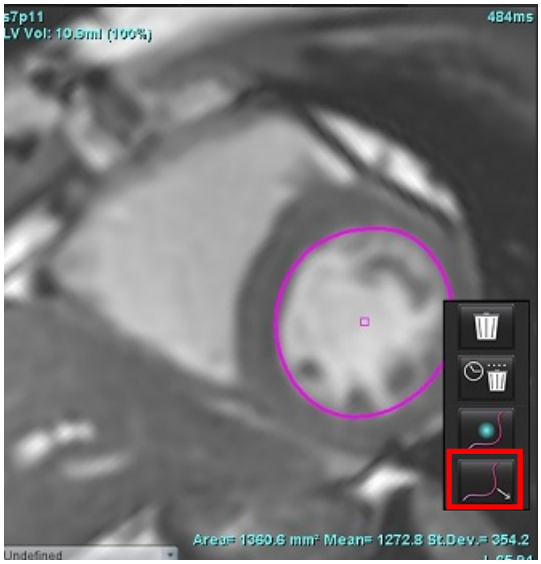
FIGURE 4. Nudge Tool Deactivation

NOTE: The default on/off state of the nudge tool can be set in Preferences.

Contour Pull Tool

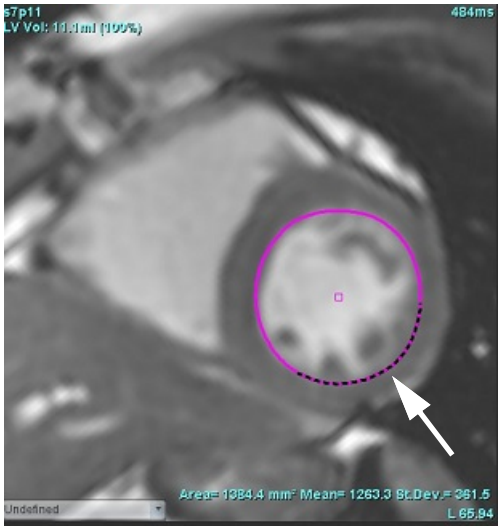
1. To activate the pull tool, left mouse click on the contour to select it. Then right mouse click and select the pull-tool from the pop-up menu, as shown in Figure 5. It allows for the adjusting of a contour segment by dragging portions of the contour to make small adjustments.

FIGURE 5. Pull Tool Activation



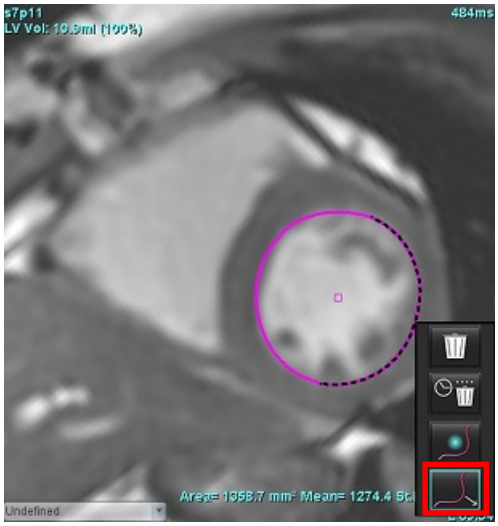
2. Left click directly on the segment of the contour to be edited. The length of the black dashed segment can be controlled by the middle mouse wheel. The position of the mouse cursor from the black dashed line will control the change of the edit for that segment of the contour.

FIGURE 6. Pull Tool



3. To deactivate the pull tool, left mouse click on the contour, then right mouse click and select the pull tool from the pop-up menu, as shown in Figure 7.

FIGURE 7. Pull Tool Deactivation



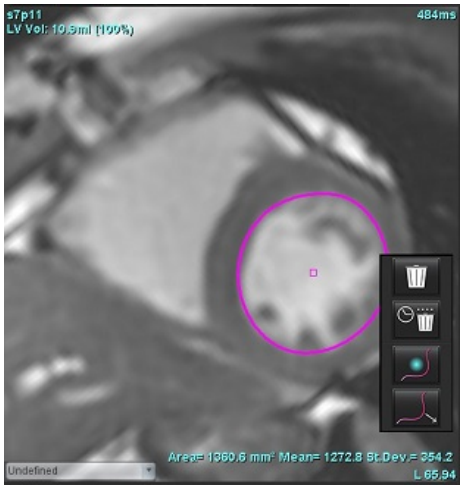
Delete a Contour

1. Left mouse click on the contour to select it and press the delete key on the keyboard.

or

2. Left mouse click on the contour to select it, then right mouse click and choose either  to delete a single contour or  to delete contours from all phases or all time points, as shown in Figure 8.

FIGURE 8. Contour Deletion



NOTE: The point spline functionality applies to all analyses except for 3D/4D Flow Viewer.

The following copy/paste and translate functionality is available in all analysis modes with the exception of PFO analysis.

- Ctrl+C = Copy ROI
- Ctrl+V = Paste ROI
- Ctrl+S = Smooth ROI

ROI Threshold Tool

To create an ROI using thresholding select  then press and hold the Alt key and left click on the image and drag the mouse.

NOTE: The state of the threshold tool is based upon the rough or smooth mode for function segmentation.

NOTE: The threshold tool is optimized for functional SSFP techniques.

Additional Editing Tool

Displayed in the Editor viewport are selections for toggling between the three edit modes.

Tool	Description
	Limit ROI
	No Limit ROI
	Overlap

Function Analysis

The user is responsible for the accurate and complete placement (and correct assignment) of all regions of interest (ROIs), including those generated or modified by the auto segmentation algorithms. The quantitative values generated by the software depend on the accurate and complete placement (and correct assignment) of these regions of interest.

The study preprocessing feature allows for the preprocessing of function analysis. Refer to the suiteDXT Instructions for Use.

This section details the typical steps used for a cardiac function analysis. The sample workflows provide an overview of the steps used in the application to complete a cardiac function analysis. The procedures describe how to perform quantitative analysis.

IMPORTANT: It is recommended that you are qualified in performing cardiac analysis, if the analysis results are to be used to reach a diagnosis.

WARNING: Following preprocessing the user is responsible for assessing the accuracy of the entire analysis and making any necessary corrections. A comprehensive review should include:

- ROI placement/identification
- ED/ES assignments
- MV/TV annulus placement
- RV insertion location

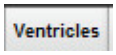
WARNING: The application assists in the analysis of the images only and does not automatically produce a clinical interpretation of the results. The use and placement of quantitative measurements is at the discretion of the user. Misdiagnosis can occur if measurements are inaccurate. Measurements should only be created by a properly trained and qualified user.

WARNING: Incorrect scan plane may cause inaccurate analysis results. See Appendix B on page 209.

NOTE: Retrospective 2D series created from 4D Flow may require manual segmentation.

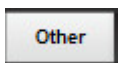
NOTE: Functional analysis is supported for multiple series. The results that are present on the report reflect the current series selected under functional analysis.

Select  There are three categories for analysis:



- Includes volume analysis for the left ventricle (LV) and right ventricle (RV)

- Includes volume analysis for the left (LA) and right atrium (RA).



- Includes pre-defined linear measurements and user defined measurements that can be added.

Ventricles

Select the analysis type:

	
Short Axis	Long Axis

Click  to delete contours.

NOTE: Matrix mode can be used for the deletion of contours.

Calculate Index Measurements

1. Click  .
2. Enter patient **Height** and **Weight**.

   The end-diastolic volume index, end-systolic volume index, mass end-diastolic index, mass end-systolic index, mass index phase, cardiac output index and stroke volume index measurements are calculated on the Measurement table.

NOTE: The BSA calculation method can be selected on the Reporting interface.

Auto LV & RV Segmentation

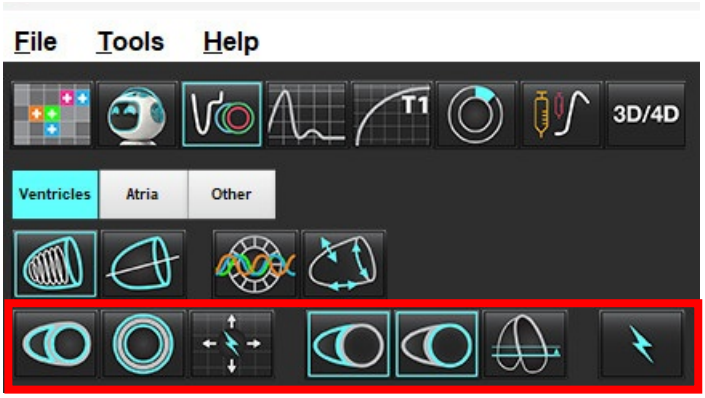
The auto segmentation feature calculates standard parameters of cardiac function without anatomical input. After segmentations results are generated, ROI types can be selected or deselected for viewing. Segmentation editing can also be performed from user input.

NOTE: For regional analysis, dyssynchrony and valve plane analysis segmentation for all slices and all phases should be performed.

To start LV & RV segmentation perform the following:

1. Select the short axis series and adjust the window/level.
2. Click **Ventricles**.
3. Click  for auto segmentation.
4. Make the appropriate selections from the segmentation tool bar, as shown in Figure .

FIGURE 1. Segmentation Toolbar



5. Click  to auto segment both LV and RV. Use  for LV only and  for RV only.

NOTE: For optimal RV segmentation, select both the epicardial and endocardial traces.

Review Segmentation Accuracy and Editing

1. Play the short axis series in cine mode and review the accuracy of the contours.
2. Edit any contours that are inaccurate.

NOTE: Contour editing is supported for smooth mode. Perform a contour edit and select start auto segmentation.

To reassign ED or ES, click on either the ED or ES buttons and select either the left or right side of the matrix cell. Refer to Matrix View on page 76.

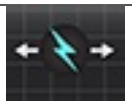
NOTE: The phase assignments of ED and ES are determined by the segmentation. The largest volume calculated is assigned ED and the smallest volume calculated is assigned ES.

3. Review placement of inferior RV insertion point on each slice. Adjust for each slice if needed.
4. Review matrix mode and confirm ED and ES assignments.

Table 1: Auto Segmentation Contour Types

						
Smooth Mode – Includes the papillary muscles in the ventricular volume.	Rough Mode – Excludes the papillary muscles from the ventricular volume.	Rough LV, Smooth RV.	Smooth LV, Rough RV	Show endocardial and epicardial contours.	Show endocardial contours.	Show chords.

Table 2: Auto Segmentation Propagation* Types

			
Propagate all slices all phases or show all slices all phases	Propagate all slices; single phase	Propagate all phases; single slice	Propagate showing contours for ED/ES phases only

*Propagation functionality will be swapped when the preference is checked for flip x(slice) and y(phase) axis for matrix mode.

Table 3: Segmentation Display

	
Right Ventricle	Left Ventricle

Perform Auto Segmentation for All Slices in a Single Phase

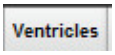
1. Select the short axis series and adjust the window/level.
2. Click Ventricles.
3. Click  .
4. From the segmentation bar select either smooth  or rough mode  .
5. To generate myocardial mass results, select  .
6. Review the short axis images and select the end-diastolic phase.
7. Select  for all slices in a single phase.
8. Click  to auto segment both LV and RV. Use  for LV only and  for RV only.
9. Review the short axis images and select the end-systolic phase, repeat step 9 to segment.

Review Segmentation Accuracy/Editing

1. Play the short axis series in cine mode and review the accuracy of the contours.
2. Edit any contours that are inaccurate.
3. Review the matrix and confirm ED and ES assignments.
4. Review all results on the measurement table.

Manual LV and RV Function Analysis Procedure

NOTE: It is recommended that the end-diastolic and end-systolic phases are used. Processing should begin on the end-diastolic phase. The analysis workflow is typically performed from the base to the apex.

1. Select  .
2. Select the appropriate short axis series from the Image View.
3. Click  .
4. Click  button for Volume measurements.
5. Locate the end-diastolic phase.

Define the Endocardium

1. Select  for LV or  for RV.
2. Trace the endocardial contour.
3. Proceed to the next slice using  , the left and right arrow keys, the mouse scroll wheel or select the thumbnail.
4. Repeat steps 2 and 3 until the entire left and/or right ventricle is segmented.

   The Endocardial contour tool will stay selected to expedite the segmenting of multiple slices.
5. Locate the end-systolic phase.
6. Repeat steps 2 and 3 on the end-systolic phase until the entire left and/or right ventricle is segmented.

NOTE: The software automatically defines the end-diastolic phase as the phase with the largest volume, and the end-systolic phase as the phase with the smallest volume. The end-diastolic and end-systolic phase assignments are updated during segmentation.

Review Segmentation Accuracy and Editing

1. Play the short axis series in cine mode and review the accuracy of the contours.
2. Edit any contours that are inaccurate.
3. Review the matrix and confirm ED and ES assignments.
4. Review all results on the measurement table.

Manual LV and RV Myocardial Mass Procedure

1. Select the appropriate cardiac phase.
2. Select  for LV epicardium or  for RV epicardium.
3. Trace the epicardial contour.
4. Proceed to the next slice using  or use <-- and --> or select the thumbnail.
5. Repeat steps 3 and 4 until the entire left and/or right ventricular epicardium is segmented.
   The mass results are automatically updated as the epicardial contours are defined.

Review Segmentation Accuracy/Editing

1. Play the short axis series in cine mode and review the accuracy of the contours.
2. Edit any contours that are inaccurate.
3. Review matrix mode and confirm ED and ES assignments.
4. Review all results on the measurement table.

Basal Interpolation

To perform interpolation for the basal slices, identify either the mitral or tricuspid valve annulus on a long axis view.

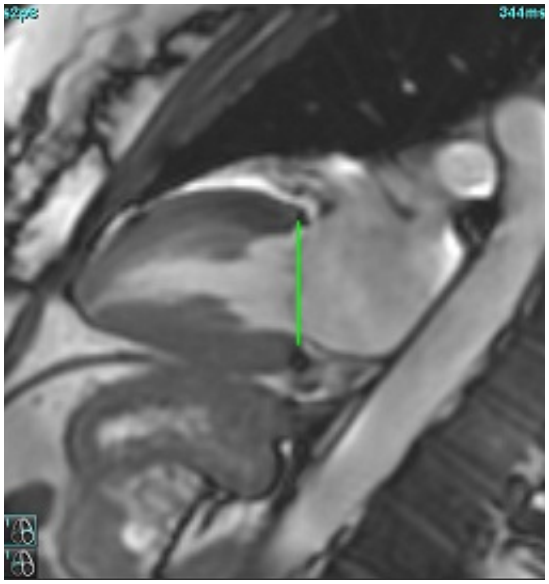
NOTE: The automatic basal interpolation feature is turned “off” unless the **Apply MV and TV Annulus** and **Apply Basal Line Interpolation** is checked in preferences. Select **Tools > Preferences > Edit System.** (**Admin Only**)

1. For LV basal interpolation, select a 2-Chamber view in the cross-reference mode.
2. Select  .
3. Define the MV annulus, as shown in Figure 2. Review the placement of the line on the appropriate end-systolic and end-diastolic phases using the cine controls.

NOTE: Multi-plane basal interpolation is supported. For example, the MV annulus can be identified on 2-chamber and a 4-chamber views; fit is done between the two planes.

NOTE: Locate the series of either the MV or TV annulus placement by clicking  or  located in the lower left on the viewport.

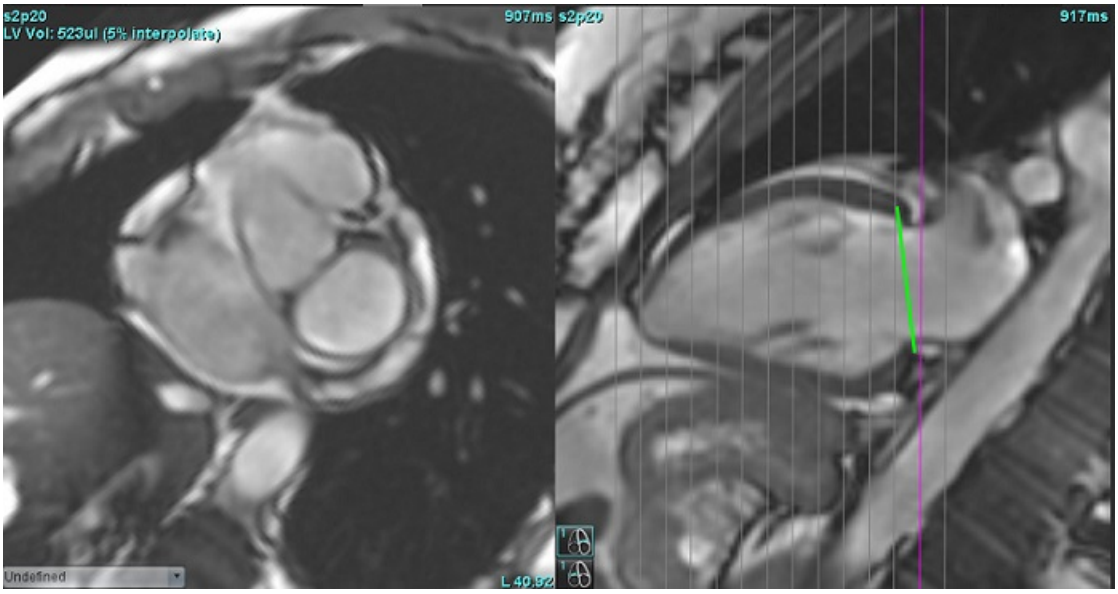
FIGURE 2. MV Annulus



4. Review the updated calculation by reviewing the cross-reference slices in relationship to the line.

As shown in Figure 3, the interpolated volume calculation is based upon the relationship of the line intersection with the slice (pink line) this volume is now included in the volume results. The actual region of interest will not be shown. Slices that have been interpolated will state the volume amount with the percentage of interpolation in left hand corner of the image, as shown in Figure 3.

FIGURE 3. Volume Calculation

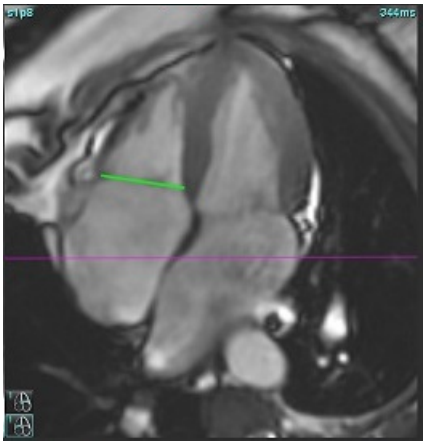


5. For RV basal interpolation, select a 4-Chamber view in the cross-reference mode.

6. Select  .

7. Define the TV annulus, as shown in Figure 4. Review the placement of the line on the appropriate end-systolic and end-diastolic phases using the cine control.

FIGURE 4. TV Annulus



8. Review the updated calculations by reviewing the cross-reference slices in relationship to the line and review the ED and ES assignments in the matrix view.
9. To reset the result back to the original value, right mouse click and hold directly on the line to select delete or left mouse click on the line and use the delete key on the keyboard.

Review Accuracy

1. Play the long axis series in cine mode and review the placement of the line.
2. Adjust the line placement as needed.
3. If automatic insertion has been performed, check for proper series selection and line placement. If not properly placed perform a right mouse click on the line and delete.

Motion Correction Between Series

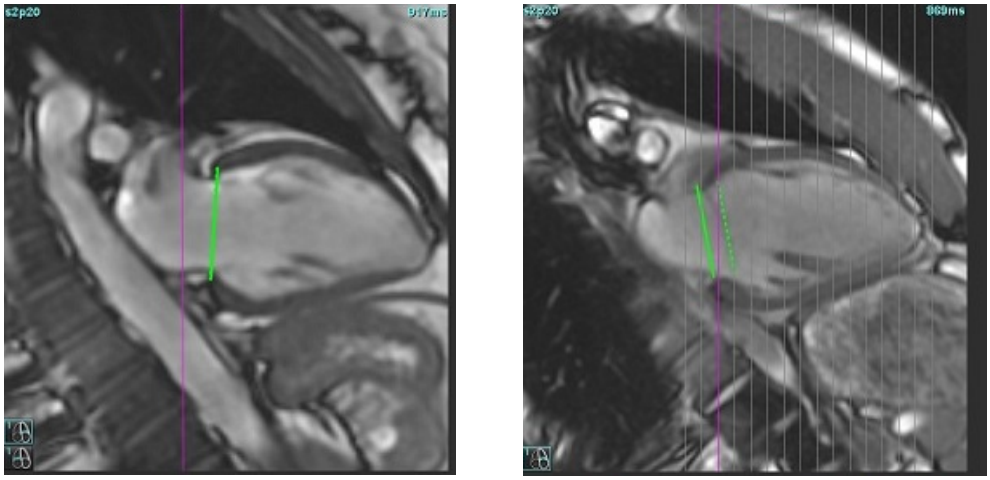
Motion Correction Between Series compensates for cardiac translation that may occur between the acquisition of long axis images and short axis images. Errors in chamber volumes can occur if annular planes are derived from long axis images that do not spatially register with short axis images that contain the endocardial contours used for volumetric analysis. The error may occur if the short and long axis images are acquired in different stages of the respiratory cycle or if the patient changes position (i.e. translates) between the acquisition of the long and short axis images. When **Motion Correction Between Series** is selected, the end-diastolic center of the atrioventricular valve plane is defined by the most basal end-diastolic ventricular endocardial contour. The angulation of the annulus valve plane and the relative position of its center on other cardiac phases are determined by the angulation of the annulus lines and the relative position of the annulus centers as defined on the long axis images.

NOTE: To access the feature in Function Analysis mode. Select **Tools > Preferences > Edit System**. (**Admin Only**) Select **Motion Correction Between Series** under Function.

1. Perform LV and RV auto segmentation for all phases all slices.
2. Perform the Basal Interpolation for the LV and RV.
3. Select  .

4. Agreement can be confirmed when the dashed line appears superimposed over the MV annulus line placement, as shown in Figure 5 (left).

FIGURE 5. Confirmed Agreement (left) Cardiac Translation (right)



5. Figure 5 (right) shows a gap between the solid and dashed annulus lines.
6. The solid line represents the annulus plane drawn on the long axis image. The dashed line represents the translated annulus plane based on the location of the most basal endocardial contour.

NOTE: It is the responsibility of the user to determine the reason for the gap between the solid and dashed line, and to correct the analysis if necessary. Possible reasons for a gap include:

- The most basal endocardial contour on the short axis image is not drawn on the correct slice. If not corrected, the software will incorrectly compensate for translation.
- The annulus line does not represent the position of the annulus. If not corrected, the software will incorrectly compensate for translation.
- Cardiac translation between the long axis acquisition and the short axis acquisition.

If the most basal endocardial contour is drawn on the correct slice and the annulus line is drawn correctly on the long axis image, then the gap between the solid and dashed line represents true cardiac translation and the software will correct for that translation.

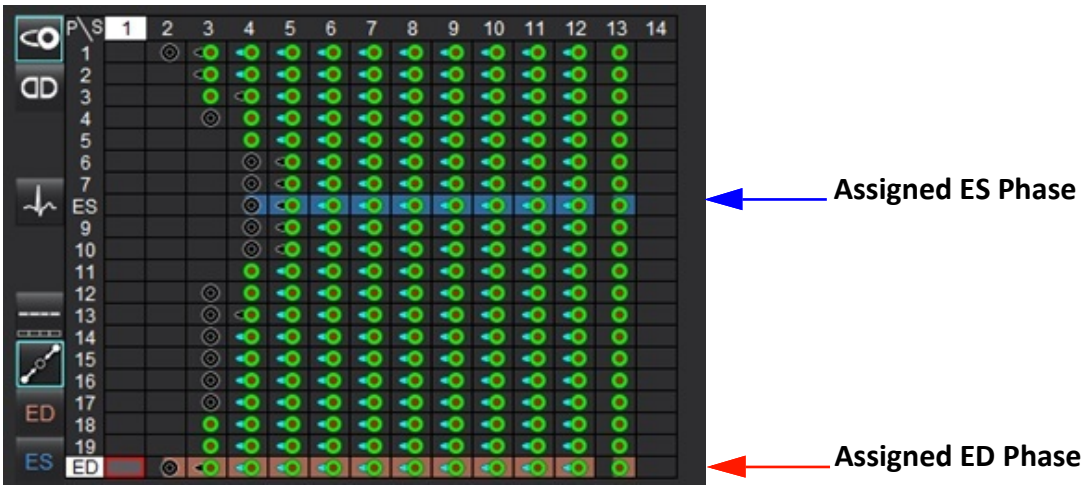
7. Review the translation if the RV segmentation has been performed and the TV annulus has been placed.

Matrix View

NOTE: The x (slice) and y (phase) axis can be swapped. Select **Tools > Preferences > Edit**. Select **Flip X (slice) and Y (phase) axis for matrix mode** under Function. If the preference is changed the application should be restarted.

The matrix is used to review and assign the end-systolic and end-diastolic phases and for navigation between phases and slices. Assigned ED and ES phases are indicated as solid color blocks of red for ED or blue for ES as shown in Figure 6.

FIGURE 6. Matrix View for LV and RV



Ventricular Assignment

The ED (Figure 7) or ES (Figure 8) assignment for the left ventricle is made by selecting the right side of an individual matrix cell.

FIGURE 7.

FIGURE 8.

The ED (Figure 9) or ES (Figure 10) assignment for the right ventricle is made by selecting the left side of an individual matrix cell.

FIGURE 9.

FIGURE 10.

Atrial Assignment

The ED (Figure 11) or ES (Figure 12) assignment for the left atrium is made by selecting the right side of an individual matrix cell.

FIGURE 11.

FIGURE 12.

The ED (Figure 13) or ES (Figure 14) assignment for the right atrium is made by selecting the left side of an individual matrix cell.

FIGURE 13.

FIGURE 14.

Matrix Functionality

The deletion of contours can be performed by ether selecting a phase or slice row or an individual matrix cell and performing a right mouse click.

Interpolation is noted by the non-colored indicators. Interpolation can be applied for the following conditions:

- If the same cardiac phase is traced across slices for either end-systole or end-diastole and a slice has been skipped.
- If the same cardiac phase is traced across slices for either end-systole or end-diastole and/or a slice has been skipped the basal interpolation can be applied.

NOTE: To apply slice interpolation, select Tools > Preferences > Edit. Check **Apply Mid Ventricular Interpolation**.

Display Options

Display LV/RV Matrix

Display RA/LA Matrix

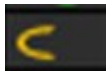
Selections

One Heartbeat per Slice		Analysis mode for non multiple heartbeat acquisitions.
Multiple Heartbeats per Slice		Analysis mode for multiple heartbeat acquisitions.
Global ED/ES		When global is selected, the combined volume is based upon the ED and ES assignments having the same phase.
Single ED/ES		When single is selected, the combined volume is based upon the largest and smallest volume per phase for each slice. Must select Propagate All Slices, All Phases mode to activate. Basal interpolation is not supported in this mode.
Basal Interpolation		Select to turn "On" or "Off." Indicated directly on the volume curve.
ED		Click directly on the left side of the matrix cell for the RV or the right side of the cell for the LV to assign the End-diastolic phase. Click directly on the left side of the matrix cell for the RA or the right side of the cell for the LA to assign the End-diastolic phase.
ES		Click directly on the left side of the matrix cell for the RV or the right side of the cell for the LV to assign the End-systolic phase. Click directly on the left side of the matrix cell for the RA or the right side of the cell for the LA to assign the End-systolic phase.
Max		Selection for maximum atrium volume*
Min		Selection for minimal atrium volume*

*Refer to the note under Atria on page 84.

Chamber Indicators

Ventricular Segmentation Indicators

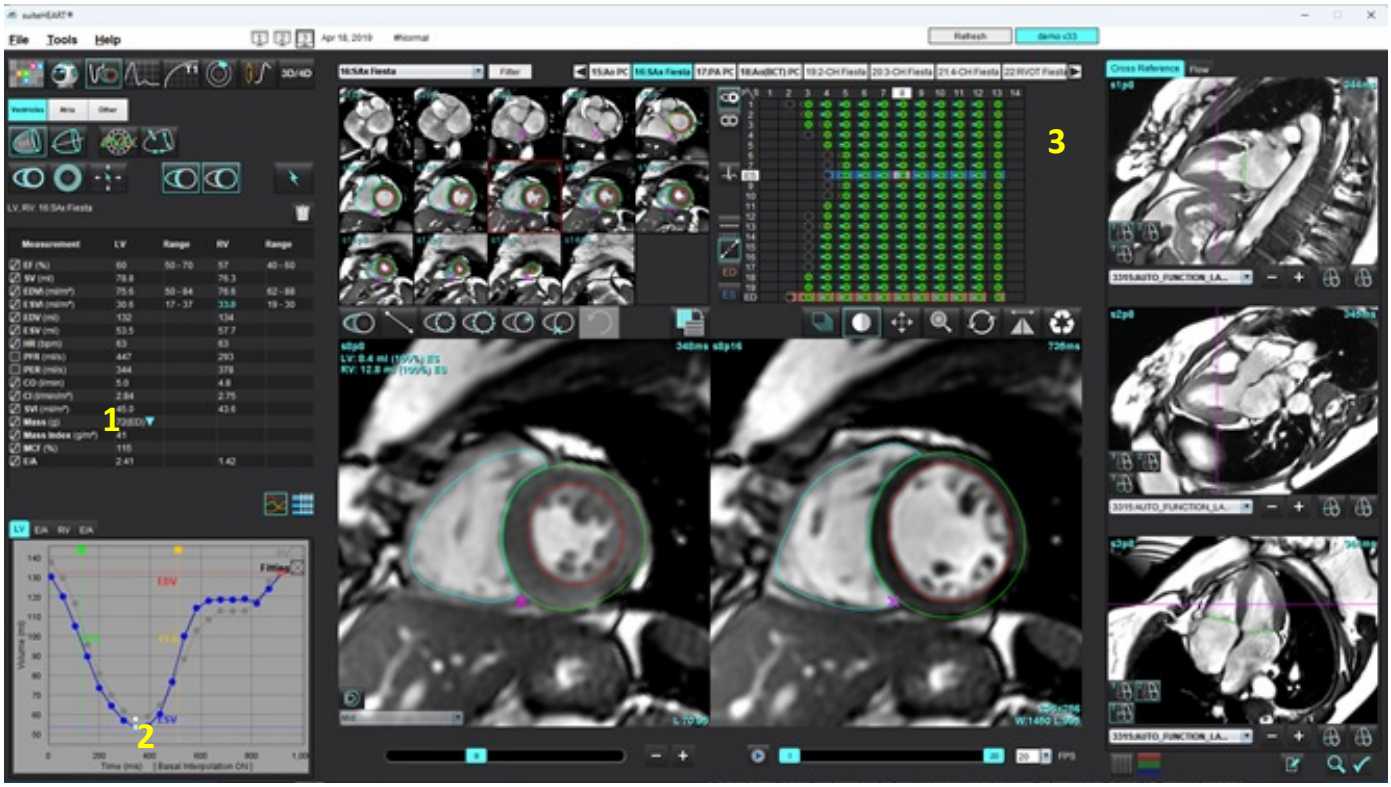
			
LV Endocardium	LV Epicardium	RV Endocardium	RV Epicardium

Atrial Segmentation Indicators

	
RA Endocardium	LA Endocardium

Ventricular Function Analysis Results

FIGURE 15. Ventricular Auto-Segmentation Results



1. Volumetric results, 2. Volume curve, 3. Matrix

Volume Curve

When auto segmentation is performed for all phases and all slices for either the LV or RV, a ventricular volume versus time curve is generated, as shown in Figure 15. Right mouse click to include the volume curve on the report.

- The red circle indicates end-diastolic (labeled ED on image viewport).
  - Click and drag the red circle to reassign ED.
- The blue circle indicates end-systolic (labeled ES on image viewport).
  - Click and drag the blue circle to reassign ES.
- The green cursor indicates Peak Ejection Rate (PER) ml/sec. (Interactive Vertical Cursor).
- The yellow cursor indicates Peak Filling Rate (PFR) ml/sec. (Interactive Vertical Cursor).
- Corresponding image phase selection is indicated by the white circle on the volume curve.
- To view the E/A curve click on the tab for LV E/A or RV E/A.

Volumetric results are displayed on the measurement table.

- To review the ventricular mass results or mass index, left-click on the inverted triangle for either the LV or RV.
- The phase selected from the phase list is shown in the report. The default is ED.

FIGURE 16. Mass Results

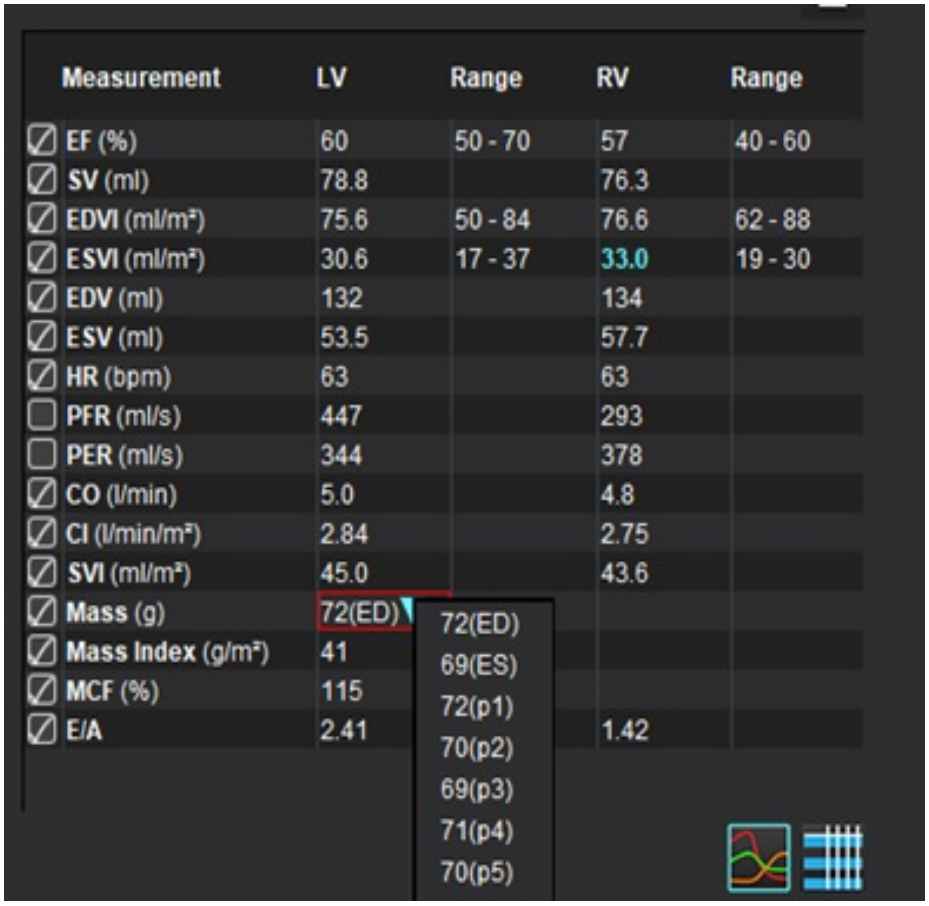
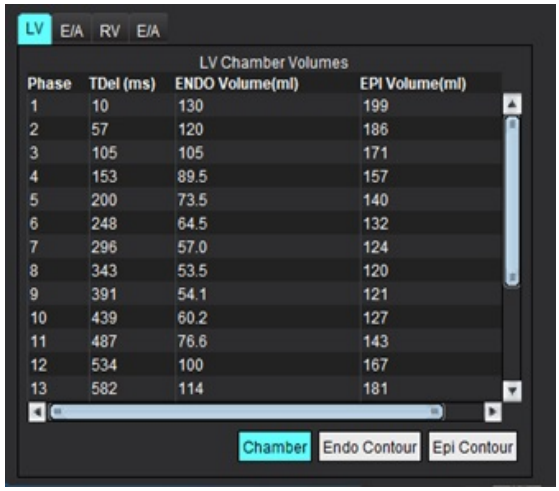


FIGURE 17. Chamber Volume Table



LV and RV volumes are displayed in the Chamber Volume table.

Left Ventricular Regional Analysis

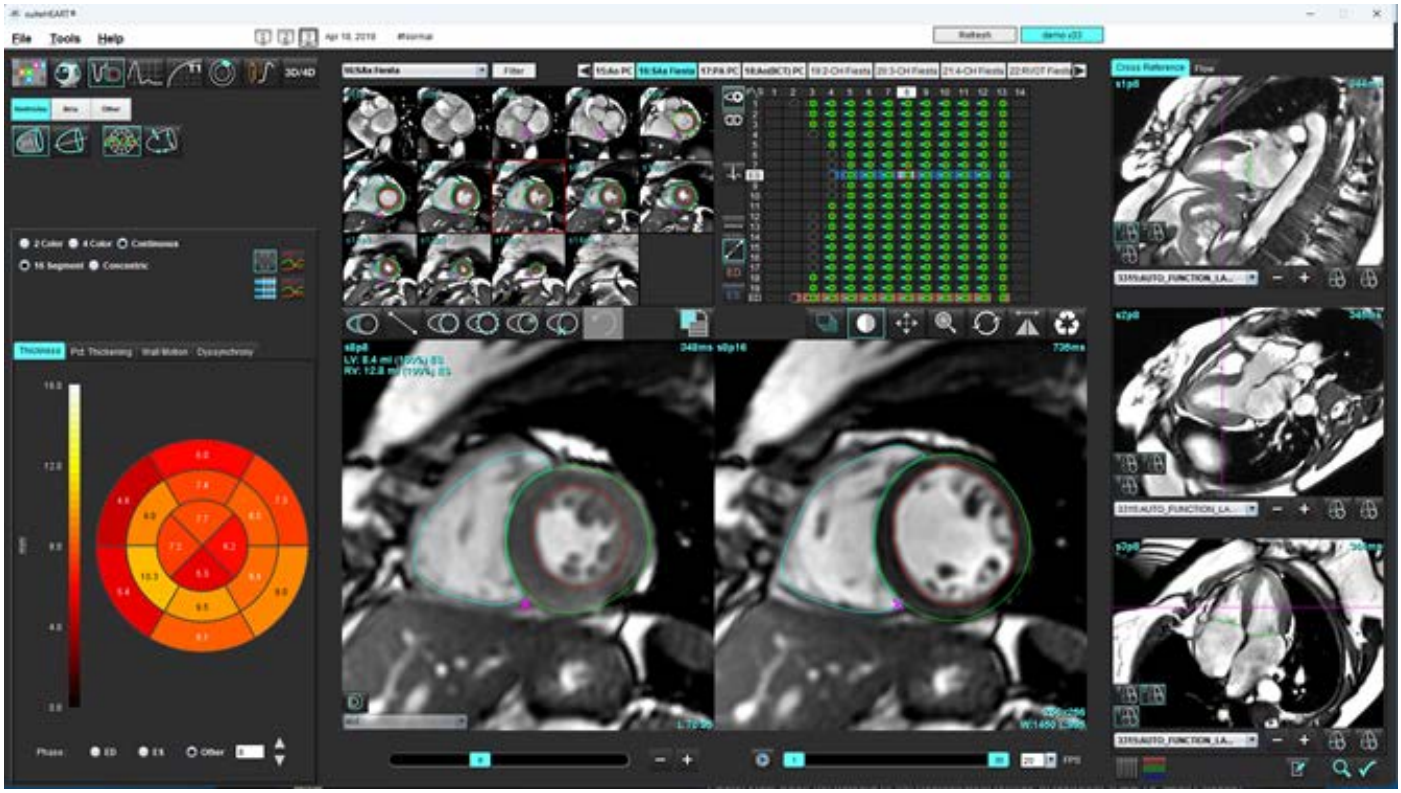
LV Regional Analysis allows for the review of wall motion, wall thickness, wall thickening and wall thickness results.

NOTE: If the LV and RV buttons in Function Short Axis are both deselected or if the chamber selection button in Long Axis is deselected, the Start Auto Propagation button will be disabled.

1. Perform Auto LV segmentation for all slices in all phases (refer to page 70).
2. Review the placement of the RV insertion point on each slice and adjust the RV insertion point for the basal slices.
3. To add an RV insertion point to a slice location, click RV insertion point  , select an auto segmented slice and deposit the RV insertion point.
4. Confirm basal, mid and apical classification. 

5. Click Regional Analysis  . Thickness, Percent Thickening and Wall Motion will display in a plot, graph or table formats.

FIGURE 18. Regional Analysis



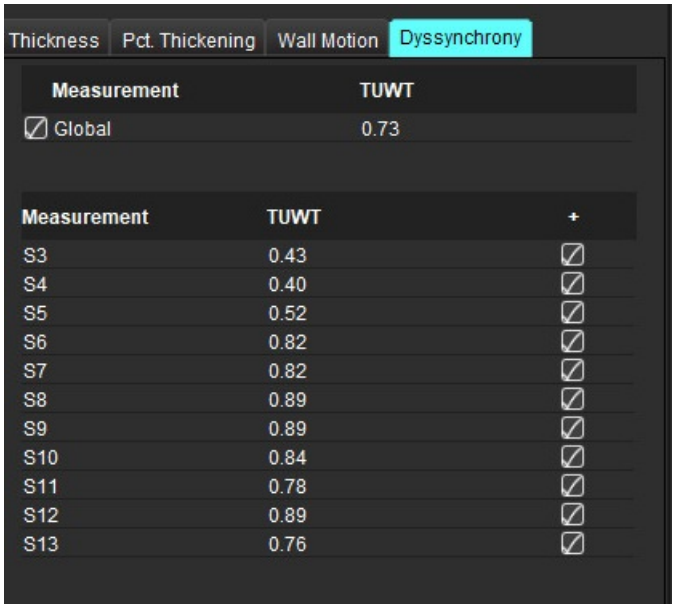
Dyssynchrony Analysis

Dyssynchrony is an extension of the Regional Analysis results allowing for the calculation of the Temporal Uniformity of Wall Thickness (TUWT) base upon circumferential information obtained from the Regional Analysis.

Dyssynchrony Analysis Procedure

1. Perform LV auto segmentation (See Perform Auto Segmentation for All Slices in a Single Phase on page 70.).
2. Select Regional Analysis  .
3. Select the Dyssynchrony tab.
4. The measurement table will show the results for each slice and the mean global result.
5. The global result calculation is optimal when only LV mid-ventricular slices are included. To remove a slice result from the global result calculation, click directly on the box with the checkmark in the far right column (Figure 19).

FIGURE 19. Global Result Calculation



Recommended References

Bilchick et al, “Cardiac Magnetic Resonance Assessment of Dyssynchrony and Myocardial Scar Predicts Function Class Improvement Following Cardiac Resynchronization Therapy”, JACC, Vol.1:No 5: 2008 p.561-8

Helm RH, Leclercq C, Faris OP, Ozturk C, McVeigh E, Lardo AC, Kass DA. Cardiac dyssynchrony analysis using circumferential versus longitudinal strain: implications for assessing cardiac resynchronization. Circulation. 2005 May 31;111(21):2760-7. doi: 10.1161/CIR-CULATIONAHA.104.508457. Epub 2005 May 23. PMID: 15911694; PMCID: PMC2396330.

Auto Long Axis Segmentation

1. Select  .
2. Select a long-axis series.

   NOTE: If preprocessing has been performed the AUTO_FUNCTION_LAX series will be used for analysis. If different long axis views are preferred, a new series can be created in the viewer.

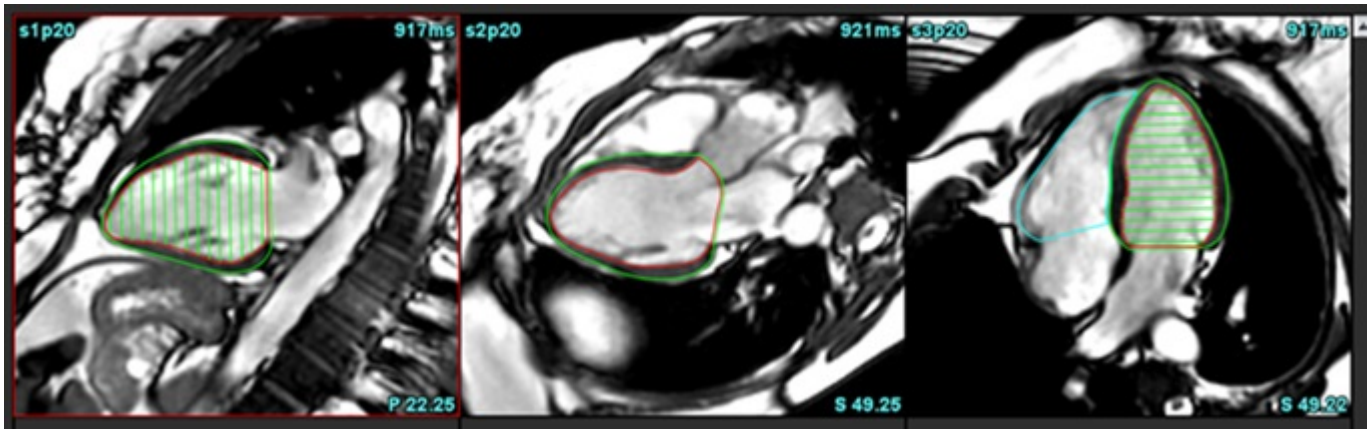
   NOTE: The number of phases need to match for all long axis views. If they do not match, only the 4ch will be segmented.

3. Select  .
4. Select the  to propagate all slices, all phases.
5. Click  to auto segment both LV and RV. Use  for LV only and  for RV only.

   NOTE: Volume results are only obtained from the 2ch and 4ch. The segmentation for 3ch LV and 4ch RV are used for Strain analysis (research only). The Fractional Area Change (FAC) will be obtained from the 4ch RV.

6. Review all traces.
7. To manually trace, click  to trace the left ventricular endocardium and click  to trace the right ventricular endocardium for both end-diastole and end-systole.
8. For the calculation of mass, trace the left ventricular epicardium  .

FIGURE 20. Long-axis Segmentation



The results are displayed on the Measurement table.

NOTE: The centerline will only be displayed if the algorithm cannot find the annulus line.

NOTE: The default measurement labels for atrial volumes are EDV which refers to the maximum atrial volume and ESV which refers to the minimal atrial volume. To set the labels as MaxV and MinV, select **Tools > Preferences > Edit**. Select **Atrial Volume Label: MaxV, MinV under Function**.

Manual LA and RA Analysis

1. Select the appropriate series from the Image View.

   NOTE: For optimal results, it is recommended to use a 4-chamber stack for analysis. The 4-chamber view better delineates the atrial anatomy.

2. Click 

.

3. Select the  button.

4. Locate the end-diastolic phase.

Define the Endocardium

1. Select  for LA Endocardium or  for RA Endocardium.

2. Trace the endocardial contour.

3. Proceed to the next slice using  , use the left and right arrow keys, the mouse scroll wheel or click the thumbnail.

4. Repeat steps 2 and 3 until the entire atrium is segmented.

5. Locate the end-systolic phase.

6. Repeat steps 2 and 3 on the end-systolic phase until the entire atrium is segmented.

   NOTE: The software automatically defines the end-diastolic phase as the phase with the largest volume, and the end-systolic phase as the phase with the smallest volume. The end-diastolic and end-systolic phase assignments are updated during segmentation.

7. If a short axis view has been used, identify the MV and/or TV annulus.

Auto LA or RA Analysis

1. Click 

.
2. Select a long-axis series.

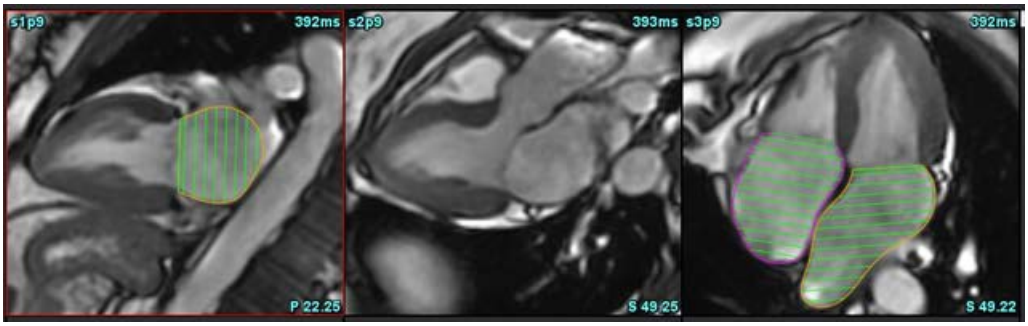
   NOTE: If preprocessing has been performed the AUTO_FUNCTION_LAX series will be used for analysis. If different long axis views are preferred, a new series can be created in the viewer.

3. Select  .
4. Select  to propagate all slices, all phases.
5. Click  to auto segment both LA and RA. Use  for LA only and  for RA only.
6. Review all traces.

   NOTE: The centerline will only be displayed if the algorithm cannot find the annulus line.

7. To manually trace, click  to trace the RA endocardium and click  to trace the LA endocardium for both end-diastole and end-systole.

FIGURE 21. Centerline Placement



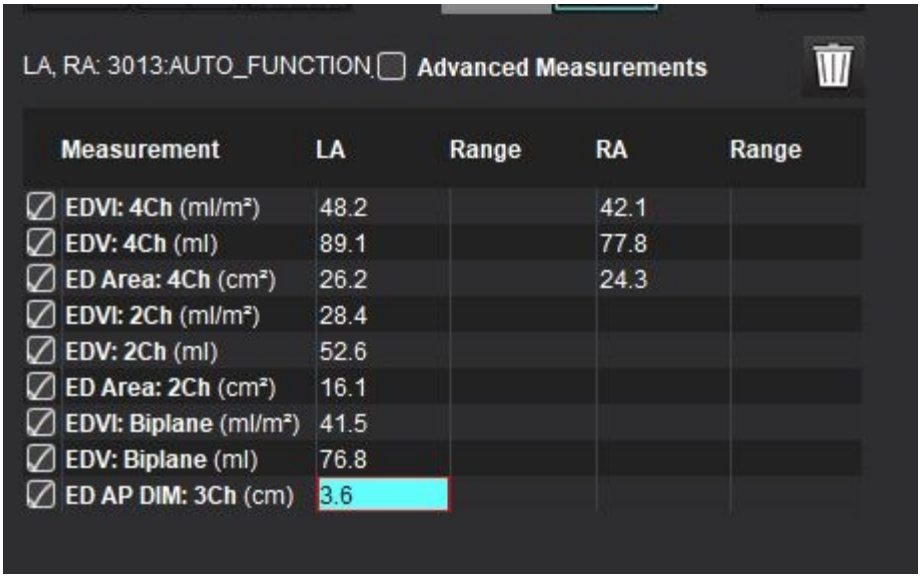
Atrial Measurements

1. Click 

.
2. Select the appropriate series.
3. To perform an LA dimension, click directly on the table in the column for ED AP DIM:3ch and then deposit two points. See Figure 22.
4. Check 

for more detailed results.

FIGURE 22. Atrial Measurement

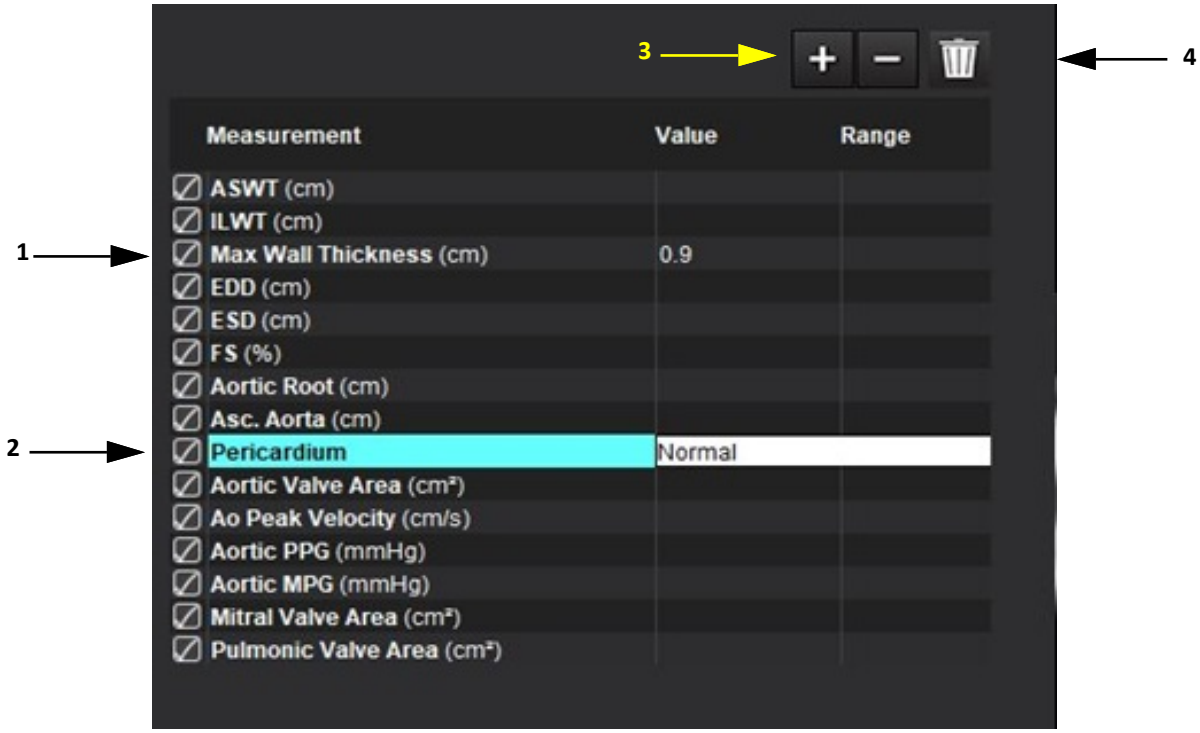


NOTE: Atrial ED areas are automatically obtained from the ED assignment. Use the matrix to change.

User Defined Measurements

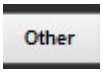
The application allows for the reporting of linear and area measurements. Tool tips are available by placing the cursor over the measurement listed on the table.

FIGURE 23. Default Measurements



1. Auto Max Wall Thickness, 2. Type-in Field for Pericardium, 3. Add/Remove Custom Measurement, 4. Delete all Measurements

Perform a Measurement

1. Select  .
2. Select the series.
3. Click 

button.

   NOTE: The max wall thickness is automatically measured. Click directly on the result to locate the measurement. If edits to the endo or epi are performed, the measurement location will update.

4. Locate the image with the anatomy to be measured.
5. Click the desired measurement, which will highlight to indicate the selection is active.

CAUTION: Accurate placement of the line is critical to measurement results. Misdiagnosis may occur if measurements are inaccurate. Measurements should only be created by a properly trained and qualified user.

6. To edit, click on annotation and when the color changes to purple it is active. Place the cursor over one of the endpoints and adjust the endpoint.

   The measure distance value updates accordingly in the Measurements table when you move the cursor outside of the Image Editor window.

   Place the cursor over the center marker to move the entire measure distance line to another location.

NOTE: To reset the measurement, select the measure distance line and access the right mouse menu and select trash can; or use the Delete key on the keyboard.

NOTE: Custom measurements can be reordered in the Print Preferences Other tab in Preferences, select **Tools** > **Preferences** > **Edit** then select **Print** tab.

Delete Measurements

Click  to delete all measurements.

Add Custom Measurement

1. Click the  .
2. Enter a unique label in the Add Custom Measure pop-up window.
3. Select the measurement type as either Linear or Area.
4. Select **OK**.

Remove Custom Measurement

1. Click the  .
2. Select the custom measurement(s) to be removed from list.
3. Choose **Select**.

NOTE: Custom measurements created will be present for all future analysis until removed from the listing.

Aortic Valve Plane Analysis

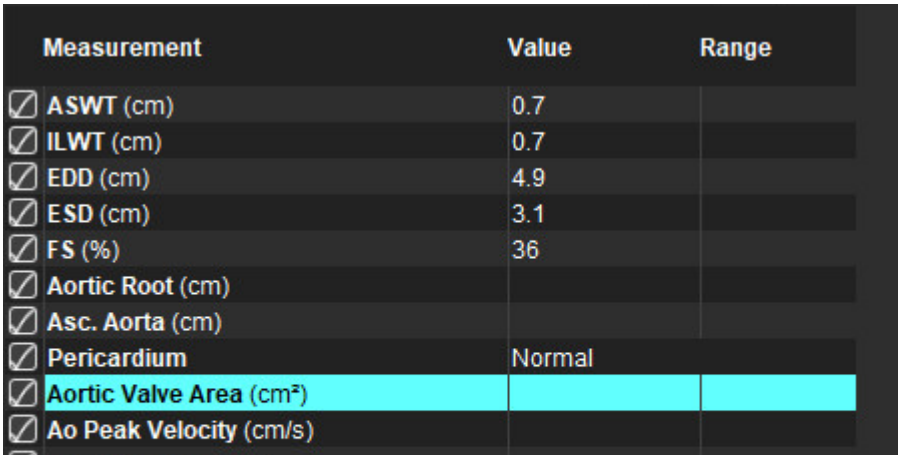
The aortic valve plane analysis feature allows for the calculation of peak velocity, peak pressure gradient and mean pressure gradient for the aortic valve.

Using the results from the LV auto segmentation, the pressure gradient is computed from the cardiac output, based on the frame-by-frame changes in left ventricular systolic volume.

Aortic Valve Plane Analysis Procedure

1. Perform LV auto segmentation on all slices in all phases (see page 70).
2. Select a series that demonstrates valve anatomy.
3. Select Aortic Valve Area from the measurement table (Figure 24) and perform planimetry of the aortic valve, as shown in Figure 25.

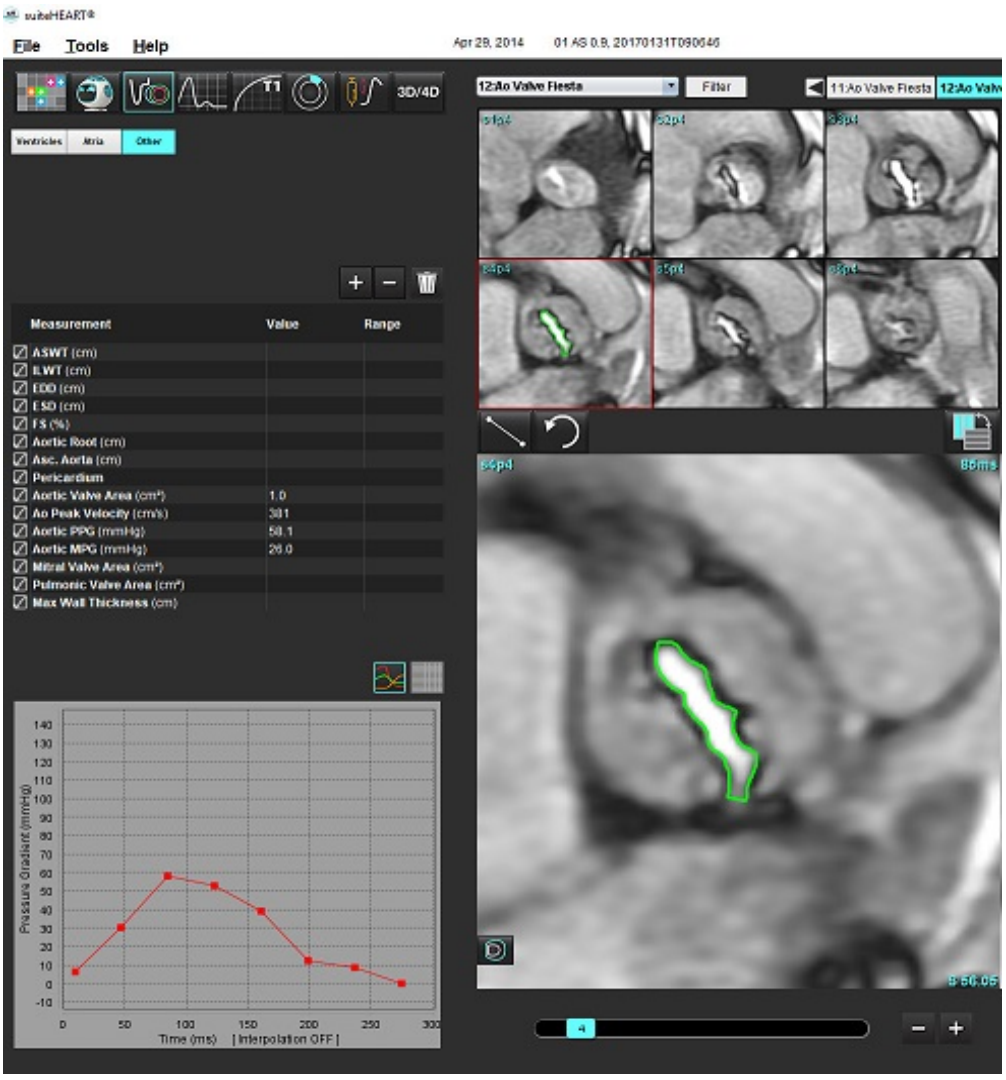
FIGURE 24. Aortic Valve Area



4. Upon completion of the ROI, the table will update with the results and present a graph showing the pressure gradient over time.

Click  to delete all measurements.

FIGURE 25. Aortic Valve Plane Analysis



WARNING: It is recommended that you are qualified in performing cardiac analysis, if the analysis results are to be used to reach a diagnosis.

NOTE: The results of Peak Velocity, Peak Pressure Gradient, and Mean Pressure Gradient obtained by Aortic Value Plane Analysis are not valid in patients with mitral regurgitation or a shunt.

Recommended References

Hakki, A. H. et al. “A Simplified Valve Formula for the Calculation of Stenotic Cardiac Valve Areas.” Circulation 63 (1981): 1050–1055.

Patel, K., Uretsky, S., Penesetti, S. et al. COVA (cardiac output valve area): a reliable method for determining aortic transvalvular pressure gradients that does not use phase contrast imaging. J Cardiovasc Magn Reson 16 (Suppl 1), P247 (2014). https://doi.org/10.1186/1532-429X-16-S1-P247

Myocardial Contraction Fraction

The myocardial contraction fraction (MCF) requires complete endo and epi LV segmentation of the short axis and is reported on the result table for short axis function. It is the user's responsibility to establish their own normal ranges for MCF.

Recommended References

Abdalla M, Akwo EA, Bluemke DA, Lima JAC, Shimbo D, Maurer MS, Bertoni AG. Association between reduced myocardial contraction fraction and cardiovascular disease outcomes: The Multi-Ethnic Study of Atherosclerosis. Int J Cardiol. 2019 Oct 15;293:10-16. doi: 10.1016/j.ijcard.2019.07.040. Epub 2019 Jul 11. PMID: 31327521; PMCID: PMC7175692.

Arenja N, Fritz T, Andre F, Riffel JH, Aus dem Siepen F, Ochs M, Paffhausen J, Hegenbart U, Schönland S, Müller-Hennessen M, Giannitsis E, Kristen AV, Katus HA, Friedrich MG, Buss SJ. Myocardial contraction fraction derived from cardiovascular magnetic resonance cine images-reference values and performance in patients with heart failure and left ventricular hypertrophy. Eur Heart J Cardiovasc Imaging. 2017 Dec 1;18(12):1414-1422. doi: 10.1093/ehjci/jew324. PMID: 28165128.

Maurer MS, Packer M. How Should Physicians Assess Myocardial Contraction?: Redefining Heart Failure With a Preserved Ejection Fraction. JACC Cardiovasc Imaging. 2020 Mar;13(3):873-878. doi: 10.1016/j.jcmg.2019.12.021. PMID: 32139035.

Estimated LVFP (Left Ventricular Filling Pressure)

NOTE: This parameter only applies to certain types of heart failure, not applicable for hypertrophic cardiomyopathy or mitral insufficiency. It is the user's responsibility to determine clinical interpretation.

The estimated LVFP requires complete endo and epi LV segmentation of the short axis for left ventricular mass at end-diastole and the atrial biplane result. The result is reported under function measurement table. It is the user's responsibility to determine clinical interpretation.

CMR PCWP (mmHg) = 5.7591 + (0.07505*LAV) + (0.05289*LVM)-(1.9927*sex)

Where:

sex [female=0, male =1]
LAV is left atrial maximum volume
LVM is left ventricular mass in diastole

Recommended References

Pankaj Garg, Ciaran Grafton-Clarke, Gareth Matthews, Peter Swoboda, Liang Zhong, Nay Aung, Ross Thomson, Samer Alabed, Ahmet Demirkiran, Vassilios S Vassiliou, Andrew J Swift, Sex-specific cardiac magnetic resonance pulmonary capillary wedge pressure, European Heart Journal Open, Volume 4, Issue 3, May 2024, oeae038, https://doi.org/10.1093/ehjopen/oeae038

Thomson R. J., Grafton-Clarke C., Matthews G., Swoboda P. P., Swift A. J., Frangi A., Petersen S. E., Aung N., and Garg P. (2024) Risk factors for raised left ventricular filling pressure by cardiovascular magnetic resonance: Prognostic insights, ESC Heart Failure, doi: https://doi.org/10.1002/ehf2.15011

MAPSE/TAPSE

The MAPSE/TAPSE analysis feature allows for the evaluation of ventricular function.

MAPSE uses the perpendicular distance of the end-systolic mitral annular plane midpoint to the end-diastolic plane. TAPSE uses the perpendicular distance of the end-systolic lateral tricuspid annular plane to the end-diastolic plane

The E' results are derived from the ventricular volume curve along with annular line placement on the 4-chamber SSFP cine view.

NOTE: To obtain MAPSE/TAPSE results during preprocessing, select **Tools > Preferences > Edit System**. (**Admin Only**) Check **Apply MV and TV Annulus** under Function. To apply auto Basal Interpolation for the short axis function check **Apply Basal Line Interpolation**.

Table 4: Terminology

Parameter	
MAPSE	Mitral Annular Plane Systolic Excursion
TAPSE	Tricuspid Annular Plane Systolic Excursion
E/A (LV & RV)	Ratio of the E Wave and A Wave from the derivative of the LV Volume curve (Figure 26)
e' Lateral	Most negative velocity near the end-diastolic time interval using the lateral end of the mitral annulus line (Figure 27)
e' Septal	Most negative velocity near the end-diastolic time interval using the septal end of the mitral annulus line (Figure 27)
e' Average	Average of the e' Lateral and e' Septal (Figure 27)

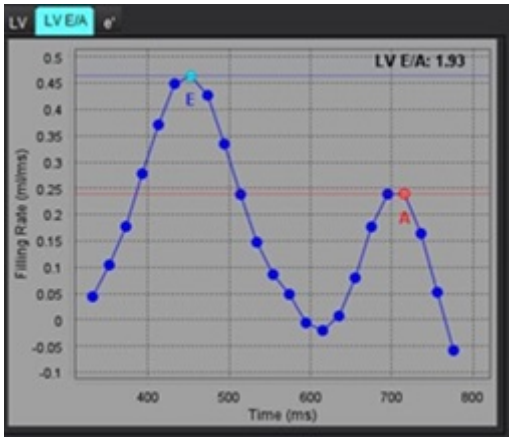
Analysis Procedure

1. Perform LV auto segmentation on all slices in all phases for the 4-Chamber view (Auto LV & RV Segmentation on page 67).

   NOTE: To auto obtain MAPSE/TAPSE results, select **Tools > Preferences > Edit System**. (**Admin Only**). Check **Apply MV and TV Annulus** under Function. (see Basal Interpolation on page 72)

2. To change the E (blue) designation click directly on the blue dot and move to another phase point on the graph. (Fig. 26)
3. To change the A (red) designation click directly on the red dot and move to another phase point on the graph. (Fig. 26)

FIGURE 26. LV Long Axis E/A Curve



4. Select the e’ tab, click directly on the blue dot for **Lateral** or the red dot for **Septal** and drag to the desired phase to reassign, if necessary (see Figure 27).

   e’ is designated as the most positive velocity. The values will be displayed on the long axis result table as shown in Figure 28.

FIGURE 27. e' Curve

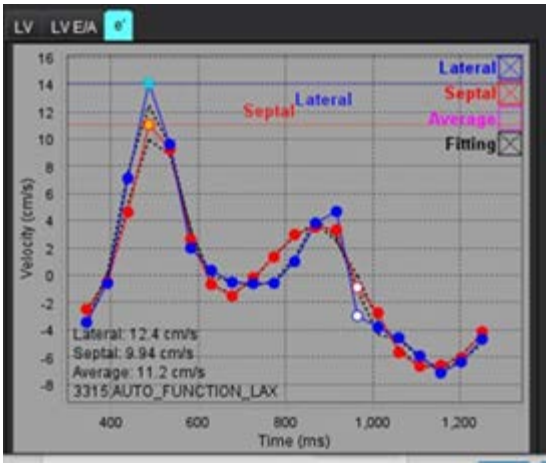
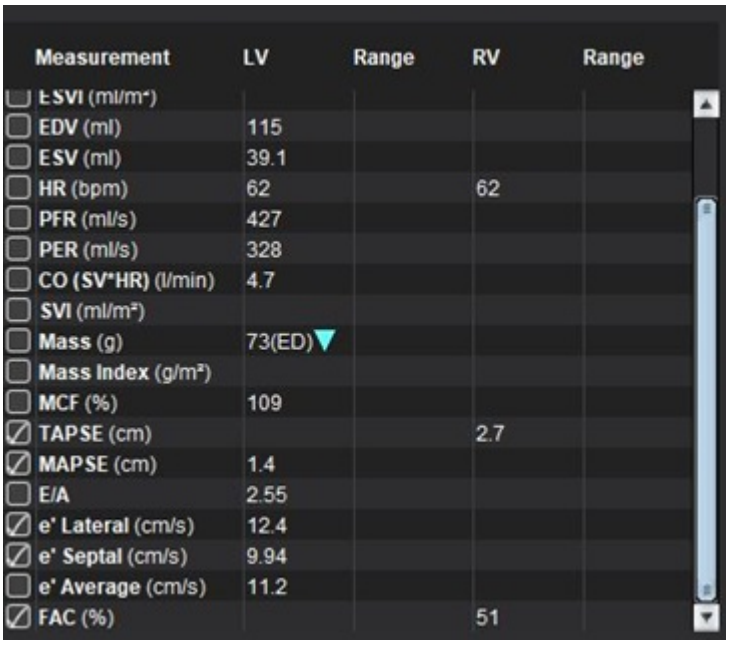


FIGURE 28. Long Axis Result Table



Measurement	LV	Range	RV	Range
ESVI (ml/m²)				
EDV (ml)	115			
ESV (ml)	39.1			
HR (bpm)	62		62	
PFR (ml/s)	427			
PER (ml/s)	328			
CO (SV*HR) (l/min)	4.7			
SVI (ml/m²)				
Mass (g)	73(ED)			
Mass Index (g/m²)				
MCF (%)	109			
TAPSE (cm)			2.7	
MAPSE (cm)	1.4			
E/A	2.55			
e' Lateral (cm/s)	12.4			
e' Septal (cm/s)	9.94			
e' Average (cm/s)	11.2			
FAC (%)			51	

Recommended References

Bulluck, H., Ngamkasem, H., Sado, D. et al. A simple technique to measure TAPSE and MAPSE on CMR and normal values. J Cardiovasc Magn Reson 16 (Suppl 1), P22 (2014). https://doi.org/10.1186/1532-429X-16-S1-P22

Real-Time Analysis

Required Images: Short axis SSFP acquisitions with multiple heartbeats per slice with no cardiac or respiratory gating.

It is recommended that each slice is imaged for a long enough time to cover at least one complete inspiration-expiration respiration cycle. The temporal resolution should be sufficient to visualize cardiac motion.

The software will auto-detect a real-time, multi-heartbeat acquisition based on the number of phases.

NOTE: Long Axis, Strain, Dyssynchrony, Aortic Valve Plane analysis, Basal Interpolation, and Auto Max Wall Thickness are not supported for real-time acquisitions.

NOTE: Regional Analysis for Pct Thickening and Wall Motion are only supported for End Systolic.

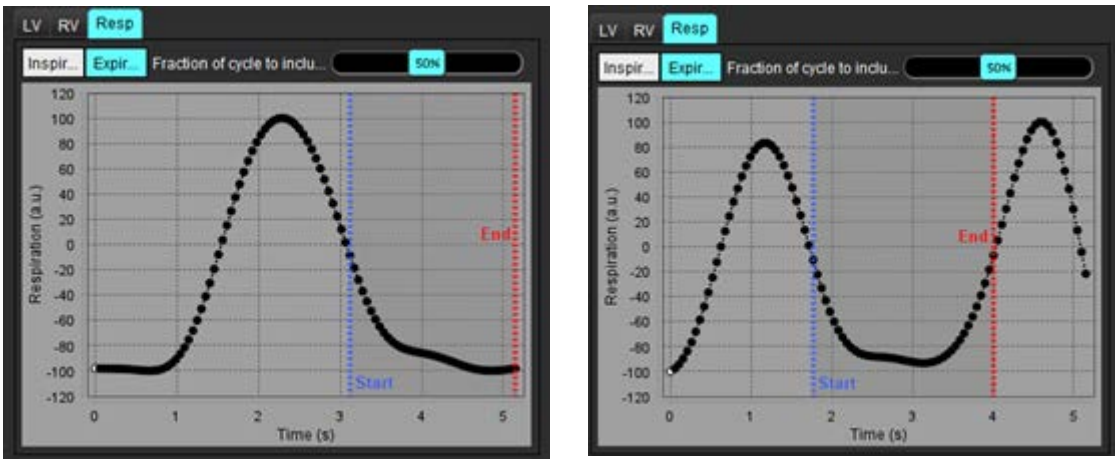
Analysis Procedure

1. Perform short axis auto segmentation on all slices all phases refer to page 67.
2. If a real-time acquisition is detected the  will be displayed on the matrix as shown in Figure 29.

FIGURE 29.

3. Review the Resp Tab, end-expiration analysis is recommended as shown in Figure 30.
4. The respiratory curve can be reviewed for each slice location by changing the slice. If the respiration window is changed, ED and ES assignment might also be changed so that they are within that new window. Clicking and dragging on the vertical lines on the graph changes the respiration window on the current slice only and it overrides the global respiration settings.
5. The fraction of the respiratory cycle to be included can be changed for all slices simultaneously by the slider bar (default 50%) except those slices which have been manually adjusted.

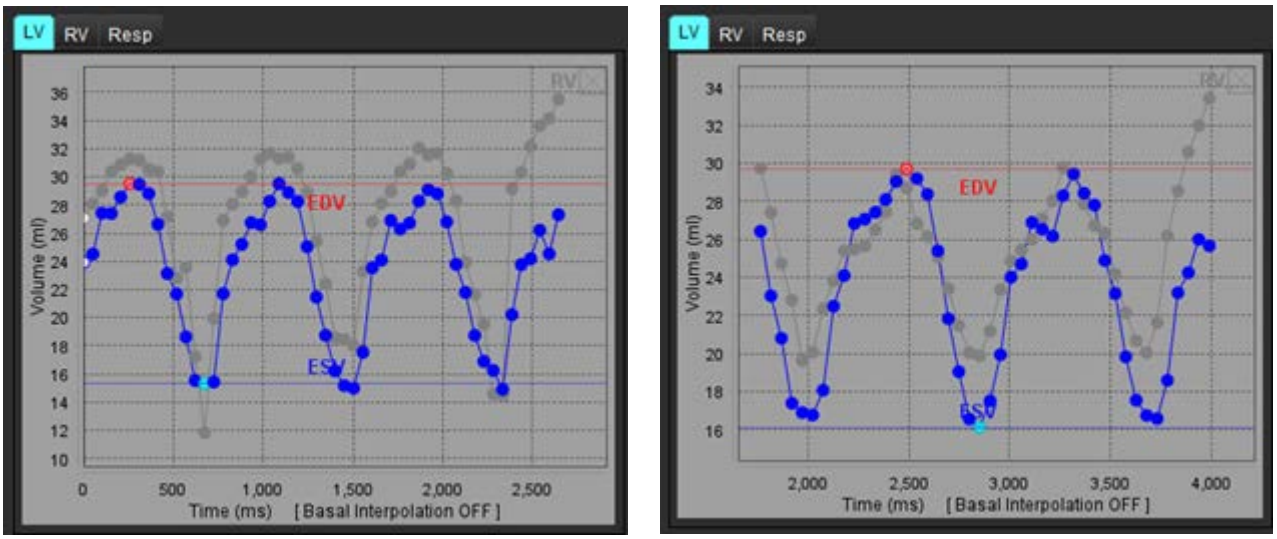
FIGURE 30. Respiratory curve examples from two different slices



6. The matrix view will show the limits used, ▼ is the start and the red arrow ▲ indicates the end of the part of the respiratory cycle used in the analysis.
7. Click on the LV or RV tab to review the ED and ES assignments for each slice (Figure 31).

   The ED and ES phases are auto detected for each slice. ED or ES phase assignments can be changed by clicking or dragging the circle for ED or ES. (The RV assignment is based on the LV phase assignments.)

FIGURE 31. LV volume curve examples from two different slices. Red dot = ED; blue dot = ES



NOTE: Each short axis slice has its own volume curve to review.

8. To calculate cardiac output enter the heart rate then click directly on the result table.

Recommended Reference

Chen C, Chandrasekaran P, Liu Y, Simonetti OP, Tong M, Ahmad R. Ensuring respiratory phase consistency to improve cardiac function quantification in real-time CMR. Magn Reson Med. 2022 Mar;87(3):1595-1604. doi: 10.1002/mrm.29064. Epub 2021 Oct 31. PMID: 34719067; PMCID: PMC8776600.

Flow Analysis

The Flow Analysis mode supports both 2D and 4D Flow acquisitions. Both manual and fully automatic segmentation with the quantification of flow volume, velocity, regurgitant volume, pressure gradient, pressure half-time, and Qp/Qs are supported. Based on user method selection(s), automatic calculation of aortic, mitral, pulmonic, and tricuspid regurgitation can be obtained. Accurate flow results depend on images being acquired using the correct scan plane, the appropriate acquisition parameters, and through-plane flow encoding.

NOTE: Auto segmentation may be less accurate in cases where image quality is poor. In those cases, the user is responsible for editing the contours or performing manual segmentation.

NOTE: If both 2D phase contrast and inline 4D Flow analysis has been performed, all results will be available in Flow Analysis Mode.

The Preprocessing feature supports the identification of vessel types for 2D phase contrast, as listed in Table 1, and auto aliasing detection and correction. Refer to the suiteDXT Instructions for Use.

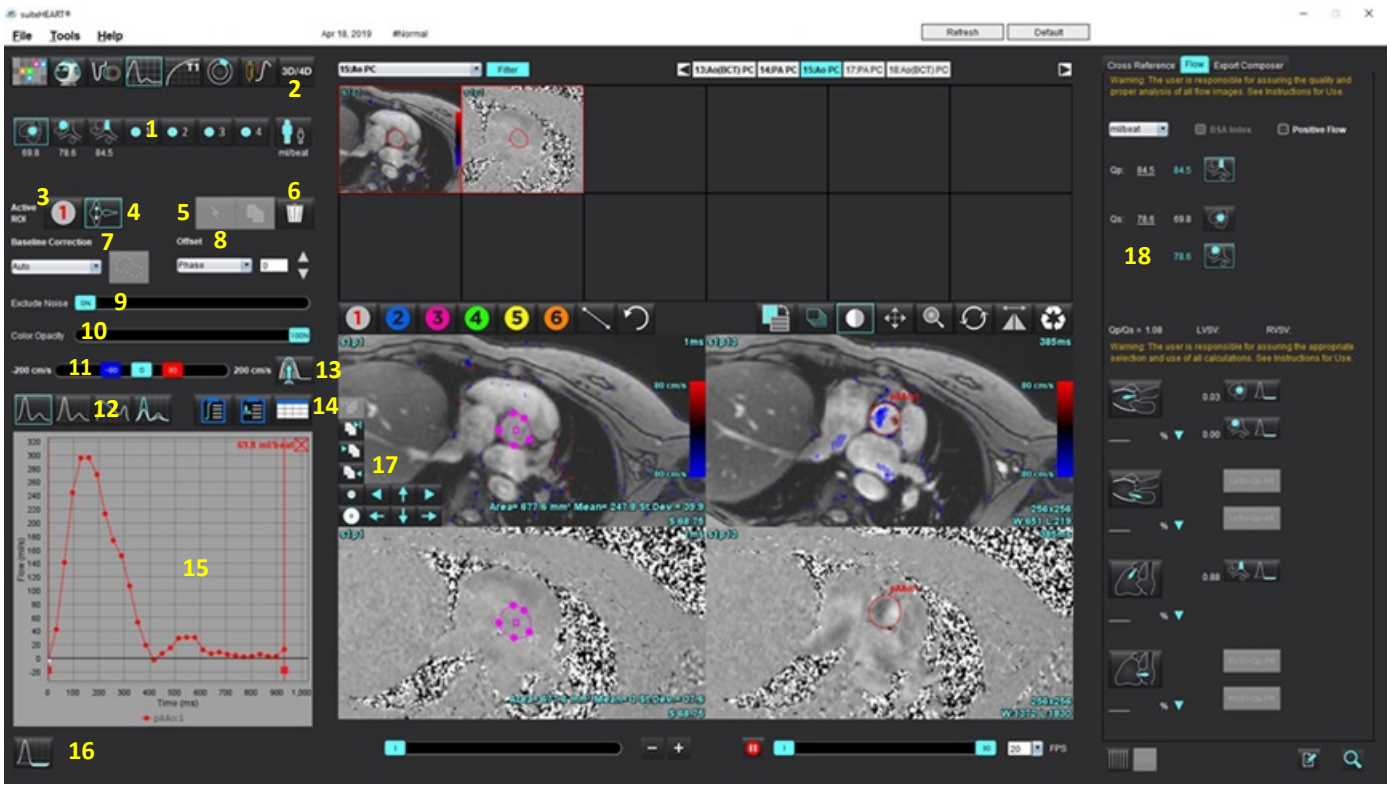
WARNING: Following preprocessing, the user is responsible for assessing the accuracy of the entire analysis and making any necessary corrections. A comprehensive review should include:

- ROI placement
- Correct vessel identification for each category
- Baseline correction
- Auto aliasing correction and detection

WARNING: The user is responsible for the accurate placement and correct category assignment of all regions of interest (ROIs), including those generated or modified by the auto segmentation algorithms. The quantitative values generated by the software depend on the accurate placement and correct vessel category assignment of all regions of interest.

WARNING: The application assists in the analysis of the images only and does not automatically produce a clinical interpretation of the results. The use and placement of quantitative measurements is at the discretion of the user. Misdiagnosis can occur if measurements are inaccurate. Measurements should only be created by a properly trained and qualified user.

FIGURE 1. Flow Analysis Interface Overview



1. Vessel Categories, 2. Adult/Pediatric Selection, 3. Active ROI selection, 4. Invert Graph, 5. Propagate selections, 6. Delete options, 7. Baseline, correction drop- down menu 8. Offset: Phase, Dilation, Flow, 9. Exclude Noise Pixels, 10. Color Opacity Control, 11. Aliasing Correction, 12. Curve Mode Selections, 13. Auto Aliasing, 14. Result table selections, 15. Curve Result/Display, 16. Regurgitant Mode, 17. Editing tools, 18. Integrated Analysis

NOTE: Flow Analysis displays the magnitude and phase images in a side-by-side image display. Other image types acquired at the same scan location are not displayed and should be reviewed in the Viewer.

NOTE: The heart rate can be obtained by hovering over the flow result on the curve display.

Flow Analysis Using Auto Segmentation

If preprocessing has been completed, based on the 2D phase contrast series present in the study, the segmentation will be performed automatically on the 2D phase contrast series and assigned to the appropriate vessel category (Table 1). Auto segmentation does not require an initial ROI to be placed on the vessel just select the appropriate vessel category and the proper series displaying that vessel. If preprocessing is not performed It is important to select the appropriate category that correlates to the vessel anatomy that has been acquired.

WARNING: The user is responsible for the accurate placement and correct category assignment of all regions of interest (ROIs), including those generated by preprocessing.

NOTE: If there are more than six vessels acquired for phase contrast per tab, the Preprocessing feature will only keep the six most recent results.

NOTE: The net flow result will be displayed under each vessel category. If there is more than one flow measurement in a vessel category the average result will be shown. To hide this value, select **Tools > Preferences > Edit System** (**Admin Only**) and set the flow unit to **NONE** under Flow.

Table 1: Vessel Categories

Vessel Category	Tool Tip	Label
	LVOT	Left Ventricular Outflow Tract (Pediatric)
	pAAo	Proximal Ascending Aorta
	mAAo	Mid Ascending Aorta
	pDAo	Proximal Descending Aorta (Pediatric)
	SVC	Superior Vena Cava (Pediatric)
	MPA	Main Pulmonary Artery
	RPA	Right Pulmonary Artery (Pediatric)

Table 1: Vessel Categories

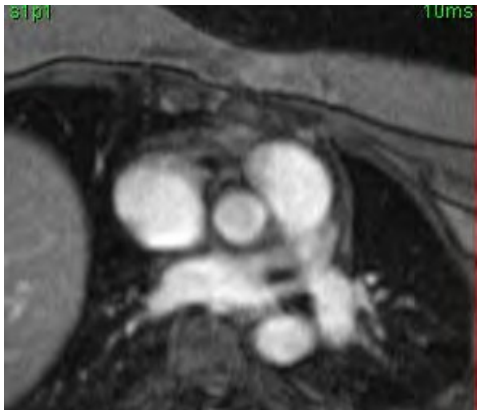
Vessel Category	Tool Tip	Label
	LPA	Left Pulmonary Artery (Pediatric)
	IVC	Inferior Vena Cava (Pediatric)
	dDAo	Distal Descending Aorta (Pediatric)
 	Flow 1, Flow 2 Flow 3, Flow 4	User defined categories. Right click and enter a new label for the category. The label will appear as a tool-tip.

Perform Auto or Manual Segmentation

(Example of Proximal Ascending Aorta Segmentation)

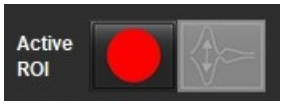
1. Select either Adult or Pediatric  .
2. Select the  category.
3. Select the appropriate phase contrast series that demonstrates the proximal ascending aorta, as shown in Figure 2.

FIGURE 2. Proximal Ascending Aorta



4. Select the Active ROI color, as shown in Figure 3.

FIGURE 3. Active ROI Selection



Six ROIs are available, numbered 1 - 6. The color coding remains consistent across the analysis view, image viewports and graphs.

5. Select  .
6. Review the segmentation on the vessel. Confirm that the correct vessel was segmented.

   If the incorrect vessel is segmented perform manual segmentation.

7. To perform manual segmentation select  .
8. Create a contour around a vessel by depositing 4 points around the vessel of interest, move the cursor out of the editor window to close the ROI.

   - Choose  for automatic segmentation over all phases in the slice.

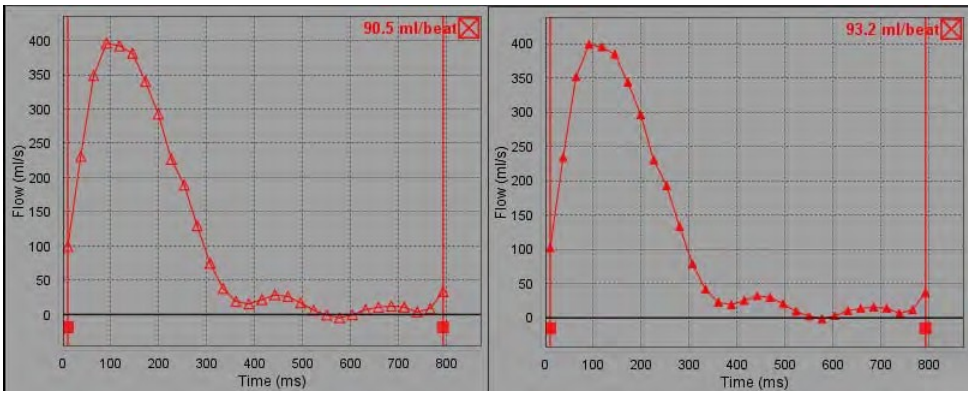
   or

   - Choose  to propagate the same contour over all phases in the slice. This is useful when analyzing small stationary vessels.

9. To edit, click on a contour, perform the edit and click  . Refer to Contour Editing on page 101.
10. Flow results are displayed on the graph and results tables. Click the check box beside the flow result to remove the associated curve from the graph.
11. Select a Baseline Correction option from the file pull-down.

    Curves with a Baseline Correction applied will have solid phase data points, as shown in Figure 4. Refer to Baseline Correction Options on page 104.

FIGURE 4. Flow Graph - No Correction (left graph); Correction Applied (right graph)



All flow curves generated are displayed in a positive direction. Inverted curves are indicated by  .

Vessel Category Move

Upon review, if a completed flow result is not in the correct vessel category it can be moved to the appropriate category.

Left click on the contour, right click and release; then cursor over the vessel type and select the appropriate vessel category as shown in Figure 5. (Pediatric categories are shown.) The flow result will now be shown in that category.

FIGURE 5. Vessel Category Move Selection

Contour Editing

1. Select the desired phase to edit.
2. Left click on the contour to activate it for editing.
   The contour will turn purple indicating it can be edited.
3. If displayed, edit the contour by moving the points for point spline contours.
4. Perform a free hand edit by clicking and tracing.
5. Left mouse click on the contour to select, then right mouse click to use tools, as described in Table 2.
6. Use the viewport editing tools as described in Table 3.

Table 2: Right Mouse Click Options

Tool	Description
	Delete a single ROI on current phase
	Delete all ROIs on all phases

Table 2: Right Mouse Click Options

Tool	Description
	Nudge Tool selection
	Pull tool selection
 Current vessel category will be shown.	Move flow results to a different category

Edit a Range of Phases

1. Select the desired slice.
2. Select  to display thumbnails of all the phases of a given slice location.
3. Select the first phase of the range of phases to be edited.
4. Depress and hold the shift key and select the last phase of the range to be edited.
5. Edit the contour in the image editor window.
6. Deselect the contour by either clicking on the image away from the selected contour or by moving the cursor out of the editor window.

Table 3: Viewport Editing Tools

Tool	Description
	Copy edit to end of phases
	Copy edit to start of phases
	Copy ROI from previous phase
	Copy ROI to next phase
	Decrease ROI size

Table 3: Viewport Editing Tools

Tool	Description
	Expand ROI size
	Navigate to Previous and Next Phase
	Shift ROI right or left
	Shift ROI up or down

Baseline Correction Options

There are three flow baseline corrections methods for 2D phase contrast. Flow curves that have a correction method applied will have solid phase data points.

NOTE: Phase contrast images that are used for analysis should not have image phase wrap. Phase wrap present in the image will invalidate the auto baseline correction.

Auto Baseline Correction

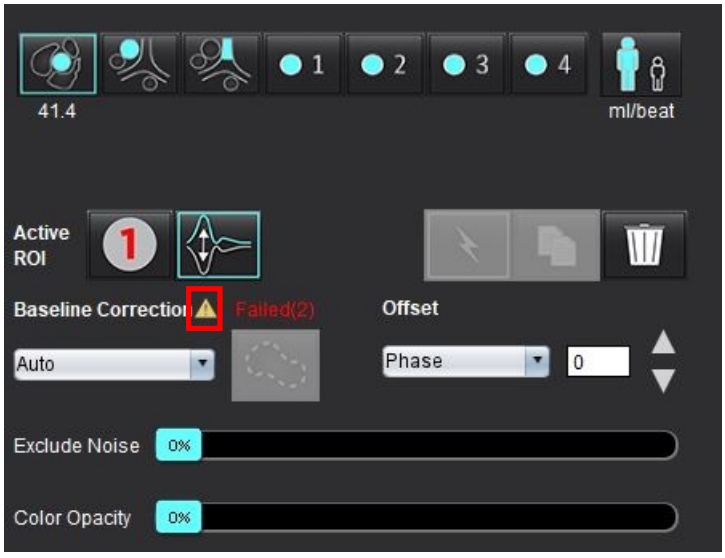
The Auto baseline correction corrects for phase errors that occur during image acquisition by examining the phase error in distant stationary organs (e.g., chest wall, liver, etc.) and spatially fitting the data using linear or higher order interpolation.

NOTE: If a 2D magnitude and phase series is created by using the 3D/4D Flow Viewer, the application will create an uncorrected series and a second series to which phase error correction has been applied. Do not apply Auto from the baseline correction pull-down to the series labeled “Corrected.”

1. Generate a flow curve using the appropriate phase contrast series.
2. Select Auto from the Baseline Correction pull-down.

   NOTE: Auto baseline correction will be automatically applied for 2D and 4D if **Auto Baseline Correction** is selected in Preferences. (**Admin Only**)
3. The correction will be applied with the updated results displayed directly on the flow graph.
4. Series which fail the fitting analysis will be indicated by a warning symbol, as shown in Figure 6.

FIGURE 6. Baseline Correction Failure



Failure Types:

1 – Wrap in the Image
2 – Noise in the Image
3 - Image is invalid

NOTE: Phase wrap present in the image will cause inaccurate flow results, as shown in Figure 7. 2D Cine Phase Contrast images that are used for flow analysis should not have image phase wrap, as shown in Figure 8.

FIGURE 7. Example Images Showing Phase Wrap (White Arrows)

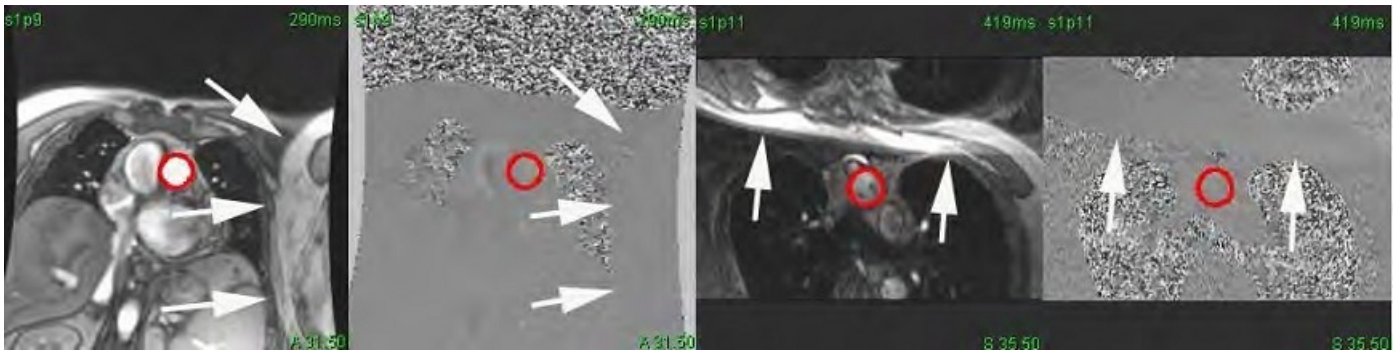
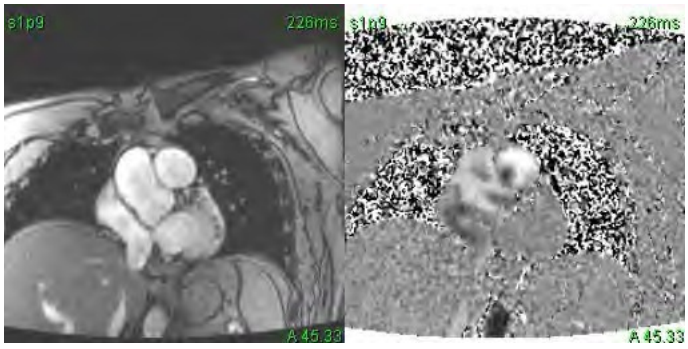


FIGURE 8. Example Images with No Phase Wrap



Phantom Correction

To improve the accuracy of phase contrast results and to correct for baseline phase shift errors, a phantom acquisition can be used to calculate this error.

NOTE: The phantom correction series must have been acquired with the same scan prescription and parameters as the original phase contrast series. There must be signal from a stationary object filling the entire contour on the phantom series.

1. Generate a flow curve using the appropriate phase contrast series.
2. Select the corresponding phantom series from the Baseline Correction pull-down.
3. The correction will be applied with the updated results displayed directly on the flow graph.

Background Contour Correction

This correction method can be considered for vessels that are surrounded by static tissue.

NOTE: For optimal correction the background contour must be placed in static tissue directly adjacent and surrounding the region of flow.

1. Generate a flow curve using the appropriate phase contrast series.
2. Select the Background ROI from the Baseline Correction pull-down.
3. Click  to draw a contour.
4. The correction will be applied with the updated results displayed directly on the flow graph.

Flow Tools

Offset Options

The file pull-down has 3 options: Phase, Flow, Dilation

Table 4: Offset Options

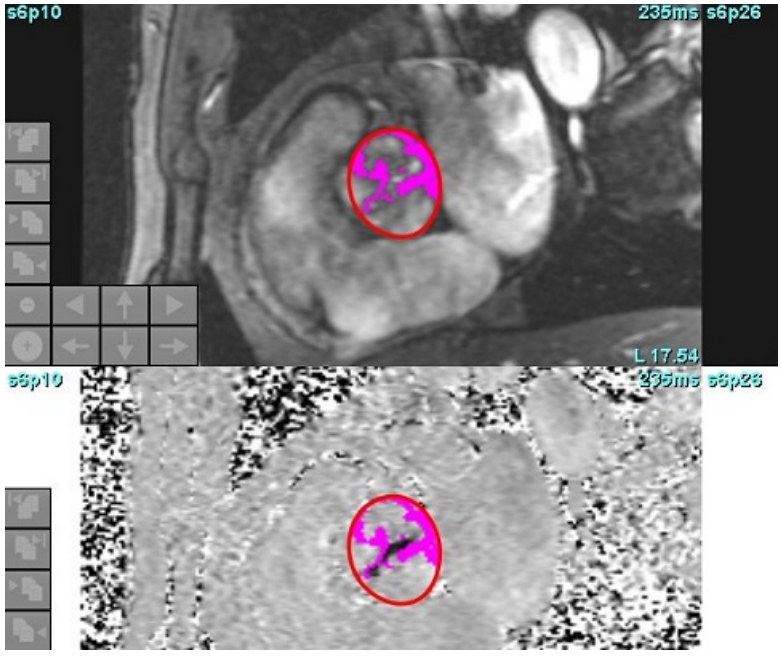
Selection	Description
Phase	Changes the ordinate of the flow curve.
Flow	Changes the abscissa value of the flow curve which changes the baseline values of the flow result.
Dilation	Uniformly changes the radius of the segmented vessel for all phases by a specified pixel amount to include valid flow pixels.

Exclude Noise Pixels

This option identifies low intensity pixels (high fluctuation of velocities) if present within the ROI, identified by the pink overlay as shown in Figure 10 and excludes them from the flow calculation. The percentage of noise pixels can be adjusted by the slider bar.

FIGURE 9. Noise Pixels

FIGURE 10. Noise Pixels Identified by Pink Overlay



Color Overlay

To display a red/blue color overlay representing velocities on the magnitude image click and drag the color opacity slider bar. Adjust the velocity range by setting the blue or red markers as shown in Figure 11. Select **Tools > Preferences > Edit** on the Global tab under Flow to adjust the color opacity. To remove the color overlay set the opacity to 0%.

FIGURE 11. Color Overlay Controls

Auto Velocity Aliasing Correction

Aliasing correction can be performed without a ROI present on the image. If more than one slice location is present in the series performing auto or manual will affect all slice locations. If performing manual correction to change a single slice location in a stack use the Ctrl or Alt key on the keyboard when changing the slider bar control.

FIGURE 12. Manual Correction

NOTE: Manual correction can be performed by using the slider bar control marker. If auto is applied, manual correction is disabled.

Configure Auto Aliasing Detection/Correction

NOTE: The user is responsible to visually review the phase image to confirm aliasing correction. There maybe instances where noise pixels along the edge of a vessel will be detected which are not true aliasing.

NOTE: There maybe instances where aliasing cannot be corrected therefore the acquisition should be acquired with a higher VENC.

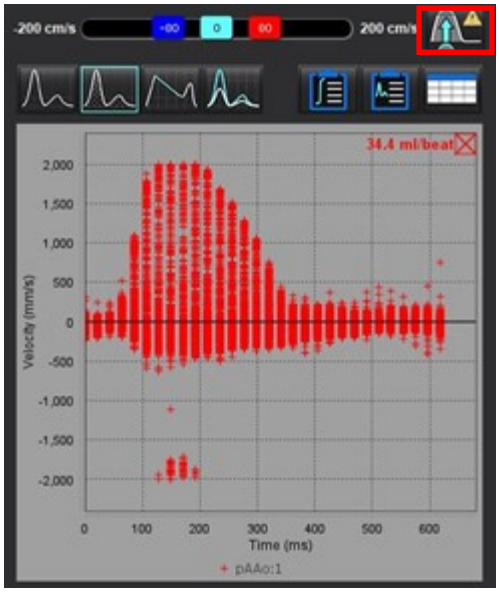
If aliasing is detected during preprocessing or auto segmentation, it will be indicated by a yellow triangle as shown in Figure 13.

1. Select **Tools > Preferences > Edit System**. (**Admin Only**)
2. Under Flow, check **Aliasing Automatically Detected**.

   Upon preprocessing each 2D phase contrast series and 4D Flow will be evaluated for aliasing.

If aliasing is detected it is shown as a yellow triangle: 

FIGURE 13. Aliasing detected (single yellow triangle)

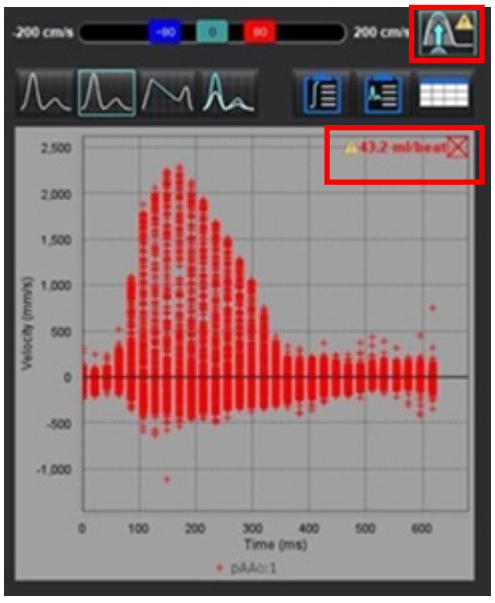


3. Select **Tools > Preferences > Edit System**. (**Admin Only**)
4. Under Flow, check **Aliasing Correction On By Default**.

   Upon preprocessing, aliasing detected will be corrected automatically.

If correction has been applied, a yellow triangle will be present by the flow result. 

FIGURE 14. Aliasing detected and corrected (Yellow triangle shown by flow result and highlighted icon.)



NOTE: If the correction preference is not turned on click  to apply correction. When selected, the icon will be highlighted as indicated by the blue outline. 

Recommended Reference

Phase unwrapping in 4D MR flow with a 4D single-step laplacian algorithm - Loecher - 2016 - Journal of Magnetic Resonance Imaging - Wiley Online Library.

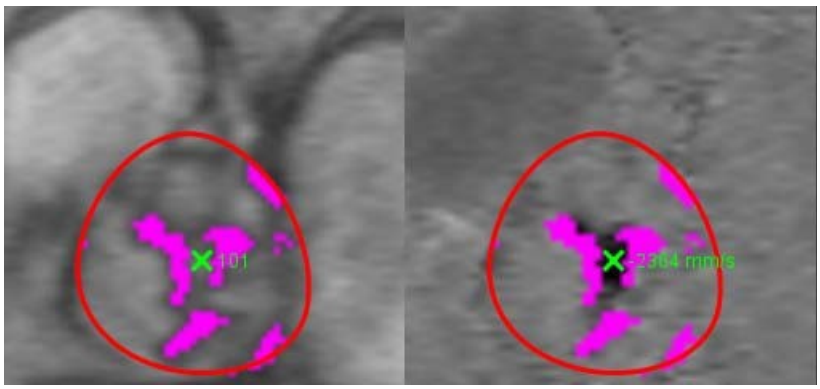
User Defined Peak Velocity

1. Select the appropriate phase of the cardiac cycle.

2. Use  to position the cursor on the phase image.

   The cursor is synchronized with both the magnitude and phase images. The velocity result appears in mm/s on the phase image next to the cursor.

FIGURE 15. Pixel Flow Velocity



Curve Mode Selections

Table 5: Curve Model Selections

Selection	Mode	Description
	Flow	Curve represents the flow volume of each phase in the entire cardiac cycle (default). Each point on the curve represents flow for that phase. Net flow result is displayed.
	Histogram	Displays a plot of the velocity of each pixel within each region of interest for every phase of the cardiac cycle. Peak and mean pressure gradient results are displayed.
	Pressure Half-Time (PHT)	The time it takes for the peak transmitral pressure gradient to decrease by half. Allows for the identification of slope of the graph to calculate the PHT and mitral valve area (MVA).
	Compare	Allows for the display of curves from two different categories.
	Regurgitant	Calculates the net negative flow (below x-axis).

Histogram Mode

Select histogram mode to display a plot of velocities per pixel and the calculation of the peak and mean pressure gradient.

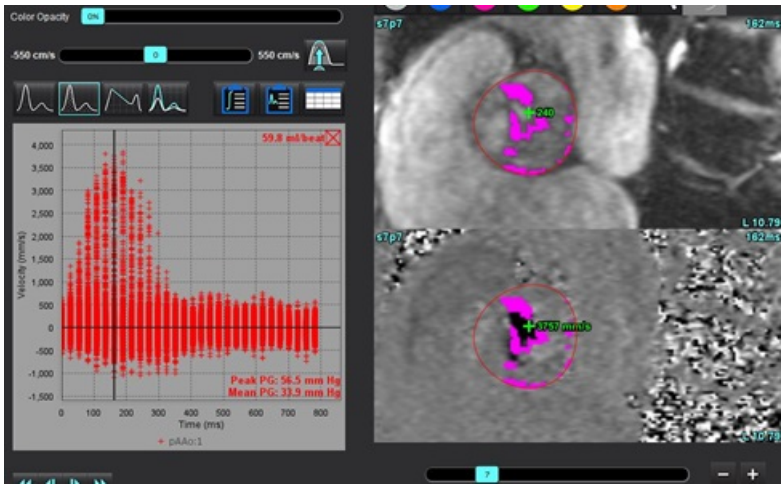
1. Generate a flow curve using the appropriate phase contrast series.
2. Select  .
3. Click directly on the graph to activate a cross hair cursor on the phase image, which indicates the corresponding location of that pixel.
4. Use the double arrow controls at the bottom of the graph to locate the highest or lowest velocity value, (Figure 16).
5. Use the single arrow controls to increment discretely through the velocity values, as shown in Figure 16.

NOTE: The series locate functionality, when clicking directly on the flow curve, is disabled when in histogram mode. Switch to flow mode to enable the locate functionality.

NOTE: To ensure that the corresponding magnitude and phase image are displayed, work with one flow curve at a time, deselect the other histogram curves from the graph display.

NOTE: Studies analyzed using histogram mode with a previous version of suiteHEART® Software may need to be reanalyzed.

FIGURE 16. Histogram Mode



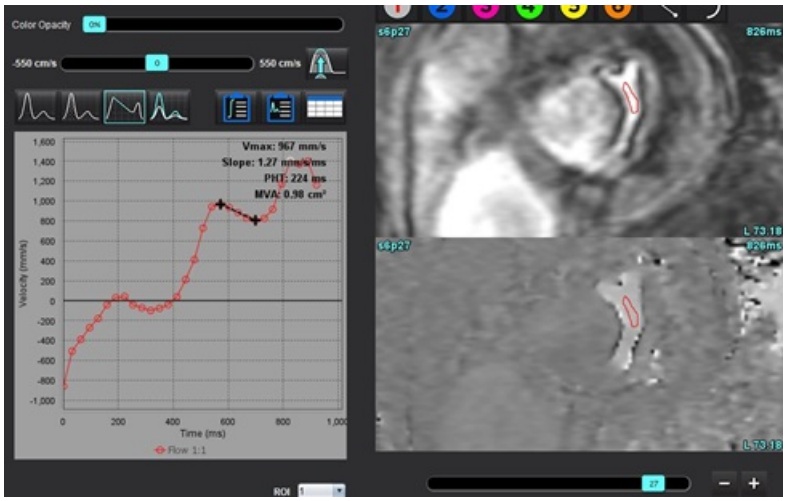
Pressure Half-Time

The Pressure Half-Time (PHT) can be obtained by measuring the deceleration slope of the E-wave on phase contrast images acquired of the mitral valve. This mode allows for the identification of slope of the graph to calculate the PHT and mitral valve area (MVA).

1. Generate a flow curve using the appropriate phase contrast series of the mitral valve.
2. For the ROI propagation use the copy paste option.
3. Select  .

4. Click directly on the plot to identify the highest velocity of the deceleration portion of the curve.
5. Click an end point to calculate the slope of the curve as shown in Figure 17.
6. To reset the calculation, place the cursor over an end point, right mouse click and select the trash can.

FIGURE 17. Pressure Half-Time Results



NOTE: Mitral Valve area (MVA), Pressure Half-Time (PHT) results are not valid in patients with aortic insufficiency, cardiac shunt or decreased ventricular compliance.

NOTE: The series locate functionality, when clicking directly on the flow curve, is disabled when in PHT mode. Switch to flow mode to enable the locate functionality.

Recommended Reference

http://www.csecho.ca/mdmath/?tag=mvaph

View Flow Results

Select one of the following options to review flow results in a table format.

Table 6: Result Table Options

Selection	Label	Description
	Integrated Analysis	Displays the analysis results from the flow panel. Includes results for aortic, mitral, pulmonic, and tricuspid regurgitation and Qp/Qs. Refer to Integrated Analysis on page 115.
	Flow Analysis	Summary of results per flow curve.
	Data Table	Lists detailed flow parameters for each phase per flow curve.

Change Category Label for Flow

Only the labels for the categories of Flow 1 - Flow 4 can be changed.

FIGURE 18. Flow 1 - Flow 4

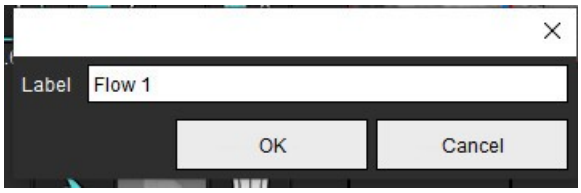
Change Label

1. Right mouse click on 

(as shown in Figure 18).
2. Enter the new label name (Figure 19).
3. The new labels will appear as tool tips.

NOTE: The curve legend label will be assigned the same label.

FIGURE 19. Edit Category Label



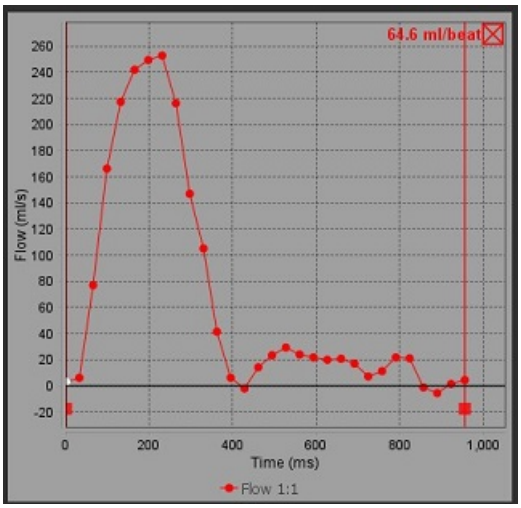
NOTE: Changing the flow category labels changes the flow header label for the report.

Edit Curve Legends

1. Right mouse click on Flow 1:1 on the bottom of the flow graph (Figure 20).

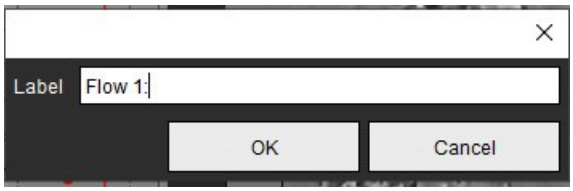
   NOTE: If the category label has been changed then that label will be shown.

FIGURE 20. Edit Curve Legends



2. Enter the new label name.

FIGURE 21. Change Flow Curve Legends Label



NOTE: The new flow curve legends will be saved with the current template.

Integrated Analysis

Based on a user selected method, Integrated Analysis calculates Qp, Qs, Qp/Qs, aortic, mitral, pulmonic, and tricuspid regurgitant volumes and regurgitant fractions (RF%).

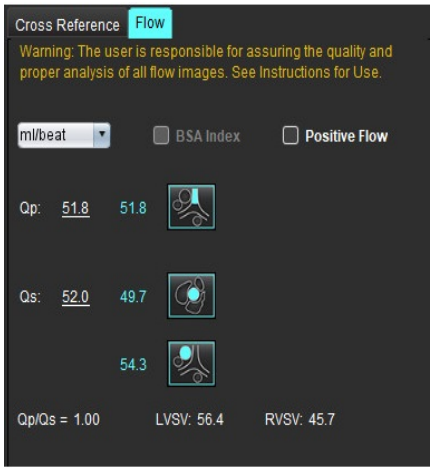
WARNING: The user is responsible for selecting the method for determining Qp, Qs, and aortic, mitral, pulmonic, and tricuspid regurgitant volumes and regurgitant fractions.

WARNING: Some or all methods may not be appropriate, depending on patient pathology. The user is responsible for determining, which if any method is valid for interpretation.

WARNING: The user is responsible for the accurate placement and correct category assignment of all regions of interest (ROIs), including those generated by preprocessing.

NOTE: The user can set the default calculation method for Integrated Analysis by selecting Tools > Preferences > Edit from the file pull-down menu. Default Method selections are: None, All, or Last.

Integrated Analysis Overview (Adult is shown)

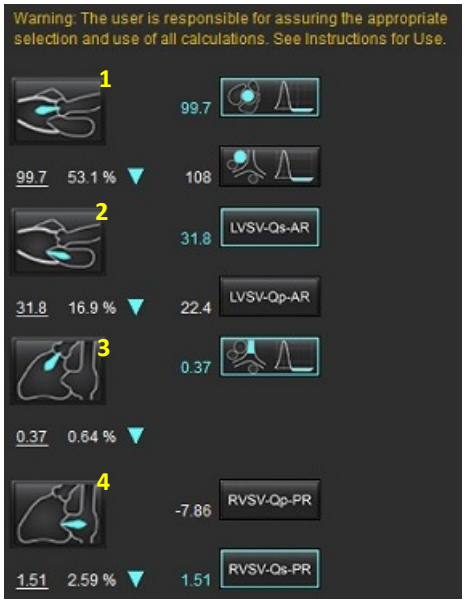


- ml/beat or l/min unit selection
- Index to BSA selection (height and weight must be entered on Reporting interface)
- Positive Flow result selection

Selections for Qp and Qs

- Qp: Displays the flow values from the MPA category
- Qs: Displays the flow values from either the pAAo or mAAo categories
- Qp/Qs result
- LV and RV stroke volume results displayed from the short axis function analysis

Underlined Qp or Qs values can be manually entered. To reset, delete the value and press enter on the keyboard.



Calculation method can be selected for the following:

- 1- Aortic regurgitation and RF%
- 2- Mitral regurgitation and RF%
- 3- Pulmonic regurgitation and RF%
- 4-Tricuspid regurgitation and RF%

Underlined regurgitant values can be manually entered. To reset, delete the value and press enter on the keyboard.

Table 7: Qp/Qs Selections

NOTE: If a vessel category has more than one measurement the average will be used.

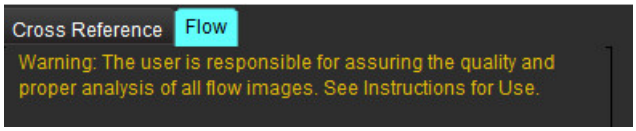
NOTE: For Qp or Qs, the value can be obtained from a single or a combination of the selections described in the table.

Result	Selection	Description
Qp		Flow result from the MPA category.
Qp (Pediatric)		Flow result from LPA + RPA
Qs	 	Flow result from the pAAo or mAAO category. Select both vessel types to average the Qs result.
Qs (Pediatric)		Flow result from the LVOT category.
Qs (Pediatric)		Flow result SVC + pDAo
Qs (Pediatric)		Flow result SVC + IVC
Qs (Pediatric)		Flow result SVC + dDAo
Qp/Qs=		Result is based upon the above selections.

Calculate Qp/Qs

1. To use the Integrated Analysis feature, select FLOW in the upper right as shown in Figure 22.

FIGURE 22. Flow Tab



2. Prior to using the Integrated Analysis, confirm all vessel assignments and accurate contours in all categories.
    - If the vessel segmented is in the incorrect category perform a right mouse click and move to the correct category.

- If the vessel segmented is the incorrect vessel for that category, delete the Active ROI and click  .
- If after using auto segmentation and the vessel is not identified correctly perform manual segmentation. Refer to Perform Auto or Manual Segmentation on page 99.

WARNING: The user is responsible for the accurate placement and correct category assignment of all regions of interest (ROIs), including those generated by preprocessing.

3. For Qp select  .
4. For Qs select  or  or both vessels categories (the values from the two categories will be averaged).
5. The Qp/Qs result will be calculated as shown in Figure 23.

FIGURE 23. Qp/Qs Results (Adult shown)

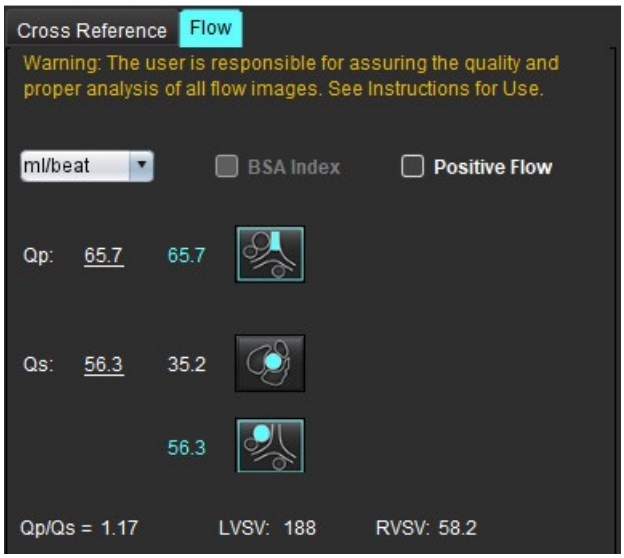


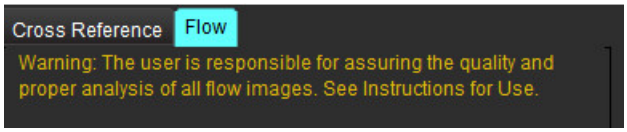
Table 8: Calculation Methods for Regurgitant Volume

Selection	Valve Type	Method Description
	Aortic	Direct from Flow Curve (Proximal)
	Aortic	Direct from Flow Curve (Mid)
	Aortic (Pediatric)	LVOT positive flow rate - Qp
	Mitral	Indirect (LVSV used is obtained from short axis function results)
	Mitral	Indirect (LVSV value used is obtained from short axis function results)
	Pulmonic	Direct from flow curve (MPA)
	Pulmonic (Pediatric)	Direct from flow curve LPA + RPA negative flow
	Tricuspid	Indirect (RVSV used is obtained from short axis function results)
	Tricuspid	Indirect (RVSV used is obtained from short axis function results)

Calculate Regurgitant Volume and Regurgitant Fraction (RF%)

1. To use the Integrated Analysis feature, select FLOW in the upper right as shown in Figure 24.

FIGURE 24. Flow Tab

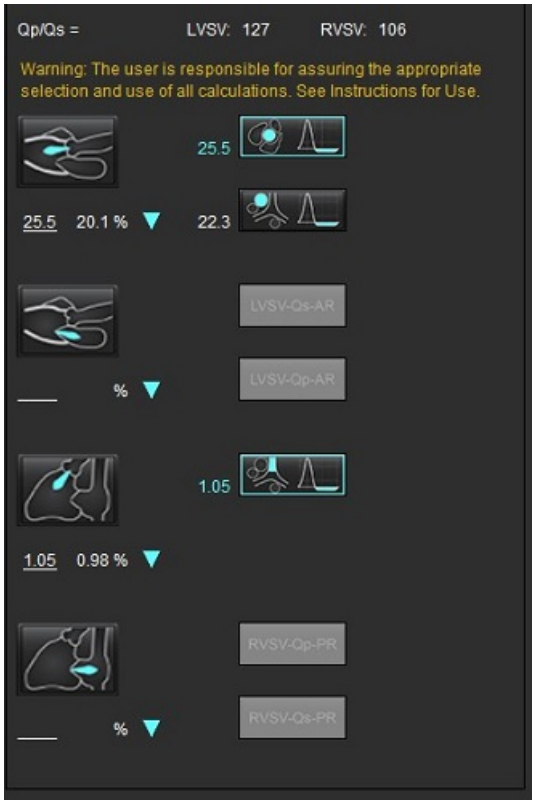


2. Prior to using the Integrated Analysis, confirm all vessel assignments and accurate contours in all categories.
   - If the vessel segmented is in the incorrect category perform a right mouse click and move to the correct category.
   - If the vessel segmented is the incorrect vessel for that category, delete the Active ROI and click  .
   - If after using auto segmentation and the vessel is not identified correctly perform manual segmentation. Refer to Perform Auto or Manual Segmentation on page 99.

WARNING: The user is responsible for the accurate placement and correct category assignment of all regions of interest (ROIs), including those generated by preprocessing.

3. Select the calculation mode. Shown in Figure 25 the aortic regurgitation and regurgitant fraction is calculated by selecting  and the pulmonic regurgitation and regurgitant fraction is calculated by selecting  .

FIGURE 25. Method Selections for Aortic and Pulmonic (Adult Shown)



4. The regurgitant volume and RF% is calculated as shown in Figure 26. The denominator value used is the LVSV for aortic and mitral the RVSV for tricuspid and pulmonic. To enter a different value left click on the triangle and type in a new value into the field. To reset to the original value just clear the field and press enter on the keyboard, as shown in Figure 26.

FIGURE 26. RF Denominator

5. If more than one calculation method is selected the values are averaged for the regurgitant volume result.

6. For the calculation of mitral regurgitation and RF% there needs to be a Qp, Qs and an aortic regurgitation method selected, as shown in Figure 27.
7. For the calculation of tricuspid regurgitation and RF% there needs to be a Qp, Qs and a pulmonic regurgitation method selected, as shown in Figure 27.
8. Any result that is negative is considered an invalid result and will be indicated by a yellow triangle as shown in Figure 27.

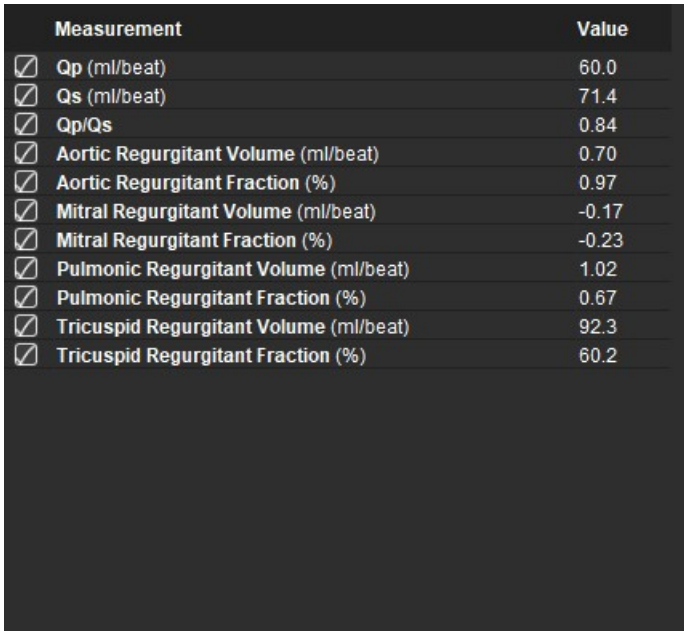
FIGURE 27. Method Selections (Adult Shown)

To review all results select  .

NOTE: The selection of the flow units are at the top of the Integrated Analysis panel, select ml/beat or l/min.

NOTE: The results can be index to BSA by selecting the Index to BSA at the top of the Integrated Analysis panel. Both height and weight must be entered in the History tab.

FIGURE 28. Integrated Results



Measurement	Value
Qp (ml/beat)	60.0
Qs (ml/beat)	71.4
Qp/Qs	0.84
Aortic Regurgitant Volume (ml/beat)	0.70
Aortic Regurgitant Fraction (%)	0.97
Mitral Regurgitant Volume (ml/beat)	-0.17
Mitral Regurgitant Fraction (%)	-0.23
Pulmonic Regurgitant Volume (ml/beat)	1.02
Pulmonic Regurgitant Fraction (%)	0.67
Tricuspid Regurgitant Volume (ml/beat)	92.3
Tricuspid Regurgitant Fraction (%)	60.2

Myocardial Evaluation

The user is responsible for the accurate and complete placement of all regions of interest (ROIs), including those generated or modified by the auto segmentation algorithms. The quantitative values generated by the software depend on the accurate and complete placement of these regions of interest and applied thresholding.

The study Preprocessing feature allows for the preprocessing of Late Enhancement. Refer to the suiteDXT Instructions for Use.

The Myocardial Evaluation (ME) analysis tool aids in the quantitative determination of areas of different signal intensities within the myocardium.

There are four analysis tabs available:

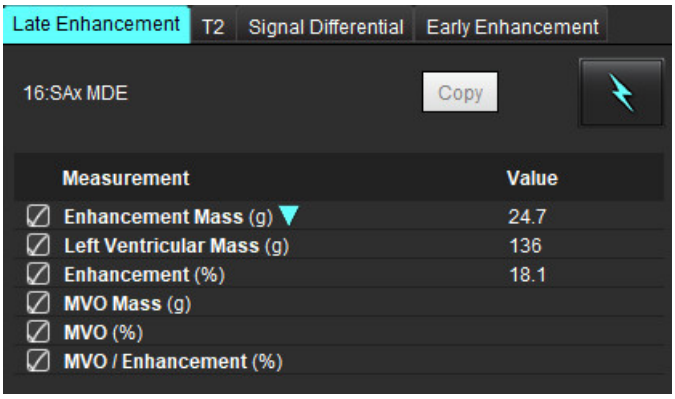
- **Late Enhancement** - Determines myocardial segments of increased and low signal intensity.
- **T2** - Determines myocardial segments of increased signal intensity from black-blood imaging techniques.
- **Signal Differential** - Displays the Salvage Mass results using both Late Enhancement and T2 analysis and the T2 signal intensity (SI) ratio.
- **Early Enhancement** - Determines the ratio of the signal intensity of the myocardium and the percent of absolute myocardial enhancement from T1 weighted images.

WARNING: Following preprocessing, the user is responsible for assessing the accuracy of the entire analysis and making any necessary corrections. A comprehensive review should include:

- ROI placement/identification
- RV insertion location
- Signal intensity threshold

WARNING: The application assists in the analysis of the images only and does not automatically produce a clinical interpretation of the results. The use and placement of quantitative measurements is at the discretion of the user. Misdiagnosis can occur if measurements are inaccurate. Measurements should only be created by a properly trained and qualified user.

Analysis Tabs

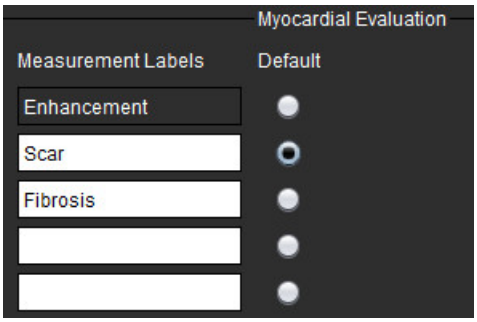


Define Result Measurement Labels

The result measurement labels can be user defined; the default label is Enhancement.

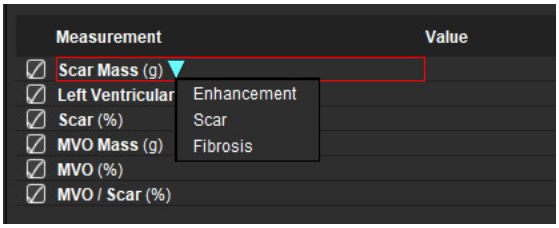
1. Select **Tools >Preferences >Edit System**. (**Admin Only**)
2. Type in additional labels in the blank fields, as shown in Figure 1.
3. Select the default label.
   This label will be used for all new analysis.
4. Click **Save and Exit**.

FIGURE 1. Define Labels



To change the label on the measurement table, left click on the arrow to select a new label.

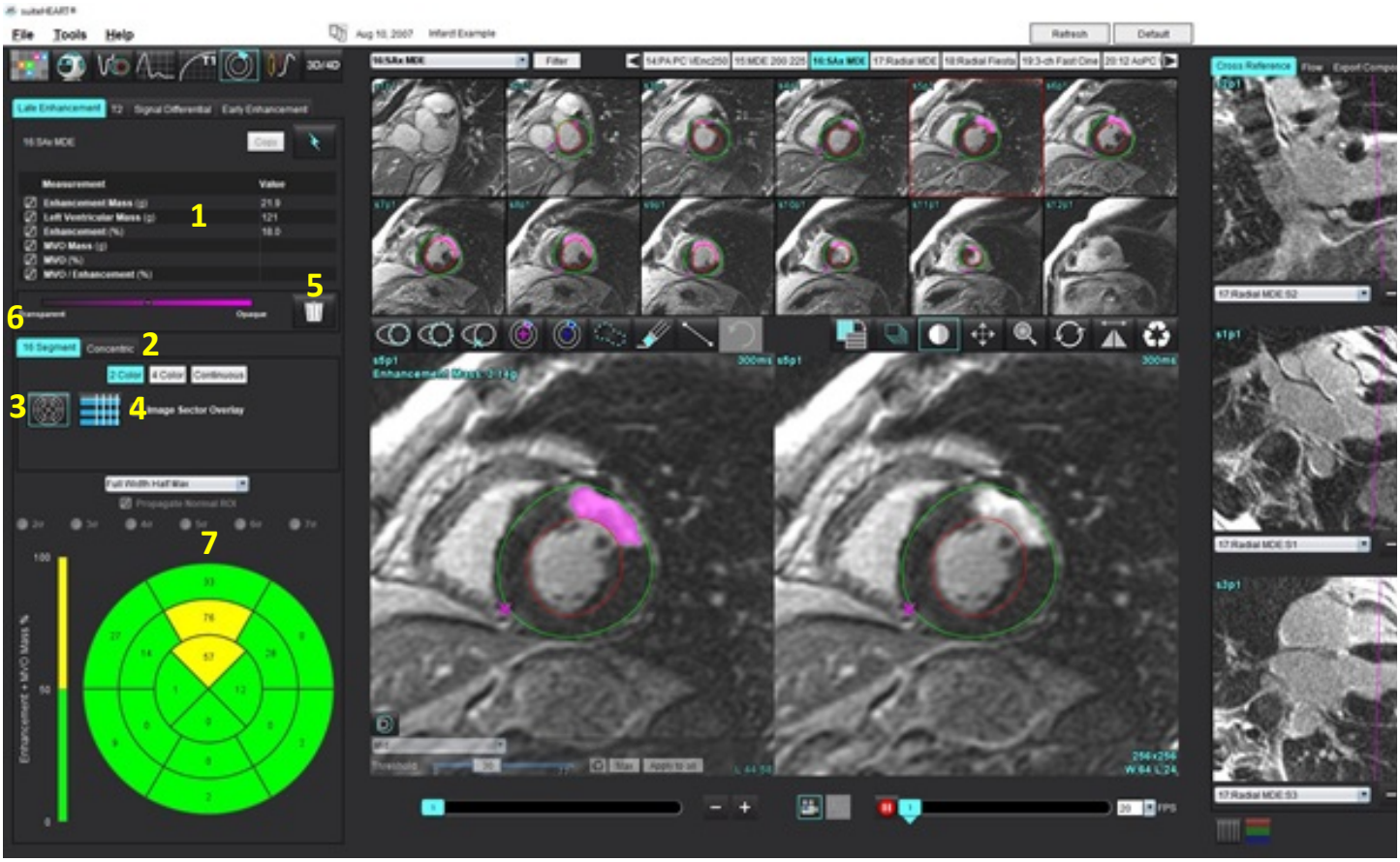
FIGURE 2. ME Measurement Labels



Late Enhancement Analysis Procedure

1. Select  .
2. Select Late Enhancement tab.
3. Select the appropriate short axis series.
4. Select  to perform Auto Segmentation.
5. Review all endocardial and epicardial traces, RV insertion point and the thresholding on each slice. Edit thresholding as necessary.

FIGURE 3. Myocardial Evaluation Analysis



1. Result table, 2. Polar Plot Selection, 3. Polar Plot Display, 4. Result Table Display, 5.Delete, 6. Opacity, 7. Polar Plot

6. To perform manual segmentation, trace the LV endocardium on the most basal slice by selecting  .

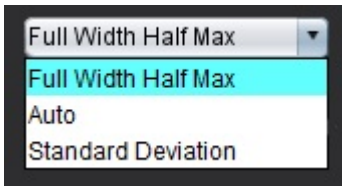
7. Trace LV epicardium by selecting  .

8. Place the inferior RV insertion point by selecting  .
9. Move the cursor outside of the editor window to complete the ROI.
10. Repeat steps 6 - 9 until the entire ventricle is segmented.
11. Confirm the base, mid and apical classification.

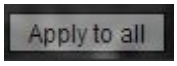
Algorithm Selection

1. Select the appropriate algorithm from the file pull-down menu (Figure 4).

FIGURE 4. Algorithm Selection



2. If required, click 

to maximize the threshold value for that slice. Click 

to apply that value to all slices. Use the slider bar to adjust the threshold algorithm for each slice, if needed. Click  to reset the threshold.
3. For Standard Deviation, select 

.
4. Place a normal ROI  in a normal myocardium segment. This ROI is copied to all slices if the Propagate Normal ROI is checked.
5. For Auto, adjusting the threshold gives the probability of enhancement.

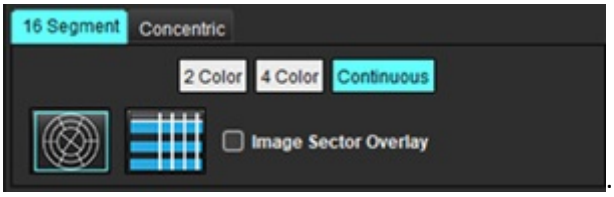
Threshold Editing

1. To add high signal intensity regions select  .
2. To add low signal intensity regions select  .
3. To delete either signal intensity regions select  small eraser tool or  large eraser tool.

Polar Plot Display Formats

The ME analysis tool provides 2 polar plot formats: 16 Segment and Concentric

Option 1: 16 Segment polar plot

1. Select the **16 Segment** tab 

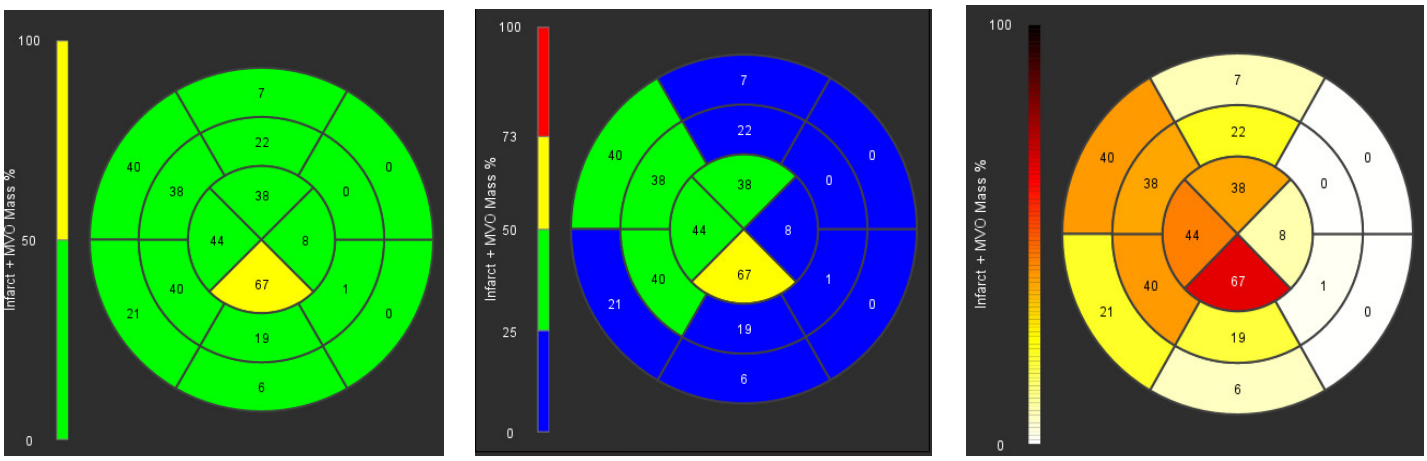
.
2. Select 2 Color, 4 Color, or Continuous.

   Color assignments can be defined by clicking on the color scale bar.

   To change the percent values, click and drag directly on the color divider.

FIGURE 5. Polar Plots

2 Color Polar Plot **4 Color Polar Plot** **Continuous Color Polar Plot**

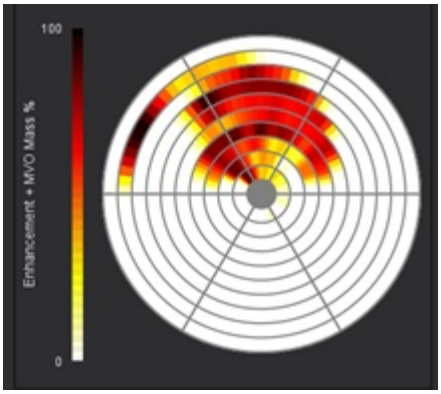


3. Select  to display the Polar Plot Summary Table.

Option 2: Slice-by-Slice format

1. Select the **Concentric** tab.

FIGURE 6. Concentric Tab



The Concentric tab provides the preferences that change the format of the Polar Plot to a slice-by-slice format, where each ring represents a slice. The number of rings is determined by the number of slices analyzed.

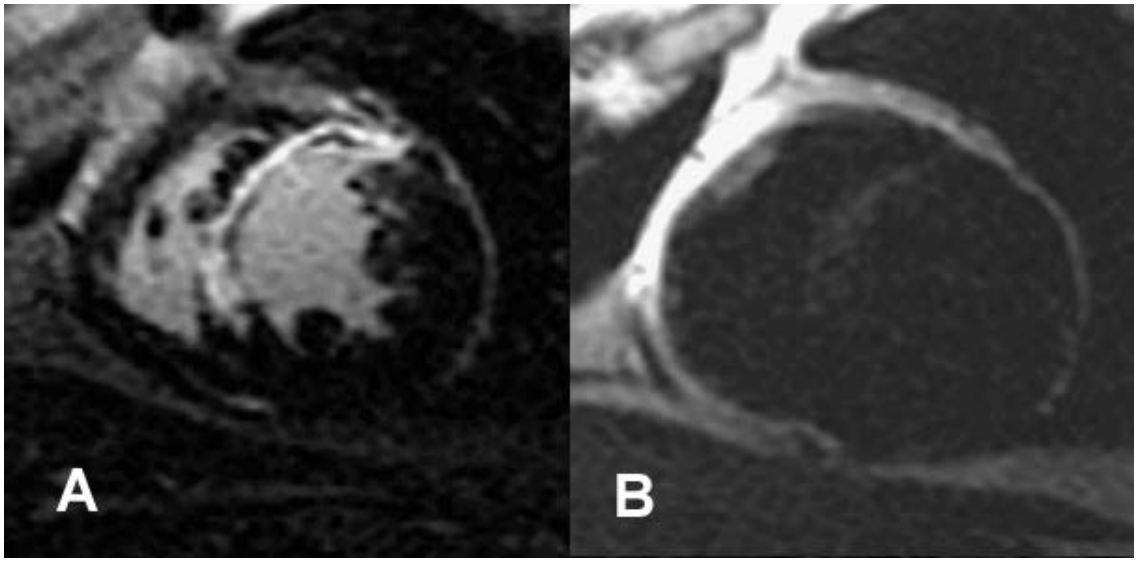
2. Select the number of sectors.
3. Check the subsectors to show the ROI mass percent changes within the sector.

   A smoothing function is applied when subsectors is selected.
4. Click the **Continuous** check box to change the Polar Plot to percent signal intensity and color code the values on a continuous spectrum from 0-100%.

Click  to delete contours.

NOTE: The semi-automatic thresholding for Late Enhancement analysis works optimally on high quality myocardial evaluation images as shown below (Image A). In images acquired without signal from the blood pool (Image B) or incorrect Inversion time, the threshold will need to be subjectively set by the user.

FIGURE 7. Myocardial Late Enhancement Images

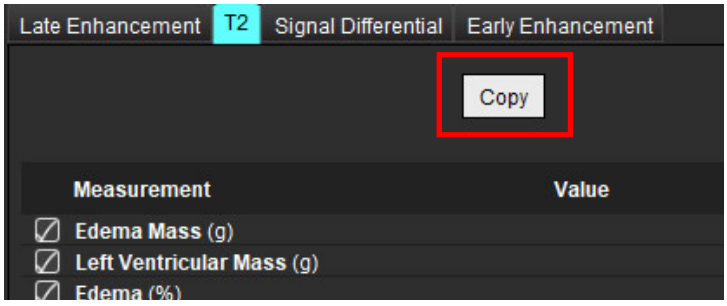


T2 Analysis

1. Select the **T2** tab.
2. If the Late Enhancement series has been previously analyzed, the ROIs can be copied to the T2 series by selecting copy (see Figure 8).

NOTE: To copy ROIs it is required that the number of slices match for each series to get accurate results; if the number of slices does not match, the copy button will not be available. The DICOM import process can be used to create the appropriate series that contains the same number of slices.
Acquisition parameters, such as matrix and FOV, should be the same for each series for best results. After performing a copy, review the ROIs carefully on all of the slice locations and make appropriate edits.

FIGURE 8. Copy Button



3. If there is no previous Late Enhancement analysis, the ROIs can be created manually.
4. Trace the LV endocardium on the most basal slice by selecting  .
5. Trace the LV epicardium by selecting  .
6. Mark the inferior RV insertion point by selecting  .
7. Move the cursor outside of the editor window to complete the ROI.
8. Repeat steps 4-7 until the entire ventricle is segmented.
9. To perform a 2 Standard deviation thresholding, select the Add Normal ROI  and place an ROI in a normal myocardium segment. This ROI is copied to all slices if the Propagate Normal ROI is checked. Review each slice location and adjust the ROI as necessary.

   NOTE: When the skeletal muscle ROI and Normal ROI are provided, the software performs the following calculation:
   Normalized myocardial T2 SI = SI myocardium / SI skeletal muscle;
   Threshold calculation: Threshold = 2 * STD NORMAL + AVG NORMAL
10. Select the first basal slice and use the slice classification pull-down to select Base. Confirm the classifications for the remaining slices. Use the slider bar to adjust the threshold algorithm for each slice, if needed.
11. To perform T2 Signal Intensity analysis, select the Add Skeletal muscle ROI  and place an ROI in the skeletal muscle. This ROI is copied to all of the images. Review each slice location and adjust the ROI as necessary.

    NOTE: Black-blood images may have insufficient flow suppression which could result in inaccurate signal intensity analysis and thresholding. Insufficient flow suppression can result in high signal intensity which may be confused with myocardial edema. Low signal intensity artifacts can cause a false low result.

Editing

To add regions of high T2 signal intensity, select  .

To remove regions of high T2 signal intensity, select  small eraser tool or  large eraser tool.

Click  to delete contours.

Late Enhancement and T2

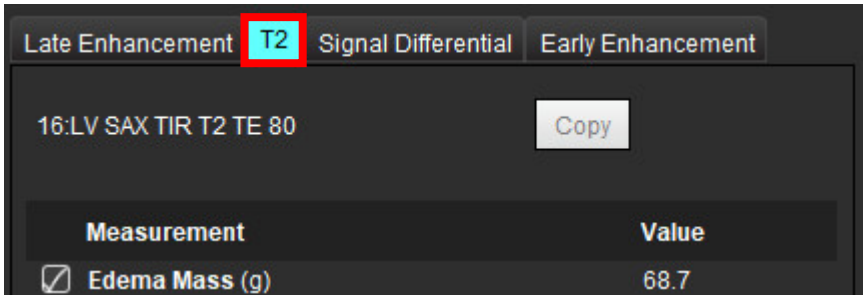
The combined analysis mode allows for side-by-side analysis with editing tools for Late Enhancement and T2 (Edema) images.

NOTE: To enable the combined analysis mode, the analysis of a short axis Late Enhancement series must be completed first using the Late Enhancement tab. T2 (Edema) images must be present in the same study.

1. Select  .
2. Select an appropriate study with both Late Enhancement and T2 (edema) images. Complete the analysis procedure for Late Enhancement.

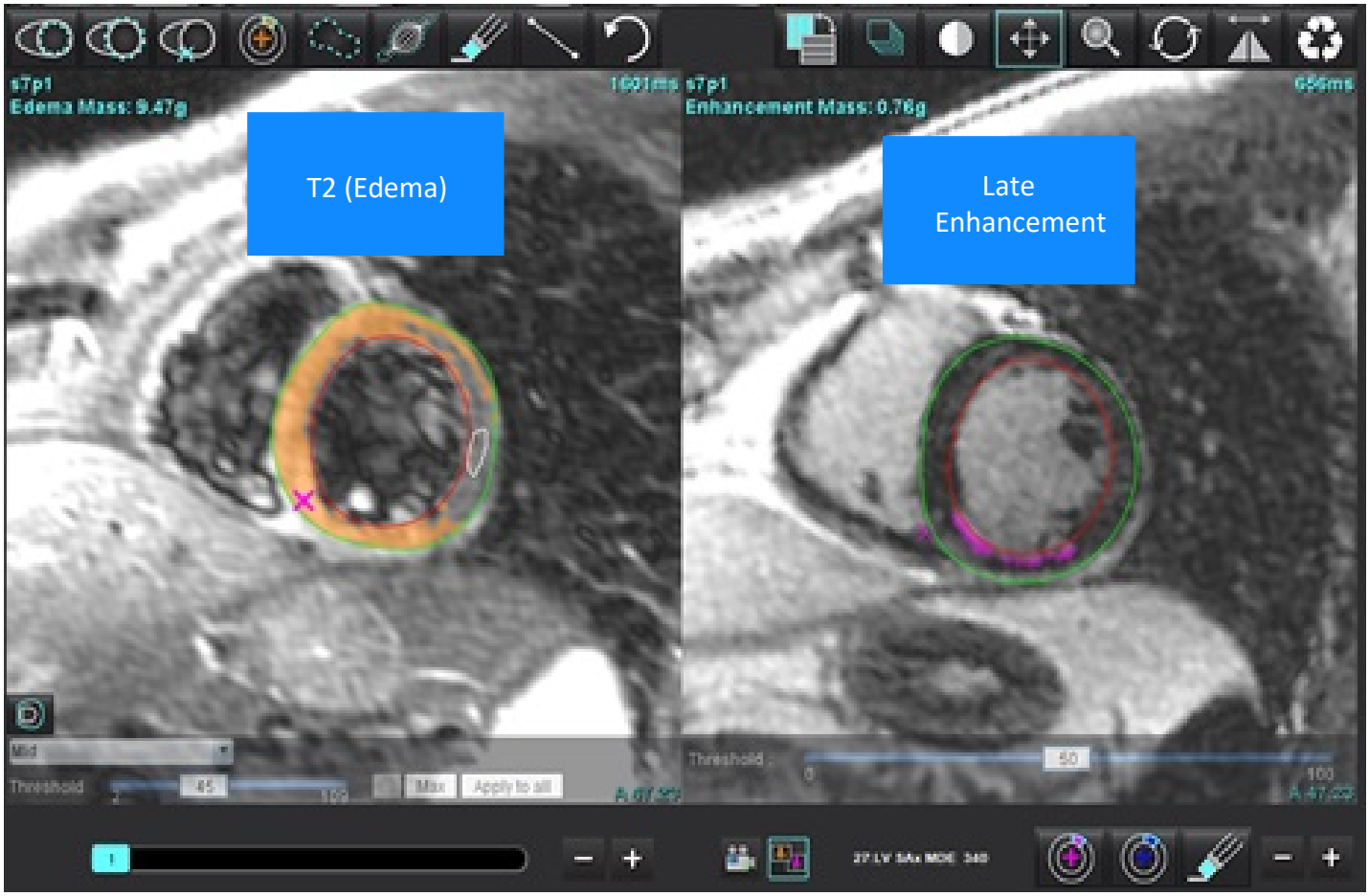
   NOTE: Review the thresholding for each short axis slice on the Late Enhancement tab prior to selecting combined analysis mode.

3. Select the T2 tab and complete the analysis procedure for the T2 series.



4. Select  to start combined analysis, as shown in Figure 9.

FIGURE 9. Combined Analysis Mode

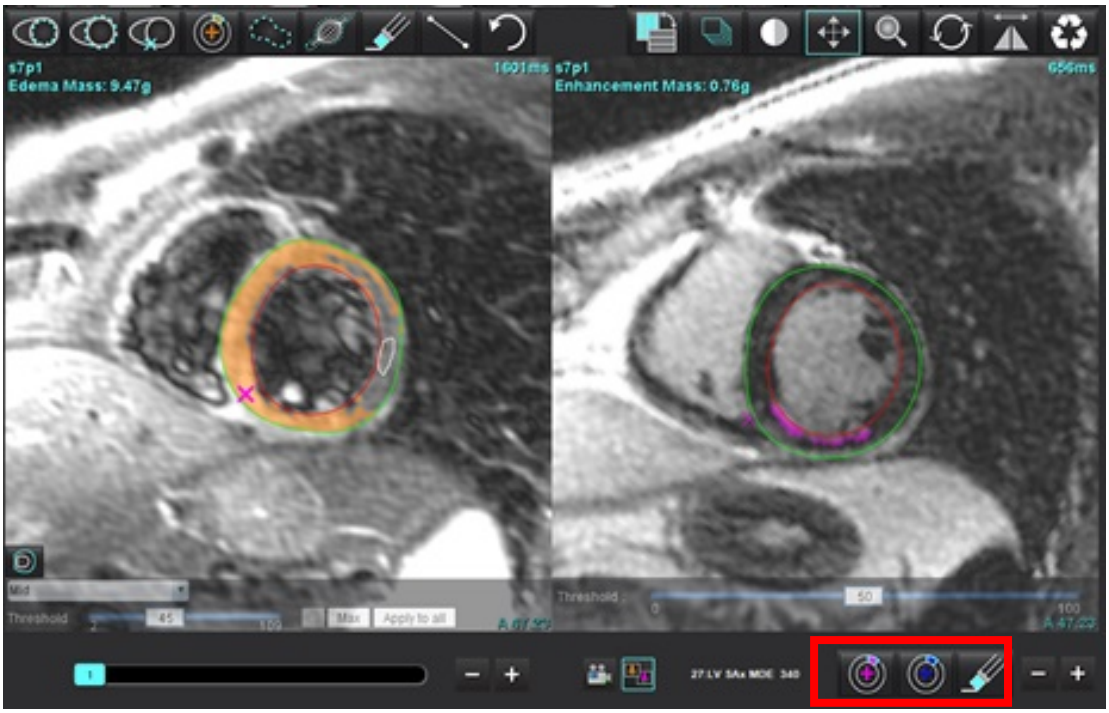


5. Upon selection, the previously analyzed Late Enhancement series will appear in the mode view window. This window then becomes an editor window for the Late Enhancement images.
6. For editing of the Late Enhancement images, use the editing tools located below the image viewport as shown in Figure 10.

NOTE: Confirm all updates to the results directly on the Late Enhancement tab.

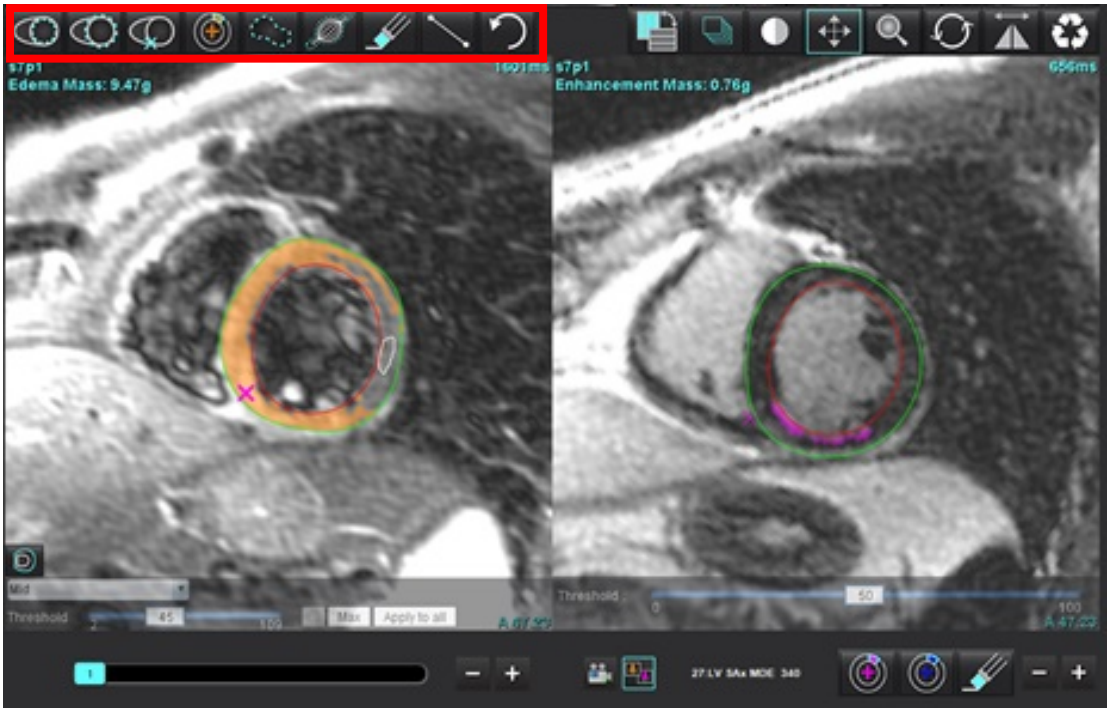
NOTE: If the LV endocardium or LV epicardium ROIs are deleted, go back to the Late Enhancement tab to retrace.

FIGURE 10. Late Enhancement Editing Tools



7. For editing of the T2 (Edema) series on the left, use the editing tools located above the image viewport, as shown in Figure 11.

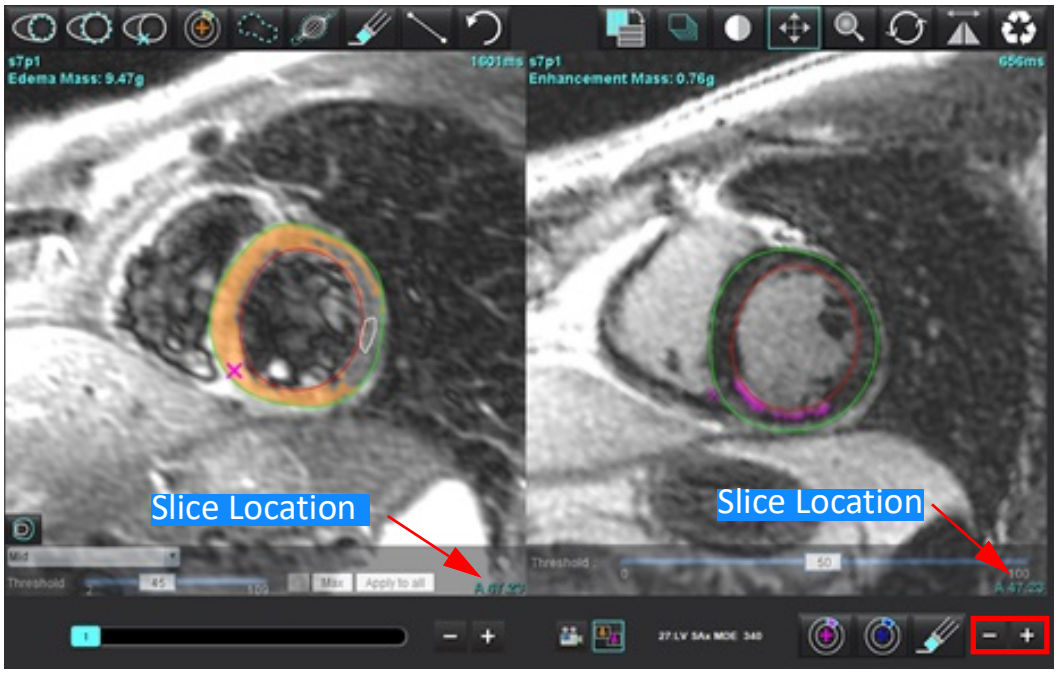
FIGURE 11. T2 (Edema) Analysis Tools



8. Use the minus and plus buttons to navigate to a different slice level for the Late Enhancement series, as shown in Figure 12.
    - Slice location information is located in the lower righthand corner of each viewport.

NOTE: The slice location displayed for the Late Enhancement is determined by the slice location in the T2 (Edema) editor window. Use the minus/plus buttons to override this selection.

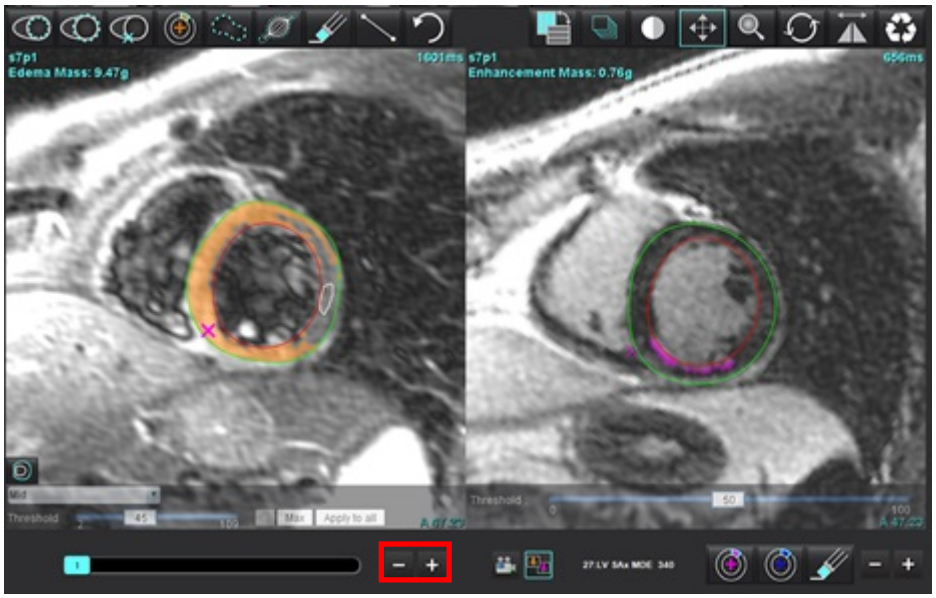
FIGURE 12. Slice Navigation Controls Late Enhancement



9. Use the minus and plus buttons located below the T2 (edema) editor viewport to navigate to a different slice level for both the Late Enhancement and T2 (Edema) series, as shown in Figure 13.

NOTE: In combined analysis mode the plus and minus buttons on the left link slice navigation for both viewports.

FIGURE 13. Combined Slice Navigation Controls



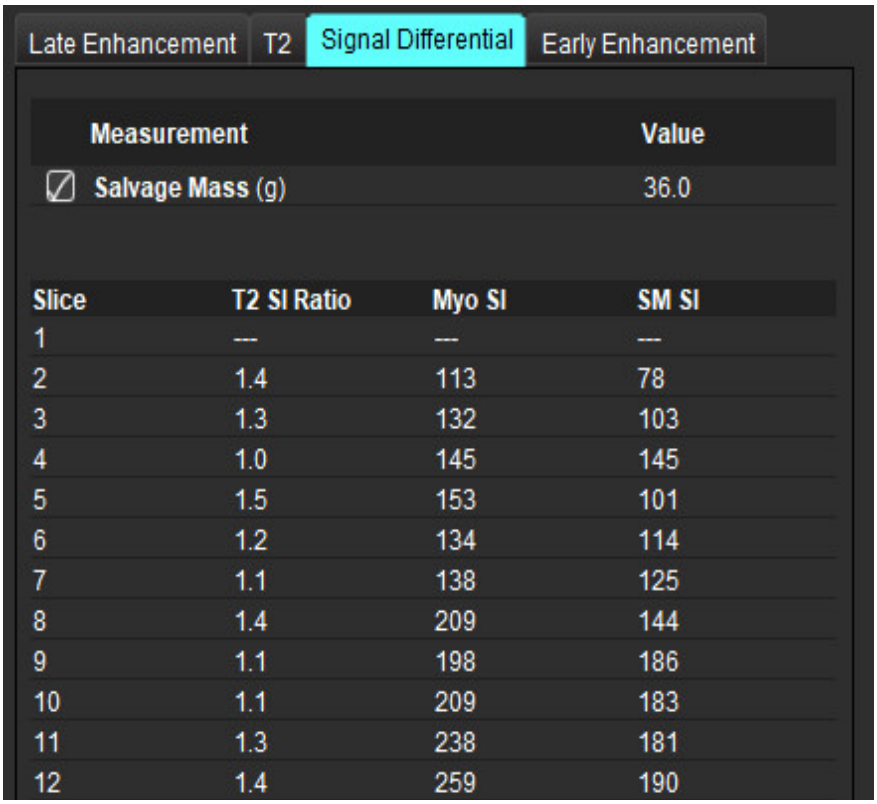
Signal Differential Results

Select the Signal Differential Tab

NOTE: Late Enhancement and T2 analysis must be completed to obtain the Salvage Mass Results. The T2 analysis must be completed with the placement of the Skeletal muscle ROI for T2 Signal Intensity (SI) analysis.

NOTE: If the T2 (Edema) result is less than the Late Enhancement result (Infarct + MVO) the Salvage Mass result will be blank.

FIGURE 14. Signal Differential Tab

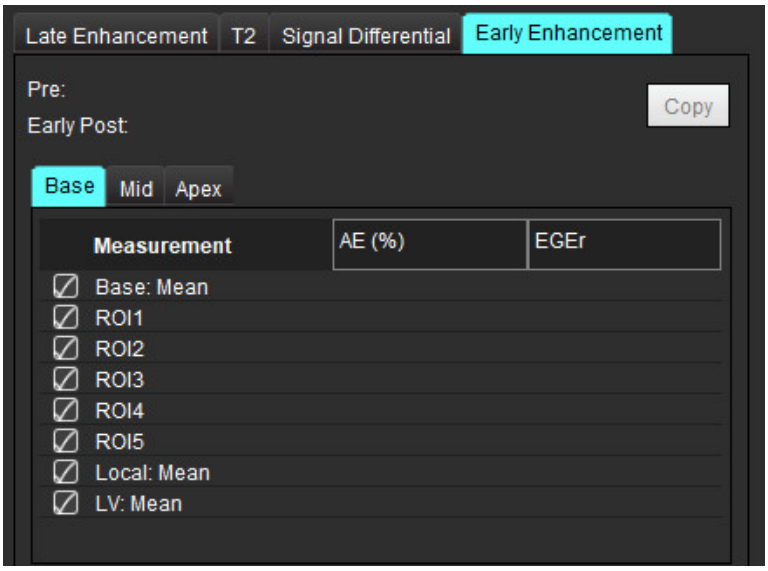


Early Enhancement Analysis

Images required for the analysis is a short axis stack using a gated spin echo T1 sequence, Pre- and Post Enhancement. The analysis allows for the manual segmentation of the epicardium and endocardium on the initial series with a copy function for the calculation of Absolute Enhancement % (AE) and Early Gd Enhancement Ratio (EGEr). A local ROI can be used to analyze regions in the myocardium.

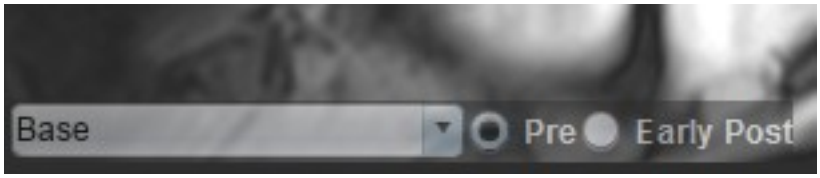
NOTE: Black-blood images may have insufficient flow suppression which could result in inaccurate signal intensity analysis and thresholding.

1. Select the Early Enhancement Tab.
2. Select the appropriate short axis T1 weighted series.



3. Trace the LV endocardium on the most basal slice by selecting  .
4. Trace the LV epicardium by selecting  .
5. Mark the inferior RV insertion point by selecting  .
6. Move the cursor outside of the editor window to complete the ROI.
7. Repeat steps 3-6 until the entire ventricle is segmented.
8. Add an ROI in the skeletal muscle by selecting  .
9. Select a basal slice location. Click the Slice Classification pull-down menu and select Base.
10. Confirm the base, mid and apical classifications for each slice.
11. To analyze a specific myocardial region, select  and trace an ROI in the myocardium.

FIGURE 15. Slice Classification and Series Type Selection



12. Select the series type of Pre.

    If the Early Post series was segmented first, select Early Post.

13. Select the appropriate short axis T1 weighted Early Post series type.

    If the Early Post series was segmented first, select the Pre series.

14. Select Copy.
15. Review all endocardial and epicardial traces, RV insertion and skeletal muscle placements and edit as necessary.
16. ROIs can only be copied when all ROIs and RV insertion, slice classification, series type (steps 3-12) have been completed on the selected series.

    NOTE: If an Endocardial or Epicardial trace is deleted use the Undo.

    NOTE: The skeletal ROI can be adjusted on each slice location. If deleted, the analysis will need to be redone.

17. Click  and select **ALL: Early Enhancement** to remove all analysis.

    NOTE: To copy ROIs it is required that the number of slices match for each series to get accurate results; if the number of slices does not match, the copy button will not be available. The DICOM import process can be used to create the appropriate series that contains the same number of slices.

    NOTE: Acquisition parameters, such as matrix and FOV should be the same for each series for best results. After performing a copy, review the ROIs carefully on all of the slice locations and make appropriate edits.

Local ROI Tool

1. Select the appropriate Pre-enhancement short axis T1 weighted series.
2. Trace a local ROI in the specific myocardium region by selecting  .
3. Add an ROI in the skeletal muscle by selecting  .
4. Select the proper slice classification and the series type as shown in Figure 16.

FIGURE 16. Slice Classification and Series Type Selection

5. Select the appropriate short axis T1 weighted Early Post series type.
6. Select Copy.
7. Click  and select **ALL: Early Enhancement** to remove all analysis.

Recommended References

Abdel-Aty H, Boyé P, Zagrosek A, Wassmuth R, Kumar A, Messroghli D, Bock P, Dietz R, Friedrich MG, Schulz-Menger J. Diagnostic performance of cardiovascular magnetic resonance in patients with suspected acute myocarditis: comparison of different approaches. J Am Coll Cardiol. 2005 Jun 7;45(11):1815-22. doi: 10.1016/j.jacc.2004.11.069. PMID: 15936612.

Amado LC, Gerber BL, Gupta SN, Rettmann DW, Szarf G, Schock R, Nasir K, Kraitchman DL, Lima JA. Accurate and objective infarct sizing by contrast-enhanced magnetic resonance imaging in a canine myocardial infarction model. J Am Coll Cardiol. 2004 Dec 21;44(12):2383-9. doi: 10.1016/j.jacc.2004.09.020. PMID: 15607402.

Berry C, Kellman P, Mancini C, Chen MY, Bandettini WP, Lowrey T, Hsu LY, Aletras AH, Arai AE. Magnetic resonance imaging delineates the ischemic area at risk and myocardial salvage in patients with acute myocardial infarction. Circ Cardiovasc Imaging. 2010 Sep;3(5):527-35. doi: 10.1161/CIRCIMAGING.109.900761. Epub 2010 Jul 14. PMID: 20631034; PMCID: PMC2966468.

Ferreira VM, Schulz-Menger J, Holmvang G, et al. Cardiovascular Magnetic Resonance in Nonischemic Myocardial Inflammation: Expert Recommendations. J Am Coll Cardiol. 2018;72(24):3158-3176. doi:10.1016/j.jacc.2018.09.072.

Galea N, Francone M, Fiorelli A, Noce V, Giannetta E, Chimenti C, Frustaci A, Catalano C, Carbone I. Early myocardial gadolinium enhancement in patients with myocarditis: Validation of “Lake Louise consensus” criteria using a single bolus of 0.1mmol/Kg of a high relaxivity gadolinium-based contrast agent. Eur J Radiol. 2017 Oct;95:89-95. doi: 10.1016/j.ejrad.2017.07.008. Epub 2017 Jul 27. PMID: 28987703.

T1 Mapping Analysis

This feature allows for the signal quantification of the longitudinal spin-lattice relaxation time (T1). The application supports T1 analysis for both Native (non-enhanced) and Post enhancement images and the calculation of the extracellular volume fraction (ECV).

Required Images: Inversion or saturation recovery images with varying inversion times (TI) or inline maps. Series that have motion correction applied are recommended for analysis. Representative slice locations for the left ventricular base, mid and apex are recommended.

For further guidance on performing T1 Mapping please refer to the following article:

Messroghli, D.R., Moon, J.C., Ferreira, V.M. et al. Clinical recommendations for cardiovascular magnetic resonance mapping of T1, T2, T2* and extracellular volume: A consensus statement by the Society for Cardiovascular Magnetic Resonance (SCMR) endorsed by the European Association for Cardiovascular Imaging (EACVI). J Cardiovasc Magn Reson 19, 75 (2017). https://doi.org/10.1186/s12968-017-0389-8

WARNING: Follow preprocessing the user is responsible for assessing the accuracy of the entire analysis and making any necessary corrections. A comprehensive review should include:

- ROI placement/identification
- RV insertion location

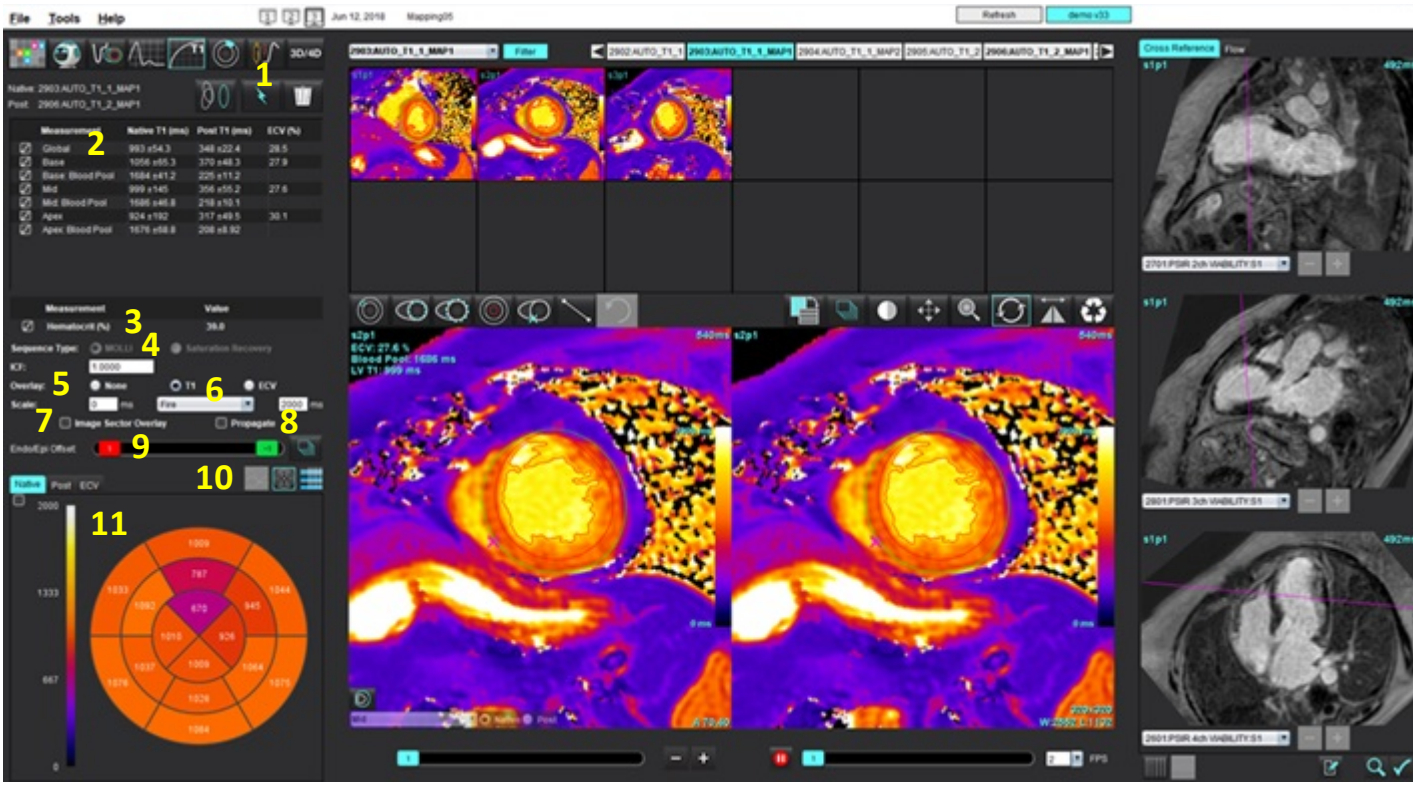
WARNING: The application assists in the analysis of the images only and does not automatically produce quantifiable results. The use and placement of quantitative measurements is at the discretion of the user. Misdiagnosis can occur if measurements are inaccurate. Measurements should only be created by a properly trained and qualified user.

WARNING: The user is responsible for the accurate placement of all regions of interest (ROIs), including those generated by auto segmentation.

NOTE: To set the T1 Mapping preferences, Select **Tools > Preferences > Edit**. Select the **T1/T2/T2*** tab.

NOTE: It is recommended to set the **Auto Compose Series for Analysis** in preferences for your scanner type. The analysis requires that all slice locations are in a single series. Select **Tools > Preferences > Edit**. Select the **Auto Compose Series** tab.

FIGURE 1. T1 Mapping Interface



1. Auto Segmentation, 2. T1 Results, 3. Hematocrit entry, 4. Sequence Type selection, 5. Colormap overlay selections, 6. Colormap options, 7. Display sector overlay, 8. Editing propagation, 9. Endo/Epi Offset, 10. Curve, 16-Segment Polar plot or Table, 11. T1 Curves, Polar Plots, Tables

Perform Analysis

1. Select 

.
2. Select the appropriate time series or map series.
3. Click  to perform motion correction if required. A new series will created labeled MOCO. This series can be used for analysis.

   NOTE: Motion correction can be configured for preprocessing.
4. The color map will be displayed automatically if the preference for overlay has been selected.
5. To select a different color scale use the file-pull down menu.
6. To create a Global T1 result select  .
7. Review all endocardial and epicardial traces, RV insertion point and blood pool placement.
8. Edit any inaccurate contours.
9. Use the Endo (red) or Epi (green) offset to adjust contours 

 Propagate offset to all slices.  Offset single slice.

10. To edit a single inversion time click off the 

.
11. Confirm slice classification for each slice location and series type.

NOTE: If a stack of short axis images are segmented the T1 result for the Base, Mid or Apex and the 16-segment polar plot sectors will be averaged based upon the slice classification. The blood pool T1 result will not be averaged.

12. To calculate the ECV perform auto segmentation on both the Native and Post Series.
13. Review all endocardial and epicardial traces, RV insertion point and blood pool placement on both series.
14. To measure a segment of the myocardium select  .

NOTE: Use copy/paste to copy a local ROI from the native image to the post image if the ECV is to be calculated.

NOTE: Up to five Local ROI measurements can be created on an image for Base, Mid and Apex.

15. Select  to place a blood pool ROI, if needed.
16. Enter the Hematocrit (HCT) value.
17. The ECV result (%) will be displayed in the result table.
18. Manual segmentation can be performed.
    - Trace the LV endocardium by selecting  .
    - Trace the LV epicardium by selecting  .
    - Mark the RV insertion point by selecting  .
    - If the ECV is to be calculated place the blood pool ROI by selecting  .
    - Confirm slice classification for each slice location and series type.

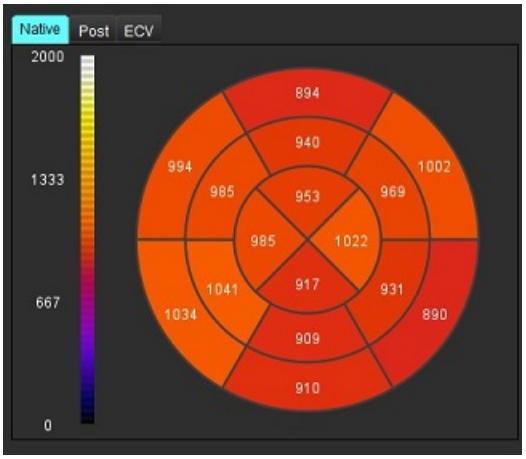
Recommended Reference

Wong. et al,. “Association Between Extracellular Matrix Expansion Quantified by Cardiovascular Magnetic Resonance and Short-Term Mortality.” Circulation (2012):126:1206-1216.

16-Segment Polar Map

NOTE: ECV Polar Plot requires that the ECV analysis is completed.

1. Complete the Global T1 analysis for Base, Mid and Apex.
2. Confirm the RV insertion point for each slice location.
3. Confirm the correct slice classification and series type.
4. Select the 16 Segment Polar Plot  .



5. Select 

to show the sector overlay directly on the image.
6. Select Graphs  to return to the T1 curves, if the time series was analyzed.

T1 Result Values Format

Result	DICOM Images		Map Images
Global	mean +/- std		mean +/- std
Base/Mid/Apex	value +/- error		mean +/- std
Local ROIs	value +/- error		mean +/- std
Local	mean +/- std		mean +/- std
Blood Pool	value +/- error		mean +/- std

NOTE: The global result is an average of the T1 values by pixel.

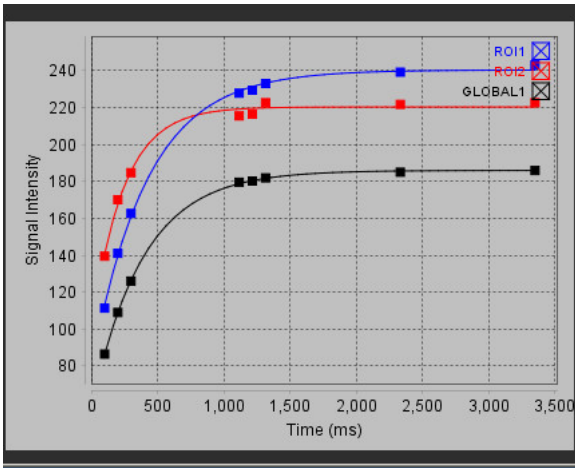
Delete Contours

Click  on the interface to delete **ALL** contours on the series selected.

Left mouse click on a contour followed by a right mouse click to delete a single contour or select  to delete contours on all time points.

Review the T1 Curves

1. The curve fitting results show the signal behavior from the image data. In cases of image artifacts due to misregistration, breathing artifacts or arrhythmias the curve fit may not be optimal.
2. A signal intensity point can be eliminated from the calculation by clicking directly on the point on the graph and selecting the contour on the image, which turns purple.
3. Select delete from the right mouse (click and hold) or select the keyboard delete.



NOTE: Curve display is only generated by using the time series for analysis.

WARNING: The results of the T1 curve fit should be reviewed by a properly trained and qualified user.

Result	Equation Reference	Fit Type
T1 Look-Locker (MOLLI)	y=A-B exp(-t/T1*)	Nonlinear curve fitting using a Levenberg-Marquardt algorithm*

Recommended Reference

*Messroghli D. R. et al,. “Modified Look-Locker Inversion Recovery (MOLLI) for High Resolution T1 Mapping of the Heart.” Magnetic Resonance in Medicine (2004) 52: 141-146.

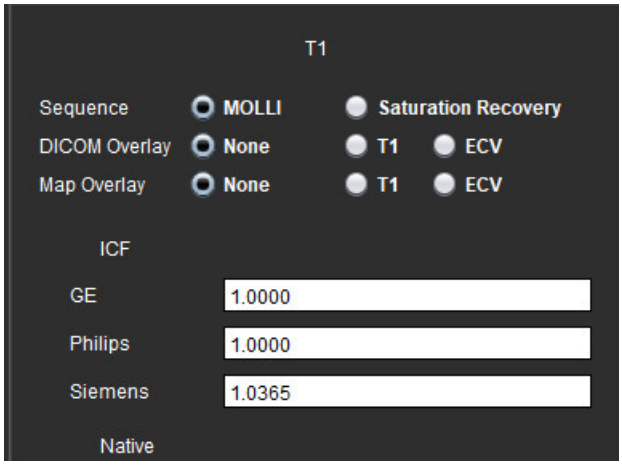
Inversion Correction Factor (ICF) Siemens MyoMaps

To obtain T1 results when analyzing the time series images that are similar to the generated scanner T1 map, confirm the efficiency inversion pulse used for MyoMaps MOLLI protocols. If indicated as "Non-sel IR T1 Map" on the scanner under the Contrast/Common card under Magn Preparation, the recommended inversion correction factor ICF=1.0365. For further clarification it is recommended to contact your Siemens Applications Support Specialists.

If analyzing the time series images enter the appropriate ICF in preferences as shown in Figure 2.

1. Select **Tools > Preferences > Edit System**. (**Admin Only**)
2. Select the **T1/T2 Mapping** tab.
3. Enter the ICF according to vendor type.

FIGURE 2. T1 Mapping Preferences



Recommended Reference

Kellman, P., Hansen, M.S. T1-mapping in the heart: accuracy and precision. J Cardiovasc Magn Reson 16, 2 (2014). https://doi.org/10.1186/1532-429X-16-2

T2 Mapping Analysis

This feature allows for the signal quantification of the T2 relaxation time. T2 mapping is a tissue characterization technique.

Required Images: T2 preparation sequence with a steady-state free precession readout with varying echo times (TE) or inline maps. Series that have motion correction applied are recommended for analysis. Representative slice locations for the left ventricular base, mid and apex are recommended.

For nonlinear 2-point, the equation is y = a * exp(-TE/T2), where TE is echo time or T2 prep duration, depending on the sequence.

For nonlinear 3-point, the equation is y = a * exp(-TE/T2) + c, where a, T2, and c are coefficients (parameter to be calculated by the fitting).

For linear 2-point, the equation is Y = A - TE/T2, where Y = log(y) and A = log(a).

NOTE: For 2 point fitting for either linear and nonlinear, background subtraction is not performed.

For further guidance on performing T2 Mapping please refer to the following article:

Messroghli, D.R., Moon, J.C., Ferreira, V.M. et al. Clinical recommendations for cardiovascular magnetic resonance mapping of T1, T2, T2* and extracellular volume: A consensus statement by the Society for Cardiovascular Magnetic Resonance (SCMR) endorsed by the European Association for Cardiovascular Imaging (EACVI). J Cardiovasc Magn Reson 19, 75 (2017). https://doi.org/10.1186/s12968-017-0389-8

WARNING: Follow preprocessing the user is responsible for assessing the accuracy of the entire analysis and making any necessary corrections. A comprehensive review should include:

- ROI placement/identification
- RV insertion location

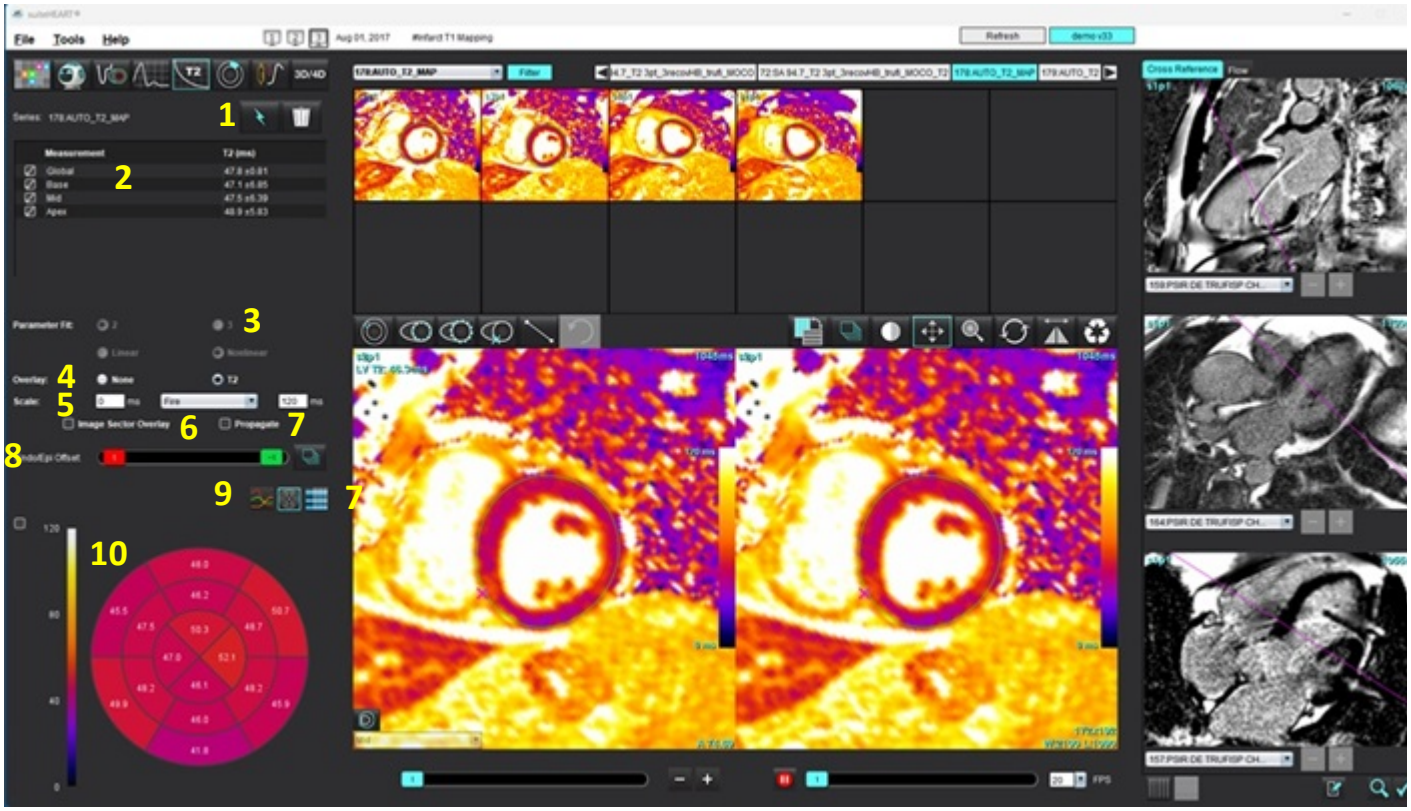
WARNING: The application assists in the analysis of the images only and does not automatically produce quantifiable results. The use and placement of quantitative measurements is at the discretion of the user. Misdiagnosis can occur if measurements are inaccurate. Measurements should only be created by a properly trained and qualified user.

WARNING: The user is responsible for the accurate placement of all regions of interest (ROIs), including those generated by auto segmentation.

NOTE: To set the T2 Mapping preferences, Select **Tools > Preferences > Edit**. Select the **T1/T2/T2*** tab.

NOTE: It is recommended to set the **Auto Compose Series for Analysis** in preferences for your scanner type. The analysis requires that all slice locations are in a single series. Select **Tools > Preferences > Edit**. Select the **Auto Compose Series** tab.

FIGURE 1. T2 Mapping Interface



1. Auto Segmentation, 2. T2 Results, 3. Parameter fit selections 4. Colormap overlay selections, 5. Colormap options 6. Display sector overlay, 7. Editing propagation, 8. Endo/Epi Offset, 9.Curve, 16-Segment Polar plot or Table, 10. T2 Curves, Polar Plots, Tables

Perform Analysis

1. Select 

.
2. Select the appropriate time series or map series.
3. If analyzing the time series, select the fitting method.

   NOTE: The nonlinear fitting algorithm does not estimate the background noise.

   NOTE: To obtain T2 results using Siemens original DICOM images that are similar to the generated Siemens scanner T2 map select Linear Fitting.
4. Set the overlay preference to automatically display the color map, if desired.
5. Use the file-pull down menu to select a different color scale.
6. Create a Global T2 result by selecting 
.
7. Review all endocardial and epicardial traces and the RV insertion point.
8. Edit any inaccurate contours.

9. Use the Endo (red) or Epi (green) offset to adjust contours 

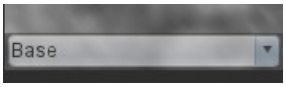
.

 Propagate offset to all slices.  Offset single slice.

10. To edit a single echo time click off the 

.

11. Confirm slice classification for each slice location and series type.



NOTE: If a stack of short axis images are segmented the T2 result for the Base, Mid or Apex and the 16-segment polar plot sectors will be averaged based upon the slice classification.

12. To measure a segment of the myocardium select  .

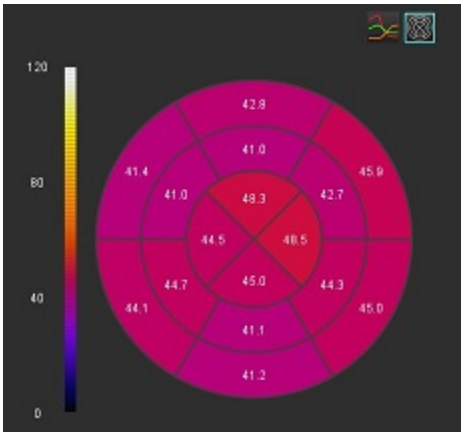
NOTE: Up to five Local ROI measurements can be created on an image for Base, Mid and Apex.

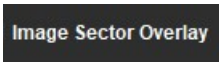
13. Manual segmentation can be performed.

- Trace the LV endocardium by selecting  .
- Trace the LV epicardium by selecting  .
- Mark the RV insertion point by selecting  .
- Confirm slice classification for each slice location.

16-Segment Polar Map

1. Complete the Global T2 analysis for Base, Mid and Apex.
2. Confirm the RV insertion point for each slice location.
3. Confirm the correct slice classification.
4. Select the 16 Segment Polar Plot  .



5. Select 

to show the sector overlay directly on the image.
6. Select Graphs  to return to the T2 curves if the time series was analyzed.

T2 Result Values Format

Result	DICOM Images		Map Images
Global	mean +/- std		mean +/- std
Base/Mid/Apex	value +/- error		mean +/- std
Local ROIs	value +/- error		mean +/- std
Local	mean +/- std		mean +/- std

Delete Contours

Click  on the interface to delete **ALL** contours on the series selected.

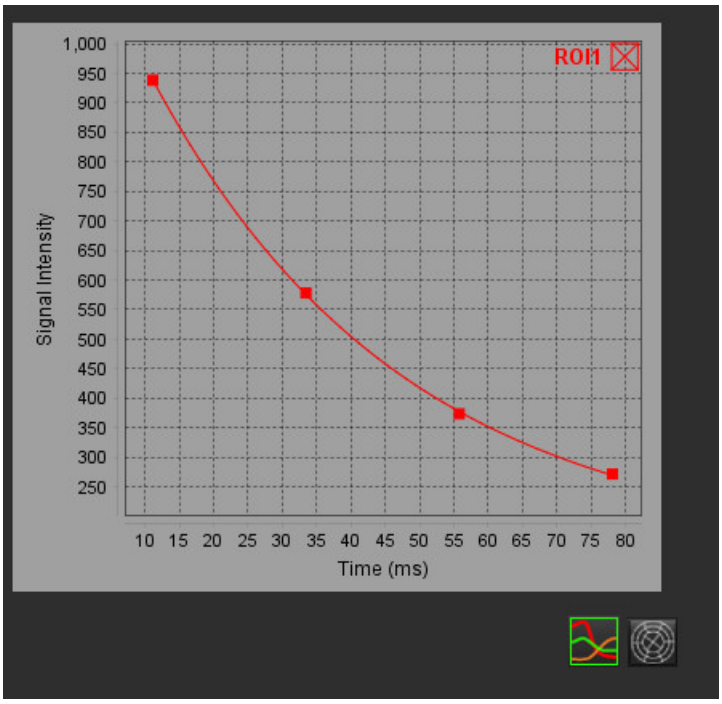
Left mouse click on a contour followed by a right mouse click to delete a single contour or select  to delete contours on all time points.

Review the T2 Curves

1. The curve fitting results show the signal behavior from the image data. In cases of image artifacts due to wrap, misregistration, breathing artifacts or arrhythmias the curve fit may not be optimal.
2. A signal intensity point can be eliminated from the calculation by clicking directly on the point on the graph and selecting the contour on the image, which turns purple.
3. Select delete from the right mouse (click and hold) or select the keyboard delete.

NOTE: Curve display is only generated by using the time series for analysis.

WARNING: The results of the T2 curve fit should be reviewed by a properly trained and qualified user.



Myocardial Perfusion

The Myocardial Perfusion analysis mode allows the user to review and analyze myocardial perfusion images. Series that have motion correction applied are recommended for analysis.

NOTE: Semi-quantitative analysis is supported. If a dual sequence series is available a shading correction can be applied.

NOTE: It is recommended to create a single series with the stress perfusion motion corrected images and a single series with the rest motion correction images.

CAUTION: Parameters of upslope and relative upslope may not be accurate on images that shading correction has not been performed.

WARNING: The application assists in the analysis of the images only and does not automatically produce a clinical interpretation of the results. The use and placement of quantitative measurements is at the discretion of the user. Misdiagnosis can occur if measurements are inaccurate. Measurements should only be created by a properly trained and qualified user.

FIGURE 1. Myocardial Perfusion Analysis Interface

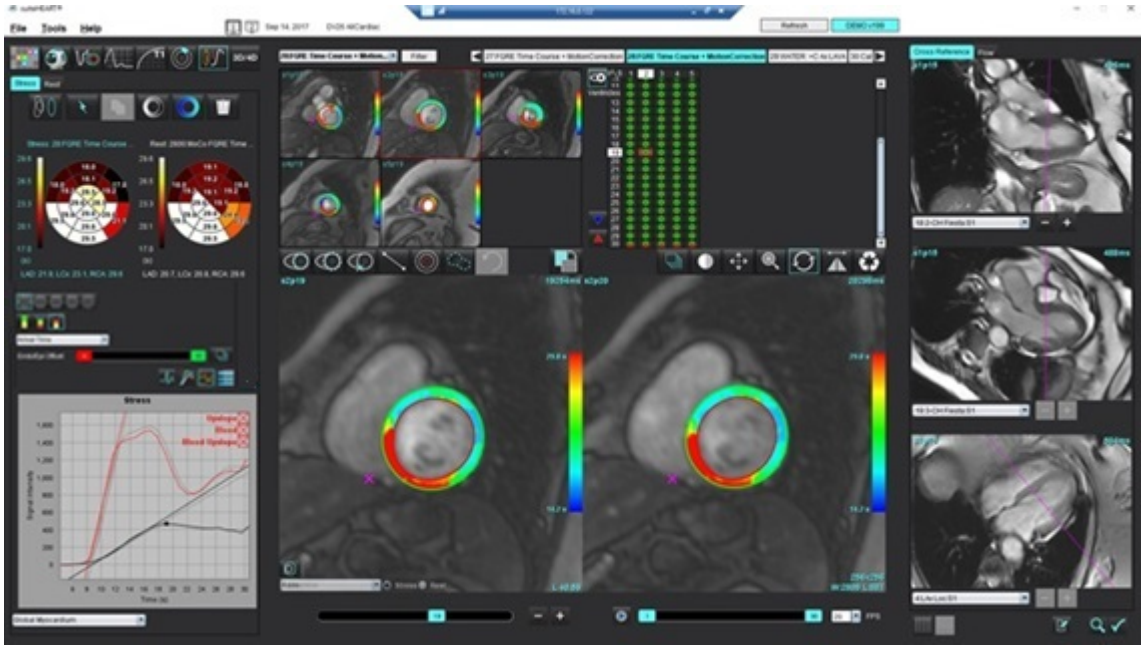
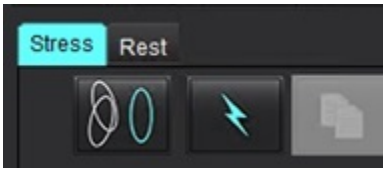


Table 1: Analysis Tools

	Perform motion correction.
	Propagate all slices, all phases.
	Propagate all phases, single slice.
	Perform auto-segmentation.
	Recalculate analysis after edit. (Only if auto segmentation has been performed.)
	Copy / paste contours over all phases.
	Recalculate analysis after edit. (Only if copy / paste has been performed.)
	Shading correction applied.
	Display Segment color overlay.
	Display no overlay.
	Display pixel-wise color overlay for calculated parameter.
	Display R to R interval.
	Display graphs of stress and rest.
	Graph display.
	Display parameter results table.
	16, 32, 48, 96 Segment or Concentric Polar Plot selection.
	2-Color, 4-Color or Continuous Polar Plot color selection.
	Concentric Polar Plot Selections.

Perform Myocardial Perfusion Analysis

1. Select  .
2. Select the tab for either Stress or Rest.



3. Select the myocardial perfusion series.
4. Click  to perform motion correction if required. A new series will created labeled MOCO. This series can be used for analysis.

   NOTE: Motion correction can be configured for preprocessing.

5. Select  to perform Auto Segmentation and analysis calculation.
6. Review all endocardial and epicardial traces, RV insertion point on each slice and edit as necessary.
7. Confirm the base, mid and apical classification.
8. To perform manual segmentation, select  to draw the endocardial contour on a single slice or all slices.
9. Select  to draw the epicardial contour on a single slice or all slices.
10. Select  to copy / paste the contours to all phases.
11. Place the inferior RV insertion point by selecting  .
12. Review all endocardial and epicardial traces, RV insertion point on each slice and edit as necessary.
13. Confirm the base, mid and apical classification.
14. The start and end frames used for the analysis are automatically determined by the arrival time and peak time. To adjust, select  .

    - Click  to assign the start phase, then click directly on the cell in the matrix.
    - Click  to assign the end phase, then click directly on the cell in the matrix.

Contour Editing

When an edit is performed the analysis must be recalculated. The edit warning symbol will appear. Click  to perform the recalculation.

Review Results

1. Select to review the calculated parameters in a polar plot format from the file pull-down menu. See Figure 2.

   Placing the cursor over a segment on the polar plot will highlight the corresponding graph for that segment.

FIGURE 2. Calculated Parameters Pull-down Menu

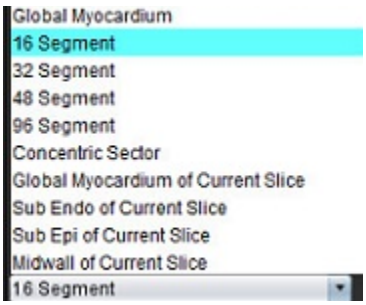
Review Graph/Table Results

1. Click  to review the RR interval plot.
2. Click  to display both stress and rest curves.
3. Click  to display the graphs.

   When displaying the segment color overlay on the image, placing the cursor directly on a colored segment will highlight the corresponding graph for that segment.

4. Click  to display the parameter results.
5. Select to review graph results from the file pull-down menu, Figure 3, located on the lower left under the graph display.

FIGURE 3. Graph Results



Calculate Relative Upslope (RU) and Reserve Index (RI)

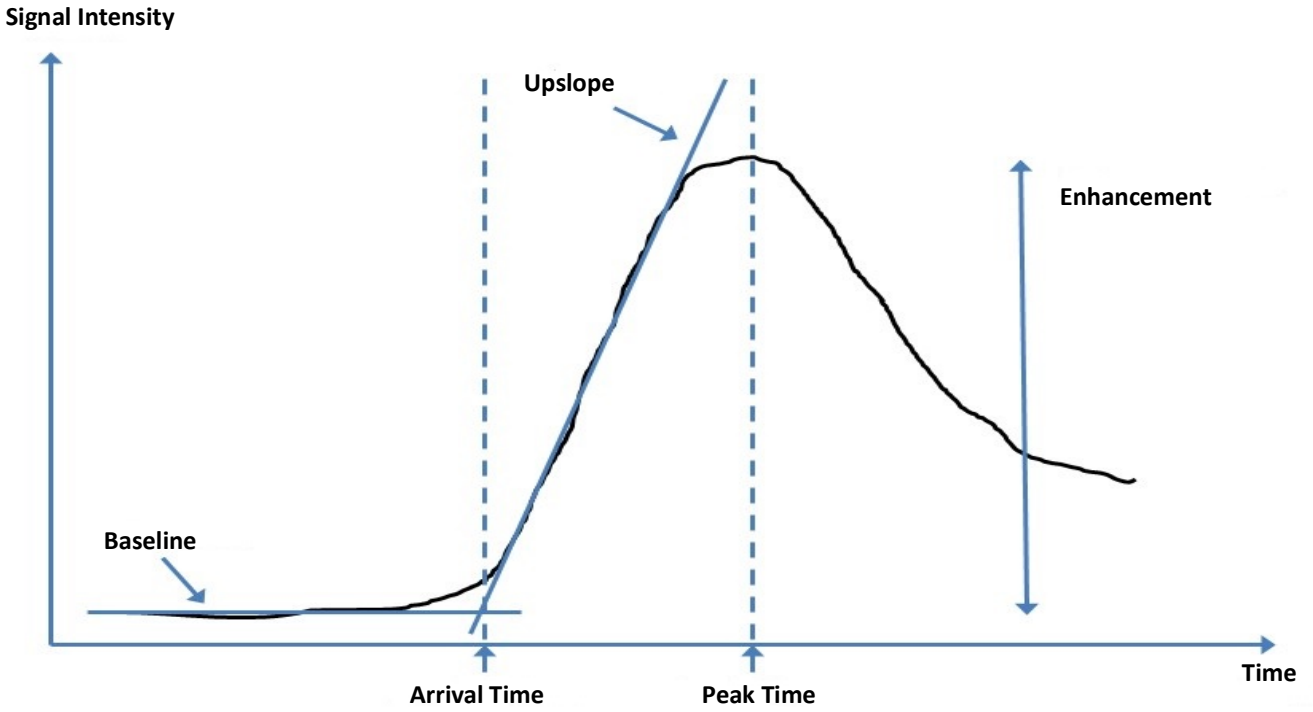
1. The blood pool ROI is placed automatically during the auto segmentation.
2. To change the slice location of the blood pool, use the thumbnail view to select a different slice location. To auto create a new blood pool ROI, select  or select  .
3. To place the blood pool ROI manually, select  , trace an ROI then select  or  .

   Basal slice level is recommended.
4. To delete the blood pool ROI right mouse click and select 

NOTE: For the calculation of the reserved index, both Stress and Rest analysis must be present.

CAUTION: Myocardial Perfusion result parameters of upslope and relative upslope may not be accurate on images that shading correction has not been performed.

Definition of Parameters Calculated from the Myocardial Perfusion Curve



Arrival Time	time (in seconds) of the intersection of the baseline and upslope
Peak Time	time (in seconds) of which the signal intensity reaches maximum
SI Ratio	SI(peak time - baseline)/ baseline
Upslope	The upslope is calculated by the weighted linear fitting using points between arrival time and peak time
Relative Upslope	RU = myocardial upslope / blood pool upslope
Reserve Index	The myocardial reserve index (RU) is defined as: RI = RU STRESS / RU REST

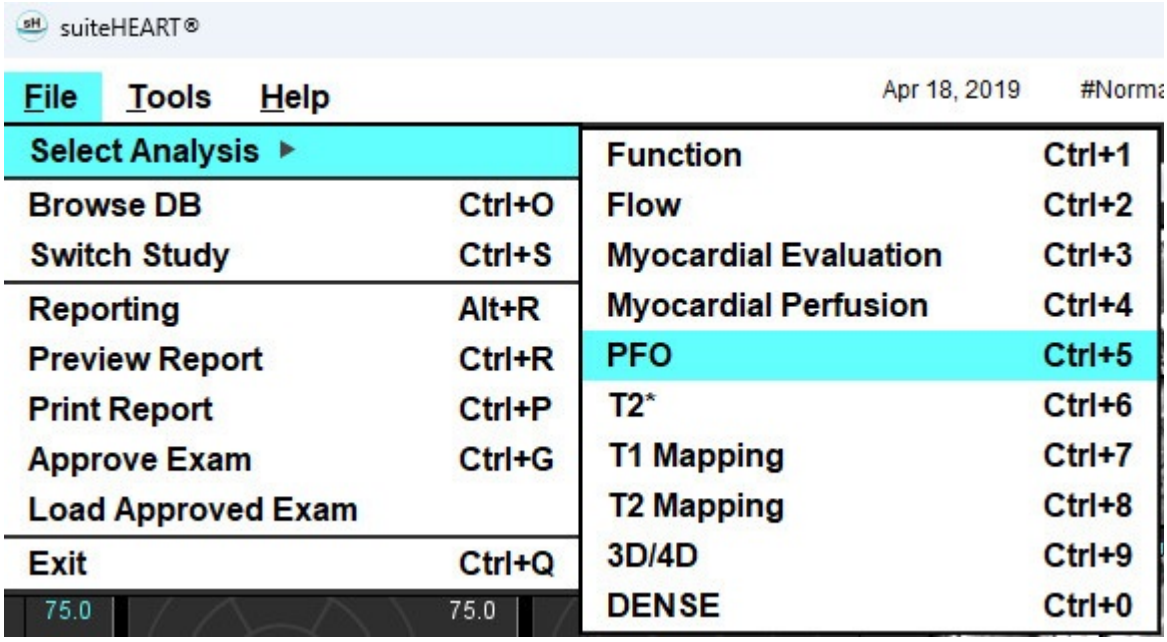
Patent Foramen Ovale (PFO) Analysis

The PFO analysis tool allows the generation of signal versus time curves to demonstrate an early peak for the detection of a PFO.

WARNING: The application assists in the analysis of the images only and does not automatically produce a clinical interpretation of the results. The use and placement of quantitative measurements is at the discretion of the user. Misdiagnosis can occur if measurements are inaccurate. Measurements should only be created by a properly trained and qualified user.

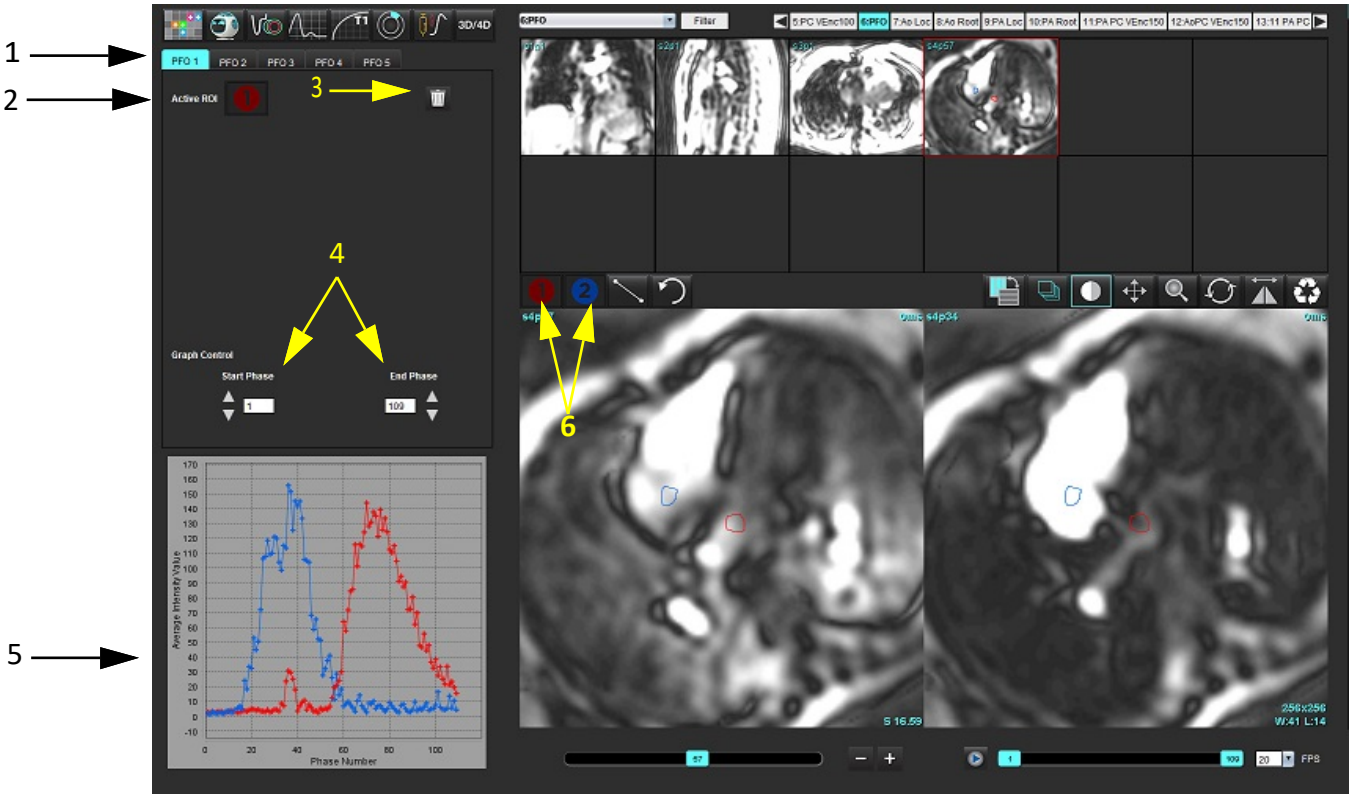
Launch PFO

1. Select **File > Select Analysis > PFO**.



2. Select a realtime series.

FIGURE 1. PFO Analysis Window



1. PFO editable tabs, 2. Active ROIs, 3. Delete, 4. Start and End phase, 5. Signal Intensity vs Phase curve, 6. PFO Analysis icons

Select Atrial Anatomy

Select an image where the anatomy of the left atrium (LA) and right atrium (RA) can be appreciated.

Generate Left Atrial (LA) Intensity Curve

1. Draw the curve by selecting  .
2. Trace a contour on the LA in the Image Editor window.
3. Move the cursor out of the Image Editor window.
4. Generate LA intensity curve.

   The signal intensity curve for the LA is automatically generated.

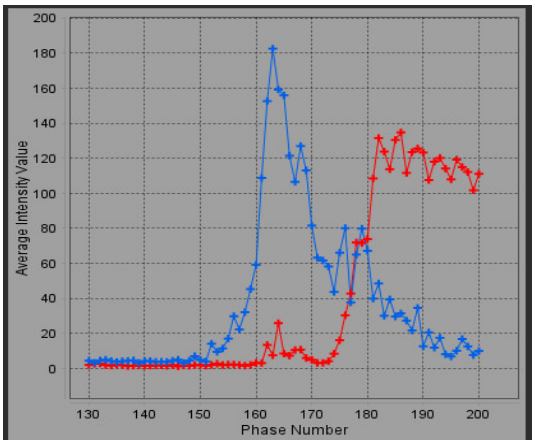
Generate Right Atrial (RA) Intensity Curve

1. Generate the RA intensity curve following the same steps previously listed to generate the LA intensity curve while using  .

   The curves are overlayed and displayed in the curve results display window.

NOTE: If a ROI has been placed on phase 1, for example, and the start phase is changed, the user drawn ROI will still be present on the original image where the ROIs were placed.

FIGURE 2. PFO Curve Results



Review Curve Data and Select Phase Range

1. Review the curves in the report window and adjust the **Start Phase** and **End Phase**.
2. Use the up and down arrows to select the **Start Phase** and **End Phase** to set the phase range for curve display.

Adjusting the start and end phases affect the display of the PFO curves.

Clicking on a point on the graph updates the phase displayed in the Image Editor window.

FIGURE 3. Start and End Phase Selection Screen

NOTE: If there are two acquisitions in the same series, you can set the Start and End Phases for the first acquisition, draw the LA and RA ROIs (resulting in automatic generation of curves), and then repeat the process on another PFO tab for the second set of images. All PFO tab labels are editable.

Editing Contours

Editing multiple phases at a single slice location:

1. Select the slice location
2. Select 
3. Select the first phase of the range of phases to be edited.
4. Depress and hold the shift key and select the last phase of the range to be edited.

   The selected thumbnails will appear highlighted with a red border.

5. Edit the contour in the image editor window.
6. Deselect the contour by either clicking on the image away from the selected contour or move the cursor out of the editor window.

ROI editing can be controlled by setting the scope.

Select the proper scope function from the Image View.

 Scope All – Applies ROI edits to all phases.

 Scope Current to End – Applies ROI edits from the current phase to the end.

 Scope Current Only – Applies ROI edits to the current phase only.

Delete Contours

Click  to delete **ALL** contours.

Left mouse click on an image followed by a right mouse click select  to delete contours on all time points.

Review Final Curve Results

A graph is generated from the contours showing pixel intensity versus time. Right mouse click on  to send to the report.

T2*

The T2* analysis tool calculates the T2* values of tissue from a multi-echo fast gradient echo sequence.

The T2* curve is a graph of the signal intensity versus echo time using an exponential decay curve formula. The T2* fitting algorithm is based on Levenberg-Marquardt non-linear least square algorithm.

The calculation for the T2* decay curve is: $y = a * \exp(-TE/T2^*) + c$

Where:

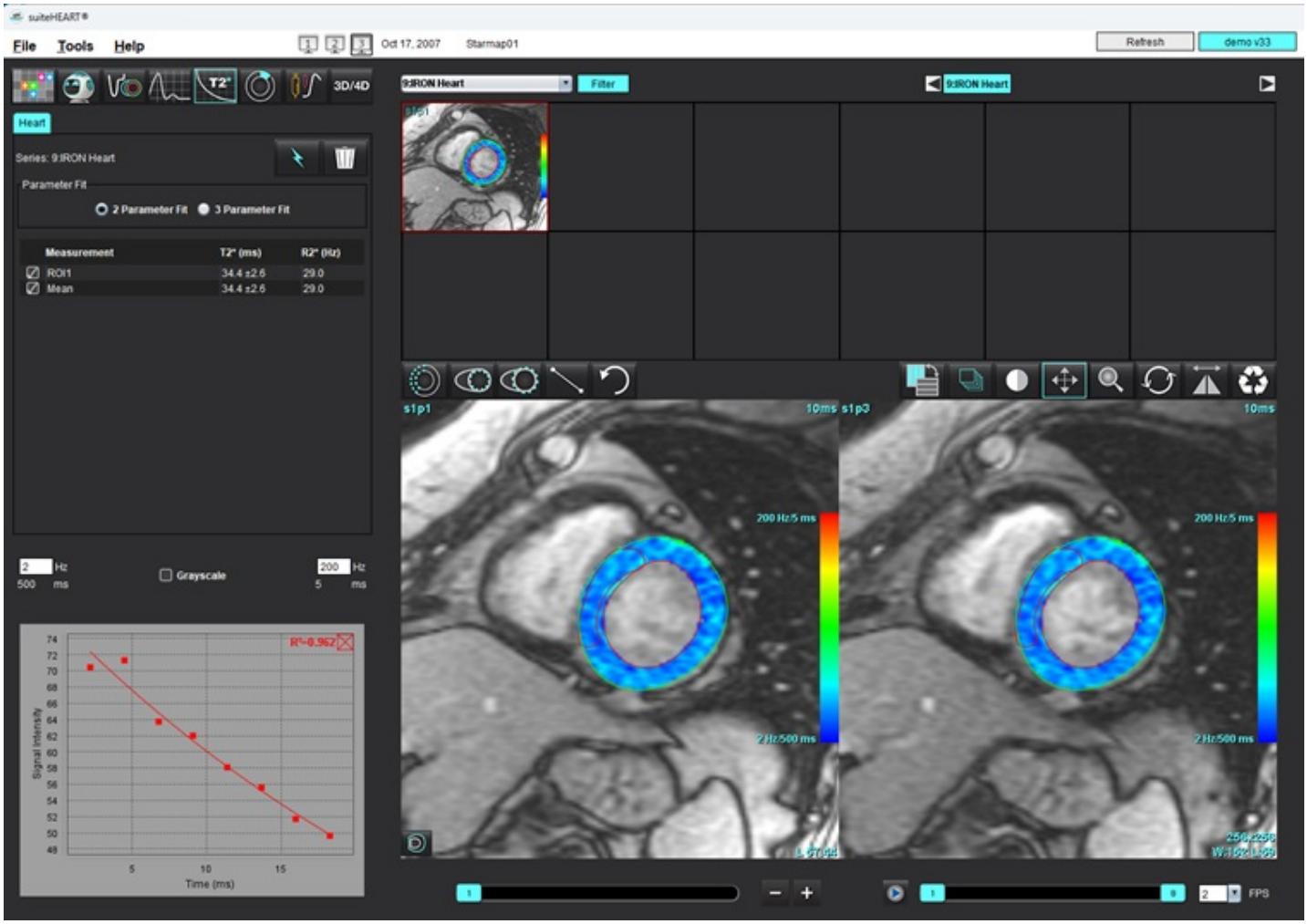
Table 1:

y	is the signal intensity at time TE
a	is the transverse magnetization at time 0 (zero)
TE	is the echo time
T2*	is the decay constant, and
c	is the background noise

WARNING: The application assists in the analysis of the images only and does not automatically produce a clinical interpretation of the results. The use and placement of quantitative measurements is at the discretion of the user. Misdiagnosis can occur if measurements are inaccurate. Measurements should only be created by a properly trained and qualified user.

Heart Analysis Procedure

FIGURE 1. T2* Analysis Interface



1. Select  .
2. Select the appropriate series.
3. Select  to perform auto segmentation.
4. Review the placement of the septal ROI.
5. To perform manual segmentation, draw a contour that encompasses the interventricular septum using  .

   The T2* and R2* are calculated and are displayed in the result table.

   The R^2 value is calculated and displayed on the graph.

Create Myocardial Colormap

1. Trace LV endocardium by selecting  .
2. Trace LV epicardium by selecting  .

   The T2*/R2* colormap is overlayed on the image.
3. The R2* colormap value can be changed.

NOTE: The default range for 1.5T images is 5ms - 500ms for T2*. The default range for 3.0T images is 2.5ms - 1000ms for T2*.

4. Right mouse click and select  to adjust the dynamic color range for the color map.

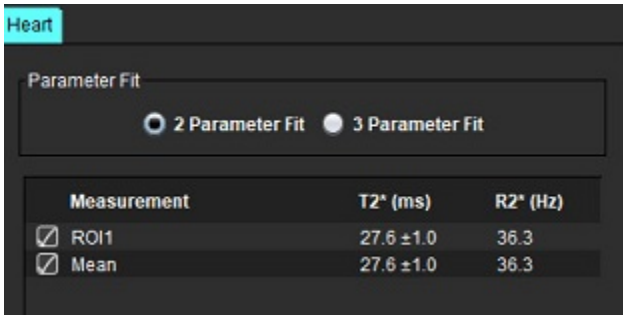
   The color overlay on the Image Editor changes dynamically.

   The Hz and ms values also change dynamically.
5. The T2* and R2* values can be determined by selecting the  and placing it over the color map overlay on the image.

Fitting Parameters

Select either the 2 Parameter or 3 Parameter Fit for the T2* decay curve.

FIGURE 2. Parameter Fit



The 2-parameter fit is widely accepted based on peer review literature [1]. In this model, the background noise, c, is calculated using a histogram-based algorithm and subtracted from the signal intensity, after which a non-linear fit is performed.

The 3-parameter fit is also available as referenced in peer review literature [2]. This model is a non-linear approach that works directly from the original input signal.

For both models, the initial T2* value is estimated using a trial linear fitting.

1. D.J Pennell, et al. “Cardiovascular T2-star (T2Star) magnetic resonance for the early diagnosis of myocardial iron overload,” Eur Heart J 2001; 22: 2171-2179.
2. Ghugre NR, et al. “Improved R2* Measurements in Myocardial Iron Overload,” Journal of Magnetic Resonance Imaging 2006; 23: 9-16.

Review the T2* Results

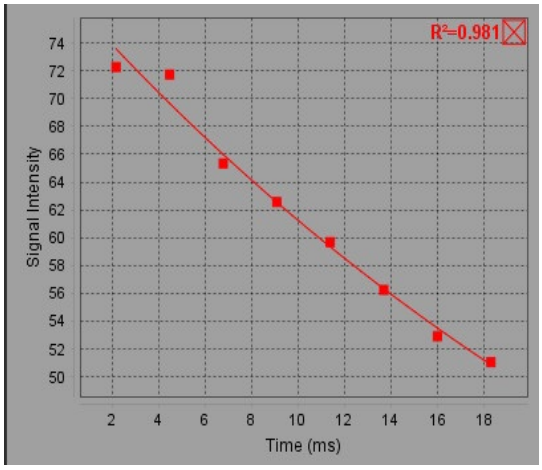
1. Review the contour position on all of the images.
2. The table lists the individual T2*/R2* measurements and also calculates a mean value.

NOTE: The T2* curve is a graph of the signal intensity versus echo time using an exponential decay curve formula. On occasion, it may be necessary to remove later echo points from the decay curve for a better curve fit. This may occur in extreme cases of iron overload when the signal intensity can be very low.

To delete a single contour from an image

1. Left mouse click to select the contour, which turns purple.
2. Right mouse to select the trash can or use the Delete key on the keyboard to remove a contour.
   - The contour is deleted and the curve fit is recalculated.

FIGURE 3. T2* Curve



WARNING: The results of the T2* curve fit should be reviewed by a properly trained and qualified user.

Table 2: R2*/T2* Conversions

Result	Unit	Conversion
R2*	Hz	R2*=1000/T2*
T2*	ms	T2*=1000/R2*

The factor of 1000 is used as the T2 and T2* are reported in units of milliseconds (ms) and R2 and R2* are Hertz (or s-1).

3D/4D Flow Viewer

Provides interactive oblique reformatting of 3D and 4D flow images. The Vessel tab allows for the auto segmentation of the thoracic aorta along with tools for editing and measurement reporting. Tools are available to create 2D phase contrast and 2D function images from 4D that can be analyzed. Inline flow analysis can be performed with auto segmentation of vessels.

NOTE: A 3D series with isometric voxels and overlapping slices improves the quality of the reformatted images.

NOTE: The 3D/4D Flow Viewer shall display a 4D series only if 4D is licensed.

NOTE: If both 2D phase contrast and inline 4D flow analysis have been performed all results will be available in Flow Analysis Mode.

CAUTION: 3D or image reformats only provide additional supplemental information in the formulating of a diagnosis and should always be used in conjunction with conventional imaging techniques.

WARNING: Always correlate any 3D reformats with the original acquisition data.

WARNING: Following preprocessing, the user is responsible for assessing the accuracy of the entire analysis and making any necessary corrections. A comprehensive review should include:

- ROI placement
- Correct vessel identification for each category
- Baseline correction

Table 1: 3D/4D Tabs (see Figure 1)

Tab	Description
Display	Image view visualization tools and DICOM image saving.
Vessel	Auto segmentation and editing tools.
Analysis	Inline 4D Flow analysis.

FIGURE 1. 3D/4D Tabs

Display Tab

Table 2: Display Tab

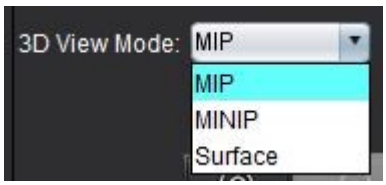
Tool	Description
	**Crosshair Cursor** - synchronizes navigation between all viewports. Use for seed point for pathlines.
	**Orientation Buttons** - changes the image plane in the 3D and oblique viewports. **S = Superior** **I = Inferior** **A = Anterior** **P = Posterior** **L = Left** **R = Right**
	**Oblique Mode** - displays the plane of the oblique reformat and the perpendicular intersection to display desired anatomy.
	**Double Oblique Mode** - displays three oblique planes defined by three adjustable color axis - blue, yellow, green. Adjust any axis to update the two other oblique planes.
	**3D View Mode** - provides image render modes in the 3D viewport **MIP** - Maximum intensity projection (Default). **MINIP** - Minimum intensity projection. **Surface** - Refer to Surface Mode on page 177.
	**Display Mode** - displays segmentation Visualization tools (see Table 6, “Visualization Tools (Display or Vessel Tab),” on page 174).
	**Streamlines**- global visualization of 3D velocity fields at a specific temporal phase. Settings: **Stream Filter** - adjusts the intensity of the stream lines.
	**Pathlines** - the trajectories of individual blood particles as they move through the cardiovascular system over time. **Path Filter** - adjusts the blood speed threshold.

Table 2: Display Tab

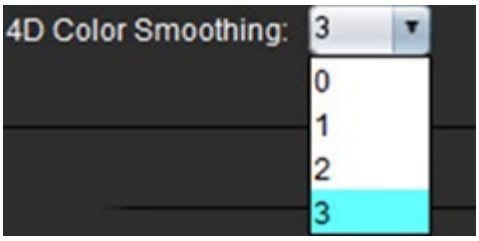
Tool	Description
	**Vectors**- arrows representing speed and direction of blood flow. Settings: **Vector Filter** - adjusts the blood speed threshold. **Spacing** - adjust the density of the arrows. **Size** - adjust arrow scale to the local speed.
1  2  3  4 	**1 Color Speed Overlay*** (disabled when Streamlines and Vectors are selected.) **2 Color Speed Overlay Removal*** **3 Phase Visualization*** **4 Angiogram*** *Available for 4D Flow only.
	**Speed Range** - adjusts the color speed assignment of the direction of flow. Available for 4D Flow images only. The Speed Range color bar legend is displayed on the right hand side of each viewport. The value is an estimate.
	**Opacity** - controls the color speed opacity on the image to improve the visualization underlying anatomy. Available for 4D flow images only.
	**4D Color Smoothing** - degree of smoothing for the color speed overlay.
	**Cine** - controls frames per second and defines start and end frame of the cine movie. Available for 3D time-resolved magnitude and 4D flow images only. Use space bar on keyboard to play or pause cine.
	**Save DICOM Series - Screenshot** - saves the viewport images as displayed, including visualizations. 1 - Active viewport 2 - All viewports **NOTE:** Image type is determined from 3D view mode selection.

Table 2: Display Tab

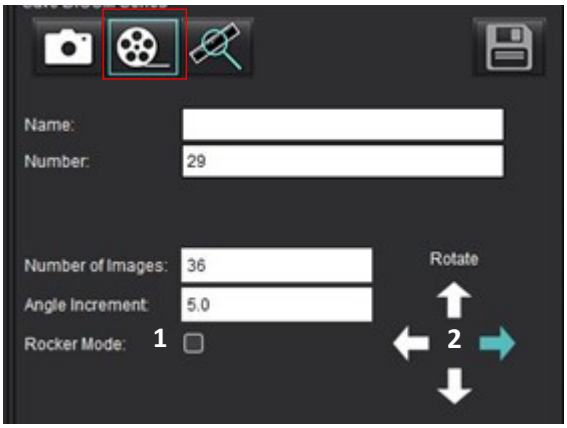
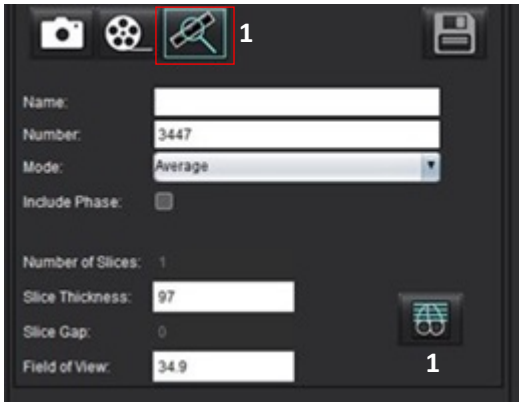
Tool	Description
	**Save DICOM Series- Rotational Cine** - saves the active viewport image as a rotational cine. 1 - Rocker Mode - select to save images in rocker cine. 2 - Select the arrow for the direction of the rotation.
	**Save DICOM Series- Further Analysis -** For 3D acquisitions saves images as MIP. For 4D acquisitions saves images as conventional cines with magnitude and/or phase. Series created can be used for future analysis. 1 - Multi slice Rx tool **NOTE:** For each magnitude and phase series a baseline corrected series is created.
	**Save** - saves all image series types created by the series definition to the local database.

Table 3: Viewport Tools

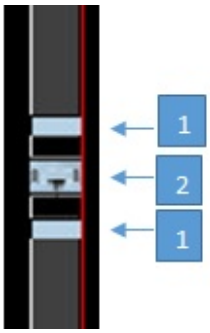
Tool	Description
	**Paging and Thickening** - changes the thickness of the MIP image and pages through the image set. 1= click and drag either side buttons to change the thickness of the MIP image 2= click and drag the slider to page through the image set or use the scroll wheel. Controls are found on the right hand side of the selected viewport.
	**Linear** - provided measurement of a straight line distance. Click directly on the measurement then right mouse to perform Delete, Locate, or Label. (Quick Key Alt + 1)
	**3D Rotate** - tilts or rotates the images in the 3D viewport. Middle mouse and drag directly in the viewport to tilt or rotate.
	**Flow Direction** - displays the perpendicular plane in oblique viewports. Right mouse click in viewport, left mouse click select Flow Direction. Left mouse click directly on the anatomy of interest. Available for 4D flow only.
	**Window/Level** - right mouse click in viewport.
	**Pan** - right mouse click in viewport.
	**Zoom** - right mouse click in viewport.
	**Rotate** - available for the 3D viewport and oblique viewports.
	**Undo** - removes the last action on the viewport

Table 3: Viewport Tools

Tool	Description
	**Reset**
	**Hide 3D Image** - click to hide volumetric image data, in 3D view, to only show ISO surface.
	**Send image to report** - right mouse click in viewport.
	**Scan Parameters** - right mouse click in viewport.

Table 4: Quick Key

Function	Action
Target Cursor	Position the cursor on the desired anatomy and press Shift.
1 x 1 Layout	Double clicking on any 2 x 2 viewport toggles the layout to 1 x 1 and back to 2 x 2.
Linear Measurement	Perform by clicking the Shift + 1.

FIGURE 2. Quick Keys

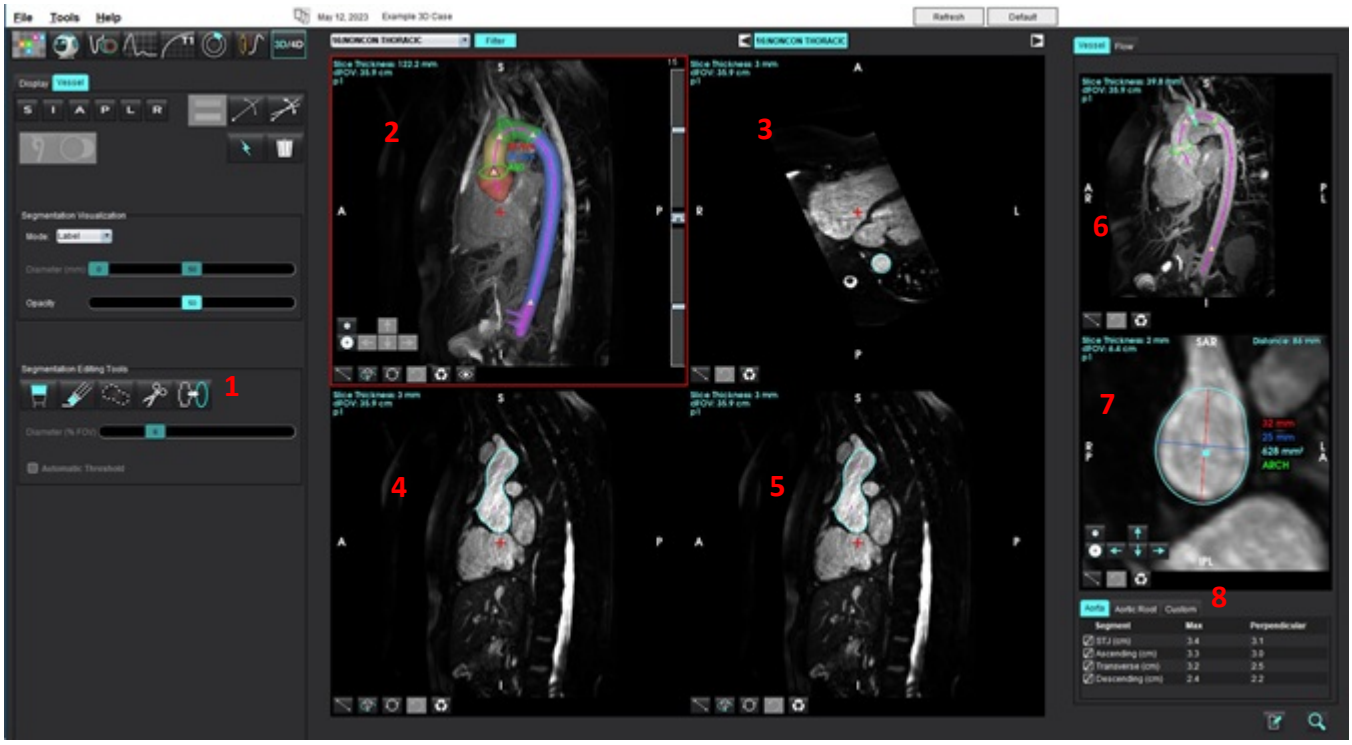
3D/4D Editing Tools	
3D Rotate	Ctrl + Alt + Middle Mouse Button
Image Zoom	Ctrl + Middle Mouse Button
Window/Level	Alt + Middle Mouse Button
Move Crosshair Cursor	Shift
Brush	Alt+A
Erase	Alt+E
Trace	Alt+T
Cut	Alt+C
Smooth	Alt+S
Brush Size	Alt + Mouse Wheel
Quit Editing	Alt+Q
Toggle Display Mode	Alt+D

Vessel Tab

The Vessel tab allows for the auto segmentation of the thoracic aorta along with tools for editing and measurement reporting.

Required Images: Automatic 3D Vessel Segmentation is optimized for bSSFP sequences but supports contrast enhanced 3D MRA and contrast enhanced dual-echo water reconstructed image types.

FIGURE 3. Vessel Analysis Interface (3D)



1. Editing Tools, 2. 3D Viewport, 3. Axial Viewport, 4. Oblique Viewport, 5. Oblique Viewport, 6. Centerline View, 7. Orthogonal View, 8. Measurement Tables

3D Segmentation with Measurements

1. Select 3D/4D.
2. Select the **Vessel** tab.
3. Select the appropriate 3D series from the series navigation pull-down.

   The image type selected will be indicated on the button.
4. Click  to perform auto segmentation, calculate the centerline, place aortic landmarks as yellow triangles, and record maximum diameter measurements in the landmarked segments shown in green. See Figure 4.

NOTE: Vessel segmentation can be configured for preprocessing.

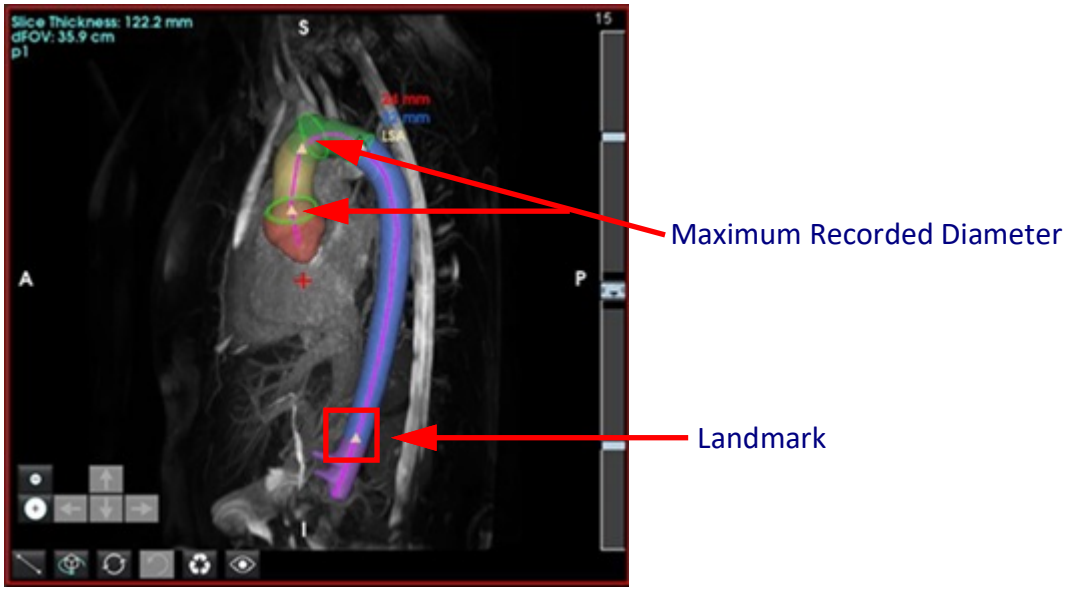
NOTE: Landmarks: Sinotubular Junction (STJ), Brachiocephalic Artery (BCA), Left Subclavian Artery (LSA) Celiac Artery (CA).

Maximum diameters and a perpendicular measurement passing through the maximum diameter's midpoint are automatically calculated along the centerline.

Scrolling with the mouse wheel in the Orthogonal View will advance the view forwards/backwards along the centerline.

NOTE: It is possible to scroll 'off the end' of the centerline - the Orthogonal View will display slices extrapolated in the direction of the final centerline point. This can be useful for navigating beyond the centerline endpoints, especially near the root.

FIGURE 4. 3D Segmentation View



5. Review the measurements results on the Aorta tab in the bottom right. Clicking directly on the measurement result table will locate the placement of the measurement in the viewports. See Figure 5.

NOTE: The measurement unit selected in preferences will be the unit for the report.

NOTE: Click the Custom tab and click  to add a custom measurement.

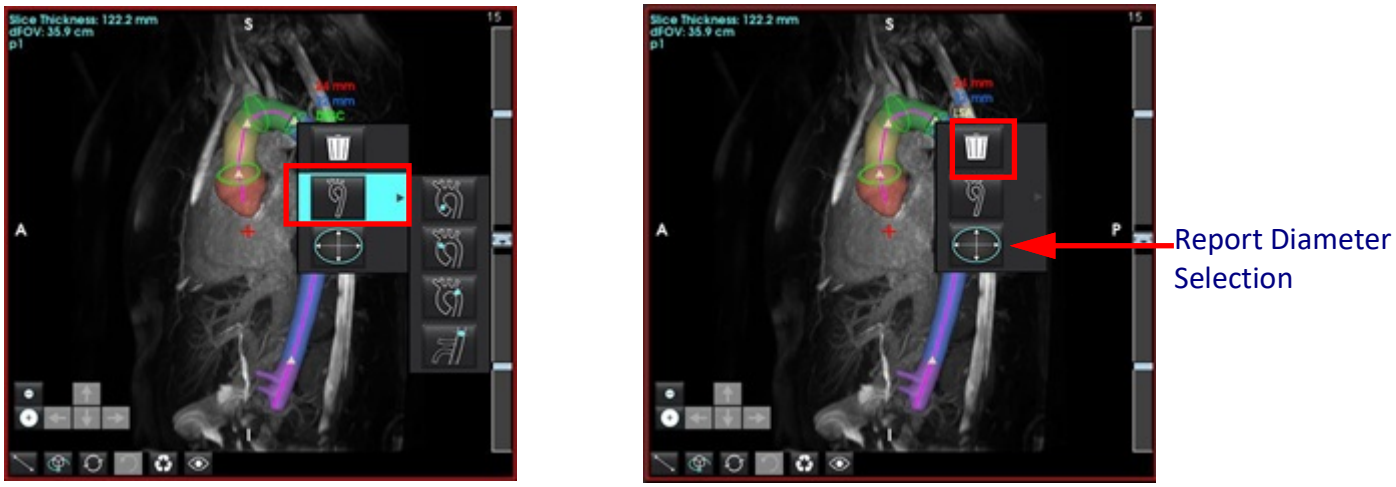
FIGURE 5. Measurement Tables

6. Review the landmark segments. To change, click and drag the yellow triangle along the centerline or right mouse click on the centerline and place a landmark at the selected centerline point.

   Landmarks can be deleted by right mouse clicking over the landmark and selecting the trash can icon. See Figure 6.

NOTE: Automatic measurements at the maximum will be recalculated.

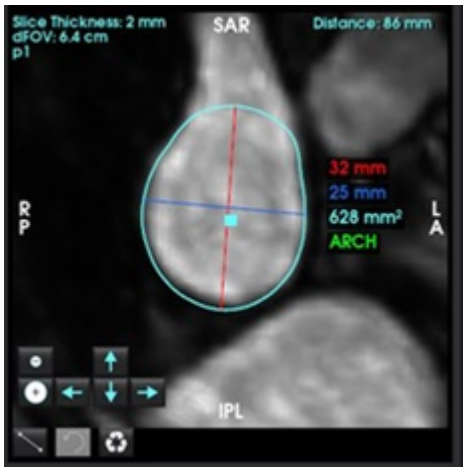
FIGURE 6. Right Mouse Click Change Landmark (left) Right Mouse Click Delete (right)



NOTE: The STJ measurement is a landmark. Moving the landmark will update the recorded measurement.

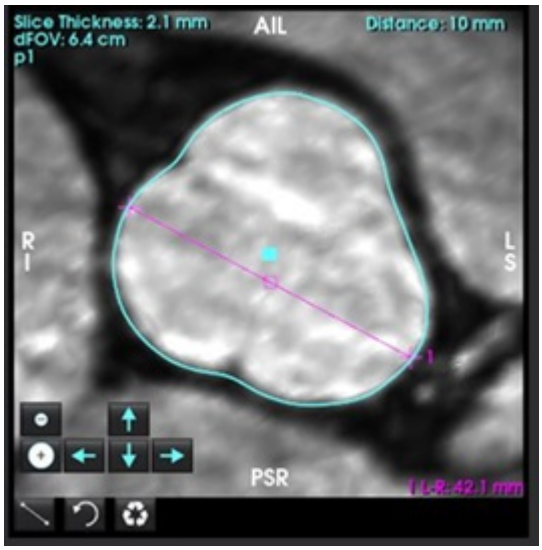
7. The maximum recorded measurement position can be manually changed by right mouse clicking along the aorta within a segment and selecting  to change the measurement position.
8. The recorded measurements can be manually overridden in the Orthogonal View by clicking on the linear annotation and dragging either end (see Figure 7). Linear measurements can be reset by right mouse clicking on the annotation and selecting  .

FIGURE 7. Orthogonal View



9. The Aortic Root tab has six predefined measurements. Localize the aortic root and click directly on the measurement in the table and then click on the orthogonal view to create linear measurements. See Figure 8.

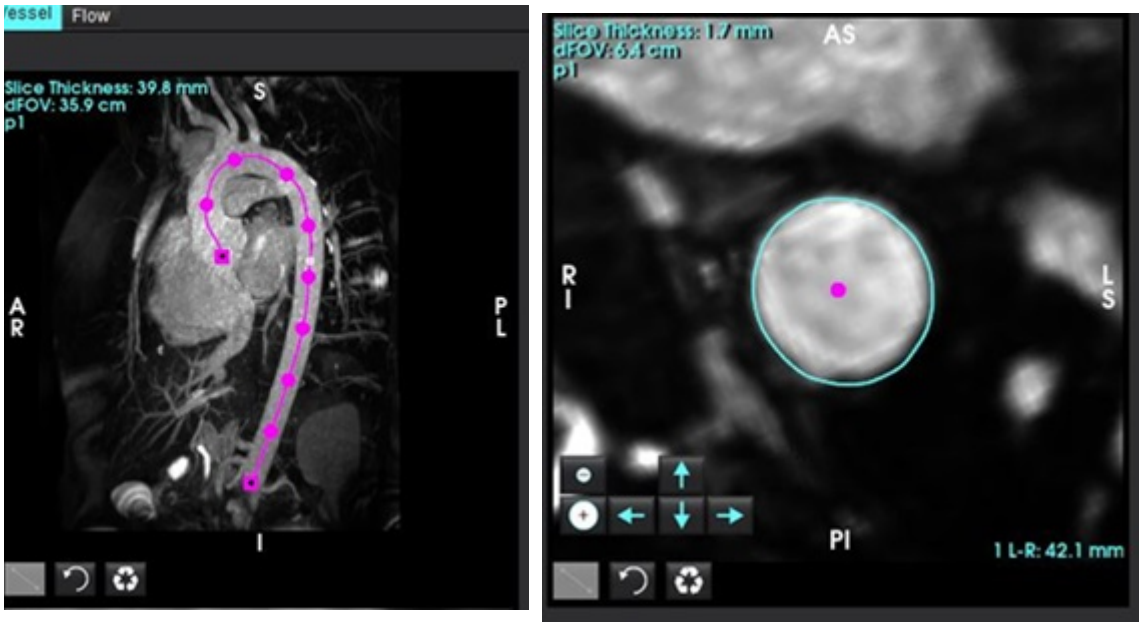
FIGURE 8. Aortic Root Tab showing Orthogonal View



10. Clicking the centerline in the Centerline View will convert it to a Spline, to edit click and drag on a point. Double click on either end of the centerline to extend it. See Figure 9.

IMPORTANT: Overriding the centerline directly will prevent future update of the centerline from segmentation edits!

FIGURE 9. Centerline Viewport and Orthogonal Viewport



11. Review segmentation, making minor changes using dilate, erode, shift existing contour (Table 7) or major changes using brushes, lasso, smooth (Table 8).

NOTE: Prior to performing any major segmentation editing it is recommended to review measurements first as the centerline maybe accurate and only minor measurement adjustments would be needed.

Table 5: Segmentation Controls (Vessel Tab)

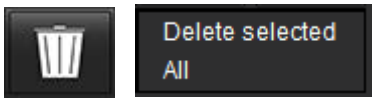
Selection	Description
	Vessel Selection Dropdown-Select the active vessel for segmentation editing. **NOTE:** Performing auto-segmentation will segment all vessels regardless of the selected vessel. **NOTE: Options for PA, SVC, IVC will only appear in 4D.**
	Automatic Vessel Segmentation **3D**: Thoracic Aorta **4D**: Thoracic Aorta, PA, SVC, and IVC
	Delete active, selected or all segmentation(s). **NOTE:** For 3D, no drop-down will appear and only the aorta will be deleted.
	Limit / No Limit ROI. Toggle the ability for the actively selected vessel to override (claim voxels from) other vessel segmentations. **NOTE:** Only available for 4D.

Table 6: Visualization Tools (Display or Vessel Tab)

Selection	Description
	Open the Segmentation Visualization panel in Display tab.
	Toggle visibility of each vessel isosurface (Display tab only).
	**Label** - colors the active vessel in teal, inactive vessels in grey. **Vessel**- all vessels are colored brightly with different colors. **Diameter (3D only)** - active vessel is colored according to cross sectional diameter. **Area (3D only)** - active vessel is colored according to cross sectional area.
	In diameter and area mode, the slider can be adjusted to scale the color bar.
	Adjusts opacity for all segmentations (%).

Table 7: Viewport Editing Tools

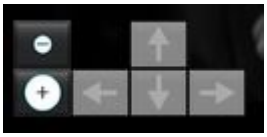
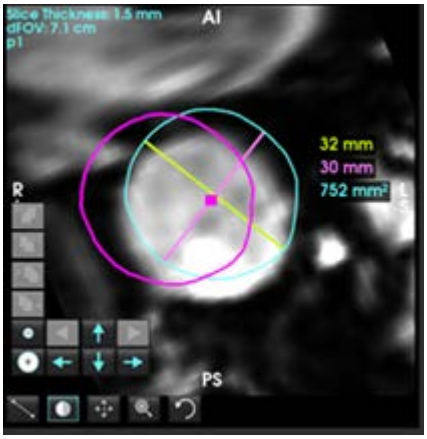
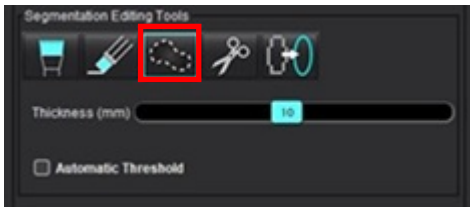
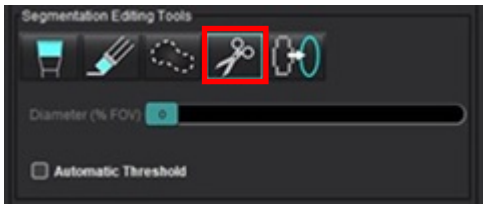
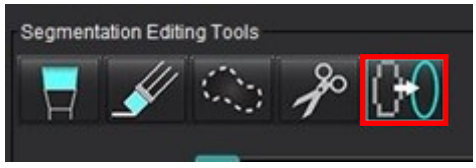
	**3D View**- Global erode and dilate.
	**Orthogonal View** The arrow keys allow single voxel displacement of the contour. The erode and dilate buttons will apply to the contour. Erode, dilate, and shift will all be propagated to slices above and below the current slice proportional to the amount of displacement applied.
	Click and drag the contour in the orthogonal view (starting at the blue square) to apply combined shifts instead of clicking the arrow keys multiple times.

Table 8: 3D Editing Tools

Tool Selection	Description
	**Brush Add** Paints a 3D Sphere. The size of the brush is a percentage of the FOV. (Diameter defaults to 6% FOV. (30 cm FOV ~ 1.8 cm diameter).
	**Brush Erase** Diameter defaults to 6% FOV. (30 cm FOV ~ 1.8 cm diameter).
	**Trace Add** Thickness defaults to 10mm through-plane Effects a stack not a curved volume.
	**Cut** Can be used in the 3D view, applies to entire slice thickness.
	**Smooth** Applied as a brush directly on the isosurface Without drawing ROI, Press ALT+S after selecting the tool to apply global smoothing. After drawing ROI, press ALT+S repeatedly for iteratively stronger smoothing. Transforms into a spherical smoothing brush for interaction with 3D surface model.

NOTE: These tools will affect through-plane stack. Brush and erase will affect the current slice and the slices within the radius above/below. Default thickness for trace is 10 mm. Cut and smooth operations' effective thickness is the active view's slice thickness.

NOTE: Selecting the **Automatic Threshold** will calculate the optimal threshold to separate background from vessel within the interaction. This tool requires the user to draw along/near the vessel boundary and will calculate the optimal threshold for adding or erasing. For best results, use in regions where the vessel is not surrounded by tissue of similar brightness.

Surface Mode

Required images: Contrast-enhanced 3D acquisitions or other angiographic sequences in which intravascular signal is significantly higher than background tissue. See Figure 10.

1. Select **Display** tab.
2. Select **Surface** (3D Only) from the drop-down menu.

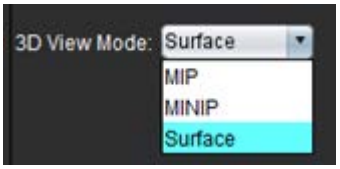


FIGURE 10. Surface Mode

3. Use the opacity slider on the left panel to change the depth of the surface to be visible.

   Decreasing the opacity will reveal inner anatomical structures with higher signal intensity, while increasing the opacity will include more surrounding background tissue with lower image intensities.

4. Right mouse click to change the color-mapping and select  .

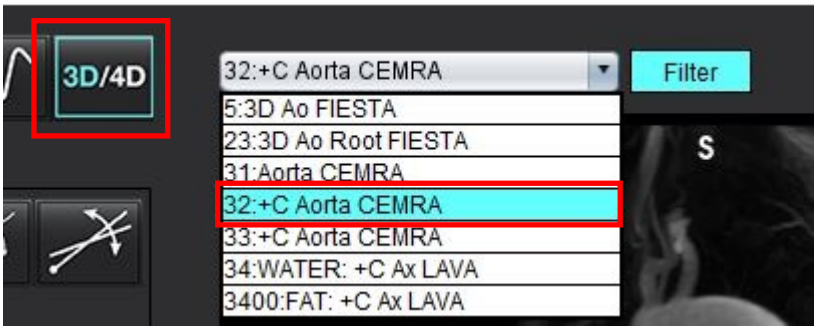
   Window width adjusts the range of the color while window level determines the brightness.

Example Workflow: Create MIP Images from a 3D Image Series

1. Select the appropriate study and launch suiteHEART® Software.
2. Select 

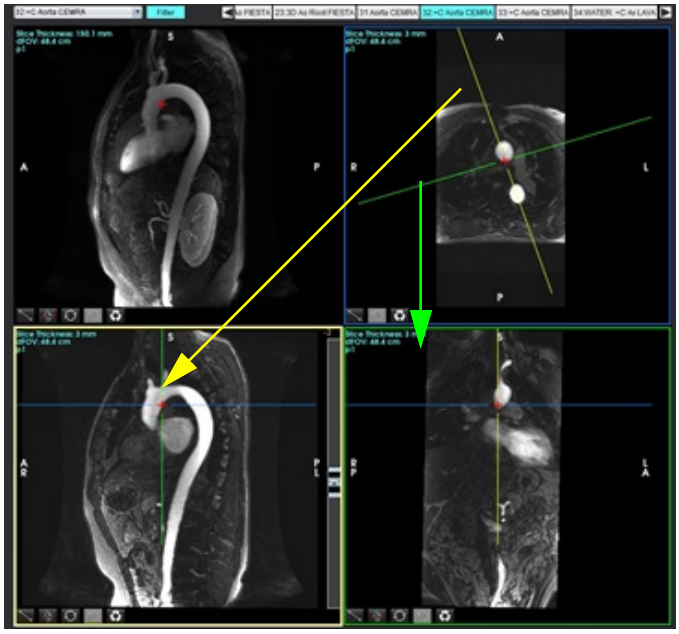
.
3. Select the appropriate 3D series from the series navigation pull-down. The image type selected will be indicated on the button, as shown inFigure 11.

FIGURE 11. Series Navigation



4. Select  and click on the desired viewport. Reformat lines will appear as shown in Figure 12.

FIGURE 12. Double Oblique Mode



5. Click on the solid line, left mouse click and drag and tilt the line to display the desired anatomy.
    a.) Click on the desired viewport for saving.
    b.) Adjust the MIP thickness using the controls on the right hand side of the viewport.
    c.) Complete the series definition entries, as shown in Figure 13.
    d.) Click the save button to save the MIP image to the local database.

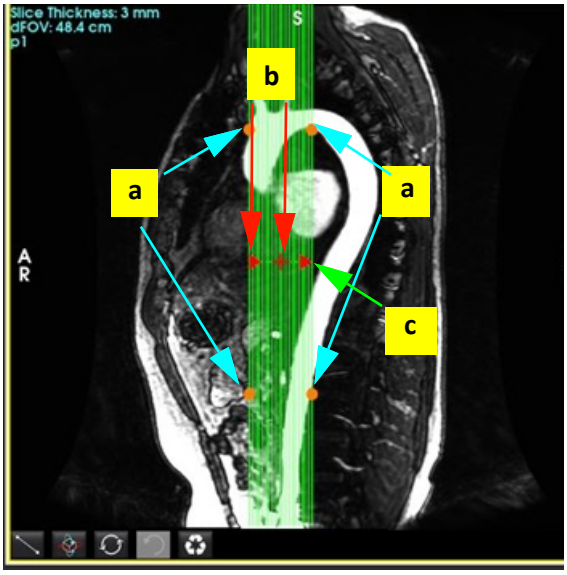
FIGURE 13. Save for Further Analysis

6. Create a stack of MIP images by selecting  .

   NOTE: The maximum number of post-processed MIP images that can be created is 512.

7. Click on the viewport to be used as the reference image and define a stack of batch images, as shown inFigure 14.
   a.) Extend the range of the slice coverage.
   b.) Adjust the angle and arrows indicate slice direction.
   c.) Move the Rx.

FIGURE 14. Rx Planning



8. Enter the series definition options and click  to save the image stack to the local database.
9. To view the created series, switch to function analysis mode, select review mode and click refresh.

Example Workflow: Create 2D Series for Analysis

The creation of conventional 2D phase contrast or 2D functional images requires a 4D Flow series that has both time-resolved magnitude and flow conventions of R/L, A/P and S/I.

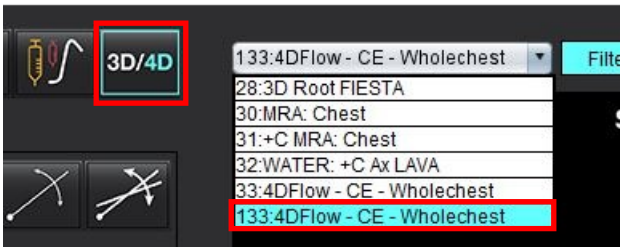
Series created as magnitude alone or magnitude and phase from 4D flow images are a valid 2D conventional series that can be used in function or flow analysis.

Series that are created as post-processed from 4D Flow will have a color flow overlay.

1. Select the appropriate study and launch suiteHEART® Software.
2. Select 

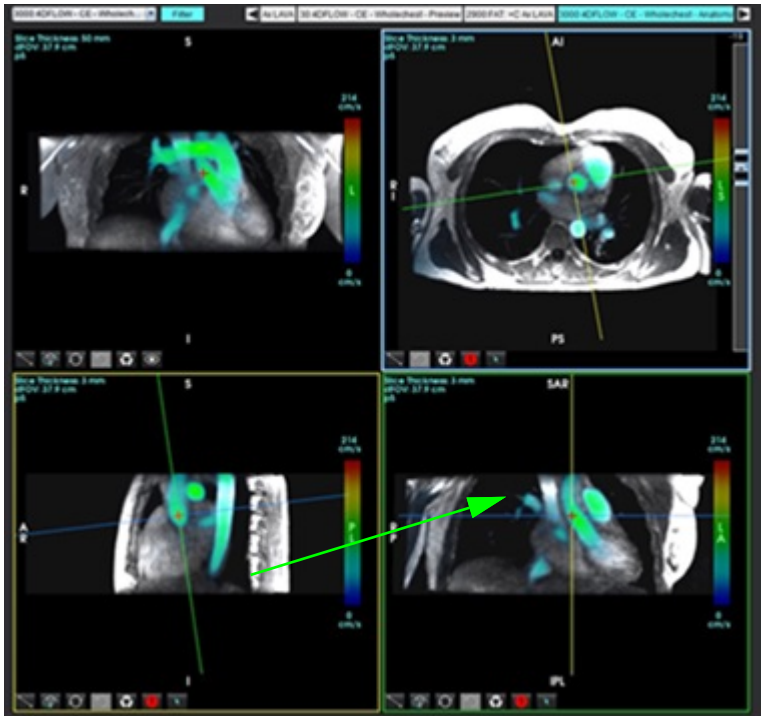
.
3. Select the appropriate 4D series from the series navigation pull-down, as shown inFigure 15. The image type selected will be indicated on the button, as shown inFigure 15.

FIGURE 15. Series Navigation



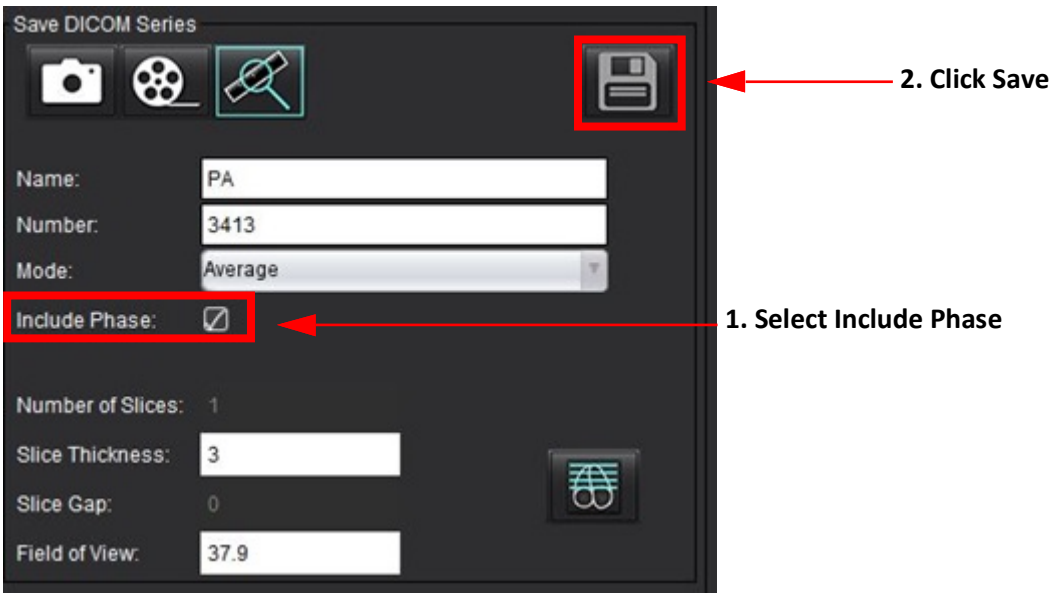
4. Select  and click on the desired viewport. Reformat lines will appear as shown in Figure 16.

FIGURE 16. Double Oblique Mode



5. Click on a solid line, left mouse click and drag and tilt the line to display the desired anatomy.
   a.) Click on the desired viewport for saving and select Magnitude and Phase mode to create a 2D phase contrast series or select Magnitude to create a functional series.
   b.) Adjust the slice thickness using the controls on the right hand side of the viewport.
   c.) Complete the series definition entries, as shown in Figure 17, and click the save button to save the series to the local database.

FIGURE 17. Series Definition and Save

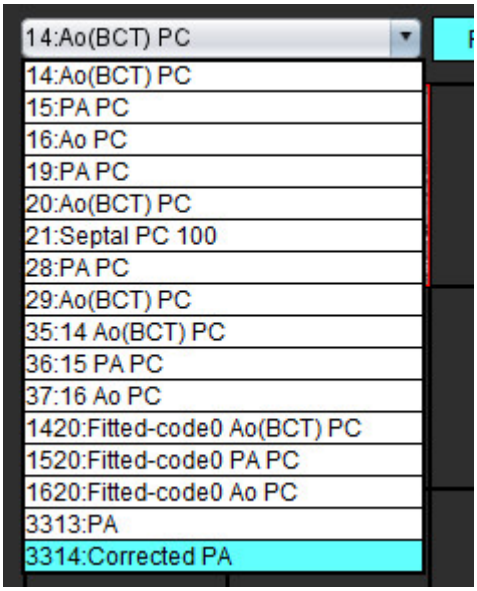


6. To create a stack of multi-slice multiphase images select  .

NOTE: The maximum number of multiphase images that can be created is 32.

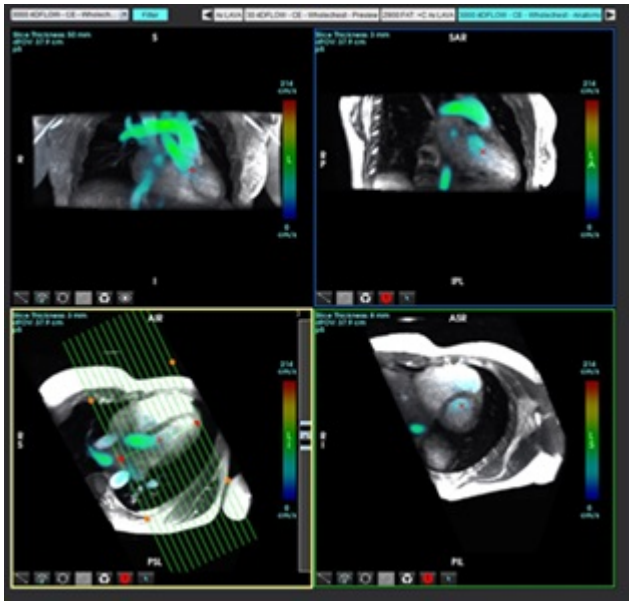
NOTE: When saving magnitude and phase series, the second series will have auto baseline correction applied. The series will be labeled “corrected” as shown in Figure 18.

FIGURE 18. Auto Phase Offset Error Corrected Series Example



7. Click on the viewport to be used as the reference image and define a stack of batch images, as shown in Figure 19.

FIGURE 19. Rx Planning



8. Select the Series Definition options and click  to save the image stack to the local database.
9. To analyze the created series, switch to the appropriate analysis mode and click refresh.

Example Workflow: 4D Flow Segmentation With Flow Analysis

1. Select 

.
2. Select the appropriate 4D Flow series from the series navigation pull-down.

   The image type selected will be indicated on the button 

.
3. Select the **Vessel** tab.
4. Click  to perform auto segmentation.

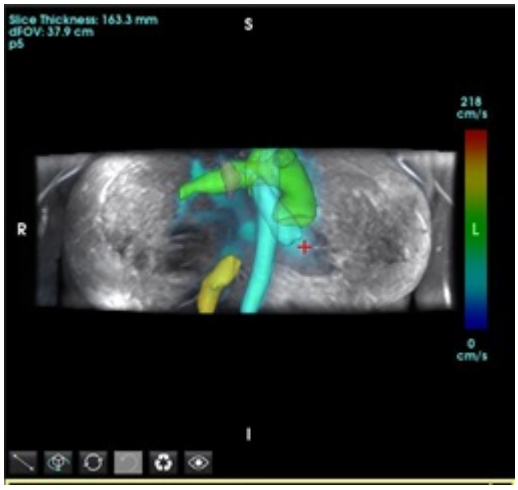
   This will segment, landmark, and place 2D flow planes for the Aorta, PA, IVC, and SVC. Select the Display tab to view. See Figure 20.

NOTE: Vessel segmentation can be configured for preprocessing.

NOTE: Refer to See Table 1 on page 98 for vessel categories definitions.

NOTE: Segmentation is performed on estimated systole phase.

FIGURE 20. 4D Flow Segmentation

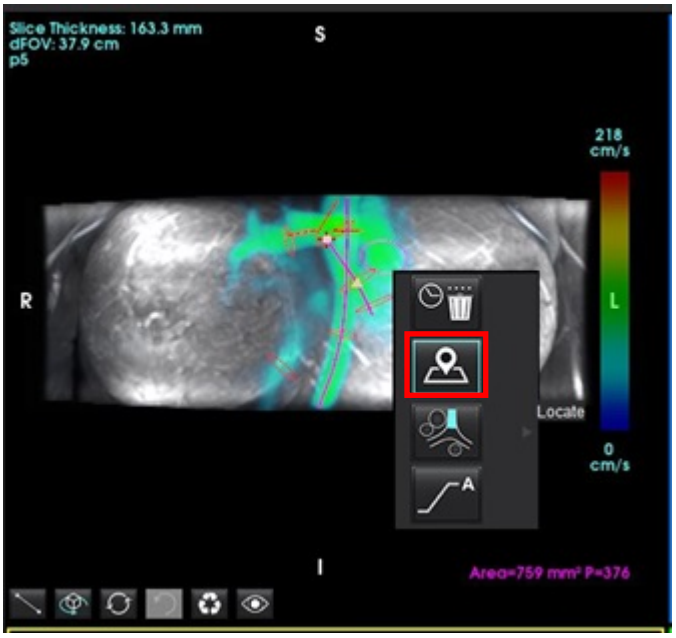


5. Select the appropriate vessel for editing. Vessel tab allows segmentation editing like in 3D mode. Refer to Table 8 on page 176.
6. Review segmentation and edit if desired.

   The objective of the segmentation is placement of the flow planes shown on the Analysis tab.
7. The Analysis tab shows the flow results; review each category and the flow contours in the Orthogonal view.
8. Press Crtl + middle mouse to review the contours in all phases.
9. To locate the placement of an ROI in a vessel, left click on the ROI and then right click and select  .

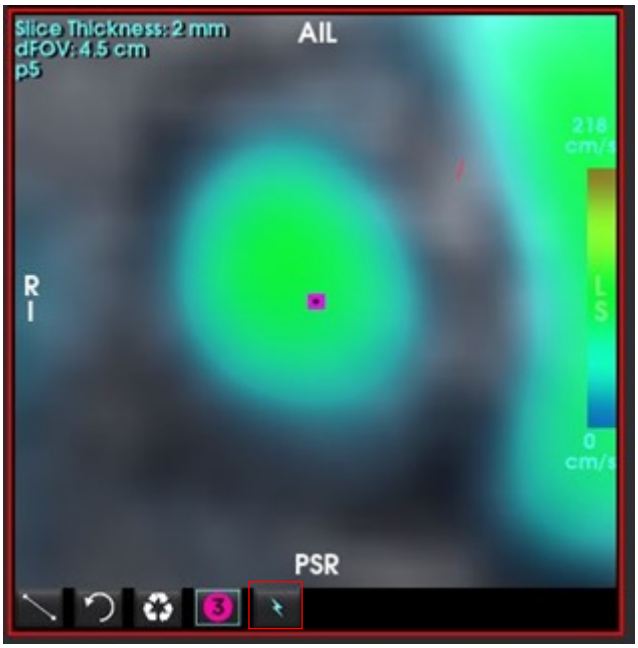
WARNING: The user is responsible for the accurate placement and correct category assignment of all regions of interest (ROIs), including those generated by preprocessing.

FIGURE 21. Locate ROI Placement on Vessel



10. In the Orthogonal view scroll along the centerline and click the lightning bolt for rapid adjustment of flow plane position. Confirm vessel category on the Analysis tab. Figure 22

FIGURE 22. Orthogonal View



11. Left click on the contour to drag the spline points, copying from adjacent phases, and shift/erode/dilate. Figure 23

FIGURE 23. Edit Tools

Streamlines are emitted from the selected flow contour when on the Analysis tab. For global streamline emission, change to the Display tab.

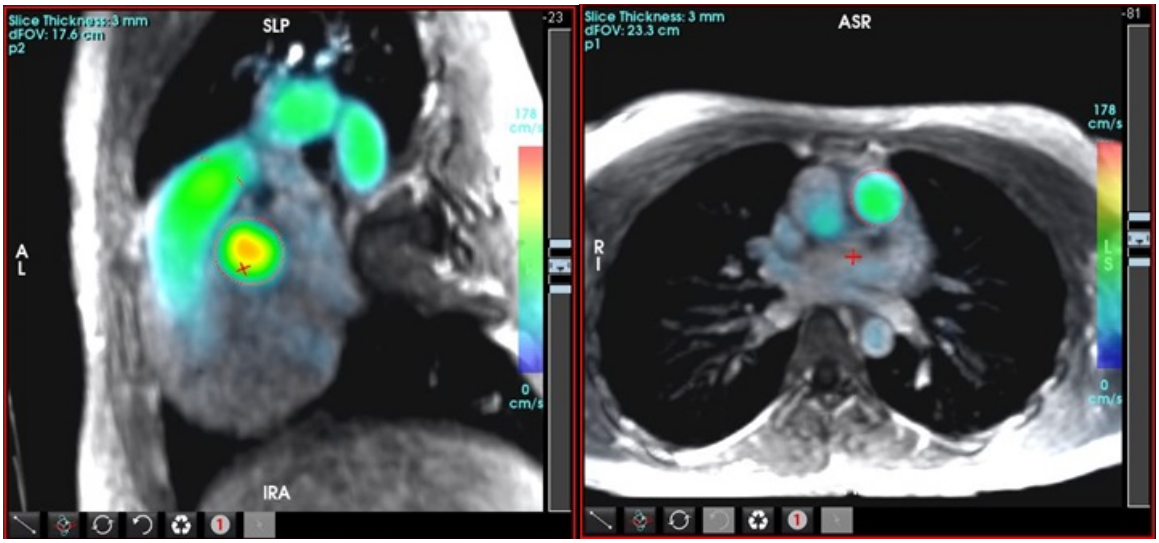
Example Workflow: Manual Flow Measurement

For detailed information on the flow analysis interface tools, see Flow Analysis on page 96.

1. Select the **Analysis Tab**.

2. Localize the vessel of interest. Click the  to generate a flow curve.

FIGURE 24. Aortic and Pulmonic Vessels Example



WARNING: The user is responsible for the accurate placement and correct category assignments of all regions of interest (ROIs), including those generated by preprocessing.

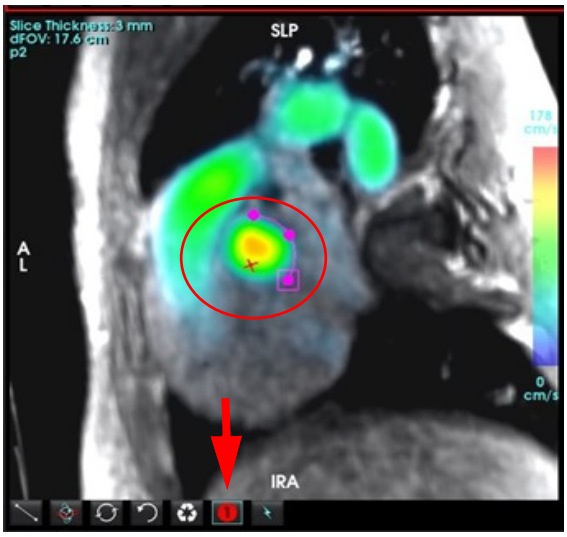
3. For manual segmentation, localize the vessel of interest and click on the  as shown in Figure 25.

Six ROIs are available, numbered 1 - 6. The color coding is consistent across the analysis view, image viewports and graphs.

4. Create a contour around a vessel by depositing 4 points around the vessel of interest.

5. Click  for segmentation over all phases.

FIGURE 25. Manual ROI Placement

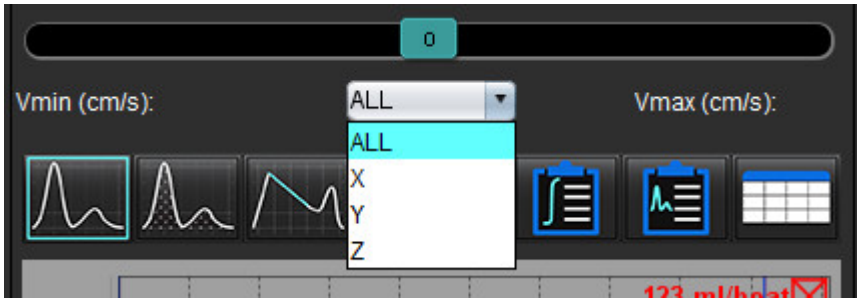


Perform Velocity Aliasing Correction

For Auto Velocity Aliasing Correction see page 107.

To correct for velocity aliasing, drag the slider bar control button to perform phase unwrapping. The effect of the change will be updated directly on the phase image and the results displayed directly on the flow graph. To check each of the three velocity-encoded images along the three orthogonal (x,y,z) directions select from the pull-down menu, as shown.

FIGURE 26.



Reporting

WARNING: The report should be inspected prior to approval and distribution to ensure that the content matches the analysis. Delayed or misdiagnosis may occur should the report contents be erroneous. Analysis and interpretation should be done by properly trained and qualified users.

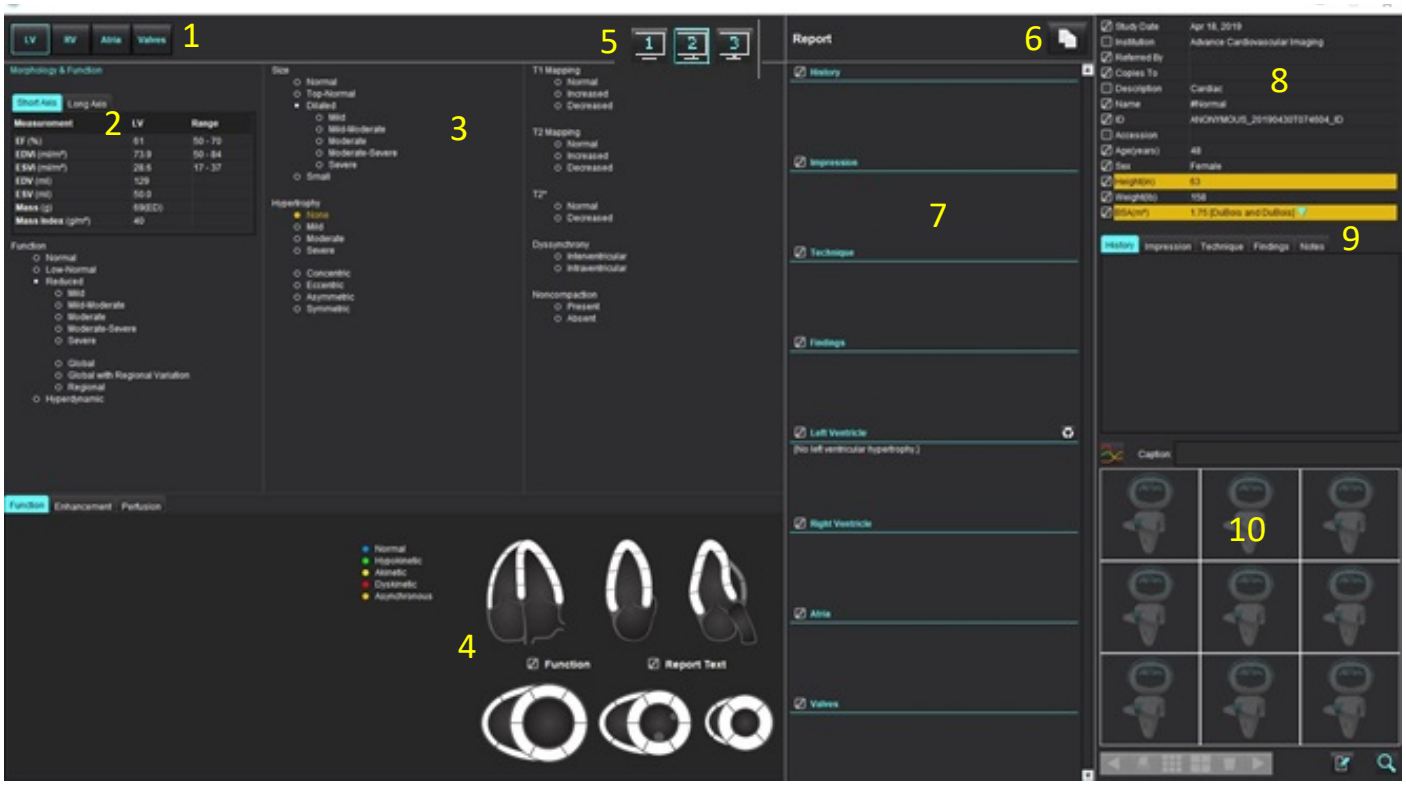
NOTE: Functional analysis is supported for multiple series. The results that are present on the report reflect the current series selected under functional analysis.

The Reporting interface can be access by clicking  in the lower right had corner of the interface or by performing Alt+R. It is recommended to have two monitors to facilitate the reporting of cardiac images.

If multiple monitors are present select the monitor  from the upper middle right of the interface.

The Reporting interface (Figure 1) provides a menu driven selection. Selections can be made directly on the interface with the appropriate report section populating with text. Reporting text and categorical ranges for parameter results can be user defined under preferences. Select **Tools > Preferences >Edit System** (**Admin Only**) select **Reporting** tab.

FIGURE 1. Reporting Interface



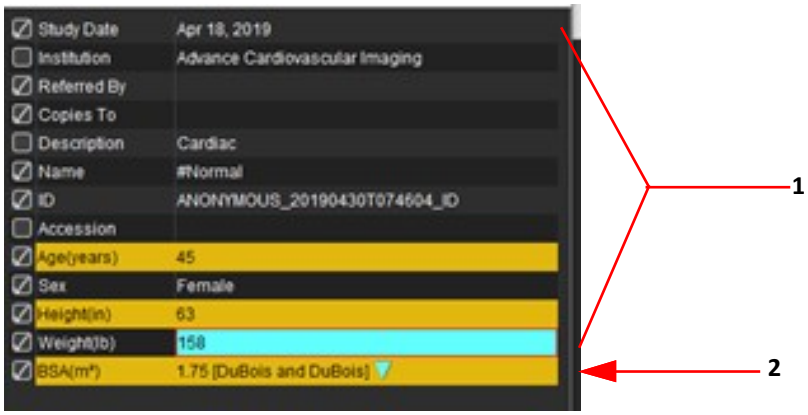
1. Cardiac Anatomy Selection, 2. Results, 3. Menu Selections, 4. Schematics for Polar Plots, 5.Monitor Selection, 6. Copy Report as HTML, 7. Report Content, 8. Patient Demographics, 9. Macro Tabs, 10. Add Images, Graphs, Tables to Report

Patient Demographics

The demographics section contains patient information from the DICOM header. Fields can be edited (highlighted) as shown in Figure 2.

NOTE: Editing does not change the DICOM header.

FIGURE 2. Demographics



1. DICOM Header Information, 2. BSA Selection

The BSA calculation type can be selected by performing a left-mouse click on the inverted triangle.

BSA Calculation Method	Formula
DuBois and DuBois	BSA (m2) = 0.20247 x Height(m)0.725 x Weight(kg)0.425
Mosteller	BSA (m2) = SQRT([Height(cm) x Weight(kg)]/3600) BSA (m2) = SQRT([Height(in) x Weight(lbs)]/3131)
Gehan and George	BSA (m2) = 0.0235 x Height(cm)0.42246 x Weight(kg)0.51456
Haycock	BSA (m2) = 0.024265 x Height(cm)0.3964 x Weight(kg)0.5378
Boyd	BSA (m2) = 0.0003207 x Height(cm)0.3 x Weight(grams)(0.7285 - (0.0188 x LOG(grams))

Reference: http://halls.md/formula-body-surface-area-bsa/

The appropriate cardiac anatomy to be reported can be selected from the upper left of the interface as shown in Figure 3.

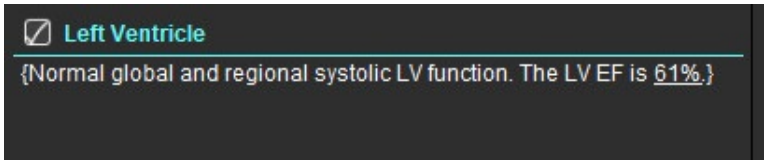
- LV: Left Ventricular
- RV: Right Ventricular
- Atria
- Valves

FIGURE 3. Cardiac Anatomy Selection

NOTE: Completing categorical ranges will enable the auto prefill functionality for the report. Text will prefill according to the user defined values. If a selection is made from the menu interface during the reporting process the prefilled functionality is no longer enabled.

1. From the menus, select relevant findings for the study. If LV has been selected then the report section for Left Ventricle will populate with text as shown in Figure 4.

FIGURE 4. Example Selection for Left Ventricle

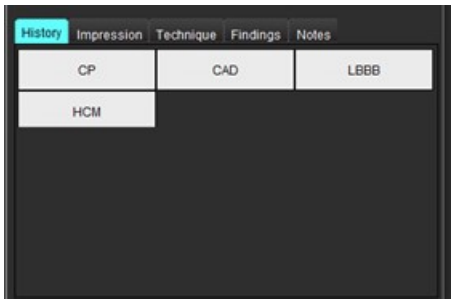


2. Place the cursor outside of the bracket and press the back arrow on the keyboard to remove the entire bracketed line or place the cursor inside the bracket for manually adding or editing text.

NOTE: All appropriate analysis needs to be completed prior to generating result parameters.

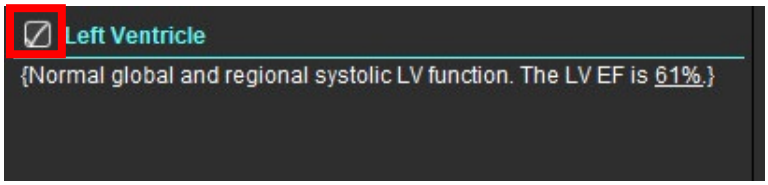
3. All reporting sections can be manually edited. Macros can be created for the report sections of History, Impression, Technique and Findings. Configure macros, select **Tools > Preferences >Edit** select **Macro** tab.

FIGURE 5. History Tab shown with User Defined Macros



4. In the report section, click the check boxes to include or exclude content in the report. See Figure 6.

FIGURE 6. Report Content



5. Click  to export the report in HTML format.

Add Images, Graphs or Tables to the Report

1. Right mouse click on any image viewport, graph or table and select  .

2. View graphs or tables by selecting  .

NOTE: Multi-slice images can be sent to the report. Select **Tools > Preferences > Edit**. Check Multi-slice Image to Report under General.

In review mode, right mouse click on  ; note cine must be paused.

FIGURE 7. Images, Graphs, Tables

1. View Graphs and Tables, 2. Caption Type-in, 3. Controls

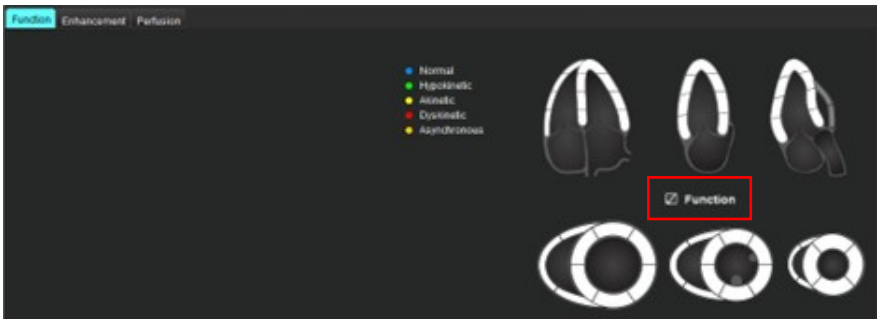
Controls

	Step through each image, graph or table
	Include in report when enabled
	Image format small or large
	Remove image, graph or table
	Image locate

Polar Plots

Polar Plots can be added to the report by completing the appropriate schematic. Polar Plots are available for Function, Enhancement and Perfusion. To include Polar Plots on the report click the box shown in Figure 8.

FIGURE 8. Schematics



Segment Selection

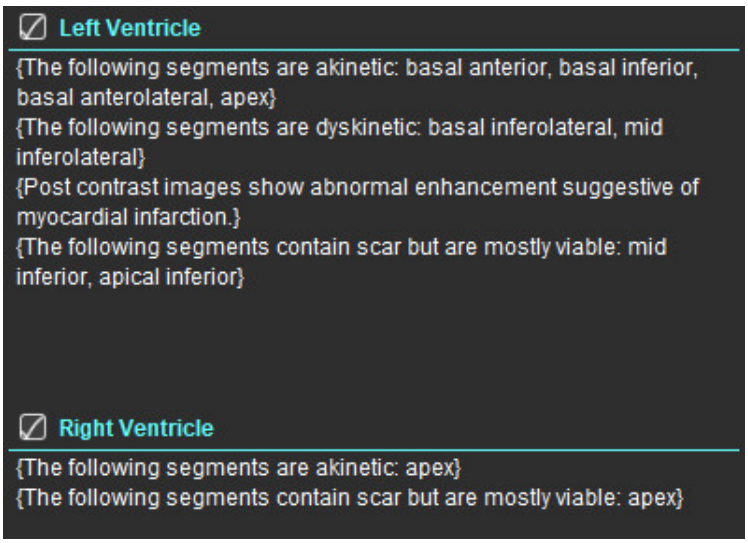
1. Left-mouse click on a color coded descriptor and left click on the segment or -
   right mouse click directly on a segment to select from the list or -
   select away from the segment to set for all segments.
2. Segment selections for function and enhancement will populate the appropriate report section for either Left or Right Ventricle with text descriptors of the selection as shown in Figure 9.
3. Configure the default label, Enhancement, by selecting **Tools > Preferences > Edit System** (**Admin Only**) and enter the desired label under Myocardial Evaluation. Select the appropriate label from Myocardial Evaluation Analysis tab.

NOTE: If the long axis apical segment is completed the 17 segment Polar Plot will be formatted on the report.

NOTE: The Enhancement schematic can be toggled when viewing the Perfusion schematics.

4. To set Polar Plot to 4-color, select **Tools > Preferences > Edit System** (**Admin Only**) > **Reporting** > **Polar Plot** and select **4-color.**

FIGURE 9. Segment Selections

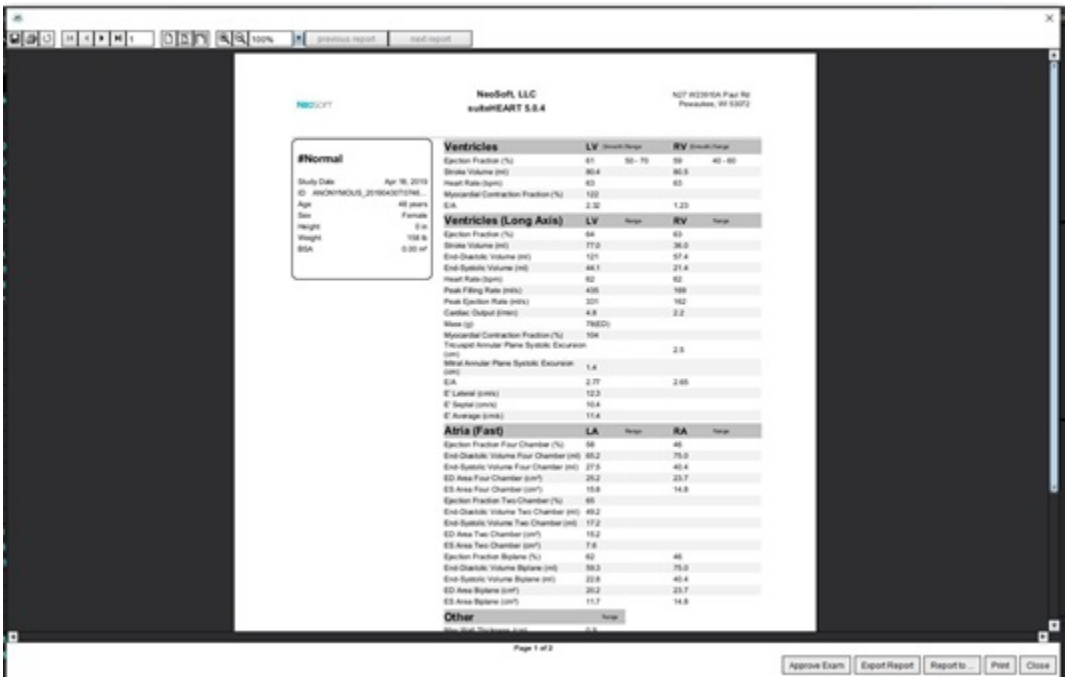


Preview and Approve the Report

1. Select File > Preview Report or select  from the lower right.
2. Review the report to ensure that all the desired analysis results and structured information is included.
3. Select  to save the report as a PDF, RTF, XLS, or TIFF.
4. Select the destination and file type.

NOTE: The report file name can be configured in Preferences. See Selections for Report Preferences on page 30.

FIGURE 10. Preview Report



5. Select **Export Report** to create a DICOM secondary capture series.
6. Select **Report to...** to export results to a third party reporting system.

WARNING: The report should be inspected prior to approval and distribution to ensure that the content matches the analysis. Delayed or misdiagnosis may occur should the report contents be erroneous. Analysis and interpretation should be done by properly trained and qualified users.

Approve the Exam

The application has a feature that approves and locks reports. The approved report is saved and can be viewed but it cannot be changed. Approving can only be performed on the Preview Report screen.

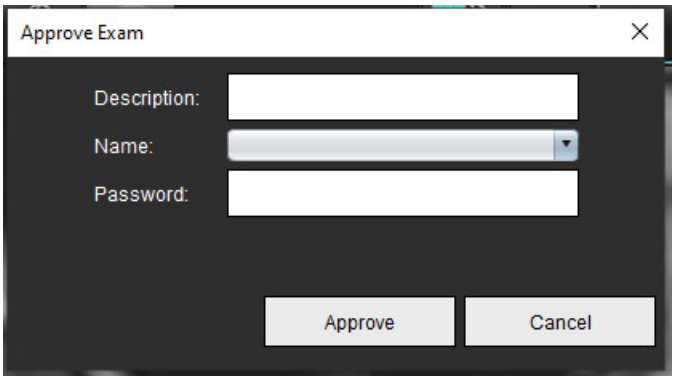
NOTE: Prerequisites: The user must be an authorized report signatory. See Authorized Report Approvers on page 31. (**Admin Only**)

NOTE: Auto Export destination can be configured, see Manage Report Approvers on page 32. (**Admin Only**)

NOTE: To automatically export as DICOM upon approving the exam see page 33. (**Admin Only**)

1. From the Preview window, select **Approve Exam**.

FIGURE 11. Approve Exam Window



2. Enter a signature description, if desired.
3. Select your user name from the **Name** pull-down menu.
4. Type in your password.
5. Click **Approve** to confirm and close the window. Click Cancel to close the window without completing the sign-off procedure.

   Using the description provided, a series is created.

NOTE: When an approved exam has been performed the report will have the date and time stamp.

Export Options

1. Select **Tools > Export > Report to Excel**.

   Exports report as an Excel file.
2. Select **Tools > Export > Report to XML**.

   Exports report as an XML file.
3. Select **Tools > Export > Data to Matlab**.

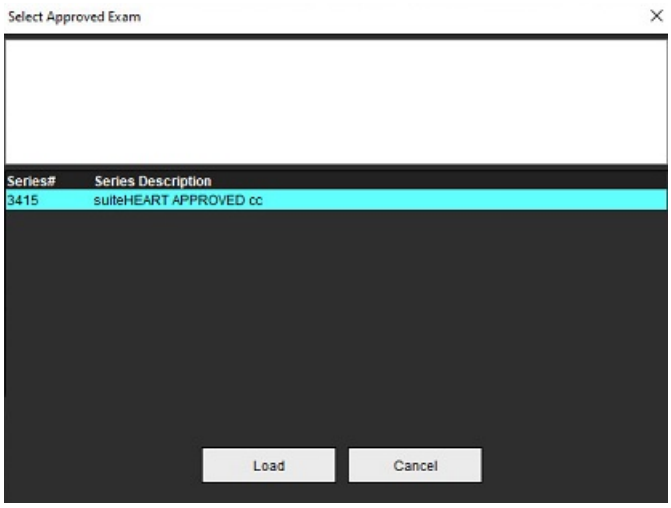
   Exports a Mat-file in binary form.
4. Select **Tools > Export > Segmentation to NRRD**.
5. Select **Tools > Export > Isosurface to STL**.

Review an Approved Exam

1. Select **File > Load Approved Exam**.

   This displays the Select Approved Exam window. All the approved exams related to the exam are displayed in the list.

FIGURE 12. Approved Exam Selection Window



2. Select the series from the list.
3. Click Load to load and display the approved exam and it's accompanying analysis.
   - An approved exam can be viewed only.
   - A new exam can be generated from an approved exam by editing an approved report and saving those changes to a new exam. The new exam is saved as a secondary capture series.

NOTE: Loading an approved exam and analysis will overwrite the information in the current analysis session.

NOTE: When restoring exams that have been analyzed with prior versions of suiteHEART® Software, and if a "Load Approved Exam" has been performed, the report will not have the name of the approver or the date and time stamp. **It is recommended to review all analysis and confirm all results prior to reissuing the report.**

Report Database

The Report Database allows you to perform a search on the contents of previously approved reports. A report is only entered into the report database after it has been approved.

Report Database Tool Procedure

1. Select **Tools > Report Database**.

Select Search Criteria

2. Select the correct template for the search from the Search template drop-down menu.
3. Select the search query from the History drop-down menu. The current query bar displays your selected values.

FIGURE 1. Search Options

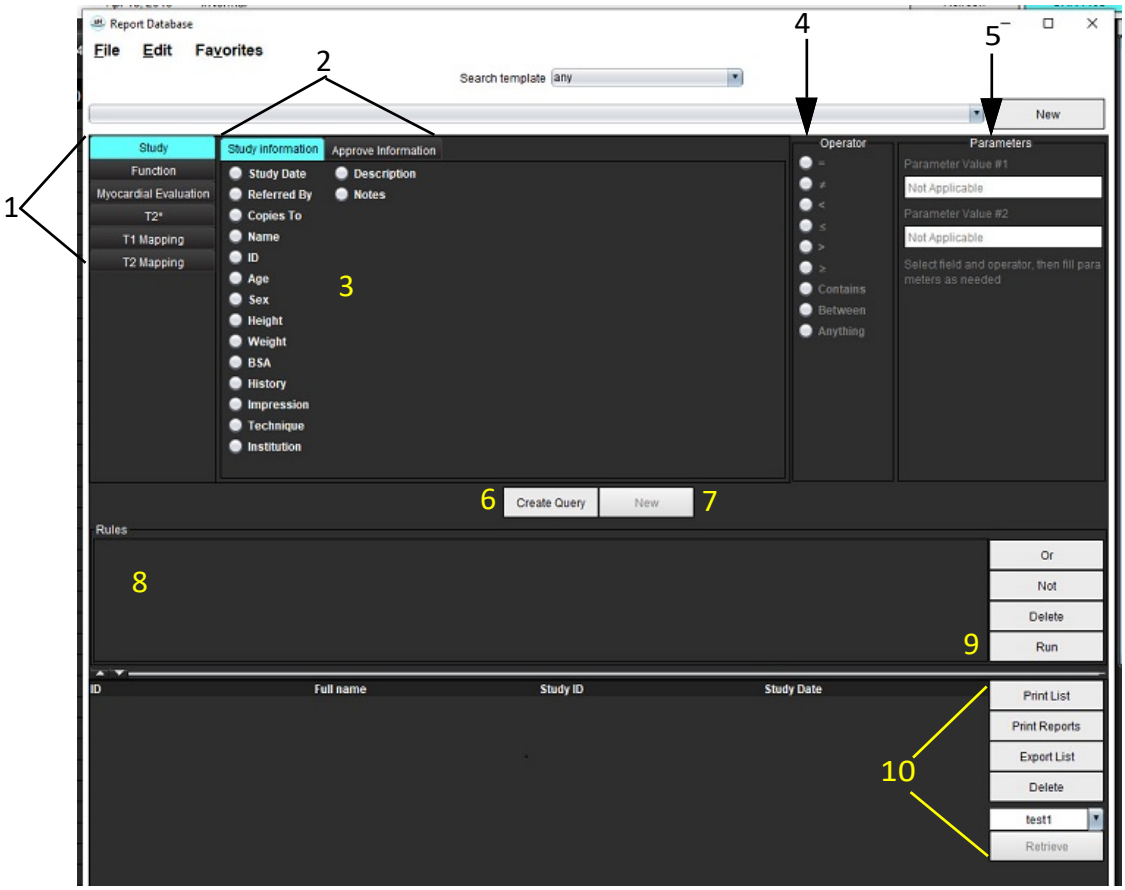
NOTE: If the desired query does not exist already, create a new query.

Perform a Query

1. Select **New** to the right of the History bar, as shown in Figure 1.

   The create query panels are displayed in the Report Database window.

FIGURE 2. Database Query Panel



1. Query Analysis Tabs, 2. Query Group, 3. Query Fields, 4. Query Operators, 5. Query Parameters, 6. Create Query, 7. New Query, 8. Query Rules, 9. Query Run, 10. Query Options

2. Select the query category tab from Study, Function, ME, T2*, T1 Mapping and T2 Mapping. The query groups and fields update accordingly.
3. Select the query group.
4. Select the query field.

   NOTE: The Report Database cannot perform a search on custom measurements.

5. Select the operator to define the query search parameters.
6. Enter parameters to provide values for the search criteria.
7. Select **Create Query** to display the query in the Rules panel. Multiple queries can be executed during a single search operation. Repeat steps 1 through 7 for each additional rule.

   The **Not** button will negate a query value.

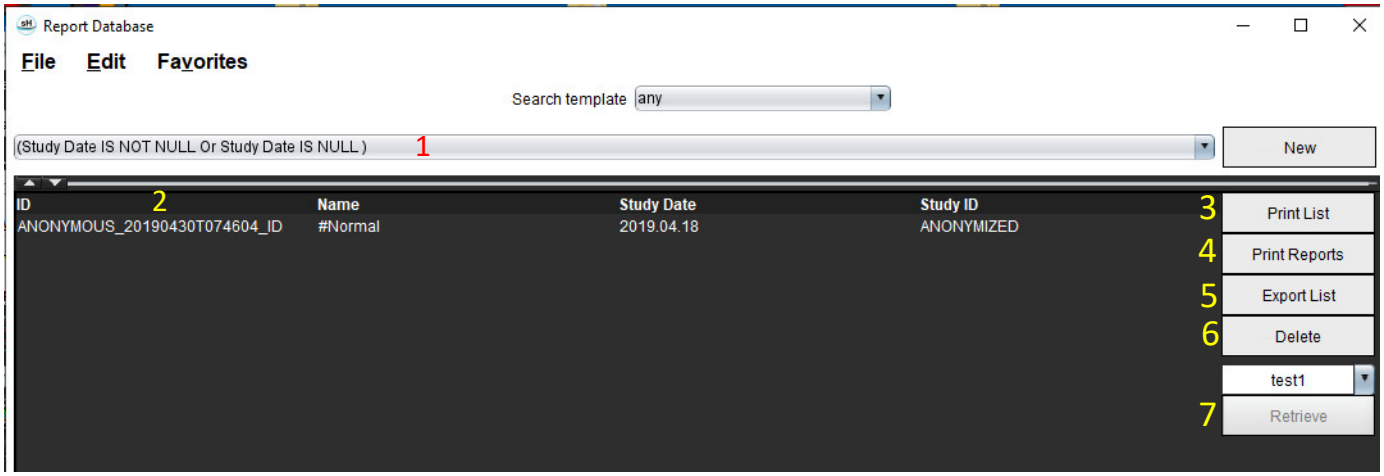
The **Or** button will concatenate multiple queries while satisfying the search with only one of the queries. The **Or** function applies to the query rule above the selection.

The **Delete** button provides a means to select and delete a query rule.

8. Select **Run** to search the database.

   The search results are displayed in the Query result window. The query values that satisfy the search are displayed in the right most column of the result window.

FIGURE 3. Query Result Window



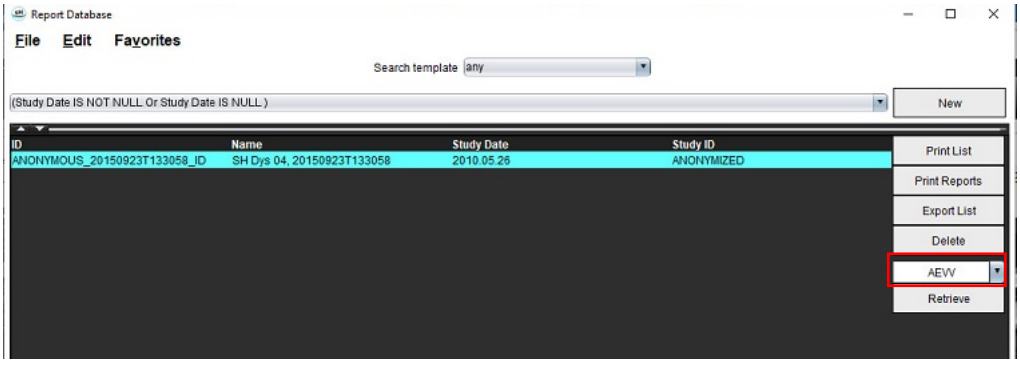
1. History Bar, 2. Query Results, 3. Print List, 4. Print Reports, 5. Export List, 6. Delete, 7. Retrieve Studies

NOTE: New query results are only created based on a unique combination of exam ID, exam date, authorized signature and report template. If a duplicate of these fields is recognized, the old report is replaced by the new report.

Retrieve Studies

1. From the Query Result window, select the **DICOM source**.
2. Select the **studies** from the result list.
3. Click **Retrieve**.

FIGURE 4. Query Result Window

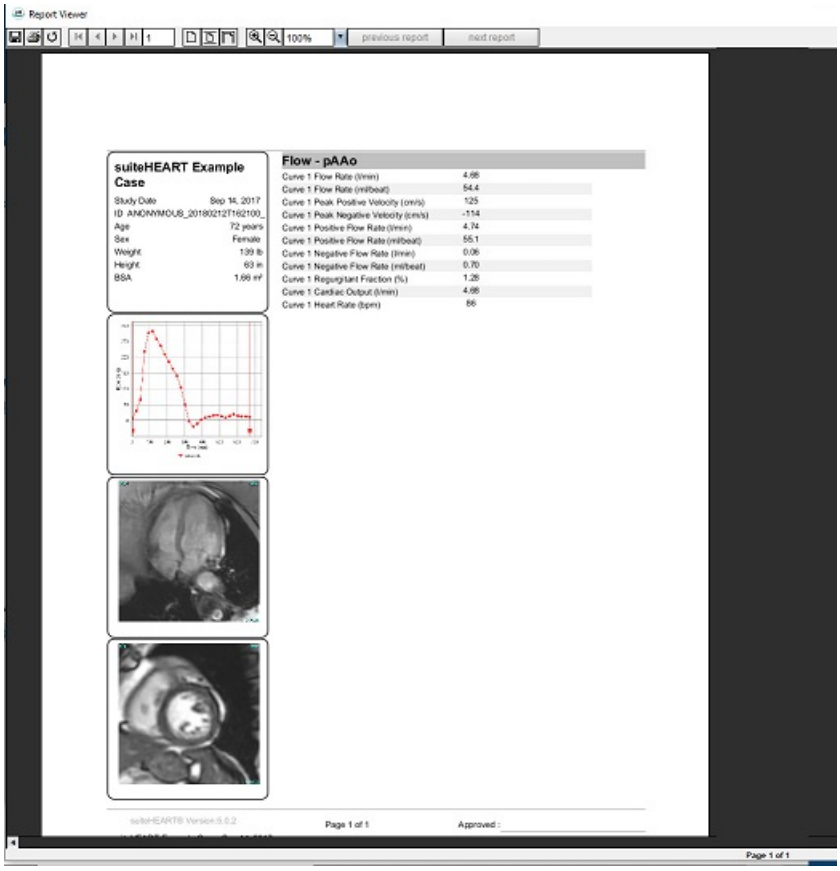


View the Results

1. To view a report, double click an entry in the Query result window.

   A new window opens displaying the selected report. If more than one report is available, use **Next Report** and **Previous Report** to step through the reports. Click the close window marker ✕ to close the Report Review window.

FIGURE 5. Report Viewer



2. From the main report, database interface:

   Edit > Select All selects all search results.

   Edit > Clear Selection deselects all search results.

   Edit > Invert Selection toggles the selection state of each result.

   Edit > Clear History deletes record of previous queries.

3. Select **Print List** to send the query list to the printer.
4. Select **Print Reports** to send the selected reports to the printer.
5. Select **Export List** to save the list as an html file and the report as a pdf.
6. Select **Delete** to remove the selected report(s) from the report database

Save a Query

1. Select **Favorites > Add to Favorites**.
2. In the Add To Favorites text box, type in a label for the query and click **OK**.

FIGURE 6. Favorites Menu

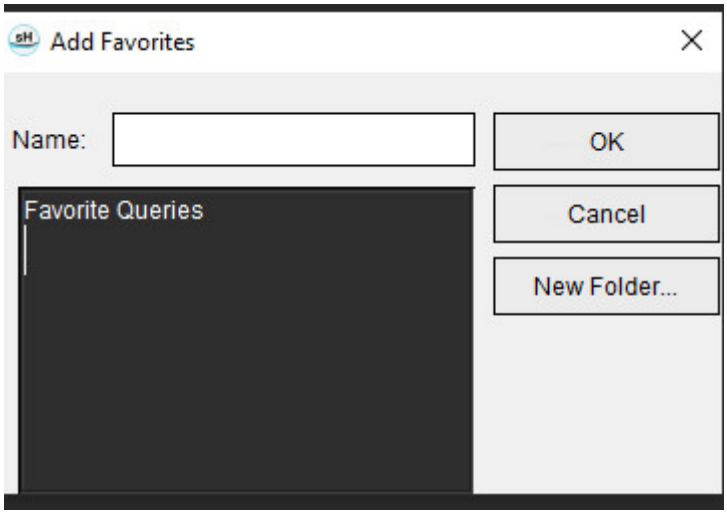
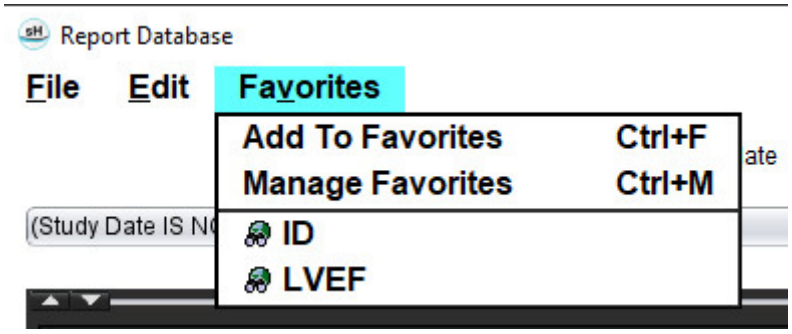


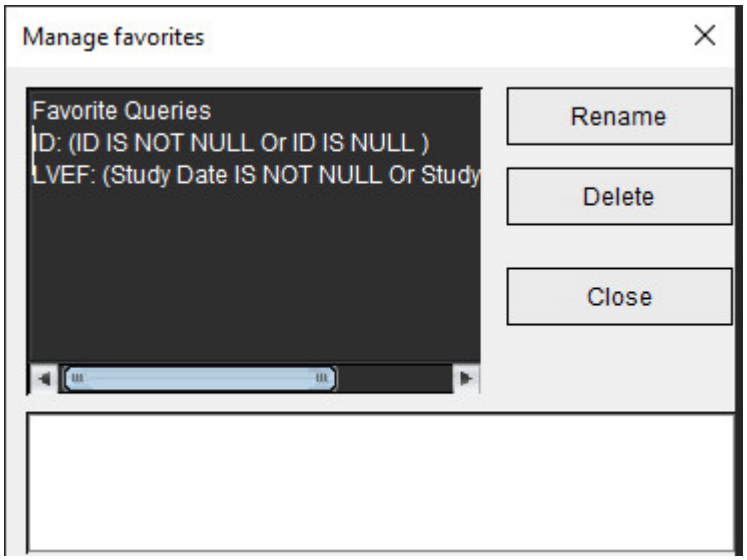
FIGURE 7. Favorites Pull-down



Delete a Favorite

1. Select **Favorites > Manage Favorites** from the Report Database window.

FIGURE 8. Manage Favorites Window



2. Select the favorite item.

   The entire query formula is displayed in the Result window.

3. Click **Delete**.

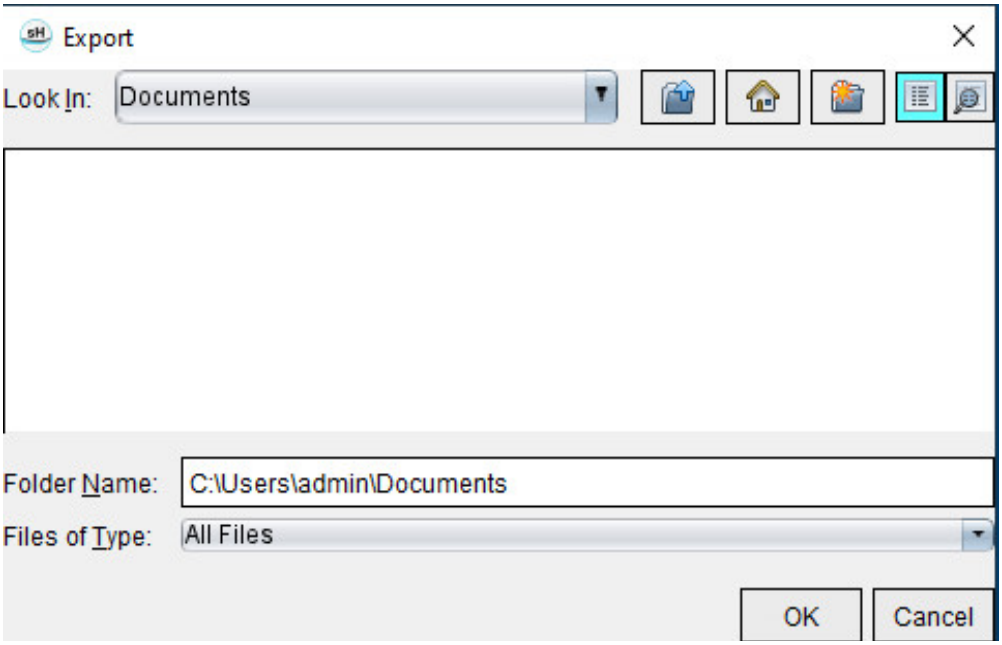
   A confirmation popup will verify your delete selection. Select **Yes**.

4. Select **Close**.

Export Search Results to an HTML File

1. Select **Export List** on the right hand side of the Report Database window.

FIGURE 9. Export Window



2. Select the directory to which to export the list.
3. Select **OK**.
    - A popup window inquires whether the reports should be included.
    - The listing and reports are exported to an HTML file.

Export the Database

As the database becomes larger it is advisable to archive the data.

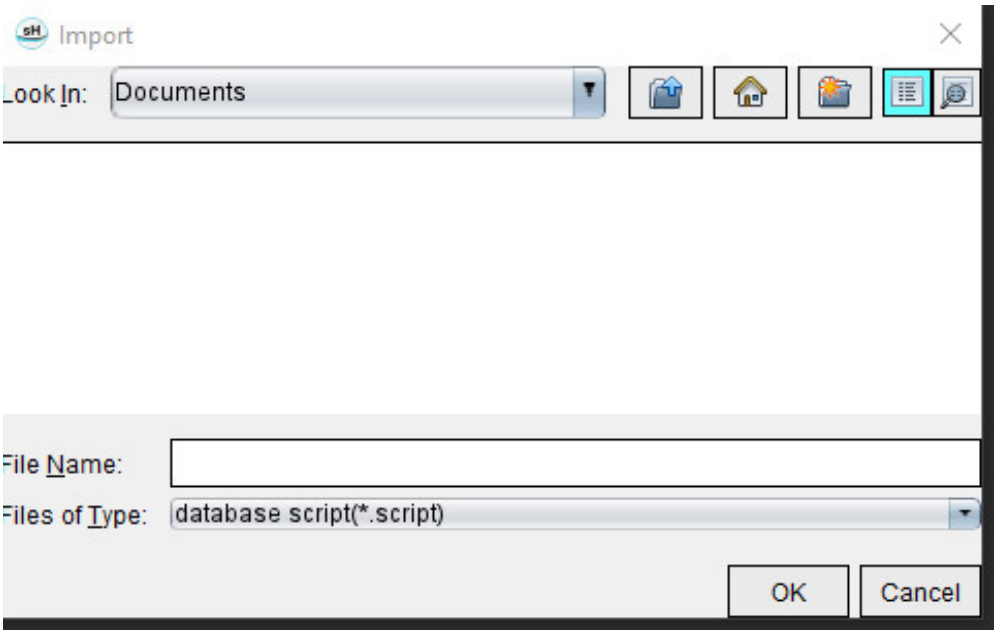
1. Select **File > Export** from the Report Database menu bar.
2. Select the directory to which to export the list.
3. Select **OK**. The database is exported to the external storage device.

Import a Database

The database can be imported from another PC to which it was exported.

1. Select **File > Import**.

FIGURE 10. Import Window



2. Select the directory from which to import the database.
3. The imported database is merged with the existing database.

Appendices

Appendix A: User Level Preferences

The application allows individual users to configure a subset of preferences.

Admin privileges are determined by your IT department. Whether you are a user with access to suiteDXT admin and suiteDXT non-admin log in depends on the install. An admin launch of suiteDXT can be identified through the shortcuts. (Figure 1)

FIGURE 1. Launch Selections

System Upgrade: Previous preferences settings and templates will be available for all users whether it is a single user or multi-user environment.

NOTE: After any changes to preferences or templates it is recommended to close suiteHEART and relaunch.

The menu selections found in the following table are available under **Tools > Preferences**.

Table 1: User Level Menu Selections

Selection	Level	Description
Edit	User/Admin	Allows a user to change their own preferences and templates; grayed out options affect all users and can only be changed by Admin Edit System functionality.
Edit System	Admin Only	Allows editing of all preferences unavailable to standard editing. Additionally allows editing the set of preferences used for default preprocessing.
Import	Admin Only	Restores all preferences and templates for all users from an exported file. Importing preferences from a release prior to User preferences will import preferences to the System set. Upon import all current preferences and templates will be deleted.
Copy	User/Admin	Copy preferences from other users (template ownership will not be copied).
Export	User/Admin	Exports all preferences and templates for all users.

Admin Functions

Add new user as Authorized Report Approvers

1. Run suiteDXT as Admin.
2. Launch suiteHEART.
3. Select Tools->Preferences->Edit System.
4. Enter user under Authorized Report Approvers.
5. Assign a password. Users can change their password.
6. Select the appropriate auto export destination if configured.
7. Click Apply.
8. Click Save and Exit.

Changing system wide preferences

1. Run suiteDXT as Admin.
2. Launch suiteHEART.
3. Select **Tools > Preferences > Edit System**.
4. Make appropriate changes to analysis preferences as listed in Table 2.

NOTE: Making any changes to system preferences affects all users.

Table 2: Admin controlled Analysis Preferences

Tab	Section	Preference
General	Report	All Preferences within section, consisting of report headings, logos, etc.
General	Authorized Report Approvers	Authorized Report Approvers (add, delete)
General	General	Automatically Export Approved Exam
General	Flow	Auto Baseline Correction
General	Flow	Regurgitant Mode: Auto
General	Flow	Aliasing Automatically Detected
General	Flow	Aliasing Correction On By Default
General	Flow	Flow Unit
General	Flow	Default Method
General	Idle Timer	Idle Timer
General	Myocardial Evaluation	All Preferences within section
Virtual Fellow	Apex Direction	2ch, 3ch, 4ch directions
Function	General	Apply MV and TV Annulus
Function	General	Apply Basal Line Interpolation
Function	General	Apply Mid Ventricular Interpolation
Function	General	Motion Correction Between Series
Function	General	Enable Preprocessing for multiple series
T1/T2/T2*	T1	Sequence, ICF
T1/T2/T2*	T2	Parameter Fit
T1/T2/T2*	T2*	Parameter Fit
T1/T2/T2*	Endo/Epi Offset	T1,T2 Endo/Epi Offset
Reporting	Reporting	All Preferences within Reporting tab, including any custom text and text selection criteria for the Reporting Interface
Auto-Compose Series	Auto-Compose Series	GE Combine T1, Philips T1/T2, Siemens T1/T2

Templates

Template titles that are bolded cannot be edited.

Managing previous templates from 5.1.2.

Admin can assign existing 5.1.2 templates to specific users. To change ownership:

1. Run suiteDXT as Admin.
2. Launch suiteHEART.
3. Select Tools->Preferences->Edit System.
4. Select Template tab.
5. Select the template name you want to assign.
6. Use the Username dropdown to assign the template to a specific user.
7. Click Save and Exit.

Delete Templates:

1. Run suiteDXT as Admin.
2. Launch suiteHEART.
3. Select Tools->Preferences->Edit System.
4. Select Template tab.
5. Select the Current template name.
6. Click Delete.
7. Click Save and Exit.

User Functions

Single User Environment

In a single user configuration, the copy function is not available. Only applicable in a multi-user environment where a user wants to copy an existing user preference.

Multi-User Environment

Users can copy other users preferences.

1. Launch suiteHEART.
2. Select **Tools > Preferences > Copy**.
3. The file pull-down will show user names (templates are not copied).
4. Select the user.
5. Click OK.

NOTE: The admin controls changes to analysis preferences as listed in Table 2.

Templates

Templates are available to all users for use in suiteHEART including previous templates and templates provided by Neo-Soft (predefined). Users can edit/change their own templates and not edit templates created by other users.

Users can copy existing templates. Copied templates can be edited by the user performing the copy.

Each user can select their own template after study launch. Previous template selection is applied for future cases.

Users can create new templates themselves or use a predefined template.

Change Authorized Report Approvers Password

NOTE: Users will need their original password assigned from the Admin person.

1. Launch suiteHEART.
2. Select **Tools > Preferences > Edit**.
3. Enter Old Password.
4. Enter New Password.
5. Enter the new password again in Confirm Password.
6. Click Apply.
7. Click Save and Exit.

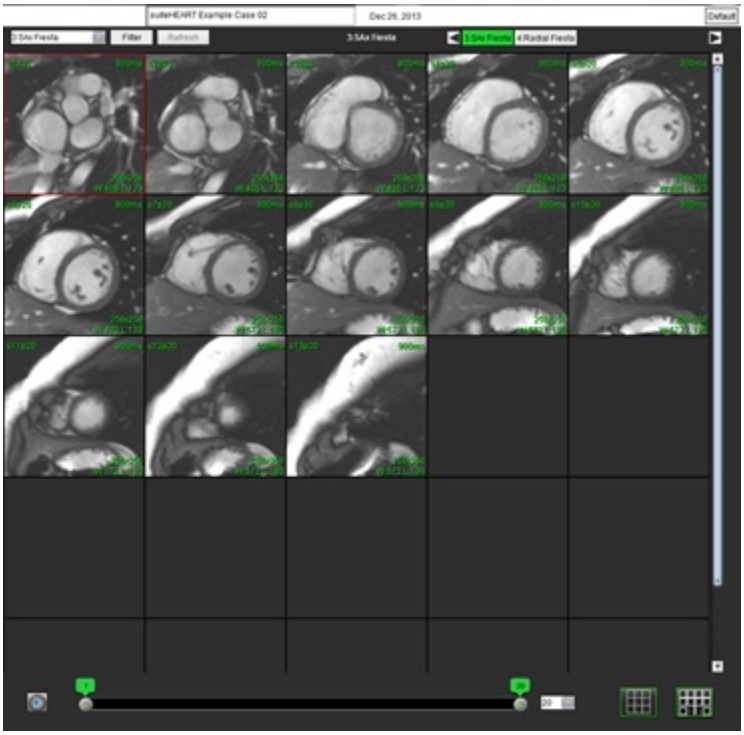
Changing system preferences

1. Launch suiteHEART.
2. Select **Tools > Preferences > Edit**.
3. Make appropriate changes to analysis preferences.

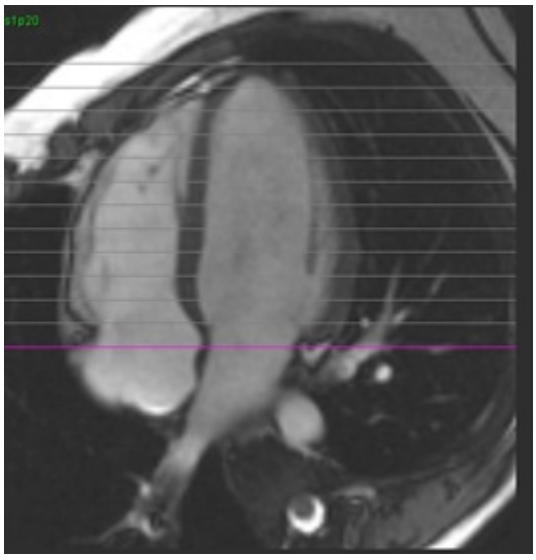
NOTE: Grayed out options can only be changed by Admin.

Appendix B: Functional Analysis Scan Plane Example

For accurate function results, analysis should be performed on a short axis view as shown in the first figure below.



Correct scan plane prescription for the acquisition of the short axis view. Slices should be prescribed perpendicular to the long axis of the left ventricle with at least 2 slices above the base and 1 slice after the apex included in the series.



Appendix C: GE 2D Cine Phase Contrast Parameters

1. Flow Direction = **Slice**
2. Collapse = **off**
3. Flow analysis = **on**
4. Flow recon = **phase diff**

Appendix D: Function Volume Analysis Methods

View	Method
LV/RV Short Axis Stack	Simpsons Rule
LV Long Axis Multiple Views (2Ch, 4Ch)	Biplane Simpsons Rule
RV Long Axis Views 4Ch	Fractional Area Change (FAC)
LV Long Axis Single View	Simpsons Rule
LA/RA Short Axis or Axial Stack	Simpsons Rule
LA Multiple Views (2 Ch & 4 Ch)	Biplane Simpsons Rule
RA View (4 Ch)	Simpsons Rule
LA/RA Long Axis Single View	Simpsons Rule
LV Mass	Myocardial Density = 1.05

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