

GenIQ

User Guide



GenIQ
User Guide, English
5757796-1EN (09/2016) Rev.1
© 2016 General Electric Company
All rights reserved.

This page is intentionally left blank

Applicable Regulations and Standards

Medical Device Directive

This product complies with the regulatory requirements of the following:

- Council Directive 93/42/EEC concerning medical devices: the CE Mark of Conformity affixed to the product testifies compliance to the Directive.



- For a system, the location of the CE Mark of Conformity is described in the system manual.
- Medical Device Good Manufacturing Practice Manual issued by the FDA (Food and Drug Administration, Health and Human Services, USA).
- International Electrotechnical Commission (IEC), international standards organization, when applicable.
- USA/HHS:



CAUTION:

United States Federal law restricts this device to use by or on the order of a physician.

- GE Medical Systems SCS is ISO 9001 and ISO 13485 certified.
- The original document is written in English.

Manufacturer address

GE Medical Systems SCS
283, rue de la Minière
78530 Buc
FRANCE
Telephone: +33 1 30 70 40 40

Legal notices

GE and the GE Monogram are trademarks of General Electric Company.

Advantage Workstation is a trademark of General Electric Company or one of its subsidiaries.

DICOM is the registered trademark of the National Electrical Manufacturers Association for its standards publications relating to digital communications of medical information.

All other trademarks are the property of their respective owners.

Indications for use

GenIQ is an automated post-processing software option that is indicated for use on dynamic magnetic resonance imaging data sets to generate parametric images from the image intensity variations over time. This dynamic change in signal intensity is used to calculate functional parameters related to tissue flow and leakage of the contrast agent from the intravascular to the extracellular space.

GenIQ provides information that when interpreted by a trained physician, can be useful for assessing tissue vascular properties.

Revision history

Revision	Date	Reason for change
1	9/2016	First release of GenIQ user guide 5757796.

About this manual

This topic explains the purpose and design of this manual. It is an introduction to the manual, providing information on the purpose, intended use, graphic conventions, and safety notices that may appear throughout the manual.

This operator manual is to be used for the following product:

- GenIQ



The manual does not identify components or features that are standard or purchasable options. **Therefore, if a feature or component included in the manual is not on your system, it is either not available on your system configuration or your site has not purchased the option.**

Purpose and scope

This manual is written for health care professionals (namely, the radiologist, oncologist and technologist) to provide the necessary information relating to the proper operation of the included software applications. The manual is intended to teach you the features necessary to use the software applications to their maximum potential. It is not intended to make any type of clinical diagnosis.

This user guide is originally written in English.

GenIQ is a software extension of the Volume Viewer application and uses several of the features of this application. When using GenIQ, you should be fully familiar with these features and the relevant safety information from the Volume Viewer user documentation.

Graphic conventions and legends

Please note that the screen captures in this document are intended for demonstration purposes only and may not always be fully identical to the actual user interface (e.g., in color scheme). Use these screen captures as guides.

This manual uses special conventions for images and legends to make it easier for you to work with the information. The table below describes the conventions used when working with menus, buttons, text boxes, and keyboard keys.

Figure 2-1: Graphic conventions

Example	Description
Select Shared Segmentation option	Selecting an option in a check box or radial button and selecting a tab.
Press Enter	Pressing a hard key on the keyboard.
Press and hold Shift	Pressing and holding down a hard key on the keyboard.
Click Compute	A button label or Interface button name.
In the Kernel Spatial Smoothing text box ...	The name of text box in which you can select or type text.
Type <i>series name</i> in the Registered Gated text box	Text you enter into a text box.
Select Clip Min & Max > Ktrans	The pathway of selecting option(s) in a pull-down menu.
Ctrl + X	Press and hold the Control button on the keyboard and press the X button on the keyboard. Ctrl is the abbreviation used for the Control keyboard button, and ALT is the abbreviation used for the Alternative keyboard button.

Example	Description
Select items in a list	Press and hold the Control button and click each item. Press and hold the Shift button and click the first and last item in a contiguous list to select all items.

Safety notices

The following safety notices are used to emphasize certain safety instructions. This manual uses the international symbol along with the danger, warning, or caution message. This section also describes the purpose of an Important notice and a Note.



DANGER:

Danger is used to identify conditions or actions for which a specific hazard is known to exist that will cause severe personal injury, death, or substantial property damage if the instructions are ignored.



WARNING:

Warning is used to identify conditions or actions for which a specific hazard is known to exist that may cause severe personal injury, death, or substantial property damage if the instructions are ignored.



CAUTION:

Caution is used to identify conditions or actions for which a potential hazard may exist that will or can cause minor personal injury or property damage if the instructions are ignored.



Important indicates information where adherence to procedures is crucial or where your comprehension is necessary to apply a concept or effectively use the product.



Note provides additional information that is helpful to you. It may emphasize certain information regarding special tools or techniques, items to check before proceeding, or factors to consider about a concept or task.



Troubleshooting tips provide information that allow you to investigate the resolution of some type of problem, locate the difficulty, and make adjustments to solve the problem.

This page is intentionally left blank

Table of contents

Applicable Regulations and Standards	i
About this manual	iii
Chapter 1: Read me first	1-1
Overview	1-2
GenIQ - an introduction	1-2
Product Description	1-2
Prerequisites	1-2
Chapter 2: Safety	2-1
Safety messages	2-2
General GenIQ safety messages	2-2
Image Reliability	2-2
Considerations	2-2
GenIQ warnings and cautions	2-2
Model-based VIF maps	2-4
PSDs	2-4
Processing time	2-4
Software messages	2-5
Chapter 3: GenIQ	3-1
GenIQ Algorithms	3-2
Equations of the GKM (with a 2-parameter fitting algorithm)	3-3
Semi-quantitative parameters	3-4
GenIQ parametric maps	3-5
GenIQ general information and procedures	3-6
GenIQ work area	3-7
Review steps area	3-7
Tools panels	3-11
Protocol selection screen	3-13
General GenIQ procedures	3-14
Window width and level	3-14
Region of Interests	3-14
Modify and save a protocol	3-14
Graphs	3-14
Fitted curve	3-17
GenIQ high level workflow	3-20
Step 1: Open GenIQ	3-21
Step 2: Review Images and Settings	3-23
Localized VOI	3-23
Motion correction	3-24
Modify phase range	3-25

Select the VIF mode	3-26
Step 3: Review All Maps	3-28
Adjust the threshold	3-29
Clip Min & Max values and select permeability map	3-30
Step 4: Advanced settings	3-31
GenIQ final settings	3-31
GenIQ T1 settings	3-31
Physiologic parameters	3-32
Parametric images	3-32
Downsampling	3-33
Compute	3-33
Step 5: Review permeability maps	3-34
Step 6: Close GenIQ application	3-36
DCE MRI protocol considerations	3-37
Glossary	Glossary-1
Index	Index-1

Chapter 1: Read me first

GenIQ is a software application running on AW (Advantage Workstation™) and AWS (AW Server) on the VolumeShare platform. This manual is specific for concepts, procedures and screens that relate to GenIQ. For details on the following topics, see the Volume Viewer user guide:

- Getting Started: simple exam review in 5 steps
- Protocols Page Description
- On View Controls
- Yellow annotation on an Image
- Keyboard Shortcuts and Tips
- Right-mouse click selections
- Reformat

To facilitate your understanding of GenIQ and for ease of use when executing the procedures, click the hyper-links that often link to a screen from which the step is executed.

The Safety chapter provides information about safety precautions and procedures. It is important for you to read and understand the contents of this chapter so the correct precautions and procedures are followed.

- [Safety cautions and warnings](#)

Before using your system, familiarize yourself with the purpose and design of this manual and the overview of the system user interface.

- [Overview](#)
- [GenIQ work area](#)

READ ME FIRST

Overview

GenIQ - an introduction

This User Guide describes how to use the GenIQ software application for the pharmacokinetic analysis of DCE¹-MRI data sets. The application is used to perform a General Kinetic Model (GKM)-based pharmacokinetic modeling of DCE-MRI data. The goal of GenIQ is to extract functional parameters describing tissue vascular properties such as forward and backward transfer constants, plasma volume, and volume of extra-cellular space.

This document assumes that you have read and understood the AW VolumeShare User's Manual describing the basic operation of the AW VolumeShare tool, working with files, and the various tool boxes. This document only describes the use of the GenIQ software.

GenIQ workflow

GenIQ only processes the following:

- Patient data from a single date.
- Single type of post-processing, which means that you can only compute one series per GenIQ session. If the exam has two series (for example pre- and post-contrast series), the maps must be computed for one series and then quit GenIQ and relaunch it to compute the second series.

Product Description

GenIQ is an application on the AW VolumeShare platform on the AW² and AWS³ systems.

Prerequisites

To view GenIQ, the following must be installed on your AW or AWS system:

- DICOM image data sets
- AW VolumeShare 7 or later
- READY View license

¹Dynamic Contrast Enhanced

²Advantage Workstation

³AW Server

Chapter 2: Safety

This section presents information necessary to successfully work safely with GenIQ.

Safety information includes the following:

- [General GenIQ safety messages](#)
- [Image Reliability](#)
- [Considerations about PURE and other filters](#)
- [All GenIQ warnings and cautions](#)
- [Software messages](#)

Safety messages

Read all cautions and warnings before you use GenIQ.

General GenIQ safety messages

- Use the Advanced review tool to review all the input images for motion artifact or incorrect geometry before processing.
- Use the Advanced review tool to review all the input images for the presence of artifacts before processing.
- Ensure recomputation of maps after modification of input parameters.
- Ensure that there is no discrepancy between functional maps, graphs, statistics, and ROI numbers due to various screen saves taken after re-computation of the maps or modification of the ROIs.
- Software shall not be used alone as a basis for diagnostic or treatment purposes.

Image Reliability



Review outputs of processing to ensure image orientation integrity.

Considerations

PURE

Keep the following important points in mind when using PURE¹ with scans that are post processed or displayed in a viewer.

The PURE feature changes the pixel intensity in the image while providing a more uniform image in the process. This may lead to altered results when GenIQ is used in conjunction with PURE for processing MR images. It is recommended to either disable PURE for dynamic studies or apply the PURE feature uniformly across all the dynamic series.

The output of post processing can be modified with any change to the scan protocol. For optimal image quality, keep consistency with scan protocols and use PURE² for both pre and post contrast imaging.

SCIC, ClariView and other filters

SCIC³ and other image filters are not supported by GenIQ.

GenIQ warnings and cautions



CAUTION:

If the **Compute** button is available, always click it to re-compute the functional maps after making changes to the input parameters. The changes are not taken into account automatically.

¹Phased array UniforMity Enhancement

²Phased array UniforMity Enhancement

³Surface Coil Intensity Correction

**CAUTION:**

Measurements are calculated and displayed by the software to one decimal place (0.1 mm square). You should be aware that the real measurement accuracy is generally considerably less for several reasons. The main factors are image set resolution, display resolution, acquisition accuracy and display settings.

**CAUTION:**

Ensure that you review and if necessary correct the position and signal characteristics of detected vessels in automatic and semi-automatic mode before reviewing the computed functional maps. Switch to a different vessel detection mode if results are not optimal.

Be sure to place manual vessel pixels in appropriate areas of the image based on anatomy and signal characteristics.

**CAUTION:**

Be aware that removing phases, particularly during peak enhancement, can impact the accuracy of the results.

**CAUTION:**

ROIs¹ must be defined and deposited on GenIQ parametric images with a degree of caution to ensure that the following areas are excluded from the ROI:

- Noise-inducing areas.
- Anatomical regions with delayed contrast uptake such as the bladder.

**CAUTION:**

Turning off the Algorithm Threshold results in the following:

- An increased number of computed pixels.
- It may substantially increase computation time.
- A potential increase in the number of noise pixels, which can possibly degrade measurement reliability.

**CAUTION:**

The registration algorithm in GenIQ provides optimal results under the following conditions:

- Images that are the result of a 2 or 3-dimensional volume acquisition and reconstructed as a stack of slices acquired in the same orientation, preferably axial plane.
- Inter-slice spacing is within the range of 0 (contiguous slices) to 3 mm maximum.

¹Regions Of Interest

- The number of slices are sufficient to completely cover the region-of-interest along each dimension.

Model-based VIF maps



The model-based VIF method does not account for patient specific uptake differences in flow and cardiac output. Between-subject variation of tissue physiology measurements cannot be taken into account, when the model-based curve is used.



Pixels are not displayed on Dynamic Contrast Enhanced images. The curve displayed in the graph view does not come from detected pixel(s) vessels. The curve is a population-averaged standard VIF¹.



The Model-Based VIF method is a standardization approach of the VIF and may not be accurate enough to be used in combination with the 3-parameter fitting algorithm. fPV parameter, especially may be of poor quality. Switch to Auto, Semi-Auto or Manual VIF mode, if 3-parameter fitting algorithm is selected.

PSDs

For details related to the recommended PSDs, see [Open GenIQ](#).



The following is a 3D fast spoiled gradient recalled echo technique consideration used to acquire dynamic images. The slice locations at the start and end of the multi-phase series give inaccurate results due to wraparound artifact and variability in the excitation pulse profile. Begin Image analysis once you have discarded these start and end slices.



GenIQ requires the acquisition of at least 3 baseline phases before arrival of the contrast agent. Fewer time points in the baseline may lead to inaccurate estimation of the contrast agent concentration.



If TRICKS is the DCE series used for the GenIQ analysis, be aware that the pulse sequence is interpolated and thus may not provide optimum or accurate GenIQ values.



Vessels can potentially be saturated and therefore the quality and accuracy of the functional maps can be effected for LAVA , VIBRANT and other PSDs that are acquired with flip angle values smaller than 30°.

Processing time



DCE² Image acquired with a 512 matrix (or interpolated to 512) may result in a long processing time. The processing time can be on the order of several minutes.

¹Vascular Input Function

²Dynamic Contrast Enhanced

Software messages

Messages that provide information and warnings related to the current system status are displayed on the screens. Some of these messages may be related to safety issues. For example, a message may warn that a screen or printed image will be enlarged or reduced, and this must be taken into consideration when making a diagnosis. It is important that you take note of and act on the information given in these messages.

The table below shows safety-related messages which may be displayed. In manuals intended for use in countries in which the on-screen language is different from the local language, the table shows the displayed messages and gives a translation in the local language. In manuals intended for use in countries in which the on-screen language is available in the local language, the table is not present.

Table 2-1: GenIQ software safety messages

#	English	Translation
1	Be aware that removing phases, especially vascular phases, could impact the accuracy of results.	
2	After performing this operation, data are interpolated.	
3	Skipping two contiguous phases is not allowed.	

This page is intentionally left blank

Chapter 3: GenIQ

Angiogenesis is the physiological process of new blood vessel growth from pre-existing vessels. This is a normal process for growth and development, wound healing, etc. It is also a transition stage of tumors that move from a dormant to malignant state. GenIQ is an AW¹ software application used to assess DCE²-MRI images for tissue flow, permeability, and contrast leakage from the vascular space into the extravascular-extracellular space (EES) and then slowly leak back into the vascular space.

Permeability is a parameter that is related to the rate of leakage of contrast agent from the blood plasma space (captured by VIF³) to EES. Tumors have a higher and faster uptake of MRI contrast agents. Images acquired with T1 based scan parameters are sensitive to the accumulation of contrast in EES⁴.

¹Advantage Workstation

²Dynamic Contrast Enhanced

³Vascular Input Function

⁴Extra-vascular Extra-cellular Space

GenIQ Algorithms

Pharmaco-Kinetic modeling values are derived by converting DCE¹-MRI data to contrast concentration, to which a pharmacokinetic model is fitted. The General Kinetic Model (GKM) is used in the generation of the GenIQ map. The GKM divides each single voxel in two compartments (see figure below):

- the blood plasma (or intravascular space) and
- the extracellular extravascular space (EES or interstitial space).

In other words, any given voxels of the MRI images contains fractions of both compartments, the VS and the EES.

Figure 3-1: General Kinetic Model

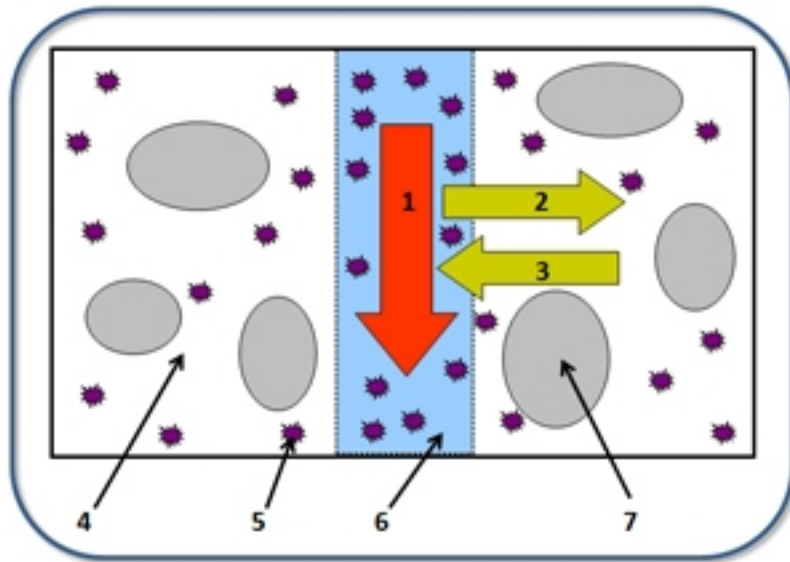


Table 3-1: Image legend

#	Description
1	Blood flow
2	K^{trans}
3	K_{ep}
4	Extravascular-extracellular space (EES) Fractional Volume: V_e Tracer concentration: $C_e(t)$
5	Represents contrast agent molecules
6	Capillary vascular plasma space Fractional Volume: V_p (or f_{pV}) Tracer concentration: $C_p(t)$ Input VIF: $V_p = (1-Hct)V_b$
7	Intracellular space Fractional Volume: V_i

¹Dynamic Contrast Enhanced

Equations of the GKM (with a 2-parameter fitting algorithm)

Figure 3-2: General Kinetic Model equations

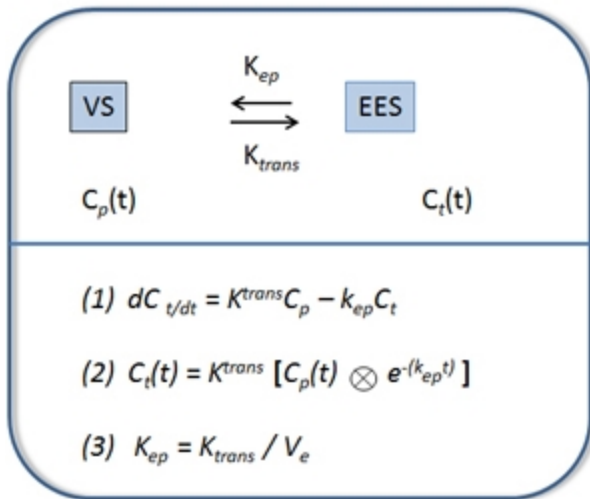


Table 3-2: Equation legend

Item	Description
VS	Vascular Space (VIF)
EES	Extra-vascular extra-cellular space
$\otimes$	Convolution
C_t	Tissue factor concentration
C_p	Plasma tracer concentration
K_{trans}	Volume transfer constant, Vascular Space (VS) to Extra-vascular Extra-cellular Space (EES)
K_{ep}	Rate Transfer Constant, EES to VS
F_{pv}	Fractional Plasma Volume
V_e	Volume of EES per unit volume of tissue

Any given single voxel may have different fractions of the VS and EES compartments. To account for this fact, an additional term, the fractional plasma volume (fPV) can be integrated in the final equation using a 3-parameter fitting algorithm.

Figure 3-3: 3-parameter fitting algorithm

$$C_t = C_p K_{trans} \otimes e^{-K_{ep} t} + f_{pv} C_p$$

Semi-quantitative parameters

The semi-quantitative parameters do not require the knowledge of a model. They have the advantage of being relatively straightforward to calculate, but have significant limitations. The semi-quantitative parameters may not accurately reflect contrast agent concentration in the tissue of interest and can be influenced by the contrast agent injection procedure and the scanner settings (including the pulse sequence, gain and scaling factors) and target position in the image.

Figure 3-4: Semi-quantitative parameters

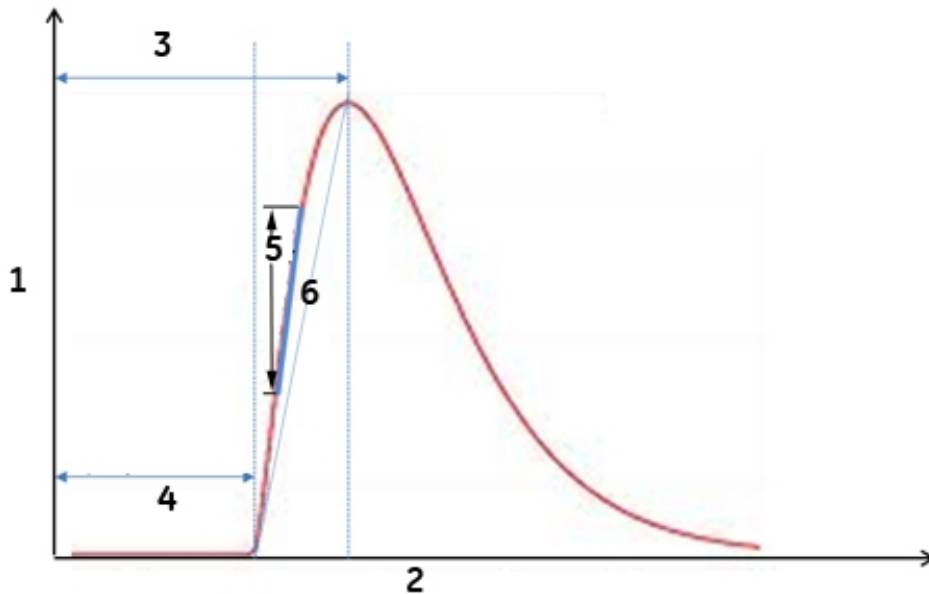


Table 3-3: Image legend

#	Description
1	Concentration (mM)
2	Time (seconds)
3	Time to Peak (TTP)
4	Bolus Arrival Time (BAT) is the time from scan start to tracer bolus arrival at tissue.
5	Maximum slope is the slope of the steepest part of the concentration curve.
6	Slope is the slope of the line joining the bolus arrival time point to the peak point.

$IAUGC^1_{90} = \text{Area under tissue concentration curve from time BAT to BAT+90 Seconds} / (\text{Area under AIF concentration curve from time BAT to BAT + 90 Seconds}).$

$CER^2 = (\text{Peak Signal} - \text{Baseline Signal}) / (\text{Baseline Signal})$

Note that CER is calculated from signal curves and not concentration curves, as baseline concentration is ~ 0 mM.

¹Initial Area Under Gadolinium contrast agent Concentration

²Contrast Enhancement Ratio

GenIQ parametric maps

The following parametric maps are generated in GenIQ.

Table 3-4: GenIQ maps

GenIQ map	Definition	Units
IAUGC	It is an abbreviation for: Initial area under the gadolinium contrast agent concentration time curve.	none
BAT	It is an abbreviation for: Bolus Arrival Time.	second
CER	It is an abbreviation for: Contrast Enhancement Ratio.	none
K_{ep}	The transfer constant (often called wash-out rate) is a measure of the movement of contrast agent from the extravascular extracellular to the intravascular space: fPV Fractional plasma volume (= vp).	min-1
K^{trans}	It is the transfer constant (frequently called wash-in rate), which is a measure of the movement of the contrast agent from the intravascular to the extravascular extracellular space. It describes the forward leakage rate of the contrast medium.	min-1
Max slope	It is an abbreviation for: Maximum Slope of Increase.	mMol/sec
V_e	It is the volume of the extravascular extracellular space. It is the leakage space.	none

GenIQ general information and procedures

The GenIQ software package is a general post-processing software application to create graphs (time curves, spectrum) and color parametric maps. These are specified from processing algorithms that provide additional clinical information for diagnosis purposes. It permits overlay of color parametric maps on to anatomical reference images using a simple “drag and drop” functionality. GenIQ offers default protocols for processing MRI¹ DCE² data sets. Protocols and layouts can be customized.

GenIQ only processes the following:

- Patient data from a single date.
- Single type of post-processing, which means that you can only compute one series per GenIQ session. If the exam has two series (for example pre- and post-contrast series), the maps must be computed for one series and then quit GenIQ and relaunch it to compute the second series.

Procedures

- [GenIQ work area](#)
- [Protocol selection screen](#)
- [General GenIQ procedures](#)

GenIQ Workflow

- [High level workflow](#)
- [Step 1: Open GenIQ](#)
- [Step 2: Review Images and Settings](#)
- [Step 3: Review All Maps](#)
- [Step 4: Advanced settings](#)
- [Step 5: Review permeability maps](#)
- [Step 6: Close GenIQ application](#)

¹Magnetic Resonance Imaging

²Dynamic Contrast Enhanced

GenIQ work area

Open **GenIQ** to display the work area.

Figure 3-5: GenIQ work area

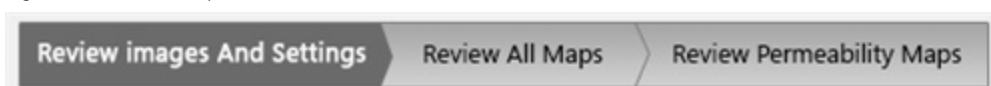


Table 3-5: Image legend

#	
1	List of review steps.
2	GenIQ panels.
3	Graph view displays a concentration or signal intensity over time graph when an ROI is deposited on an image viewport. You can change the display by selecting another series/map view from the active annotation.
4	Source images. You can change the display by selecting another series/map view from the active annotation.
5	The series view is an image view that displays the source image. You can change the display by selecting another series/map view from the active annotation.

Review steps area

Figure 3-6: Review steps area screen



Review steps area displays the following selections:

- Review Images And Settings, which displays the following screens:
 - Localized VOI
 - Preprocessing
 - VIF mode
 - T1 corrections
- Review All Maps, which displays the following screens:
 - Threshold
 - Clip Minimum and Maximum values
 - Final settings
 - Physiological parameters
 - Parametric images
 - Downsampling
- Review Permeability Maps, which displays the same screens as Review All Maps except for Permeability Maps rather than All Maps.

Click **Patient List icon**  to return to the patient list or main AW browser. To return to the current session from the Patient list, click on any Volume Viewer, READY View, GenIQ or custom protocol from the applications list.

The **+ icon**  opens/closes the Protocol List screen from which you can select another review step. Protocol list is the list of all the protocols and review steps compatible with your data set. The list is filtered based on the selections made from the Protocol Filters menus.

Click **My Protocols** to only display protocols you have chosen as favorites.

Click **Show Incompatible protocols** to display all the protocols and review steps even if they are not compatible with your data set.

Summary table

The Summary table displays ROI statistics for each deposited ROI. To expand the table, click the arrow icon to the right of Summary Table. Click the Summary Table icon on the Export tool panel to view the summary table.

Figure 3-7: Export tool panel

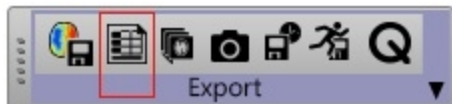
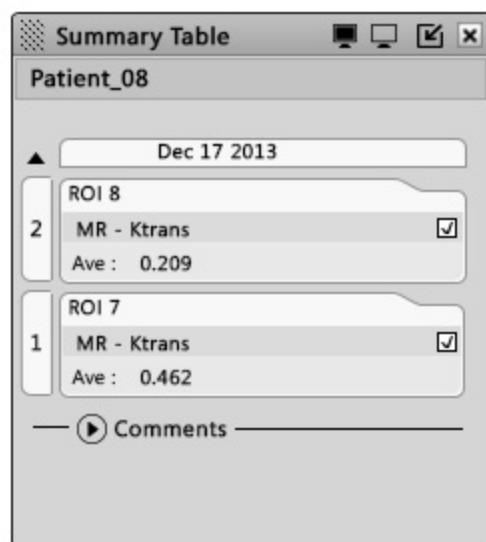


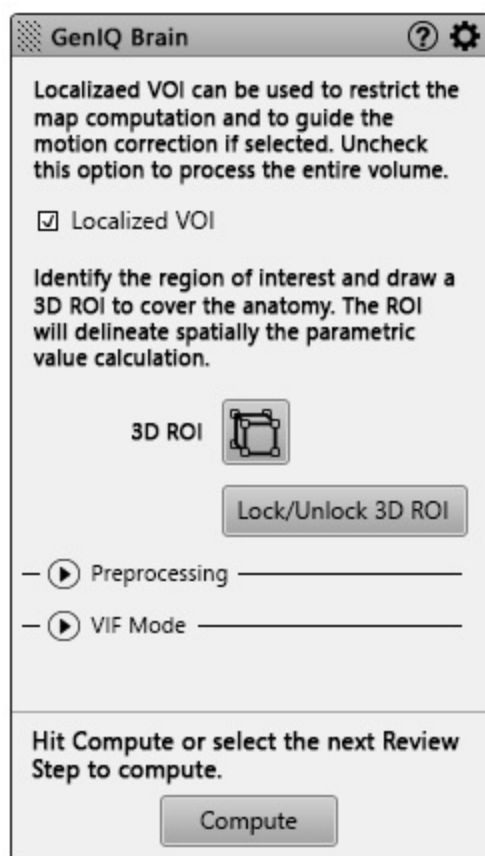
Figure 3-8: Sample summary table



Application screen area

The content in this panel changes based on the opened GenIQ protocol and the selected review step.

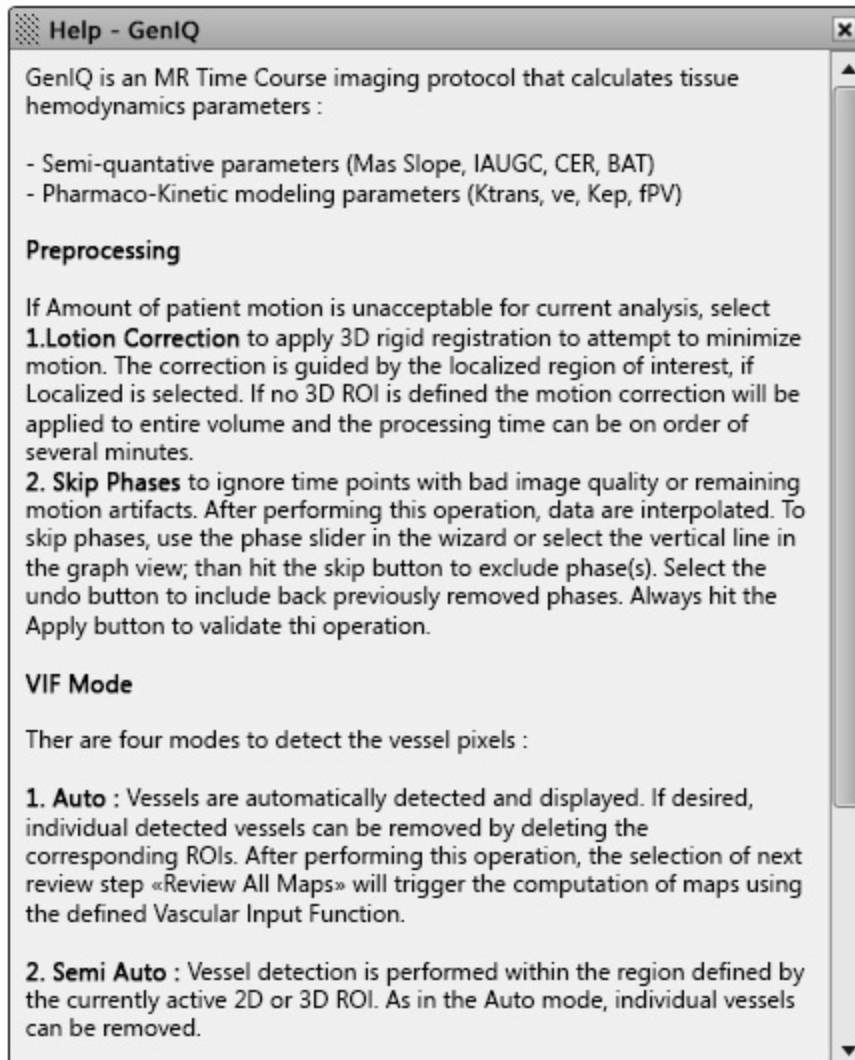
Figure 3-9: Example of an application screen area



- Click the arrow to open new areas of the screen.

- The screen has a **hash-marked symbol**  that allows the screen to be picked up and moved to a new location on the monitor.
- The **Tools icon**  displays additional selections. It is a toggle button that moves the screen area between two sets of screens.
- The **Help icon**  opens a screen with explanations about the application screen.

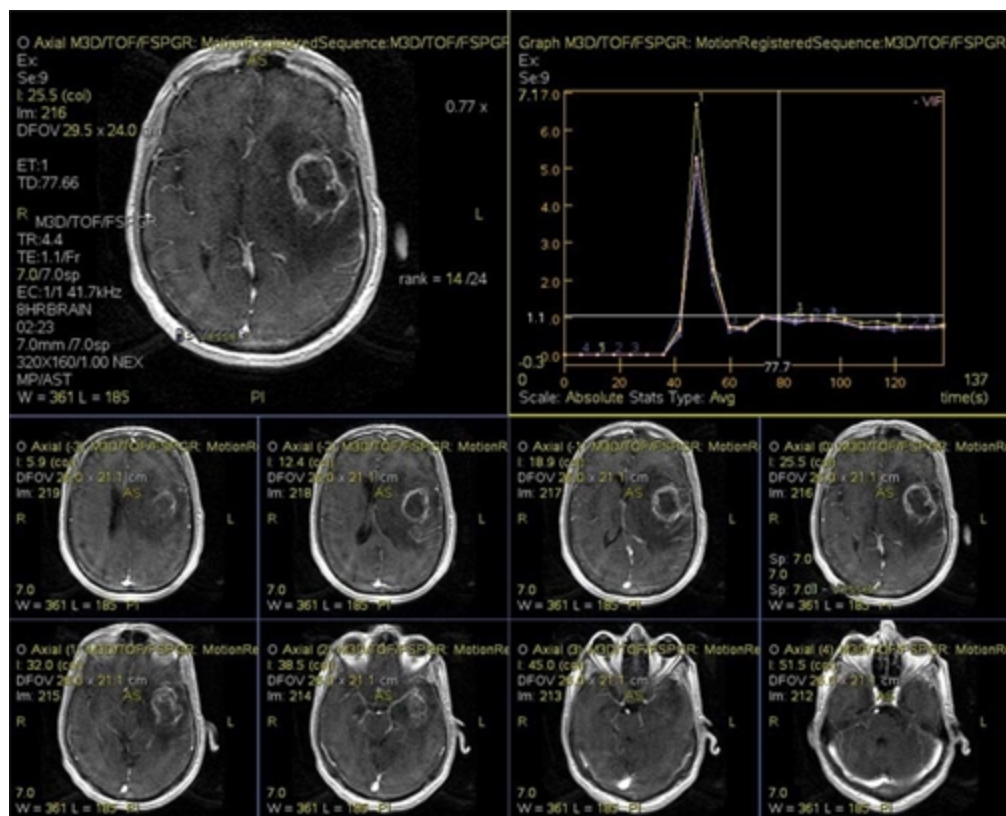
Figure 3-10: Example of a help screen



Source image/ image maps/graph viewports

The content in the viewports changes based on the currently active exam and selected review step. The viewport can display images, functional maps, graphs, etc.

Figure 3-11: Example of viewport area

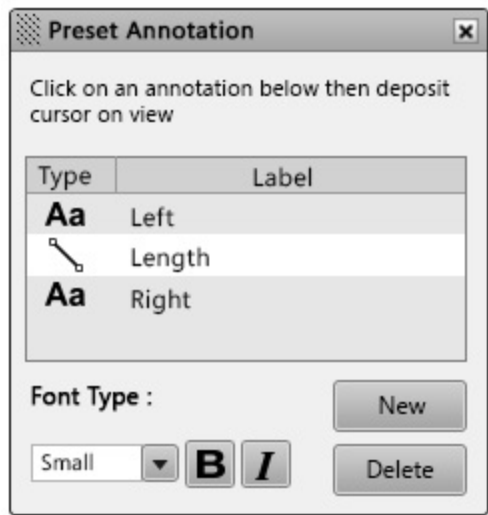


Tools panels

Refer to your Volume Viewer manual for details. Note that this panel may be placed either on the user interface at the top of the screen (horizontal display) or at the side of the screen (vertical display).

Each tool panel has an arrow in the lower right corner. Click on the arrow to see other icons in that tool group. Some icons, when selected, display a screen in the upper right corner of the user interface.

Figure 3-12: Example of a display screen when Preset Annotation icon is activated



Related topics

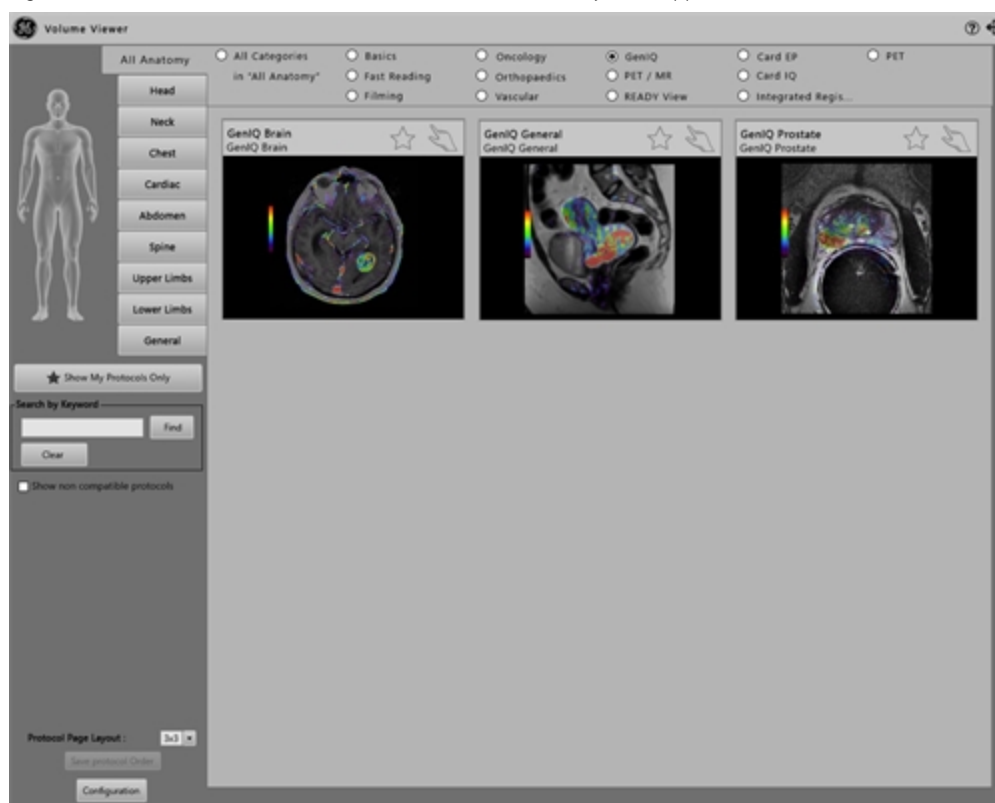
- [GenIQ](#)
- [GenIQ high level workflow](#)

Protocol selection screen

The Protocol Selection screen appears if you do not have a one-touch protocol for GenIQ.

The GenIQ protocols appear when the GenIQ filter is applied. The list of protocols is modified if an anatomical filter is applied.

Figure 3-13: Protocol Selection screen with GenIQ and All Anatomy filters applied



Related topics

[GenIQ work area](#)

[GenIQ high level workflow](#)

General GenIQ procedures

Window width and level

Auto W/L

Auto Window Width and Level (WW/WL) is applied to all protocols.

GenIQ computes an optimal Window Width and Level for the functional map display in the viewports. The optimal WW/WL is computed based on the noise levels present in the volume and using the histogram data of the functional volume. Auto WW/WL ensures that the functional volumes are presented well in the viewports but does not exclude minor user manual adjustments.

W/L shortcut

- Press “w” on the keyboard to come back to the defaults window W/L settings (the one from the maps when they are calculated for the first time).
- Automatically set window width and level of the view currently pointed to by the mouse cursor (on the basis of the histogram of the pixel values in the view).

Adjust the W/L of an image

1. Click the desired viewport to make it active.
2. To adjust the W/L, middle-click and drag over the image.



Adjusting the range will not affect the quantitative values when executing an ROI¹ analysis.

Region of Interests



CAUTION:

ROIs² must be defined and deposited on GenIQ parametric images with a degree of caution to ensure that the following areas are excluded from the ROI:

- Noise-inducing areas.
- Anatomical regions with delayed contrast uptake such as the bladder.

Modify and save a protocol

Please refer to your READY View user guide: Chapter 3 > General information and procedures.

Graphs

The graph view displays the image intensity and concentration curves of regions of interest.

The ROI image intensity curves represent the same information for the pixels within the area of each ROI defined on the image views (series, function, and composite views). Each image intensity curve is annotated with the corresponding ROI number.

¹Region Of Interest

²Regions Of Interest



! Pixels are not displayed on Dynamic Contrast Enhanced images. The curve displayed in the graph view does not come from detected pixel(s) vessels. The curve is a population-averaged standard VIF¹.

Adjust the graph

Use these steps to adjust the graph characteristics. Use the graph to simultaneously change the phase (rank) on all viewports.

- To update the graph, press and hold **Alt + g**.
- Any viewport can be changed to a graph view.

Figure 3-14: Graph display

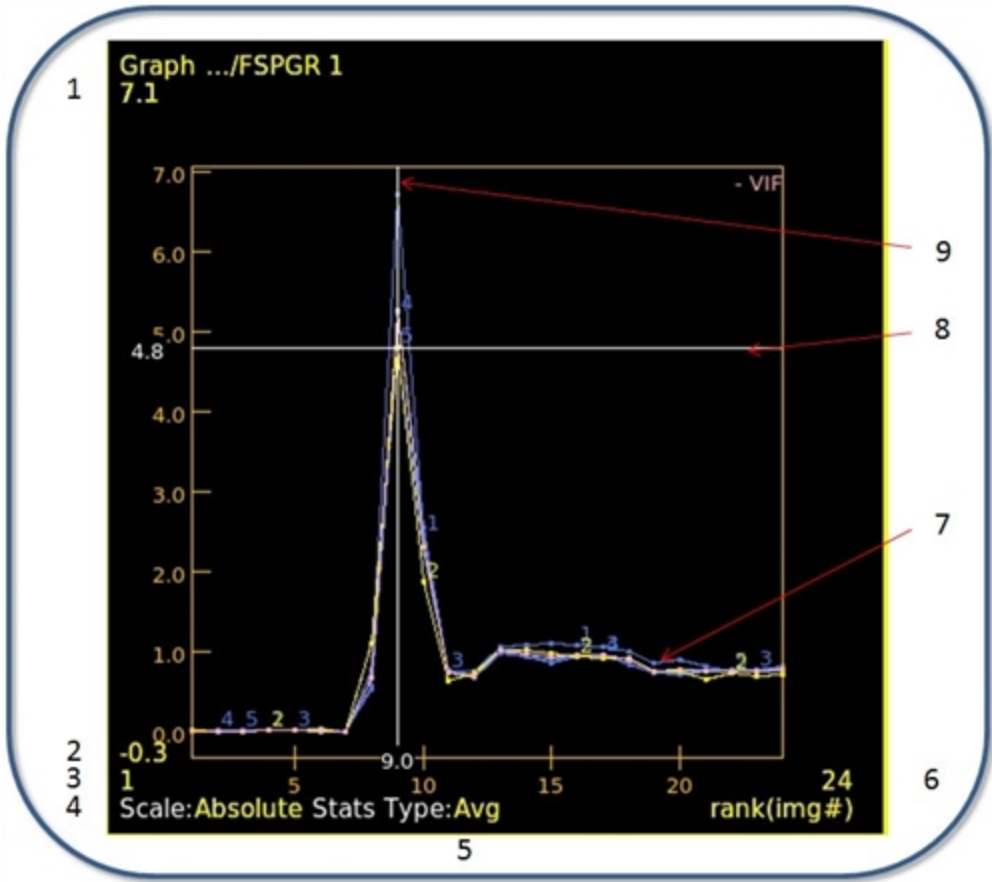


Table 3-6: Image legend

#	Description
1 and 2	Vertical-axis upper/lower limit annotation Place the cursor over the active vertical annotation and left-click, right-click or middle-click and drag to change the scale values of the graph's vertical axis. • The vertical axis can represent pixel intensities in MR units (absolute, relative, or as a percentage) or Gadolinium concentration in mmol/L. • The vertical axis represents the signal point spread plotted to the graph. • The graph can also be re-scaled for curve shape comparison. This can be useful if there are two ROIs deposited and you cannot see both time/intensity curves on the graph.

¹Vascular Input Function

#	Description
3 and 6	Horizontal-axis upper/lower limit annotation Place the cursor over the active horizontal annotation and left-click, right-click, or middle-click and drag to change the scale values of the graph's horizontal axis. - The horizontal axis (number scale) represents the phase range. - The horizontal axis can represent either image numbers (rank) or image time in seconds or milliseconds.
4	Scale type Place the cursor over the active scale type annotation. Click and select an option: absolute, relative, percentage, or shape comparison.
5	Type of statistic Place the cursor over the active ROI type. Click and select the ROI pixel values as average curve, max (maximum) curve, or min (minimum) curve. An ROI number annotation is displayed whenever an ROI is selected. You can use this annotation to select an ROI. You can also select an ROI by clicking on the curve in the graph view. Note that each time you click an ROI, the curve is annotated with the corresponding ROI number.
6	Place the cursor over the active rank/time annotation and left click to select either time or rank. The horizontal axis changes accordingly.
7	ROI curve. - The cursor ROI¹ image intensity curve represents the change in pixel values for the pixels under the cursor of every image in the data set. This curve is automatically displayed and updated with each cursor movement. - The ROI image intensity curves represent the same information for the pixels within the area of each ROI defined on the image views (series, function, and composite views). Each image intensity curve is annotated with the corresponding ROI number. - Each phase is denoted by a dot on the curve. You can place the white bar cursor over each dot and correlate it with the phase value on the horizontal scale.
8 and 9	Deposit an ROI on an image viewport and then select it. The ROI and image intensity curve display in yellow. Use the white moveable bars (cross hairs) on the graph view to identify the image intensity value (horizontal bar) for a given image number (vertical bar) at any point. - Select the image number (or time) and middle-click and drag the cursor to the left or right on the graph. - View or move the cursor to the desired location and left-click. - The vertical bar follows the cursor, and the horizontal bar automatically indicates the corresponding image intensity value. - The reference image corresponding to that rank point (time) is displayed in the series viewport. - The Horizontal reference line correlates a point on an image intensity curve with the vertical scale.

¹Region Of Interest

Fitted curve

pK modelling [both two-parameter (Ktrans, ve)/ three parameter Toft's model (Ktrans, Ve, fPV)] is done on the concentration curve obtained from signal DCE data.

Once pK model fit computation is triggered, the fitted concentrated curve can be displayed to evaluate the goodness of fit with the GKM (General Kinetic Model).

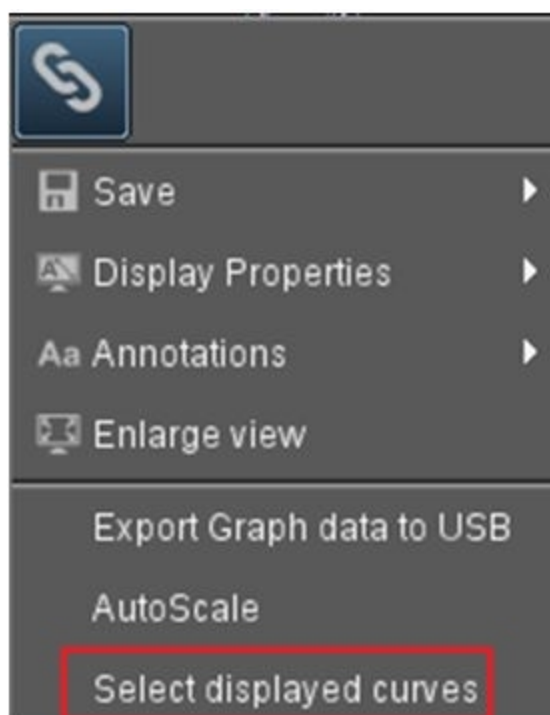
Fitted curve reflects the concentration curve generated by using bolus time-point value, BAT, Ktrans, Ve and (fPV) from the PK fitting module. This will help the user gauge the fidelity of pK model fitting procedure and identify errors (such as BAT does not match, Ktrans unreasonable).

Procedure

Use these steps to display a Fitted Curve.

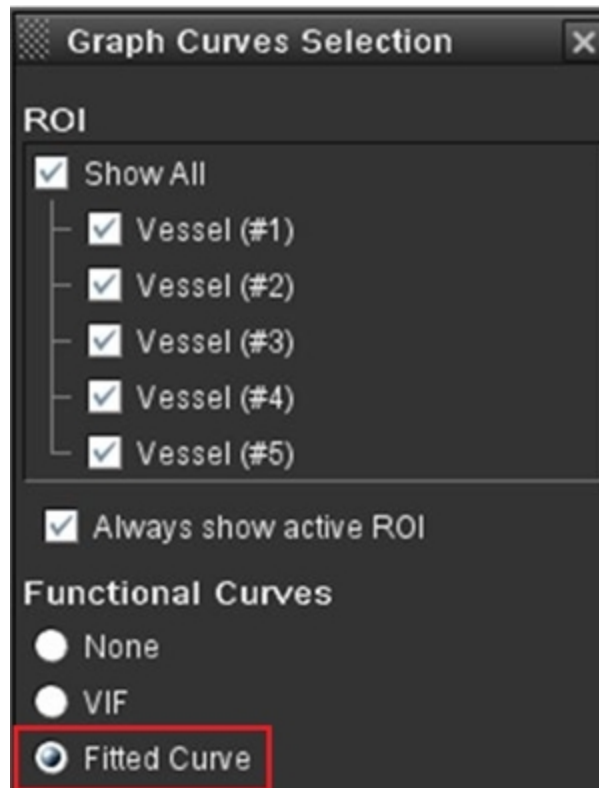
1. From the Graph View screen, right-click to display the Graph View menu.
2. From the Graph View menu, click **Select displayed curves**.

Figure 3-15: Graph View menu



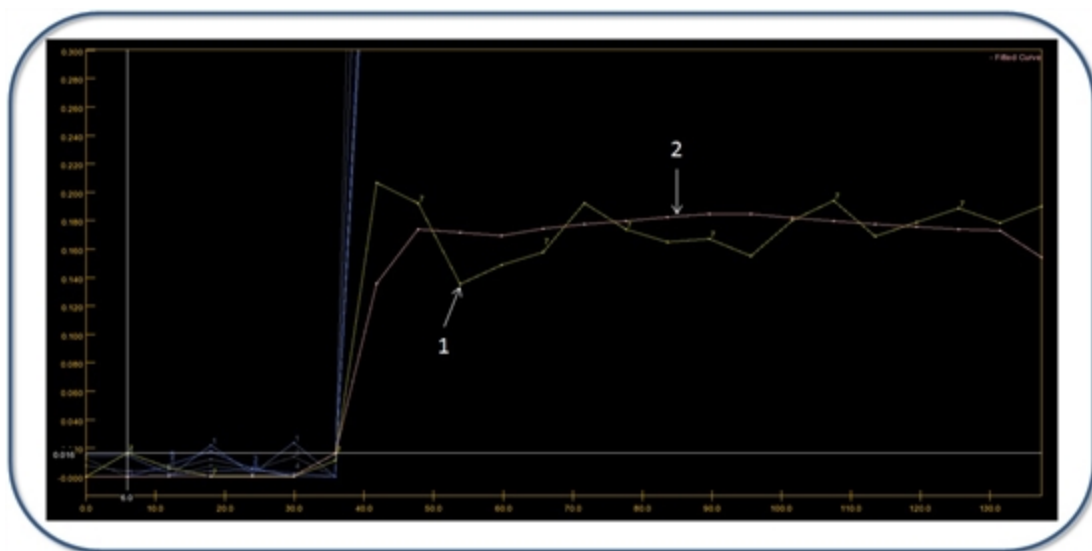
3. From the Graph Curves Selection screen, Functional Curves area, click **Fitted Curve** option.

Figure 3-16: Graph Curves Selection screen



- The Fitted Curve is colored pink.
- Adjust the Y axis scale as needed.

Figure 3-17: Concentration Curve and Fitted Curve



#	Description
1	Yellow curve is the original Concentration Curve.
2	Pink curve is the Fitted Curve.

Considerations

- If an active ROI is on display, selecting the Fitted Curve option will calculate it from the ROI graph curve.
- If no active ROI is on display, selecting the Fitted Curve option will calculate it from the current cursor location.
- The Fitted Curve can only be selected when the graph shows a Concentration Curve and not when it shows a Signal Intensity curve.

GenIQ high level workflow

Use these steps to generate GenIQ graphs and parametric maps.

1. **Open GenIQ application** on your AW¹ or AWS system.
 - Refer to **General GenIQ procedures** to execute any of the general GenIQ procedures.
2. Review images and settings. From the Review Steps screen, note that **Review Images & Settings** is automatically selected. Complete the selections on the Review Images and Settings screen.
 - a. **Apply motion correction**, if needed.
 - b. **Skip phases**, if needed.
 - c. **Select the VIF mode**, if needed.
 - d. **Define T1 Correction value for tissue**, if needed
3. Select the next Review step (**Review All Maps**) to compute functional maps. Optional: review the maps and change the following parameters, if needed.
 - a. **Adjust the threshold**.
 - b. **Select a particular map**.
 - c. **Adjust Clip Min and Max values** if you want to segment a lesion.
4. Optional: review Advanced Settings. Click the **Advanced Settings icon**  and adjust the following parameters if needed.
 - a. **Adjust Physiological parameters** for Blood Hematocrit.
 - b. **Adjust Parametric image values** for the fitting algorithm, algorithm threshold activation, IAUGC and kernel smoothing.
 - c. **Adjust Resolution size slider Downsampling** to reduce computation time at the expense of reduced resolution.
5. Review permeability maps. From the Review steps screen, click **Review Permeability maps**. Complete the selections on the **Permeability Maps** screen.
 - a. Optional: click the **Advanced Settings icon**  and adjust the following parameters as defined in step 3.
6. **Close the GenIQ application**.

¹Advantage Workstation

Step 1: Open GenIQ

Use these steps to launch the GenIQ application.

Considerations

- A warning message is posted if the selected series may not be acceptable for use.
"The selected data has been acquired with low temporal resolution. Please ensure that the results are acceptable for use."

Quality review considerations before post processing data with GenIQ

- Review the images to confirm that all imaging parameters were correct, data structure is correct and artifact free before the data is post processed and analyzed.
 - For any longitudinal study, at each subsequent time-point, input data must be consistent over time. Therefore, the DCE protocol must be acquired with the same parameters (pulse sequence parameters and injection protocol).
1. From the Patient List, select an MRI ¹DCE² series with GenIQ compatible criteria.
 - For protocol criteria details, see [DCE MRI protocol considerations](#).
 2. From the applications list, click **GenIQ**.
 - If GenIQ does not appear on the application list, click **More** to view a complete list of applications and click **GenIQ**.
 3. Select the desired protocol from the [Protocol Selection screen](#).
 - GenIQ Brain protocol has the following characteristics:
 - Preset T1 correction value is 800 ms for 1.5T images and 1200 ms for 3.0T images.
 - Auto VIF³ is the default VIF mode.
 - Semi-auto and Manual VIF modes are available.
 - GenIQ General protocol is used for DCE series acquired at any other location in the body. GenIQ General protocol has the following characteristics:
 - Preset T1 correction value is 860 ms for 1.5T images and 900 ms for 3.0T images.
 - Model-based VIF is the default VIF mode.
 - Semi-auto, and Manual VIF modes are available.
 - GenIQ Prostate protocol has the following characteristics:
 - Preset T1 correction value is 1317 ms for 1.5T images and 1597 ms for 3.0T images.
 - Model-based VIF is the default VIF mode.
 - Auto, Semi-auto, and Manual VIF modes are available.
 4. From the Loading panel complete the following steps.
 - a. Review the checked contents.
 - The Loading Panel displays the source series first, followed by the in-line processed series (generated during the exam procedure), and last, the secondary capture series in a separate zone.

¹Magnetic Resonance Imaging

²Dynamic Contrast Enhanced

³Vascular Input Function

- Once the session is launched, it is still possible to add series into the session through the Mini-Patient List.
- b. Select the desired series and secondary capture series that you want to use in the analysis.
- c. If there are multiple series that you want to work as a single, continuous data set, then use the Link Series option, as follows. For example, you may want to combine the pre and post contrast series into a single data set.
 - First, deselect all series at the exam level.
 - Next, select the box of the 1st series, and click the (+) button beside the box, which opens the series content. For example, in the scenario of a multi-phase pre and post-contrast acquisition, it may show the individual phases. Note that you cannot select a subset of images within the series.
 - Next, select the box of the 2nd series, and also click the (+) button.
 - Click **Link Series**. The second linked series is no longer listed and its content is added to the content of the first linked series. Click the (+) button to see the new series content.
 - Continue and select all other desired series.
- d. Click **OK**. The system loads the selected images into the GenIQ work area.
- 5. The images display with the DCE source files and graph view. The parametric maps are not displayed yet. The [Review images and Settings](#) review step is launched.
 - The layout can be customized. See your AW VolumeShare operator manual for details.
 - Auto VIF (GenIQ Brain protocol) automatically displays the slice that includes vascular pixels.
 - Model based VIF mode (GenIQ Prostate and GenIQ General protocols) do not display artery vascular pixels.
- 6. Use the AW review controller tools and active annotation to review the image data. Refer to your AW manual for details.

Related topics

[Step 2: Review Images and Settings](#)

[Step 3: Review All Maps](#)

[Step 4: Advanced settings](#)

[Step 5: Review permeability maps](#)

[Step 6: Close GenIQ application](#)

[General GenIQ procedures](#)

Step 2: Review Images and Settings

- Review the Loading panel content and click **OK** to start the **Review Images And Settings** Review step.
 - For AW systems with two monitors, the second monitor displays the DCE source images.
 - The Review Images and Settings review step displays the following default layout.



NOTE that for some acquisitions, the default layout displays the same image for two locations instead of one image per location. This rarely occurs and is related to the slice acquisition.

Figure 3-18: Review Images and Settings layout

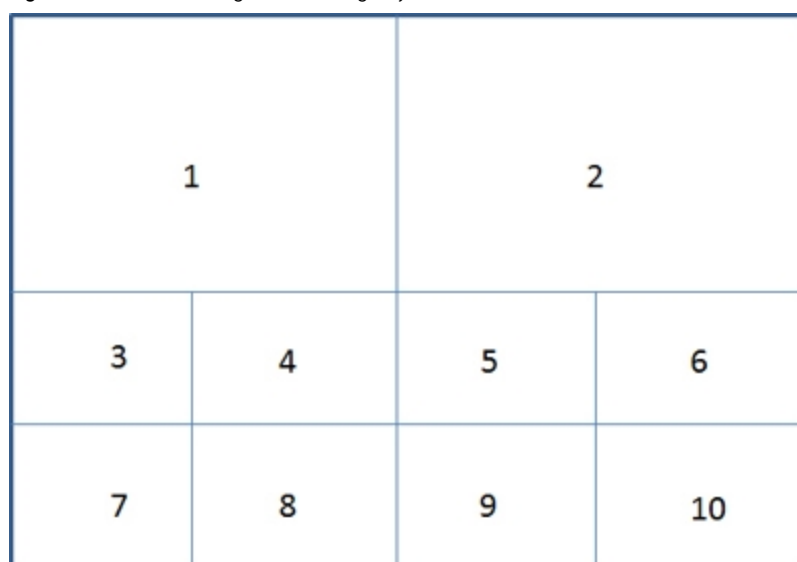


Table 3-7: Image legend

#	Description
1	Displays the DCE ¹ source images.
2	Displays the graph view of the DCE images.
3-10	Displays the DCE image source images at different locations.

Use these steps to minimize the effects of patient motion, adjust the phase range and select the VIF mode.

Localized VOI

From the Review Images and Settings screen, **Localized VOI** option is selected by default. Typically use Localized VOI to select an area of interest around a lesion. This means the map computation is done inside the specific user defined 3D ROI.

To define the Localized VOI, follow these steps:

- Click the **3D ROI icon**  to define the Localized VOI.
- Click and drag the 3D ROI edges to size it.
- In all three planes, check and make adjustments as needed to the 3D ROI size and position.

¹Dynamic Contrast Enhanced

4. Once you are satisfied with the 3D ROI cursor position and size, click **Lock/Unlock 3D ROI**.
 - This action creates the Compute Mask.
5. Click **Unlock 3D ROI** if you need to readjust the size or position of the 3D ROI.



Uncheck the Localized VOI if you prefer to compute maps on the entire volume. This is not recommended because of the computation time.

Motion correction

Use these steps to minimize the effects of patient motion. GenIQ uses a rigid motion correction algorithm. It can either be applied to a localized area of interest or over the whole volume. The computation time is based on the size of the region of interest: the smaller the ROI the faster the computation time. Motion Correction creates a new series.

1. If the images exhibit motion with respect to the reference image, complete the following from the Review Images & Settings screen,
 - a. Click the **Preprocessing** arrow to open the Preprocessing screen area.
 - b. Click **Motion Correction** option box.
 - c. Click **Apply** to start the correction process.
 - If **Localized VOI** is selected (the default option), the computation time is based on the ROI size; the smaller the ROI the faster the computation time.
 - If no **Localized VOI** is defined, motion correction occurs over the entire anatomy of interest. Note that the computation can take several minutes for the entire volume of interest.
 - The correction time is a function of the localized region size. Therefore, it may take several minutes to complete. To terminate the motion correction calculation and proceed without it, click **Stop**.
2. From the Tools area Export panel, click the **Quick Export icon**  to save the new set of processed images, which allows access to the corrected series from the patient browser.



CAUTION:

The registration algorithm in GenIQ provides optimal results under the following conditions:

- Images that are the result of a 2 or 3-dimensional volume acquisition and reconstructed as a stack of slices acquired in the same orientation, preferably axial plane.
- Inter-slice spacing is within the range of 0 (contiguous slices) to 3 mm maximum.
- The number of slices are sufficient to completely cover the region-of-interest along each dimension.

Modify phase range

Use these steps to remove phases that demonstrate significant motion between phases or images that have poor image quality. The slider is synchronized with the vertical line in the graph view.



CAUTION:

Be aware that removing phases, particularly during peak enhancement, can impact the accuracy of the results.

1. Click and drag the slider and overlay it on the phase you want to remove from the analysis.
 - Respond to any warnings that may appear.
 - Note that you cannot skip two contiguous phases.

Figure 3-19: Vertical line positioned over phase you want to remove

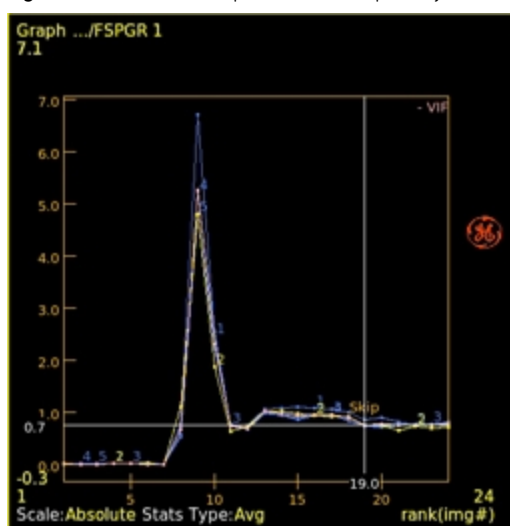


Figure 3-20: Display box updates as the slider is moved

2. Use the slider and select the **Skip** button to ignore the phases with bad quality. Then, select **Apply to interpolate data**. Select **Undo** to include removed phases.

25

Skip Undo

22 25

Be aware that removing phases, especially vascular phases, could impact the accuracy of results.

2. From the Preprocessing selection area, click **Skip**.
 - Skip phases can be done before Motion Correction is started for more accurate results.
3. Repeat the above two sub-steps for each phase you want removed from the data set.

- The skipped phase numbers appear in the display box.
 - If needed, move the slider to a phase skipped and click **Undo** to restore this excluded phase.
4. Click **Apply** to register the new slice range and data interpolation.

Select the VIF mode

Prior to analysis and generation of graphs and parametric maps, use these steps to define the regions of interest for the VIF¹. Gen IQ allows four methods for defining a region of interest.



CAUTION:

Ensure that you review and if necessary correct the position and signal characteristics of detected vessels in automatic and semi-automatic mode before reviewing the computed functional maps. Switch to a different vessel detection mode if results are not optimal.

Be sure to place manual vessel pixels in appropriate areas of the image based on anatomy and signal characteristics.



The model-based VIF method does not account for patient specific uptake differences in flow and cardiac output. Between-subject variation of tissue physiology measurements cannot be taken into account, when the model-based curve is used.

1. From the Preprocessing selection area, click **VIF Mode** to view the VIF selections.
2. Select a VIF Mode option button.
 - **Auto**
 - It is the optimal mode for neuro DCE² exams.
 - Vessels (arteries, veins, sagittal sinus) are automatically detected and displayed. If desired, individual vessels can be removed by deleting the corresponding ROI³.
 - It automatically displays the slice that includes the VIF pixels.
 - **Semi-auto**
 - a. From the Tools area, under the **Measure/annotate** toolbar, select either the 2D or 3D icon.
 - b. Draw one ROI on the region of interest and click **Search**.
 - c. Place the cursor over the area of interest and left-click to deposit the ROI.
 - For Semi Auto mode, vessel detection is performed within the region defined by the currently active 2D or 3D ROI.
 - If desired, individual vessels can be removed by deleting the corresponding ROI.
 - **Model-based**
 - It is recommended when a reliable VIF cannot be located in any image.
 - An internal population-averaged standard VIF curve is used as the Vessel Input Function.



The Model-Based VIF method is a standardization approach of the VIF and may not be accurate enough to be used in combination with the 3-parameter fitting algorithm. fPV parameter, especially may be of poor quality. Switch to Auto, Semi-Auto or Manual VIF mode, if 3-parameter fitting algorithm is selected.

¹Vascular Input Function

²Dynamic Contrast Enhanced

³Region Of Interest

- **Manual**

VIF can be manually defined by clicking candidate vessel pixels within major vessels, preferably close to the region of interest. For body applications, these pixels should be selected in arteries. For brain applications, typically select the manual VIF pixels in the sagittal sinus.

To minimize errors in VIF estimation that are due to general motion or flow and saturation effects, when ever possible, select the pixels from vessels that are in-plane in the imaging slice. Pixels should also be selected in the central part of the vessel to minimize errors due to motion and due to flow near the boundaries of the vessel.

- a. From the VIF Mode screen area, click the **Pixel ROI icon** .
 - b. Place the cursor over the vessel and examine the pixel value on the concentration curve. If the peak concentration in the selected vessel pixel is greater than 10 mM, then that pixel does not provide a usable measurement of blood concentration.
 - c. Left-click to deposit the ROI.
 - d. Click **Mark VIF**.
 - e. The following warning message appears if the peak concentration in the selected vessel pixel is greater than 10 mM. Select **Yes** to accept the blood concentration measurement or **No** to discard the blood concentration measurement.
 - "The signal characteristics of the selected voxel do not appear to correspond to a valid VIF. Are you sure you wish to mark this voxel as a VIF?"
 - f. Repeat the above steps to deposit up to 6 Pixel ROIs.
3. From the Review Steps area, click **Review All Maps** to generate parametric images.
-  Note that map computation can take several minutes based on the matrix size and the volume of interest.

Related topics

[Step 1: Open GenIQ](#)

[Step 3: Review All Maps](#)

[Step 4: Advanced settings](#)

[Step 5: Review permeability maps](#)

[Step 6: Close GenIQ application](#)

[General GenIQ procedures](#)

Step 3: Review All Maps

Use these optional steps to change default settings that are used to calculate the parametric maps. Once all settings have been changed, you must click **Compute** to generate a new set of parametric images.

- From the [Review Steps area](#), click **Review All Maps**.
 - For AW systems with two monitors, the second monitor displays the DCE image fused with the Ktrans map.
 - The Review All Maps review step displays the following default layout.

Figure 3-21: Review Images and Settings layout

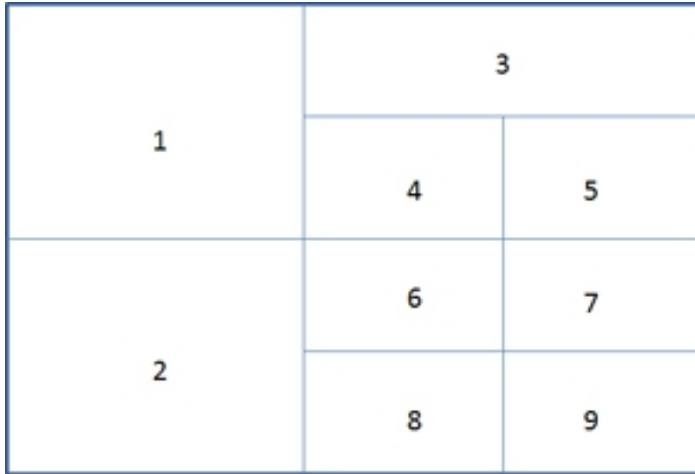


Table 3-8: Image legend

#	Description
1	Displays the DCE ¹ source images.
2	Displays the DCE image fused with the K_{trans} map.
3	Displays the graph view of the DCE images.
4	Displays the V_e map.
5	Displays the IAUGC ² map.
6	Displays the K_{ep} map.
7	Displays the CER ³ map.
8	Displays the maximum slope map.
9	For a 2-parameter fitting algorithm layout, displays the ktrans map. For a 3-parameter fitting algorithm layout, displays the fPV map.

¹Dynamic Contrast Enhanced

²Initial Area Under Gadolinium contrast agent Concentration

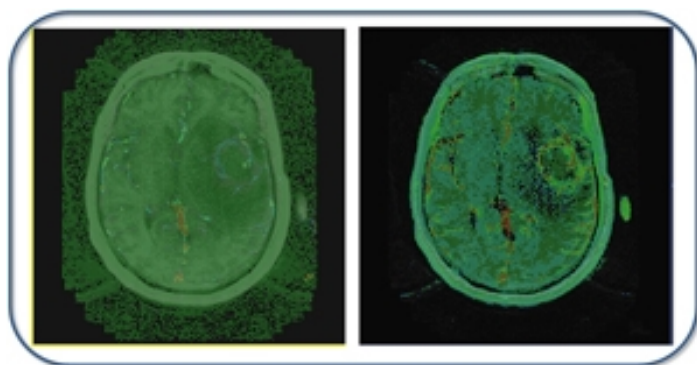
³Contrast Enhancement Ratio

Adjust the threshold

Use these steps to adjust the threshold. GenIQ computes, by default, the functional values for the entire data set. You can dynamically update the threshold for both the source and maps.

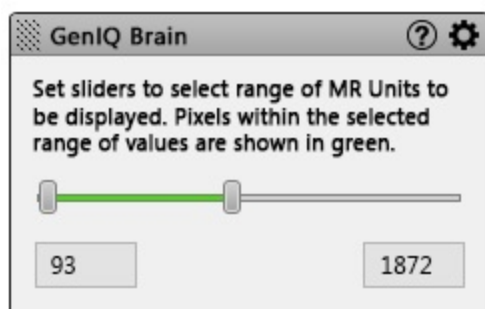
1. From the threshold adjustment screen area, adjust the threshold, if needed.
 - The low and high threshold sliders allow you to define the range of MR values (pixel values) that will be processed by the protocol (shown by green hatching on the image).

Figure 3-22: Example of threshold set too wide(left) and then corrected (right)



2. Display a source image in a viewport.

Figure 3-23: Threshold slider, left slider = low threshold, right slider = high threshold



3. Adjust the left **Threshold** slider to set the low ("air" or "noise") threshold. Alternatively, enter a value in the text box. For finer control, click inside one of the text boxes and use the up/down arrow keys to increment/decrement one unit at a time.
 - The default setting may, at times, exclude some of the data inside the volume of interest. Adjust as necessary. Note that the maps update dynamically as the threshold changes.
4. Adjust the right **Threshold** slider to set the high threshold. Alternatively, enter a value in the text box. For MR exams, this can usually be left at the default value.
 - All pixels with MR values outside the defined range are masked out, that is they are not processed and appear black in the functional views. Non-relevant image data, such as air spaces (including the empty space outside the patient), do not appear on the functional maps, making for easier interpretation of the resulting image.

Clip Min & Max values and select permeability map

Use these steps to set a minimum and maximum threshold to visualize a particular anatomy or pathology and then overlay it on another image or map.

1. Click the **Clip Min & Max values** arrow to view the selections.
2. From the menu, select the permeability map for which you want to define a threshold, for example **Ktrans**.
 - For parametric map details, see [GenIQ parametric maps](#)
3. In one of the viewports, from the active annotation, select the same map as selected in the menu.
4. From the Clip Min & Max values area, adjust the upper and lower threshold to visualize the anatomy/pathology of interest.
5. Fuse the segmented image to an anatomy image or any other image.
 - a. Click an image and drag it over another image and drop it in the "Drop here to mix the views" box.
 - b. To remove the fusion from an image, click the map portion of the series/map active annotation (the content that is to the far right) and select **No Fusion**.
6. If desired, select **Shared Segmentation** option to propagate the segmentation to all other maps.

Related topics

[Step 1: Open GenIQ](#)

[Step 2: Review Images and Settings](#)

[Step 4: Advanced settings](#)

[Step 5: Review permeability maps](#)

[Step 6: Close GenIQ application](#)

[General GenIQ procedures](#)

Step 4: Advanced settings

Use these optional steps to change default settings that are used to calculate parametric maps. Once all settings have been changed, you must click **Compute** to generate a new set of parametric images.

1. From the Review All Maps or the Review Permeability Maps review steps, click the **Advanced Settings icon**  to view the advanced settings panel.
2. Click the **Advanced Settings icon**  again, to close the Advanced Settings panel.

GenIQ final settings

Use these steps to view the selected processing settings.

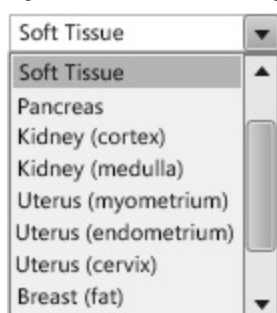
1. Click the **GenIQ Final Settings** arrow to display the final settings.
2. If you want to change any of the settings, click the appropriate selection from the GenIQ wizard to edit the value in the table.
3. When all changes have been made, click **Compute** to update the maps.

GenIQ T1 settings

Use these steps to define the T1 correction values for Tissue, which is only available for GenIQ General protocols. It is not available for GenIQ Brain nor GenIQ Prostate protocols. It is only available from the Review Images and Settings review step.

1. Click the **GenIQ T1 Settings** arrow to view the selections.
 - a. The Blood T1 value is automatically selected and it is based on the magnetic field strength of the MR system.
 - b. The Tissue T1 value is automatically selected for Brain and Prostate GenIQ protocols, and it can be modified in the General protocol. If desired, select a tissue from the menu. The T1 time is automatically entered. Please note that these values are only recommendations.

Figure 3-24: Advanced Settings menu



2. To select a different value, click **Other** and type and enter a value, if desired. Please note that these values are only recommendations.

Table 3-9: Sample tissue T1 values

Anatomy	1.5T T1 value	3.0T T1 value
Brain	800 ms	1200 ms
Prostate	1317 ms	1597 ms
Soft Tissue	860 ms	900 ms

Anatomy	1.5T T1 value	3.0T T1 value
Blood	1320 ms	1600 ms
Pancreas	584 ms	725 ms
Kidney cortex	966 ms	1142 ms
Kidney medulla	1412 ms	1545 ms
Uterin myometrium	1309 ms	1514 ms
Uterin endometrium	1274 ms	1453 ms
Uteric cervix	1135 ms	1616 ms
Breast fat	296 ms	366 ms
Breast grandular	1266 ms	1444 ms

Reference: Relaxation Times of Abdominal and Pelvic Tissues, de Bazelaire et al. Radiology March 2004
 Relaxation Times of Breast Tissue at 1.5T and 3T, Rakow-Penner et al. Measured Using IDEAL JMRI 23:87–91 (2006)

Physiologic parameters

Use these steps to change the physiological parameters from the default settings. It is only available from the Review All Maps and Review Permeability Maps review steps.

1. Click the **GenIQ Physiological parameters** arrow to view the selections.
2. The Blood hematocrit is a physiological parameter that is independent of the magnetic field. From Review All Maps and Review Permeability Maps review steps, type and enter a different value, if desired.

Parametric images

Use these steps to select the parametric fitting algorithm, IAUGC value and the kernel smoothing value.

1. Click the **GenIQ Parametric images** arrow to view the selections.
2. The default fitting algorithm is 2-parameter. If desired, change the fitting algorithm to 3-parameter, which results in computation of the fPV¹ parametric map.
3. If desired, turn **Off** the Algorithm Threshold selection button to display parametric values for all voxels.



CAUTION:

Turning off the Algorithm Threshold results in the following:

- An increased number of computed pixels.
 - It may substantially increase computation time.
 - A potential increase in the number of noise pixels, which can possibly degrade measurement reliability.
4. If desired, change the IAUGC value. Type and enter a value that represents the bolus arrival time in seconds. This value defines the integral of the area under the concentration curve.
 - The default value for the area under the curve is 90.
 5. If desired, change the kernel spatial smoothing value.

¹Fractional Plasma Volume

- The kernel spatial smoothing defines the radius of the spatial smoothing applied to the original data before functional processing.
- The default value is 1.
- As the kernel size increases, voxel averaging occurs and the image maps appear smoother.
- a. Click **Apply** to smooth the map without executing computation.
 - **Reset** changes the selections to the factory default values.
 - **Save** saves your selections as the new default values.

Downsampling

Use these steps to reduce computation time at the expense of reduced resolution.

1. Click the **GenIQ Downsampling** arrow to view the selections.
 2. Move the slider to the right to decrease processing time at the expense of decreased resolution.
Move the slider to the left to increase the resolution at the expense of increased processing time.
- The XY and Z resolution values as defined by number of voxels, are updated as the slider is moved.

Compute

1. Click **Compute** to generate the parametric maps with the new selections.

-  Note that map computation can take several minutes based on the matrix size and the volume of interest.

Related topics

[Step 1: Open GenIQ](#)

[Step 2: Review Images and Settings](#)

[Step 3: Review All Maps](#)

[Step 5: Review permeability maps](#)

[Step 6: Close GenIQ application](#)

[General GenIQ procedures](#)

Step 5: Review permeability maps

- From the [Review Steps area](#), click **Review Permeability Maps**.
 - For AW¹ systems with two monitors, the second monitor displays the DCE image fused with the Ktrans map.
 - The Review Permeability Maps review step displays the following default layout.

Figure 3-25: Review Permeability layout

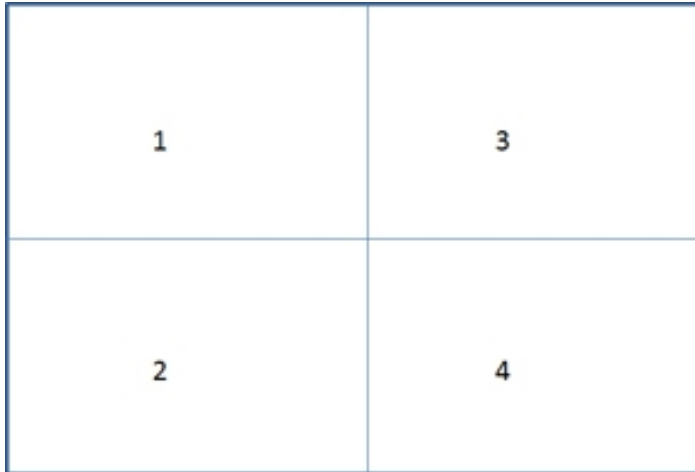


Table 3-10: Image legend

#	Description
1	Displays the DCE ² source images.
2	For a 2-parameter fitting algorithm, displays the Ktrans map. For a 3-parameter fitting algorithm, displays the Ve map.
3	For a 2-parameter fitting algorithm, displays the IAUGC map with 90 value. For a 3-parameter fitting algorithm, displays the Ktrans map.
4	For a 2-parameter fitting algorithm, displays the Ve map. For a 3-parameter fitting algorithm, displays the fPV map.

- For parametric map details, see [GenIQ parametric maps](#)
- The screen areas for the Review Permeability Maps are the same as Review All Maps. For details, see the following:
 - [Adjust the threshold](#)
 - [Clip Min & Max values and select permeability map](#)
 - [Step 4: Advanced settings](#)
 - [Physiologic parameters](#)
 - [GenIQ T1 settings](#)
 - [Parametric images](#)
 - [Downsample](#)
 - [Compute](#)

¹Advantage Workstation

²Dynamic Contrast Enhanced

Related topics

[Step 1: Open GenIQ](#)

[Step 2: Review images and settings](#)

[Step 3: Review all maps](#)

[Step 4: Advanced settings](#)

[Step 6: Close GenIQ application](#)

[General GenIQ procedures](#)

Step 6: Close GenIQ application

Use these steps to exit the GenIQ application. Prior to exiting the application consider the following:

- Save any desired output series.
- Make sure the progress bar is not currently showing activity.

1. From the control panel, click the *Exit icon* .
 - The application closes and returns to the patient list.

Related topics

[Step 1: Open GenIQ](#)

[Step 2: Review images and settings](#)

[Step 3: Review all maps](#)

[Step 4: Advanced settings](#)

[Step 5: Review permeability maps](#)

[General GenIQ procedures](#)

DCE MRI protocol considerations

To get optimum and accurate results in GenIQ, consider the following information when acquiring the MRI protocol that will be post processed with GenIQ.

At a minimum, the protocol used to acquire the images for GenIQ should include:

- An anatomic series for tissue of interest.
- A DCE¹ series that collects dynamic data during the passage of the contrast agent must have the following characteristics:
 - Pulse Sequence: 2D or 3D fast spoiled gradient recalled echo or equivalent
 - Coils: Body transmit coil, phased array receive coil
 - Imaging Options: Do not use Mag Transfer
 - TE as short as possible (1.5-2.0 ms)
 - TR as short as possible (3-5 ms)
 - The minimum temporal resolution must be less than 30 seconds and ideally less than 10 seconds.
 - The series must have a positive enhancement curve.
 - SCIC² and other image filters are not supported by GenIQ.
 - Flip angles: Select the maximal allowed flip angle when SAR limitations occur. High flip angles (20-30°) are recommended in order to minimize saturation of the signal intensity versus gadolinium concentration, particularly in vessels. Note that SAR limits may affect the maximum allowable flip angle.
 - The series must have a minimum of 10 phases. Select a number of phases that results in a scan time of 5 minutes or longer. The number of phases must allow for acquisition of post injection data, excluding baseline images).
 - In order to get accurate measurements on the parametric maps, it's recommended to synchronize the injection and the start of the multiphase scan. If it happens that the scan protocol acquires the pre-contrast data followed by a time pause before resuming with the multi-phase acquisition, it is then recommended to exclude Phase #1 from the series loading panel upon session launch.
 - It is recommended to start the post-contrast multi-phase series early enough so that three temporal phases are acquired before the bolus arrives in the scanned area. This action stabilizes the pre-contrast baseline signal intensity for the GenIQ computation.
 - DCE Image acquired with a 512 matrix (or interpolated to 512) are not recommended as it may result in a long processing time.
 - When the total number of images per dynamic series becomes very high, resulting from the # of slices locations and # of temporal phases, it will start affecting the execution performance of the application. An information message is displayed at the session launch when this situation occurs.

¹Dynamic Contrast Enhanced

²Surface Coil Intensity Correction

- GenIQ Compatible PSD¹s:
 - 2D Fast SPGR² PSD
 - 3D Fast SPGR PSD
 - 3D Fast TOF³-SPGR
 - 2D FGRE-ET⁴
 - FSE⁵
 - FSE-XL⁶
 - BRAVO⁷
 - DISCO⁸
 - LAVA⁹ PSD
 - LAVA-XV PSD
 - LAVA-Flex PSD
 - **TRICKS**¹⁰
 - VIBRANT¹¹ PSD
 - VIBRANT-XV PSD
 - VIBRANT-Flex PSD



GenIQ requires the acquisition of at least 3 baseline phases before arrival of the contrast agent. Fewer time points in the baseline may lead to inaccurate estimation of the contrast agent concentration.

¹Pulse Sequence Data base

²SPoiled GRAdient echo

³Time Of Flight

⁴Fast Gradient Recalled Echo - Echo Train

⁵Fast Spin Echo

⁶Fast Spin Echo EXcel

⁷BRain VOlume Imaging

⁸Differential Subsampling with Cartesian Ordering

⁹Liver Acquisition with Volume Acceleration

¹⁰Time Resolved Imaging of Contrast Kinetics

¹¹Volume Imaging for BReast AssessmeNT

Glossary

A

AIF

Artery Input Function

AW

Advantage Workstation

AWS

AW Server

B

BRAVO

BRain VOlume Imaging

C

CER

Contrast Enhancement Ratio

D

DCE

Dynamic Contrast Enhanced

DISCO

Differential Subsampling with Cartesian Ordering

E

EES

Extra-vascular Extra-cellular Space

F

FGRE-ET

Fast Gradient Recalled Echo - Echo Train

FPV

Fractional Plasma Volume

FSE

Fast Spin Echo

FSE-XL

Fast Spin Echo EXcel

G

Gd

Gadolinium

GKM

General Kinetic Model

I

IAUGC

Initial Area Under Gadolinium contrast agent Concentration

L

LAVA

Liver Acquisition with Volume Acceleration

M

MRI

Magnetic Resonance Imaging

My Term

My definition

O

OC

Operator Console

P

PSD

Pulse Sequence Data base

PURE

Phased array UnifoRmity Enhancement

R

ROI

Region Of Interest

ROIs

Regions Of Interest

S

SCIC

Surface Coil Intensity Correction

SPGR

SPoiled GRadient echo

T

TOC

Table Of Contents

TOF

Time Of Flight

TRICKS

Time Resolved Imaging of Contrast Kinetics

V

VIBRANT

Volume Imaging for BReast AssessmeNT

VIF

Vascular Input Function

VS

Vascular Space

This page is intentionally left blank

Index

1

1.5T T1 tissue times	3-31
----------------------------	------

3

3-parameter fitting algorithm	3-3
3.0T T1 tissue times	3-31
3DFSPGR caution	2-2

A

about this manual	iii
Adjust threshold	3-29
Algorithm Threshold	3-32
Algorithm Threshold caution	2-4
Algorithms	3-2
Angiogenesis	3-1
Auto VIF mode	3-26
Automatic VIF caution	2-2
AW VolumeShare	1-1, 1-2

B

BAT parametric map	3-5
Blood flow	3-2
Blood hematocrit	3-32
Blood T1	3-32

C

Capillary vascular plasma space	3-2
Caution	v
Cautions	2-2
CER	3-28
CER parametric map	3-5
ClariView	2-2
Clip Min & Max	3-30
Close GenIQ	3-36
compatible PSDs	3-21
compatible series parameters	3-21
Compute	3-33
Convolution	3-3
Ctrl + X	iii

D

Danger	v
Display of permeability maps	3-34
Downsample	3-33
Dynamic contrast enhanced images	2-4

E

EES	3-1, 3-2, 3-3
exit GenIQ	3-36

F

Final settings	3-31
Fitting algorithm	3-28, 3-32
fPV	3-3, 3-34
fractional plasma volume	3-3
Fractional plasma volume	3-3
Fractional Volume	3-2
Fuse images	3-30

G

General Kinetic Model	3-2
GenIQ algorithms	3-2
GenIQ applications	3-1
GenIQ overview	3-1
GenIQ procedures	3-6
GenIQ work area	3-7
GKM model	1-2, 3-2
Graph display	3-15
Graphic conventions and legends	iii

H

hard key	iii
----------------	-----

I

IAUG	3-32
IAUGC	3-28, 3-32, 3-34
IAUGC parametric map	3-5
Image Filters	2-2
Important notice symbol	v
Input VIF	3-2
Intracellular space	3-2
items in a list	iv

K

K ep	3-28
Kep parametric map	3-5
Ktrans	3-2, 3-28, 3-30, 3-34
Ktrans parametric map	3-5

L

launch GenIQ	3-21
Localized VOI	3-24

M

Manual VIF mode	3-26
Max slope	3-28
Max slope parametric map	3-5
Model based VIF mode	3-26
Modify phase range	3-25
Motion Correction	3-24
Motion correction caution	2-4

N

Note symbol	v
-------------------	---

O

open GenIQ	3-21
option in a check box	iii

P

Paqrametric images selections	3-32
parameter fitting algorithm	3-34
Parametric maps	
BAT	3-5
CER	3-5
IAUGC	3-5
K trans	3-5
Kep	3-5
Max slope	3-5
Ve	3-5
permeability map	3-30, 3-34
Pharmaco-Kinetic model	3-2
Phase range	3-25
Physiological parameters	3-32
Plasma tracer concentration	3-3
Procedures	3-6

Processing time important message	2-4
Protocol selection	3-21
Protocol selection screen	3-13
PSDs	3-38
PSDs cautions	2-4
PURE	2-2
Purpose and scope	iii

R

radial button	iii
Rate transfer constant	3-3
Removing phases caution	2-2
review image setting display	3-23
Review step	3-8
ROIs caution	2-4

S

Safety notices	v
SCIC	2-2
Screen work area	3-7
Screens	
Protocol selection	3-13
review steps	3-8
Select final settings	3-31
Select permeability map	3-30
Select VIF mode	3-26
selecting a tab	iii
Semi-automatic VIF caution	2-2
Semi auto VIF mode	3-26
Shared Segmentation	3-30
Skip phases	3-25
Software application	1-2
Software messages	2-5
Summary table	3-8

T

T1 tissue correction	3-31
T1 tissue types	3-31
T1 tissue values	3-31
text box	iii
Threshold adjustment	3-29
Tissue factor concentration	3-3
Tracer concentration	3-2
Troubleshooting symbol	v

type text	iii
-----------------	-----

V

Ve	3-34
Ve parametric map	3-5
VIF cautions	2-4
VIF modes	3-26
Volume transfer constant	3-3
VS vascaular space	3-3

W

W/L	3-14
auto	3-14
shortcut	3-14
Warning	v
Warnings	2-2
Window width and level	3-14
Work area	3-7
workflow	3-20
step 1	3-21
step 2 review images and setings	3-23
step 3 advanced settings	3-28, 3-31
Step 5 close GenIQ	3-36
WW/WL	3-14

This page is intentionally left blank