DynaCAD 3.2
Viewer Application Guide

MRI Study Review, Analysis and Reporting Software

DTM125 Rev. A

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ABOUT THIS DOCUMENT

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DynaCAD 3.2	DynaLOC Prostate Interventional
DynaCAD Breast Diagnostic DynaCAD Prostate Diagnostic DynaCAD Advanced PK Analysis DynaLOC Breast Interventional	
CE 0473	CE 0123
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How to Use This Manual

This application guide contains setup and operational instructions for the DynaCAD MRI Study Review, Analysis and Reporting Software. Review it thoroughly before attempting to set up and operate the software. Keep it in a convenient location for easy reference during the operation of this software.

This guide does not attempt to cover all the details or provide for every possible condition that could occur during setup, operation, or maintenance. Should further information be necessary or particular problems arise which are not covered sufficiently in this document, please contact Invivo technical support operations. Invivo contact information can be found at the end of this manual.

Explanation of Symbols used marking the DynaCAD and MR Analysis Software:

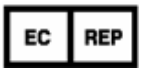
Symbol	Description
	Manufacturer
	Date of Manufacture
	Refer to Manual
	WARNING Warnings are directions which, if they are not followed, can cause fatal or serious injuries to a patient or users.
	CAUTION Cautions are directions which, if they are not followed, can cause damage to the equipment described in this manual.
	NOTE Notes provide advice and highlight unusual points. A note is not intended as an instruction.
	CE Mark
	Authorized representative in the European Community
SN	Serial Number
REF	Model or Catalogue Number

TABLE OF CONTENTS

1 OVERVIEW OF MANUAL 1-2

2 DYNACAD 3 DEVICE LABELING 2-1

2.1 BRIEF DEVICE DESCRIPTION 2-1

2.2 INDICATIONS FOR USE 2-1

2.3 CONTRAINDICATIONS 2-1

2.4 WARNINGS 2-2

2.5 CAUTIONS 2-3

2.6 ADVERSE EFFECTS 2-4

2.7 HOW SUPPLIED 2-4

2.8 OPERATING SYSTEM REQUIREMENTS 2-4

2.9 HARDWARE REQUIREMENTS 2-4

2.9.1 DYNACAD CLIENT REQUIREMENTS 2-4

3 INTRODUCTION AND GENERAL DESCRIPTION 3-1

3.1 INTENDED PURPOSE 3-1

3.2 PRODUCT OVERVIEW 3-1

3.3 DATA FLOW 3-1

3.4 SOFTWARE OPERATION 3-2

3.4.1 KEY TERMS 3-2

3.5 SYSTEM OVERVIEW 3-2

3.6 DYNACAD TOOLS AND FUNCTIONS 3-3

4 USER LOGIN 4-1

4.1 LOG IN AND PASSWORDS 4-1

4.2 LOG OUT 4-1

4.3 SESSION EXPIRY 4-2

5 STUDY MANAGEMENT 5-1

5.1 STUDY MANAGER 5-1

5.1.1 THE STUDY MANAGER MAIN SCREEN 5-1

5.1.2 HEADER COLUMNS IN THE STUDY LIST 5-2
5.1.3 STUDY LIST FILTER 5-3
5.2 DICOM Q/R 5-4
5.3 GET PRIOR STUDIES 5-5
5.4 IMPORTING STUDIES 5-5
5.5 EXPORTING STUDIES TO MEDIA 5-6
5.6 ROUTING STUDIES OR SERIES 5-7
5.7 ONE-CLICK DICOM SEND 5-8
5.8 DELETING STUDIES AND SERIES 5-10
5.9 RE-PROCESS A STUDY FROM THE STUDY MANAGER 5-11
5.10 MARKING STUDIES AS READ 5-11
5.11 OPENING STUDIES 5-11
5.11.1 PATIENT WITH MULTIPLE STUDIES 5-12
5.11.2 SELECT MULTIPLE PATIENTS 5-12
5.12 CLOSING STUDIES 5-13
6 BASIC OPERATION 6-1
6.1 BASIC IMAGE CONTROL 6-1
6.1.1 2D/ MPR KEYBOARD AND MOUSE SHORT-CUTS 6-1
6.1.2 2D/ MPR RIGHT MOUSE CONTEXT MENU 6-2
6.1.3 2D/ MPR IN-VIEWPORT (LEFT) TOOLS 6-5
6.1.4 3D KEYBOARD AND MOUSE SHORT-CUTS 6-6
6.1.5 3D RIGHT MOUSE CONTEXT MENU 6-7
6.1.6 3D IN-VIEWPORT (LEFT) TOOLS 6-9
6.2 VIEWPORT LAYOUT 6-11
6.3 RENDERING MODE 6-11
6.4 SELECTING AN IMAGE OR CHART VIEWPORT 6-12
6.5 SELECTING A NEW SERIES 6-12
6.6 IMAGE INFORMATION 6-13
6.6.1 VIEWPORT OVERLAY TEXT 6-13
6.6.2 IMAGE INFORMATION 6-14

6.6.3 PK PROCESSING PARAMETERS....6-15
6.7 COLOR OVERLAY....6-16
6.7.1 PK, IAUGC, T10 COLOR OVERLAYS....6-16
6.7.2 QUICKTP COLOR OVERLAY....6-17
6.7.3 ONCAD COLOR OVERLAY....6-24
6.7.4 FUSION COLOR OVERLAYS....6-27
6.8 IMAGE SUBTRACTION....6-34
6.9 IMAGE SCROLLING....6-34
6.10 ROTATING AND SCROLLING OBLIQUE MPR IMAGES....6-35
6.11 ROTATING 3D IMAGES....6-35
6.12 WINDOW LEVEL/WIDTH, ZOOM AND PAN....6-36
6.13 LINKING....6-36
6.13.1 SPATIAL LINKING....6-36
6.13.2 TEMPORAL LINKING....6-37
6.14 CORRELATE....6-38
6.15 VOXEL PROBE....6-39
6.16 RULER, ARROW AND TEXT....6-40
6.16.1 ANNOTATION TOOL....6-40
6.16.2 RULER....6-41
6.16.3 ARROW POINTER....6-41
6.17 FREE HAND ROI, LESION 2D AND LESION 3D....6-42
6.18 CREATE MOVIE....6-42
6.18.1 2D IMAGES CAPTURE....6-42
6.18.2 3D IMAGES CAPTURE....6-43
6.18.3 SAVING....6-43
6.19 NIPPLE LOCATION....6-44
7 PROSTATE GLAND SEGMENTATION....7-1
7.1 PROSTATE EDITOR USER INTERFACE....7-1
7.1.1 TOOLBAR....7-2
7.1.2 IN-VIEWPORT TOOLBAR....7-3

7.2 INITIAL PROSTATE BOUNDARY 7-3
7.2.1 AUTOMATIC SEGMENTATION 7-4
7.2.2 MANUAL PLACE MODEL 7-5
7.3 PROSTATE EDITING 7-5
7.3.1 GRAB AND DRAG 7-5
7.3.2 REGION OF INFLUENCE 7-6
7.3.3 SMOOTHING 7-7
7.3.4 PAN, RESIZE AND ROTATE 7-8
7.3.5 UNDO AND RESET 7-8
7.4 SAVE AND APPROVAL 7-8
7.5 PROSTATE GLAND INFORMATION DISPLAY 7-8
8 REGION OF INTEREST (ROI) 8-1
8.1 ROI CREATION 8-1
8.1.1 LESION 2D 8-1
8.1.2 LESION 3D 8-3
8.1.3 FREEHAND ROI 8-4
8.2 ROI EDITING 8-7
8.2.1 EDIT BOUNDARY 8-7
8.2.2 REMOVE BOUNDARY 8-7
8.2.3 CLEANING FUNCTION FOR ROI'S 8-8
8.2.4 PROPAGATING AN ROI 8-8
8.2.5 DELETING AN ROI 8-8
8.2.6 ROI LABEL 8-8
8.2.7 GO TO WORST WASHIN, WASHOUT OR WASHIN/OUT 8-9
8.2.8 PROBE FOR WORST CURVE 8-9
8.2.9 SHOW AUTO KEY IMAGES 8-11
8.3 SUB-ROI 8-11
8.3.1 SUB-ROI CREATION 8-11
8.3.2 SUB-ROI VISIBILITY 8-12
8.3.3 SUB-ROI EDITING 8-12

8.4 ROI ANALYSIS 8-13
8.4.1 DISPLAYING CHARTS 8-13
8.4.2 CHART TYPES 8-13
8.5 PI-RADS 8-23
8.6 AUTO NAVIGATION WITH MULTIPLE ROIS 8-25
9 HANGING PROTOCOLS 9-1
9.1 INTRODUCTION 9-1
9.2 CREATING, EDITING, OR DELETING A HANGING PROTOCOL 9-1
9.3 HANGING PROTOCOL MATCHING 9-2
9.3.1 CREATE, EDIT AND DELETE MATCHING RULE 9-3
9.3.2 DEFAULT HANGING PROTOCOL 9-4
10 KEY IMAGES AND REPORTS 10-1
10.1 CREATING REPORTS 10-1
10.2 CREATING KEY IMAGES 10-1
10.2.1 CAPTURE IMAGE INDIVIDUALLY 10-1
10.2.2 CAPTURE ALL DISPLAYED IMAGES 10-1
10.3 REVIEW AND SAVE KEY IMAGES 10-2
10.4 4 OR 6 IMAGE LAYOUT REPORT 10-2
10.5 LESION BASED AUTO REPORT 10-4
10.6 PI-RADS REPORT 10-5
10.7 CONFIGURING THE AUTO REPORT TEMPLATE 10-5
11 USER OPTIONS 11-1
11.1.1 DISPLAY 11-1
11.1.2 HANGING PROTOCOL 11-2
11.1.3 CROSS CORRELATION 11-2
11.1.4 PK ANALYSIS 11-3
11.1.5 MEASUREMENTS 11-5
11.1.6 MISCELLANEOUS FUNCTIONS 11-6
12 STUDIES COMPARE 12-1

12.1 LOADING MULTIPLE STUDIES....12-1
12.2 HANDLING OF DIFFERENCES IN PATIENT NAME AND ID....12-2
12.3 COMPARE DISPLAY MODE....12-2

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1 Overview of Manual

This manual is intended to describe the DynaCAD MRI study review, analysis, and reporting software and to provide training to radiologists using the DynaCAD for review of processed MRI images.

- Chapter 1 includes the DynaCAD device labeling, providing a brief description of the software, indications for use, contraindications, warnings and precautions, adverse effects and how the system is supplied.
- Chapter 3 provides an overview of intended purpose, product overview, architecture and DynaCAD 3 tools and functions.
- Chapter 4 discusses application login.
- Chapter 1 discusses study management.
- Chapter 6 provides a detailed description of the tools available in the viewer.
- Chapter 1 describes the prostate boundary editing.
- Chapter 1 describes the tools for defining and analyze region of interest.
- Chapter 1 discusses setting up and modifying hanging protocols.
- Chapter 10 discusses generating key images and reports.
- Chapter 1 describes the user options and preferences.
- Chapter 1 discusses how to compare studies.

2 DynaCAD 3 Device Labeling

2.1 Brief Device Description

DynaCAD is used to review, analyze, and generate reports for MRI studies. Post-processed and raw MR images directly from the scanner may be viewed. When used in conjunction with DynaCAD Breast, Prostate and Advanced processing, the viewer displays and provides tools to analyze the post processed image series generated from the analysis performed by the DynaCAD Breast, Prostate and Advanced Analysis software using all the available time points. DynaCAD allows a small application to be placed on any computer which enables thin client communication to a visualization server for review and analysis of images across a network.

2.2 Indications for Use

The DynaCAD 3 software consists of the MR Analysis Server software and the viewer Workstation software.

The MR Analysis Server software, which includes DynaCAD Breast, DynaCAD Prostate and Advanced PK for other MR Analysis modules, is intended to be used as a post-processing software package designed to provide a reliable means for analyzing MR datasets. The software facilitates the analysis of dynamic and non-dynamic MR datasets to provide study review and additional mathematical and/or statistical analysis. The resulting analysis can be displayed in a variety of formats, including parametric images overlaid onto source MRI images.

The DynaCAD Workstation software is intended for use in conjunction with the MR Analysis Server software and facilitates the analysis and presentation of datasets generated by the MR Analysis Server software and incorporates the following functions: Region of Interest (ROI) curve, Pixel of Interest (POI) curve, Report Card, Volume Calculation, Statistical Analysis, 3-D visualization of image series, and DICOM reporting, among other capabilities.

The DynaCAD Software serves as a workflow roadmap tool that organizes and guides the radiologist through the series of sequential tasks that must be performed in order to arrive at a diagnosis. The specific configuration of product features drives the DynaCAD's underlying workflow solution for lesion characterization and reporting. This inherent workflow regimen integrates easily into the radiologist's existing departmental workflow and can be adapted to fit the needs of each user, thereby streamlining diagnosis. In the hands of a trained physician the information provided by the data analysis could yield information that may assist in the interpretation of dynamic and non-dynamic MR studies.

2.3 Contraindications

There are no contraindications for this device.

2.4 Warnings

- When interpreted by a physician, DynaCAD 3 software provides information that may be useful in screening, diagnosis, intervention planning and monitoring. Patient management and all other clinical decisions are the responsibility of the interpreting physician and should not be made based solely on the results of DynaCAD 3 Software analysis. When reviewing a case, all image sequences should be reviewed and taken into account for interpretation. Images should be interpreted only by trained physicians.

- Please review and edit the nipple location if necessary the nipple location prior to drawing an ROI. Failure to do so may cause some measurements in the lesion analysis summary to be inaccurate.

- Please review and edit if necessary the Prostate boundary prior to drawing an ROI. Failure to do so may cause some measurements in the lesion analysis summary to be inaccurate.

- When reviewing Split Sagittal Breast images verify the left and right images are loaded correctly in the image viewport. This can be done by checking the location text information in the upper left viewport.

- Always send studies first to a DICOM 3 storage device or PACS archive, since the DynaCAD 3 workstation is not intended to serve as a primary storage archive.

- Take care to note the Study Date and Time in the image overlay when comparing studies.

- Significant patient motion or differences in acquisition resolution between MRI sequences may impact the image position accuracy when using the correlate feature. If the image position appears to be incorrect between different sequences, manually scroll one of the image stacks to make them inline.

- When reviewing Breast images in the 3D rendering mode, verify the left and right images are loaded correctly in the image viewport when selecting the left/right shortcut icon. This can be done by checking the location text information in the upper left viewport.

- Pharmacokinetic and QuickTime Point (QuickTP, QTP) analysis requires a pre-contrast dataset; verify that the dynamic sequence to be used has at least one pre-contrast dataset. Erroneous outputs will occur if pre-contrast phase/time points are missing. DynaCAD's MR Analysis Server should not be used with manipulated settings to process a study, as it will result in erroneous output.

- Confirm the dynamic curve of the known anatomical region(s); they should be evaluated to ensure that the correct dynamic phases were used in the analysis, for example, an expected contrast dynamic in the heart.

- The colorization on every slice should be carefully examined along with subtraction images. If there is no colorization in the areas that significantly enhance, use the Pixel of Interest (POI) tool for viewing the dynamic curves to analyze the cause.

- Hardware used shall meet the minimal hardware specifications.

- Hardcopy printouts shall not be used for diagnostic interpretation.

- AVI movie clips and secondary capture images are to be used for presentation only.
- For optimal performance of the MR Analysis Software it is recommended not to load additional software onto the MR Analysis Server Hardware.

2.5 Cautions

- Federal law restricts the sale, distribution, and use of this device to or on the order of a physician.
- Do not place liquids on or near the hardware components which contain the DynaCAD 3 software. If a liquid is accidentally spilled on electrical components, immediately shut down the hardware system to prevent any potential electrical shock. Contact your authorized Invivo service provider for further instructions.
- Ensure that the voltage and current requirements are within system specifications to avoid bodily injury from electrical shock or fire hazard.
- Temperature and Humidity Warning – DynaCAD 3 software operations must be performed within the following hardware temperature and humidity ranges.

  Temperature: 50°-95° Fahrenheit (10°-35° Celsius)
  Humidity: 20-80%

- Altitude Warning– DynaCAD 3 software operations must be performed within the following altitude ranges:

  Altitude: -50-10,000 feet

  For altitudes above 2950 feet, the maximum operating temperature is derated 1°/550 ft.

- Operating Noise – DynaCAD 3 computer hardware (when provided by Invivo) will operate within a range of 30-44 dB and not exceed a noise level of 65 dB while in operation.

Software Installation and Maintenance

- This software product contains no independently user-serviceable parts.
- Only trained personnel are qualified to install software.
- The software shall be installed on supported Operating systems only.
- DICOM Configurations information: AE Title: DYNACAD_DIAG, Port: 1602
- Do not load additional software onto the MR Analysis Server hardware.

2.6 Adverse Effects

The use of DynaCAD 3 review workstation adds no known additional patient risks, as there is no direct contact with the patient.

2.7 How Supplied

DynaCAD 3 is supplied as software only or optionally with computer hardware. Please ask your Invivo representative for the most up to date recommended hardware specification.

2.8 Operating System Requirements

The DynaCAD Client workstation software runs on Microsoft® Windows® XP, Windows 7 and Windows 8 Professional Edition or above. The operating system should be patched with the latest Windows Service Packs and Windows hotfixes.

2.9 Hardware Requirements

2.9.1 DynaCAD Client Requirements

Recommended Specifications for DynaCAD Client

Intel Xeon E5 CPU, 4 GB Memory, 100 GB HDD, 27" 2560x1440 monitor

1 Gigabit network card

Minimum Specifications for DynaCAD Client

Intel Core™ 2 Duo 2 GHz CPU, 2GB memory, 100 GB HDD

1280x1024 resolution monitor, 100 Mbps network card, Windows XP

3 Introduction and General Description

This Application Guide describes how to use the DynaCAD software.

3.1 Intended Purpose

This Application Guide focuses on how to use the DynaCAD MRI study review, analysis, and reporting software. The DynaCAD MRI study review, analysis, and reporting software provides the radiologist with a comprehensive set of tools to assist in lesion characterization and reporting of MRI datasets.

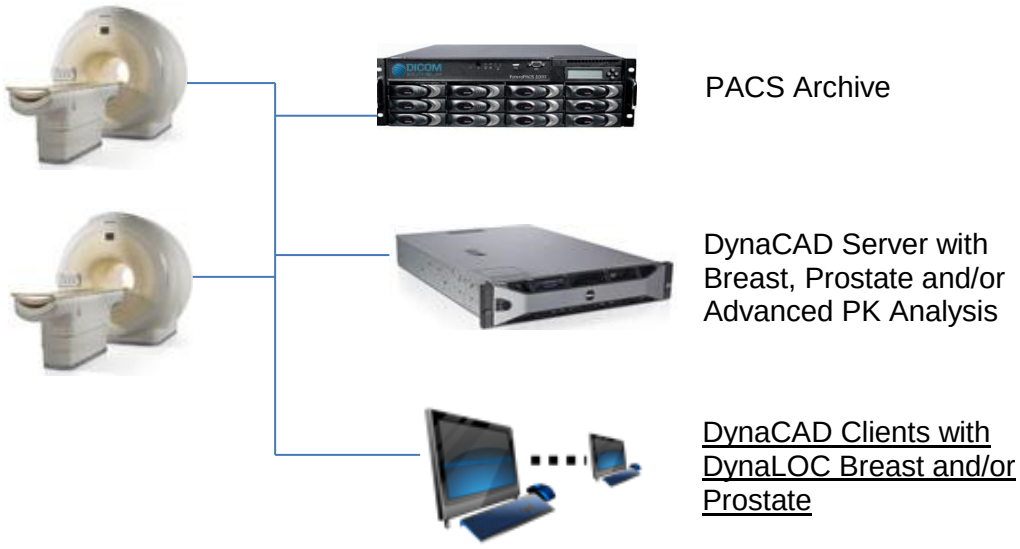
This Application Guide will help you configure your system, guide you through the basic configuration steps, explain the use and operation of the software, and assist in troubleshooting the software in study of problems.

3.2 Product Overview

DynaCAD is a DICOM 3.0 compliant review and post-processing software intended for use in viewing Magnetic Resonance Imaging (MRI) datasets. It supports viewing and post-processing of non-contrast and Dynamic Contrast Enhanced MRI data, as well as secondary capture data. It contains several interactive functionalities which facilitate the detection and identification of suspicious areas, such as segmentation algorithms, multi-planar reconstruction, three-dimensional display, and dynamic curve visualization.

3.3 Data Flow

An example of dataflow using DynaCAD is shown below:



3.4 Software Operation

3.4.1 Key Terms

DynaCAD – A digital imaging software application with an extensive set of quantitative image analysis tools for performing real-time analysis utilizing MRI patient exam data.

To utilize the system to its full potential, it is helpful to review some terms and understand their applications.

Viewport – A window that displays images in the DynaCAD area, providing a variety of display options. It is compatible with MRI and other modalities that produce DICOM 3.0 formatted images.

Chart Viewport – A window that displays analysis graphics/data in the DynaCAD area, providing a variety of Region of Interest (ROI) specific information.

Hanging Protocol – A customized, user-specific arrangement of images and associated data, placement of Viewports, Chart Viewports, Reports, and settings for window/level and other parameters.

Series – Organizational unit of an examination comprised of one or more DICOM images.

Study – An organizational unit of an examination comprising one or more series, which in turn comprise individual images.

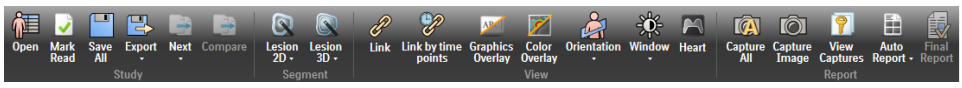
Window – A view in the DynaCAD application with images, data, or charts in it.

3.5 System Overview

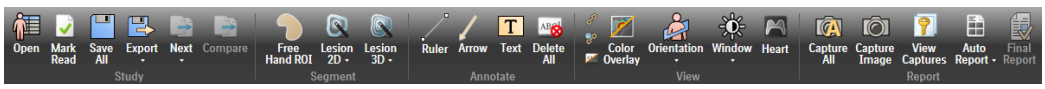
In order to become familiar with the user interface and DynaCAD, refer to the icons described in this section while navigating through the various tools. Note that Toolbar menus are context specific and may change slightly depending upon the status of the displayed viewports.

Main Menu Toolbar

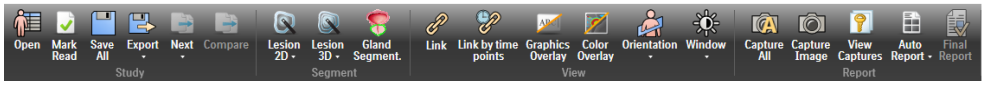
Home Shortened Toolbar for Breast



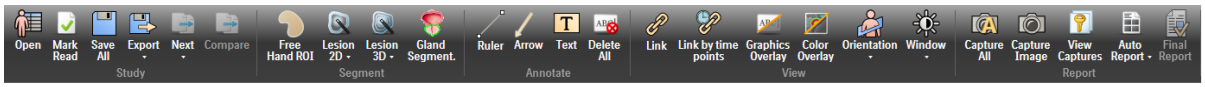
Home Shortened Toolbar for Prostate



Home Expanded Toolbar for Breast

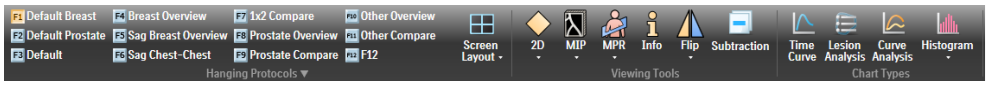


Home Expanded Toolbar for Prostate

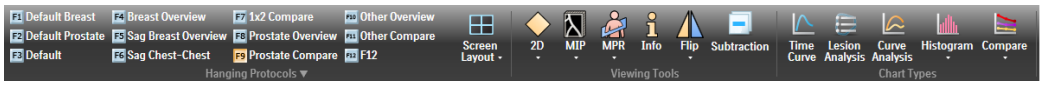


Hangings Shortened Toolbar

Hangings Expanded Toolbar

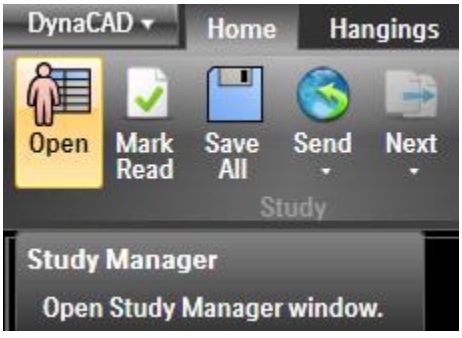


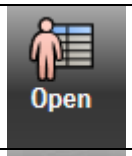
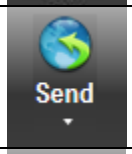
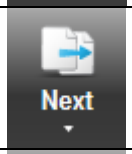
Hangings Expanded Toolbar for study comparison

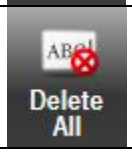
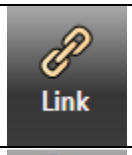
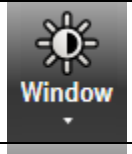


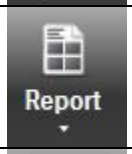
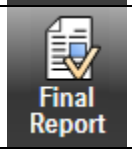
3.6 DynaCAD Tools and Functions

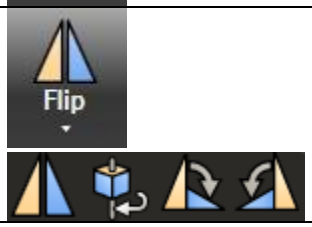
In order to become familiar with the user interface and Invivo DynaCAD, refer to the icons described in this section while navigating through the various tools. Note that toolbar menus are context specific. When the cursor is placed over button, a tooltip message appears to explain the function.



ICON	FUNCTION
Study Group Icons	
	Left click opens the Study Manager displaying the list of patients
	Left click marks the current study as read in the Study Manager
	Left click saves all measurements, annotations and 2D, 3D ROIs
	Left click sends pre-configured series to a DICOM destination. Left click on the text or arrow displays the list of series and allows the user to choose the specific series to be DICOM export.
	Left click on the icon loads the next selected patient. Left click on the text or arrow displays the list of the selected patient, allowing the user to choose a specific patient to be loaded.
	Left click switches the layout to compare multiple studies. Only enabled when more than one studies are available.
Segment Group Icons	
	Left click enables the free hand ROI function.
	Left click on the icon enables the last selected 2D ROI Segment function based on the color overlay. Left click on the text or arrow displays a list of 2D ROI Segment functions.
	Left click on the icon enables the last selected 3D ROI Segment function based on the color overlay. Left click on the text or arrow displays a list of 3D ROI Segment functions.
	Left click opens the Prostate edit window.
Annotate Group Icons	

ICON	FUNCTION
	Left click activates the ruler tool in an active viewport.
	Left click enables arrow drawing in an active viewport.
	Left click enables an annotation to be written in an active viewport.
	Left click deletes all measurements, annotations and ROIs.
View Group Icons	
	Left click enables spatial linking of all image viewports. This function can also be enabled or disabled by using the right mouse button in a viewport and selecting the function in the drop down menu.
	Left click enables linking of all image viewports that display time series such as original and motion corrected DCE, subtraction series.
	Left click enables or disables graphic overlays in all viewports. Clicking once turns off the text in each corner of the viewport. Clicking a second time removes measurements, annotations and ROIs. Clicking a third time restores all text, measurements, annotations and ROIs.
	Left click toggles on and off PK color overlays for all viewports.
	Left click on the icon displays the image of the active viewport in the acquisition plane. Left click on the text or arrow displays the MPR options.
	Left click on the icon applies auto-window levelling to the active viewport. Left click on the text or arrow displays a dropdown menu that lists the related functions including window presets and inversion for the user to select.
	Left click toggles on/off the heart mask. Only available for breast study.

ICON	FUNCTION
Report Group Icons	
	Left click captures all images in current layout and places them in the Key Images clipboard or reports.
	Left click captures an image or chart of the active viewport.
	Left click displays captured key images and charts.
	Left click creates an ROI based automatic report. Left click on the text or arrow displays a dropdown that list report options: Auto Report, PI-RADS (for prostate exam), and 4 and 6 image fix layout.
	Left click displays the Final Report. Only enabled when a Final Report is available.
Hanging Protocols Group Icons	
	Left click on one of the twelve F keys applies the associated user definable hanging protocol. Right click to save the current layout assignment or the edit the hanging protocol name.
	Left click on the text or arrow displays multiple options of screen layouts.
Viewing Tools Group Icons	
	Left click on the icon applies 2D display mode to the active viewport. Left click on the text or arrow displays multiple layout options for the 2D viewport.
	Left click on the icon appies MIP mode to the active viewport. Left click on the text or arrows displays multiple layout options for the MIP viewport.
	Left click on the icon applies MPR mode to the active viewport. Left click on the text or arrows displays the option of Axial, Coronal, Sagittal and Oblique MPR.

ICON	FUNCTION
	Left click displays DICOM header information of the image in the selected Viewport. It only displays the information when the display mode is either 2D or MPR displaying in the original acquisition plane.
	Left click on the icon flips image based on the last chosen options. Left click on the text or arrow displays the different flip options. Once selected, the icon and text label will be updated accordingly.
	The Subtraction button will be available if the active viewport is a dynamic series, including original and motion corrected DCE. Left click will create a DCE subtraction that enables scrolling through time at different slices. Right clicking on this icon will allow selecting and saving the reference time point for displaying the subtractions.
Chart Types Icons	
	Left click displays a Time Curve in a selected viewport. The time axis will display post injection timing when a processed color overlay is displayed or timing from the DICOM header if an image with no color overlay is displayed.
	Left click displays a Lesion Analysis summary report in a selected viewport.
	Left click displays a Curve Analysis in a selected viewport.
	Left clicking displays a list of all the histograms that can be displayed in a selected viewport when selected. The histograms include WashIn, WashOut, QuickTP (QTP), PK Joint Histogram, K^{trans}, V_e, K_{ep}, V_p, T10, iAUGC and ADC
	Left clicking displays a list of all the Compare charts that can be displayed in a selected viewport when selected. The Compare charts include K^{trans}, V_e, K_{ep}, V_p, T10, iAUGC and Volume Compare.

4 User Login

4.1 Log in and Passwords

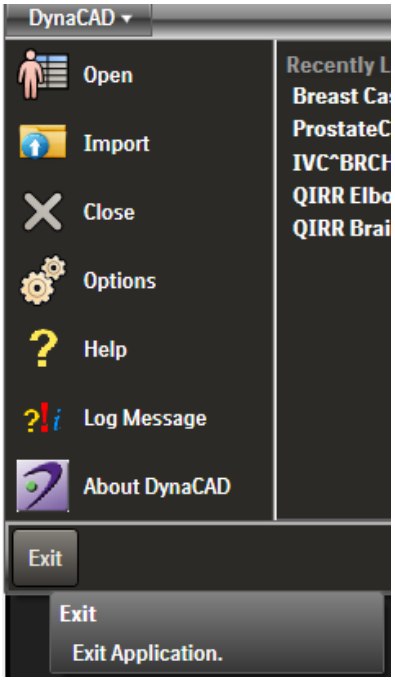
A user must be logged into DynaCAD to read any cases. To log into the DynaCAD:

- Log in to Windows using your personal Windows user account.
- Double click the DynaCAD icon on the desktop.
- The DynaCAD login window is displayed.
- Enter your DynaCAD username and password.
- Click the **Login** button to continue logging into the DynaCAD software.

4.2 Log out

To log out of the application:

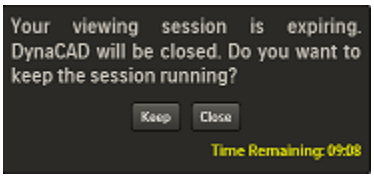
Left-click the DynaCAD button of the DynaCAD main application window, and select **Exit** to close the application.



Alternatively, the application can be closed by left clicking the standard windows close window function, **X,** in the upper right hand corner of the application window.

4.3 Session Expiry

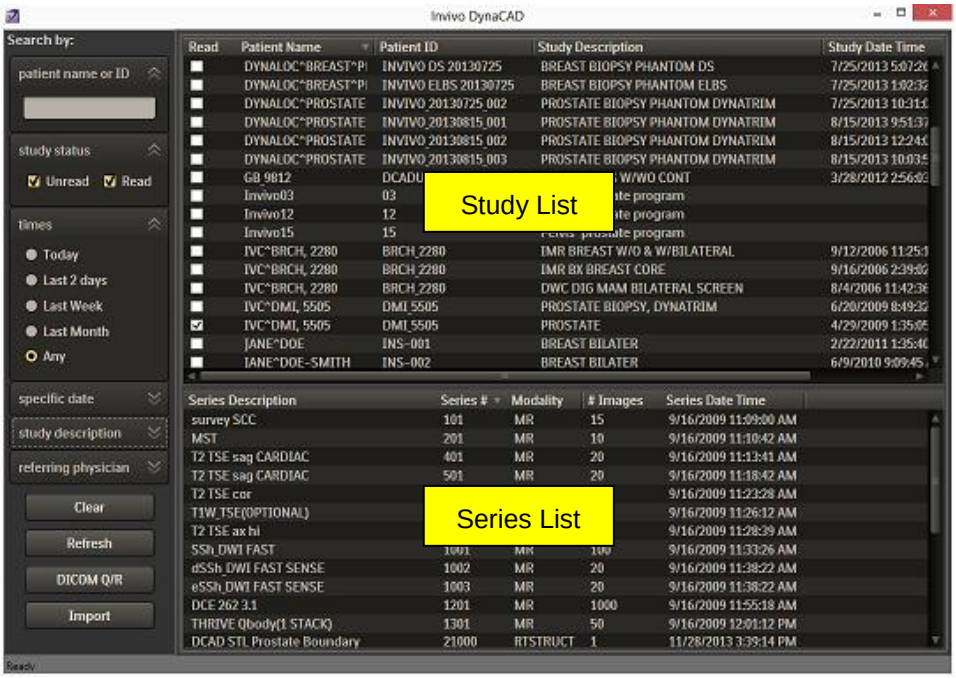
If the session is idled for more than a pre-defined time limit (defined in the DynaCAD Admin Web page), the reading session will automatically be closed. A warning dialog will be displayed 10 minutes prior to the session expiry. Choose **Keep** to keep the session open and continue using DynaCAD, or **Close** to logout of the application.



5 Study Management

5.1 Study Manager

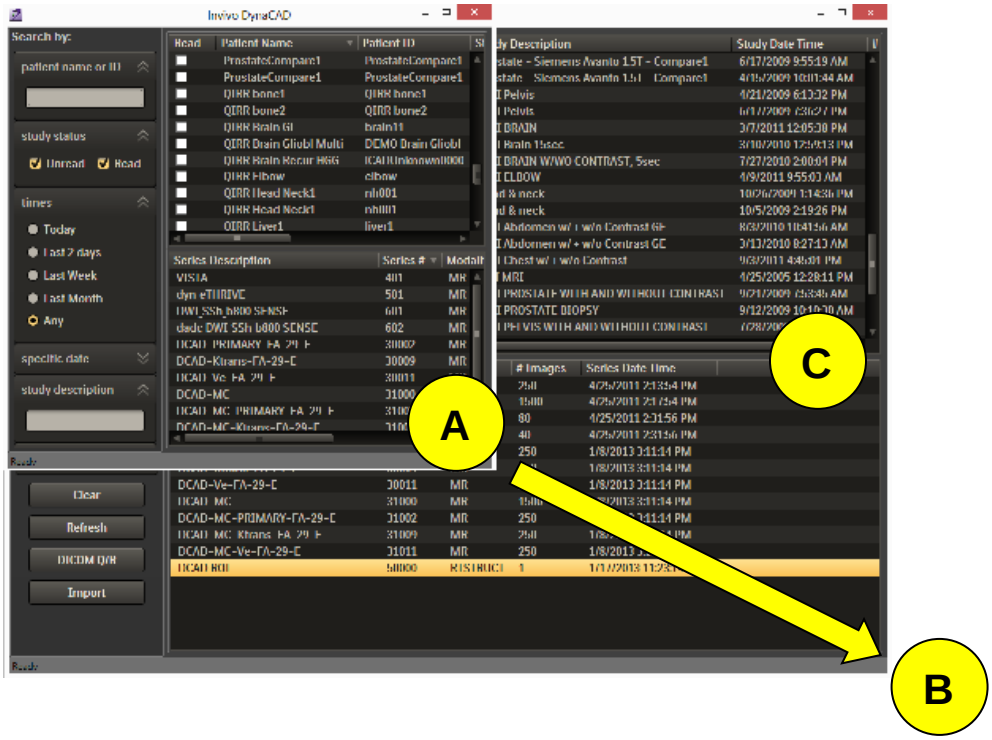
The Study Manager displays the list of available studies to the user and allows them to select and load into the viewer. The Study Manager queries the DynaCAD Server based on the user chosen search criteria and the results are displayed in the Study List in the top panel. If a study is still transferring to the DynaCAD Server, the study will not display in the Study List. When the study in the Study List is single-clicked, all data pertaining to that study will appear in Series List in the bottom panel.



NOTE: *Always send studies to a PACS archive since DynaCAD is not intended to serve as a storage archive.*

5.1.1 The Study Manager Main Screen

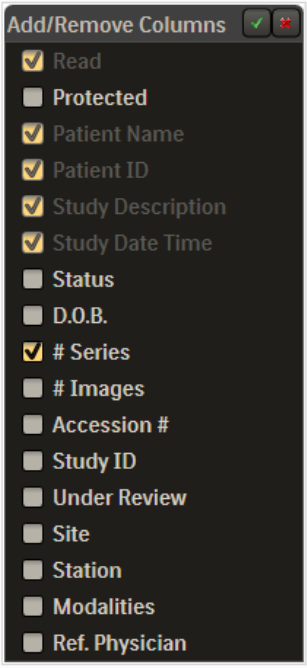
The Study Manager window can be resized or enlarged to display all information by clicking and dragging the window border, e.g. left click and drag from (A) to (B) as shown below



The vertical height of the Study and Series List pane can be adjusted by left click and drag the horizontal separator (C).

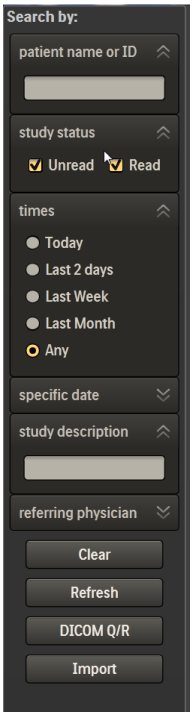
5.1.2 Header columns in the Study List

Additional information can be added to the header columns for display. Right click in a header field and a drop menu will appear. Check the field name to be added and choose the green check, this will add the field to the Study Manager. Deleting a field name can be accomplished by unchecking a field and selecting the green check.



5.1.3 Study List Filter

Finding MRI Exams can be facilitated by using the search tool shown below, which is located on the left side of the Study Manager. Information can be sorted by clicking on column headers (i.e., patient name, patient ID, study description, date, etc.).



Patient name or ID: Typing in letters (last name) or ID numbers will begin to display the matching names or ID #.

Study Status: Checking read or unread displays the corresponding list of studies.

Times: Checking the choices displays the corresponding list of studies.

Specific Date: Selecting a date displays the corresponding list of studies.

Study Description: Typing in letters will begin to display matching study descriptions.

Referring Physician: Typing in letters will begin to display matching physician names.

Clear: Left clicking this option will clear the search criteria and display the entire list of studies.

Refresh: Left clicking this option will update the Study Manager list, especially convenient when new patient data is added or being processed.

NOTE: *When data is being reprocessed, it is important to select the* ***Refresh*** *button in the Study Manager to update the entire Study List and associated sequences in the Series List.*

5.2 DICOM Q/R

DICOM Q/R (Query/Retrieve) allows the user to retrieve patient data from another DICOM device, such as a PACS system. This feature is particularly useful when wanting to review and compare a prior study to an existing study.

Left clicking the **DICOM Q/R** button will open a new window to enable searching by particular fields. This function can also be launched by right clicking a study in the Study List and selecting **Get prior studies**.

A list of patient names will appear in the top field, right clicking on a patient name will allow the user to **Expand series** or begin the **Retrieve** process. Selecting the **Expand series** option will list all the series associated with the selected study in the middle pane. Selecting **Retrieve** will begin the process and the study being retrieved will be displayed in the bottom pane with the retrieval status information updated during the process.

The **Available** column indicates if a study is already available in the DynaCAD Server.

DICOM Source: Selecting the drop down arrow will list all the available devices that can be searched to retrieve patient data. Devices can be added by going to the DynaCAD Admin Web page and adding them in the DICOM **Destination Management** tab.

Patient name: Typing the patient name in this field will query the DICOM Source when the **Query** button is selected.

Patient ID: Typing the patient ID in this field will query the DICOM Source when the **Query** button is selected.

Accession number: Typing the Accession Number in this field will query the DICOM Source when the **Query** button is selected.

Study description: Typing the study description in this field will query the DICOM Source when the **Query** button is selected.

From/To: Typing the beginning and end dates will query the DICOM Source when the **Query** button is selected.

Query: Selecting this button will begin to query the DICOM Source based on the information provided in the above fields.

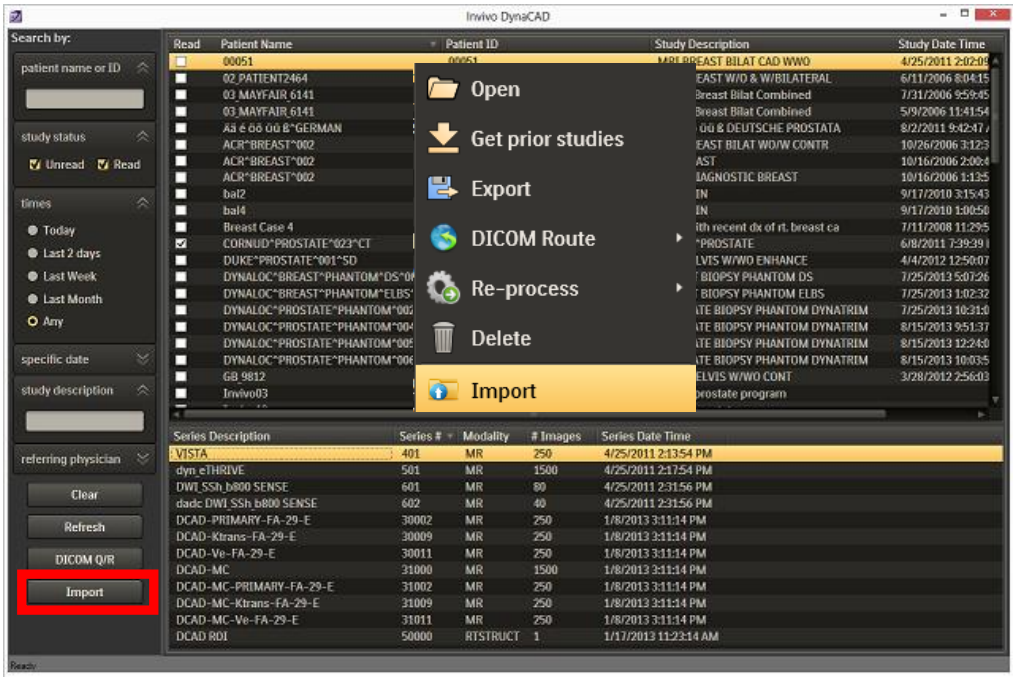
5.3 Get Prior Studies

Right clicking on a study item in the Study Manager will allow a user to Query/Retrieve studies of that patient by selecting the **Get prior studies** option. This will open the **DICOM Q/R** window and automatically copy the patient name and ID to the corresponding search box. Refer to section 5.2 for detailed information on how to Query/ Retrieve a patient. The **DICOM Q/R** window can also be opened by selecting the **DICOM Q/R** button on the left panel of the Study Manager.

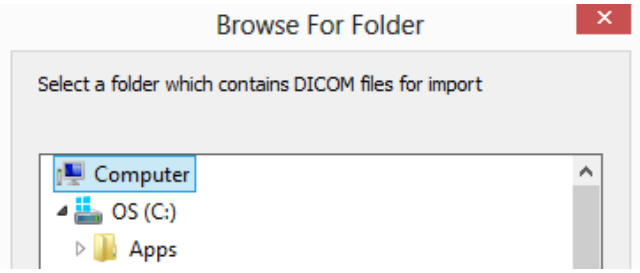
5.4 Importing Studies

This function imports DICOM files that are located in a media such as CD/ DVD/ USB. To import:

- Left click on the **Import** button, or right click on the Study List pane, and select **Import** from the Right Mouse Menu.



- This will open the **Browse for Folder** dialog.



- Select the folder from the appropriate location in the computer, on the CD/DVD, USB Drive or from other available media and locations.
- Click **OK** at the bottom of the **Browse for Folder** dialog to begin the import.

  The progress bar at the bottom of the Study Manager will indicate import progress. When the import is complete a pop-up window will read **"Import DICOM folder completed,"** and the studies of the newly imported files will appear in the Study Manager.

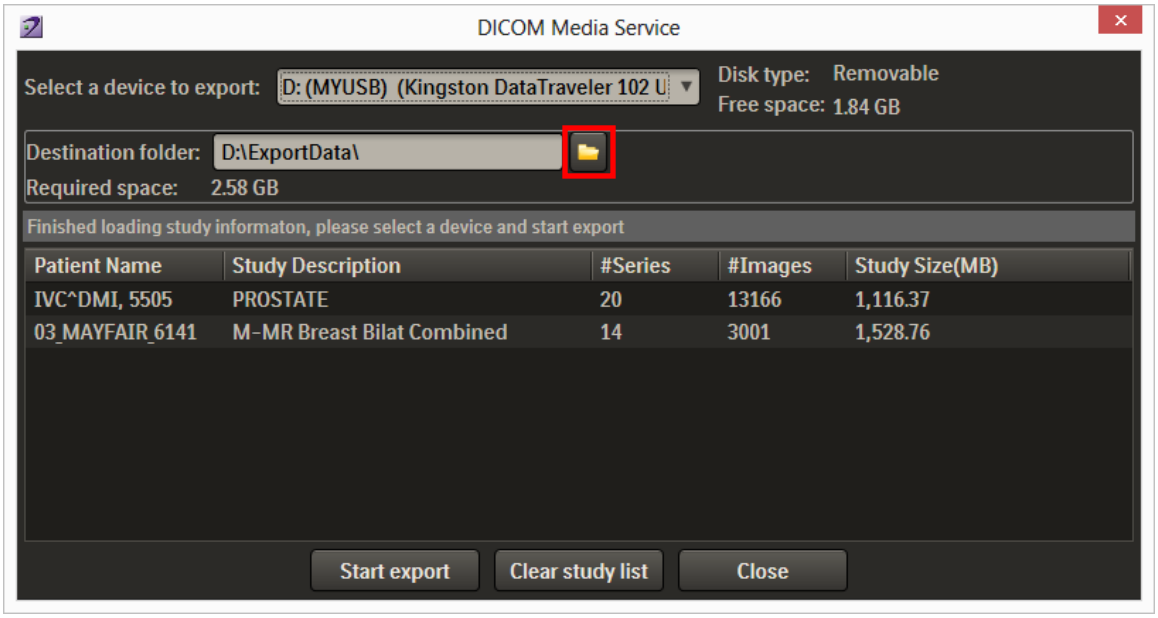
5.5 Exporting Studies To Media

One or more studies can be written to the hard disk or portable media as DICOM files.

To export studies:

- Either select one or more studies from the Study List pane, or one or more series from the Series List pane.
- Right click to open the Right Mouse Menu.
- Click **Export** to display the DICOM Media Service menu.

The DICOM Media Service dialog will be displayed.



- Click the folder icon at the end of the **Destination folder** line to select the Destination Folder if different from the one shown.
- Check to make sure the correct case(s) are in the list.
- Click **Start export** button to begin exporting the selected files, **Clear study list** to clear the cases currently displayed, or **Close** to remove the export screen.

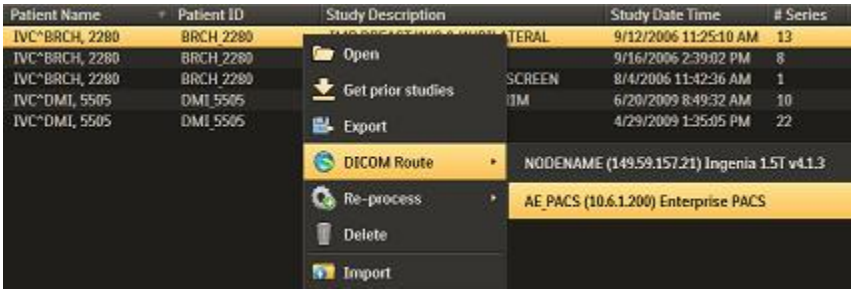
The progress bar in the center of the **DICOM Media Service** screen will indicate export progress, and when the export is complete, an information window displays "*Completed export successfully.*" The exported files will appear in the destination folder.

NOTE: *Once an export begins, you will not be able to open or modify studies until the export is complete. After the export is in process, however, you can click the* ***Cancel Export*** *button which now replaces Start Export at the bottom of the screen, to stop the export. You can also click* ***Close*** *to remove the screen, but if an export is in process, exporting will continue until complete.*

NOTE: *Only series available in the study manager's series list are available for study export and routing, i.e. a study can be exported or routed while there are still remaining tasks in the MR processing queue.*

5.6 Routing Studies or Series

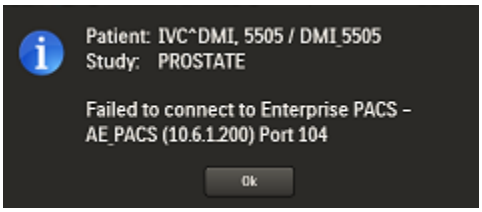
In addition, cases or series can be routed to a DICOM destination. Within the Study Manager, select one or more studies or series. Right click on the select item(s), select **DICOM Route** from the Right Mouse Menu and then select the DICOM destination. Only destinations that have been added to the DICOM Destination Management table in the DynaCAD Admin Web are available in the route list. Please refer to the DICOM Destination Management section in the DynaCAD Server manual to add routing destinations that will be displayed in the Study Manager.



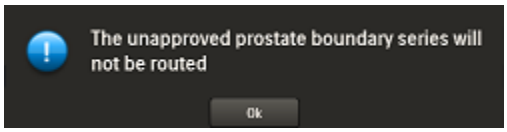
Routing a series or multiple series selected from the Series List of the Study Manager can be achieved by the same method as above. To select multiple series in a row depress the SHIFT key and select the last series, to select non-consecutive series, depress the CTRL key and select them one at a time.

When done, a message will appear indicating the successful completion of the routing.

In the event that the studies or series were not transferred successfully, an error message similar to the one shown below will be displayed.

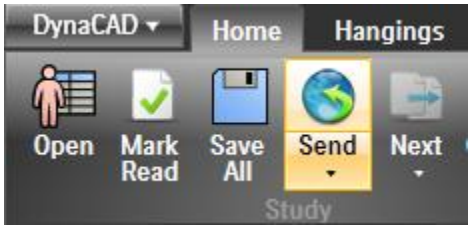


Attempting to route studies or series with an unapproved prostate boundary will result in the following warning message. The unapproved prostate boundary will not be DICOM export, but the rest of the study will be sent. To send the prostate boundary, it has to be approved first (see Section 1), and then select the series "*DCAD STL Prostate Boundary*" and export.

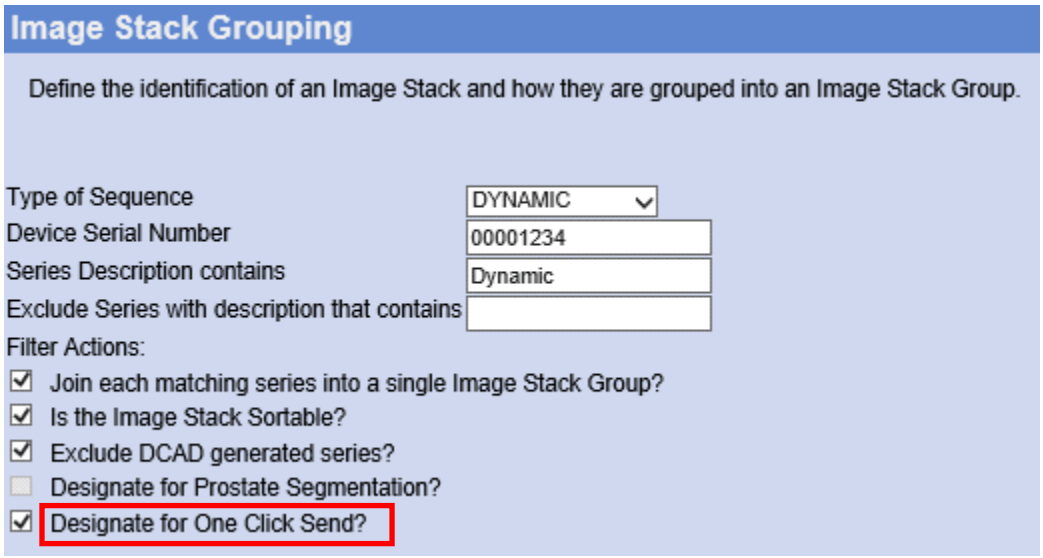


5.7 One-Click DICOM Send

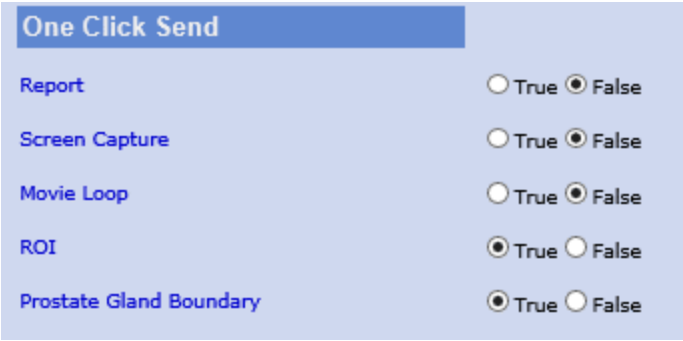
One-Click DICOM Send is a convenient feature in the application that allows the user to DICOM send a list of preconfigured series including user generated data such as ROI, key images and report to a DICOM destination such as a PACS by just clicking the **Send** button in the **Home** tab of the application toolbar.



One-Click Send automatically selects the series to be sent based on the corresponding setting defined in the Image Stack Group filter. When an Image Stack Group is defined using the DynaCAD Admin Web page, there is an option to indicate if it is included for the One-Click Send automatically:



For the user generated date, the Routing Service tab of the DynaCAD Admin Web's Application Settings contains settings to include/ exclude those series:

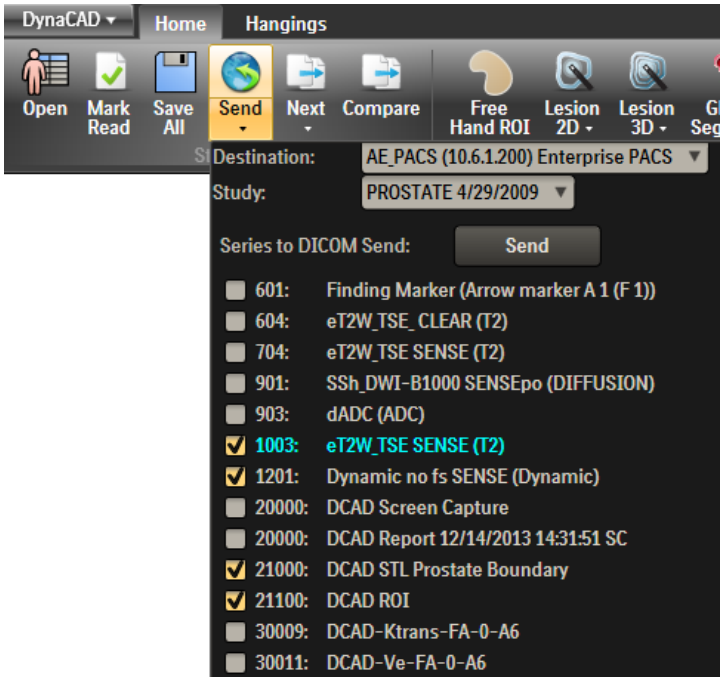


In addition, two special built-in rules are defined:

- Un-approved prostate boundary will not be included in DICOM Send even the Prostate Gland Boundary setting above is set to True. If the prostate boundary is not approved, it will appear in **Red** in the One-Click Send series list to warn that it will not be exported.
- The prostate boundary reference series will be added to the list automatically if the prostate boundary is included in the export list. It will be highlighted in **Cyan** in the One-Click Send series list.

Left click on the **Send** button icon (top portion of the button) will automatically send all the selected series.

Left click on the **Send** button label (bottom) will display the list of available series and the current selections.



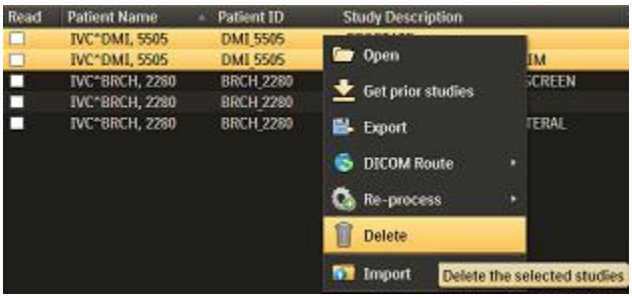
It allows the user to:

- Select a new DICOM destination
- Select the study to be DICOM Send if the patient has two or more studies.
- Include/ exclude series to be sent. This will override the default selection.

Once the DICOM Send is invoked, the series selection will be remembered for the current study.

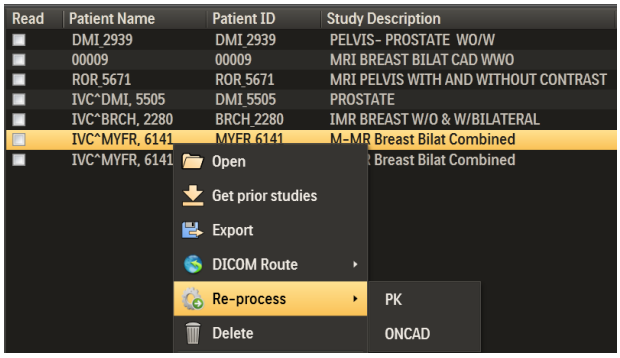
5.8 Deleting Studies and Series

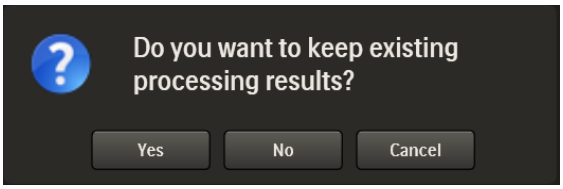
To delete one or more studies or series, select the item to be deleted according, and right click to display the Right Mouse Menu. Select **Delete**. Once selected, a confirmation dialog will be displayed.



5.9 Re-process a Study from the Study Manager

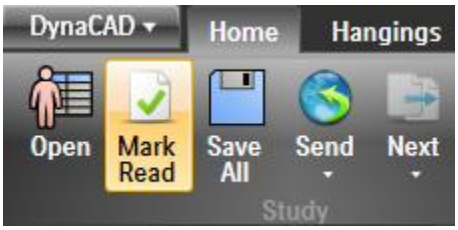
The right drop down menu allows a study to be re-processed using the Pharmacokinetic model or by ONCAD as set up in the DynaCAD Profile Editor. It will also re-run any other items that are setup in the Profile Editor, e.g. subtractions and motion correction. Once selected, a dialog box will appear to allow the option to keep or delete the existing processing results.



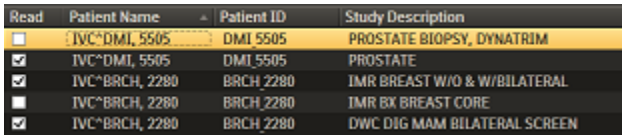


5.10 Marking Studies as Read

To mark a study as *read*, left-click the **Mark Read** button in the **Home** tab of the application toolbar.



Alternatively, a study can be marked *read* from the Study Manager by clicking on the checkbox under the **Read** column of the Study List.



To filter the *read* and *un-read* studies, select the appropriate choice under the **study status** under the Search panel in the Study Manager.

5.11 Opening Studies

To open a study in the application, perform either of the following optional procedures:

Option 1

- Place the mouse cursor over a study shown in the Study List.
- Double-click to open the study and load the exam series into the default hanging protocol displayed in the image viewports.

Option 2

- Place the mouse cursor over a study shown in the Study List.
- Right-click the mouse button to display a pop-out menu.
- Select **Open** with the left mouse button to open the study and load the exam series into the default hanging protocol displayed in the image viewports.

5.11.1 Patient with Multiple Studies

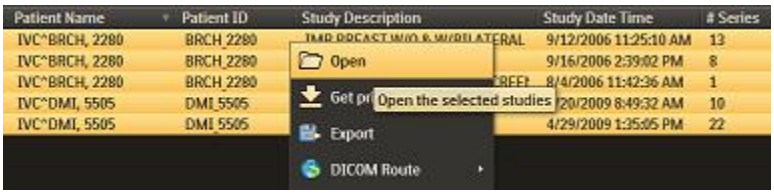
If there are multiple studies associated with the patient, e.g. prior studies are available, it is not necessary to select all the studies. Always select only the current study to be read and open it in the viewer. The associated studies of the patient will be made available automatically. Please refer to Section 1 for opening multiple studies for reading multiple studies together.

Similar, for loading into DynaLOC Breast or Prostate for biopsy, select the newly acquired biopsy study instead of the diagnostic studies. This will allow loading into the corresponding DynaLOC module automatically if configured.

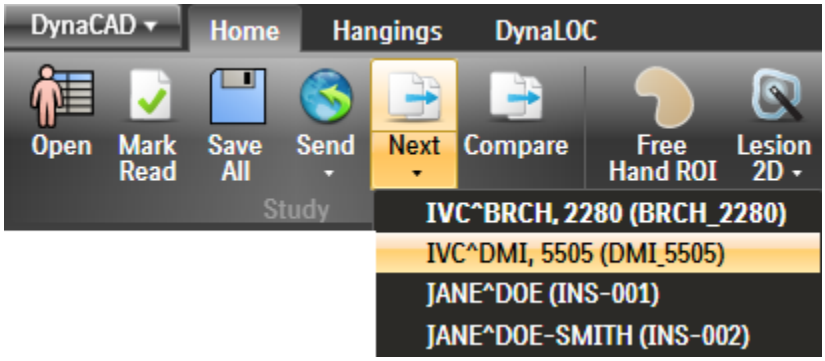
5.11.2 Select Multiple Patients

Multiple studies from different patients can be selected and pre-loaded in a list without returning to the Study Manager. To do this:

- Depress the SHIFT key on the keyboard and left click on the select studies.
- Once selected, right click and select **Open**. This will load the first patient to the application. The rest of the patient studies will be in the **Next** Patient list.



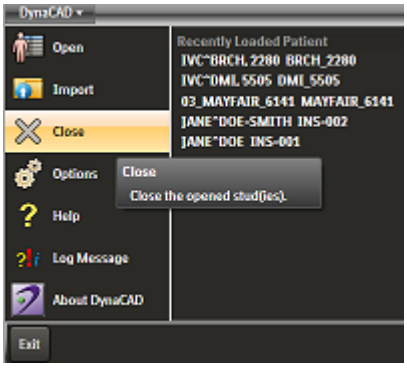
- To display the next case, click the **Next** button in the **Home** tab of the application toolbar.



- Optionally, left click the **Next** button label. A drop down menu will display the selected patients. Click on the desired patient to open it.

5.12 Closing Studies

To close studies in the DynaCAD application: left-click the DynaCAD button and select **Close**.

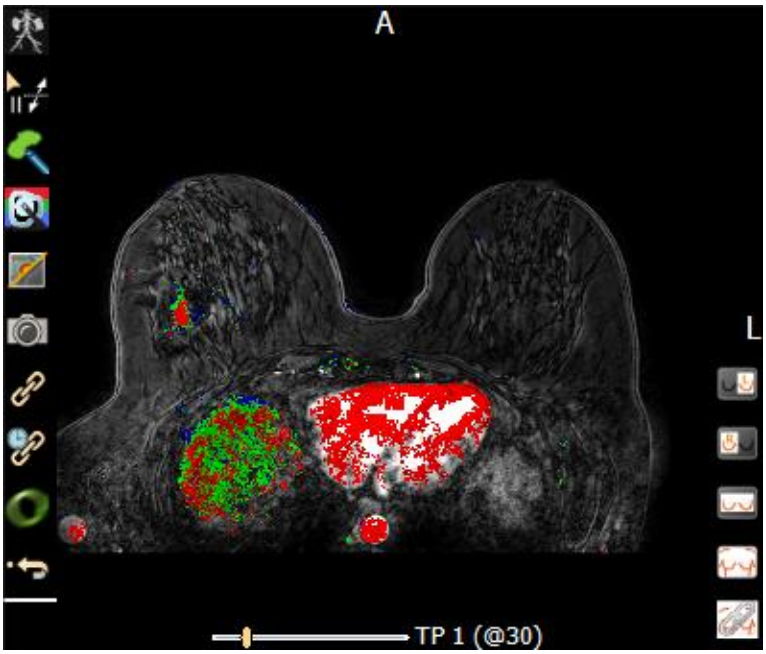


6 Basic Operation

6.1 Basic Image Control

The general mouse cursor will display an arrow in the left upper portion of the cursor icon. The icon will change to a different symbol with a “+” in the left upper portion of the cursor icon signifying the hot spot where actions such as the ruler measurement will begin.

Two in-viewport toolbars are available in the image viewport. They are located in the left and right bottom side of the viewport as shown below. A number of tools are available, and they can be different depending on the rendering mode, i.e. 2D, MPR and MIP, of the viewport.

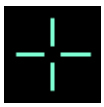


When displaying a time sequence series, i.e. DCE including motion corrected DCE, a slider will be available in the mid bottom of the viewport to allow scrolling between the dynamic time phases. Using the left/right keyboard arrows will also scroll through the time phases.

6.1.1 2D/ MPR Keyboard and Mouse Short-cuts

Keyboard and mouse short-cuts are available to make certain often used tools to be available without explicitly changing the mouse interaction mode:

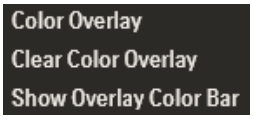
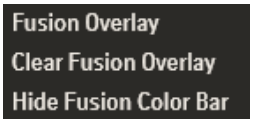
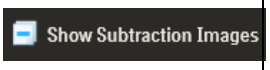
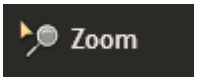
Cursor	Mouse and Keyboard Shortcut	Action

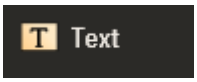
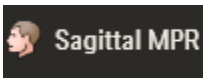
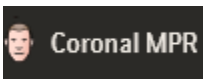
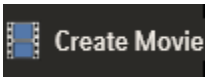
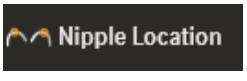
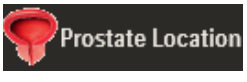
Cursor	Mouse and Keyboard Shortcut	Action
	Keyboard arrow left/right	Scroll through the time phases for DCE series.
	Keyboard arrow up/ down	Scroll through image series slice by slice.
	Keyboard Home/ End	Scroll to the first/ last image
	Mouse wheel scroll	Scroll through the images spatially
	CTRL+ Mouse Wheel scroll, or Press and hold right and left mouse button, or Press and hold right mouse button and mouse wheel	Zoom location under mouse cursor. ***Note**: Left button will be reserved when the mouse interaction mode is Correlate.*
	Press and hold left and center mouse button	Pans the image up/down and left/right to position the image. ***Note**: Left button will be reserved when the mouse interaction mode is Correlate.*
	Press and hold middle mouse wheel, then drag in horizontal and vertical to change window width and level	Changes window/level settings.
	Press ALT and left click over image	Correlate images in viewports by superimposing crosshairs. Moving crosshair in one viewport moves crosshair in other viewports to indicate same location.
	Press CTRL and left click over image	Set the Oblique MPR rotate pivot to the click location. Only applicable in Oblique MPR.
	Double Left click	Toggle between current layout and 1x1

6.1.2 2D/ MPR Right Mouse Context Menu

Clicking the right mouse button will display the Right Mouse Context Menu. It provides different options depending on the organ, color overlay on/off, image sequence and viewport (image vs. chart). The options are described in the following table:

Right Mouse Context Menu for 2D/ MPR Viewport

Right Mouse Context Menu for 2D/ MPR Viewport	
Study label at top of menu.	Move mouse over study label to display a pop-out menu from which you can select another image series for display.
	Move mouse to highlight **Color Overlay** to open a pop-out menu from which you can select the type of PK or QuickTP data to be superimposed as color overlay on the image. Left click **Clear Color Overlay** to remove an existing color overlay. Left click **Show/Hide Overlay Color Bar** to remove the color bar in the viewport.
	Move mouse to highlight **Fusion Overlay** to open a pop-out menu from which you can select from a list of available ADC and Diffusion data to be superimposed as color overlay on the image. Left click **Clear Fusion Overlay** to remove an existing fusion overlay. Left click **Show/Hide Fusion Color Bar** to show/hide the fusion color bar in the viewport.
	When the DCE series, including motion corrected DCE, is the active viewport, selecting this icon will create a DCE subtraction that enables scrolling through time at different slices.
	Left click to display the Scroll icon, and then hold down the left mouse button while moving the mouse up/down to scroll through the images of the series.
	Left click to display the Window icon, and then hold down the left mouse button while moving the mouse left/right and up/down to change window width and level.
	Left click to display the Zoom icon, and then hold down the left mouse button while moving the mouse up/down to zoom in/out the image.
	Left click to display the Pan icon, and then hold down the left mouse button while moving the mouse up/down and left/right to position the image.
	Left click to enable the Correlate function, which displays cross hairs on the image(s) to permit quick comparison of displayed images. Moving the mouse positions the cross hairs as desired.
	Left click to enable the Voxel Probe function, which allows you to click anywhere in an image to display an intensity analysis showing values for the intensities and PK values at the selected point, i.e. Pixel Value, K^{trans}, V_e and ADC values as relevant.

Right Mouse Context Menu for 2D/ MPR Viewport	
	Left click enables the free hand ROI function. Left click, hold and drag to follow the lesion boundary, release the mouse to finish
	Left click enables 2D ROI function.
	Left click enables 3D ROI function.
	Left click activates the ruler tool.
	Left click enables arrow drawing. The mouse mode will change back to its original mode after drawing an arrow.
	Left click enables an annotation to be written. The mouse mode will change back to its original mode after drawing an annotation.
	Left click to change the current viewport to MPR and display in the Sagittal orientation..
	Left click to change the current viewport to MPR and display in the Coronal orientation.
	Left click to change the current viewport to MPR and display in the Axial orientation.
	Left click changes to change the current viewport to Oblique MPR.
	Left click to spatially **Link Stack/Unlink Stack** to link or unlink the viewports. **Note:** *Label changes from **Link** to **Unlink** to indicate applicable operation.*
	Left click displays the Create Movie dialog.
	On breast exam, click to impose circles indicating the left and right nipple locations. Once nipple locators are displayed, **the Nipple Location** label changes to **Cancel Nipple Location Edit,** which removes the nipple graphics.
	Left click to enable the Prostate contour to be displayed in a viewport.

Right Mouse Context Menu for 2D/ MPR Viewport	
	Left click **Chart** to display a pop-out menu of charts available to display in the viewport.

6.1.3 2D/ MPR In-viewport (left) Tools

2D/ MPR In-viewport (left) Tools	
	**Image Setting:** Allows setting the image to an average (X-ray) or to a MIP. Clicking on the button will toggle between average and MIP. The rendering slice thickness (see next button) needs to be 2x of the acquisition slice thickness to observe the effort of average and MIP rendering.
	**Slice Thickness:** While over the thickness icon, press and hold left mouse button. Advancing to the right increases slice thickness, to the left decreases slice thickness. Left click once will reset the slice thickness. The “Thickness” text in the upper left area will display the change of slice thickness from the original image.
	**Free Hand ROI:** Left click over icon to activate. Left click, hold and drag to follow the lesion boundary, release the mouse to finish.
	**Automatic ROI:** Left click over icon to activate 2D ROI calculation. Right click over icon to activate 3D. While mouse is over icon scroll mouse wheel to change to use Red, Red+Green or Red+Green+Blue regions in the ROI analysis. Click the colorized area to calculate.
	**Colorized overlays:** Click left mouse over icon to enable or disable colorized overlays. Click middle mouse to display different color analysis (primary, K^{trans}, K_{ep}, V_e). This toggling overlay function is available with spatial series data.
	**Capturing key images:** Clicking the left mouse button over the camera icon will take a picture of the current viewport and automatically place the image in the report or key images clipboard.
	**Spatial Link:** Clicking the left mouse button over the icon will enable or disable spatial linking of all viewports that display spatial series.
	**Temporal Link:** Clicking the left mouse button over the icon will enable or disable temporal linking of all viewports that display DCE and related series.
	**Motion Correction:** Left click will toggle between original and motion corrected series. This function is only available for DCE and related series.

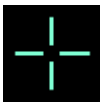
2D/ MPR In-viewport (left) Tools	
	**Reset:** Left click will reset the image to original pan, zoom, window and Level.

In-viewport (right) Tools for 2D/ MPR Breast	
	**Left Breast Zoom:** Clicking on the button will zoom and center the left breast. If viewports are linked, the relevant viewports will also be updated.
	**Right Breast Zoom:** Clicking on the button will zoom and center the right breast. If viewports are linked, the relevant viewports will also be updated.
	**Both Breasts Zoom:** Clicking on the button will zoom to display both breasts. If viewports are linked, the relevant viewports will be updated. This function applies only when showing axial breast acquisition in 2D rendering.
	**Whole Image:** Clicking on the button will display the entire image. If viewports are linked, the relevant viewports will be updated..
	**Left–Right Link Scroll**: Left clicking this icon will enable or disable linking of left and right sagittal images. When this function is disabled, the image in the active viewport can be scrolled to a different position. If this function is enabled the images will scroll together with the offset. This function applies only when left and right breasts are hung side by side. And the display orientation is sagittal

6.1.4 3D Keyboard and Mouse Short-cuts

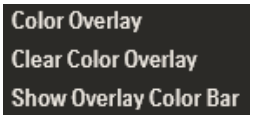
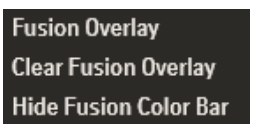
Keyboard and mouse short-cuts are available to make certain often used tools to be available without explicitly changing the mouse interaction mode::

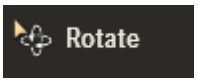
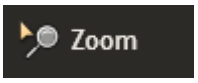
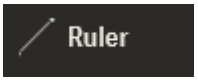
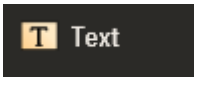
Cursors	Mouse and Keyboard Shortcut	Action
	Keyboard arrow left/right	Scroll through the time phases for DCE series.
	Mouse wheel scroll	Rotate 3D rendering.
	CTRL+ Mouse Wheel scroll, or Press and hold right and left mouse button, or	Zoom location under mouse cursor. ***Note**: Left button will be reserved when the mouse interaction mode is Correlate.*

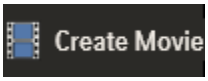
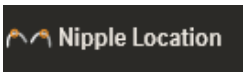
Cursors	Mouse and Keyboard Shortcut	Action
	Press and hold right mouse button and mouse wheel	
	Press and hold left and center mouse button	Pans the image up/down and left/right to position the image. ***Note**: Left button will be reserved when the mouse interaction mode is Correlate.*
	Press and hold middle mouse wheel, then drag in horizontal and vertical to change window width and level	Changes window/level settings.
	Press ALT and left click over image	Correlate images in viewports by superimposing crosshairs. Moving crosshair in one viewport moves crosshair in other viewports to indicate same location.
	Double Left click	Toggle between current layout and 1x1

6.1.5 3D Right Mouse Context Menu

Pressing the right mouse button will display the Right Mouse Context Menu. The options are described in the following table.

Right Click Context Menu for 3D Viewport	
Study label at top of menu.	Move mouse over study label to display a pop-out menu from which you can select another image series for display.
	Move mouse to highlight **Color Overlay** to open a pop-out menu from which you can select the type of PK or QuickTP data to be superimposed as color overlay on the image. Left click **Clear Color Overlay** to remove an existing color overlay. Left click **Show/Hide Overlay Color Bar** to remove the color bar in the viewport.
	Move mouse to highlight **Fusion Overlay** to open a pop-out menu from which you can select from a list of available ADC and Diffusion data to be superimposed as color overlay on the image Left click **Clear Fusion Overlay** to remove an existing fusion overlay. Left click **Show/Hide Fusion Color Bar** to show/hide the fusion color

Right Click Context Menu for 3D Viewport	
	bar in the viewport.
	When the DCE image series is the active viewport, selecting this icon will create a DCE subtraction that enables scrolling through time at different slices.
	Left Click and hold over image, then move mouse freely in any direction to rotate the image in space. The Axis of rotation depends on where the cursor is placed while pressing the mouse button. (See 6.9.)
	Left click to display the Window icon, and then hold down the left mouse button while moving the mouse left/right and up/down to change window width and level.
	Left click to display the Zoom icon, and then hold down the left mouse button while moving the mouse up/ down to zoom in/out the image.
	Left click to display the Pan icon, and then hold down the left mouse button while moving the mouse up/down and left/right to position the image.
	Left click to enable the correlate function, which displays cross hairs on the images to permit quick comparison of displayed images. Moving the mouse positions the cross as desired.
	Left click to enable the Voxel Probe function, which allows you to click anywhere in an image to display an intensity analysis showing values for the intensities and PK values at the selected point, i.e. Pixel Value, K^{trans}, Ve and ADC values as relevant.
	Left click activates the ruler tool.
	Left click enables arrow drawing. The mouse mode will change back to its original mode after drawing an arrow.
	Left click enables an annotation to be written. The mouse mode will change back to its original mode after drawing an annotation.
	No action for 3D/ MIP.

Right Click Context Menu for 3D Viewport	
	Left click displays the Create Movie dialog.
	On breast exam, click to impose circles indicating the left and right nipple locations. Once nipple locators are displayed, **the Nipple Location** label changes to **Cancel Nipple Location Edit,** which removes the nipple graphics.
	Left click to enable the Prostate mesh to be displayed in a viewport.
	Left click **Chart** to display a pop-out menu of charts available to display in the viewport.

WARNING: Significant patient motion or differences in acquisition resolution between MRI sequences may impact the image position accuracy when using the correlate feature. If the image position appears to be incorrect between different sequences, manually scroll one of the image stacks to make them inline.

6.1.6 3D In-viewport (left) Tools

3D in-viewport (left) Tools	
	**Render mode:** Left Clicking to toggle between MIP and volume rendering.
	**Windowing/ opacity/ threshold:** Left Clicking this icon will activate, while over the icon press & hold left mouse button and drag up/down and left/right will change the window level/width settings in MIP rendering mode and opacity in volume rendering mode. The same function can be done by pressing and holding mouse wheel button over the image and dragging in up/down and left/right direction.
	**Presets menu:** This tool is only enabled when the render mode is volume rendering. It provides a number of opacity presets for rendering.
	**Clip front of plane:** Left clicking this button will enable or disable this function. While over the button press and hold left mouse button and drag up/down to move the clipping away or towards the front of the volume. Clicking the right button will reset the clipping plane to half way in the volume
	**Ellipsoid/ cylinder/ box clippers:** Left/ middle/ right mouse clicking this button will activate the type of clipper respectively. Use left mouse button and drag ruler

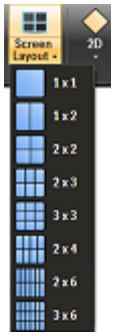
3D in-viewport (left) Tools	
	over the area to clip.
	**Disable clipper:** Left click this button to disable the clipper function.
	**Texture on cuts:** This function only applies to volume rendering. Click left mouse button to enable or disable. When active, press and hold left mouse button and drag in any direction to adjust the window level/ width of the cut surface**.**
	**Colorized overlays:** Click left mouse over button to enable or disable colorized overlays. Click middle mouse to display different color analysis (primary, K^{trans}, K_{ep}, V_e).
	**Capturing key images:** Clicking the left mouse button over the button captures the viewport and automatically place the image in the report or key images clipboard.
	**Spatial Link:** No action in 3D.
	**Temporal Link:** No action in 3D.
	**Motion correction:** Left click will toggle on and off the motion corrected image
	**Reset:** Clicking the left mouse button over the icon will reset the image to original pan, zoom, window and Level.

3D In-viewport (right) Tools	
	**Left Breast Zoom:** Clicking the Left Breast button will zoom and center the left breast.
	**Right Breast Zoom:** Clicking the Right Breast button will zoom and center the right breast image.
	**Whole Image:** Clicking the Whole Image button will display the entire image.

3D In-viewport (right) Tools	
	**Front-Back view:** Left clicking this button will switch image to front view, right click switches image to back view.
	**Bottom-Top view:** Left clicking this button will switch image to bottom view (looking from the patient's feet), right click switches image to top view (looking from patient's head).
	**Left-Right view:** Left clicking this button will switch image to a left view, right click switches image to a right view.
	**Flip back-front:** Click this button flips the image vertically.
	**Horizontal Swivel:** Left/ right clicking horizontal swivels the image ± 10°, SHIFT and click swivels image ± 30°. Clicking and holding will auto advance.
	**Vertical Swivel:** Left/ right clicking vertical swivels the image ± 10°, SHIFT and click swivels image ± 30°. Clicking and holding will auto advance.

<u>WARNING</u>: When reviewing Breast images in the 3D rendering mode, verify the left and right images are loaded correctly in the image viewport when selecting the left/right shortcut button. This can be done by checking the location text information in the upper left viewport.

6.2 Viewport Layout



To add a new image or change the viewport layout in the application:

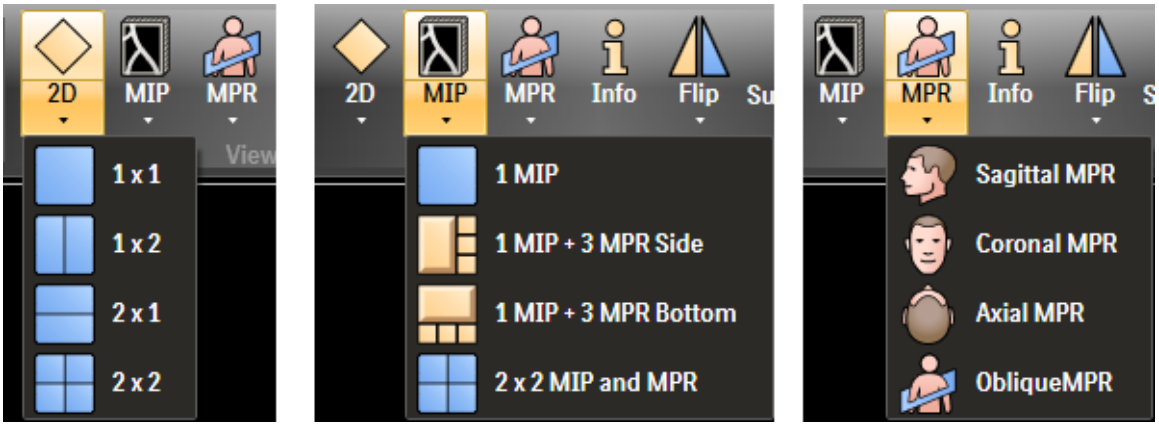
- From the **Hangings** tab of the application toolbar, left-click the **Screen Layout** drop-down arrow, select the image viewport layout **with** the left mouse button.

The chosen layout will be displayed. The content of the existing layout will be preserved.

6.3 Rendering Mode

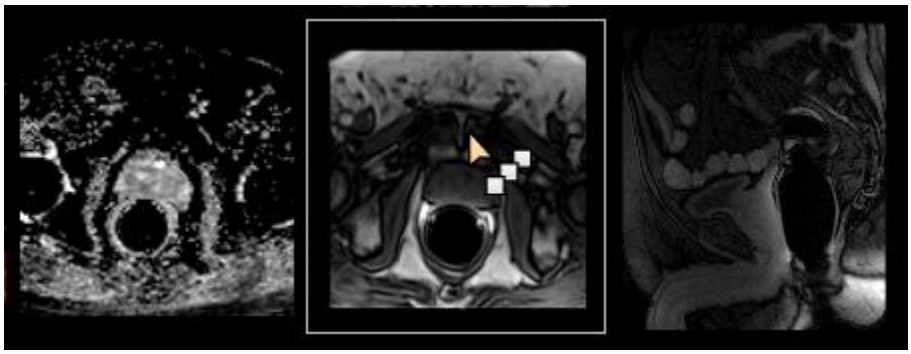
To change an image viewport in the application:

From the **Hangings** tab of the application toolbar, left-click one of the image viewing tools; **2D, MIP & MPR**. A drop down list will display, select a layout option and this will re-draw the active viewport.



6.4 Selecting an Image or Chart Viewport

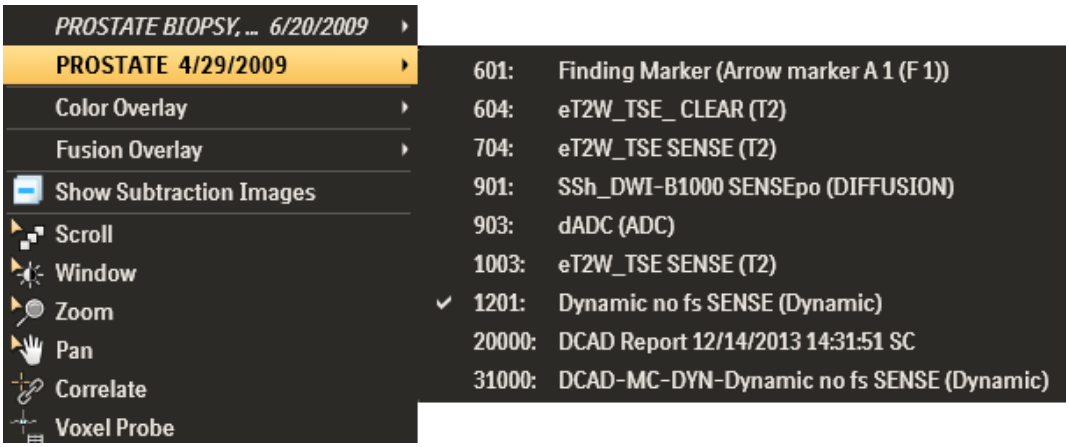
To select the image or chart viewport, left click on the viewport. A white border box indicates that the selected viewport is active as shown below.



6.5 Selecting a New Series

To select a new series, do the following:

- Position the mouse pointer in the desired viewport.
- Right-click the mouse button to display the Right Mouse Context Menu.
- Move the mouse to one of the study items. The list of series is displayed.
- Select the desired series with the left mouse button.



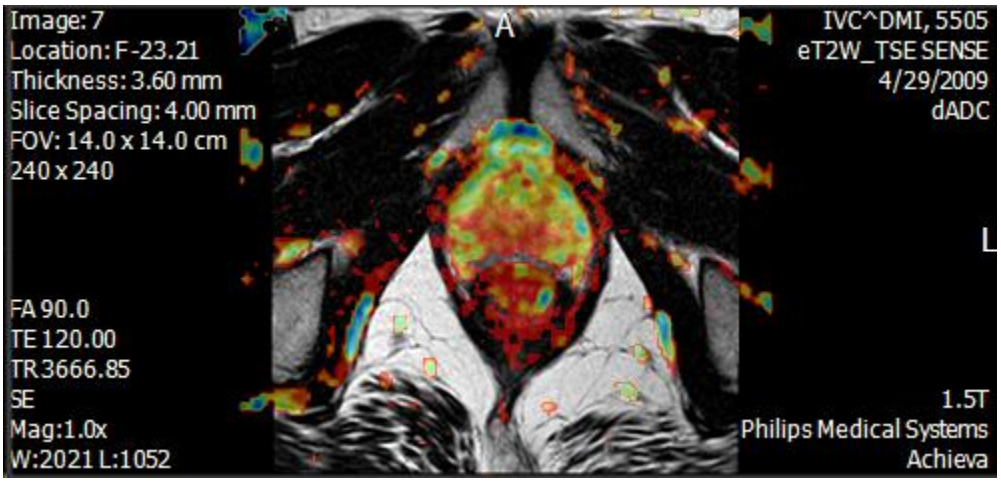
Note: *The currently selected series is indicated by the checkmark. The motion corrected DCE series is identified by "DCAD-MC-DYN-" + <series description of the original dynamic> + "(Dynamic)"*

6.6 Image Information

6.6.1 Viewport Overlay Text

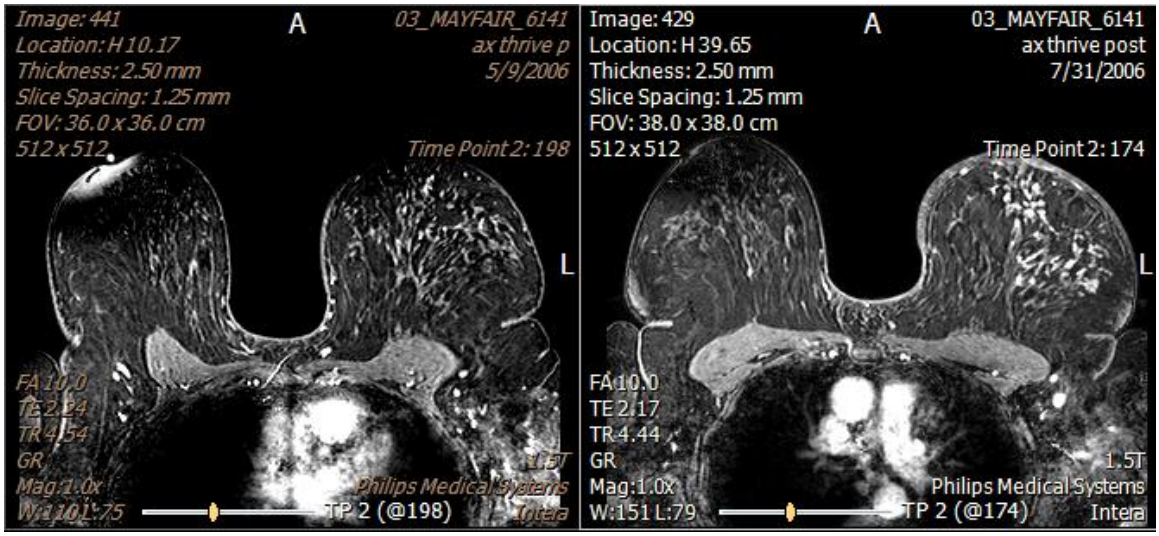
In each corner of a viewport text information will be displayed.

- Upper left area: displays Image slice number, location, slice thickness, slice spacing, field of view (FOV) and size of matrix.
- Upper right area: displays patient name, sequence, date of exam, color overlay and time point of dynamic phase (if displaying a dynamic sequence).
- Lower left: displays acquisition parameters (FA, TE, TR, GR) magnification of the image and window level values.
- Lower right: displays scanner strength, scanner manufacturer and model.

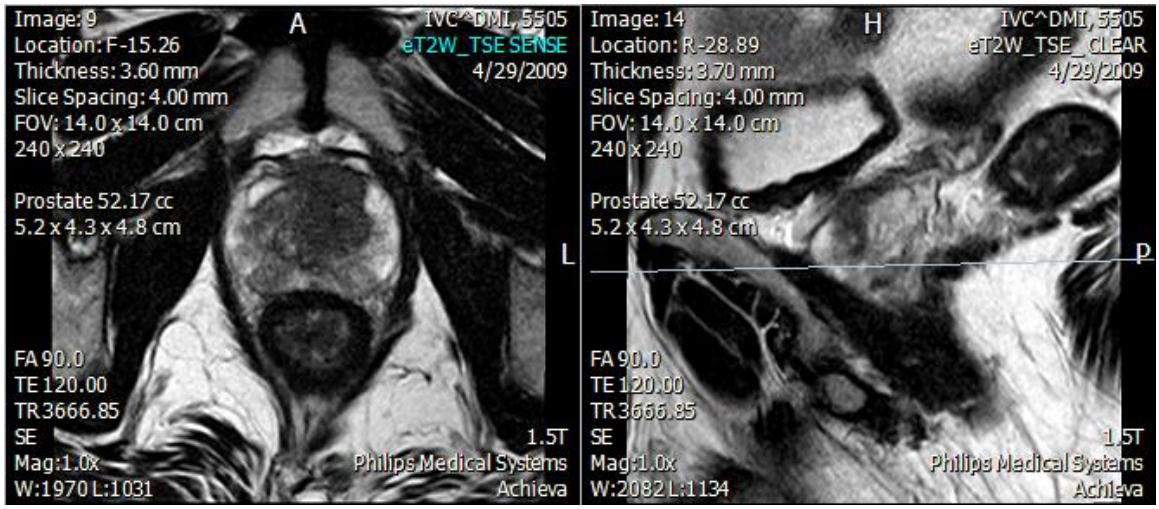


When there are multiple studies loaded, it is important for the user to be able to visually distinguish the specific study they manually selected from the Study Manager from the other

studies of the same patient, e.g. priors. The selected stud(ies) will have the text in white color whereas the non-selected ones will have the text overlay appears in **beige**.

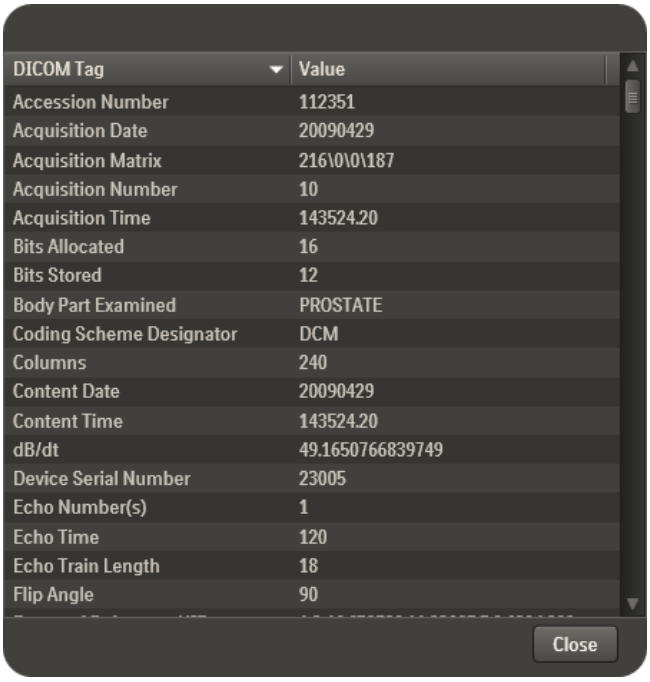


For prostate study, the series that is referenced by the prostate boundary, i.e. the series from which the prostate boundary is based on, will have the Series Description displayed in **cyan** color.



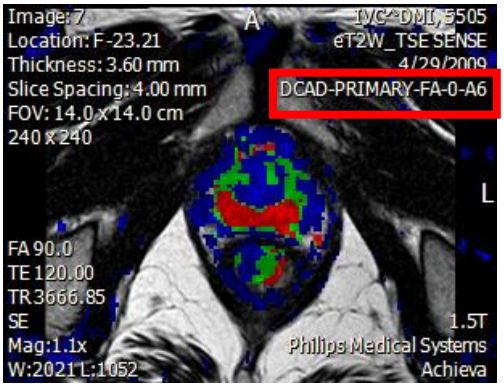
6.6.2 Image Information

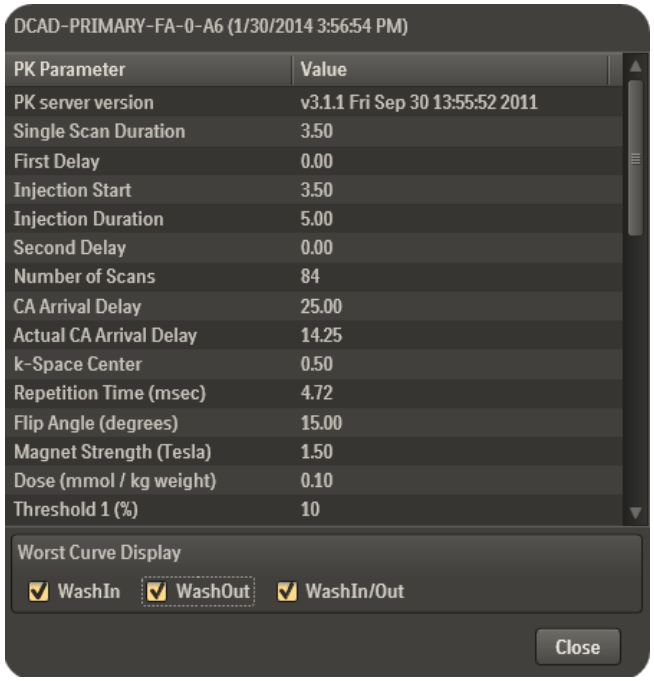
Information about an image displayed in a viewport can be displayed by clicking the **Info** button under the **Hangings** tab.



6.6.3 PK Processing Parameters

Sometimes it is useful to review the PK processing parameters, e.g. during initial setup or trouble shooting. To view the PK processing parameters, apply one of the PK data as color overlay and right click the **DCAD** Series Description in the upper right corner of viewport highlighted in the red box below.





The PK processing parameters will be displayed in a pop-up window. In the bottom pane of the window, options are available for displaying the different worst curves for a ROI:

Worst WashIn: The voxel within the selected ROI passing the thresholds that has the largest percent enhancement between the baseline and phase1.

Worst WashOut: The voxel within the selected ROI passing the thresholds that has the largest washout between phase1 and the last dynamic phase.

Worst WashIn/Out: The voxel within the selected ROI passing the thresholds that has the largest product of WashIn and WashOut percent enhancements.

Where “phase1” is: for breast - the dynamic phase closest to the 90sec post contrast arrival dynamic phase; for prostate - the dynamic phase closest to the 45 sec post contrast arrival dynamic phase; for other – closest to the “Peak Time (in seconds)” post contrast arrival dynamic phase.

6.7 Color Overlay

The main categories for color overlay are pharmacokinetic (K^{trans} ,V_e, K_{ep}), iAUGC, T10, QuickTP and Fusion (ADC, DWI).

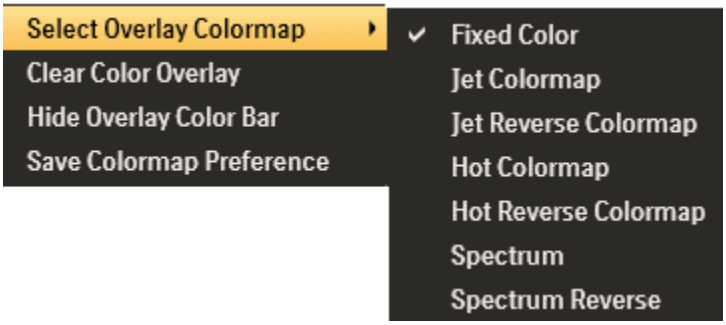
6.7.1 PK, iAUGC, T10 Color Overlays

PK Color overlays can be enabled or disabled by selecting **Color Overlay** or **Clear Color Overlay** in the drop down menu. In addition, the color bar can be enabled or disabled by selecting **Show Overlay Color Bar** or **Hide Overlay color Bar**. PK results based on motion corrected series will have an MC appended to the name of the series, for example: *DCAD-MC-Primary*.

Moving the mouse over the **Color** choice opens a pop-out menu from which you can select from the available PK data as overlay.

PK, iAUGC and T10 are setup and pre-processed by the MR Analysis software before being available for display in the DynaCAD Viewer. Please refer to the DynaCAD Server manual for setup.

Right clicking the color bar provides several options to the user; most notably, it allows them to choose one of the colormap presets.. Saving colormap preference allows the same parameters to apply to subsequent studies with the same study and series description.

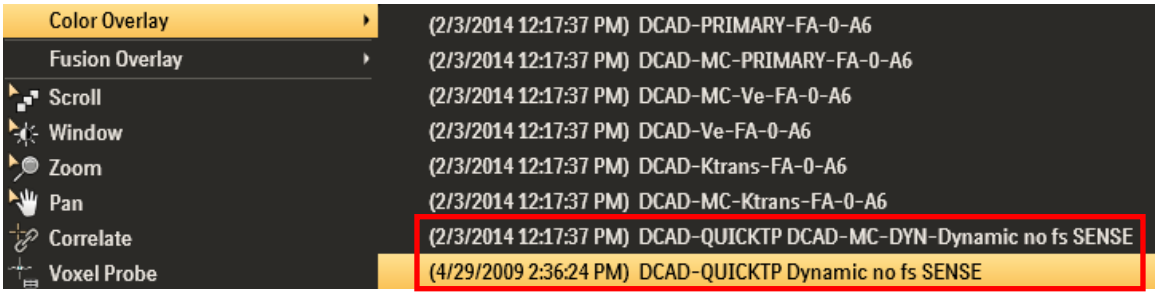


NOTE: *Changing the colormap does not apply to the Primary PK color map.*

6.7.2 QuickTP Color Overlay

QuickTP analyzes the early uptake and delayed phase pattern using three time points within a DCE series and creates an associated color overlay series, which can be displayed over any grayscale series.

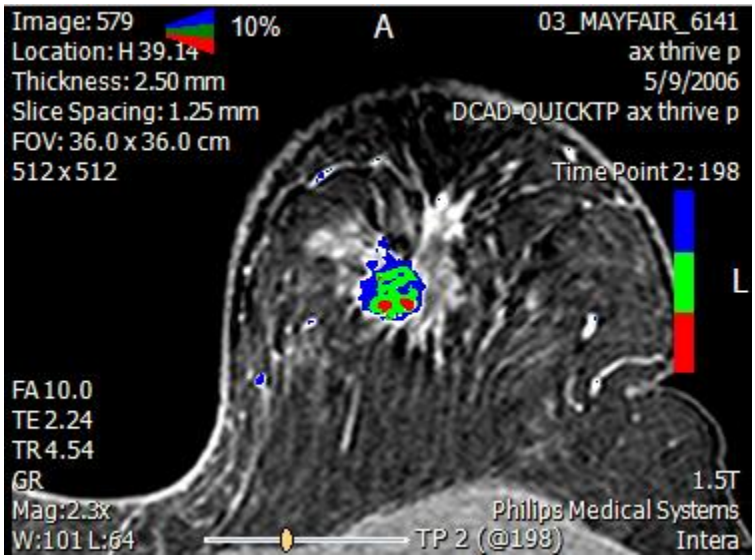
QuickTP Color Overlays are available in the viewer when a series has been categorized as "Dynamic" through the Image Stack Group Filter. Motion corrected DCE is also available for QuickTP processing. From the **Color Overlay** item of the Right Mouse Context Menu, select the corresponding QuickTP item:



The QuickTP data will be superimposed on the image after the user selects it from the list. The QuickTP label is displayed in the upper right hand corner of the viewport to notify users of the dynamic series used to create the QuickTP color overlay.

A color bar can be displayed by selecting **"Show Overlay Color Bar"** on the RMM. Alternatively, this color bar can be displayed by default by enabling the **"Display Overlay Color Bar"** under User Options.

NOTE: *The date associated with the QuickTP color overlay will reflect either the date of the original DCE series or the date when the study was processed in the case of motion correction.*

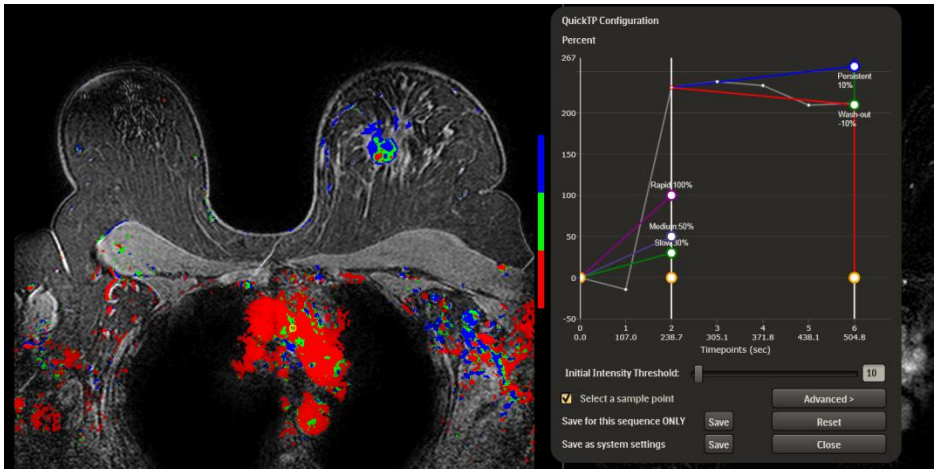


QuickTP Configuration

A QuickTP Configuration window is displayed when the user right clicks the QuickTP label displayed in the upper right hand corner of the viewport. This window provides maximum control of the color overlay display including the ability to choose the desired time points for QuickTP analysis, as well as configuring the delay\washout characteristics. The **"Advanced"** button provides noise removal options in addition to the common QuickTP configuration settings described below. The **"Save"** buttons will only save QuickTP parameters for this sequence alternately it can be saved as system settings, which allows the same parameters to be used on subsequent studies with the same Series Description from the same scanner. The "Reset" button will reset parameters back to the last saved parameters.

NOTE: *The QuickTP Configuration window is designed to help users Configure QuickTP settings and is not meant to evaluate 'hot-spots", which should be accomplished using the Time Curve Chart as well as the QuickTP histogram chart*.

Users can populate the chart with data from the dynamic series by enabling "Select a sample point" on the QuickTP Configuration menu. An orange sample point is dropped in the viewport, which can be dragged to the desired sample voxel location. It is located at the center of the lesion in the screen shot.



Time Point Selection – The vertical time point selection lines are configurable by clicking and dragging the respective orange circles on the X-axis.

- **TP0:** Represents the pre-contrast baseline time point for QuickTP Analysis.
- **TP1:** Represents the desired uptake time point.
- **TP2:** Represents the desired delayed time point past TP1.

Initial Intensity Threshold – This represents the initial intensity cut off value at TP0, which is used to identify voxels for colorization. In the provided screen shot, voxels with an intensity of 0 or less are excluded from QuickTP Analysis because they are not bright enough in the baseline time point. The grey line represents the intensity of the Sample Time Point.

***NOTE**: Voxels that have intensity smaller than the Initial Intensity Threshold are excluded from QuickTP processing.*

Uptake Percentage Thresholds – The slanted Minimum, Medium, and Rapid lines connecting TP0 and TP1 are configurable by clicking the respective circle and raising\lowering the threshold.

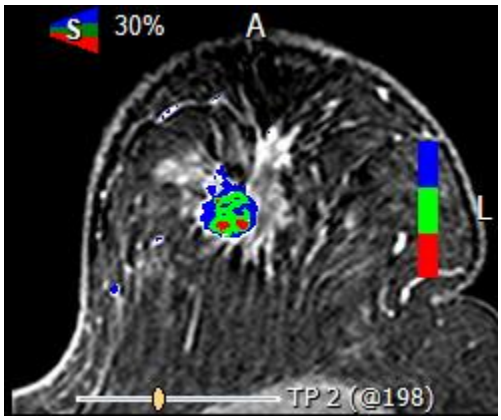
The Minimum Uptake Percentage Threshold is used to identify the voxels that are considered for colorization based on their uptake between TP0 and TP1. The Medium and Rapid settings help to categorize voxel's contrast uptake behavior and do not influence coloring.

- **The "Slow" Line:** Represents the minimum contrast uptake of a voxel between TP0 and TP1 that is considered for colorization. Voxels that fall below this uptake threshold are excluded from QuickTP Analysis.
- **The "Medium" Line:** This setting is used only to categorize voxel's contrast uptake and does not influence color overlay. Voxels with an uptake % between the "Minimum" and up to the "Medium" setting are considered to have "Slow" uptake.
- **The "Rapid" Line:** This setting is used only to categorize voxel's contrast uptake and does not influence color overlay. Voxels with an uptake % from the "Medium"

setting up to the “Rapid” setting are considered to have “Medium” uptake characteristics. Voxels with an uptake threshold greater than the “Rapid” setting are considered to have “Rapid” uptake.

NOTE: *If the voxel washes out below the baseline it is considered noise and excluded from processing (i.e. intensity at TP2<=TP0).*

Users can choose the color display of voxels in uptake groups by clicking the “S, M, and R” button within QuickTP viewport: when “S” is selected, all the voxels passing the Minimum Uptake Threshold will be shown in the overlay, when “M” is selected, only voxels with Medium and Rapid behavior will be shown in the overlay, and when “R” is selected, only voxels with Rapid uptake will be displayed in color.



Delayed Phase Percentage Thresholds – Are represented by the slanted Blue Persistent and Red Washout lines connecting the uptake TP1 point to the selected delayed phase TP2. Each respective setting is configurable by clicking the circle and raising\lowering the threshold.

The Delayed Percentage Threshold settings are used to define the color of a colorized voxel.

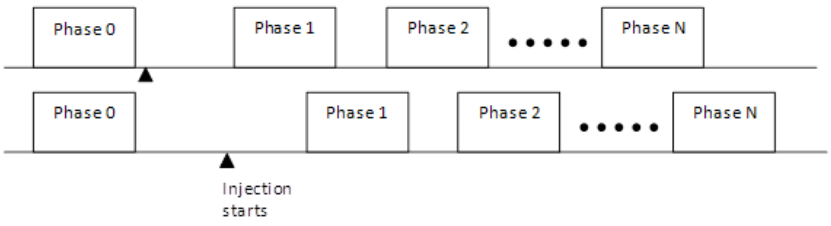
- **Persistent Threshold:** The voxels with persistent enhancement pattern above the specified threshold between time points TP1 and TP2 will be colored Blue (for RGB and RYB colormaps) or the corresponding color range depending on the other Colormap choices.
- **Between Persistent & Washout Thresholds:** Represent voxels with “Plateau” behavior. These will be colored Green (if RGB colormap if chosen) or Yellow (if RYB) or the corresponding color range depending on the other Colormap choices.
- **Washout Threshold:** The voxels with washout/decline pattern above the specified threshold between time points TP1 and TP2 will be colored Red (for RGB and RYB colormaps) or the corresponding color range depending on the other Colormap choices.

The **“Advanced”** button provides noise removal options in addition to the common QuickTP Configuration settings described above.

Time Points

- **Use Phases:** Selecting this option allows choosing which time point to use for TP0, TP1 and TP2. Selecting the time points from this page or the QuickTP configuration page will update the parameters for both pages.

  The Use Phase option can be used for any acquisition, and it is the recommended option when the injection start from the beginning of the DCE sequence varies and/ or there are no two consecutive dynamic phases without a time gap in between. For example, it will work in both of the cases below that it is the same type of acquisition, but the timing is different, e.g. different injection start time.

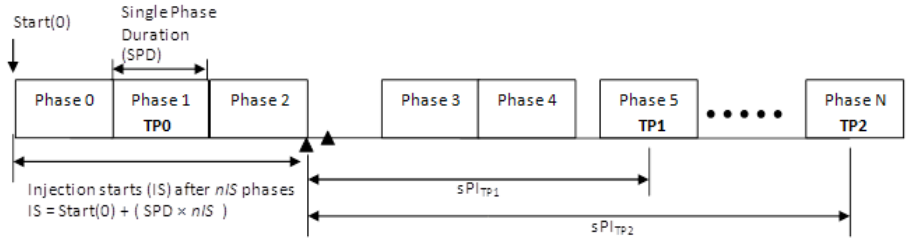


- **Use Time – Post Injection:** Selecting this option allows the Post Injection time and the Injection Start phase or time to be specified. It is used for acquisitions where the injection start is always fixed with regards to the beginning of the DCE sequence, or where there are the same amount of pre-contrast phases, and there are at least two consecutive dynamic phases without a gap.

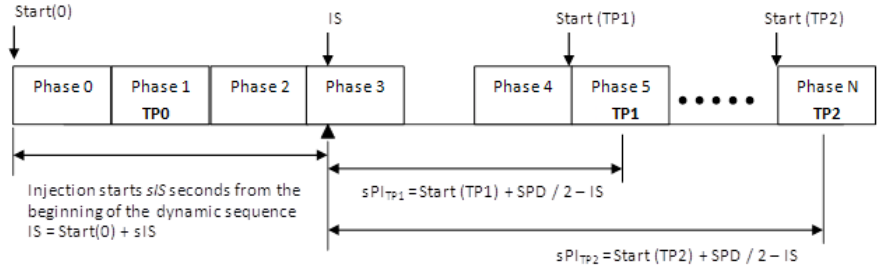
  - TP0 is specified by the phase index.

- PITP1 and PITP2 are the Post Injection time of the TP1 and TP2 measured from the Injection Start (IS) time to the center of the TP1 and TP2 phase correspondingly.

- The Injection Phase Number (nIS) or the Injection Time (sIS) are specified to define the Injection Start (IS) time. They are respectively represented in a) and b) on the diagram below which allows choosing which time point to use for TP0, TP1. Selecting the time points from this page or the QuickTP configuration page will update the parameters for both pages.



a) Injection Phase Number is specified



b) Injection Time is specified

A. The center of a phase is defined as the Start time (from DICOM header) plus the Single Phase Duration (SPD)

   - When the Injection Phase Number (nIS) is specified, the following is to determine the TP1 and TP2

   - Injection Start IS = Start Time at Phase 0 + (Single Phase Duration × Injection Phase Count)

   - TP1 is defined as the center of a phase that is closest to the IS + Post Injection Time of TP1.

   Start (TP1) = IS + sPITP1 – SPD / 2

   Same applies to TP2

B. When the Injection Time (sIS) is specified, the following is to determine the TP1 and TP2

   - Injection Start IS = Start Time at Phase 0 + Injection Start Time sIS

- TP1 and TP2 are defined using the same formula as the above case for the Injection Phase Count is specified.

Uptake Threshold In Percent Enhancement

- **Current:** Specifies the current displayed threshold in an active viewport. The values can be modified by moving the horizontal bar or typing in the specific value to the right of the bar. The value can also be changed in the viewport.
- **Slow:** Specifies the current set threshold for the “Slow” enhancement setting which can see in an active viewport. The values can be modified by moving the horizontal bar or typing in the specific value to the right of the bar. The value can also be changed by dragging the “Slow” circle on the QuickTP configuration page. The values will only increase or decrease by 5.
- **Medium:** Specifies the current set threshold for the “Medium” enhancement setting which can see in an active viewport. The values can be modified by moving the horizontal bar or typing in the specific value to the right of the bar. The value can also be changed by dragging the “Medium” circle on the QuickTP configuration page. The values will only increase or decrease by 5.
- **Rapid:** Specifies the current set threshold for the “Rapid” enhancement setting which can see in an active viewport. The values can be modified by moving the horizontal bar or typing in the specific value to the right of the bar. The value can also be changed by dragging the “Rapid” circle on the QuickTP configuration page. The values will only increase or decrease by 5.

Delayed Phase Threshold in Percent Enhancement

- **Persistent:** Specifies the current set threshold for the “Persistent” delayed phase enhancement setting which determines what voxels are colored blue in a color overlay. The values can be modified by moving the horizontal bar or typing in the specific value to the right of the bar. The value can also be changed by dragging the “Persistent” circle on the QuickTP configuration page.
- **Wash-out:** Specifies the current set threshold for the “Wash-out” delayed phase enhancement setting which determines what voxels are colored red in a color overlay. The values can be modified by moving the horizontal bar or typing in the specific value to the right of the bar. The value can also be changed by dragging the “Wash-out” circle on the QuickTP configuration page.

Subtraction Intensity Threshold

Subtraction refers to the absolute value of the difference between voxels at TP0 and TP1. Voxels are not considered for colorization if their value in the subtraction calculation is less than the subtraction intensity threshold.

- **Intensity Threshold:** Voxels are not considered for colorization if their value in the subtraction series is less than the subtraction intensity threshold. Saving the QuickTP configuration stores the pre intensity threshold factor and pre subsampling factor, which are used to calculate the subtraction intensity threshold for each

dynamic sequence during subsequent loading. When the application classifies a dynamic series for the first time it will automatically estimate a value for the subtraction intensity threshold using a histogram of the subtraction series. Users can manually adjust the subtraction intensity threshold using the slide bar, or by updating the Pre Intensity Threshold Factor.

- **Pre Intensity Threshold Factor:** This multiplier is used when automatically determining a subtraction intensity threshold using the formula:
- **Subtraction Intensity Threshold:** Average (subtraction histogram) + Pre Intensity Threshold Factor * standard deviation (subtraction histogram)
- **Pre Subsampling factor:** Refers to the down-sampling factor of the input data for the estimation of the subtraction intensity threshold. Increasing the factor allows for faster computations but a less accurate calculation of the subtraction intensity threshold.

Spatial Noise Filtering

The “Noise Filtering” option can be enabled to reduce the amount of noise in the color overlay result. When this option is enabled, each time point that is selected for analysis is processed using a median filter. The grey-level voxel values from each select time point are then replaced by the median of the grey-level values in a neighborhood (window). Users can choose between 3x3, 5x5, and 7x7 window sizes as well as two dimensional and three dimensional filtering.

Worst Curve Display

These options allow users to select which worst curve will be identified and displayed when an ROI is drawn. Checking the box will configure the system to display the type of worst curve to display. The following are definitions of the various choices for worst curve:

- **Worst WashIn:** The voxel within the selected ROI passing the thresholds that has the largest percent enhancement between TP0 and TP1.
- **Worst WashOut:** The voxel within the selected ROI passing the thresholds that has the largest washout between TP1 and TP2.
- **Worst WashIn/Out:** The voxel within the selected ROI passing the thresholds that has the largest product of WashIn and WashOut percent enhancements.

6.7.3 ONCAD Color Overlay

ONCAD is an optional product provided by Invivo Corporation. Please refer to the document “Information for Use Invivo Clinical Solutions Products” (p/n 4535-303-12111).

Workflow

In the standard configuration, incoming cases are automatically pre-processed and forwarded to ONCAD for analysis based on the DynaCAD Server processing configuration

(see DynaCAD MR Analysis Server Application Guide DTM126). Breast cases that include DCE images with at least four time points qualify for ONCAD analysis. During this analysis process, ONCAD processing times may vary and primarily depend on the number of spatial slices in the dynamic sequence, the volume of studies performed at your site, and the processing capabilities of the network and ONCAD Server. Upon completion, the ONCAD analysis results will be sent back to the DynaCAD system for display.

Checking ONCAD Results

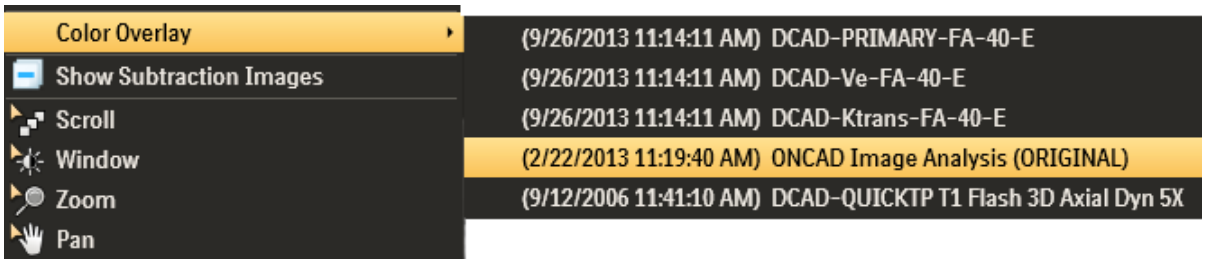
Since the ONCAD analysis takes place after the study first arrives at the DynaCAD workstation, look for the following visual cue to verify that the ONCAD analysis has completed.

Consult the Study Manager to verify that the ONCAD results have been attached to the original study. This can be done by checking the Series List of the Study Manager; the Series Description is *ONCAD Image Analysis*.

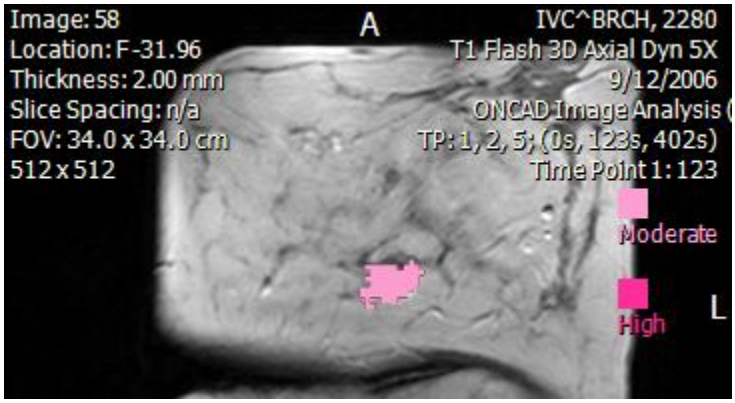
Series Description	Series #	Modality	# Images
rt sag	10	MR	39
lt sag	11	MR	39
ONCAD Image Analysis (ORIGINAL)	1500	MR	80
DCAD-Ktrans-FA-40-E	30009	MR	80
DCAD-Ve-FA-40-E	30011	MR	80

Apply ONCAD Color Overlay

To apply the ONCAD overlay to a viewport display the DCE series, select the ONCAD data from the Right Mouse Context Menu as shown below.



The selected ONCAD data will be applied as a color overlay:

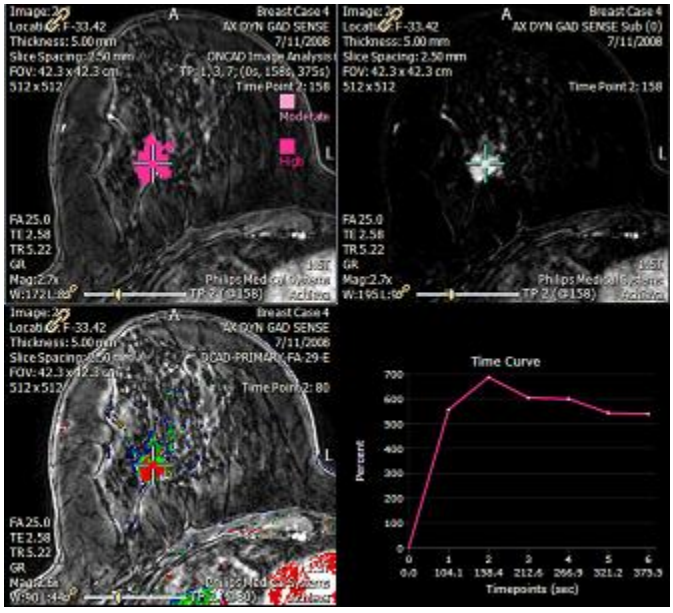


NOTE: *The ONCAD colors have been chosen to minimize confusion with the DynaCAD display of kinetic parametric analysis..*

For each detected mass, ONCAD calculates a “blooming” parametric value in the range 0 to 25; higher values correspond to higher degrees of blooming. The parametric color overlay shows both the magnitude of the blooming value and the distribution of the lesion that exhibits positive blooming.

ONCAD Colorization	
7-9	Moderate
10-25	High

DynaCAD can be configured to automatically display the ONCAD overlay as part of the Hanging Protocol when the case is opened in the viewer. Below shows a sample 2x2 hanging with ONCAD color overlay displayed in the top left viewport.

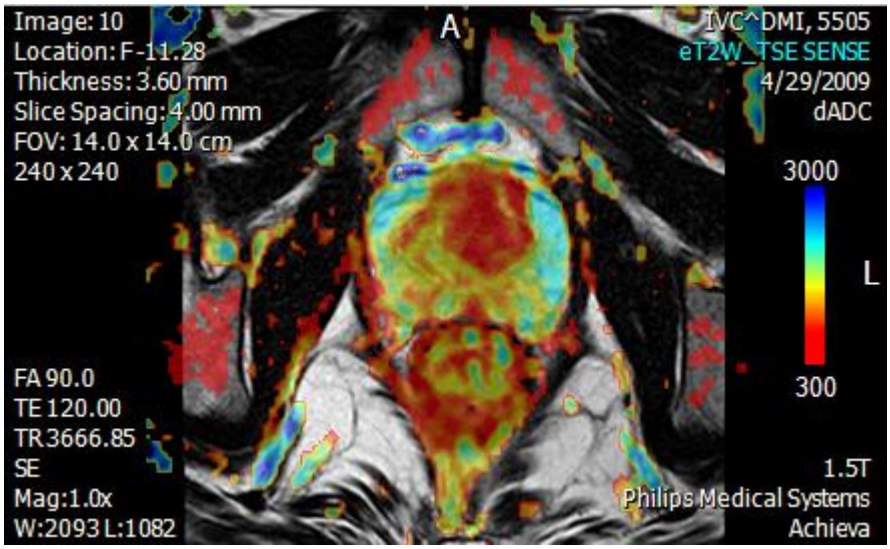


6.7.4 Fusion Color Overlays

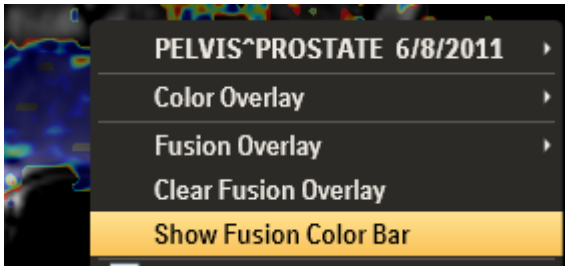
Fusion Color overlay options superimpose a ADC or DWI data onto any grayscale series as color overlay. This provides clinicians with a simple way to correlate “hot” spots found in ADC\ DWI imagery with the associated contrast uptake or structural information found in the DCE or T2 weighted imagery.

Color Fusion Overlays are available in the viewer when a series has been categorized as “ADC” or “Diffusion” through the Image Stack Group Filter. The Right Mouse Context Menu provides access to the available fusion overlays. A submenu is available for choosing different B-value data of the DWI.

The color fusion overlay is displayed in the viewport after the user selects the desired overlay. The ADC or DWI Series Description is displayed in the upper right hand corner of the viewport to notify users of the color overlay display.



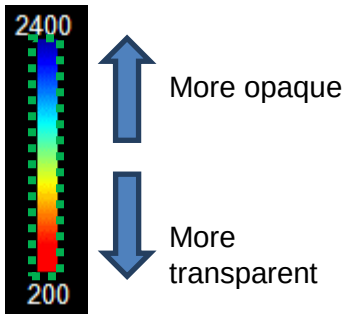
A color bar can be enabled or disabled by selecting **Show Fusion Color Bar** or **Clear Fusion Overlay** on the RMM. Alternatively, this color bar can be displayed by default by enabling the **Display Fusion Color Bar** under user options.



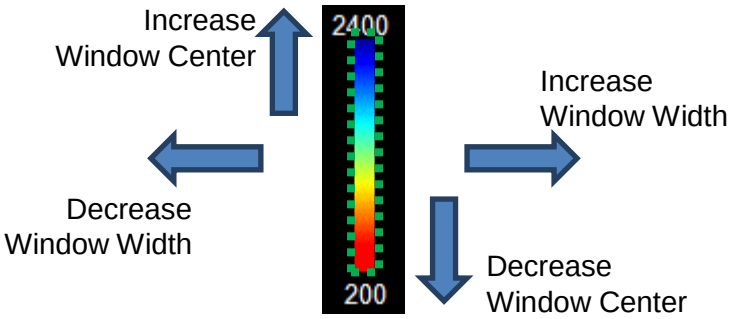
Interactive Control

Transparency, Window Center and Width and Threshold Min/ Max can be adjusted directly within the color bar displayed in the viewport.

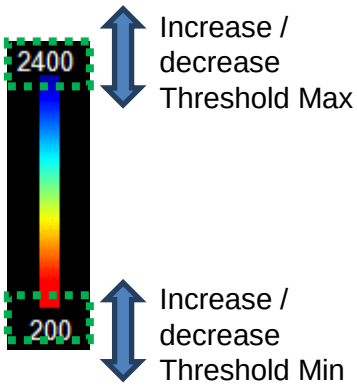
Transparency: Left mouse click and drag on the color bar changes the transparency (Blending) of the overlay. Left click and drag downwards within the color bar (dotted green box below) makes the overlay more transparent, upwards makes it more opaque.



Windowing Center and Width: The Windowing Center and Width can be controlled without using the Fusion Configuration dialog. With the Color bar displayed in the viewport, middle mouse click and drag within the color bar (dotted green box below) will modify the Center (vertical motion) and Width (horizontal motion).



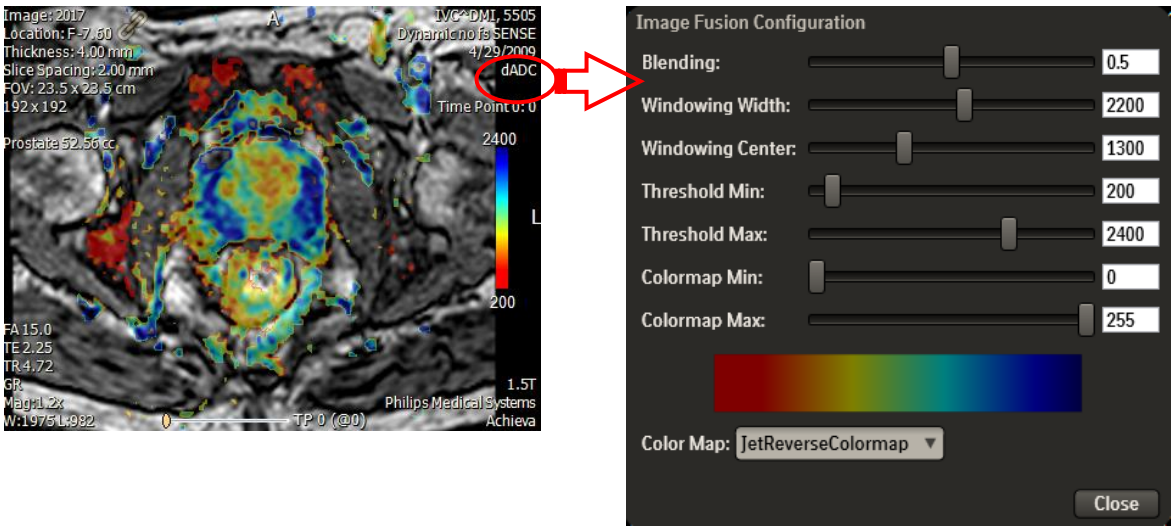
Threshold Min and Max: The number below and above the color bar (see picture below) represents the Threshold Min and Max respectively. They can be modified by moving the mouse cursor to the number (dotted green box below) and then left click and drag. The value increases if the mouse drags upwards, it decreases if the mouse drags downwards.



There are a number of built-in colormaps that can be applied to the color overlay. The available list is available by right clicking on the colorbar. The menu will be display as below:

Configuration Dialog

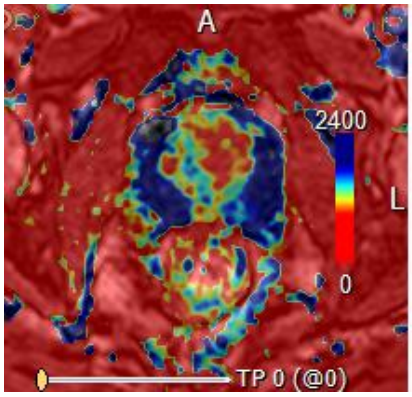
The Fusion Configuration dialog exposes a number of controls to allow the Fusion parameters to be changed interactively. The dialog can be displayed by right mouse click on the Fusion overlay label on displayed on the top right corner of the viewport.



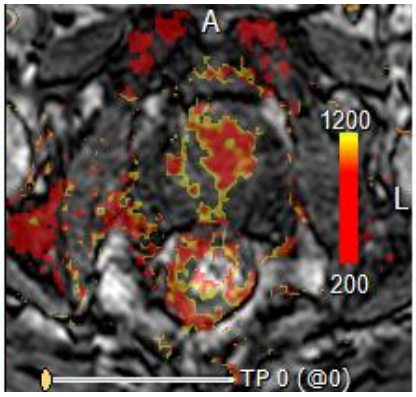
Step 1: Threshold Min and Max

The Threshold Min and Max controls the range of ADC values that will be colorized. Voxels lower than the Threshold Min and higher than the Threshold Max will be excluded in the color overlay. Tuning the Min and Max should allow you to exclude the background, allowing the prostate to be colorized. Care should be taken to set the Threshold Min; setting it too high may exclude the low ADC values that will be of interest. Note: use Voxel Probe to interrogate the ADC value.

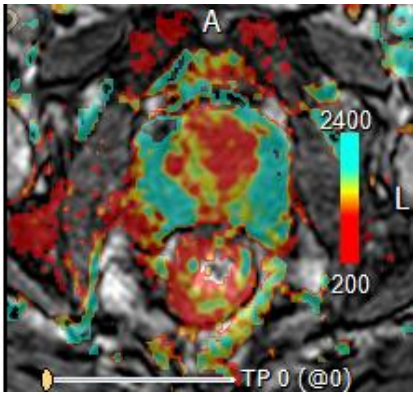
For example:



Threshold Min too low, the background is colorized



Threshold Max too low, prostate is not colorized properly



Reasonable Threshold Min and Max to allow prostate to be colorized

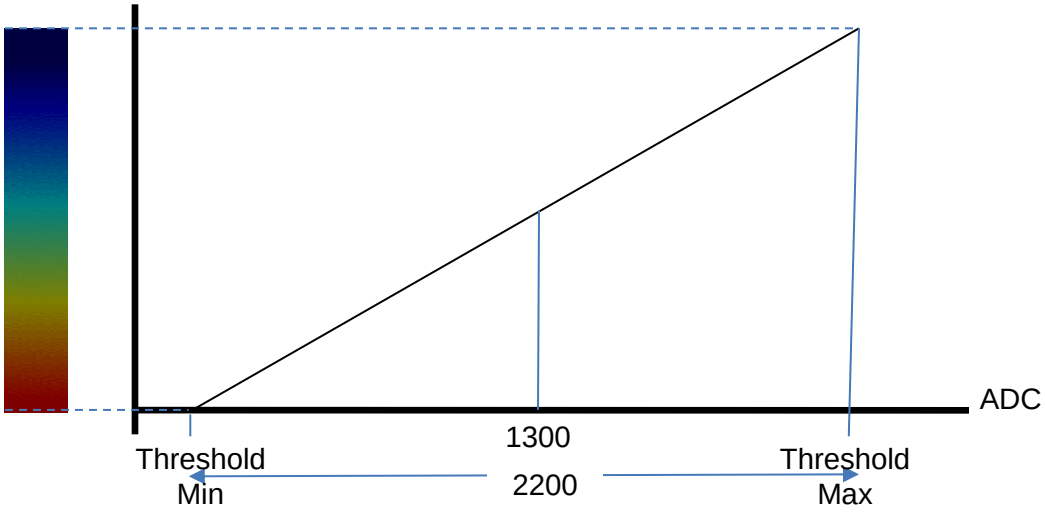
Step 2: Windowing Width and Center

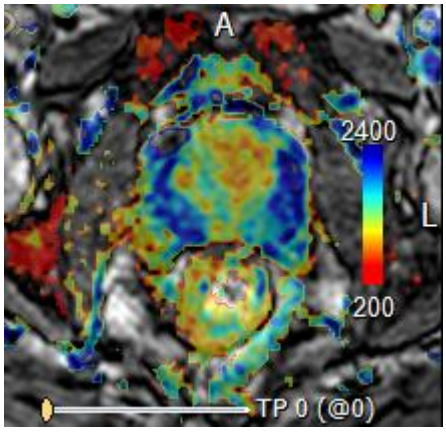
The Colormap Windowing Width and Center map the chosen ADC range, i.e. between Threshold Min and Max, to the colormap scale [0, 255]. To map the chosen ADC range to the full colormap scale:

Windowing Center = Threshold Min + (Threshold Max – Min) / 2

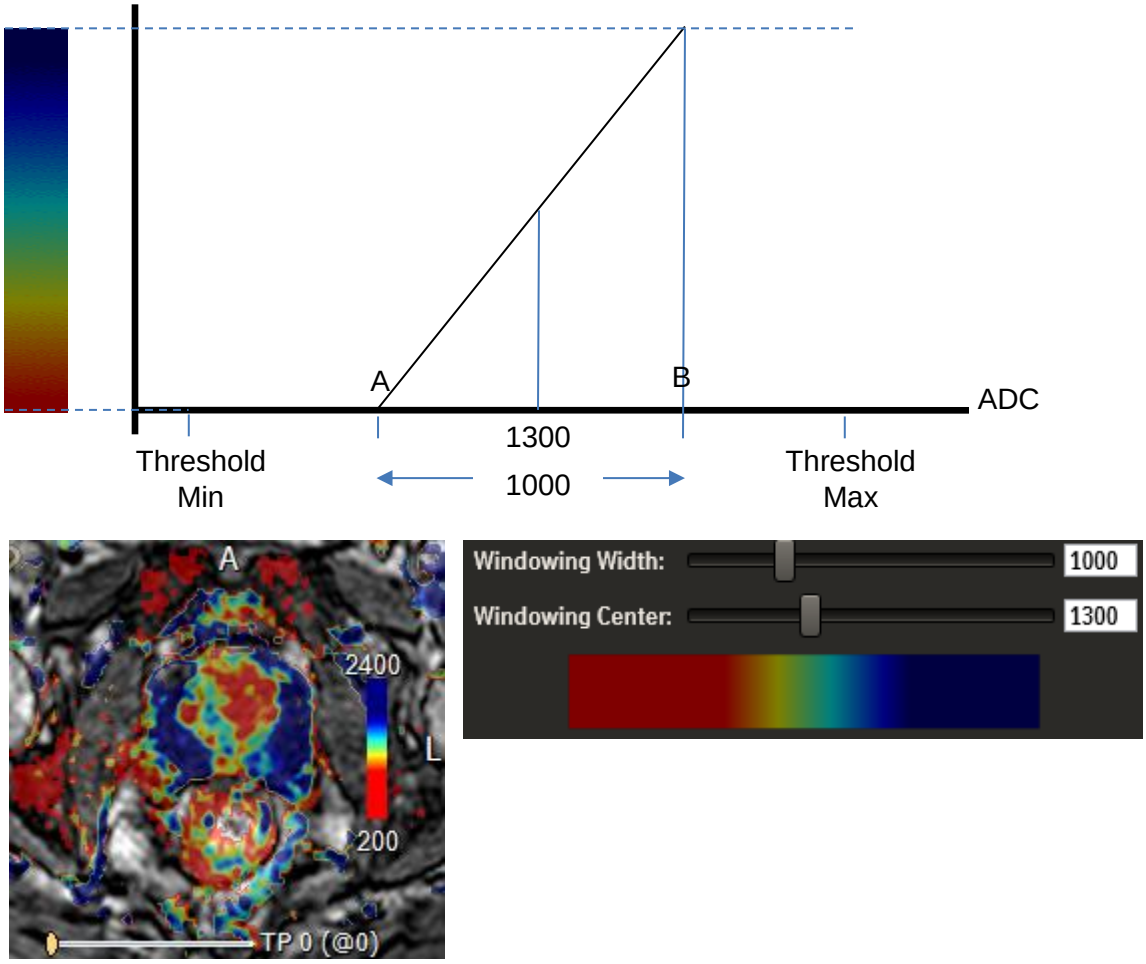
Windowing Width = Threshold Max – Min

In the above example that the Threshold Min and Max are 200 and 2400 respectively, the Window Center and Width can be set to 1300 and 1200. The full colormap will be used as shown below.



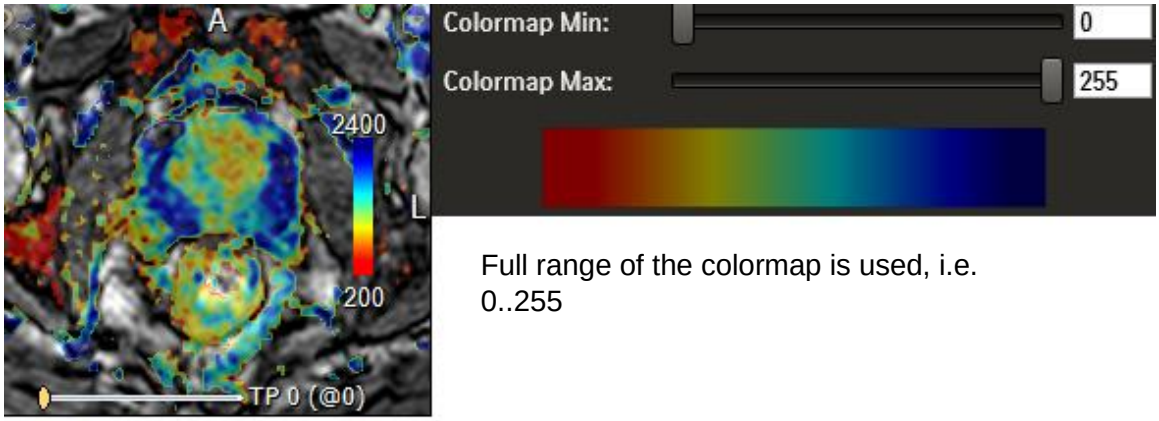


If the width is reduced from 2200 to, say, 1000, voxels with ADC values between the Threshold Min and point ‘A’ (see picture below) will be mapped to the first color of the colormap, i.e. Red in the example colormap. Similarly, voxels values between point ‘B’ and the Threshold Max will be mapped to the last color of the colormap.

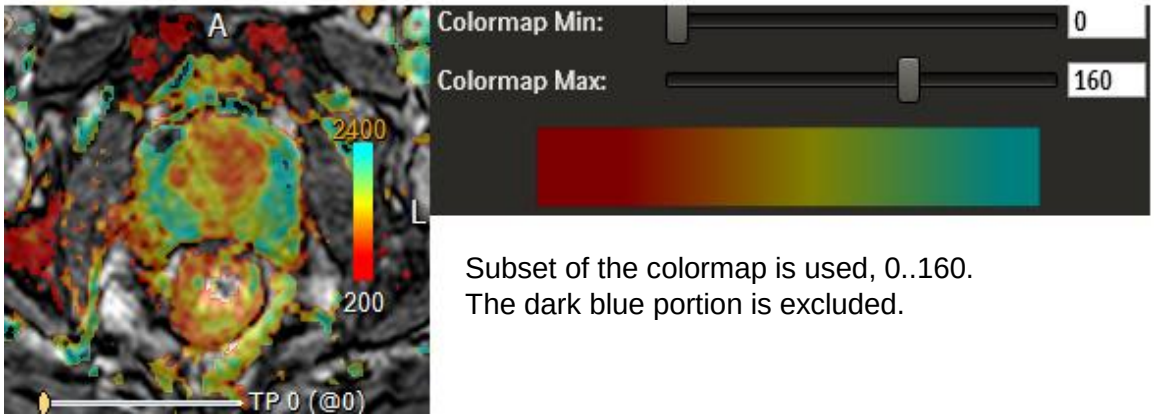


Step 3: Colormap Min and Max

If the user prefer to use only a subset of the color, e.g. only red to green, then the Colormap Min and Max can be used to scratch and move the colormap. For example, if the user doesn't want to use the blue portion of the colormap, then Colormap Max can be lowered:



Full range of the colormap is used, i.e. 0..255



Subset of the colormap is used, 0..160. The dark blue portion is excluded.

Note that the same voxels, i.e. ADC values between Threshold Min and Max (as seen in the numbers in the bottom and top of the in-viewport color bar), are colorized in the example above. They are mapped to different color based on the colormap settings.

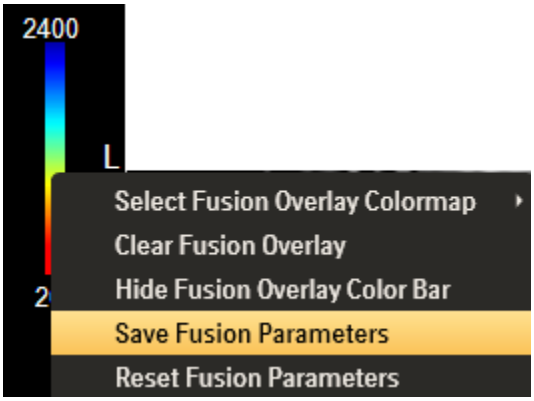
Step 4: Blending

Blending controls the transparency of the color overlay. It ranges from 0.0 to 1.0. 0.0 is transparent and 1.0 is opaque

Saving Fusion Parameters

After the fusion overlay is configured, it has to be saved to so that the new setting will be applied in subsequent application of the same type of ADC, i.e. same Series Description from the same scanner. It is important to use multiple datasets to ensure the configuration setting is optimal and the color overlay appears as expected in the representable datasets, than tuning it based on one dataset.

To save the setting, right mouse click on the color bar, and select “Save Fusion Parameters”.

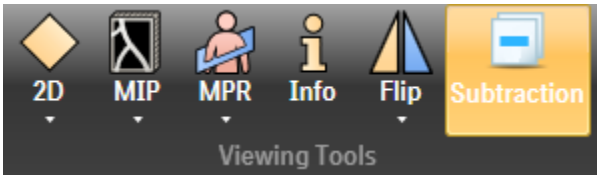


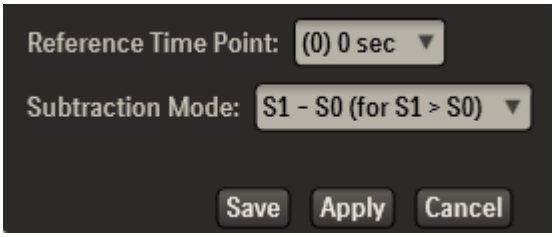
If there are more than one type of ADC series, and/or there are multiple scanners, each ADC series will need to be configured and saved.

6.8 Image Subtraction

DCE images can be converted on-the-fly to a subtraction series by left clicking on the Subtraction button under the **Hangings** tab of the application toolbar or the **Show Subtraction Images** of the Right Mouse Context Menu... This will convert the DCE images displayed in the active viewport to a subtraction series.

The subtraction time points can be configured by right clicking the **Subtraction** button under the **Hanging** tab of the application toolbar.





From the **Reference Time Point** dropdown, select the desirable time point.

Baseline averaging is a pre-processing step in the PK analysis. If configured in the Profile Editor, it will create a baseline series with Series Description *DCAD-BLA-...*. If it is available, then it will be used as the baseline for subtraction, and the **Reference Time Point** setting in the Subtraction dialog will be ignored.

If the DCE temporal slider is set to time point zero the display will look very black because the conversion is subtracting the zero time point from each other. Moving the temporal slider bar to another time point will use that time point to subtract from the baseline time point.

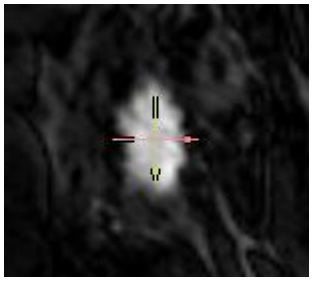
6.9 Image Scrolling

To scroll images displayed in a 2D or MPR (axial, coronal or sagittal) viewport, do one of the following:

- Position the mouse in the image viewport and left-click to make the viewport active. Then scroll thru the images by scrolling the middle mouse wheel.
- Position the mouse in the image viewport and left-click to make the viewport active. Then scroll thru the images by using the up/down keyboard arrows.
- Select **Scroll** from the Right Mouse Context Menu. Then scroll through the images by pressing and holding the left mouse button and moving the mouse up and down. This action will move the image much faster but will not display every image as it scrolls through the slices.

6.10 Rotating and Scrolling Oblique MPR Images

Oblique MPR allow the MPR plane to be rotated interactively. To rotate the plane, the center of rotation should be optimally set, e.g. on the lesion, so that the Oblique MPR plane will be rotated about the region of interest. After selecting **Scroll** from the Right Mouse Context Menu, press and hold the CTRL button, a cross hair representing the rotation pivot will be displayed in the viewport. Drag the cross hair to the desirable location. The center of rotation will be set.

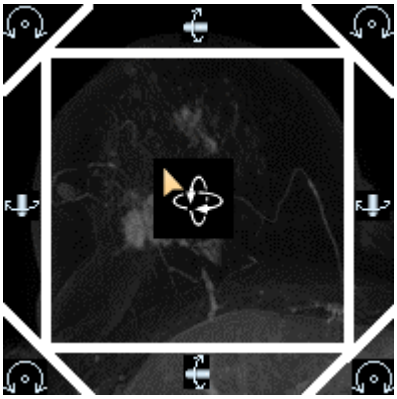


Rotate the Oblique MPR plane can be done by left click and drag.

Oblique MPR can be scrolled by scrolling the mouse wheel. This will move the image perpendicular to the oblique plane.

6.11 Rotating 3D Images

3D rendering allows the user to freely rotate the image in any direction to obtain the desirable view. To allow the user to control the view angle easily, the 3D viewport is divided into different regions.



Once you move the mouse outside the established limits, the cursor changes to a shape indicating the type of rotation possible at the current mouse location.

Cursor	Indicates
	Freeform rotation in any direction
	Horizontal rotation around a vertical axis
	Up/down rotation around a horizontal axis.
	Rotation about the image plane

NOTE: *Rotation boundaries vary according to the image being displayed. In some cases you may be able to rotate the image freely at any cursor location.*

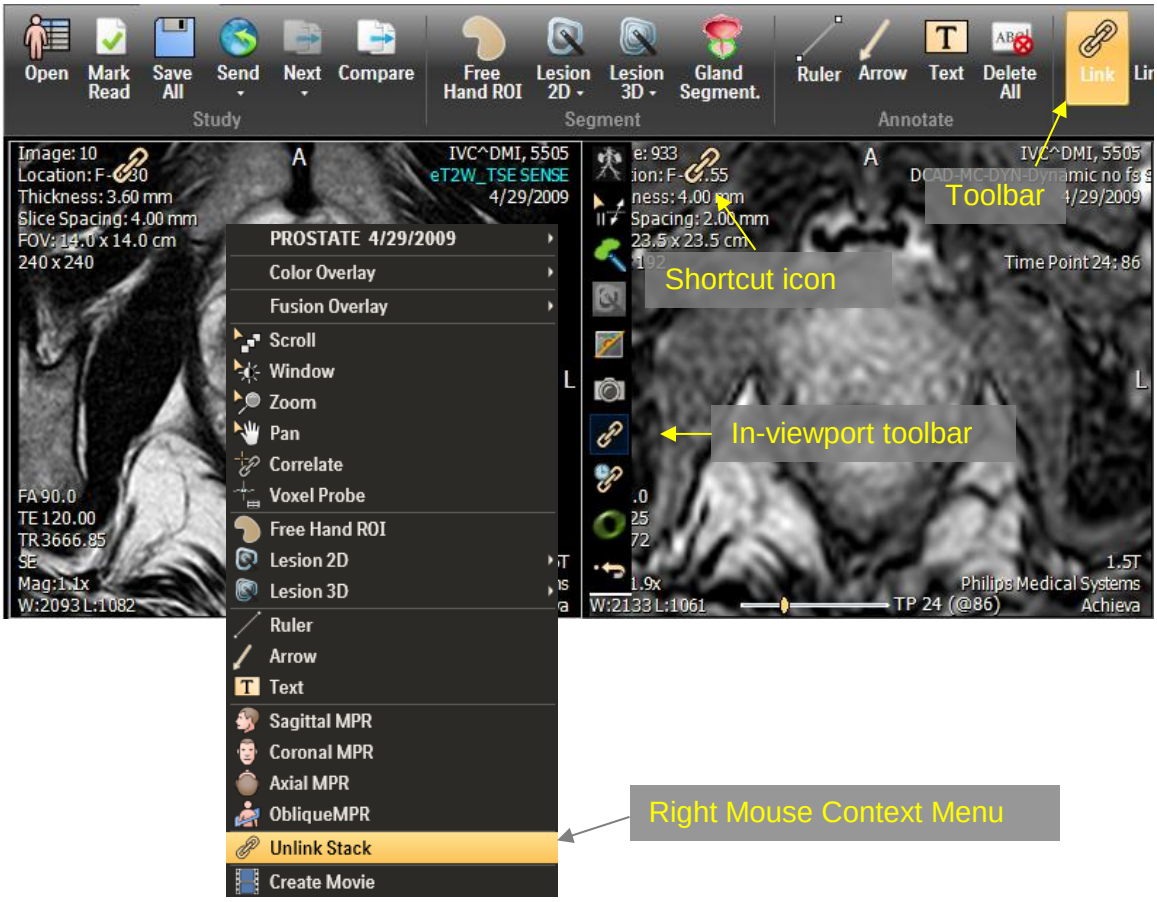
6.12 Window Level/Width, Zoom and Pan

These functions can be enabled by selecting the function in the Right Mouse Context Menu. Once selected, click and drag the left mouse button to adjust the corresponding settings interactively.

6.13 Linking

6.13.1 Spatial Linking

Spatial series of the same study can be spatially linked so that they can be scrolled, zoomed or panned together. The linking can be activated using the **Link** button from the application toolbar, viewport shortcut icon, in-viewport toolbar or the Right Mouse Context Menu.



Toolbar: Click on the **Link** toolbar button to link/ unlink all viewports. When it is highlighted, all spatial series of the same study currently displayed are linked.

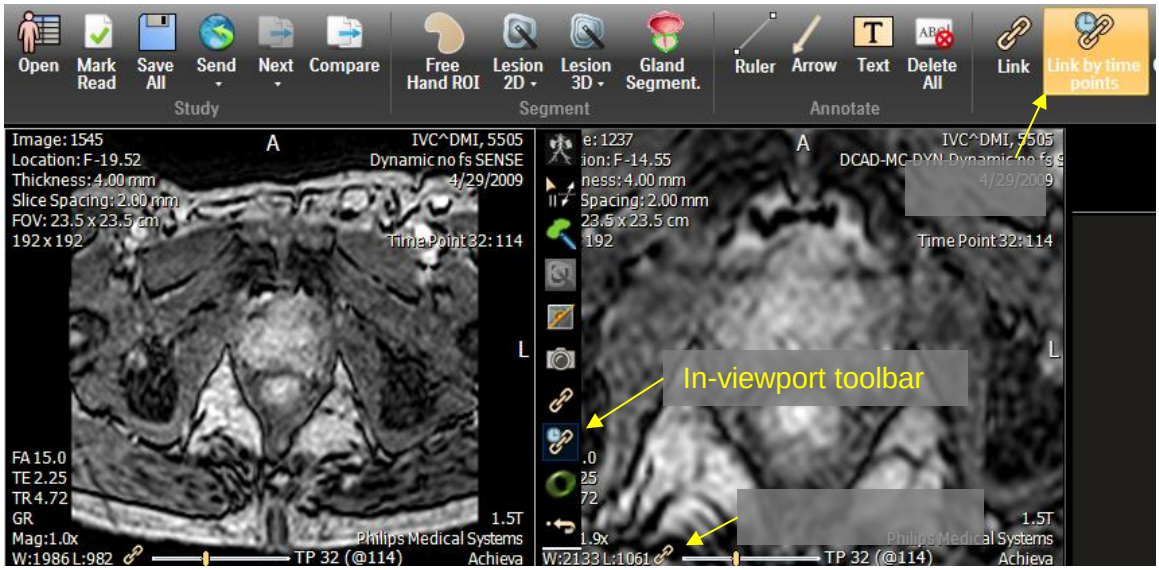
Shortcut icon: Click on the Link icon to link/ unlink the series displayed in the current viewport.

In-viewport toolbar: Click on the Link button to link/ unlink all viewports.

Right Mouse Context Menu: Click on the **Link/ Unlink Stack** menu item to link/ unlink all viewports.

6.13.2 Temporal Linking

DCE series, including motion corrected and subtraction DCE series, of the same study can be temporally linked so that the same time phase is displayed automatically when the user scrolls through the time sequence. The linking can be activated using the **Link by time points** button from the application toolbar, viewport shortcut icon, or in-viewport toolbar.



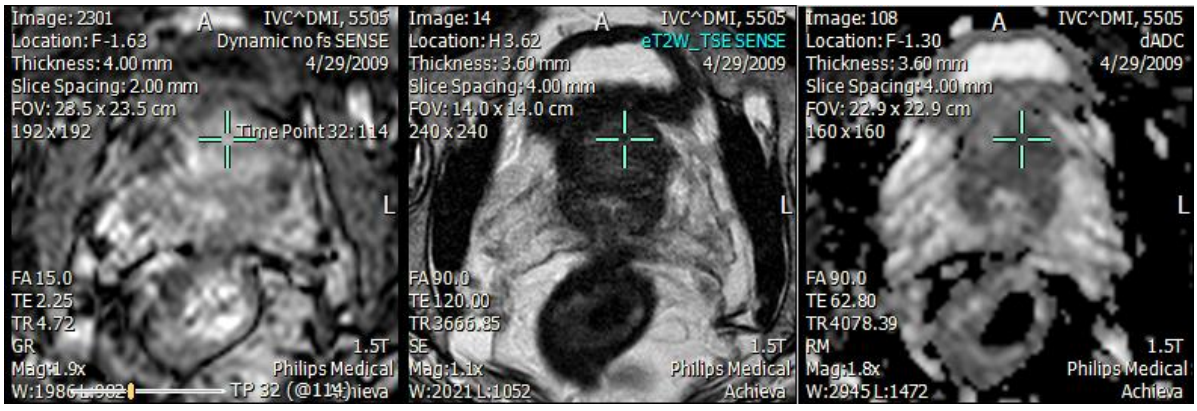
Toolbar: Click on the **Link by time points** toolbar button to link/ unlink all viewports. When it is highlighted, all time series of the same study currently displayed are linked.

Shortcut icon: Click on the **Link** icon besides the temporal slider to link/ unlink the time series displayed in the current viewport.

In-viewport toolbar: Click on the **Link** button to link/ unlink all viewports.

6.14 Correlate

The Correlate function helps the user to correlate between series of the same study by auto-scrolling and displaying a cross hair at the user chosen 3D coordinates.



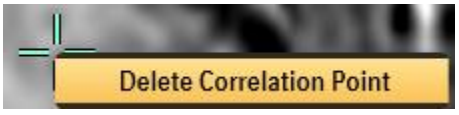
Correlate can be activated through the Right Mouse Context Menu. Once the user selects the **Correlate** menu item, Correlate becomes the active mouse interactive mode. Left clicking the mouse on an image will auto-scroll all relevant series, i.e. 3D or 4D series of the same study, currently displayed, to the same 3D coordinates of the location of the mouse click.

To disable the function, select another option from the Right Mouse Context Menu, e.g. Scroll.

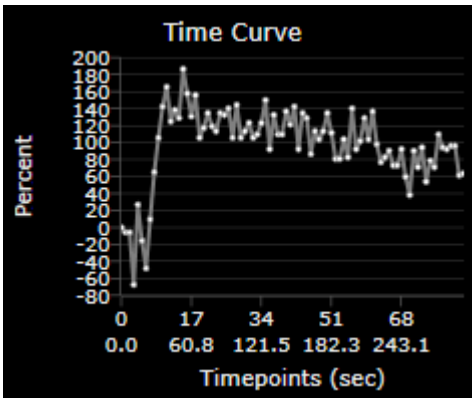
A keyboard short-cut is also available to invoke Correlate while the mouse interaction mode is set to other operation such as Scroll. Press and hold the ALT key changes the mouse cursor to Correlate, and then left click will set the Correlate 3D point to the cursor location.

Existing Correlate location can be modified by hovering the mouse near the center of the Correlate cursor. The mouse cursor will change shape to Correlate. Left click and drag the Correlate crosshair to the desirable location.

The Correlate location can be deleted by right click on the Correlate crosshair, and select Delete Correlation Point.



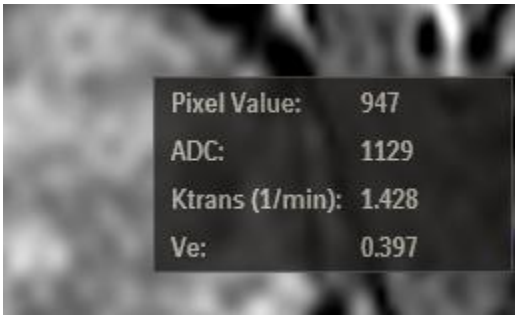
Correlate can be configured to display different information of the voxel. To configure, see Section 11.1.3 Cross Correlation for setting up the user option.



If the Time Curve chart is displayed, the time curve of the DCE data at the Correlate location will be shown.

6.15 Voxel Probe

When the **Voxel Probe** function from the Right Mouse Context Menu is selected, left click at any point on an image will display an intensity analysis showing values for the intensities and PK processing data at the selected point, i.e. Pixel Value, K^{trans} ,V_e and ADC as relevant.



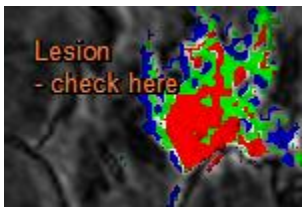
6.16 Ruler, Arrow and Text

These functions can be enabled by selecting the corresponding item under the Right Mouse Context Menu.

6.16.1 Annotation Tool

- Select the **Text** button of the application toolbar with the left mouse button or from the Right Mouse Context Menu.

- Left-click in the active image viewport window to display a "text window."
- Left-click inside the newly create text window. Type the desired text and press the [Enter] key on the keyboard to display the text.

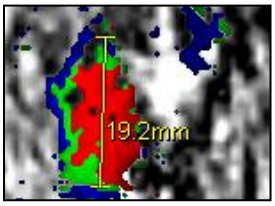


- To move the text location, position the pointer in the text box, then left-click in the text box while holding the mouse button and then drag the text box to the desired location.
- To delete the annotation, right-click on the text box border and select **Delete** with the left mouse button.

6.16.2 Ruler

- Select the **Ruler** button of the application toolbar or from the Right Mouse Context Menu.

- Click and hold the left mouse button in the active viewport, then drag the mouse in any direction to display the measurement.



- Release the left mouse button.
- The Ruler can be repositioned by left-clicking the Ruler and dragging to the new location.
- The Ruler value can be updated by selecting either endpoint and dragging it.
- The Ruler value can be repositioned by left-clicking the value and dragging to the new location.
- To delete the Ruler, place the cursor over the Ruler and right-click the mouse and select **Delete** with the left mouse button.

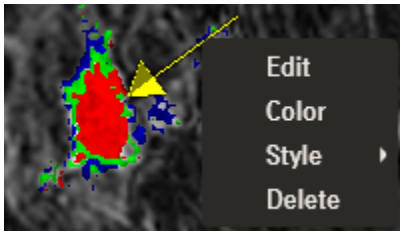
6.16.3 Arrow Pointer

- Select the **Arrow** button of the application toolbar with the left mouse button or from the Right Mouse Context Menu.

- Click and hold the left mouse button in the active viewport, then drag the mouse in any direction to display the arrow pointer.
- Release the left mouse button.
- The arrow pointer can be repositioned by left-clicking the arrowhead endpoint or the opposite endpoint and dragging the mouse.

- To change the arrow style or color, right-click on the arrow to display the Arrow Mouse Context Menu. Select **Style** or **Color** will allow changing to a different arrow style or color. The arrow can also be edited by selecting the **Edit** option.

- To delete the arrow pointer, right-click on the arrow to display the Arrow Mouse Context Menu. Select **Delete** with the left mouse button.

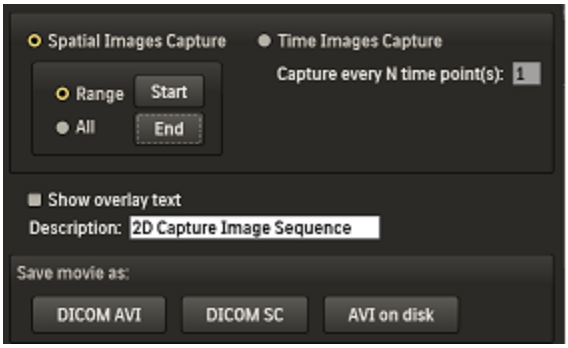


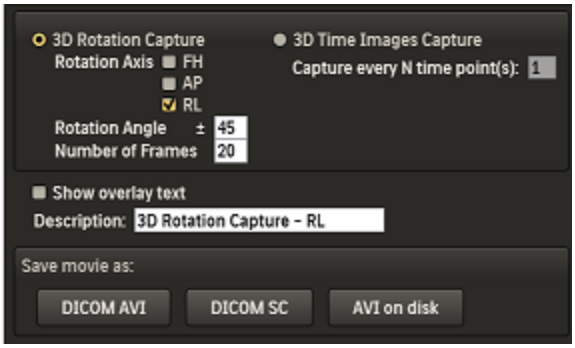
6.17 Free Hand ROI, Lesion 2D and Lesion 3D

These functions can be enabled by selecting the function in the drop down menu. More detailed discussion on these features is described below under Section 8.

6.18 Create Movie

Selecting **Create Movie** from the Right Mouse Context Menu will display the Create Movie dialog to create a movie with 2D or 3D captured images, depending on the rendering mode in the active viewport.



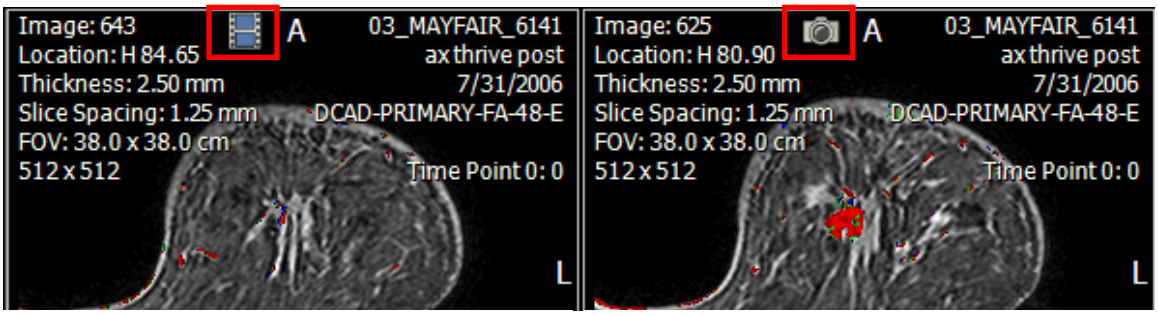


6.18.1 2D Images Capture

Two options are available:

- **Spatial Images Capture –** Capture a series of 2D images. If the active viewport series is a DCE, then the images from the displayed time point will be captured.

  Range: When **Start** is clicked it will record the image currently displayed in the active viewport. Scroll to the location the capture should be ended, then click the **End** button. The images between the Start and End inclusively will be captured. An icon will be displayed in the top left of the viewport to indicate if the current displayed image is included in the capture:



Not included in the capture Included in the capture.

All: When **All** is selected it will record the entire stack of images.

- **2D Time Images Capture –** Capture image from every N time points at the location displayed in the active viewport.

6.18.2 3D Images Capture

Two options are available:

- 3D Rotation Capture – Capture a rotation sequence based on the **Rotation Axis**, **Rotation Angle** and **Number of Frames** specified.
- 3D Time Image Capture – Capture the 3D rendered images at every **N time point** using the settings, e.g. viewing angle, as shown in the active viewport.

6.18.3 Saving

The **Show overlay text** option allows the user to include/ exclude burn-in overlay text on the capture images.

Description is the Series Description if the data is to be saved as one of the DICOM format.

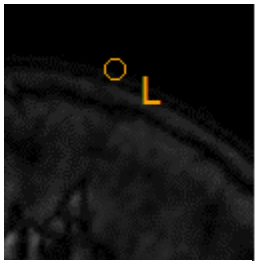
Once the above selection are done, choose to select one of the option for saving:

- **DICOM AVI:** The capture images will be packaged in an AVI file and embedded into a DICOM object. It will be stored in the DynaCAD Server, and will be available for export.
- **DICOM SC:** The capture images will be saved as a series of DICOM Secondary Capture images.
- **AVI on disk:** The capture images will be packaged in an AVI file. It will prompt for the location to be saved.

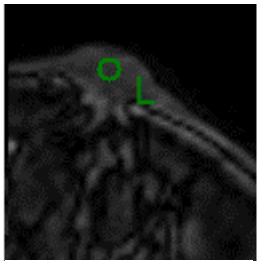
6.19 Nipple location

On breast images, selecting this function will display a circle on each breast where the software identified the nipple. While scrolling through the slices, the circle will change from orange to green at the slice where it identified the nipple location. The nipple location is used to calculate the nipple to ROI lesion measurement that is reported in the ROI lesion analysis chart.

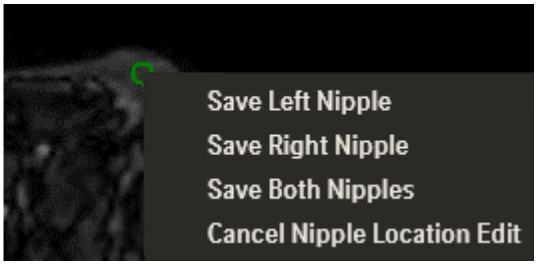
To adjust the nipple location, place the mouse cursor over the nipple circle, depress and hold the left mouse button and move the circle to the new location. If the new location is on a different slice, scroll to the new slice and follow the same instructions as above. Note that the nipple location is where the **green** circle is. If the circle is in **orange** color, then it indicates the nipple location is in the same location but on a different image. To save the new location, with the cursor in a nipple circle, right click the mouse button and select the appropriate save functions. Once the new location is saved the nipple to lesion measurement will be updated.



Orange circle indicates nipple is on another plane



Green circle indicates nipple is at the location as shown.



***WARNING*: Please review and edit the nipple location if necessary the nipple location prior to drawing an ROI. Failure to do so may cause some measurements in the lesion analysis summary to be inaccurate.**

7 Prostate Gland Segmentation

DynaCAD is capable of providing a radiologist with a visual representation of the three dimensional prostate boundary. The prostate boundary provides useful clinical information such as prostate dimensions and volume. It can also be visualize in 3D together with the lesions identified by the user. The information can be captured in the report, as well as DICOM exported..

A series with Series Description *DCAD STL Prostate Boundary* is created in the form of a DICOM RTSS object. This series is available in the Study Manager's Series list and helps users know that the prostate boundary is available.

Series Description	Series #	Modality	# Images
DCAD STL Prostate Boundary	21000	RTSTRUCT	1

It is very important the prostate boundary created is inspected by the user so that any misalignments with the actual anatomy are corrected. To ensure this is always done, it is required to approve the boundary by the user before the prostate information can be used and DICOM export. The Prostate Editor is the tool to create inspect, edit and approve the prostate boundary.

<u>WARNING</u>: Please review and edit if necessary the prostate boundary prior to drawing an ROI. Failure to do so may cause some measurements in the lesion analysis summary to be inaccurate.

7.1 Prostate Editor User Interface

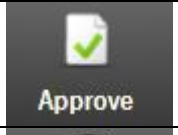
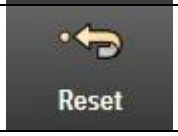
The Prostate Editor can be invoked by left clicking on the **Gland Segment** button in the application toolbar.

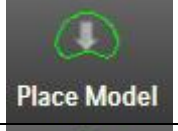
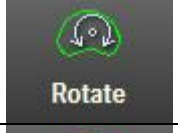
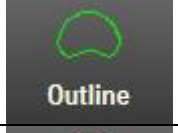
The Prostate Editor will be displayed:

It contains a toolbar and a 2x2 image display area. There are two in-viewport toolbars within each viewport as well as a Right Mouse Context Menu to allow easy access to the various tools.

7.1.1 Toolbar

The Prostate Editor toolbar provides the following functions:

ICON	FUNCTION
	Save the current prostate boundary as DRAFT.
	Save and approve the prostate boundary.
	Delete the current prostate boundary.
	Undo the previous editing action(s).
	Reset the prostate boundary to the last saved boundary.

ICON	FUNCTION
	Invoke the prostate boundary auto segmentation. The boundary will be updated once it completes the action.
	Manually place an initial prostate boundary by specifying one axis of the prostate.
	Pan the prostate boundary about the image plane.
	Increase/ decrease the size of the prostate.
	Rotate the prostate boundary about the image plane.
	Turn ON/ OFF the prostate boundary graphics (green boundary) overlay on the image.
	Cancel the editing and exit from the Prostate Editor.

7.1.2 In-viewport Toolbar

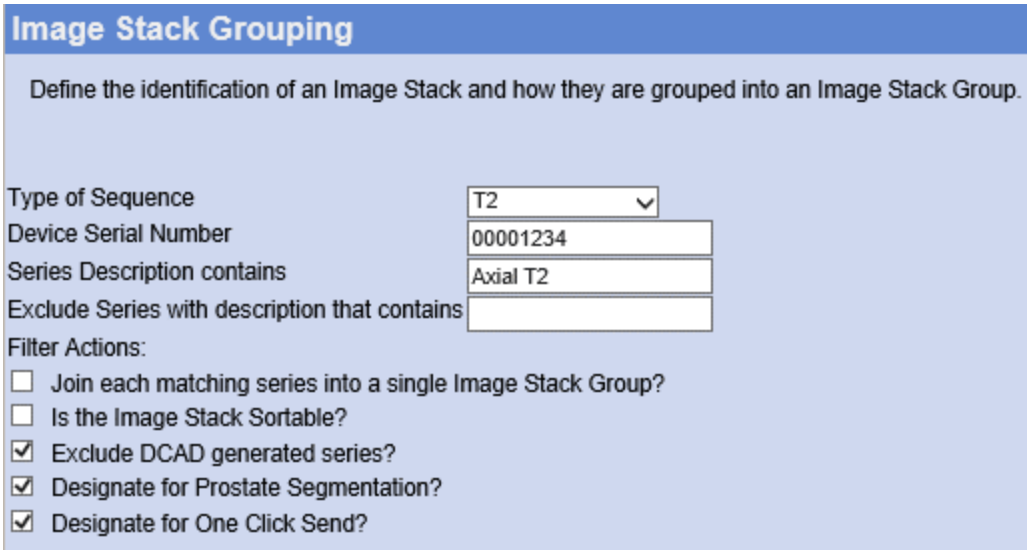
ICON	FUNCTION
	Grab and Drag the prostate boundary to move the boundary to align with the anatomy.
	Increase/ decrease the Region of Influence during the Grab and Drag action.
	Smoothing the irregularity that may be present in the prostate boundary.

7.2 Initial Prostate Boundary

The initial prostate boundary can be created by the following mechanism:

7.2.1 Automatic Segmentation

In a typical setup, a T2 weighted series is identified as the designated series for the automatic prostate boundary segmentation that takes place as one of the processing steps in the DynaCAD Server. It can be configured in the DynaCAD Admin Web's Image Stack Group filtering page. The **Designate for Prostate Segmentation** option is available in the Image Stack Group filter when the **Type of Sequence** is set to T2.



The prostate boundary algorithm will be run after the prostate study arrives in the Server, and the computed prostate boundary will be available when the study is loaded into the viewer. However, the information will not be used or display until the user approves the prostate boundary from the Prostate Editor.

In some case, the series does not get classified corrected as T2, e.g. differences in Series Description, or a different T2 weighted series is being used, e.g. same Series Description, the segmented prostate boundary may not be optimal. The user can choose the desirable T2 weighted series and run the automatic segmentation on-the-fly. The segmentation typically takes 15 seconds.

- Left click the **Delete** button to delete the current boundary.

  Note: the **Delete** button will be grayed out if no prostate boundary is available.

- Select the desirable T2 weighted series from the Right Mouse Context Menu.

- Left click the **Segment** button. This will invoke the automatic segmentation operation. A waiting icon will be displayed in the toolbar. The new prostate boundary will be displayed as overlay as soon as the segmentation is completed.

The prostate boundary will need to be inspected and approved before it can be used.

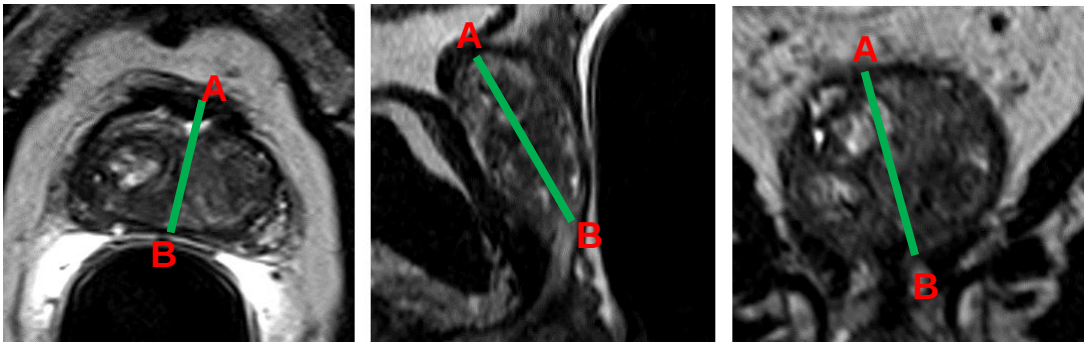
7.2.2 Manual Place Model

If the prostate boundary is not present, or the automatic segmentation does not provide desirable result, the **Place Model** option provides an alternative method to create the initial prostate boundary.

- Left click the **Delete** button to delete the current boundary.

  Note: the **Delete** button will be grayed out if no prostate boundary is available.

- Select the desirable T2 weighted series from the Right Mouse Context Menu.
- On the MPR viewports, scroll to the location approximately showing the middle of the prostate.
- Left click the **Place Model** button.
- Visually identify the major axis of the prostate. On the viewport that the prostate is the most clearly visible, click and hold the left button on the top end A of the major axis, and drag to the bottom end B of the axis. Release the left button.



- Click on the **Grab and Drag** button to edit the boundary so that it aligns with the anatomy shown in the images.

7.3 Prostate Editing

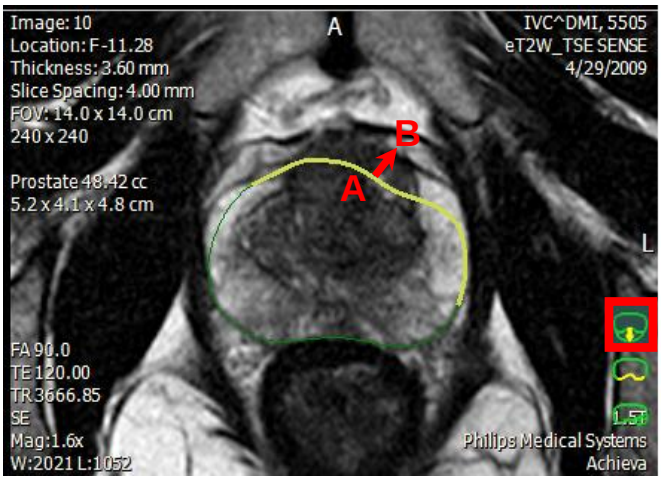
Once an initial prostate boundary is available, it can be inspected and edited if necessary.

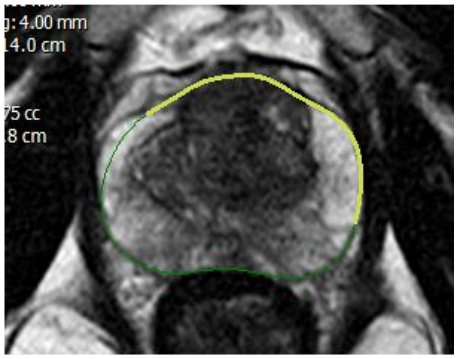
7.3.1 Grab and Drag

This is the most commonly used action. It allows you to grab the boundary to pull it to the location based on the mouse movement:

- Click on the **Grab** button in the bottom right viewport.
- Move the mouse cursor to the location to be moved – Point A below. The yellow segment shows the extent of the segment that may be affected (Region of Influence).
- Left click, hold and drag the boundary to the desired location – Point B.

- Release the mouse button



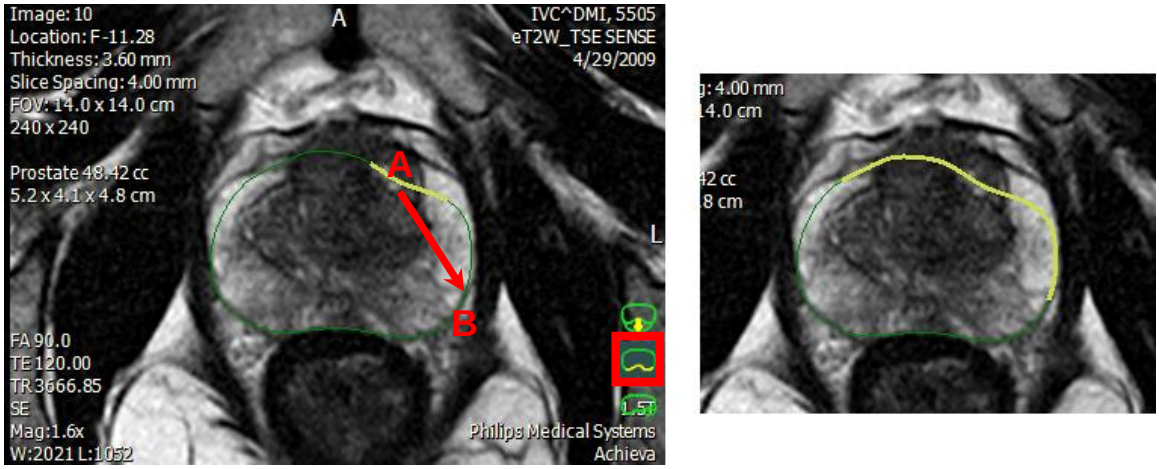


7.3.2 Region of Influence

The yellow line in the boundary represents the Region of Influence during editing, i.e. when the user grabs a point and move it to a new location. Although it is shown as a 2D segment in the viewport, it is actually a 3D region. You can change the size of the region depending the extent of the region you want to correct. To change the size of the region:

- Click the **Region of Influence** button in the bottom right viewport is pressed.
- Move the mouse cursor to the location to be moved – Point A below.
- Left click, hold and drag along the boundary.
- Release the mouse button if the yellow segment is of the appropriate length for the edit.

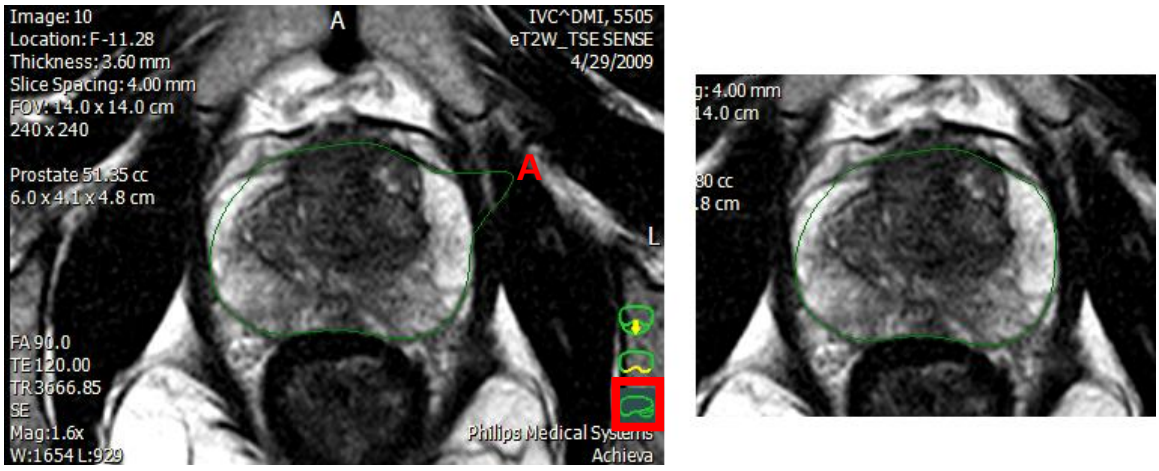
A short-cut is available to allow the Region of Influence to be changed while in Grab and Drag mode. To activate this function using the short-cut, move the mouse cursor near the boundary, and press and hold the CTRL button. The mouse cursor will change to the Region of Influence cursor. Left click, hold and drag along the boundary to define the Region of Influence.



7.3.3 Smoothing

Uneven boundary can be smoothed using the Smooth action.

- Select the **Smooth** mode by clicking on the corresponding button in the bottom right viewport.
- Move the mouse cursor to the location to be smoothed – Point A below
- Left click, hold and drag the mouse. You can drag the mouse in any direction since the smoothing is applied at Point A and does not depends on direction.
- Release the mouse when the boundary is smooth as desired.



A short-cut is available to allow Smooth to be active while in Grab and Drag mode. To activate this function using the short-cut, move the mouse cursor near the boundary, and press and hold the SHIFT button. Left click, hold and drag the mouse to smooth the boundary.

7.3.4 Pan, Resize and Rotate

Pan, **Resize** and **Rotate** buttons are available in the toolbar. When they are clicked, move the mouse cursor close to the prostate boundary, the mouse cursor shape will be changed accordingly. Click and hold the left mouse button, then drag to change pan, rotate or size of the prostate accordingly.

7.3.5 Undo and Reset

It is possible to undo the previous actions easily. Click the **Undo** button once to undo the most recent action. Click again to continue undoing previous actions.

Click the **Reset** button to reset the prostate boundary to the last saved or initial boundary.

7.4 Save and Approval

The **Save** button allows the current prostate boundary to be saved. Save should be used to save a draft, and the prostate editing has not been completed yet. The prostate boundary will still has to be approved after saving.

NOTE: *Saving the prostate boundary does not finalize and approve the prostate boundary and make it available for exporting. The prostate boundary must be approved to enable the boundary to be exported.*

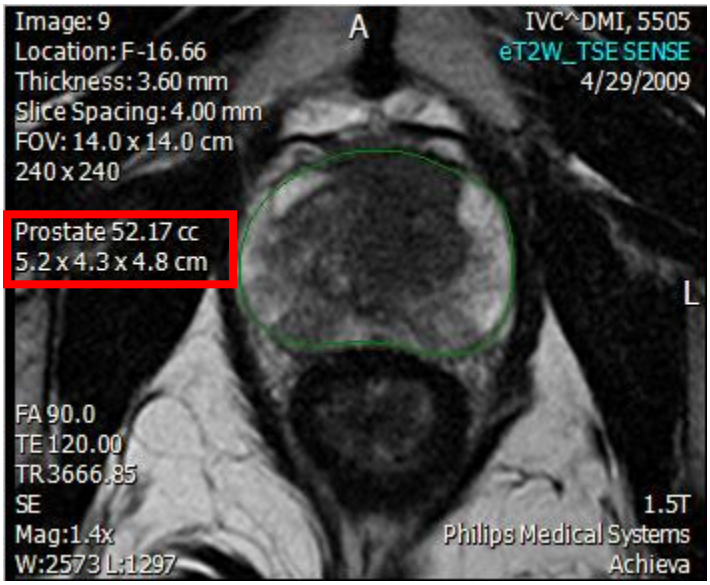
The **Approve** button allows the current prostate boundary to be saved and approved. Once approved, the prostate information will be displayed in the viewports (Note: Prostate Editor always display the prostate information) and PI-RADS report, and the DICOM RTSS object that contains the prostate boundary data will be available for DICOM export.

NOTE: *The series that is current displayed when the **Approve** button is pressed will be the reference series for the prostate boundary.*

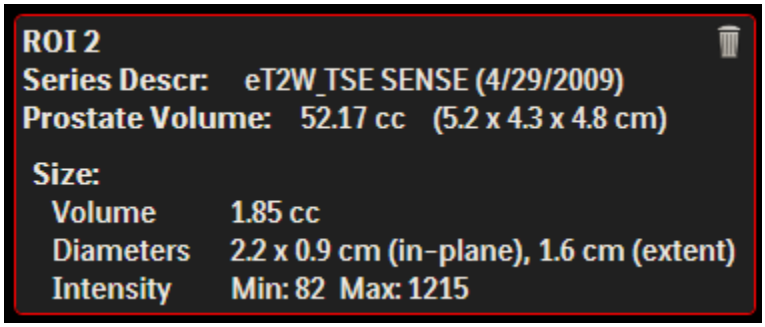
7.5 Prostate Gland Information Display

The prostate boundary and information can be displayed in the application:

- The prostate boundary is overlaid on the grayscale image when select **Prostate Location** from the Right Mouse Context Menu. It is available for both 2D, MPR and MIP rendering.
- The prostate dimensions and volume is displayed as viewport overlay once the prostate boundary is approved:



- The prostate dimensions and volume is displayed in the Lesion Analysis item:

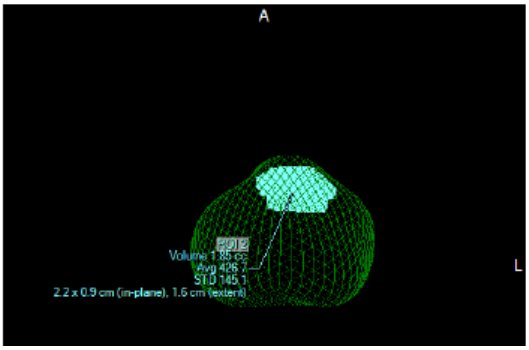


- The information is displayed in the PI-RADS report:

DynaCAD

Patient Name:	IVC, DMI, 5505	**Patient ID:**	DMI_5505
Date of Birth:	1/1/1950	**Review Date:**	2/10/2014
Study Date:	4/29/2009	**Ref. Physician:**	Dr Ref Physician
Study Description:	PROSTATE	**Created By:**	Dr Reading Radiologist

Prostate Volume:	52.17 cc
Prostate Dimensions:	5.2 x 4.3 x 4.8 cm



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8 Region of Interest (ROI)

8.1 ROI Creation

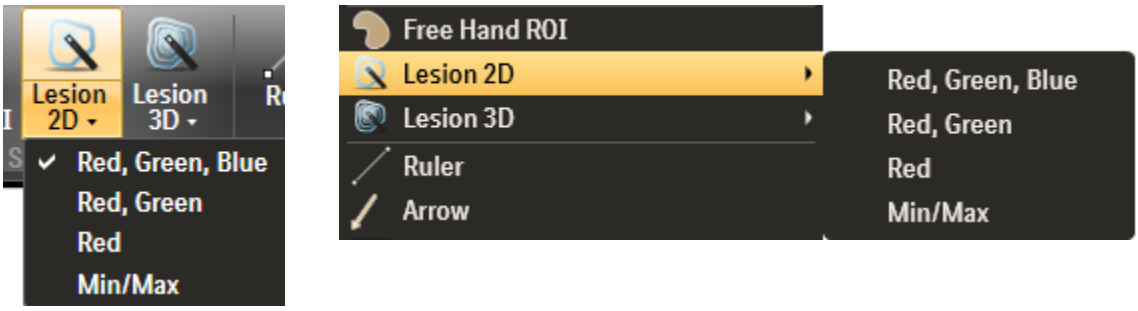
DynaCAD provides several methods to create a ROI.

8.1.1 Lesion 2D

Lesion 2D provides a one-click semi-automatic segmentation mechanism that allows a suspected lesion to be drawn on the image plane. The following type of regions are supported:

- Red, Red + Green, or Red + Green + Blue region of PK PRIMARY and QuickTP color overlay.
- Region that has voxels with intensity between a specified minimum and maximum threshold for PK, e.g. K^{trans}, and ADC color overlay.

Lesion 2D can be chosen from the application toolbar, Right Mouse Context Menu, or in-viewport toolbar. The **Lesion 2D** button from the toolbar and the Right Mouse Context Menu provides the different options for the user to choose from:



The in-viewport tool button on the left side of the viewport rotates between the different Lesion 2D options by scroll the mouse wheel. As the mouse wheel is scrolled, the icon will be changed as shown below to indicate Red, Red + Green, Red + Green + Blue, and Min/Max Threshold accordingly. Left click to select the option.

Red | Red Green | Red Green Blue | Min/ Max

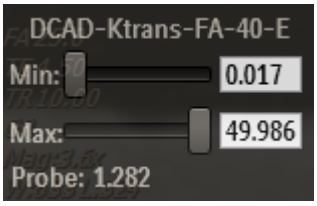
To perform the Lesion 2D Red, Red + Green, Red + Green + Blue operation:

- The rendering mode should be either 2D or one of the orthogonal MPRs. Lesion 2D cannot operate on Oblique MPR and 3D/MIP viewports.
- Apply the PK PRIMARY or the QuickTP color overlay.

- Locate the suspected lesion and then select the desirable Lesion 2D option.
- Left click on the suspected lesion. The click location should be on the selected colored region. The application may not be able to segment the region if the click location is outside the colored region.
- It will automatically segment the region. The boundary of the segmented region will then be displayed.

To perform the Lesion 2D Min/Max operation:

- The rendering mode should be either 2D or one of the orthogonal MPRs. Lesion 2D cannot operate on Oblique MPR and MIP viewports.
- Apply one of the PK parameter or the ADC overlays as desired.
- Locate the suspected lesion and then select the Lesion 2D **Min/Max** option.
- A small window will appear in the lower left viewport when the cursor is moved onto an ADC or PK color overlay image. By moving the cursor within the suspected lesion, the Probe value will be updated to show the corresponding overlay value at the mouse cursor location. The Min/ Max thresholds can be set accordingly using the sliders.



- Left click on the suspected lesion.
- It will automatically segment the region. The boundary of the segmented region will then be displayed.

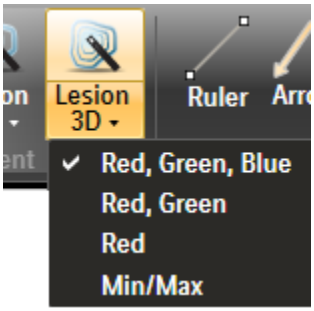
NOTE: Refer to the editing ROI's section for instructions to edit the outline. Deleting the ROI and re-adjusting the Min/Max values is another option to refine the ROI outline.

8.1.2 Lesion 3D

Lesion 3D provides a one-click semi-automatic segmentation mechanism that allows a suspected lesion to be segmented in 3D based on region growing a connected region. The following type of regions are supported:

- Red, Red + Green, or Red + Green + Blue region of PK PRIMARY and QuickTP color overlay.
- Region that has voxels with intensity between a specified minimum and maximum threshold for PK, e.g. K^{trans}, and ADC color overlay.

Lesion 3D can be chosen from the application toolbar, Right Mouse Context Menu, or in-viewport toolbar. The **Lesion 3D** button from the toolbar and the Right Mouse Context Menu provides the different options for the user to choose from:



The in-viewport tool button on the left side of the viewport rotates between the different Lesion 3D options by scroll the mouse wheel. As the mouse wheel is scrolled, the icon will be changed as shown below to indicate Red, Red + Green, Red + Green + Blue, and Min/Max Threshold accordingly. Right click to select the option.

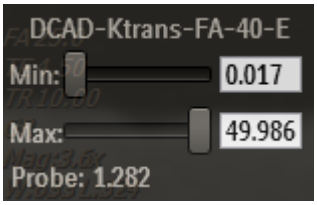
Red | Red Green | Red Green Blue | Min/ Max

To perform the Lesion 3D Red, Red + Green, Red + Green + Blue operation:

- Apply the PK PRIMARY or the QuickTP color overlay.
- Locate the suspected lesion and then select the desirable Lesion 3D option.
- Left click on the suspected lesion. The click location should be on the selected colored region. The application may not be able to segment the region if the click location is outside the colored region.
- It will automatically segment the region. The boundary of the segmented region will then be displayed.

To perform the Lesion 3D Min/Max operation:

- Apply one of the PK parameter or the ADC overlays as desired.
- Locate the suspected lesion and then select the Lesion 3D **Min/Max** option.
- A small window will appear in the lower left viewport when the cursor is moved onto an ADC or PK color overlay image. By moving the cursor within the suspected lesion, the Probe value will be updated to show the corresponding overlay value at the mouse cursor location. The Min/ Max thresholds can be set accordingly using the sliders.



- Left click on the suspected lesion.
- It will automatically segment the region. The boundary of the segmented region will then be displayed.

NOTE: *Refer to the editing ROI's section for instructions to edit the outline. Deleting the ROI and re-adjusting the Min/Max values is another option to refine the ROI outline.*

NOTE: *Lesion 2D/3D: is designed for ROI selection of well clustered and localized lesions. Please review the resulting ROI in the specified slice or all slices (in 3D case). If not satisfactory, please delete and use the Freehand ROI option.*

8.1.3 Freehand ROI

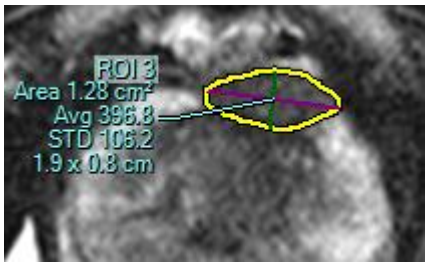
Freehand ROI allows the user to manually outline a suspected lesion using the mouse. This is useful to analyze lesions based on sequences such as T2 weighted series. User can create 2D and 3D ROI using the Freehand ROI.

To use the Freehand ROI:

- Left-click the **Freehand ROI** button in-viewport shortcut or the toolbar button.

- Move the mouse pointer to the region of interest. Left click and hold the mouse button, and drag the mouse to draw the ROI.

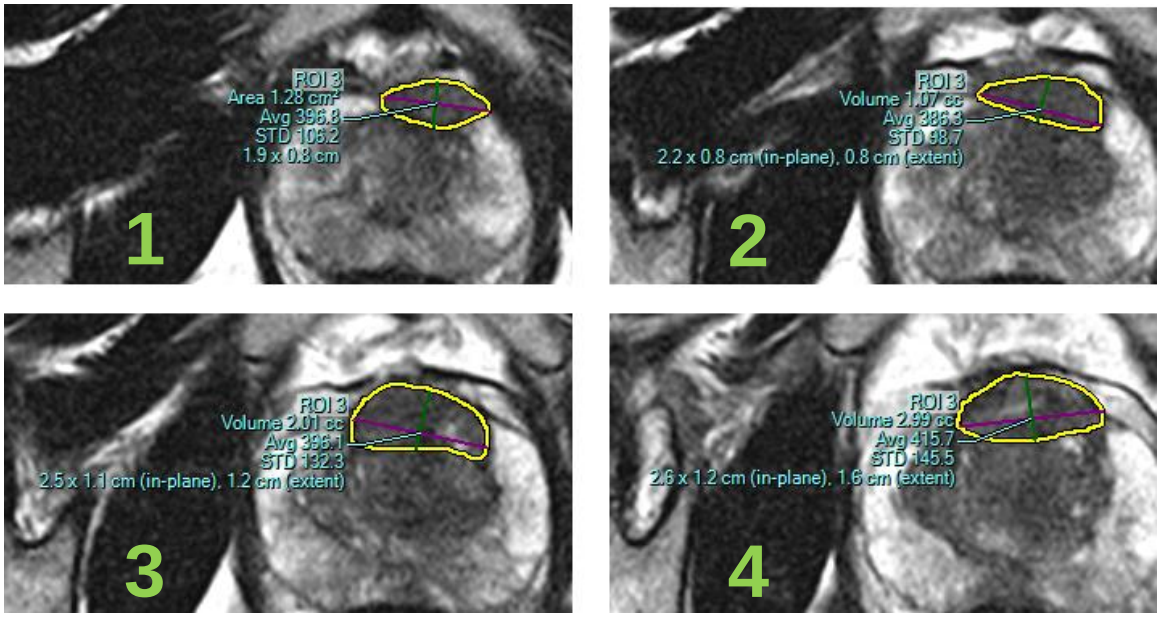
- Release the left mouse button and the ROI is automatically analyzed and the information will be shown in the viewport.



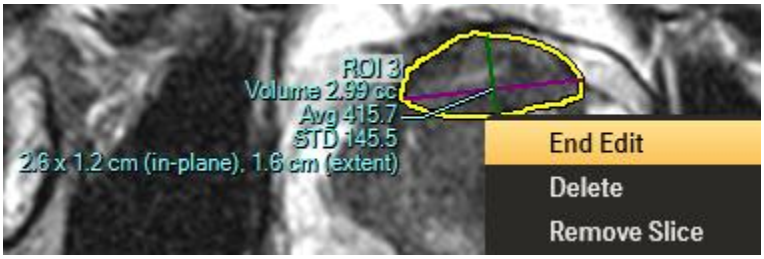
At this point, a 2D ROI is created. If a 3D ROI is to be created, continue with the following steps:

- Right click the ROI boundary the display the ROI Menu and select **Edit Make 3D ROI**.

- Scroll to the next slice and draw an ROI. Once the second ROI is drawn, the statistics under the ROI label is updated from 2D to 3D data.



- Scroll to the next image to continue defining the 3D ROI boundary.
- To complete the operation, right click on the ROI boundary again to bring up the ROI Menu. Select **End Edit**.



During the ROI creation, boundaries that are already drawn can be edited by simply moving the mouse cursor to the location to be edited. Left click and hold, move the mouse to follow the new boundary. Release the left mouse button to finish.

When all the editing is done, select **End Edit** from the ROI Menu to complete the action. It is not necessary to draw the boundary on every consecutive image throughout the extent of the ROI. Images can be skipped, and the gap will be automatically filled using nearest neighbor interpolation.

If a mistake is made in drawing the ROI and it is easier to delete the boundary on a particular image and redraw, the specific boundary can be removed by selecting the **Remove Slice** of the ROI Menu (right click on the boundary). After the boundary is removed, a new boundary can be drawn on the slice. Select **End Edit** from the ROI Menu when all editing is done.

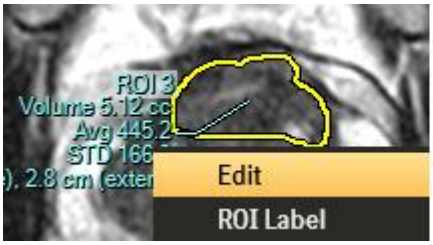
8.2 ROI Editing

8.2.1 Edit Boundary

After a ROI is created, it can still be edited regardless whether it is a 2D or 3D ROI and the method of creation.

***NOTE**: ROI Editing is only enabled when the viewport it in 2D rendering mode, i.e. showing images in their original acquisition plane.*

To start editing, right click on the boundary to display the ROI Menu. Select **Edit**.



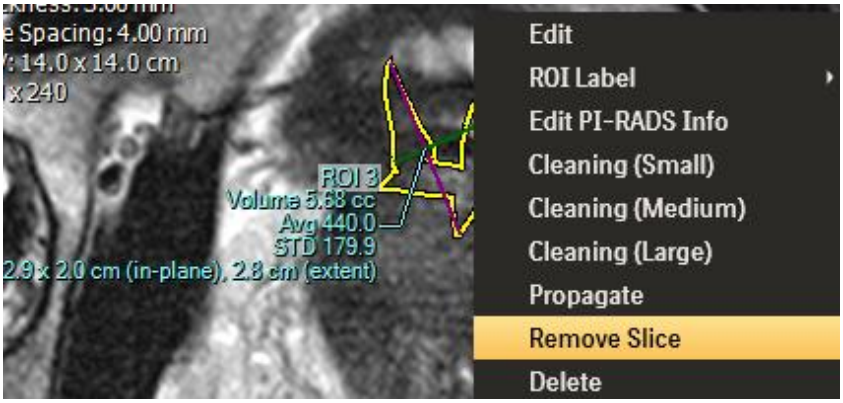
Move the mouse cursor to the location of the boundary to be edited. Left click and hold, move the mouse to follow the new boundary. Release the left mouse button to finish. When all the editing is done, select **End Edit** from the ROI Menu to complete the action.

ROI statistics will be updated to reflect the changes.

8.2.2 Remove Boundary

Boundary on a particular image can be removed by selecting the **Remove Slice** of the ROI Menu. After the boundary is removed, select **End Edit** to complete the edit. If the removed boundary is within the top or bottom of the ROI, then the boundary at that image will be interpolated.

ROI statistics will be updated to reflect the changes.



8.2.3 Cleaning function for ROI's

In the semi-automatic Lesion 2D/ 3D operation, the region grown ROI may leak into adjacent regions because of connected voxels, e.g. arteries. The Cleaning function will disconnect these regions. The Cleaning function is designed to make ROIs more accurate. Small, medium and large cleaning will eliminate more colorized voxels respectively.

Once a cleaning function is chosen, there will be an option to undo the cleaning function. Right click on the ROI boundary to bring up the ROI Menu. Select **Undo Cleaning** to undo the previous cleaning operation.

ROI statistics will be updated to reflect the changes.

8.2.4 Propagating an ROI

Selecting **Propagate** from the ROI Context Menu will display the ROI in all the viewports in the current layout.

Alternatively, click and hold the right mouse button on the ROI Label and dragging to another viewport will propagate the ROI to the chosen viewport only. Once the right mouse button is released the ROI will be displayed in the target viewport.

A propagated ROI can be hidden by selecting **Hide** from the ROI Menu. This will not delete the ROI.

8.2.5 Deleting an ROI

To remove a ROI, right click on the ROI label to display the ROI Context Menu. Select **Delete**. The ROI will be deleted. Corresponding propagated ROIs will also be removed.

8.2.6 ROI Label

Selecting **ROI Label** will allow the highlighted ROI to be renamed based on a list of pre-defined labels. Renaming the ROI will also rename the associated ROI charts.

8.2.7 Go to Worst WashIn, WashOut or WashIn/Out

***NOTE**: Go to options are only available when the PK or QuickTP overlay is applied.*

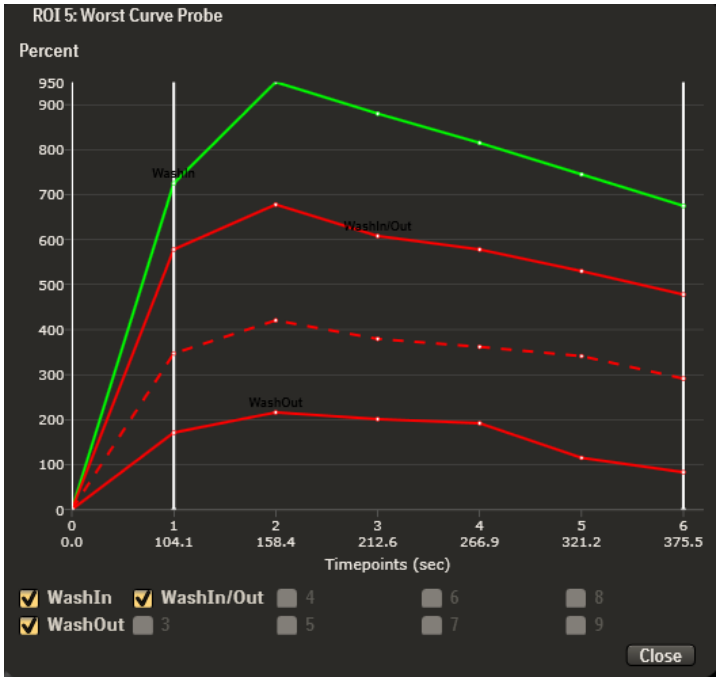
Three different choices to identify worst voxels can be configured for PK and QuickTP analysis. Once an ROI has been drawn, right clicking the mouse menu will allow options to select a **Go to Worse Curve** depending on how the system has been configured. Selecting the one of the **Go to Worse Curve** functions will display the image slice where that particular worst curve has been identified.

Configuring the worst curves for QuickTP is done in the advanced page (at the bottom) of the QuickTP configuration window (see Section 6.7.2). PK configuration is setup at the bottom of the page which displays the PK parameters (see Section 6.6.2).

8.2.8 Probe for Worst Curve

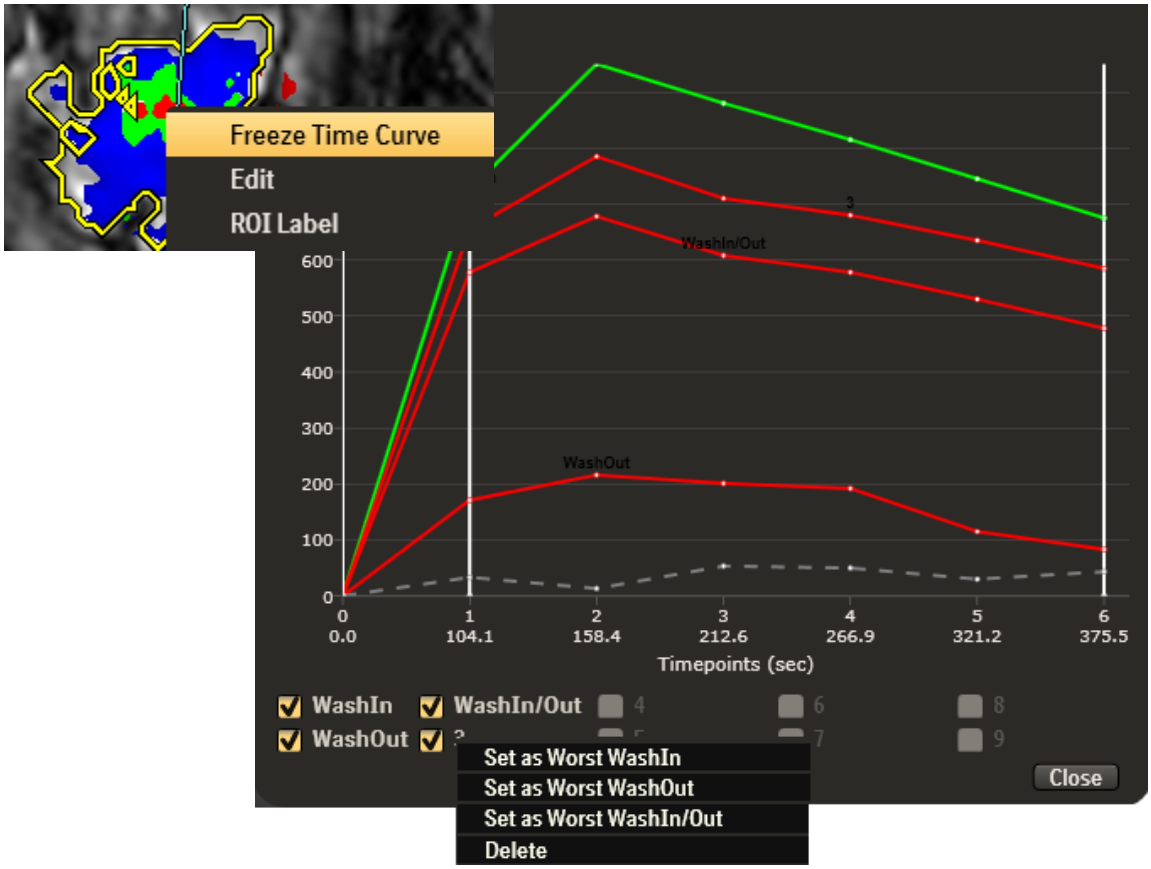
***NOTE**: **Probe for Worst Curve** is only available when the PK or QuickTP overlay is applied.*

Selecting this option displays a real time curve chart showing one of the worst curves as configured by the system (see Section 6.6.2 and Section 6.7.2 for PK and QuickTP configuration respectively). This time curve can be used as a baseline or used as a comparison while interrogating the color overlay.



The solid lines in the graph are one of the Worst Curve identified inside the ROI. The dotted line is the time curve at the mouse cursor and will be updated as the mouse moves.

If an interesting voxel is identified during the probing, the curve can be frozen on the Worst Curve Prove graph. To freeze a curve of interest, right click the mouse and select **Freeze Time Curve**. This will display the worst curves and the curve for the voxel of interest in the chart. The voxel of interest will be labeled by a number.



The frozen curve can be selected as one of the Worst WashIn, WashOut or WashIn/Out by right click on the corresponding curve label and select the **Set as** option as shown in the picture above. This will override the previous Worst Curve.

The frozen curve can be deleted by right click on the corresponding curve label and select **Delete**.

8.2.9 Show Auto Key Images

Selecting this option will automatically generate a set of key images as configured in the Report Template Editor (see Section 10.7).

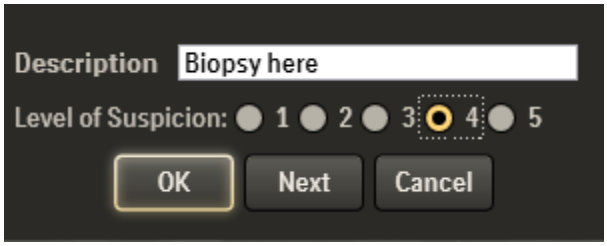
8.3 Sub-ROI

A sub-ROI is a user defined 3D Point or 2D Freehand Boundary within a ROI. An example usage is for the user to specify locations inside a ROI for target biopsy, e.g. using UroNAV. Multiple sub-ROIs can be created for a ROI.

8.3.1 Sub-ROI Creation

To create a sub-ROI:

- Create a 2D or 3D ROI.
- Right click on the ROI and select **Create Sub-ROI** from the ROI Right Mouse Menu.
- Either double left click on the desirable location for creating a 3D Point Sub-ROI, or left click, hold and drag the mouse to draw a 2D Freehand Sub-ROI.
- A popup dialog is displayed for entering a **Description** or label, as well as the **Level of Suspicion** for the Sub-ROI. Both are optional.



- Click **OK** button to complete creating Sub-ROI, or click **Next** to continue defining the next Sub-ROI.

8.3.2 Sub-ROI Visibility

Once one or more Sub-ROIs are defined, an icon will be displayed next to the ROI label to indicate one or more Sub-ROIs are available.

Visibility ON

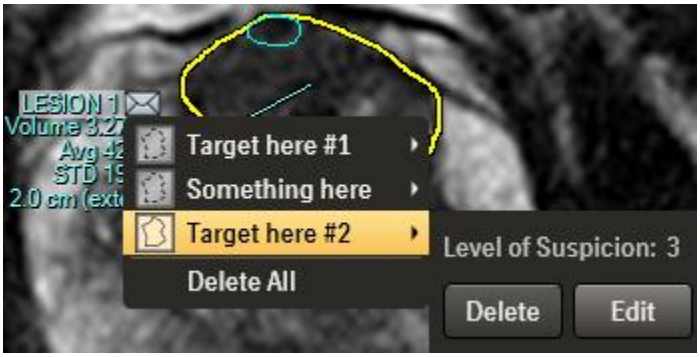
Visibility OFF

Click on the icon to show/ hide the Sub-ROI graphics.

8.3.3 Sub-ROI Editing

To edit a Sub-ROI:

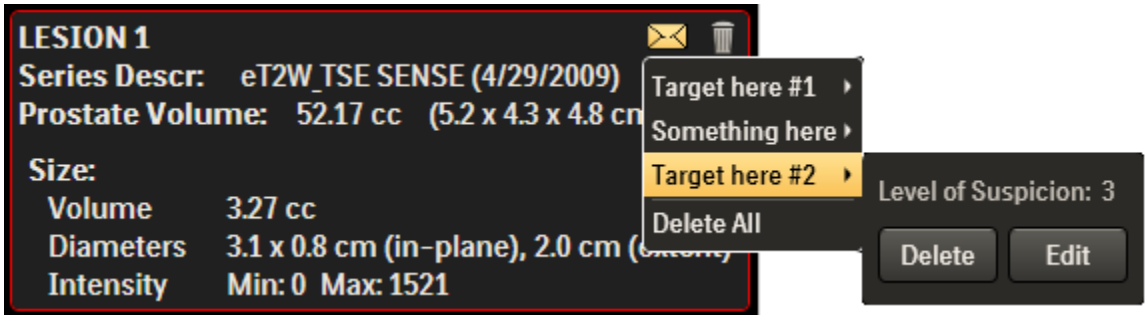
- Right click on the Sub-ROI icon to display the Sub-ROI Context Menu.
- The list of Sub-ROIs will be displayed. Highlight the Sub-ROI to be edited. Left click on the item will automatically scroll to the Sub-ROI location.



- Select **Edit** to edit the Description and/ or Level of Suspicion.
- Select **Delete** to delete the Sub-ROI.

***NOTE**: The Sub-ROI location cannot be edited. If the location needs to be modified, delete the Sub-ROI and re-create it at the new location.*

The same Sub-ROI icon is available under the ROI item of the Lesion Analysis Summary. The Sub-ROI visibility and editing can also be performed under the Lesion Analysis Summary.



8.4 ROI Analysis

8.4.1 Displaying Charts

Once an ROI is created, the corresponding analysis is then displayed in various charts.

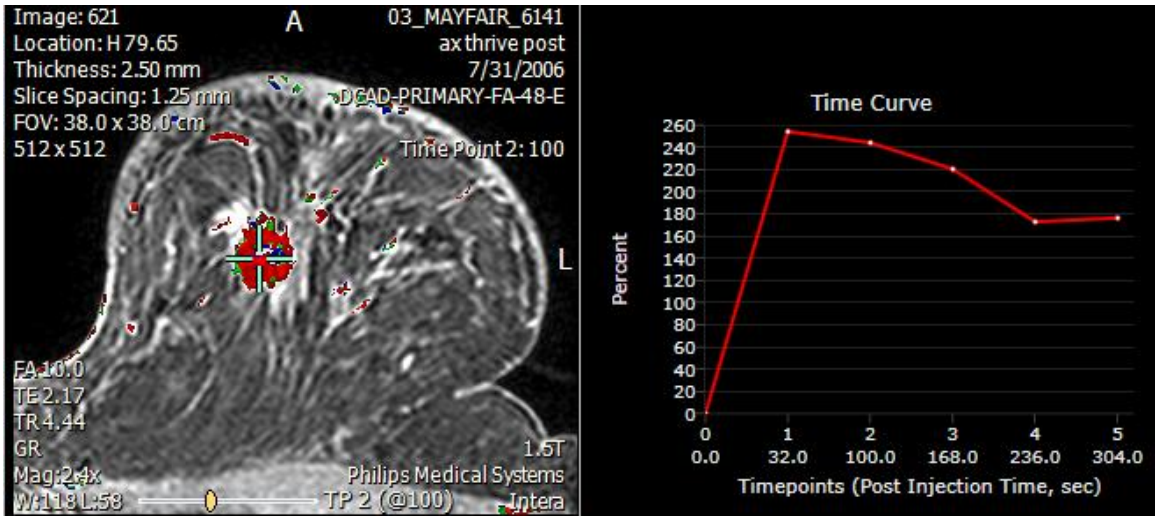
To select a chart, select the viewport where the chart is to be displayed, select the desired chart type from the **Hangings** tab of the toolbar. The chart will be displayed in the viewport.

8.4.2 Chart Types

Time Curve (Pixel of Interest, POI) – displays the intensity/ percent of a selected voxel over time.

To use the **Time Curve** tool:

- Select a viewport to display the time curve chart.
- With the left mouse button, select the Time Curve chart from the Hangings tab of the application toolbar, the Time Curve chart will display in the active viewport.
- Using the Correlate function over a voxel of interest in an image will display the intensity or percentage curve. The time axis will display post injection timing when a processed color overlay is displayed or timing from the DICOM header if an image with no color overlay is displayed. Left clicking on a particular curve's label will toggle that curve line on/off.



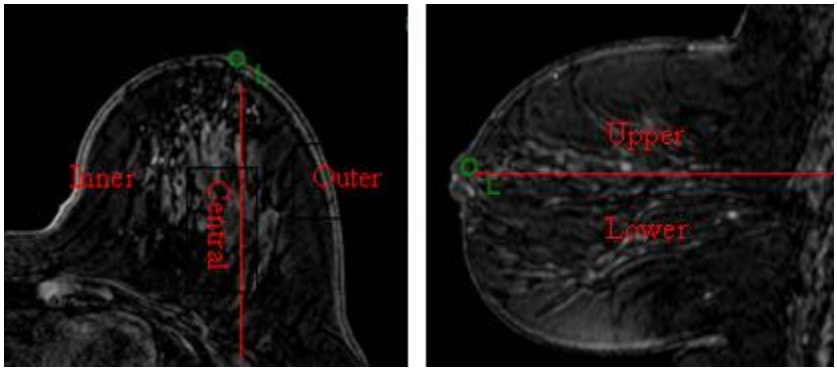
Lesion Analysis Summary - Displays a summary of the ROI measurements and distances. It automatically calculates and displays ROI information in the lesion analysis chart. A breast segmentation algorithm allows the application to automatically calculate various measurements. The algorithm uses one of the following sequences to calculate the breast segmentation; T1 axial, dynamic axial or a different T1 axial sequence in that order. It should be noted that imaginary lines are used to calculate quadrants assuming the breast nipples hang straight down to create equal quadrants. If the nipples are angled, the quadrants will not be equal, and the ROI lesion analysis may seem incorrect.

The Lesion Analysis Summary information will be slightly different for PK analysis versus QuickTP. The location and size information will generally be the same. Kinetic information for QuickTP will display information based on the 3 time point analysis and not the Pharmacokinetic analysis method.

- ROI Lesion location

  Side: left/right breast

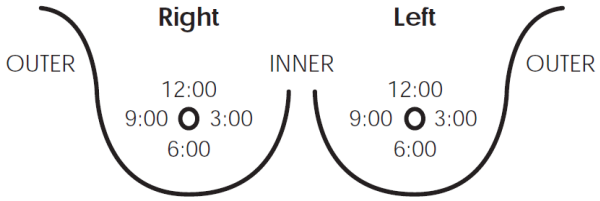
  Breast quadrant: inner, central, outer, upper and lower. These calculations are based on the breast algorithm identifying the nipple and drawing an imaginary vertical line from the nipple to the chest wall to report inner, central or outer quadrant. Upper and lower quadrants are calculated by drawing an imaginary horizontal line from the nipple to the chest wall.



Imaginary line nipple to chest wall

Nipple to lesion measurement: measured from center of lesion to the breast nipple edge.

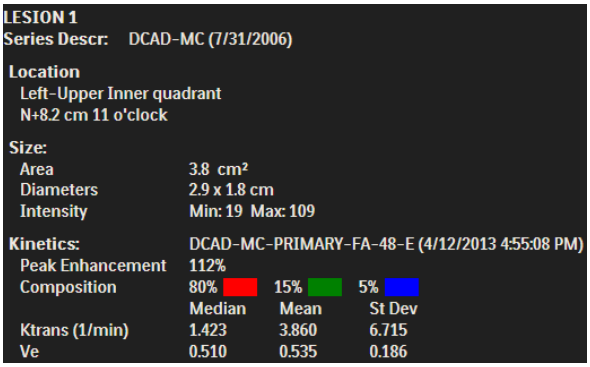
Clock face location:



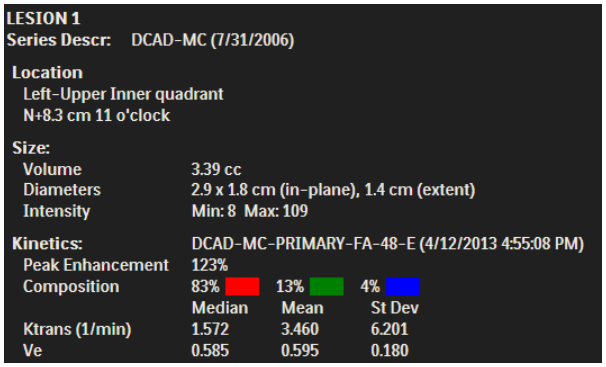
Size: Will display the Area, Diameter (2D ROI) or Volume (3D ROI) and Intensity of the ROI drawn. When a 3D ROI is drawn the diameter will report measurements for length, the diagonal in-plane width and the extent (depth). The ROI will display the slice where the measurements were calculated for the length and in-plane width.

Kinetics: Will display the peak enhancement of the drawn ROI, a percent breakdown of the drawn ROI by color and the median, mean and standard deviation of the pharmacokinetic parameters that were processed.

The Peak enhancement is defined as the greatest percentage change at one of the time points in the average curve which can be seen in the curve analysis chart.



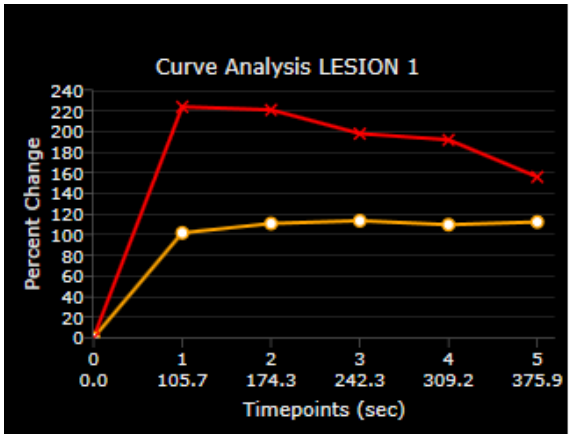
2D ROI



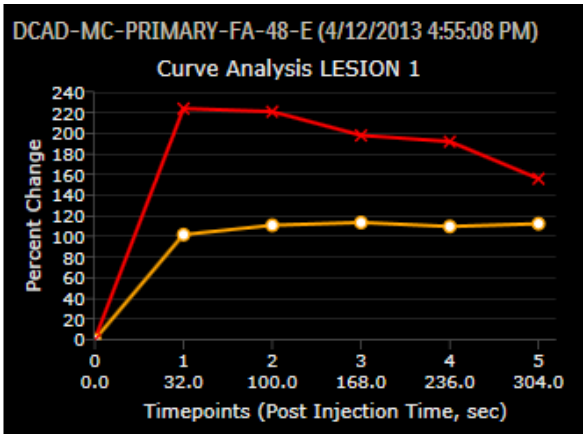
3D ROI

Curve Analysis - Displays the Percent Change Curve and Time Intensity Curve of the selected ROI.

- Left click on the **Intensity** or **Percent** label will switch the vertical scale to Intensity or Percent accordingly..
- Floating the mouse over each time point on the curve displays the data for that time point.
- QuickTP analysis will display the following information for the worse curve: percent peak enhancement, the category of the uptake threshold, curve color based on the delayed phase threshold settings and horizontal lines signifying the uptake threshold settings.

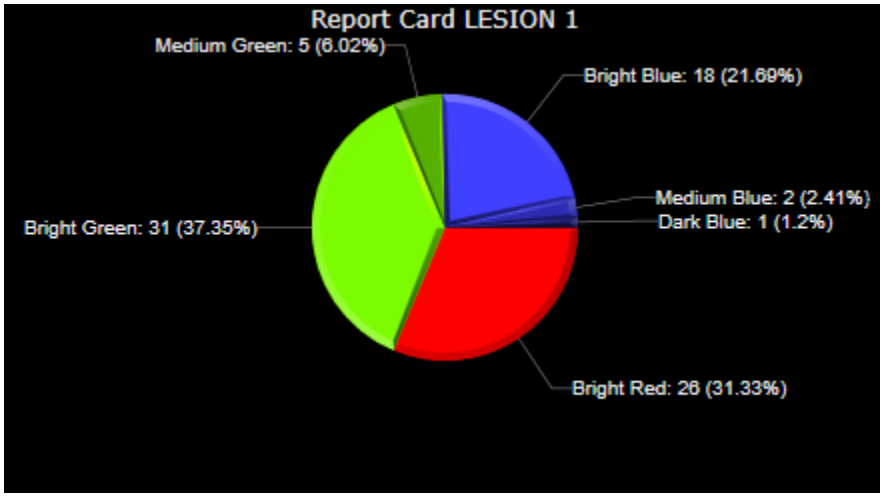


No PK overlay

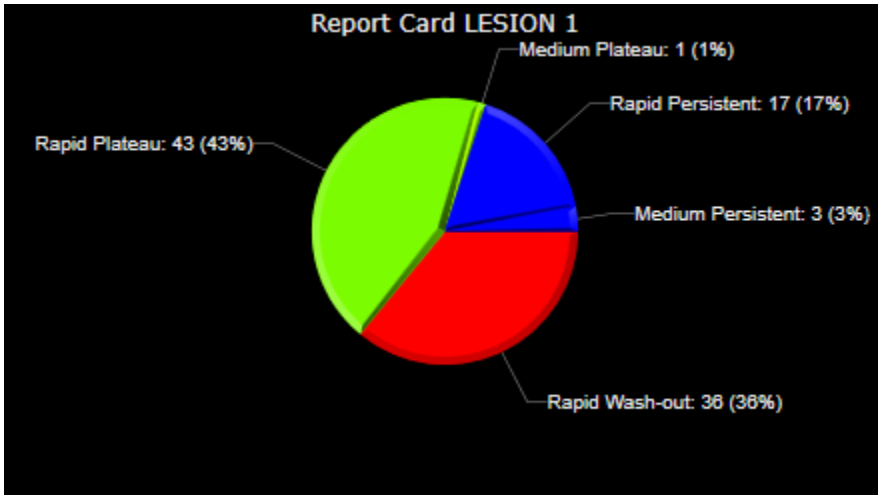


PK overlay applied

Report Card - Displays the number and percentage distribution of pixels (or voxels in an ROI) for each color and hue (PK only) of the selected ROI.

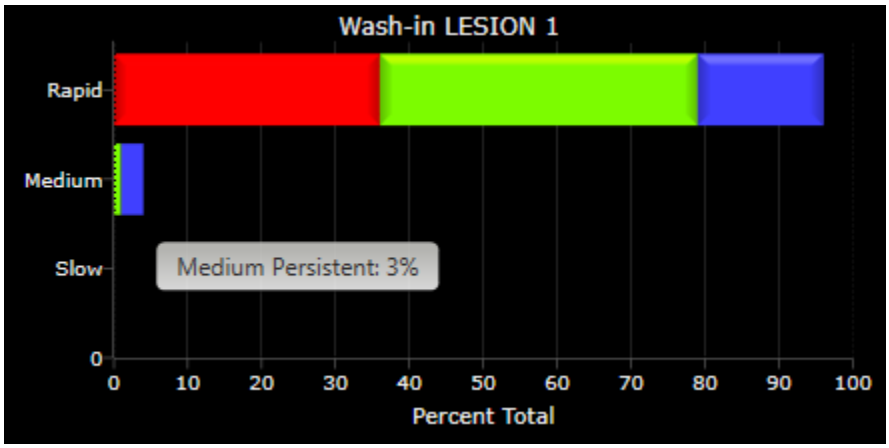


ROI with PK overlay

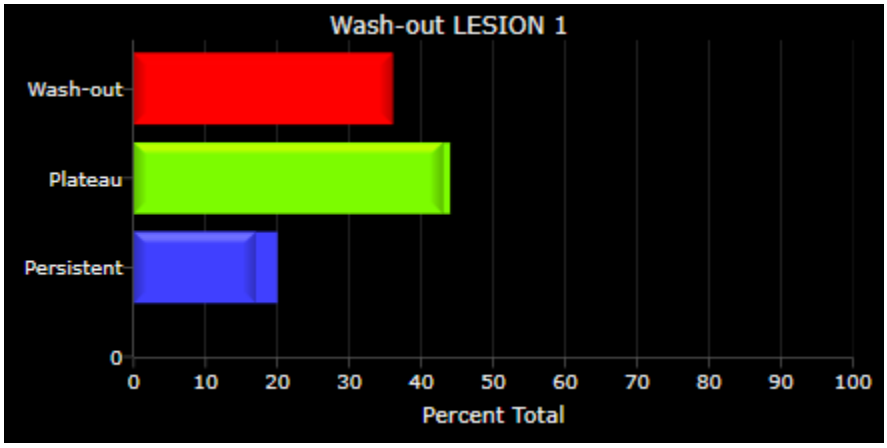


ROI with QuickTP overlay

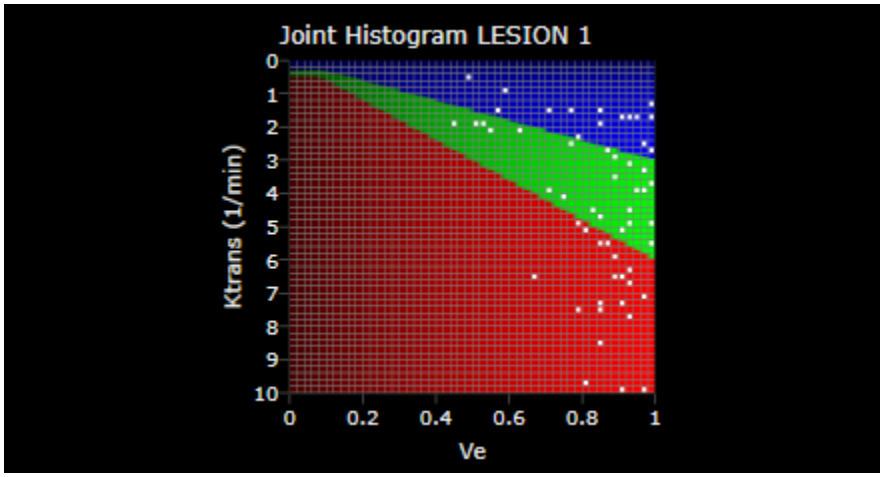
Wash-In - Displays the fast, medium, and slow wash-in components of the selected ROI. Also displays the individual and total percentage of each type of wash-in when the mouse hovers over the bar. PK displays hues of a color.



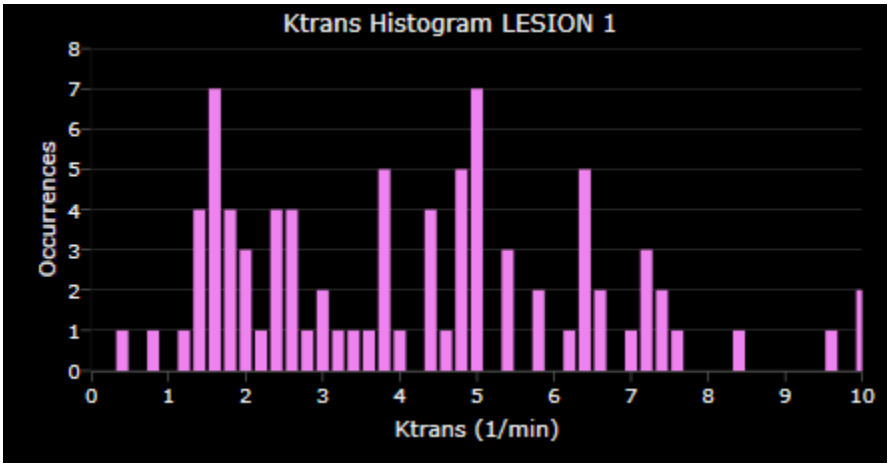
Wash-Out - Displays the Wash-out (Decline for PK), Plateau and Persistent components of the selected ROI. Also displays the individual and total percentage of each type of wash-out when the mouse hovers over the bar. PK displays hues of a color.



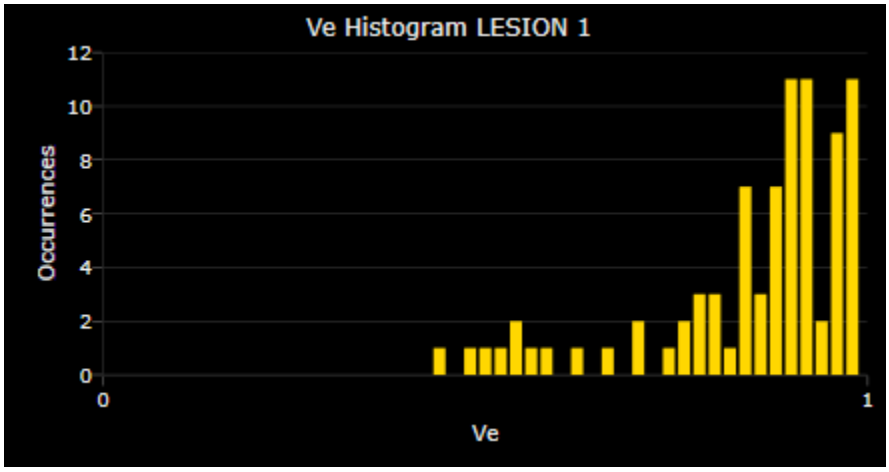
Joint Histogram - Displays the joint histogram and the number of occurrences of those combinations of K^{trans} (Permeability) and V_e pairs of the selected ROI. Specific to PK analysis.



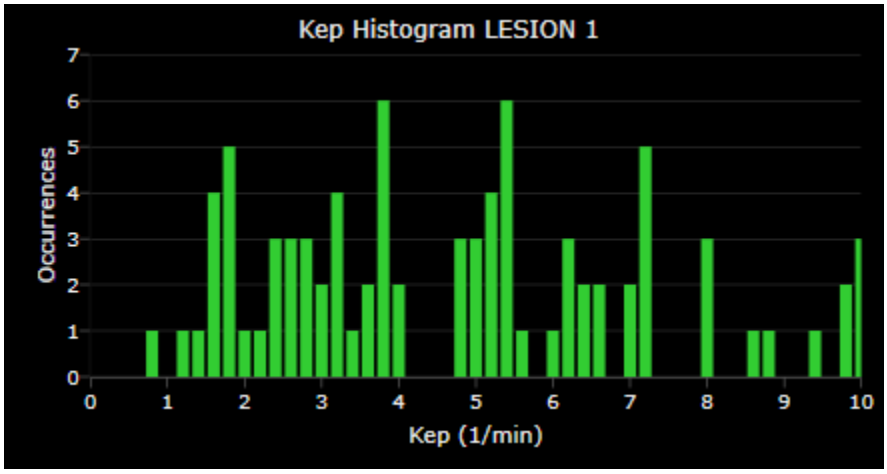
K^{trans} (Perm) Histogram - Displays the Histogram of K^{trans} (Permeability) values of the selected ROI.



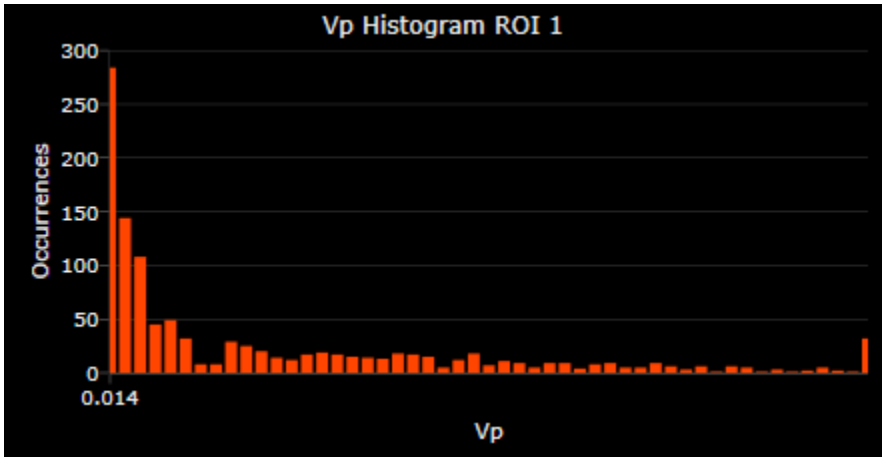
V_e Histogram: Displays the Histogram of V_e (extra-cellular volume) values of the selected ROI.



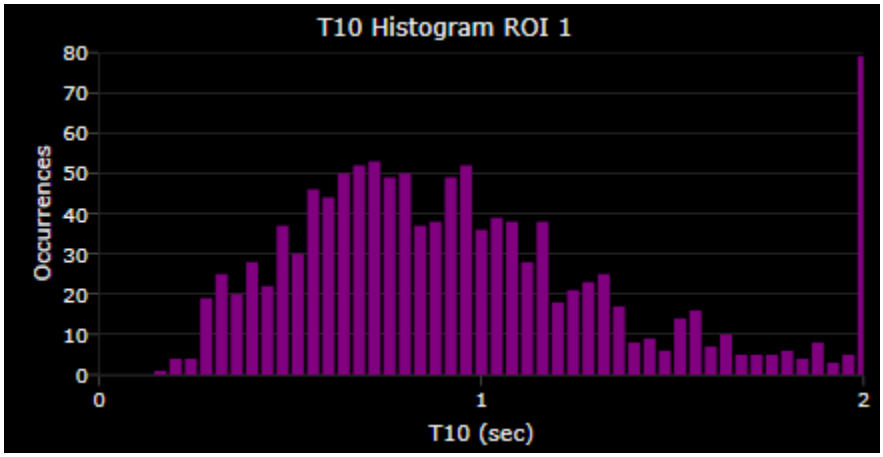
K_{ep} Histogram - Displays the Histogram of K_{ep} values of the selected ROI.



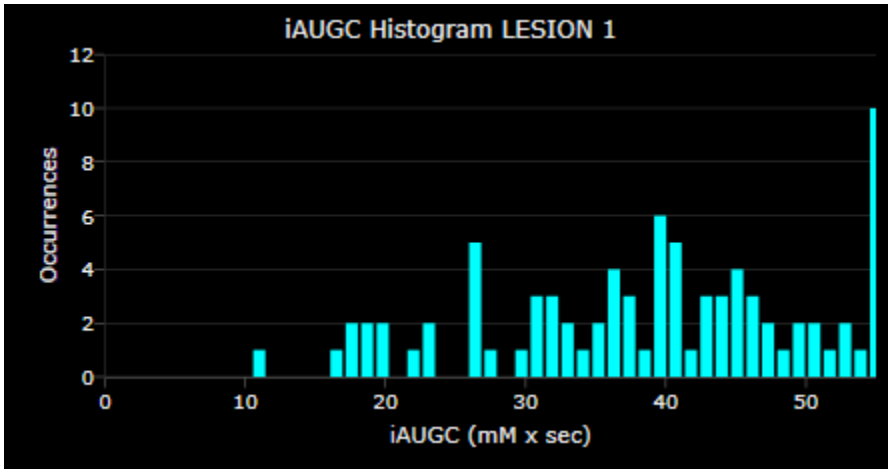
V_p Histogram - Displays the Histogram of V_p values for the selected ROI. Currently this analysis is not available.



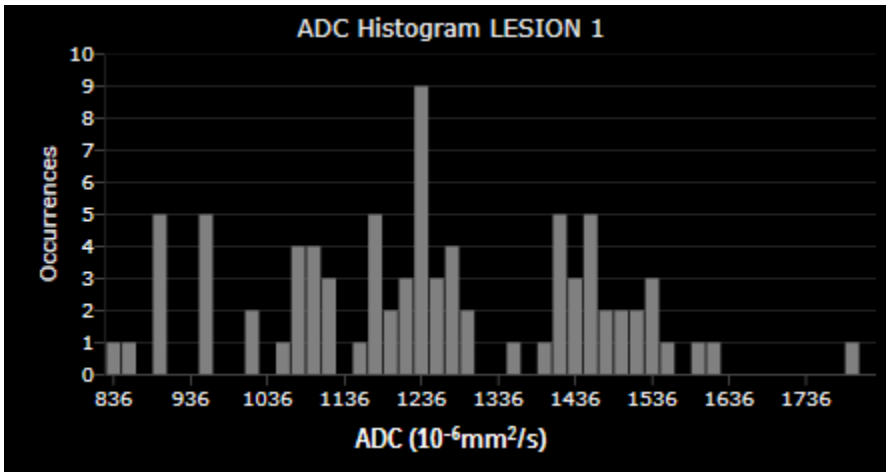
T10 Histogram - Displays the Histogram of T10 values for the selected ROI.



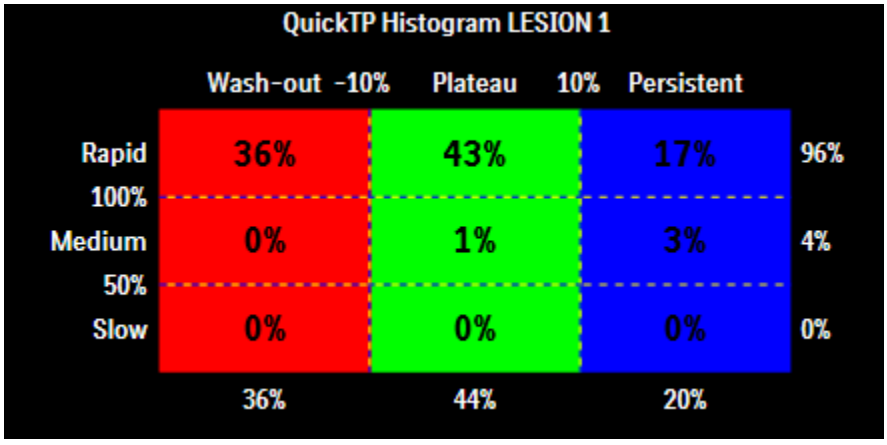
iAUGC Histogram - Displays the Histogram of iAUGC values of the selected ROI.



ADC Histogram - Displays the Histogram of ADC values of the selected ROI. DynaCAD does not do any ADC value calculations using DWI images. When an ROI is drawn over a pre-existing ADC image, DynaCAD displays the intensity statistics in a $10^{-6}mm^2/sec$ format.



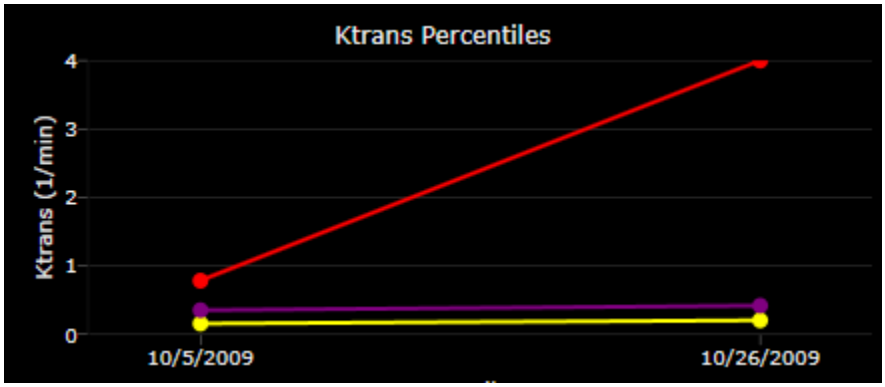
QuickTP Histogram - Displays the Histogram of the QuickTP percentage breakdown for Washout/Plateau/Persistent by Rapid/Medium/Slow of a selected ROI.



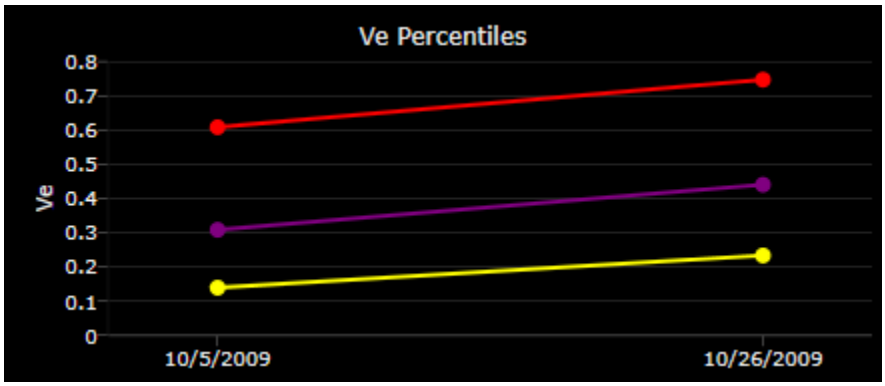
Compare Charts

A number of Compare Charts are available for displaying the 10th, 50th and 90th percentile parameters such as K^{trans}, V_e, etc. of the selected ROI for each study. One ROI has to be chosen from each study. This can be done either by clicking on the ROI label, or by clicking on the corresponding item in the Lesion Analysis Summary.

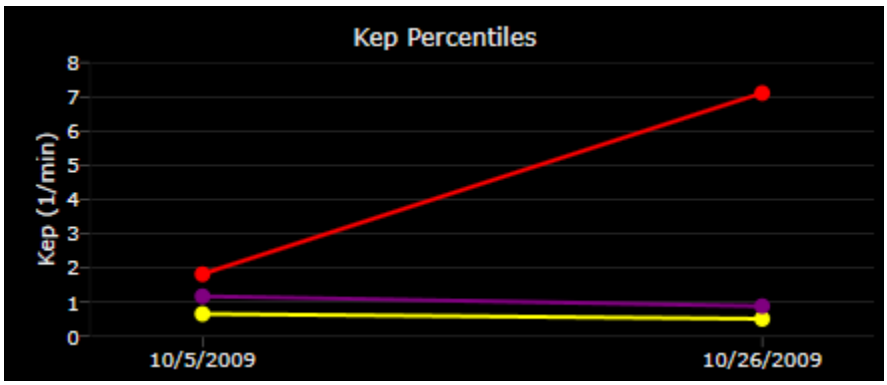
K^{trans} Compare Chart - Displays the 10th, 50th and 90th K^{trans} percentile values of the selected ROIs.



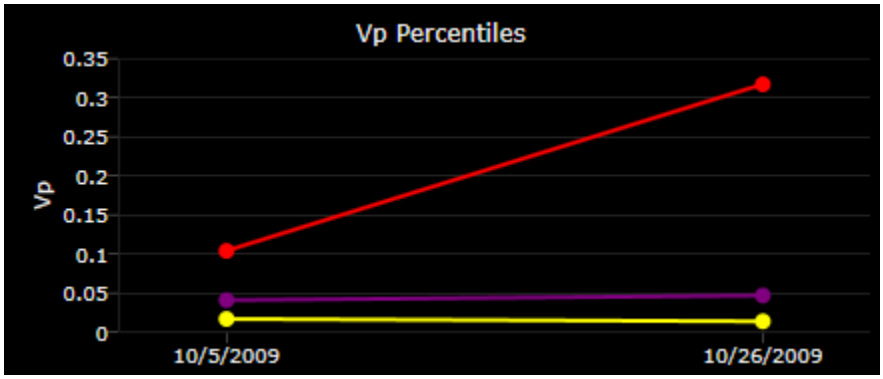
V_e Compare chart - Displays the 10th, 50th and 90th V_e percentile values of the selected ROIs.



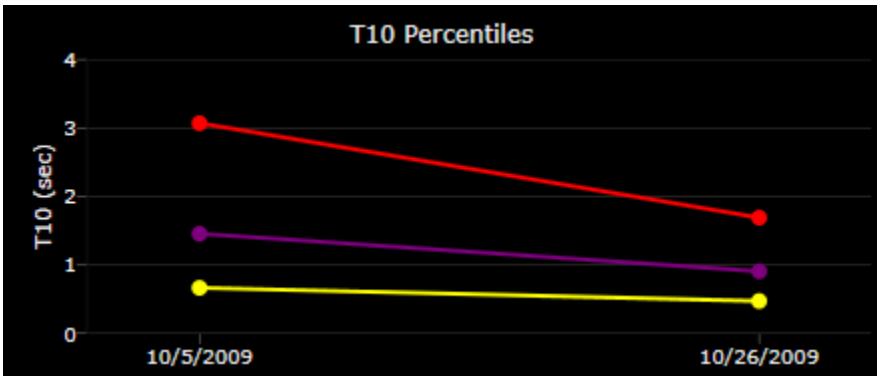
K_{ep} Compare chart - Displays the10th, 50th and 90th K_{ep} percentile values of the selected ROIs.



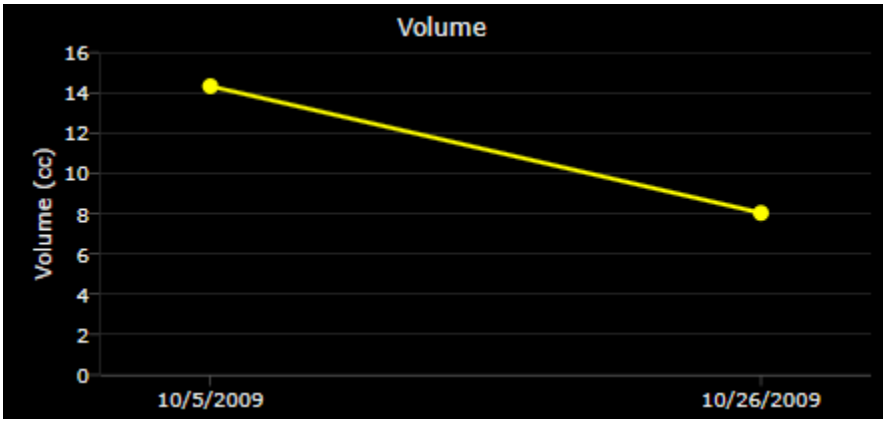
V_p Compare chart - Displays the10th, 50th and 90th V_p percentile values of the selected ROIs. Currently this analysis is not available.



T10 Compare chart - Displays the10th, 50th and 90th T10 percentile values of the selected ROIs.



Volume Compare chart - Displays the total volume values of the selected ROIs.

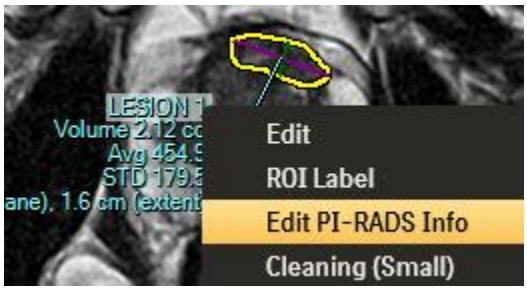


8.5 PI-RADS

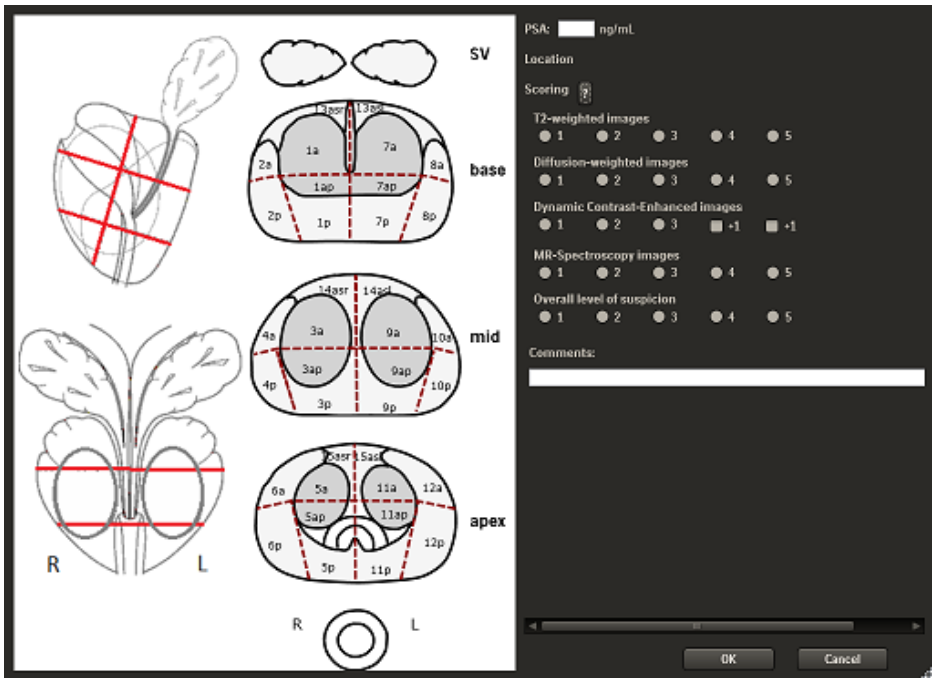
PI-RADS scoring can be entered for each suspected lesion identified:

- Create a 2D or 3D ROI.

- Right click on the ROI, and select **Edit PI-RADS** Info.



- The PI-RADS Info dialog will be displayed



On the left hand panel, the prostate schema is shown. Left click on one or more segments to indicate the location of the suspected lesion. Once selected, the **Location** text will be displayed on the right hand panel.

Scoring can be assigned based on findings on the T2-weighted, DWI, DCE and MR-Spectroscopy sequence as appropriate. However, it is not necessary to provide the scoring for each sequence type. The description for each score can be displayed by left click on the **?** button next to the Scoring label.

Comments can be added that associated with the suspected lesion. This is also optional.

In the same dialog, **PSA** can be entered. The PSA is associated with the subject study, and it will be remembered when the PI-RADS Info dialog is displayed for subsequent ROIs.

Once the PI-RADS information is entered, click the **OK** button to save. The PI-RADS information will be available in the PI-RADS report (see Section 10.6).

8.6 Auto navigation with Multiple ROIs

Performing several ROI analyses on one study produces a summary analysis for each ROI. Auto navigation helps you review all the ROIs quickly by allowing you to quickly display the source ROI for any Summary Chart.

To auto navigate back to a source ROI, left click the corresponding ROI item under the **Lesion Analysis Summary** chart. The image will immediately navigate to the ROI used to produce the report.

9 Hanging Protocols

9.1 Introduction

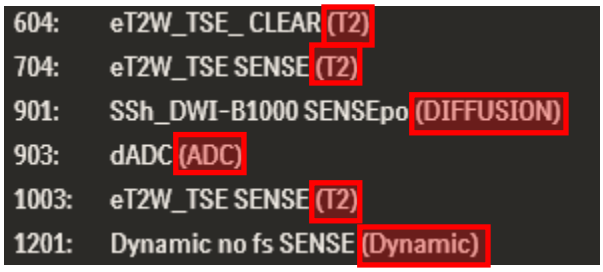
Hanging Protocol allows the user to save a layout, viewport assignment (sequence type for image series, chart type for chart) and viewport attributes (e.g. linking, color overlay, time point selection, rendering mode), and apply automatically or manually in subsequent reading of the same type of study.

Setting up Hanging Protocols consists of two steps and is simple. The first step is to define how the study should be hung. This can be achieved *in place* in the application, i.e. simply arrange the series in the viewer, and then save the settings. The second step is to define the matching criteria so that the appropriate Hanging Protocol will be applied during data loading.

9.2 Creating, Editing, or Deleting a Hanging Protocol

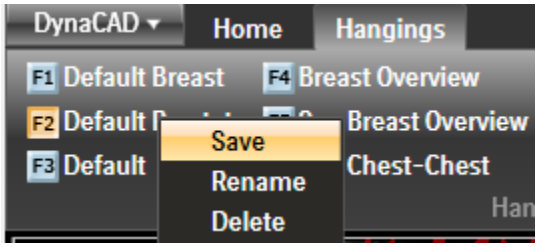
To create a new Hanging Protocol:

- Make sure the Image Stack Grouping Filter classify the series correctly for the study. Check the Right Mouse Context Menu's series list, and ensure the sequence type appended to the series are correct.. For example:

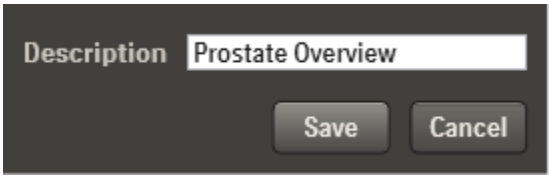


Note: *For Hanging Protocol to work correctly, those series that are included in the Hanging Protocol layout should be classified correctly. However, those series that are not included in the layout may not need to be classified.*

- Choose the desired layout from the **Screen Layout** button under the **Hangings** tab of the toolbar.
- Assign the series to each viewport by selecting the series from the Right Mouse Context Menu.
- Choose the desired viewport attributes such as rendering mode.
- Once all the parameters are set, right click on the **F**-key of the **Hanging** tab that you want to assign the Hanging Protocol to and select **Save**. Type in the name to be assigned.



- Enter the **Description** of the Hanging Protocol and click the **Save** button to save the Hanging Protocol.



To edit a Hanging Protocol:

- Open a study and left click the Hanging Protocol **F**-key to apply the Hanging Protocol.
- Change the layout and update the viewport attributes as desired.
- Right click on the desired **F**-key and select **Save**. You may use the existing Description or enter a new one. Click the **Save** button to save the new settings.

To delete an existing Hanging Protocol:

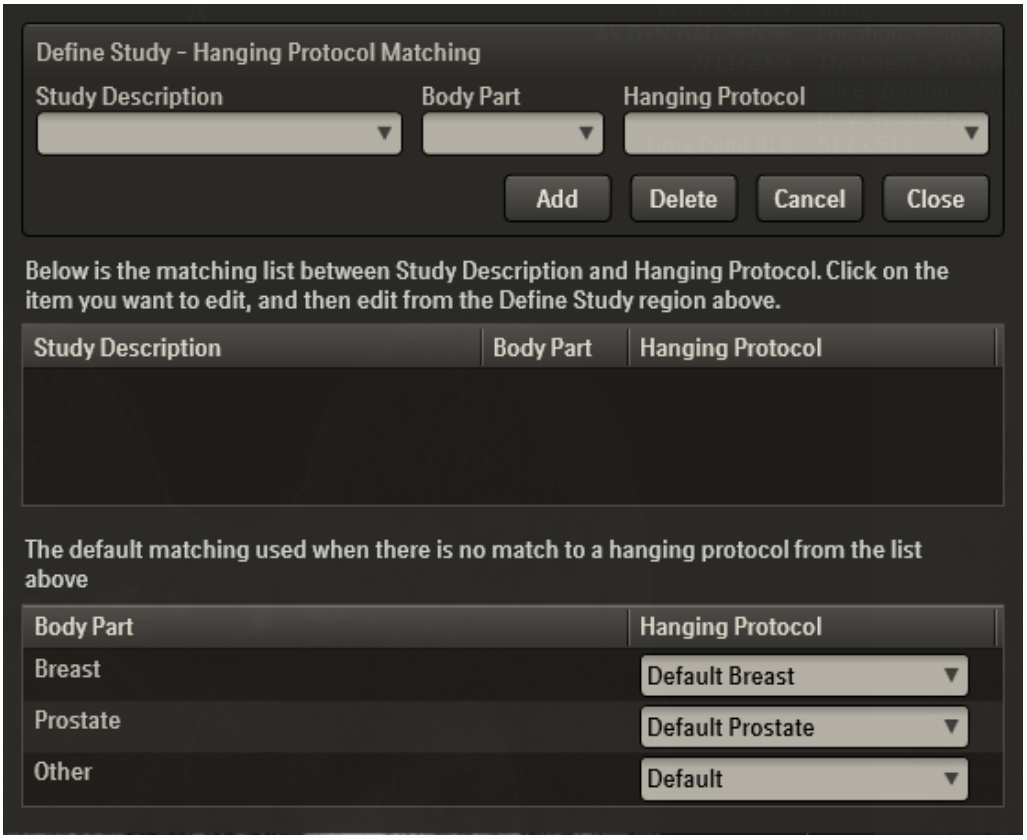
- Right click on the **F**-key Hanging Protocol to be deleted.
- Select **Delete**.

9.3 Hanging Protocol Matching

Up to twelve (12) Hanging Protocols can be defined. It is desirable that the appropriate Hanging Protocol is applied automatically during the initial loading. To achieve this, the Hanging Protocol matching rule can be defined using the Hanging Protocol Matching UI.

The Hanging Protocol Matching UI can be invoked by left click on the highlighted region indicated below:

The Hanging Protocol Matching UI will be displayed:



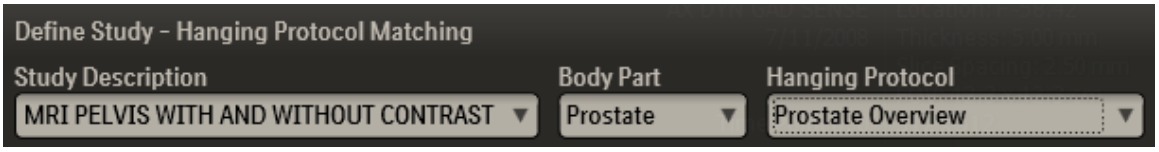
The top pane of the UI **Define Study – Hanging Protocol Matching** allows to define a matching rule. The middle pane lists the matching rules that are already defined. The bottom panel specifies the default Hanging Protocol to be applied when no match is found during loading.

9.3.1 Create, Edit and Delete Matching Rule

To define a matching rule:

- Enter the **Study Description**. It provides a dropdown list that contains all the different Study Description known to the DynaCAD database, the Study Description can be selected from the list.
- Select the **Body Part**.
- Select the **Hanging Protocol** from the dropdown list that is associated with the Study Description and Body Part.
- Click the **Add** button.

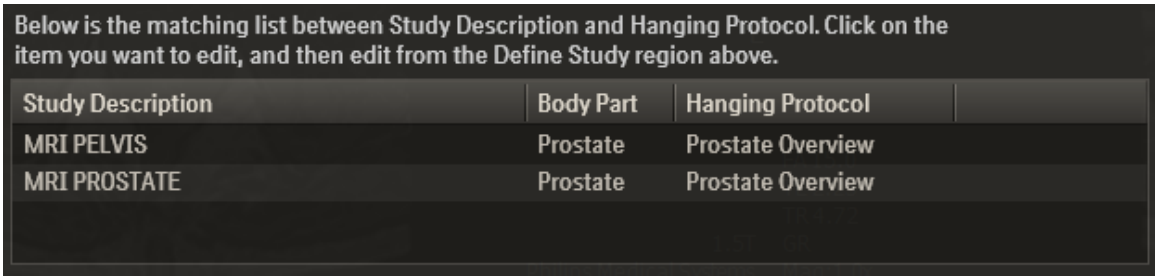
For example:



A prostate study with Study Description *MRI PELVIS WITH AND WITHOUT CONTRAST* will be mapped to the *Prostate Overview* Hanging Protocol.

The Study Description in the DICOM header may not be consistent amongst all studies of the same type. There may be typos, or there may be slight variations between the configurations in different scanners. To handle the variations, the matching algorithm supports a flexible matching scheme that is based on the best match of the Study Description. Because of this, specifying a partial Study Description may work better unless the Study Description is always consistent, e.g. using a DICOM Modality Worklist. A typical partial Study Description will contain the key portion of the entire text, e.g. *MRI PELVIS*, in the above example. This will match with Study Description that contains *MRI PELVIS*.

Multiple Study Description can be setup to match to the same Hanging Protocol. For example:



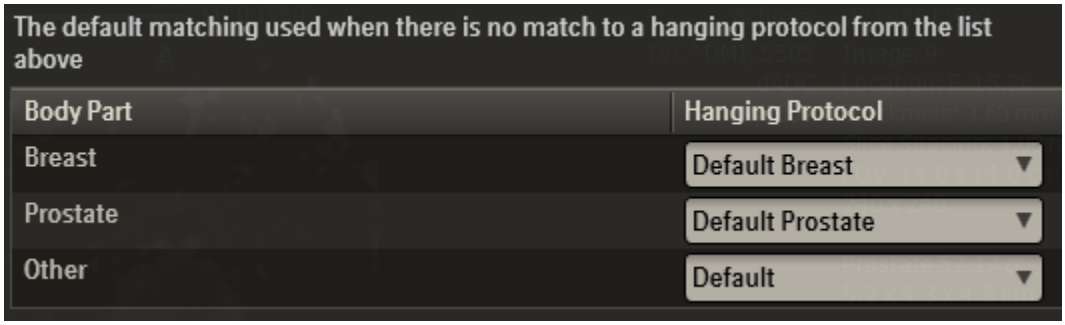
In this example, Study Description contains either *MRI PELVIS* or *MRI PROSTATE* will map to the Prostate Overview Hanging Protocol.

To edit an existing matching rule, left click on the item in the middle pane showing the matching rules. The top pane **Define Study – Hanging Protocol Matching** will reflect the selected item. Modify the matching rule as needed, and click on the **Add** button. This will add a new matching rule to the list. The original rule that was selected may still be available, e.g. the Study Description is updated because one may want to add a new rule instead of update existing one.

To delete an existing matching rule, left click on the item in the middle pane showing the matching rules. Click on the **Delete** button. The selected matching rule will be deleted.

9.3.2 Default Hanging Protocol

If no matching rule is found, then the default Hanging Protocol is applied on loading. The default Hanging Protocol for each Body Part can be specified in the bottom pane:


The default matching used when there is no match to a hanging protocol from the list above
Body Part
Hanging Protocol
Breast
Default Breast
Prostate
Default Prostate
Other
Default

10 Key Images and Reports

10.1 Creating Reports

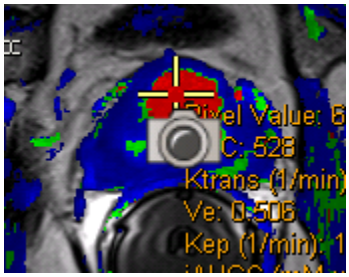
There are three ways to create a report:

- Capture images as Key images and then either save them as DICOM Secondary Capture images or bitmaps, or send them to a Windows printer to create a hardcopy. This option is usually used in the case when the actual report is created by a 3rd party dictation system, and the only requirement is to create a set of key images.
- Capture images and arrange them in a predefined image layout (2 or 3 images per row). A report header that contains patient demographic information will be appended and the report can be saved as a pdf or DICOM Secondary Capture or DICOM Encapsulated PDF.
- Using an ROI lesion based automatic template to capture key images and charts to create a general or PI-RADS report.

10.2 Creating Key Images

10.2.1 Capture Image Individually

Left click the in-viewport shortcut **Capture Image** camera button or the **Capture Image** button under the **Home** tab of the application toolbar. This will take a snapshot of the active viewport and place it in Key Images. Visual feedback in the form of a camera icon will appear briefly in the viewport to confirm the image capture.



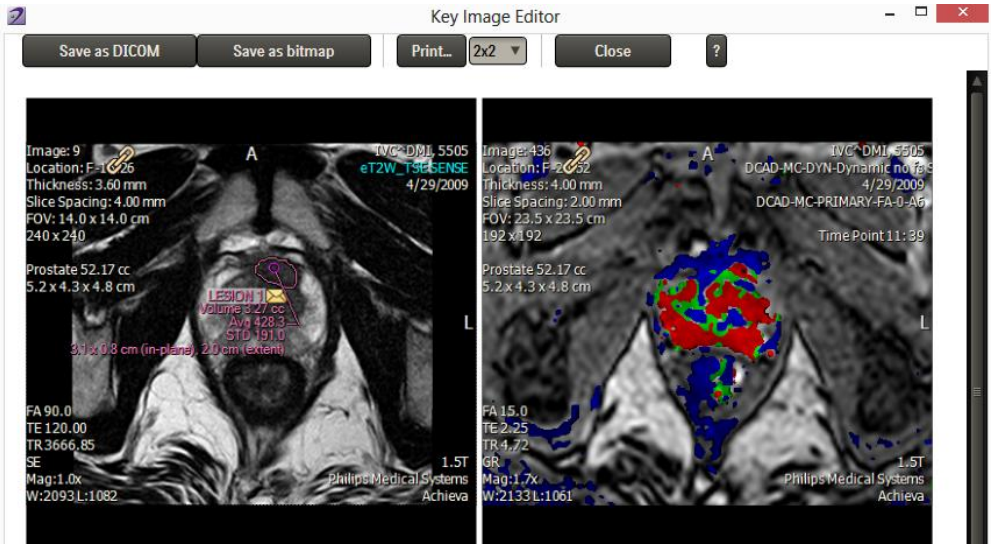
NOTE: *To capture charts, highlight the chart viewport and left click the* ***Capture Image*** *button under the* ***Home*** *tab of the application toolbar.*

10.2.2 Capture All Displayed Images

Left click the **Capture All** button under the **Home** tab of the application toolbar to take a snapshots of all the viewports in the layout and place them in key images and reports.

10.3 Review and Save Key Images

Captured key images can be displayed for review by clicking on the **View Captures** button under the **Home** tab of the application toolbar.



The **Key Image Editor** will display the captured images. Several options are available for saving and printing:

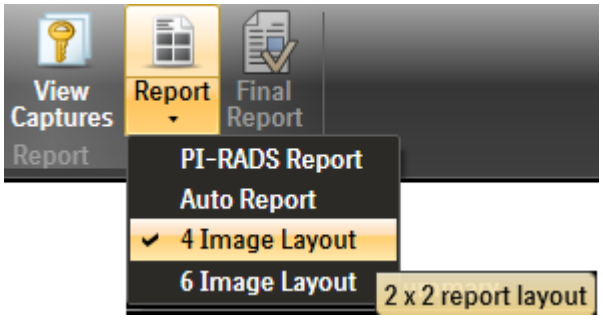
- **Save in DICOM** saves each capture in a DICOM Secondary Capture image.
- **Save as bitmap** saves each capture as a bitmap file. A prompt will be displayed for the file location and name to be saved.
- **Print…** will send the captures to a selected Windows print device. Select the layout next to the **Print** button for composing the print layout.
- The Help button, **?**, displays the mouse interactions for manipulating the capture images.

  Pan – Right Mouse click and drag
  Zoom – Mouse wheel button click and drag
  Drag and Drop – Left Mouse click and drag
  Delete – Hold Delete key and left click viewport

10.4 4 or 6 Image Layout Report

After capturing the key images, left click the **Report** button in the application toolbar. Choose either the **4 Image Layout** or the **6 Image Layout** report. The 4 Image Layout

organizes the key images in 2 columns, and the 6 Image Layout organizes them in 3 columns.



A report header with patient demographics information will be added to the report. The information can be edited.

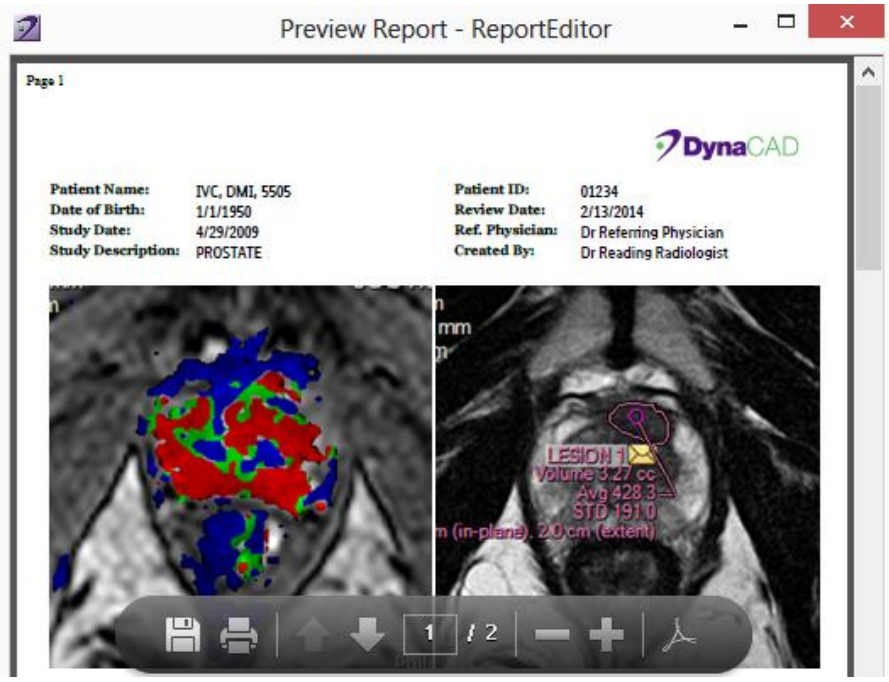
DynaCAD

Patient Name:	IVC, DMI, 5505	**Patient ID:**	01234
Date of Birth:	1/1/1950	**Review Date:**	2/13/2014
Study Date:	4/29/2009	**Ref. Physician:**	Dr Referring Physician
Study Description:	PROSTATE	**Created By:**	Dr Reading Radiologist

The current report can be saved as a draft for editing later or as a final report. Left click the **Save as draft report** or **Save as final report** button accordingly. The draft report will reside in the DynaCAD Server, and will be loaded if the **4/6 Image Layout** Report is invoked again. However it cannot be DICOM transferred. Once it is saved as a final report, it is available as a DICOM object and can be DICOM export. The final report can be displayed by clicking the **Final Report** button in the application toolbar.

The report can also be saved as a burn-in image in a DICOM Secondary Capture object by clicking the **Save as DICOM** button. The DICOM SC object can be sent to almost any DICOM viewer for viewing.

In addition to saving the report in DICOM format, it can also be saved as a pdf file, e.g. as an attachment to an email. To save the report as a pdf file, click the **Preview** button and the images will be displayed in a pdf viewer as shown below. Hover the mouse cursor to the bottom of the window, and select the Save icon. It will prompt for the folder and file name to be saved.



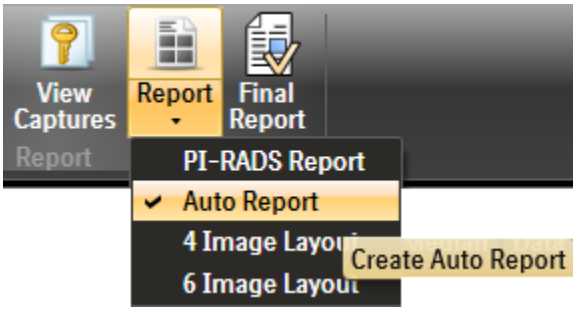
The **Print…** button in the Report Editor allows the report to be sent to a chosen Windows print device. Alternatively, print is also available in the pdf viewer.

10.5 Lesion Based Auto Report

Lesion based Auto-Report automatically captures a set of pre-configured images per lesion based on a report template, and create a report with a header containing patient demographics information.

To create an Auto Report:

- Create one or more ROIs.
- Left click on the **Report** button label in the application toolbar to dropdown the report options.



- Select **Auto Report**

It will then automatically capture the images based on the report template, and create the report accordingly. Depending on the report template, text fields may be available to enter comments and findings to the report.

In addition to the automatic captured images created for each lesion, it will also append the manual captures to the end of the report.

The report can be print and save similar to the 4 and 6 Image Layout Report.

10.6 PI-RADS Report

The mechanism of the PI-RADS report is similar to that of the Auto Report. It is also template based, and images will be captured automatically per lesion. PI-RADS scoring information will be added per lesion, as well as the prostate volume and dimensions, PSA, rendering of the prostate mesh with the suspected lesion and the prostate schema with the segment of the suspected lesion highlighted.

10.7 Configuring the Auto Report Template

The Auto Report templates are managed in the DynaCAD Server. The Report Template Editor is the tool to configure the templates for both Auto Key Image, Auto Report and PI-RADS Report. The editor is available on the DynaCAD Server and can be invoked either from the desktop icon or **Windows Start → All Programs → Invivo DynaCAD Server → Report Template Editor**.

To configure a template:

- Choose the type of report under the **Edit template for** section.
- Choose the Body Part.

***NOTE**: Body Part section will not be shown for PI-RADS Report*.

- Choose the image layout from the **Image Layout** section.

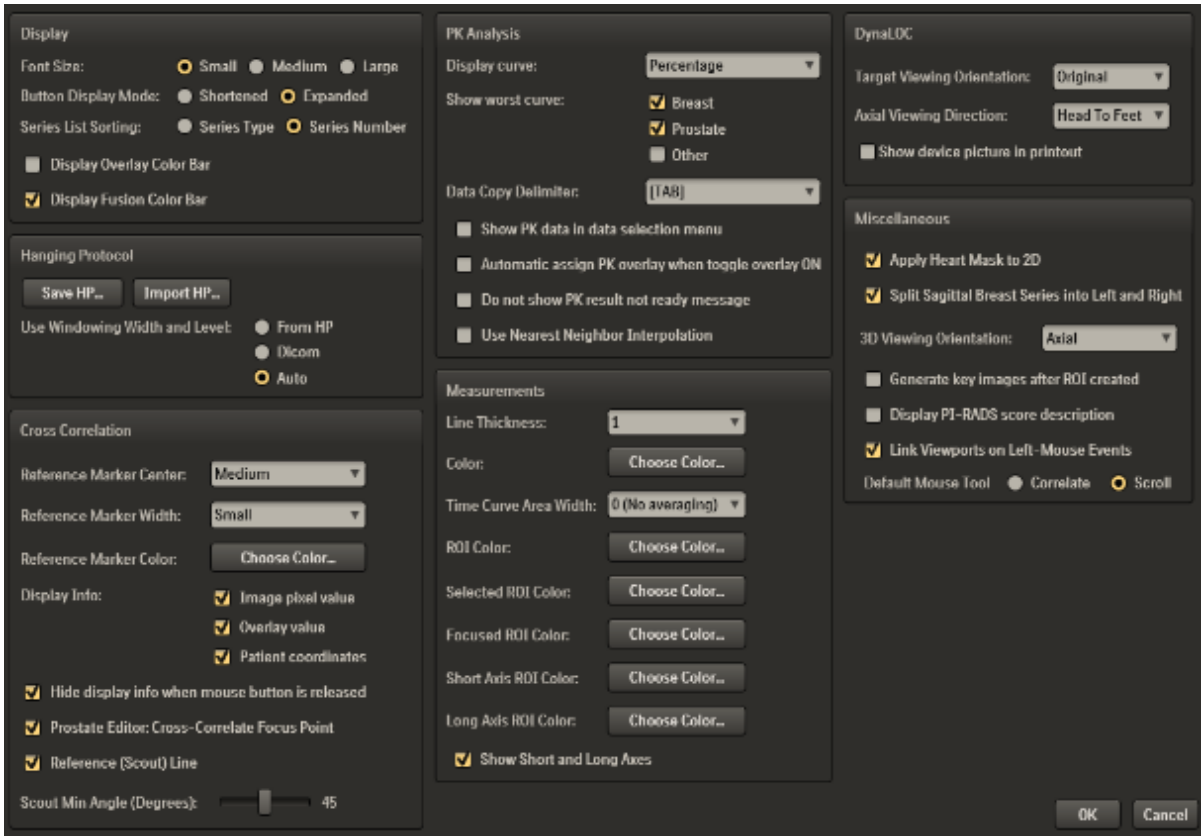
***NOTE**: Image Layout section will not be shown for Auto Key Image*.

- Left click and drag the desirable images and charts from the list under **Images and Charts** section to the **Image Layout** on the right panel. If all the viewports are filled and an addition row is required, drag and drop the desirable item to the lower border. A new row will be added.
- Left click and drag the **Text Input Items** from the left panel to the corresponding one on the right panel.
- To remove unwanted items in the report template, left click and drag the item to the **Trash** icon on the left.

Click the **Save** button when the template is configured.

11 User Options

From the main application window, left click on the DynaCAD button and select **Options**. The User Options dialog will be displayed.



11.1.1 Display

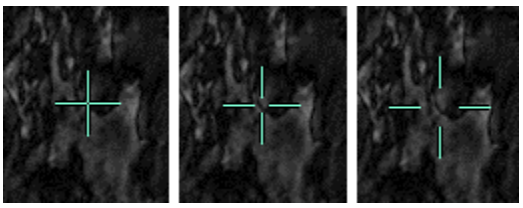
- **Font Size:** Allows changing the font size for the ribbon bar text. The default is set to small.
- **Button Display Mode:** Allows shortening or expanding the number of icons displayed in the **Home** and **Hangings** ribbon bar.
- **Series List Sorting:** Allows choosing how the series list will be displayed in viewports when the right mouse button is pressed. Selecting **Series Type** will display the list by the series description (Dynamic, T1, T2, etc.). Selecting **Series Number** displays the list by numerical order, starting from the lowest series number.
- **Display Overlay Color Bar:** Checking this box will automatically display a color bar in a viewport when a color overlay (PK PRIMARY, K^{trans}, V_e, etc.) is displayed.
- **Display Fusion Color Bar:** Checking this box will automatically display a color bar in a viewport when an ADC or DWI overlay is displayed.

11.1.2 Hanging Protocol

- **Save HP:** Selecting this option allows saving the user's hanging protocols to a file. This feature easily allows importing the hanging protocols to other DynaCAD systems.
- **Import HP:** Selecting this option allows importing a hanging protocol file from another DynaCAD system. The user's hanging protocols will be overridden.
- **Use Windowing Width and Level:** This option allows choosing from what location window/level values will be used for displayed images. The default is set to Auto.

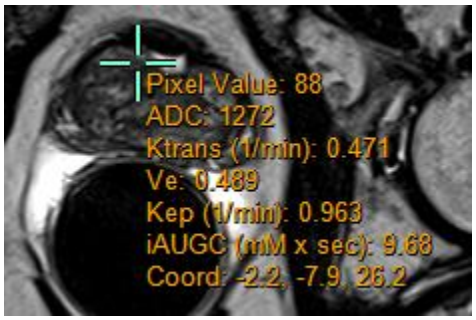
11.1.3 Cross Correlation

- **Reference Marker Center:** Allows changing the gap of the cross hair Correlate tool. The default is set to medium.



Small Medium Large

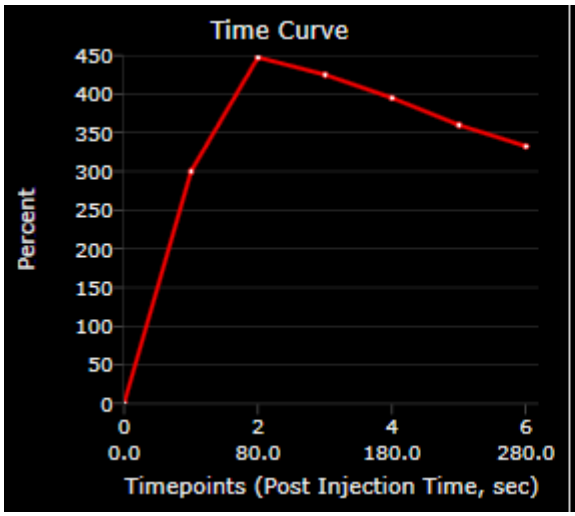
- **Reference Marker Width:** Allows changing the line thickness of the Correlate tool. The default is set to small.
- **Reference Marker Color:** Allows changing the color for the line of the Correlate tool.
- **Display Info**
    - **Image pixel value:** Checking this option will display the image pixel value when using the correlate function.
    - **Overlay value:** Checking this option will display the PK, ADC and DWI values when using the Correlate function..
    - **Patient coordinate:** Checking this option will display the image coordinates when using the correlate function.



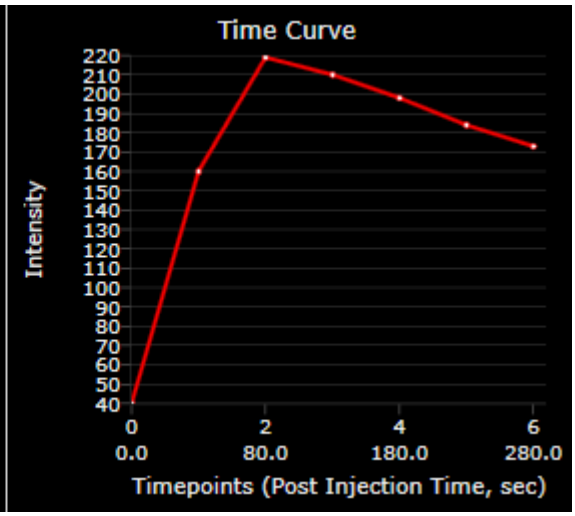
- **Prostate Editor: Cross-Correlate Focus Point:** Checking this box will automatically synchronize the other planes of the prostate editor images when clicking directly on the prostate boundary outline.
- **Reference (Scout) Line:** Checking this option will display a scout line on different image planes while scrolling an image in another plane. The default setting is checked, meaning a reference scout line will be displayed.
- **Scout Min Angle (Degrees):** This option allows setting the minimum angle for the scout line to be displayed between two images in different planes. For example, if two axial image data sets are loaded, with one axial image data set at an oblique angle compared to the first data set, the angle between them will be small. In this case, the scout line is not meaningful and the scout line will not be displayed because the images are almost parallel to each other. However, for an axial and a sagittal, the images are orthogonal to each other, i.e. large angle (or 90°) between them, the scout line will indicate the intersection between the two images being displayed. The choices of degrees are between 1° and 89°.

11.1.4 PK Analysis

- **Display curve:** Selecting this option allows choosing display of percentage or intensity time curves. The default setting is percent.



Percent Time Curve



Intensity Time Curve

- **Show Worst Curve:** This option allows displaying the worst curve for breast, prostate or other organs (currently not available) when an ROI is drawn. Checking the box enables the worst curve to be displayed in the curve analysis chart when an ROI is drawn. The following are explanations of the various worst curves:

  QuickTP:

  Worst WashIn: The voxel within the selected ROI passing the thresholds that has the largest percent enhancement between TP0 and TP1.

Worst WashOut: The voxel within the selected ROI passing the thresholds that has the largest washout between TP1 and TP2.

Worst WashIn/Out: The voxel within the selected ROI passing the thresholds that has the largest product of WashIn and WashOut percent enhancements.

PK:

Worst WashIn: The voxel within the selected ROI passing the thresholds that has the largest percent enhancement between the baseline and phase1.

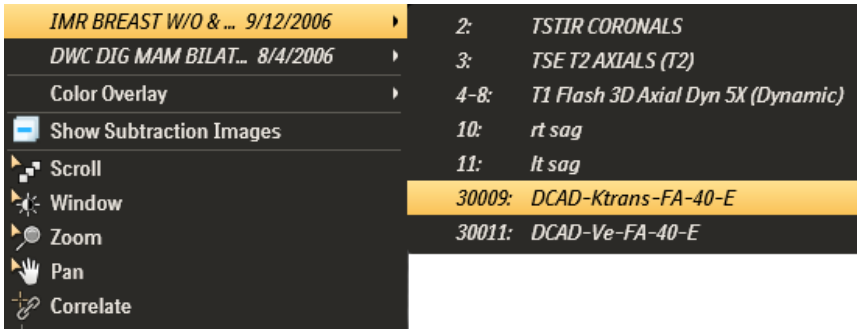
Worst WashOut: The voxel within the selected ROI passing the thresholds that has the largest washout between phase1 and the last dynamic phase.

Worst WashIn/Out: The voxel within the selected ROI passing the thresholds that has the largest product of WashIn and WashOut percent enhancements.

Where “phase1” is defined as:

- breast - the dynamic phase closest to the 90 second post contrast arrival dynamic phase
- prostate - the dynamic phase closest to the 45 second post contrast arrival dynamic phase
- other organ – closest to the “Peak Time (in seconds)” post contrast arrival dynamic phase.

- **Data Copy Delimiter:** This option is used to configure how data (e.g.: K^{trans} values) will be exported. This option makes it easier to import data into a Microsoft Excel spreadsheet. The default is set to [TAB].
- **Show PK data in data selection menu:** Checking this option will include the PK data series as part of the series list under the Right Mouse Menu. The default setting is unchecked; the PK data series will not appear in the Right Mouse Menu’s series list..



PK data series shown in the series list

- **Automatic assign PK overlay when toggle overlay ON:** Checking this option will allow turning on and off the color overlay in every viewport when toggling the **Color Overlay** button from the ribbon bar. The default setting is unchecked.

- **Do not show PK result not ready message:** Checking this option will not display a message notifying the user if the PK processing isn't complete. The default setting is unchecked; the notification message will appear.

- **Use Nearest Neighbor Interpolation:** Unchecking this option will use an algorithm to smooth the color overlays when the image is zoomed up. The default setting is unchecked.

11.1.5 Measurements

- **Line Thickness:** Selecting this option will allow changing the line thickness when drawing an ROI. The default is set to 1.

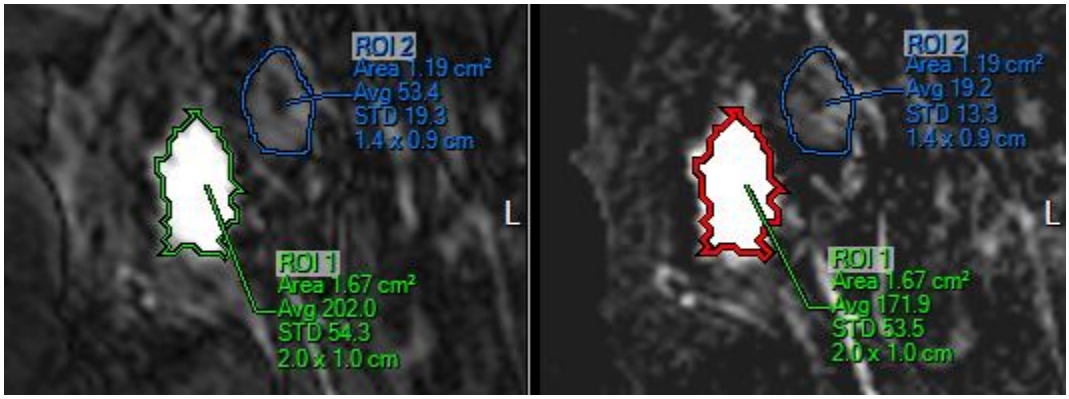
- **Color:** Selecting this option will allow choosing a different color line when drawing an ROI.

- **Time Curve Area Width:** This option is used when displaying the time curve. It allows selecting how large an area under the pointer it will use to calculate and display the curve when pointing to a voxel of interest. When using the 1 or 2 mm option it will take the average width of that area under the pointer. When using 3x3 Voxels, it will take the average of a 3x3 voxels region under the pointer. The curve display may take a few seconds to update when using the 1 or 2 mm option as it will be calculating an average of that width. The default is set to zero, no averaging.

- **ROI Color:** This option allows to select a color for the ROIs that are not currently in focused or selected.

- **Selected ROI Color:** A ROI can be propagated to other viewport(s). When the user clicks on a ROI in one viewport, the corresponding propagated ROIs in other viewports are referred to as the Selected ROIs. This option allows to select a color for the selected ROIs.

- **Focused ROI Color:** When the user clicks on a ROI, this ROI becomes the Focused ROI. This option will allow to select a color for the ROI outline and text for the Focused ROI. This feature enables users to recognize the Focused ROI (by using a different color) and is particularly useful when multiple ROIs are drawn on the same slice. Choosing this option will bring up a color palette to choose a different color.



In the example above, the Focused ROI color was set to Red, Selected ROI color was Green, and ROI color (non-focused, non-selected) was Blue. Two ROIs were drawn in one viewport and propagated to the other viewport. The user clicked on ROI 1 on the right viewport. The ROI 1 on the right viewport is now in focus, hence the outline appeared as Red. The corresponding ROI displayed in the left viewport was the Selected ROI and appeared as Green. Both label of the Focused and Selected ROI were displayed as the same color as the Selected ROI color, i.e. green, so that they can be visually correlated easily. All other ROIs outline and labels were displayed as Blue.

- **Short Axis ROI Color:** Selecting this option will allow choosing a different color line for the shortest axis (distance) within the ROI.
- **Long Axis ROI Color:** Selecting this option will allow choosing a different color line for the longest axis (distance) within the ROI.
- **Show Short and Long Axes:** Checking this option will display the line for the shortest and longest axes of an ROI.

11.1.6 Miscellaneous functions

- **Apply Heart Mask to 2D:** Checking this option will apply a mask on images when the **Heart** button is selected in the viewer.
- **Split Sagittal Breast Series into Left and Right:** Checking this option allows a single sagittal acquisition that includes both breasts to be split into Left breast and Right breast in the viewer. This allows users to create a hanging protocol to display the left and right breast separately and with breasts hung chest wall in.

  When the right and left breasts are displayed in adjacent left and right viewport respectively, they are linked by default to allow the user to compare left and right breast. For example, if the user pans or scrolls the left breast, the right breast will also be panned or scrolled in the same anatomical direction. This behavior is similar to that supported by most Mammography viewers that provide specific tools for displaying 2D MG images; DynaCAD expands the concept to 3D MR dataset. The default setting is checked.

<u>WARNING</u>: When reviewing Split Sagittal Breast images verify the left and right images are loaded correctly in the image viewport. This can be done by checking the location text information in the upper left viewport.

- **3D Viewing Orientation:** This option allows setting the displayed default orientation for images when they are loaded in a MIP viewport. The choices are Axial, Coronal and Sagittal, the default setting is Axial.
- **Generate key images after ROI created:** Checking this box will automatically generate a key image summary report when an ROI is generated or if the ROI is edited.
- **Display PI-RADS score description:** This option controls if the description for the PI-RADS to be displayed together with the score numbers. If un-checked, only the score numbers will be displayed.

- **Link Viewports on Left-Mouse Events:** This feature allows users to quickly scroll through an image series in one viewport without the other linked viewports updating. This is particularly useful when reviewing across a slow network where having a number of linked viewports will slow review speeds. Unchecking this box will enable this function. To use this feature, when viewports are linked together, click and hold the left mouse button down and scroll. When the button is released, all the linked viewports will automatically move to that spot.

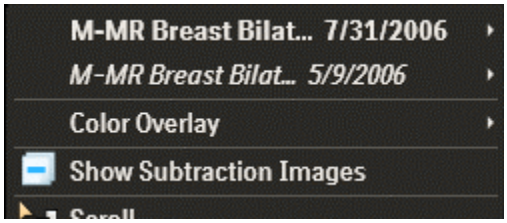
- **Default Mouse Tool:** This option allows the user to set the mouse interaction mode to either Correlate or Scroll. The default is Correlate.

12 Studies Compare

12.1 Loading Multiple Studies

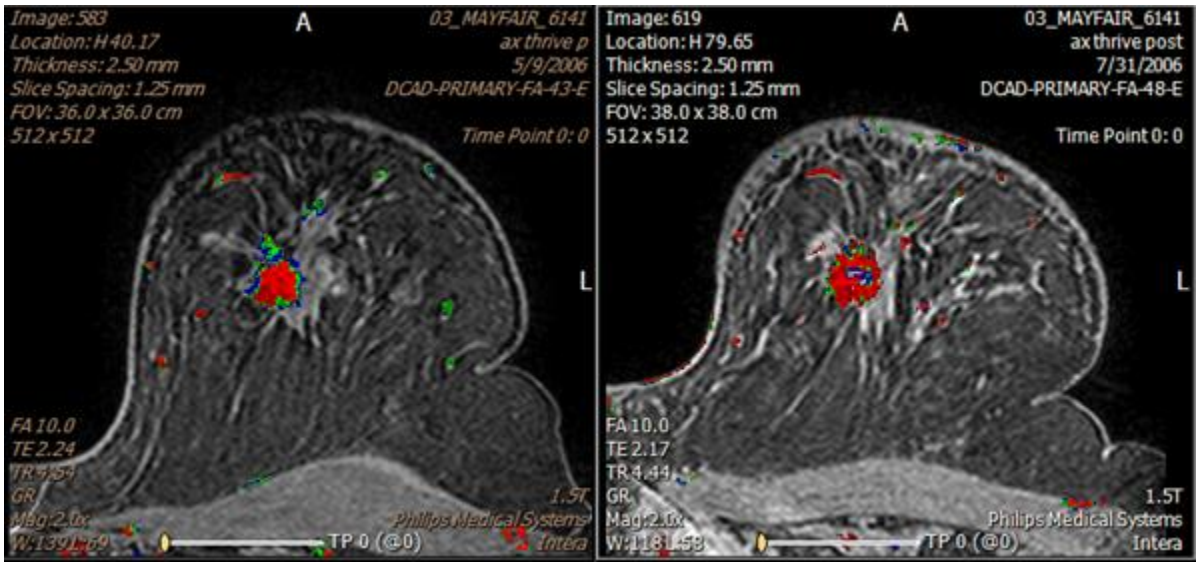
When there are more than one study associated with a patient and are already available in the DynaCAD Server, they will be made available automatically when a study is loaded into the application. If certain prior studies are not available in the DynaCAD Server, the DICOM Q/R function can be used to retrieve the prior studies – see Section 5.2 DICOM Q/R.

From the Right Mouse Context Menu:



the list of available studies will be displayed at the top of the list with the most current study at the top. The user selected study, i.e. the one highlighted in the Study Manager, is displayed in regular font, all other studies are displayed in italic.

When they are displayed on the viewport, the viewport overlay text of the user selected study is displayed in white regular font, whereas the overlay text of the other studies will be displayed in **beige** *italic* font.



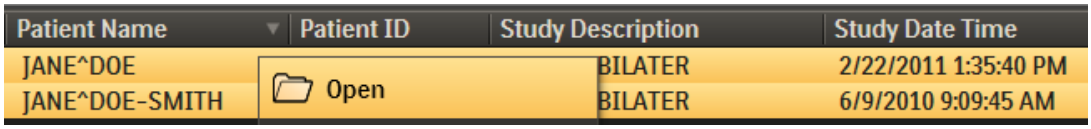
Note: When viewing multiple studies please verify the correct image data is loaded by confirming the study date in the upper right viewport text area.

12.2 Handling of differences in Patient Name and ID

Studies of the same patient may not be grouped under the same patient in the database. For example, last name may be changed after marriage, Patient ID can be different if studies are acquired in different location or institution. These studies will not be recognized as that of the same patient, and they will not be made available together automatically in the application.

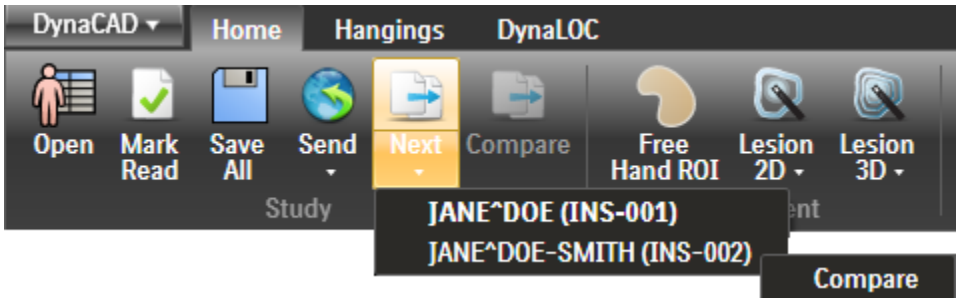
This can be overridden by the user:

- Manually select all the related studies from the Study Manager by CTRL-left click on each of the study.
- Right click and select **Open**. The studies will be loaded into the application.

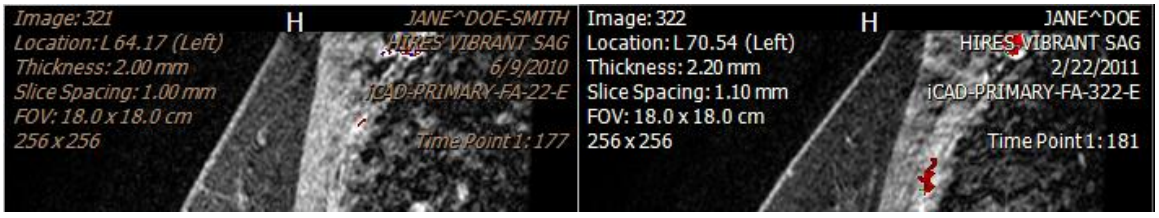


At this time, only the first study is loaded. The other study (with a different Patient Name and/or ID) is consider as the next patient to be read, and it is available under the **Next** button of the toolbar.

- To select the second study to be loaded to the same viewing session, left click on the **Next** button label.
- Right click on the second study and select **Compare**.



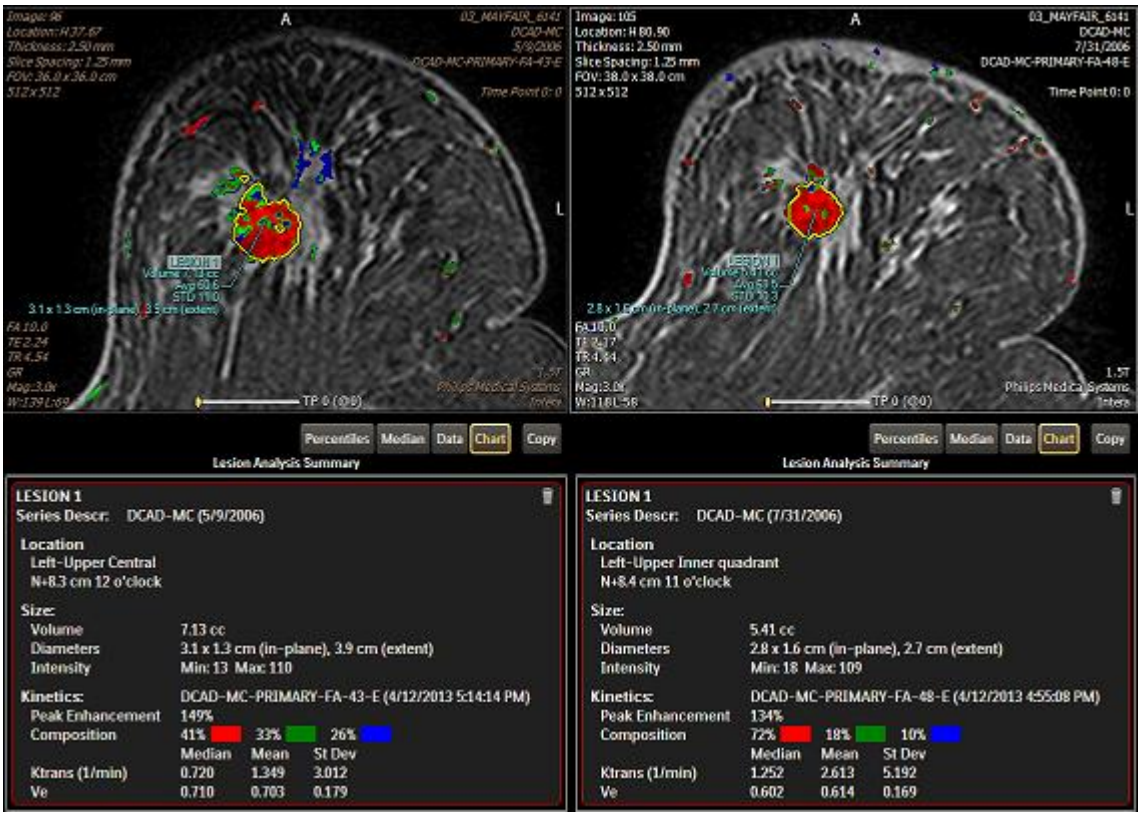
Both studies will now be loaded into the session and can be displayed side-by-side for comparison. The corresponding Patient Name will be displayed in the viewport.



12.3 Compare Display Mode

When more than one studies are loaded into the reading session, the **Compare** button will be enabled. Left click on the **Compare** button will automatically hang all the DCE studies with PK color overlay in the top row, and the Lesion Analysis Summary window for each

study will be displayed in the second row. The current study will be displayed in the leftmost viewport, followed by the most recent prior.



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A. APPENDIX A - SUPPORT

Phone support

Telephone support is available from 8:00 AM to 8:00 PM EST
1-877-INVIVO1 or 1-877-468-4861

E-mail support

Send email to dynasupport@invivocorp.com

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