

Diagnostic Workstation

English

8G7607 Rev J

Instructions for Use

Vue PACS

Version 12.2.8.x

PHILIPS

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1 Before you begin

1.1 About Vue PACS Performance Characteristics

Vue PACS is an image management device whose intended use is to provide completely scalable local and wide area PACS solutions for hospital and related institutions/sites, which will archive, distribute, retrieve, process and display images and data from all hospital modalities and information systems. The device is to be used by trained professionals including, but not limited to, physicians and medical technicians.

The device contains clinical applications that assist the processing of analyzing and comparing medical images. It is a single device that integrates review, dictation and reporting tools to create a productive work environment for the radiologists and physicians.

The Diagnostic Viewer has a variety of user profiles applicable to different stakeholders in the cycle of care such as radiologists, referring physicians, technologists, and others. With advanced streaming technology, the Diagnostic Viewer can perform well even over slow communication lines between the viewer and the server. Enterprise workflow capabilities allow users across the network to read and report from a global worklist irrespective of the image acquisition location.

The Diagnostic Viewer includes native clinical applications such as Lesion Management, CT Perfusion, MR Perfusion and MR Diffusion.

Additional display and workflow capabilities include the following:

- Native reporting module for the generation of multi-media interactive reports.
- Vue Motion uses a web browser to provide on-demand access to DICOM and non-DICOM images, to results and to other patient information on-site or to remote clinicians including referring physicians. The patient portal (MyVue) is based on Vue Motion and focused on providing access for the patient to the patient's portfolio. Patients can further manage sharing of their portfolio to others, providing them with access rights and permissions.
- Distribution capabilities to reach out to referring physicians, tele-radiology clinicians, and clinical personnel within the healthcare enterprise are available through options such as self-playing CDs, auto-routing, FAX, or e-mail.
- A DICOM conformant, on-line storage and archive environment (VNA) that ensures access, preservation, data integrity and disaster recovery options. Clinical information life cycle management is further available leading to optimal cost of ownership.
- Non-DICOM ingestion and management to support encounter-based imaging workflows.
- Scalable architecture from a single stand-alone workstation to a large multi-site distributed enterprise.
- Integration and interface options with modalities and medical information systems such as HIS, RIS, EMR, and other third-party applications based upon industry standards.

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1.2 About this guide

1.2.1 About the Instructions for Use

This Instructions for Use (IFU) is intended to assist users and operators in the safe and effective operation of the product described.

The “user” is considered to be the body with authority over the product.

The "operators" are the persons who actually handle the product.

Before attempting to operate the device, you must read this manual thoroughly, paying particular attention to all Warnings, Cautions and Notes incorporated in it. You must pay special attention to all the information given and procedures described in the Safety section.



WARNING

Warnings are directions, which if not followed, could cause moderate to serious injury to a user, patient or any other person, or could lead to a misinterpretation and/or loss or damage of patient-related data.



CAUTION

Cautions are directions, which if not followed, could cause damage to the product described in this Instructions for Use and/or any other device.

1.2.2 Usage of product

The Instructions for Use for **Vue PACS** is supplied electronically and/or in printed volumes.

The five volumes typically include:

- *Instructions for Use*. This volume explains how to use the Vue PACS device and contains information about safety, data security, system start-up, software navigation, accessing patient data, and filming.
- *Application instructions for use volumes:*
  - Review. Depending on your version of **Vue PACS**, you may have multiple, modality-specific Review volumes (for example, CT Review; NM Review: MR Review; Multimodality Review, and so on) that explain how to use the various image viewers supplied with the system. Also included in these volumes are other processing techniques for displaying and analyzing patient studies.
  - Analysis: Depending on your **Vue PACS** version you may have multiple, modality specific Analysis volumes for example, CT Analysis; NM Analysis; MR Analysis; Multimodality Analysis, and so on) that explain how to use advanced applications.

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- System Administration Guide. This volume explains how to use the **Vue PACS** device. The local site administrators and service personnel are provided the functionality required to monitor **Vue PACS** usage, check for errors, add and delete users and groups and maintain the patient database.
- Third-party applications. Different versions of Instructions for Use are available. Select the appropriate documents for your version.
- Electronic Instructions for Use. An electronic (PDF) version of the Instructions for Use is provided. Contact the administrator if you do not have access to this material.

1.3 Intended Use/Purpose

Vue PACS is an image management system whose intended use is to provide complete and scalable local and wide area PACS solutions for hospital and related institutions/sites, which will archive, distribute, retrieve, process and display medical images and data from hospital medical imaging and information systems. The system is to be used by trained professionals including, but not limited to, physicians and medical technicians

The system contains interactive tools in order to ease the process of analyzing and comparing three dimensional (3D) images. It is a single system that integrates review, dictation and reporting tools to create a productive work environment for the radiologists and physicians.

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1.3.1 Intended users

The device is to be used by trained professionals including, but not limited to, physicians and medical technicians.

- Trained radiologists – to read and review medical images as part of their routine work.
- Referring physicians and clinicians – to review the images and results created by the radiologists, or access exams for review.
- PACS Administrators – to monitor and improve the efficiency, accuracy and integrity of the image services provided to the consumers.
- Patients - to view and share their images and results created by radiologists, mainly for second opinion.

1.3.2 Patient target groups and intended patient population

Vue PACS is not limited to an intended patient population nor medical condition.

1.4 Indications for use

Vue PACS is an image management system whose intended use is to provide complete, scalable local and wide area PACS solutions for hospital and related institutions/sites, which will archive, distribute, retrieve, process and display medical images and data from hospital medical imaging and information systems. This includes the display of structured reports from CAD systems with DICOM "for presentation" mammography images. The system is to be used by trained professionals including, but not limited to, physicians and medical technicians.

The system contains interactive tools in order to ease the process of analyzing and comparing three dimensional (3D) images. It is a single system that integrates review, dictation and reporting tools to create a productive work environment for the radiologists and physicians.

The system contains a Perfusion module with interactive tools to analyze and compare Computed Tomography Perfusion (CTP) and MR Perfusion (MRP) images of adult patients. Blood perfusion parameters are automatically calculated and displayed as a set of perfusion maps and perfusion tables. The perfusion tables include the calculation of parameters related to tissue flow (perfusion) and tissue blood volume.

The system contains a Diffusion Module with interactive tools to ease the process of analyzing and comparing MR Diffusion Weighted images (DWI) and MR Diffusion Tensor Imaging (DTI) of adult patients. This module is used to visualize local water diffusion properties from the analysis of diffusion-weighted MRI data.

The system supports Subtraction with interactive tools to aid with the analysis of Digital Subtraction Angiography (DSA) images in both interventional radiology and cardiology. Subtraction automatically subtracts a mask from contrast frames of an X-Ray Angiography study for visualization of vascular anatomy and pathology of adult patients.

The Lesion Management Application is a module that works with Vue PACS for measurement of lesions or regions of interest identified by trained users; tabulation of measurements, categorization of tumor response in accordance with user-selected standards, and follow-up record of findings. Lesion Management Application is not to be used for mammography.

The Vue Motion software program is used for patient management by clinicians in order to access and display patient data, medical reports, medical data, and medical images for diagnosis from different modalities including CR, DR, CT, MR, NM, ECG, and US.

Vue Motion provides wireless and portable access to medical images for remote reading or referral purposes from web browsers including usage with validated mobile devices. This device is not intended to replace full workstations and should be used only when there is no access to a workstation. For primary interpretation and review of mammography images, only use display hardware that is specifically designed for and cleared by FDA for mammography

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1.5 Residual Risk

Information for safety in the form of warning, cautions, or recommendations for use has been added to the Instructions for Use, no reportable residual risks have been identified for Vue PACS.

1.6 Benefit

The Vue PACS system intends to provide completely scalable local and wide area PACS solutions for hospital and related institutions or sites, which will archive, distribute, retrieve and display images and data from all hospital modalities and information systems thus supporting Radiology reading. Its clinical applications support the user with interpreting clinical data by combining processing, advanced visualization and measurements.

When used as specified in the Intended Use under the circumstances and conditions as specified in the Indications for Use, the Vue PACS clinical applications assist the user with interpreting the clinical data in a structured way by offering a consistent workflow. Therefore, the expected patient benefits of the Vue PACS are a consistent way of providing diagnostic information from images and data, providing a positive impact on patient management.

The benefits of PACS systems (when compared to the traditional film-based workflow) are well established:

- Enhanced delivery of care
- Increased productivity
- No "lost films" problem
- Reduction in areas needed for archiving of Patient's film files
- Availability of patient’s file for many users at the same time
- Greater customer satisfaction

Benefit per clinical application:

3D Analysis

When used as specified in Intended Use under the circumstances and conditions as specified in Indications for Use, the 3D Analysis application assists the user with interpreting the clinical image data on par with the state of the art thus realizing a positive impact on diagnosis or patient management.

Cardiology (Cardiology and Cardiac CT)

When used as specified in Intended Use under the circumstances and conditions as specified in Indications for Use, the Cardiology application assists the user with the viewing, processing and analysis of cardiac CT datasets on par with the state of the art, thus realizing a positive impact on diagnosis or patient management. Cardiac Analysis tools also enables a user to assess cardiac morphology, mobility and functionality using echocardiographic datasets.

Coronary Artery Analysis

When used as specified Intended Use under the circumstances and conditions as specified in Indications for Use, the Coronary Artery Analysis application assists the user with interpreting the clinical image data on par with the state of the art thus realizing a positive impact on diagnosis or patient management.

Specifically, with the resulting radiological conclusions, obtained from quantitative and qualitative information of the heart and coronaries through the application and noninvasive medical imaging technique - the referring physician can advise the patient on the current condition, determine whether additional investigations are warranted, present the patient with treatment options to prevent reoccurrence or worsening of the presenting symptoms, and optionally (if diagnosed) control the evolution of the cardiac disease by taking action in controlling risk factors with heart-healthy lifestyle changes, medication, or interventional therapy.

Calcium Scoring

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When used as specified in Intended Use under the circumstances and conditions as specified in Indications for Use, the Calcium Scoring application assists the user with interpreting the clinical image data on par with the state of the art thus realizing a positive impact on diagnosis or patient management.

More specifically, coronary artery calcium (CAC) scanning assessment was incorporated into ACC/AHA Guidelines with a Class IIa status, recommendation in favor of treatment or procedure being useful or effective since 2010, CAC scoring appears to identify an important subgroup of patients with advanced subclinical atherosclerosis, who are "between" primary and secondary prevention, which may benefit from the most aggressive lipid-lowering pharmacotherapy.

Therefore, if the device is used as specified in Intended Use under the circumstances and conditions as specified in Indications for Use, the expected patient benefits are preventive pharmacotherapies, efficient follow-up by a physician that might prevent atherosclerotic cardiovascular disease (ASCVD) events.

Vessel Analysis and Digital Subtraction

When used as specified in Intended Use under the circumstances and conditions as specified in Indications for Use, the Vessel Analysis application assists the user with interpreting the clinical image data according to the clinical context and on par with the state of the art, thus providing diagnostic or treatment-decision information from images and giving positive impact on patient management. More specifically, the Vessel Analysis and Digital Subtraction applications assist the user with viewing and interpreting of a CTA or MRA vascular dataset respectively a XA dataset to confirm or rule out the presence of any vascular pathology.

The expected patient benefits are:

With the resulting radiological conclusion, the referring physician can advise the patient with options to prevent reoccurrence or worsening of the presenting symptoms and optionally (if diagnosed) control the evolution of the vascular disease by taking action in controlling risk factors with heart-healthy lifestyle changes, medication, or further investigations.

Vue Motion and ECG

When used as specified in Intended Use under the circumstances and conditions as specified in Indications for Use, the Vue Motion application assists the user with interpreting the clinical image data according to the clinical context and on par with the state of the art thus providing diagnostic or treatment decision information from images and giving positive impact on patient management.

CT Perfusion

When used as specified in Intended Use under the circumstances and conditions as specified in Indications for Use, the CT Perfusion application assists the user with interpreting the clinical image data according to the clinical context and on par with the state of the art thus providing diagnostic information from images and giving positive impact on patient management.

Specifically, the Vue PACS CT Perfusion Application assists the user in the analysis of typical brain perfusion CT medical images including the evaluation of an area of interest, to generate qualitative and quantitative information about changes in image intensity over time.

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The expected patient benefits are:

- The application provides quantitative perfusion and summary maps derived from a CT examination, a fast, painless, and noninvasive medical imaging technique.
- These quantitative maps assist the physician in the management of patients with ischemic stroke.

MR Perfusion

If the device is used under the circumstances and conditions as specified in Indications for Use, the Vue PACS Perfusion Application assists the user in the evaluation of perfusion studies and in the generation of numerical and graphical results and maps.

The application provides perfusion parameters maps from CT perfusion imaging for the assessment of alteration of blood supply to cerebral tissues. These quantitative maps assist the physician in the evaluation of stroke, or assessment and follow-up of brain tumors.

MR Diffusion

When used as specified in Intended Use under the circumstances and conditions as specified in Indications for Use, the MR Diffusion application assists the user with interpreting the clinical image data on par with the state of the art thus realizing a positive impact on diagnosis or patient management.

Volume Matching

When used as specified in Intended Use under the circumstances and conditions as specified in Indications for Use, the Volume Matching application assists the user with interpreting the clinical image data on par with the state of the art thus realizing a positive impact on diagnosis or patient management.

Specifically, the Vue PACS Volume Matching Application assists the user in the analysis of various conditions such as early diagnosis of malignant lesion, coronary artery diseases, and other diseases. The use of biological imaging enhances the success rate of correct diagnosis, which is necessary for early, effective treatment and ultimate cure.

Mammography (Mammography Image Display and Digital breast Tomosynthesis Applications)

When used as specified in Intended Use under the circumstances and conditions as specified in Indications for Use, the expected benefits of Vue PACS Mammography application are:

- Evaluation and analysis of breast tissue and potentially cancerous lesions precision
- Evaluation of a disease course over time through comparing exams over time
- Streamlining the diagnosis workflow and efficient reading with dynamic DPs and contextual tools
- Facilitation of breast tissue evaluation by supporting the visibility of CAD and other marks created on a mammography workstation

Lesion Management

If the device is used under the circumstances and conditions as specified in Indications for Use, the Vue PACS Lesion Management Application assists the user with workflows in:

- The analysis of anatomical and functional images from multiple modalities including CT, MRI, and PET/CT for a single study or over the course of multiple time points

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- The characterization of the patient's pathology using multiple imaging modalities
- The use of response imaging criteria

Expected patient benefits are:

- Facilitating a standardized and compliant radiology review and report positively affects the treatment decision-making process
- Improved diagnosis of the patient's pathology using multiple imaging modalities, helping physicians provide more adapted therapy and respond more efficiently to changes

PET/CT

When used as specified in Intended Use under the circumstances and conditions as specified in Indications for Use, the Hybrid NM Viewer application assists the user with interpreting the clinical image data according to the clinical context and on par with the state of the art thus providing diagnostic or treatment decision information from images and giving positive impact on patient management.

Specifically, the Hybrid NM Viewer Application assists the user in the analysis of lesions or heart disease and neurological disorder on the PET/CT, PET/MR, or SPECT/CT medical images including the evaluation of an area of interest, to generate qualitative and quantitative information about changes in relevant parameters over time.

The application provides as an expected patient benefit, quantitative SUV parameters derived from a PET/CT examination. These quantitative parameters assist the physician in the management of patients on the treatment decisions.

1.7 Contraindications

There are no identified contraindications

1.8 Limitations for use



WARNING

Do not use Vue PACS for any application until you have received adequate and proper training in its safe and effective operation. If you are unsure of your ability to operate this equipment safely and effectively DO NOT USE IT. Operation of this equipment without proper and adequate training could lead to clinical misdiagnosis.



WARNING

Vue PACS must be operated in an environment where the minimum specified requirements for hardware and network performance are met.

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WARNING

Do not use Vue PACS for any purpose other than those for which it is intended. Operation of Vue PACS for unintended purposes, or with incompatible equipment, could lead to clinical misdiagnosis.



WARNING

Use of this product in a way not described in these Instructions for Use could lead to clinical misdiagnosis.



WARNING

The Vue PACS system can display both lossless and lossy compressed images. The user's ability to analyze images depends on the quality of the image data the user intends to analyze. Lossy/Irreversible compression affects the quality of the image. The user is responsible to ensure that the image's quality is adequate enough for the review purpose.



WARNING

When running Vue PACS with a virtualization solution (Citrix XenDesktop®), a degradation in image quality, in addition to skipped frames, can occur, based on the network bandwidth and virtual machine configuration.



WARNING

Before the study is closed, verify that images are copied or backed up successfully.



WARNING

Before the study is deleted, verify that images are copied, archived or backed up successfully.



WARNING

Be careful when editing the report. In some parts of the report it is possible to change the information created automatically.

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WARNING

Make sure that you are using appropriate monitors and that they are properly configured and calibrated prior to using Vue PACS especially for clinical application such as Mammography.

WARNING

Never switch the IT equipment off using the POWER ON/OFF switch while the software product is still running, as this can damage data integrity, which can lead to loss or damage of patient-related data. Always exit the software product before switching off the IT equipment.

WARNING

Do not install unsupported software on the Vue PACS system because this could interfere with diagnosis or interpretation, or cause loss of or damage to patient-related data, and/or introduce computer viruses.

CAUTION

In case of a failure and images are not available via PACS, if the images need to be viewed immediately, physician/radiologist shall refer to the modality itself. When there is no onsite radiologist that can access the modality, the Institute guiding principles and procedures shall be followed.

1.9 Measurement accuracy

The Philips Vue PACS image processing technology is state-of-the-art and therefore provides sufficient accuracy to be utilized as a medical device for clinical purposes.

A major factor in determining the accuracy of manual measurements is the ability to accurately place a measurement control point on an image displayed on a monitor. In addition, the measurement accuracy is also impacted by the image quality and the user's interpretation of the image.

Factors impacting image quality:

- Scanner's calibration and quality control program, including the geometric accuracy, homogeneity, artifacts, contrast resolution, positioning and sensitometry when applicable
- Imaging protocol, including spatial resolution (for example, in-plane resolution, slice thickness), region of interest, reconstruction algorithm, data corrections (for example scatter), contrast agent, gating and acquisition sequences when applicable
- Adherence to patient management and handling procedures, including contrast administration, scan scheduling, positioning and fixation protocols

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- Pre-existing patient comorbidities
- Residual patient motion and other motion artifacts, such as organ motion

The following aspects are contributing factors to the user's interpretation of an image:

- Image viewing settings (for example, window setting, zoom)
- Visualization options (for example, MPR, MIP, or MinIP, volume rendering)
- Extent of the users' knowledge on performing measurements
- Other relevant factors

Based on their knowledge and experience, clinical users are responsible for:

- Assessing the quality and relevance of the input image interpreting the image for a proper measurement
- Judging the accuracy of the measurements based on the given image quality
- Accurately positioning the measurement control points with the mouse point

In order to obtain an accurate measurement assessment when using Vue PACS, the clinical user must take into account that patient characteristics (demographic, physiological, and so on) are not automatically processed by the Vue PACS system and that it is the clinical users' responsibility to follow the indications for use and contraindications, in conjunction with the user's expertise.

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1.10 Training

Users of the Vue PACS device must have received adequate training on its safe and effective use before attempting to use the software product described in this Instructions for Use.

Training requirements for this type of software product will vary from country to country. It is for users to make sure that they receive adequate training in accordance with local laws or regulations, which have the force of law. If you require further information about training in the use of this software product, contact your local Philips representative or the Manufacturer.

1.11 Technical Support

Should you encounter difficulty using **Vue PACS**, contact the Philips technical support group serving your area. To obtain contact information for this group, ask your local Philips representative.

When contacting Philips technical support, please have the following information available:

- Caller name, customer organization name, and location.
- Site number, if applicable.
- Detailed description of the problem, including any history of troubleshooting efforts completed before or after the problem first occurred.

For contact details, browse to http://www.philips.com/healthcare

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1.12 Safety

Philips products are designed to meet stringent safety standards. However, all software medical devices require proper operation and maintenance, particularly with regards to human safety.

It is vital that you follow strictly all safety directions under the heading Safety and all Warnings and Cautions throughout this "Instructions for Use", to help ensure the safety of both patients and operators.

In particular, you must read, understand and know the information described in this Safety section before using this device.

Also see the following information:

- Intended use of Vue PACS. See Intended Use/Purpose in this IFU.
- Contraindications. See Contraindications in this IFU.
- Training for operators of Vue PACS. See Training in this IFU.

NOTICE

Any serious incident that has occurred in relation to the device should be reported to the manufacturer or its EU Authorized Representative and also reported to the local competent authority of the European Union / European Free Trade Association member state in which the user or patient is established. Reporting in other jurisdictions must follow the applicable local regulations.

1.13 Symbols Glossary - Medical

The following symbols appear in the product documentation or on the labels attached to the product:

Symbol	Symbol Name	Symbol Description	Standard / Regulation Number & Name	Symbol Reference Number
	Manufacturer	Indicates the name and address of the manufacturer.	EN ISO 15223-1:2021 [1]	5.1.1
	Date of manufacture	Indicates the date when the device was manufactured.	EN ISO 15223-1:2021 [1]	5.1.3
	Batch code	Indicates the Software Release/ Version number.	EN ISO 15223-1:2021 [1]	5.1.5

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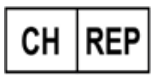
Symbol	Symbol Name	Symbol Description	Standard / Regulation Number & Name	Symbol Reference Number
	Code number	Indicates the manufacturer's catalog number so that the device can be identified.	EN ISO 15223-1:2021 [1]	5.1.6
	Consult Instructions for Use	Indicates the need for the user to consult the instructions for use.	EN ISO 15223-1:2021 [1]	5.4.3
	eIFU Indicator	When used to indicate an instruction to consult an electronic instructions for use (eIFU), this symbol is accompanied by an eIFU indicator. This indicator can represent the manufacturer's eIFU website or any other appropriate indication on the use of eIFU (for example, "Refer to IFU Kit"). The indicator can be placed either alongside, beneath, or surrounding the symbol.		

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Symbol	Symbol Name	Symbol Description	Standard / Regulation Number & Name	Symbol Reference Number
	Warning/Caution/ Notice This symbol is used on the device label to highlight the fact that there are specific warnings or precautions associated with the device, which are not otherwise found on the label.	**WARNINGS** are directions which if not followed could cause moderate to serious injury to an operator, patient or any other person, or could lead to a misinterpretation or loss or damage of patient-related data. The warning symbol is only needed if the word Warning is not translated into a local language. **CAUTIONS** are directions which if not followed could cause damage to the product described in this Instructions for Use or any other device. **NOTICES** Notes highlight unusual points as an aid to the operator.	EN ISO 15223-1:2021 [1]	5.4.4
CE 0197	CE Marking of Conformity	A marking by which a manufacturer indicates that a product is in conformity with the applicable requirements set out in European Union's harmonization legislation providing for its affixing.	European: MDD- COUNCIL DIRECTIVE 93/42/EEC of 14 June 1993 concerning medical devices, as amended. MDR: Regulation (EU) 2017/745 of the European Parliament and of the Council of 5 April 2017 on medical devices.	Annex XII of MDD Annex V of the MDR

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Symbol	Symbol Name	Symbol Description	Standard / Regulation Number & Name	Symbol Reference Number
	Prescription Device	**CAUTION** In the United States, Federal law restricts this device to sale by or on the order of a licensed healthcare practitioner.	21 CFR 801.109(b) (1) Prescription Devices	
	Medical Device Indication	An indication that the item is a medical device.	EN ISO 15223-1:2021 Regulation (EU) 2017/745 of the European Parliament and of the council of 5 April 2017 on medical devices, Annex I.	5.7.7
	Unique Device Identifier	Indicates a carrier that contains the unique device identifier information. This symbol must be placed adjacent to the Unique Device Identifier Information.	EN ISO 15223-1:2021 Regulation (EU) 2017/745 of the European Parliament and of the Council of 5 April 2017 on medical devices, Annex I.	5.7.10
	Authorized Representative in Switzerland	Indicates the authorized representative in Switzerland	N/A	N/A
	Importer	Indicates the entity importing the medical device into the locale. The symbol will be followed by the medical device importer contact details: name and address.	EN ISO 15223-1:2021 Article 13 (3) MDR	5.1.8

[1]EN ISO 15223-1:2021 Medical devices - Symbols to be used with information to be supplied. Part 1: General requirements.

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1.14 Compatibility

The software product described in this Instructions for Use must not be used in combination with other software, equipment or components unless such other software, equipment or components are recognized as compatible by Philips. A list of such software, equipment and components is available on request from your local Philips Representative or the Manufacturer. Philips is not responsible for running compatibility validation of non-supported third-party software.

Changes and/or additions to the server or workstation must only be carried out by Philips or by third parties expressly authorized by Philips to do so. Such changes and/or additions must comply with all applicable laws and regulations which have the force of law within the jurisdictions concerned, and with best engineering practice.

Changes or additions to the software product that are carried out by persons without the appropriate training or using unapproved spare parts can lead to the Philips warranty being voided.

Philips is not responsible for any malfunction of Vue PACS, if Vue PACS runs on hardware that is not according to hardware specification.

If not supplied by Philips with the Vue PACS software, Philips is not responsible for any malfunction of the hardware used.

1.15 Compliance

Vue PACS complies with relevant international and national standards and laws.

Information on compliance will be supplied on request by your local Philips Representative or by the Manufacturer.

This software product must be installed on appropriate IT equipment that complies with relevant international and national laws and standards on EMC (Electro-Magnetic Compatibility) and Electrical Safety. Such laws and standards define both the permissible electromagnetic emission levels from equipment and its required immunity to electromagnetic interference from external sources.

1.16 Network Safety, Security and Privacy_default

1.16.1 General

Philips recognizes that the security of Philips products is an important part of your facility's security-in-depth strategy. However, protection can only be realized if you implement a comprehensive, multilayered strategy (including policies, processes, and technologies) to protect information and systems from external and internal threats.

Adhering to industry-standard practice, adopt the following strategy:

- Physical security
- Operational security

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- Procedural security
- Risk management
- Security policies
- Contingency planning

The actual implementation of technical security elements varies by site and might employ several technologies, including firewalls, VLANs, NIDS, virus-scanning software, authentication methods, and other technologies.

As with any computer-based system, protection must be provided so that firewalls and other security devices are in place between the medical system and any externally accessible systems.

The USA Veterans Administration has developed a widely used Medical Device Isolation Architecture for this purpose. Such perimeter and network defenses are essential elements in a comprehensive medical device security strategy.

Any device connection to an internal or external network must be done with appropriate risk management for product effectiveness and data and systems security. Additional security and privacy information can be found on the Philips product security website.

Review Philips product security policies regarding remote service, patch management, anti-virus software and more in the “Product Security Policy Statement” and additional information sources available through this website at:

http://www.philips.com/productsecurity

NOTICE

Philips is not responsible for security of hospital-managed systems (desktop PCs, laptops) where the Vue PACS viewer is installed.

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1.16.2 Protecting Patient Health Information

One of the most important assets to protect with security measures is the patient's health related information.

Many governments require maintaining the confidentiality of this information. Therefore, strict security measures must be taken to guard this protected information.

Note: Users in the U.S.A. can find guidelines at: http://www.hhs.gov/ocr/hipaa/

1.16.3 Preventing Unauthorized Device Modification

Philips sells highly complex medical devices and systems and are required to follow government regulated quality assurance procedures to verify and validate modifications to the operation of their medical devices.

Operators of this medical device must permit only Philips-authorized changes to be made to the servers (or viewers, if applicable), either by Philips' personnel or under Philips' explicit published direction.

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1.16.4 Software Installation

CAUTION

Installation of software not authorized by Philips or not specified in the Vue PACS system documentation can adversely affect the operation and security of the system, in addition to the networks to which the system is connected. These adverse effects might not be immediately apparent to the user. Therefore, users must not install unauthorized software onto the Vue PACS Server and Workstation.

1.16.5 Off-the-shelf Software

The Vue PACS system can be used with the following customer-supplied off-the-shelf software products on local computer workstations and file servers.

Manufacturer	Name	Version
Microsoft	Windows Server	2019
Microsoft	Windows Desktop	10/11

1.16.6 About Screen

To display the About screen that displays labeling and product information, open the application, select **Help** then from the menu select **About**.

1.16.7 Software updates

Updates for this Philips software product can become available. Such updates will be communicated by Philips. Some of these updates are specific security patches and some are maintenance releases and are essential to keep the software product operating securely, safely, effectively, and reliably.

1.16.8 Security issues and guidelines

In addition to the patient information and device integrity needs discussed in the preceding section on regulatory requirements, the following topics, issues, and guidelines must be understood and addressed by operators and owners. This applies to the Vue PACS Server and Workstation and not to the diagnostic viewer PCs.

Network security

The Vue PACS system must be placed on a secure local computer network that has protections against viruses and other harmful computer system intruders. Make sure the equipment is connected to a local network that uses appropriate protection, such as a firewall, NIDS (Network Intrusion Detection System), the use of VLANs, and virus scanners.

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CAUTION

The Vue PACS system does not require open Internet connectivity for its standard Intended Use. It is strongly recommended that the Vue PACS Server/Workstation not be used for Internet browsing.

Remote service

Remote Service provides a set of tools that enable Philips to perform monitoring and service actions, entirely or partly, from a remote location. Remote Service is designed to reduce system downtime and improve investigation of systemic issues.

Remote Service features include:

- Automatic generation of alerts for Vue PACS server critical issues
- Assistance for workstations
- Remote assistance for servers
- Distribution of software
- Installation of software

Positioning of display monitors

Unauthorized visual access to protected information can be minimized by positioning the system's display monitor so it faces a wall, to prevent viewing from doorways, hallways, and other traffic areas.

NOTICE

- Monitor position is a suggestion for use with monitors of the Vue PACS viewer PCs and the Vue PACS Workstation.
- To help in limiting unauthorized visual access, an unattended computer display automatically goes blank after a set period of time.
- The Vue PACS system supports Automatic Logoff/Screen Lock. For additional information, see Automatic logoff (Lock Screen).

Room and equipment access controls

Procedures must be put in place to limit physical access to the medical device, to prevent accidental, casual or deliberate contact by unauthorized individuals.

Access to the room containing the Vue PACS server or workstation must be controlled by policy and procedures that identify who is authorized to occupy specific areas.

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The following physical controls are a recommended baseline and not a comprehensive list. Check with your hospital's Safety and Security Office for more information on what measures are in place or how to implement room access controls:

- Physically accessible computers containing personal data should be kept under lock and key.
- Require the use of physical tools or keys to access components that store data within the system.
- Employ anti-tampering mechanisms and be capable of detecting unauthorized physical access to Internal devices that store personal data, such as hard drives.
- Deploy anchors or locks to physically secure portable components or sub-components that store personal data.
- Disable or lock unnecessary I/O device interfaces and devices on physical servers and workstations (for example, network, CD, DVD USB, serial sockets, and so on).

User login and logout protections

A consistent user login process (user names and passwords) provides good security of protected information. Minimum login standards include:

- Implementing strong passwords. This is the easiest and most effective method to increase security. Strong passwords consist of at least eight alphanumeric, mixed case characters, digits and special characters like '@' or '*'.
- Never use words that can be found in the dictionary.
- Never post or share user names and passwords.
- Change system and user account passwords periodically.



CAUTION

It is strongly recommended that the password of pre-defined user accounts (OS and application) on the Vue PACS system, be changed at the time of system deployment in your facility. Consider changing these passwords on a periodic basis in accordance with your healthcare facility policy and industry standard best practices. Contact your Philips Service Engineer for more details.

Removable and portable media

When using removable media like USB storage devices, CDs, and DVDs, be aware of these security and privacy issues:

- Inserting removable media can introduce a virus to the medical device.
- If removable media is used to store patient data, protect the information from media obsolescence and potential data loss by planning and performing data migrations to newer storage technologies.

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- If the removable media is to be stored for safekeeping, protect the data from “fading” loss by performing media renewal as recommended by the media manufacturer and storing it in a secure location according to manufacturer recommended environmental settings.

CAUTION

Whenever media is inserted into the Vue PACS system, make sure that the media has not been exposed to viruses, worms, and Trojans. Make sure the media has been scanned for viruses or malware before connecting it to server or workstation and each use.

CAUTION

It is not possible to prevent the transfer of data to removable media.
Removable media used in conjunction with the Portal Server for data transfer purposes, can contain confidential patient information. Take appropriate measures to protect this information, so that unwanted access by unauthorized individuals is avoided.

CAUTION

Removable media that contains images and other medical information must be stored in a secure area that is not accessible by unauthorized individuals.

CAUTION

If the removable media containing patient data, images, or sensitive information is to be discarded, it must be destroyed (or the contained data permanently deleted) so that the data stored on it can no longer be accessed. Data that is deleted from removable media using conventional operating system or application tools will still be present on the media and data sanitization must be performed. While the Vue PACS system has data deletion capabilities, it does not provide data sanitization functionality for media that contain patient data or other sensitive information. Use appropriate data sanitization techniques and tools along with healthcare entity policies regarding media destruction and sanitization. NIST publication 800-88 Guidelines for Media Sanitization provides guidelines and best practices for media sanitization.

1.16.9 Implemented security and privacy features

It is the policy of Philips to adhere to all required standards and regulations. To assist the hospital in fulfilling security and privacy requirements such as the Health Insurance Portability and Accountability Act (HIPAA) requirements, introduced by the United States Department of Health and Human Services, functionality has been added to the Vue PACS system.

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Access control

Intended to restrict access to the system to authorized users only:

- A user log-on/log-off procedure is required to gain access to the system.
- Access to the system is granted according to a customizable list of authorized users assigned to application-based roles. Philips strongly advises to adhere to the least privilege principle.
- Access to the system is enabled through Username/password authentication, or other mechanisms like two factor authentication, smart cards, URL activation and OpenID Connect.
- Password complexity rules can be defined through the User Management tool.
- Password expiration rules can be defined through the User Management tool.
- Account Lockout Policy can be defined through the User Management tool.

  The application account Lockout Policy is:

  – Account lockout duration = 1 minute

  – Bad login attempts = 10
- This can be customized through the User Management tool
- • Philips strongly advises to remove a user from the system as soon as possible in case of termination of the contract.

Automatic logoff (Lock Screen)

The Vue PACS system provides a configurable idle time-out feature. The time-out configuration can be done using the Vue PACS tool. Only a system administrator can disable the automatic logoff feature.

After an inactivity time-out, the Lock screen appears (with the last logged in user displayed).

Additionally, automatic logoff can be accomplished through Microsoft Active Directory group policies.

Audit trail

It is required to log user activities that are information-security critical:

- This applies to logging-on, reading, or modifying clinical information.
- The system supports detailed audit trail logs, which are IHE ATNA compliant.
- The audit trail logs are either stored locally in an encrypted form on the system or can be transferred to a central Syslog server.
- Local audit logs can be viewed using the Audit Log Viewer. The Audit Log Viewer can be accessed by hospital administrators from the IT Tools folder present on the desktop of the Vue PACS system.

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1.16.10 Additional security and privacy features

HIPAA defines a number of physical and technical safeguards, which are either required or addressable.

Some features that could implement these functions are different or not implemented for reasons mentioned later. This section also lists other information related to security features that are not implemented and of which the owner of the systems must be aware.

1.16.11 Backup procedure

The system is permanently storing sensitive patient personal information, which is stored on the Oracle database and on the local storage. Personal information is encrypted.

1.16.12 Disaster recovery and business continuance

Vue PACS is a platform used in the diagnosis and treatment planning of patient care. In the event of a major outage or disaster, make sure that Vue PACS is a part of the healthcare entities Business Continuance (BC) and Disaster Recovery (DR) plan. Consider addressing the following key points for the BC and DR plan:

- Make sure that the healthcare entity has a reliable and consistent Business Continuance (BC) and Disaster Recovery (DR) plan. The Vue PACS system must be a part of DR/BC plan to ensure that it is readily recoverable and usable in the event of an unplanned outage or major disaster.
- Make sure that copies or replication is occurring for all required Vue PACS data. It is recommended to maintain the data in a separate datacenter and geographical area according to the healthcare entities DR/BC plan.
- Update the BC/DR plan as necessary to ensure that it is accurate and usable. The healthcare entity BC/DR plan must reflect any changes made to the production Vue PACS system.
- Ensure that the BC/DR plan is periodically tested and according to the healthcare entities policies and procedures. Confirm that the Vue PACS system will be recoverable within the expected Recovery Time Objective (RTO) of the healthcare entity.

1.16.13 Emergency access procedure

The Vue PACS system does not have a built-in emergency user account. However, it supports the creation of unique user accounts and assignment of permissions to users. Hospital administrators can use this function to create an emergency user account and complex password with the necessary permissions. To avoid unauthorized access to patient data, make sure that knowledge of this generic emergency user account and password is restricted and kept in a secure location with minimal access.

The Vue PACS system does not allow or enforce generic account users to enter their real names, which restricts the system's ability to track and audit the generic user account.

It is not possible to clearly mark data output (for example, screen, print-out, and exported data to DVD) as having been created during an emergency access operation.

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1.16.14 Encryption

Vue PACS supports encryption through several different methods to ensure that information is protected and secure.

Encryption at rest is supported by using SEDs (Self Encrypting Drives), which must be supplied by the healthcare facility or purchased through Philips. The use of software-based encryption at rest such as Microsoft BitLocker is not supported at this time.

Vue PACS uses three primary encryption protocols for data in transit between the endpoints and the servers. The site will need to supply SSL/TLS certificates for those services that require encrypted communications.

The following primary services or protocols offer encryption as part of their communication processes.

- CONN (proprietary protocol) for internal services
- DICOM for to communicate with devices that supports the DICOM standard
  - Vue PACS system supports the IHE ATNA profile, which enables secure transmission of ePHI between configured DICOM devices.
- HTTPS for web services

Vue PACS supports TLS 1.2 protocol for encrypted communication processes.

1.16.15 Physical access to system

The Vue PACS system must be placed in an access restricted area of the hospital.

However, the following characteristics are to be taken into account for system operation and access control when the hardware is purchased from Philips:

- The computer case is "service friendly" (for example, accessing and removing the hard drive does not require tools). However, the computer case can be locked (for example, by cable lock).
- The boot order for the system is DVD, USB, hard disk. By inserting bootable CD/DVD or connecting bootable USB memory device, the system can start up from those and thus access can be gained to the system including information stored in it.
- There is no detection of unauthorized physical access into the system (for example, through tamper-proof seals).
- Unauthorized changes to software, files or data on the Vue PACS system are not permitted and by doing so might adversely affect the operation and security of the system.
- The system BIOS is not password protected and can be accessed during startup of the system if unauthorized access to the system is possible.

1.16.16 Malware protection

The Vue PACS system incorporates protection mechanisms against the intrusion of malware (viruses and so on). Without proper cybersecurity maintenance, the effectiveness of these provisions may degrade over time, since malware is continuously altered to target newly discovered vulnerabilities.

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Despite preventive measures already implemented, a remote possibility remains that the equipment might become infected with malware. When malware is detected, or when you notice that unfamiliar behavior or degraded performance occurs repeatedly, immediately call the Philips Service Engineer for an inspection.

When the inspection confirms the infection, be sure to take measures to contain and remove the source of infection. As necessary, Philips Service can reinstall the product`s software to bring the product back into specification.

1.16.17 Whitelisting

Philips formally qualifies the Vue PACS system with CylancePROTECT®/Trend Micro, aimed at providing comprehensive malware protection using whitelisting technology.

Whitelisting identifies all trusted software that is allowed to execute on the equipment. The protection software thus prohibits the execution of untrusted software, effectively blocking malware before damage is done. Instead of relying on the frequent updates that the reactive anti-virus software needs to remain up-to-date, it offers proactive protection against a wide spectrum of malware and malware alterations by only allowing known executables. Whitelisting is not a replacement for industry standard anti-virus solutions, but it is a complementary foundation for enhanced protection against malware intrusion and unwanted code execution.

Philips certified anti-virus software

Philips formally qualifies the Vue PACS system with CylancePROTECT®/Trend Micro, aimed at providing comprehensive malware protection using whitelisting technology. Whitelisting identifies all trusted software that is allowed to execute on the equipment. The protection software thus prohibits the execution of untrusted software, effectively blocking malware before damage is done. Instead of relying on the frequent updates that the reactive anti-virus software needs to remain up-to-date, it offers proactive protection against a wide spectrum of malware and malware alterations by only allowing known executables.

The installation of anti-virus software will not automatically void the equipment warranty or service contract. Philips can provide limited support and resolve most incidents reported by the customer in a timely manner and typically within the Service Level Agreement. However, due to the dynamic nature of anti-virus software and ongoing updates, Philips cannot be held accountable for any downtime or deletion of data caused or allowed by the anti-virus applications due to subsequent updates. Any efforts to resolve issues or problems arising from the installation or actions resulting from the anti-virus software are not covered by the Service Agreement or warranty and may result in time and materials charges. In addition, Philips may request that the anti-virus software be removed or disabled to proceed with the resolution of reported issues or for system upgrade. Philips may also request that the customer provide evidence of the specific malfunction on the system without anti-virus software installed and/or enabled.

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NOTICE

The anti-virus software that is validated and approved might change over time. If you have a question related to alternate anti-virus software, contact your respective Philips Service Engineer.



CAUTION

Installing alternate anti-virus software on the Vue PACS server is an action taken by the hospital IT administrator.
The sole responsibility of such an action and its impact rests with the healthcare entity IT.

1.16.18 Endpoint Protection

CylancePROTECT comes standard on Philips for Vue PACS 12.0 and is an endpoint security product that detects and prevents various cybersecurity threats. Below is a description of cybersecurity events that CylancePROTECT can detect and how users are informed of such events:

Malware Detection:

- Event Description: CylancePROTECT can detect and block malware, including known and unknown threats, by analyzing file behavior and characteristics.
- User Notification: Users are typically informed through a real-time pop-up notification on their endpoint devices, indicating the detection and containment of the malware. The notification may provide guidance on next steps, such as isolating the affected device or initiating a malware scan.

Suspicious File Execution:

- Event Description: CylancePROTECT can flag suspicious or unauthorized file executions, such as the launching of unknown or potentially harmful applications.
- User Notification: Users will receive immediate notifications on their devices, alerting them to the suspicious activity. They may be advised to avoid interacting with the file or application and contact their IT support team for further assistance.

Script and Macro Detection:

- Event Description: The product can identify malicious scripts and macros often used in attacks like phishing or document-based threats.
- User Notification: Users may receive alerts when opening documents or running scripts containing suspicious elements. They will be instructed to exercise caution and contact IT support for guidance.

Exploitation Attempts:

- Event Description: CylancePROTECT can detect and prevent exploitation attempts targeting known vulnerabilities in software or operating systems.
- User Notification: Users may receive alerts if an exploitation attempt is detected while interacting with a vulnerable application or system. They will be advised to apply necessary updates or patches to mitigate the risk.

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Device Quarantine:

- Event Description: If a device is compromised or poses a significant threat, CylancePROTECT can automatically quarantine or isolate the affected device from the network.
- User Notification: Users will be notified of the quarantine action, typically through a notification on their device, informing them of the security measure taken. IT administrators will also be alerted to assess and remediate the issue.

Threat Intelligence Updates:

- Event Description: CylancePROTECT regularly receives threat intelligence updates to stay updated on the latest cybersecurity threats and attack patterns.
- User Notification: Users are typically not directly informed of threat intelligence updates. Instead, the product silently updates its threat database in the background to enhance its threat detection capabilities.

Policy Violations:

- Event Description: CylancePROTECT can enforce security policies and detect policy violations, such as unauthorized software installations or access to restricted resources.
- User Notification: Users will receive notifications if they attempt to violate security policies. The notification will provide guidance on complying with company policies and security best practices.

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1.16.19 Microsoft security updates

Microsoft Security Updates are routinely included with each new software release. Alternatively, Philips permits the installation of Microsoft® security updates on the Vue PACS system.

For a list of approved or validated Microsoft® security updates for Vue PACS Server/ Vue PACS Workstation, see the vulnerability evaluation report, known as the Security Status document.

The documents are accessible using the following link: http://philips.com/security.

Philips strongly advises not to apply any OS or other patches until Philips has validated it for use with the 12.0 product.

After the web page loads, click the option/image for “Cyber-security information of Philips healthcare products”. A new web page will open. Follow the guidelines provided to first request access to the product security documentation and subsequently to access the document distribution platform, Philips InCenter. In Philips InCenter, look for the product group “Radiology Informatics (RI)” to find the Security Status documents for the Vue PACS product with reference to the Security Status document. Philips permits customers to install only security updates that have the “Recommended Customer Action” as “Install recommended solution”. For each of these approved security updates, the Security Status document mentions the Knowledge Base (KB) article related to each security update. Customers can download the respective Microsoft security update referenced by the unique Microsoft® KB number from the Microsoft® TechNet website or access the same from an internal server/repository. Ensure that you download and access only the updates that are

applicable to the Microsoft® Operating System used on the Vue PACS system, that is, only updates intended for one of the following (depending on the Vue PACS product variant that you have purchased):

- Windows Server 2019 (x64) OS.

1.16.20 De-identification

The De-identify option enables you to save images while removing any identifying marks of the patient, such as patient name and patient ID.

Details of de-identified tags can be found in the Vue PACS Instructions for Use, under the Saving Images/Copying to Studies with Concealed Patient Information section.

1.16.21 Data sanitization

Vue PACS stores patient sensitive data within the system Oracle database and DICOM images. Media containing backups of the database and images will contain patient or sensitive data as well.

Patient or sensitive data can be stored in the following locations of the Vue PACS system:

- Oracle database folder
- System Oracle database backup storage folder
- Customer defined image storage locations (local or network)

If patient data, images, or sensitive information resident on the Vue PACS system are to be discarded or permanently disposed of, they must be destroyed (permanently deleted) so that the data no longer can be accessed, retrieved, or viewed at a later point in time. Data that is deleted from storage using conventional operating system or application tools will remain but not directly usable on the storage media. Data sanitization must be performed for permanent deletion. While the Vue PACS system has data deletion capabilities, it does not provide data sanitization functionality. Use appropriate data sanitization techniques and tools in alignment with healthcare entity policy and procedure for media destruction and sanitization. NIST publication 800-88 Guidelines for Media Sanitization provides reference and best practices for data sanitization.

1.16.22 Unsecured personal data transmission risks

Vue PACS transmits and receives patient images and data over a network. Data that is transmitted in an unencrypted format over a network introduce unknown risks impacting confidentiality and integrity. To reduce the risk of unauthorized data exposure, Philips strongly recommends the use of TLS (TLS 1.2) for all Web and DICOM services to ensure the secure transmission of data to the client device or modality. Please note that the healthcare entity might need to purchase or provide valid TLS certificates.

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1.16.23 Safe disposal of software components

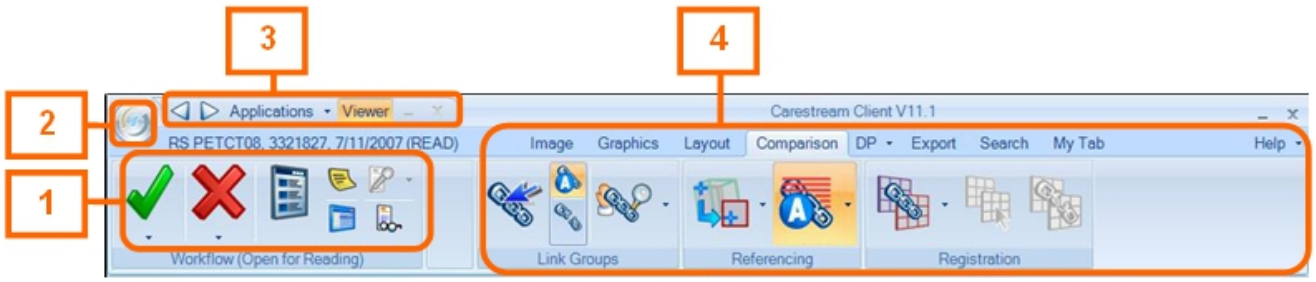
Before disposing of the Vue PACS software components, Vue PACS server and workstation drivers must be formatted in order to ensure that patient data is securely removed and cannot be recovered.

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2 User Interface

2.1 Toolbars and Tabs



1	**Workflow toolbar (static)**  Includes workflow-related icons for general reading tasks. Click Approve / Dismiss  to dismiss or confirm the study.
2	**Vue PACS icon** Contains a menu of configuration and system options including Lossless Mode, Sessions, External Applications, Application Settings, and Exit. **NOTICE! External Applications refers to any third party application integrated with the Vue PACS Client through an action button, such as ORTHOVIEW.**
3	**Applications navigation top caption** Allows you to: • Navigate between open applications such as Viewer, MPR, and 3D. • Navigate to other client applications, such as Key and Film Preview. • Launch new applications (New Application). Navigation methods to open applications: ► Press the application name displayed in the caption. ► Click Previous or Next . ► Click CTRL + TAB. ► Click View As to open the active series in the selected application. ► Click New Application to launch a new blank application.

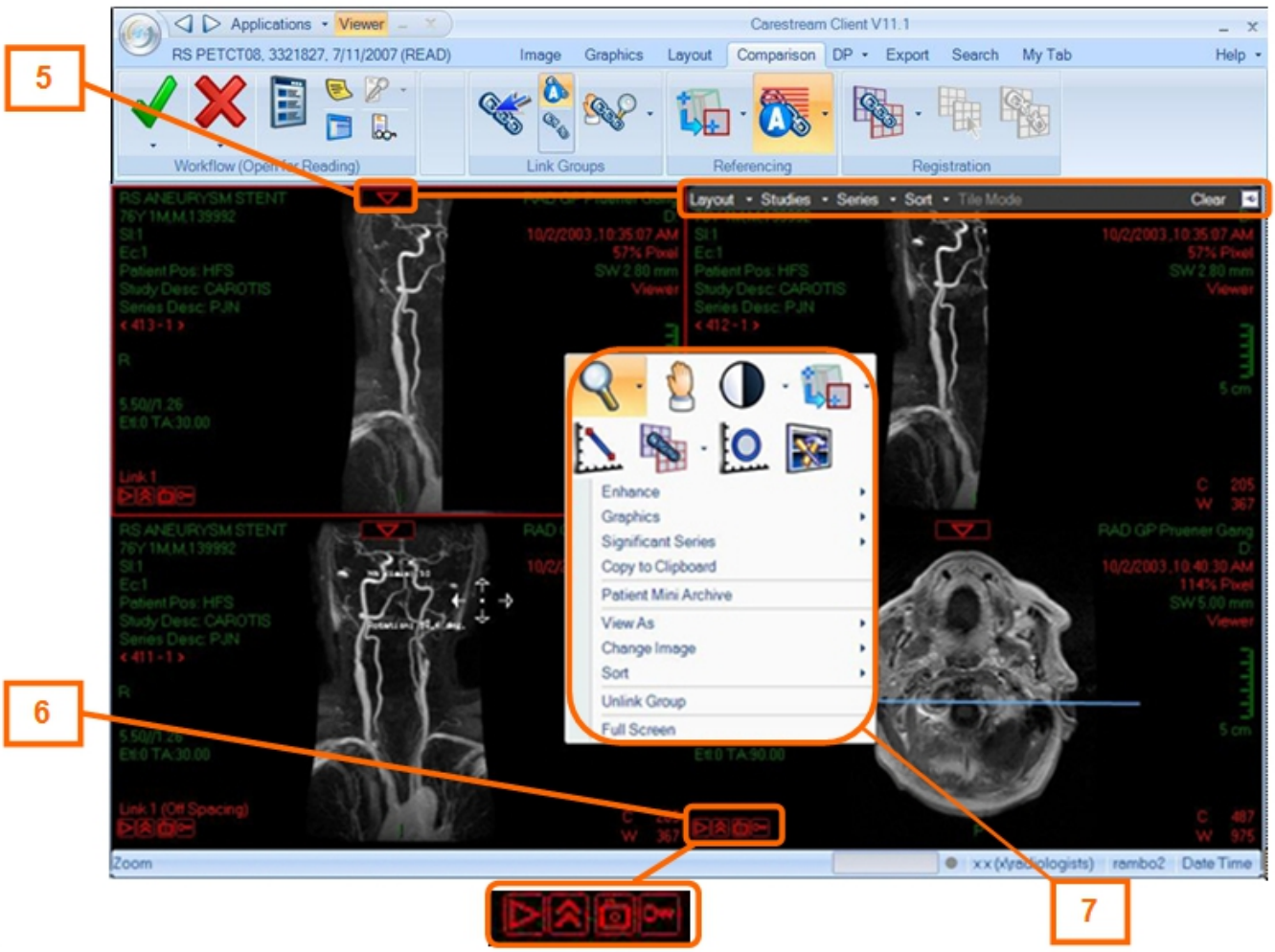
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4

Tabs toolbar (dynamic)



Allows you to access tabs that contain application functions. The tabs include Image, Graphics, Layout, Comparison, DP, Export, Search, and My Tab.



5

Group-level toolbar (dynamic)

The toolbar is available next to each Group window in the Viewer.

Click Group Drop-Down icon  to view the list of options, such as Layout, Studies, Series, Sort, and Tile Mode.

Click  to toggle between a fixed or waiving state.

NOTICE! Waiving state—the toolbar remains in a minimized state where Group Drop-Down icon only is visible. When you place your mouse cursor above the Group Drop-Down icon full toolbar is maximized automatically until you move the cursor away.

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6	**Image-level toolbar (dynamic)** Located on the bottom-left corner of the image. Allows you to perform image-related operations such as playing cine, filming, or marking key images. • **Cine**—click to start cine. Click for more cine functions. • **Film**—click to film the displayed image. • **Key Images**—click to mark or unmark a key image. The icon is highlighted when the displayed image is marked as a key image.
7	**Right-click menu toolbar** You can customize the **Right-click Menu** toolbar. You can add icons from other toolbars to put the functions that you use most frequently in one convenient location.

2.2 Defining a custom toolbar

2.2.1 Right-click Menu Toolbar

Right-click menu toolbarYou can define the contents of the **Right-click Menu** toolbar for frequently used functions.

Adding icons

1. Right-click any icon from any application toolbar.
2. Select Add to Right-click Menu.

Removing icons

1. Right-click the image.
2. From the Right-click Menu toolbar, right-click an icon.
3. Select Remove from Right-click Menu.

2.2.2 Using My Tab

You can add or remove icons from the application tabs to your personal toolbar (My Tab).

My Tab includes the following default icons: Zoom, Pan, Pointer, Line Measurement, Oval ROI, Swivel, Relate, Custom Matrix Layout, and Registration.

Adding icons

1. Right-click any icon from any application tab.
2. Select Add to My Tab.

Organizing icons

You can:

- Drag and drop the icon into the desired location in My Tab.

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- Right-click the icon and select Move Right or Move Left.

Removing icons

1. Click My Tab.
2. Right-click the icon and select Remove from My Tab.

Restoring system defaults

1. Right-click any icon in My Tab.
2. Select Reset My Tab.

Defining a default tab

1. Right-click the tab header.
2. Select Set as default tab.

2.3 Configuring shortcut keys

The system has a set of available default shortcut keys. You can configure shortcuts for any icon in the application's toolbar. Each shortcut can exist once in the system.

2.3.1 Adding or Editing a Shortcut

1. Right-click any icon from any application toolbar.
2. Select Assign Shortcut.
3. In the dialog, click the key or combination (such as CTRL + key, ALT + key, SHIFT + key). The dialog adds the shortcut or modifies the existing shortcut.

NOTICE

Click Shortcut **List** to view a printable list of the defined shortcuts.

2.3.2 Restoring the Default Shortcut

Restoring the default shortcut

1. Right-click any icon in any application toolbar.
2. Select **Reset Shortcut.**

2.4 Changing layouts (Layout Tab)

Click the **Layout Tab**.

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Viewer Application	Non-Viewer (3D) Applications
The layout is controlled on each monitor.	The layout is defined per application (either one or two monitors), rather than per monitor.

Click on any pre-defined layout icon to apply the layout depicted in the icon.

Click Custom Matrix Layout to select any layout from 1x1 to 8x8.

Drag the mouse cursor to the bottom-right corner of the matrix to choose the desired layout.

Click the mouse and drag the cursor to the left or to the bottom to expand the layout to 12x12.

NOTICE

The change applies to the monitor on which you originally clicked the layout icon. Mark the **Apply to all monitors** check box to apply the layout to all monitors.

2.4.1 Defining the Layout for Several Monitors

Click Custom Viewer Layout.

Select a default monitor configuration:

Standard—each monitor shows a different sequence. The changes apply to a single monitor only.

Tile Mode—multiple monitors show the same sequence (group or series). The layout changes that you made on a single monitor are applied to all monitors. Mark the checkbox of sequential monitors which should participate in Tile Mode.

2.4.2 Reverting from Tile Mode to Standard Mode

Click Tile Mode .

Click Layout Tab > Custom Viewer Layout > Standard.

Use the group-level toolbar and click Tile Mode.

Each monitor reverts to the original layout and original sequence.

2.4.3 Using Miscellaneous Layout Actions

Clinical applications—such as **3D**, **Vessel**, **PET/CT**—can display on up to two monitors. Decrease the application size to fit on one monitor. Increase the application size to fit on two monitors.	**Application Layout** . **NOTICE! Unavailable in the Viewer application. The Viewer is always displayed across the entire desktop.**
Changing the group layout.	Group-level toolbar.

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Applying display protocols.	Tabs toolbar > DP.
Saving presentations.	Layout tab > Save Presentations

2.5 Using a medical imaging search engine

1. Click the Search Tab.
2. Enter the medical term, clinical findings, or query in the Text to Search field.
3. Select the search engine from the Search Engines menu.

NOTICE

If the Text to Search field is blank, the engine automatically searches on the text from the Study **Description** field. The available search engines include YottaLook™, STATdx®, and Google™. (STATdx® is a licensed web site).

2.5.1 Launching the Imaging Search Engine From Report Browser

Select any word or words in the report, then right-click and select the preferred search engine.

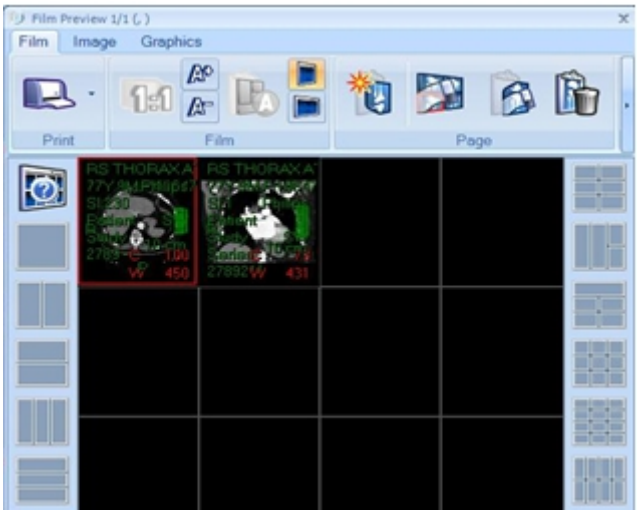
2.6 Hiding the scroll bar

Click the pin icon . In the hidden mode, the scroll emerges or “waves” when you hover the mouse cursor over the area of the scroll bar.

2.7 Using Film Preview and E-Report Preview

In the Export tab, click Film Preview  or E-Report Preview .

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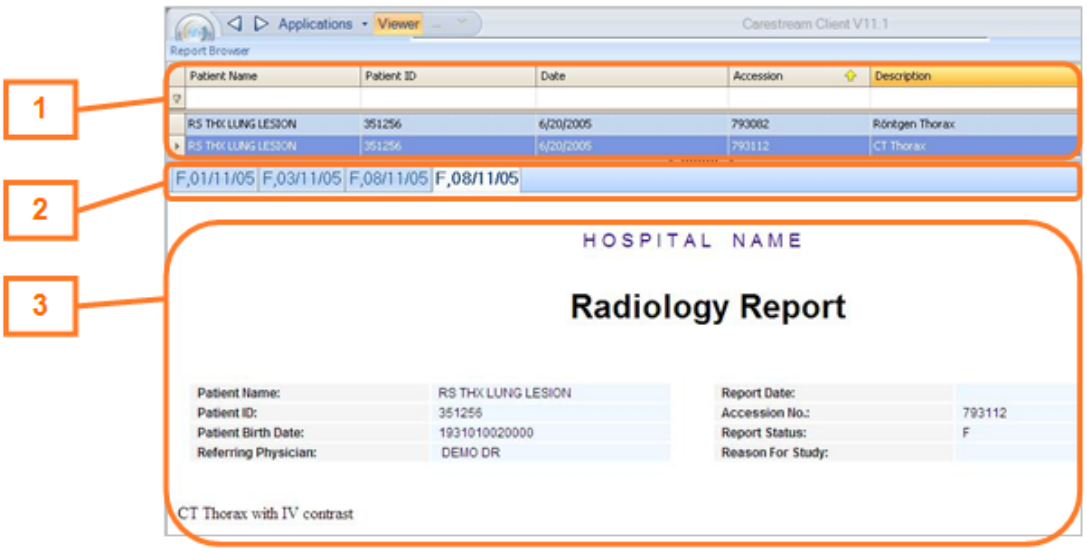


In the Film Preview or E-Report Preview window you can:

- Manipulate images.
- Click any of the layout icons on either side of the window to apply a layout.

The Film, Image, and Graphic tabs perform the same image functions as found in the Viewer.

2.8 Viewing reports, sticky notes, and teaching files



Reports and sticky notes are available in the Workflow toolbar. Teaching files are available under the Export tab.

1	**Report list** Lists the relevant patient reports. You can apply the same filters to the reports as used in the Archive Explorer for studies.

2	**Report tabs** The different tabs represent a report for the selected study in the report list. You can see the status and the date of the report inside the tab.
3	**Report** The content of the selected report.

2.9 Scrolling Options

The following scrolling options can be used to scroll through images in the Diagnostic Workstation:

- Dragging the scroll bar.
- Clicking the scroll bar arrows.
- Rotating the mouse wheel.
- Dragging the reference line.
- Right-clicking and dragging the mouse.
- Left-clicking and dragging the mouse when in Pointer/Neutral Mode

NOTICE

To perform continuous or cyclic scrolling, select the Loop scroll option in the Viewer/MPR Settings page in the Application Settings (see Choosing Viewer/MPR Settings on page 456).

2.9.1 Dragging the Scroll Bar

You can move through the images by dragging the scroll bar up and down. The image scrolling speed reflects the speed of the dragging action; a faster dragging action means that a greater number of slices is scrolled. Because of this, sometimes not all images are shown when dragging the scroll bar at speed.

2.9.2 Clicking the Scroll Bar Arrows

You can move through the images by clicking the up and down scroll bar arrows. In this case, each click moves to the next slice. Every slice is shown and none are skipped, even if the scroll bar arrows are clicked in quick succession.

2.9.3 Rotating the Mouse Wheel

You can move through the images by rotating the mouse wheel forwards and backwards. The image scrolling speed reflects the speed of the mouse wheel; a faster wheel speed means that a greater number of slices is scrolled. Because of this, sometimes not all images are shown when using the mouse wheel at speed.

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2.9.4 Dragging the Reference Line

If reference lines are shown, you can move through the images by dragging the reference line up and down. In this case, the relevant slice number is shown on the image when scrolling through original slices.

The image scrolling speed reflects the speed of the dragging action; a faster dragging action means that a greater number of slices is scrolled. Because of this, sometimes not all images are shown when dragging the reference line at speed.

2.9.5 Right-Clicking and Dragging the Mouse

You can move through the images by right-clicking and dragging the mouse up and down. The scrolling action performed depends on the scroll method defined in the Application Settings. The following options are available:

- Regular scrolling – With this option, every slice is shown and none are skipped, even if the mouse is dragged at speed. Note that the cursor is visible during the dragging action and is restricted to the boundaries of the image. If you drag the mouse to the edge of the image, the scrolling action continues at maximum speed until the end of the image stack.
- Continuous scrolling – This is similar to regular scrolling except that the cursor is invisible during the dragging action. The scrolling speed always reflects the speed of the dragging action. Every slice is shown and no image is skipped, even if the mouse is dragged at speed.
- User-defined scrolling – This is similar to continuous scrolling except that the user controls the sensitivity of the scrolling speed; a faster dragging action causes more images to be scrolled. This allows both delicate scrolling that shows every image, and fast navigation through the image stack. Because of this, not all images may be shown when using user-defined scrolling.
- Scroll bar-like scrolling – With this option, slices are shown according to the vertical location of the cursor relative to the image boundaries. When the cursor is at the top boundary, the first image is shown, when at the bottom, the last image is shown. Not every slice is shown.

2.9.6 Left-Clicking and Dragging the Mouse

When the **Enable Neutral Mode Scroll** option is selected in the Application Settings, you can use the left mouse click to scroll through a study. In this case, you must first select the **Pointer** option  to put the cursor in neutral mode. This disables the regular left-click functions, such as zooming and panning, to allow scrolling. You can then move through the images by left-clicking and dragging the mouse up and down. The scrolling action performed depends on the scroll method selected for the right-click scroll control.

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2.10 Chat

2.10.1 Chat

The chat feature enables the sending and receiving text messages between two or more users, including the ability to share screen displays.

NOTICE

This feature is enabled by your system administrator.

You can chat immediately with users who are online or send messages to users who are offline.

During a chat session, you can:

- Send Links to Exams (see Send Links to Exams on page 63).
- Share Screens (see Share Screens on page 64).
- Send Alerts (see Send Alerts on page 65).

To start a chat session

1. Click the **Chat** icon in the status bar at the bottom of the screen.
   ⇨ The **Conversations** window opens, displaying a list of chat sessions.
2. Do one of the following:
   - To begin a chat with a single recipient or group, click a specific name in the displayed list, or enter two or more characters from a person's name or a group's name to narrow down the list, and then select the desired recipient.
   - To begin a chat with more than one recipient, click **Start group chat**. Select the desired recipients from the displayed list. You can enter several characters from a person's name or a group's name to narrow down the list, and then select the desired recipients. You can perform multiple searches to add users to the same conversation.

NOTICE

The names of recipients who are online at the current time are highlighted in green.

3. Click to add additional users to a conversation. Select the desired recipients from the displayed list. You can enter several characters from a person's name or a group's name to narrow down the list, and then select the desired recipients. You can perform multiple searches to add users to the same conversation.
4. Type your message, and then click to send the message to the selected users.

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⇨ The chat thread now appears in the list of conversations. To continue sending messages in a specific chat, click the chat in the list to open it.

NOTICE

A notification is displayed when an invited user accepts a chat request.

To search for a string in a particular conversation, enter two or more characters and then click or press **Enter** to refine the list.

5. To close the chat window, click the Chat icon at the top right of the screen again.

By default, the last message in a conversation is displayed when you return to the conversation.

NOTICE

The default retention time for messages is 48 hours. See your system administrator to change this value.

To set online availability

Move the **Online/Offline** slider to **Online** or **Offline**, as desired.

If you are offline:

- Other users who search for you will see you as unavailable to participate in a conversation.
- Even if you read messages, they will still be marked as unread while you are offline.

To specify sound options

Click .

- To specify the volume of the sound for incoming chat messages, select **Loud**, **Medium**, **Quiet**, or **Mute** in the **Chat Sound** list.
- To specify whether or not a sound is played for incoming alerts, move the **Alert Sound** slider to **On** or **Mute**, as desired.

2.10.2 Send Links to Exams

While you are viewing an exam, you can send a link to the exam to another user for review.

1. Select an exam in the grid or load an exam.
2. Click the **Chat** icon at the top right of the screen.
3. Click **Start new chat**.
4. Select the user to whom you want to send the link.

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5. Click **Start conversation**.
6. Click .

The user receives a message with a link to the selected exam.

2.10.3 Share Screens

During a chat session, you can share your application with another user.

1. Load an exam.
2. Click the **Chat** icon  in the status bar at the bottom of the screen.
3. Click **Start new chat**.
4. Select the user with whom you want to share your screen.
5. Click **Start conversation**.
6. Click . The exam appears inside a border that indicates that the screen is being shared. At this time, the following occurs:
   - The priors list is hidden.
   - No additional users can join the screen sharing session.
7. The intended recipient receives a message about the shared session. Two possible situations can occur:
   - If the sender is online, the recipient can either click **LIVE SESSION** to begin the shared session immediately, or **REVIEW** to view the exam offline.
   - If the sender is offline, the **LIVE SESSION** button will be grayed out and the recipient can only click **REVIEW** to view the exam offline.

   During a shared session, screens are synchronized between the presenter and the spectator. The presenter of a shared session remains in control of the session until permission is granted to the other user by clicking **Pass Presenter Role**.

   The presenter can display the current mouse position by holding down the **L** key.
8. Click **End Session** to end the shared session.

NOTICE

During a shared session:

- Non-DICOM data cannot be shared.

ECG exams cannot be shared.

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2.10.4 Send Alerts

You can send emergency alert notifications to all users, or to specific user groups.

1. Click the **Chat** icon in the status bar at the bottom of the screen.
2. In the Conversations window, click .
3. Enter a title and type your message.
4. Select the required expiration time for the alert:

   You can select the default expiration time of 24 hours, or select **Customizable** from the drop-down list, and specify either a date or time.
5. Select one or more distribution groups for the alert.
6. Click **Distribute**.

   ⇨ A message displaying the alert automatically appears on all users' screens if they are online. For offline users the message is displayed the next time a user logs in, if the retention time for the alert has not yet passed.

⇨ To close and delete an alert message that you have received, click **Dismiss** in the message.

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3 Toolbar and Shortcut Keys

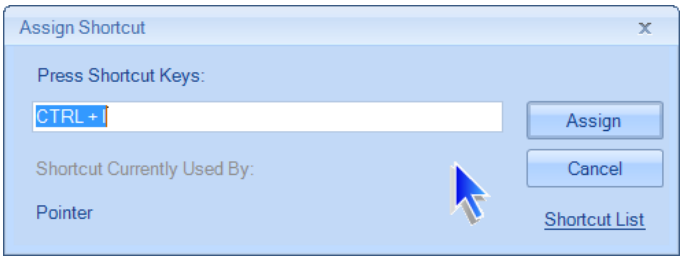
3.1 Shortcut Keys

The Diagnostic Workstation provides shortcut keys to many of the actions.

To see a list of the shortcut keys available by default, click Help at the top-right corner, and select Shortcut List.

You can assign your own shortcuts to all actions available via the toolbar icons.

1. To assign a shortcut key, right click the toolbar icon, and select Assign Shortcut or Customize --> Assign Shortcut.
2. Press the keys that are to serve as shortcuts, and click Assign.



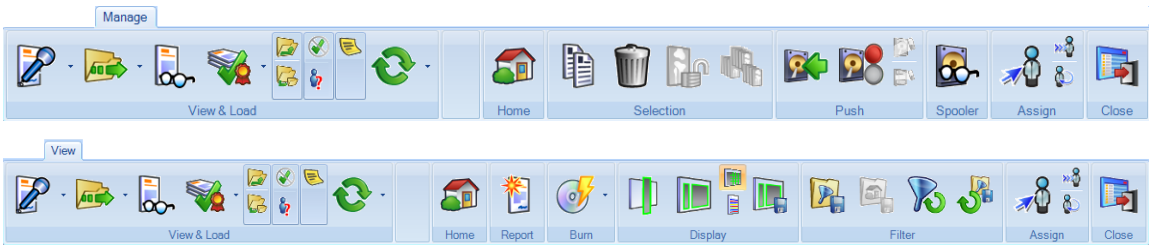
3.2 Archive Explorer Toolbar

3.2.1 Archive Explorer Toolbar

The PowerViewer toolbar comprises tabs, menus and ribbons, each offering tools to facilitate study archiving and management. The toolbar includes two tabs:

- View - contains tools designed to facilitate the radiologist with the reading flow.
- Manage - contains tools designed to facilitate the administrator with study organization and archiving.

For a description of the icons, click the various toolbar areas in the images below .



3.2.2 View & Load Toolbar - Archive Explorer

Icon	Description

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	Launch the report editor and dictate or write a report. Enabled for systems that include the Reporting module.
	Load the selected study or worklist.
	Open the report browser to view patient reports.
	Batch-sign final reports. The reports' status changes to Approved.
	Load the key images in the selected study.
	Load the images of the significant series in the selected study.
	Load Worklist.
	Load a worklist with all groups required for the defined presentation.
	Load to Vue Motion.
	Load the patient's prior studies in the global worklist, regardless of the site at which they are located.
	Navigate up one level.
	Explore the selected item by navigating down one level.
	Open a study in view only mode. In this mode, the study is not locked and may be viewed by another user. The Reporting module is disabled and you cannot create a report.
	Open a study with all the patient's identifying details concealed. Note that patient details that are burned on images may still be visible.

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	Show the study's sticky notes.
	Refresh the Archive Explorer.

3.2.3 Report - Archive Explorer

Icon	Description
	Create a report without a study (for example, when the radiology images are on a film).

3.2.4 Burn - Archive Explorer

Icon	Description
	Burn the selected data to a CD. Click on the drop-down menu to burn significant series and to select a burner.

3.2.5 Home - Archive Explorer

Icon	Description
	Go to your home folder.

3.2.6 Display Toolbar - Archive Explorer

Icon	Description
	Open the field chooser to add column headers to the list of studies.
	Reset view.
	Display grid lines in the list of studies displayed in the Archive Explorer.
	Highlight studies with various colors based on criteria defined using study-level DICOM tags.

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	Save as default settings.

3.2.7 Filter Toolbar - Archive Explore

Icon	Description
	Save filtered lists of studies as folders for easier access in the future.
	Set as home folder.
	Reset filter.

3.2.8 Assign To Toolbar - Archive Explorer

Icon	Description
	Assign studies to users or groups.
	Assign all read studies automatically to a selected user or group (useful in resident-attending situations, for example).
	Assign the selected study to yourself.

3.2.9 Close - Archive Explorer

Icon	Description
	Close the Archive Explorer.

3.2.10 Selection Toolbar - Archive Explorer

Icon	Description

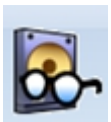
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	Copy the selected data.
	Delete the selected data.
	Unlock study.
	Mark significant series.

3.2.11 Push Toolbar - Archive Explorer

Icon	Description
	Push the selected study to a client for off-site viewing and analysis.
	Receive studies that were pushed to client.
	Remove specific studies from the cache.
	Clear cache from all studies.

3.2.12 Spooler - Archive Explorer

Icon	Description
	Open a spooler window with information about processes currently running.

3.3 Patient Mini-Archive Toolbar

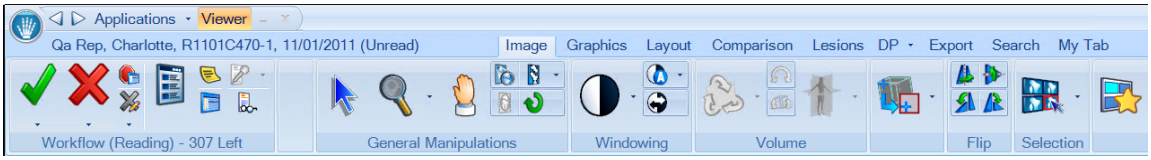
The Patient Mini-Archive toolbar lets you navigate through the displayed information in the Patient Mini-Archive.

3.4 PowerViewer Toolbar

3.4.1 About the PowerViewer Application Toolbar

About PowerViewer Toolbar

The PowerViewer toolbar comprises tabs, menus and ribbons, each offering tools to facilitate study reading.



3.4.2 Workflow Toolbar

This toolbar is static and includes workflow-related icons for general reading tasks.

Icon	Description
	Confirm and close the current study. The study status advances. This button is disabled when integrating with any third party reporting software which is fully integrated with Philips Diagnostic Workstation (such as PowerScribe) and the Confirm action is performed in the third party reporting software. Alternatively, press the shortcut keys: Ctrl+ 2
	Dismiss current study without changing its status. This button is disabled when integrating with any third party reporting software which is fully integrated with Philips Diagnostic Workstation (such as PowerScribe) and the Dismiss action is performed in the third party reporting software. Alternatively, press the shortcut keys: Ctrl+ 4
	Open the menu and select one of the following: • Mark as STAT • Save Key Images • Save Bookmarks The selected action is applied upon closing the current study.
	Stop the automatic loading of the next study. When selected, after closing the current study, the next study will not open automatically.
	Open the Patient Mini-Archive to load images, reports, orders and sticky notes.

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	Open the Sticky Notes dialog.
	Open the Archive Explorer without dismissing the study.
	Start dictating a report for the current study.
	Open the Report Browser to show reports and orders for the study.

3.4.3 Application Navigation Caption

Allows you to:

- Launch new applications such as **Viewer**, **MPR**, and **3D**.
- Navigate between open applications.
- Navigate to other client applications, such as **Film Review** and **E-Report Viewer**

To navigate between applications, use any of the following methods:

- Click Previous or Next .
- Press the application name displayed in the Navigation caption.
- Click Ctrl + Tab.
- Click View As to open the active series in the selected application.

3.4.4 Toolbar Tabs

About Toolbar Tabs

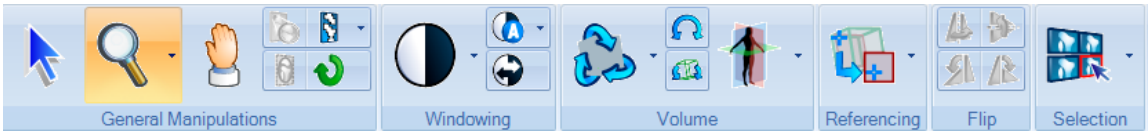
The various tabs display ribbons that contain tools for enhancing the reading process. The tabs include.

Image (see Image Tab on page 74).	Allows you to manipulate images, apply windowing, view volumetric displays, relate images, and flip them.
Graphics (see Graphics Tab on page 76).	Allows you to measure images, perform orthopedic measurements, label spine and add bookmarks
Layout (see Layout Tab on page 78).	Allows you to change screen layout, set series navigation patterns, apply Display Protocols (DPs) and save the display as presentation.
Comparison (see Comparison Tab on page 80).	Allows you to link groups for simultaneous scrolling, register volumetric studies such as CTs and RMs, create relate points and show reference lines.

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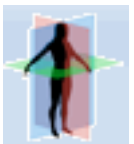
Lesiosn Tab on page 81	Allows you to segment lung, liver, lymph node and generic lesions, to detect and segment lesions on the basis of existing lesion in prior studies, to correct lesions, and to manage bookmarks.
DP Tab on page 83	Create or edit a Display Protocol or apply a pre-defined DP. You can also save a current display as a presentation.
Export Tab on page 83	Mark key images and significant series, film regions or images and manipulate filmed images, determine selection mode, save studies to a DICOM archive, designate studies as teaching files, burn studies on a CD and invoke an external application.
Search Tab on page 84	Search terms in the internet.

Image Tab



Icon	Description
General Manipulations	
	Change the cursor to neutral mode.
	Change to Zoom mode. Hold down the Shift key to pan, or the Alt key to zoom from cursor.
	Zoom in from the point clicked on the image, not from the center of the image. Use Application Settings to make this the default mode. Use the Zoom drop-down menu to zoom from cursor, zoom ROI, and set synchronized zooming of linked images.
	Pan the image. Hold down the Shift Key to zoom while panning.
	Magnify an outlined area. While left clicking, hold down the Shift key to window the magnified area, the Ctrl key to change the magnifying factor, or the Alt key to change the size of the magnified area
	Sharpen or smoothen the selected image. Select a filter from drop-down menu.
	Hide and show a shuttered area in DICOM images which were taken originally with the shutter functionality activated. The icon is disabled if the shutter functionality was not active when the image was originally taken. .

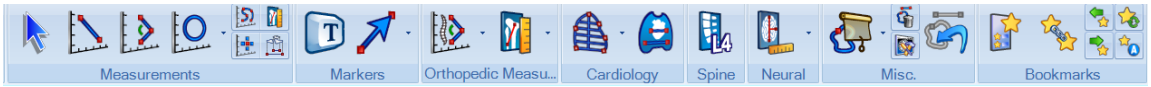
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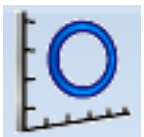
	Reset zoom, windowing and other parameters to initial display.
Windowing	
	Window the selected image to achieve optimal viewing. Use the drop-down menu to use preset windowing values, lookup table values, color maps, min and max values, and automatic windowing.
	Apply automatic windowing. Select an option from the drop-down menu to determine whether the area will be defined automatically by the application (in which case the central quarter of the image is selected), or whether you select the area manually.
	Apply automatic windowing to the selected region of interest.
Volume	
	Swivel volumetric images to view them from any desired angle. Enabled for CT, PET and MRI images. Hold down the Shift key while swiveling to roll the image (identical to using the Roll icon), or the Alt key to relate a Point of Interest. Use the drop-down menu located to the right of the Swivel icon to reset the image orientation.
	Roll the image around the center of the image.
	Roll the image automatically to the closest axial, coronal or sagittal plane.
	Change the rendition of the image. Use the drop-down menu to change the rendition to Viewer, MPR, MipPR, MinPR and set MPR Parameters.
Referencing	
	Relate a specific Point of Interest (POI) in one group to the matching location in other registered groups from the current or prior study.
Flip	
	Flip selected image horizontally.
	Flip selected image vertically.
	Rotate selected image 90° to the left.

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	Rotate selected image 90° located to the right.
Selection	
	Specify whether image manipulations are applied to a single image, a group or all images. Select the desired option from the drop-down menu.

Graphics Tab



Icon	Description
	Change cursor to Neutral mode.
	Draw a line to measure the distance between two points in an image.
	Draw an angle to measure the angle in degrees between body features.
	Draw a Region of Interest (ROI) to measure its area, average pixel value, standard deviation, and range of pixel values. Click on the pop-up menu to the right of the icon to draw an oval, a persistent oval, a sphere VOI, a square, or a freehand shape.
	Draw a curve to measure its length.
	Perform scale calibration. Define the mm/pixel settings for images.
	Draw a cursor to measure the pixel value in an image.
	Draw two lines to display the ratio between them.
Markers	

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	Place text annotations on images.
	Draw a shape. Click on the drop-down menu to draw an arrow, an oval, a line, a square, a curve, or a freehand shape.
Orthopedic Measurements	
	Draw a Cobb angle to measure a curvature. Click on the drop-down menu to draw a single Cobb angle or multiple consecutive angles.
	Measure angular alterations. Click the drop-down menu to measure angular alterations of the leg (Goniometry), assess hip-joint situations (Coxometry), measure the horizontal misalignment of the hip joint, or measure the percentage of femoral head with no acetabular coverage (Reimer's Migration Index) for one or both hips.
Cardiology	
	Measure the left ventricular ejection fraction in echocardiography cine clips. Use the drop-down list to select the view to be measured (A4Cd, A4Cs, A2Cd, or A2Cs).
	Measure the cardiothoracic ratio by drawing a midline and four points that represent the lung and heart edges.
Neural	
	Measure the distance between a manually drawn symmetry line and a shifted midline.
Spine	
	Label spine vertebrae on one series. The labeling propagates automatically to other series of the same study.
Miscellaneous	
	Click on the drop-down menu to hide all graphics added to the selected images, hide relate-point graphics created by the system, hide DICOM annotations, hide location references or hide technical references.
	Delete all graphics added to the selected images.

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	Change the text size and color of the active graphic.
Bookmarks	
	Show/hide the Bookmark List window.
	Navigate to the bookmark in the previous row in the Bookmark List window.
	Navigate to the bookmark in the next row in the Bookmark List window.
	Associate bookmarks of different studies to create a follow-up set and calculate changes over time.
	Automatically mark graphic as bookmark. When this icon is activated (highlighted yellow), graphics you draw, including line, ROI, square, rectangle, oval, freehand, curve measurement and arrow, are automatically marked as bookmarks.

Layout Tab



Icon	Description
Application Layout	
	Change layout to 1x1
	Change layout to 1x2
	Change layout to 1x2

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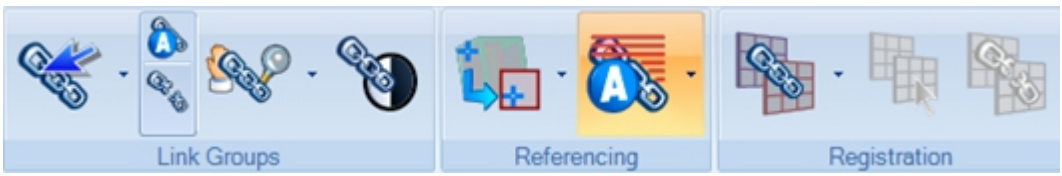
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	Change layout to 2x2
	Change layout to 2x3
	In MPR view, change to MPR dobule oblique layout. Allows you to view volumetric data in a 2x2 layout by retaining a perpendicular relationship between the planes. Press Shift to turn the perpendicular and horizontal cross section lines in the reference images to obliques.
	Define a customized layout.
	In Vessel Analysis and other applications, select a layout (display option) and save display option parameters.
	Tile the images of a series across the screen. Click again to revert to the original display.
	Toggle between the definition layout (the layout on which you define a new vessel) and the examination layout (the layout in which the resulting vessel is displayed).
	In Cardiac Analysis, select single-phase or multi-phase mode. The phase percentage is annotated on the image.
Series Navigation	
	Replace all displayed series of the selected study with the previous set of series.
	Replace the series of the selected study with the previous series by shifting the currently displayed series gradually to the right, taking away the bottom right series.
	Replace all displayed series of the selected study with the next set of series

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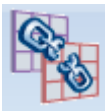
	Replace the series of the selected study with the next series by shifting the currently displayed series gradually to the left, taking away the bottom right series.
	Replace all displayed series of the selected study with the first set.
Display Protocols/Presentations	
Display Protocol Name	Click on the drop-down menu to save as display protocol, save a presentation, or change the display protocol. A display protocol allows you to save for later use a specific organization of the screen display. Saved information includes image parameters such as zoom and windowing, rendition types, links and reference lines.
	Save the current display for reloading at a later stage. A presentation captures layout, zoom and pan characteristics, windowing values, measurements, segmentation etc.
	Re-apply the display protocol with which the study was originally loaded. Alternatively, press the shortcut keys: Shift+Alt+D

Comparison Tab



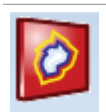
Icon	Description
Link Groups	
	Creates a link between two or more groups for simultaneous scrolling and for comparison. The drop-down offers you an option to link by slice, regardless of group orientation or planar view.
	Automatically links all groups with the same frame of reference (same study or registered studies) and the same orientation/plane.
	Breaks the links between all groups.
	Synchronizes zoom or zoom and pan between linked groups.
	Synchronizes window level changes in two or more groups. Changing the window level in one group causes the same simultaneous changes in all linked groups, provided the window level of the groups was initially the same.
Referencing	

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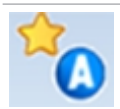
	Relates a point of interest in a study to the matching point in registered groups of the same or a prior study.
	Shows projected reference lines of the active group on other displayed groups.
Registration	
	Register volumetric studies and automatically link them, register studies according to a specific anatomical area, perform manual registration or treat two groups as registered.
	Refines registration at a specific region of interest
	Breaks registration.

Lesiosn Tab



Icon	Description
Segmentation	
	Volumetrically segment a lung lesion based on your click.
	Volumetrically segment a liver lesion based on your drawn line.
	Volumetrically segment a lymph node lesion based on your drawn line.
	Volumetrically segment a lesion located inside your drawn sphere (or spheroid). The segmentation threshold is based on the maximum value point inside the volume boundaries or on a fixed value, depending on threshold type settings.
	Volumetrically segment any lesion based on your drawn line.

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	Draw the long and short lesion diameters for a two-dimensional RECIST measurement.
	Define a lesion's contour in a semi-automatic manner in order to volumetrically measure the lesion.
Lesion Tracking	
	Locate and segment lesions in a destination study based on the location of existing lesions in a source study.
	Stop lesions in the destination group from being segmented based on the existence of source group lesions.
Corrections	
	Correct a drawn contour using the livewire mode.
	Treat two different lesions as a single one.
	Crop a lesion based on a drawn line representing a plane perpendicular to the displayed plane.
Bookmarks	
	Define an association between two bookmarks marking two occurrences of a lesion or general finding in two different studies.
	Show/hide bookmark list.
	Navigate to the previous/next bookmark on the bookmark list.
	Automatically mark graphic as bookmark. When this icon is activated (highlighted yellow), graphics you draw, including line, ROI, square, rectangle, oval, freehand, curve measurement and arrow, are automatically marked as bookmarks.
RT	

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	Show/hide Radiation Therapy (RT) dosage information on the active image.

DP Tab

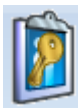
The DP Tab allows you to create a Display Protocol, Open the DP Editor, and reapply the original Display Protocol that the study was originally loaded with. You can also apply a pre-defined DP from the list of most relevant DPs and Same Modality DPs section of the DP drop down menu.

The DP drop down menu also allows you to save the current display of images to be loaded in the same manner at a later stage. The exact set of images displayed, including layout, pan and zoom properties, windowing values, segmentations, measurements etc.

See Creating a New Display Protocol on page 598.

Export Tab

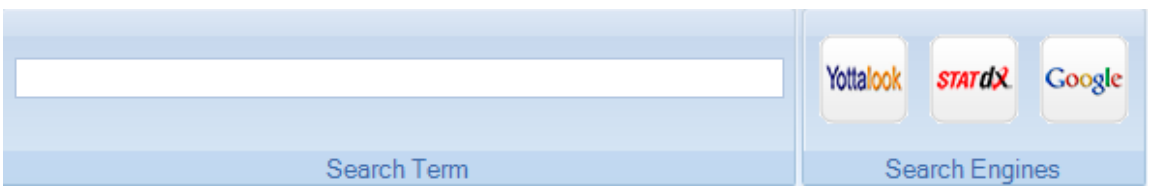


Icon	Description
Key Images	
	View and manipulate key images from the E-Report Preview window.
	Mark the active image as a key image.
	In certain applications (PET/CT for example), mark the entire layout as a key image.
Sig. Series	
	Mark the active series or a subset of images as significant. In MPR, the slice thickness, spacing and number of images of the created series can be changed.
Film	
	Preview, modify, prepare and print filmed images.

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	Crop to film a selected region of interest.
	Film selected images
	Mark an MPR group as a significant series or mark the group for filming. Number of images, spacing, thickness, series description and image label can be modified.
Selection	
	Determine whether image manipulations are applied to a single image, a group, or all displayed images.
Save	
	Save selected images to any available DICOM archive.
	Designate studies to use for teaching.
Burn	
	Send the current study to CD-Direct for burning.
External Application	
	Invoke an integrated external application (ORTHOVIEW).

Search Tab



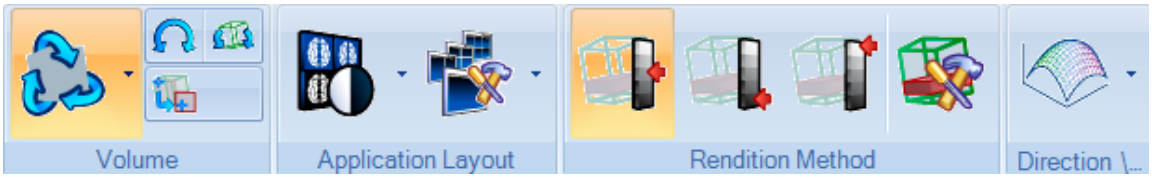
The Search tab allows you to enter terms in the text box and look them up in the Internet. You may conduct the search in Yottalook medical imaging search engine, in STATDX database or in GOOGLE.

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Philips

3.5 MPR Application Toolbar

The following tab is added to the toolbar when you open the MPR application.



Icon	Description
Volume	
	Swivel the image.
	Roll the image from side to side around the center of the volume.
	Roll the image to the closest axial, sagittal or coronal plane.
	Click a point of interest to locate the matching point in other registered groups for the same or prior study (see About Relate Mode on page 590.
Application Layout	
	Duplicate a group of result images to manipulate them individually.  None: Duplicates the group.  Vertical: Duplicates the group and displays the duplicate group adjacent to the original group.  Horizontal: Duplicates the group and displays the duplicate group under the original group.

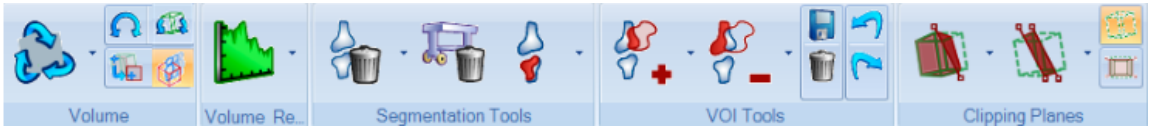
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	Select group layout: • MPR standard Layout (default). Display one result image and reference images showing the scanned volume in axial, sagittal and coronal views with default and additional cross-section lines. In this layout you can select one image, two images, 2x2 images, 2x3 images, or user defined number of images for the result display area. • MPR 2x2 layout • MPR double oblique layout. Allows you to view the data in a 2x2 layout by retaining a perpendicular relationship between the planes. Press Shift to turn the perpendicular and horizontal cross section lines in the reference images to obliques. You can also apply: • Single-phase mode • Multi-phase mode
Rendition Method	
	MPR (average MipPR) - Render the MPR slab using the average pixel value.
	MIP (maximum intensity projection) - Render the MPR slab using the maximum pixel value.
	MinPR (minimum intensity projection)- Render the MPR slab using the minimum pixel value.
	Control rendering parameters. Select rendition type, slice thickness and slice spacing.
Direction	
	Reformat plane and curve: • Axial/Sagittal/Coronal: Lets you define the planar view, or orientation, of the image. • Parallel/Concentric/Sectional/Sectional parallel: Lets you draw and manipulate curved cross-sections on the reference images, as follows: – Parallel: Curved cross-sections that are parallel to one another. – Concentric: Curved cross-sections that decrease in size towards the same central mid-point. – Sectional: Cross-sectional slices that are perpendicular (90°) to a defined curved cross-section. – Sectional Parallel: Parallel cross-sectional slices on a defined curved cross-section.

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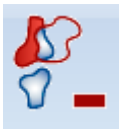
3.6 3D Analysis Application Toolbar

The following tab is added to the PowerViewer application (see PowerViewer Application on page 151) toolbar when you open the 3D application.



heading	heading
Volume	
	Swivel the image.
	Roll the image from side to side.
	Roll the image to the closest axial, sagittal or coronal plane.
	Relate a point on the MIP image to its relevant location on the MPR reference images (see About Relate Mode on page 590).
	Weighted MIP On/Off.
Volume Rendering	
	Edit Volume Rendering (VOLR) protocols, use enhanced VOLR to obtain high 3D image quality, and determine responsiveness during 3D volume manipulation by selecting image quality. See Edit the VolR parameters.
Segmentation Tools	
	Automatically remove bone tissue.
	Automatically remove scanner bed (see Removing the Scanner Bed on page 211).
	Define 3D tissues (see Building and Applying Tissues on page 205). See Tissue Definition Toolbar on page 102.
VOI Tools	
	Define volume of interest plus. See Define Volume of Interest.

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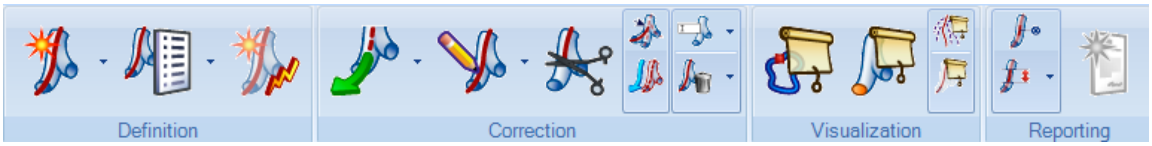
	Free VOI Plus. Lets you define a freehand region of the volume that you want to keep and discard the rest of the volume.
	Oval VOI Plus. Lets you define an oval region of the volume that you want to keep and discard the rest of the volume.
	Rectangular VOI Plus. Lets you define a rectangle region of the volume that you want to keep and discard the rest of the volume.
	Define volume of interest minus. See Define Volume of Interest.
	Free VOI Minus. Lets you draw a freehand shape on the image and then remove the shape from the image.
	Oval VOI Minus. Lets you draw an oval shape on the image and then remove the shape from the image.
	Rectangular VOI Minus. Lets you draw a rectangle shape on the image and then remove the shape from the image.
	Save VOI
	Reset VOI
	Undo Last VOI
	Redo Last VOI
Clipping Planes	
	Add a clipping pane.
	Add a slab.
	Show or hide frames.
	Create clipping plane that is perpendicular to the plane of the display.

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3.7 Vessel Analysis Toolbar

The following tab is added to the toolbar when you open the Vessel Analysis application.

See 3D Toolbar (in 3D Analysis Application Toolbar on page 87) .



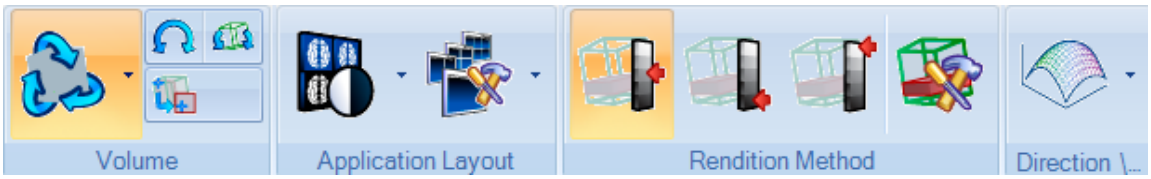
Icon	Description
Definition	
	Define a new vessel. Select a protocol type that matches the vessel to be segmented.
	Select a vessel from the list for viewing, editing and measuring.
	Mark points on any vessel and segment using the general vessel protocol.
Correction	
	Extend vessel segmentation beyond the existing end point.
	Manually edit segmented vessel center line or contours.
	Truncate the active vessel at a selected point.
	Create a new vessel by branching from the active vessel at the location of the reference marker.
	Recalculate the vessel based on manual editing.
	Rename the active vessel.
	Delete the active vessel.

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Visualization	
	Hide center line and contours of all vessels.
	Hide orange overlay indicating segmented vessels and other vessel-related suggestions in MPR displays.
	Show/hide purple overlay indicating automatic protocol suggestions that have not yet been accepted.
	Hide the rest of the 3D volume to isolate the segmented vessels and tissues.
Reporting	
	Mark a location along the vessel centerline as a bookmark.
	Mark a point of interest: Mark a stenosis type point of interest; Mark an aneurysm type point of interest.
	Generate a Vessel Analysis report.

3.8 Cardiac CT Application Toolbar

The following tab is added to the PowerViewer (see PowerViewer Toolbar on page 72) application toolbar when you open the Cardiac CT application.



Icon	Description
Volume	
	Swivel the image.
	Roll the image from side to side around the center of the volume.

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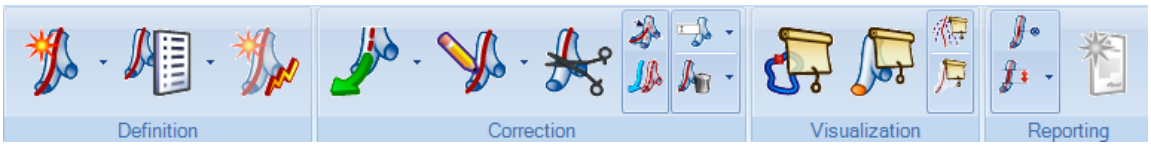
	Roll the image to the closest axial, sagittal or coronal plane.
	Click a point of interest to locate the matching point in other registered groups for the same or prior study (see About Relate Mode on page 590).
Application Layout	
	Duplicate a group of result images to manipulate them individually.  None: Duplicates the group.  Vertical: Duplicates the group and displays the duplicate group adjacent to the original group.  Horizontal: Duplicates the group and displays the duplicate group under the original group.
	Select group layout: • MPR standard Layout (default), displaying a result image and reference images showing the scanned volume in axial, sagittal and coronal views with default and additional cross-section lines. In this layout you can select one image, two images, 2x2 images, 2x3 images, or user defined number of images. • MPR 2x2 layout. • MPR double oblique layout. Allows you to view volumetric data in a 2x2 layout by retaining a perpendicular relationship between the planes. Press Shift to use the perpendicular and horizontal cross section lines in the reference images as obliques. You can also apply: • Single-phase mode. • Multi-phase mode.
Rendition Method	
	MPR (average MipPR) - Render the MPR slab using the average pixel value.
	MIP (maximum intensity projection) - Render the MPR slab using the maximum pixel value.
	MinPR (minimum intensity projection)- Render the MPR slab using the minimum pixel value.
	Control rendering parameters. Select rendition type, slice thickness and slice spacing.

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Direction	
	Reformat plane and curve: • Axial/Sagittal/Coronal: Lets you define the planar view, or orientation, of the image. • Parallel/Concentric/Sectional/Sectional parallel: Lets you draw and manipulate curved cross-sections on the reference images, as follows: – Parallel: Curved cross-sections that are parallel to one another. – Concentric: Curved cross-sections that decrease in size towards the same central mid-point. – Sectional: Cross-sectional slices that are perpendicular (90°) to a defined curved cross-section. – Sectional Parallel: Parallel cross-sectional slices on a defined curved cross-section.

3.9 Coronary Analysis Toolbar

The following tab is added to the PowerViewer (see PowerViewer Toolbar on page 72) application toolbar when you open the Coronary Analysis application.



Icon	Description
Definition	
	Define a new vessel. Select a protocol type that matches the vessel to be segmented.
	Select a vessel from the list for viewing, editing and measuring.
	Mark points on any vessel and segment using the general vessel protocol.
Correction	
	Extend vessel segmentation beyond the existing end point.

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	Manually edit segmented vessel center line or contours.
	Truncate the active vessel at a selected point.
	Create a new vessel by branching from the active vessel at the location of the reference marker.
	Recalculate the vessel based on manual editing.
	Rename the active vessel.
	Delete the active vessel.
Visualization	
	Hide center line and contours of all vessels.
	Hide orange overlay indicating segmented vessels and other vessel-related suggestions in MPR displays.
	Show/hide purple overlay indicating automatic protocol suggestions that have not yet been accepted.
	Hide the rest of the 3D volume to isolate the segmented vessels and tissues.
Reporting	
	Mark a location along the vessel center line as a bookmark.
	Mark a point of interest: Mark a stenosis type point of interest; Mark an aneurysm type point of interest.
	Generate a Vessel Analysis report.

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3.10 Mammography Application Workstation Toolbar

The following icons are added to the PowerViewer (see PowerViewer Toolbar on page 72) application toolbar when you load a mammography study. The list also presents shortcuts you can use to perform the various activities.



Icon	Shortcut Keys	Description
	**Ctrl + I**	Put the cursor in neutral mode.
	**Alt + Shift + S** **Alt + Shift + A**	Select single image for actions to be applied. Select all images in current viewbox for actions to be applied.
	**Ctrl + M**	Use the magnifying glass and select its mode.
	**Z**	Use the zoom tool.
	**P**	Use the pan tool.
	Q	A shortcut that toggles between 2D and DBT mammography views when available.
	Shift + Q	Shifts between the various suggested groups. To display a list of the suggested groups, right-click the laterality and view position annotation.
		Choose a filter to enhance the selected images.
	**Alt + Shift + R**	Resets selected mammography images with chest wall justification, nipple alignment, last applied zoom mode, originally applied windowing and VOI LUT.
	**W**	Apply the windowing mode.

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	**Alt + Shift + I**	Mask breast tissue of selected mammography images only.
	**Alt + I**	Apply inverse windowing to the selected image.
	**Alt + L**	Select Line Measurement graphic tool.
	**Alt + Ctrl + O**	Select Oval Shape graphic tool.
	**Alt + Shift + O**	Select Oval Shape with Line graphic tool. The tool draws an oval and a line measuring the distance between an oval center and nipple.
	**Alt + T**	Select Text graphic tool.
		Auto link–When Auto link is turned on, all prior studies are linked allowing simultaneous scrolling.
		Unlink–Breaks the links between linked groups.
	**Alt + U**	Justify the chest wall of mammography images against the side of the image window.
	**Alt + Q**	View segments of the mammography image at original resolution, or configured zoom, in a sequence of steps.
	**Alt + Shift + Q**	View segments of the mammography image at same size and original resolution, or configured factor of original resolution, in a sequence of steps.
	**Alt + Shift + R**	Identify a corresponding region on opposing mammography views for a selected point of interest. **NOTICE! This tool is not applicable to Breast Tomosynthesis exams at this time.**
	**Alt + Ctrl + N**	Apply or remove nipple alignment to mammography images.
	**Alt + Shift + N**	Display nipple reference lines on mammography images for identification of the nipple or for correction.

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	**Alt + C**	Display CAD Marks on mammography images. **NOTICE! This tool is not applicable to Breast Tomosynthesis exam at this time.**
	**Ctrl + S**	Save the selected (modified) image(s).
		Export selected images for viewing and printing in the Film Previewer. See Film Preview Toolbar on page 99.
	**Ctrl + T**	Mark study as a teaching study.

3.11 Cine Toolbar

The following icons are added to the PowerViewer application toolbar when you load a multi-image Ultrasound, Angiography, or Breast Tomosynthesis exam.

Icon	Shortcut Keys	Description
	**Alt + Shift + P**	Pause all cine loops in the current application.
	**Alt + Shift + L**	Play all cine loops in the current application.
		Stop all cine loops in the current application.
		Display previous image (or frame) for all cine loops in the current application.
		Display next image (or frame) for all cine loops in the current application.
		Play cine in reverse mode.
		Play cine in forward mode.
		Play cine in back and forth mode.
		Slider to adjust the frame rate.

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3.12 Image Level Toolbar



Icon	Shortcut Keys	Description
1	**Ctrl+Up Arrow** **Ctrl+Down Arrow**	Pause or Play cine loop.
2	**Up Arrow**	Display previous image (or frame) in the stack.
3	**Down Arrow**	Display next image (or frame) in the stack.
4		Display cine tools.
5		Film active image.
6	**Alt + Space**	Mark active image as a Key Image (for desktop diagnostic viewer clients only).
	` (single quote key)	Mark active image as a Key Image (for clients that have both desktop and Web environments).
	Ctrl+Alt+Space	Unmark Key Image (for desktop diagnostic viewer clients only).
	Shift +` (~)	Unmark Key Image (for clients that have both desktop and Web environments).

3.13 Cine Toolbar Group Level

The following cine toolbar controls cine behavior at a group level:



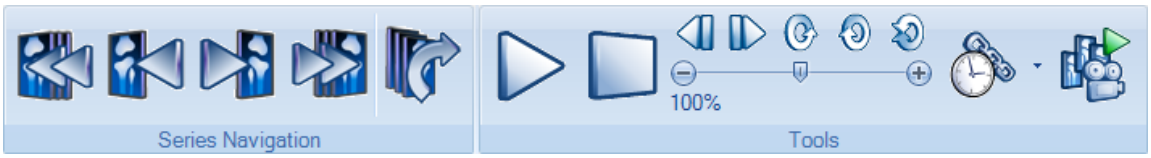
Icon	Description
	Frames per Second - Set the frame rate (frames per second) of the Cine movie.
	Preview - Preview the movie in a low resolution.
	Backwards - Play the Cine movie from end to beginning.
	Forward - Play the Cine movie from beginning to end.

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	Move backwards and forwards.
	Set States - Set the range of images to be played in the Cine movie.
	Reset - Create a new Cine movie.
	Stop the cine movie
	Save the Cine movie to a DICOM archive or to a local disk in AVI format.

3.14 Automatic Cine Toolbar

The following tab is added to the PowerViewer (see PowerViewer Toolbar on page 72) toolbar when you open an Ultrasound or Angio X-ray studies.



Icon	Description
Series navigation	
	Show previous set of series - All displayed series of the selected study are replaced with the previous set.
	Shift series left - The previous series of the selected study is shown, while shifting the currently displayed series gradually. The series are shifted to the right, taking away the bottom right series in the viewer.
	Shift series right - The next series of the selected study is shown, while shifting the currently displayed series gradually. The series are shifted to the left, taking away the top left series in the viewer.
	Show next set of series - All displayed series of the selected study are replaced with the previous set.
	Show first set of series - All displayed series are replaced with the first set.
Tools	

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	Pause all cine loops - All displayed Auto-Cine groups are paused.
	Stop all cine loops - All displayed Auto-Cine groups are stopped.
	Previous/Next frame -All groups' progress is paused one step at a time (forward or backward, respectively).
	Forward/Backward/Back and Forth - Change the direction of all groups. Play the cine movie from beginning to end/from end to beginning/back and forth.
	Changes the playing rate of all groups. The percentage is applied to the default frame rate.
	• Synchronize US or XA linked groups along the scan timeline, relative to the starting point of the scan. – Use the Sync Absolute Time option to synchronize all linked groups to the same absolute point in time, regardless of the scan start time. (Used mainly for cases when a number of scanning sources are used). • Synchronize heartbeat in linked Stress Ecocardiography US groups.
	Cine All - View all relevant series of a study continuously. The currently applied auto cine stops in all groups, and the selected group starts playing all series of the study in cine mode. When all images of the series have been played, the next series is automatically shown and played in cine mode. The PMA displays the currently playing group.

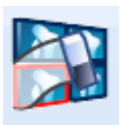
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3.15 Film Preview Toolbar

The following icons are added to the Film Preview window.



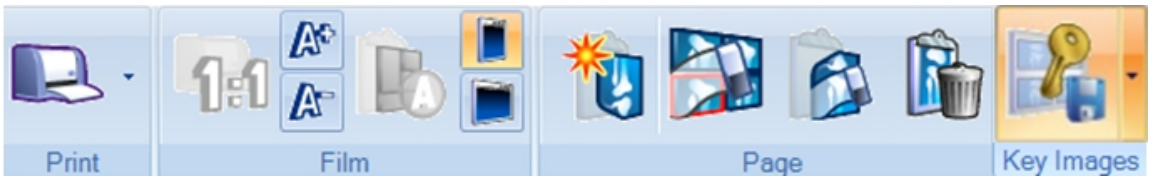
Icon	Description
Print	
	Open a print dialog box from which you can print the current content. Press the Ctrl key and click the Print icon to print to your default printer.
Print	
	Change the preview window to True-Size mode.

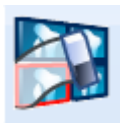
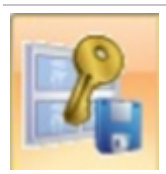
	Enlarge the font size of annotations on the images.
	Reduce the font size of annotations on the images.
	Use with automatic printing machines to achieve an optimal layout while printing the largest images possible.
	Portrait layout.
	Landscape layout.
Page	
	Insert a new page at the end.
	Clear selected images from the preview window.
	Clear current page from the preview window.
	Clear all images from the preview window.
Export	
	Mark the active image as key image.
	Save selected images or layout to any available DICOM archive.

3.16 E-Report Preview Toolbar

The following icons are added to the E-Report Preview window.

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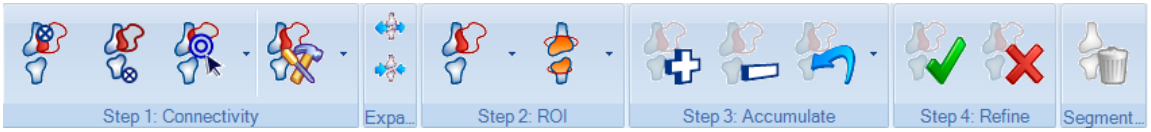


Icon	Description
Print	
	Open a print dialog box from which you can print the current content. Press the Ctrl key and click the Print icon to print to your default printer.
	Change the preview window to True-Size mode.
	Enlarge the font size of annotations on the images.
	Reduce the font size of annotations on the images.
	Portrait layout.
	Landscape layout.
Page	
	Insert a new page at the end.
	Clear selected images from the preview window.
	Clear current page from the preview window.
	Clear all images from the preview window.
Key Images	
	Save changes to key images. You can save changes made to the key images, changes made to the layout, or both changes made to the key images and to the layout.

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3.17 Tissue Definition Toolbar

The following tab is added to the toolbar when you define a new tissue using the 3D tools (see 3D Analysis Application Toolbar on page 87.



Icons	Description
Step 1: Connectivity	
	Mark a seed point on the image.
	Mark an outside point on the image.
	Mark a semi-automatic expansion seed and inflate a balloon within it.
	Define the Tissue Definition parameters.
Expand	
	Add pixels to expand the tissue border.
	Remove pixels to collapse the tissue border.
Step 2: ROI	
	Draw a freehand, oval or square Region of Interest (ROI).
	Draw a freehand, oval or square contour.

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Step 3: Accumulate	
	Remove a tissue.
	Add a tissue.
	Reset the changes to the image you are viewing.
Step 4: Refine	
	Accept a tissue.
	Dismiss a tissue.
Step 5: Segment	
	Automatically remove bone tissue. See: Adjusting the Results of Bone Removal on page 194.

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3.18 Integration Actions Toolbar

The following icons are added to the PowerViewer (see PowerViewer Toolbar on page 72) toolbar when you click Integration Actions .

Icon	Description
	Generate SRAD Report.
	Access SR Configuration.
Notepad	Open the Notepad application.

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4 Using the Archive Explorer

4.1 About Archive Explorer

When you log in to the Diagnostic Workstation, the Archive Explorer window automatically opens.

You can also open the Archive Explorer from a viewing application, such as PowerViewer or Cardiac CT (see Opening the Archive Explorer on page 106.

The Archive Explorer lets you access the images in the archives. You can:

- Load images for viewing.
- Maintain your workflow.
- Organize images in the archives.
- Select and retrieve images from the archives

4.1.1 Exploring the Contents of an Archive or Folder

From the Archive Explorer left pane, click  next to a folder.

The contents of the folder appear in the right pane and the left pane indicates the expanded folder.

Left Pane	Right Pane
The left pane consists of folders containing images as well as the location of the folders within the archive. Click a folder in the left pane and the contents of the folder appears in the right pane. • Click  to expand a folder and see more of its contents. • Click  to collapse the folder.	The contents of a folder you select in the left pane appear in the right pane. The right pane also contains filter fields that let you sort and filter data.

4.2 Refreshing the Archive Explorer Display

Refresh the Archive Explorer to ensure that you see the most recent folder content.

1. From the View tab of the Archive Explorer toolbar, click Refresh 
   ⇨ The Archive Explorer updates with the latest information.
2. Select Auto Refresh from the drop-down list to refresh the study list.

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4.3 Adding Action Buttons

Action buttons let the Diagnostic Workstation invoke external applications from within the Vue PACS application.

You can also define Action buttons to invoke external applications with shared patient and study information.

Contact the system administrator about adding Action buttons.

4.4 Opening the Archive Explorer

You can return to the Archive Explorer from a viewing application (viewbox), such as PowerViewer or Cardiac Analysis, to load additional studies.

To open Archive Explorer:	Do this:
With an icon.	In the Workflow ribbon, click Open Archive Explorer  .
With a keyboard shortcut.	Press **Ctrl + N**.

4.5 Closing the Archive Explorer

To close the Archive Explorer without exiting the Diagnostic Workstation, do one of the following:

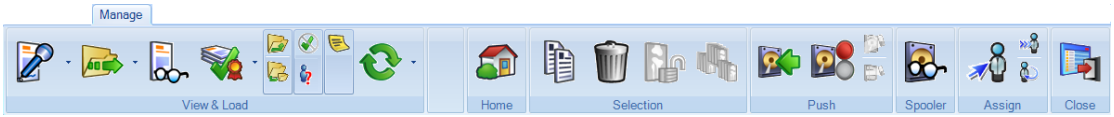
- Click the Close icon in the toolbar  .
- Click the Close icon at the top right corner.

4.6 Archive Explorer Toolbar

The PowerViewer toolbar comprises tabs, menus and ribbons, each offering tools to facilitate study archiving and management. The toolbar includes two tabs:

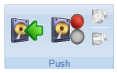
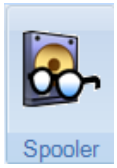
- View - contains tools designed to facilitate the radiologist with the reading flow.
- Manage - contains tools designed to facilitate the administrator with study organization and archiving.

Manage Tab

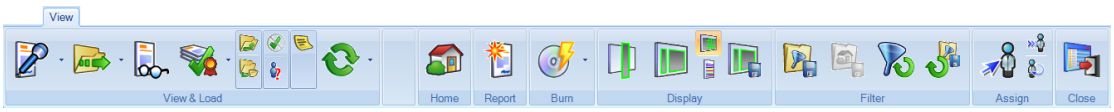


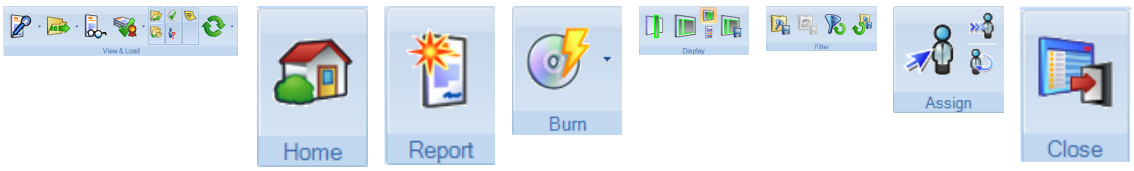
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View & Load (see View & Load Toolbar - Archive Explorer on page 67).	Home (see Home - Archive Explorer on page 69).	Selection (see Selection Toolbar - Archive Explorer on page 70).	Push (see Push Toolbar - Archive Explorer on page 71).	Spooler (see Spooler - Archive Explorer on page 71).	Assign to Toolbar (see Assign To Toolbar - Archive Explorer on page 70).	Close (see Close - Archive Explorer on page 70).

View Tab





View & Load (see View & Load Toolbar - Archive Explorer on page 67).	Home (see Home - Archive Explorer on page 69).	Report (see Report - Archive Explorer on page 69).	Burn (see Burn - Archive Explorer on page 69).	Display (see Display Toolbar - Archive Explorer on page 69).	Filter (see Filter Toolbar - Archive Explore on page 70).	Assign to Toolbar (see Assign To Toolbar - Archive Explorer on page 70).	Close (see Close - Archive Explorer on page 70).

4.7 Displaying the Contents of a Folder

The Archive Explorer window provides a two-pane layout for easy exploration of folders.

1. Select an archive in the left pane.
   ⇨ Select an archive in the left pane.
2. Select a folder.
   ⇨ The list of studies in the folder appears in the right pane.
   ⇨ You can also double-click an item in the right pane to explore its contents. For example, double-click a study to list the series in the study or double-click a series to list the images.
   ⇨ **NOTICE! The result of double-clicking at any level of the study (study, series, or image) depends on the settings defined in the Application Settings tool. For example, you can define double-clicking to load an entire study.**

3. OPTIONAL: You can manipulate contents of the right pane to show the desired set of data.

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5 Using Worklists

5.1 About Worklists

Worklists provide special options designed to streamline your workload. A Worklist folder represents work to be completed and contains a list of status levels, which are steps through which a study passes until completion. For more information about your worklist configuration, contact the system administrator.

Worklist folders differ from the other general folders within the Archive Explorer in that once a study is accepted, the next study in the worklist automatically appears. They are similar in that when the user is finished reading a study in the Worklist folder, the Diagnostic Workstation automatically assigns that study the next status.

The Diagnostic Workstation automatically keeps track of the worklist from which a study was selected and the position of the study within the worklist. The number of studies still to be reviewed by you and any other reviewers using the worklist is indicated. This number is updated each time you move to a different study. You move from one study to the next within the worklist directly from the Viewer.

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NOTICE

When you are not working within a worklist, the Archive Explorer appears automatically after a study is accepted.

Worklists can be customized to fit a user's specific needs. They can be configured according to modality, physician name, date, priority, or any other field that is accessible to the Diagnostic Workstation. For example, if a worklist contains a CT head folder, it can be configured to automatically display the relevant data.

5.2 Worklist Folder

A worklist folder is a pre-configured folder that represents work to be completed. A worklist provides special options designed to streamline your work. Each worklist folder contains a list of status levels that are a series of steps that a study goes through until completion.

Worklist folders differ from the other folders within the Archive Explorer in that after a study is accepted, the next study in the worklist automatically appears.

Like other folders in the Archive Explorer, when you finish reading a study in the worklist folder, the Diagnostic Workstation automatically selects the next study in the worklist for display.

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The Diagnostic Workstation keeps track of the worklist from which the study was selected and the position of the study within the worklist. You can use the Viewer to move from one study to the next within the worklist. When you are not working within a worklist, the Archive Explorer automatically appears after a study is accepted.

NOTICE

If a lock indicator appears next to a study on the worklist, another user has that study open. You can still load the study for viewing, but you cannot make any modifications. If someone loaded the study since you opened the Archive Explorer, you may not see the lock indicator until you refresh your display.

You can customize worklists to fit your specific needs. Worklists can be configured according to modality, physician name, date, priority, or any other valid field in the Diagnostic Workstation. For example, if you have a worklist that contains a CT chest folder, the worklist can be configured to automatically display the relevant data.

NOTICE

Worklist configuration depends on the workflow of each site. For more information, contact the system administrator.

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5.3 Global Worklist

5.3.1 Multi-Site Querying

The Global Worklist is displayed like any other regular worklist folder in the Archive Explorer. Use the Global Worklist to:

- Read studies from all sites connected to the data center.
- Fetch prior studies from other sites.

Using the Global Worklist

1. Connect directly to the data center or to your local server.
2. Select the Global Worklist to query your studies from all sites.

Multi-Site Loading

Loading speed determines whether streaming is used or not used.

The load speed is chosen automatically, depending on the best study location.

Look at the Expected Rate column to see:

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- Availability—Fast (online) or slow (nearline).
- Quality—Best (fast connection) or Progressive (slow connection).

See these topics:

About Worklists on page 109

Working with Global Priors on page 127

5.4 Creating or Viewing a Custom Worklist

Use the Custom fields to mark studies of interest or to store additional study information in a worklist folder.

To create a custom worklist:

1. Make sure the Custom Worklist field appears in the Archive. If the Custom Worklist field does not appear (see Changing Column (Filter) Headings on page 134).
2. Locate the relevant study, then click in the Custom Worklist field of that study.
3. Type a tag that will identify the worklist.
   ⇨ Use any text string that will identify the worklist as yours.
4. Click Enter.
5. Repeat this process for any additional studies you want to mark.

To view a custom worklist:

- Filter the Archive Explorer Custom Worklist column for your custom tag.

NOTICE

We recommend that you use the same Custom Worklist tag for conference purposes. You can then create a personal folder that filters for your tag and access your studies whenever needed by selecting the folder.

See these topics:

About Worklists on page 109

Worklist Folder on page 109

Loading Images in Worklist Mode on page 112

Opening the Worklist Manually on page 112

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5.5 Loading Images in Worklist Mode

When you log on to the Diagnostic Workstation, your customized worklist automatically appears in the left pane of the Archive Explorer. When you load images in worklist mode and finish the study, the images for the next study in your worklist appear. You can load worklists that were previously saved with presentations.

1. From the Archive Explorer, select a worklist folder.

   NOTICE! When you select a worklist folder, the Load tool on the Archive Explorer toolbar changes to Load Worklist.

2. Right-click and select Load Worklist or click Load Worklist  from the drop-down menu of the Load icon  in the toolbar.

See these topics:

About Worklists on page 109

Opening a Study Saved in Presentation State on page 620

5.6 Opening the Worklist Manually

From the Archive Explorer left pane, click the Worklist folder.

See this topic:

Loading Images in Worklist Mode on page 112

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6 Managing Studies in the Archive

6.1 About Study and Archive Management

The Archive Explorer provides tools to assist you with managing studies.

See these topics:

Copying Data to a Different Archive on page 113
Deleting Data from the Archive on page 114
Setting the Study Status on page 114
Setting the Study Priority on page 115
Assigning a Study to a User on page 116
Creating or Viewing a Custom Worklist on page 111

6.2 Copying Data to a Different Archive

You can select data in the Archive Explorer and copy it to another archive.

1. Select the data that you want to copy.
2. Click Copy  in the Manage tab of the View Explorer toolbar.
   ⇨ The Copy dialog box appears.
3. Click the archive you want to copy and drag it to the Copy To area.
4. To copy to additional archives, repeat step 3.

NOTICE

To copy the selected data to all archives listed in the Archives List, click Add All. All archives are moved to the Copy To list. To remove archives from the Copy To list, drag an individual archive to the Archives List, or click Remove All to remove all the archives.

To use a study for teaching/public purposes, copy the study, select the Conceal Patient Details check box, and enter a random alternative identifier.

5. When you are finished, click OK.

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6.3 Deleting Data from the Archive

You can delete studies and individual series in the Archive Explorer. The data specified will be permanently removed from the archive.

NOTICE

If you do not have permission to delete data, the Delete options are grayed out. Contact the system administrator.

1. Select the data you want to delete.
2. Click Delete  in the Manage tab of the Vue Explorer toolbar.
   ⇨ You are asked to confirm the deletion.
3. You are asked to confirm the deletion.

6.4 Setting the Study Status

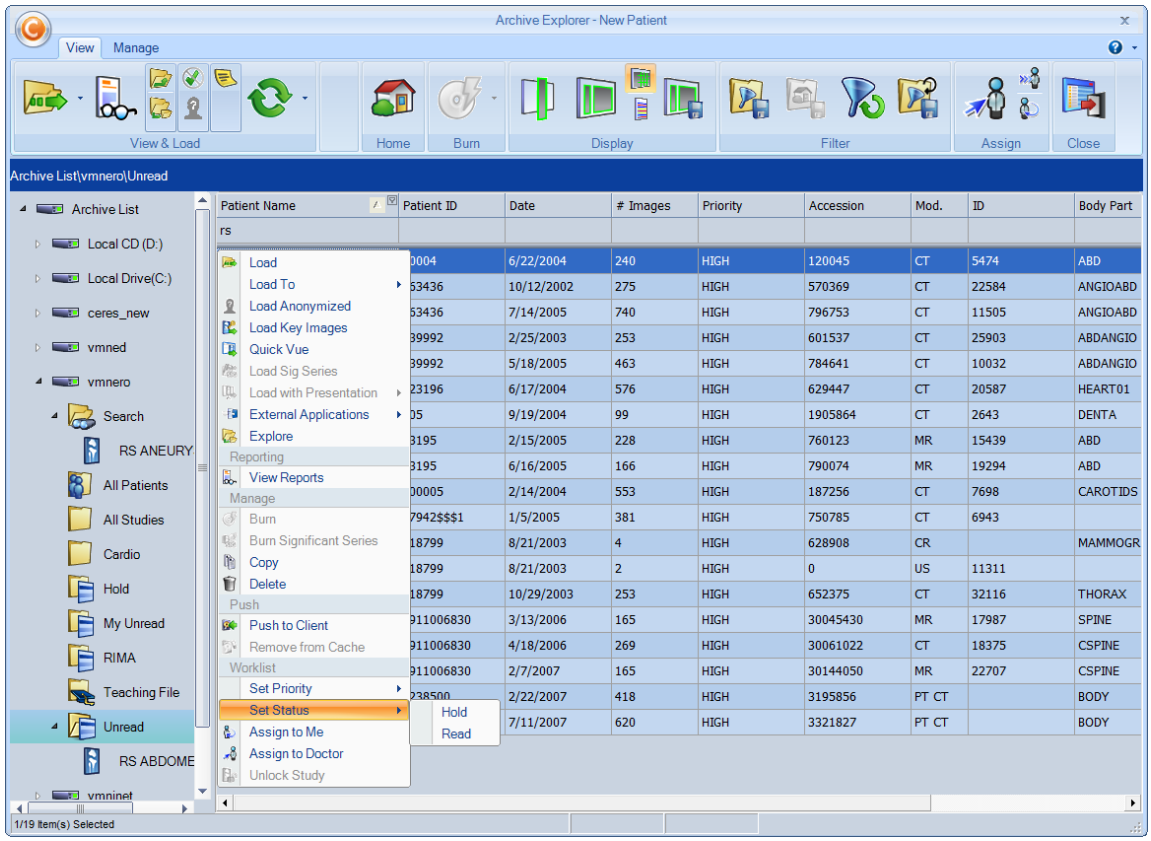
NOTICE

The options available depend on your site's configuration.

1. From the Archive Explorer, select a study.
2. From the right-click menu, select Set Status, then click the required option.

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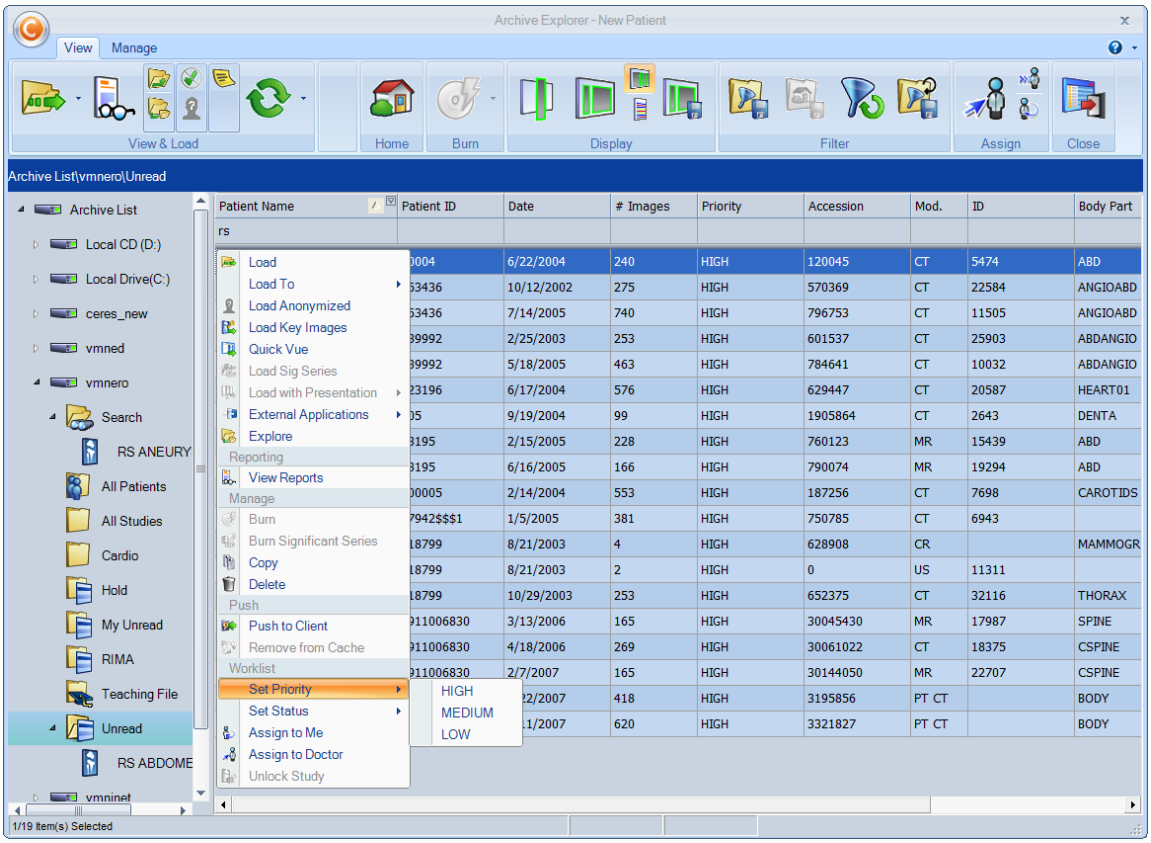


6.5 Setting the Study Priority

NOTICE

The options available depend on your site's configuration.

1. From the Archive Explorer, select a study.
2. From the right-click menu, select Set Priority, then click the required option.



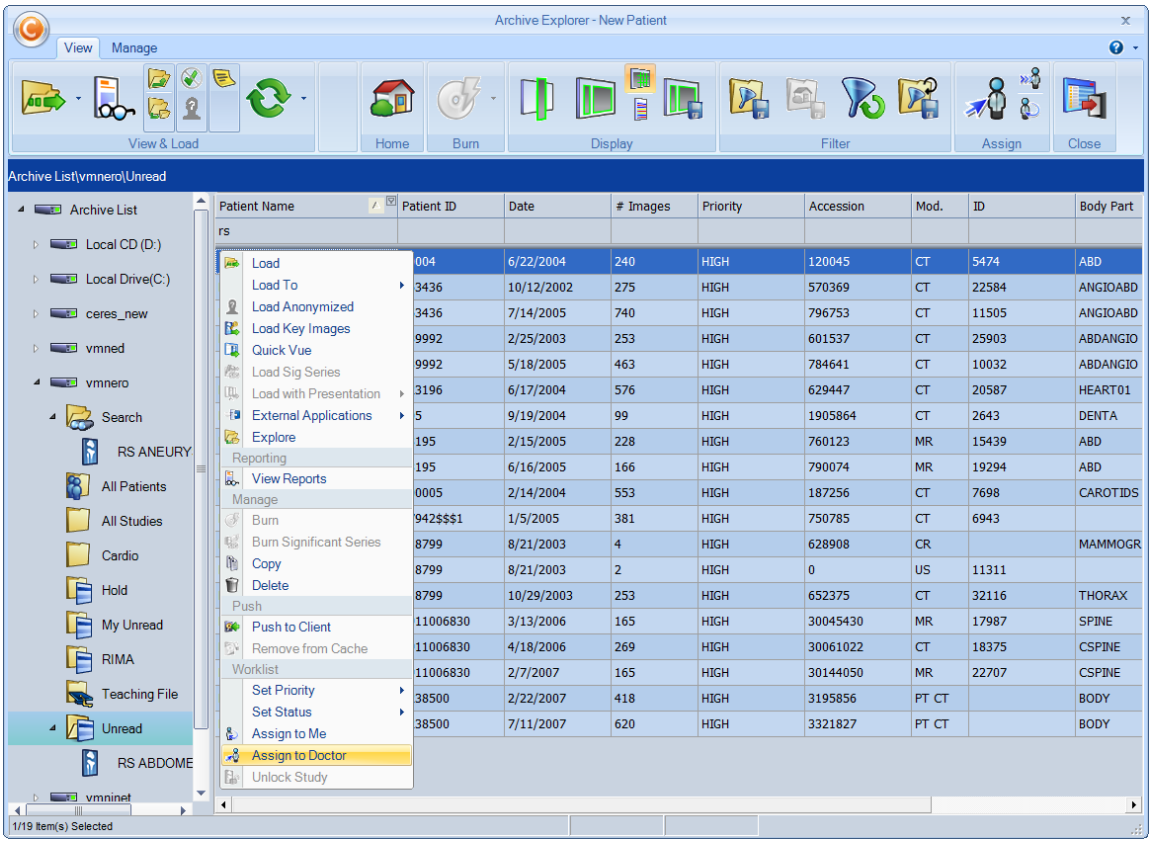
6.6 Assigning a Study to a User

You can assign studies to specific users.

1. From the Archive Explorer, select a study.
2. Do one of the following:
   - From the right-click menu, select Assign to Doctor, then click the user to whom you want the study assigned.
   - Use Assign to Doctor  in the View tab of the toolbar.

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Additionally, you can do the following:

- Use Assign to Me to assign the selected study to yourself. This saves you the need to click Assign to Doctor and select yourself from the list.
- Set a user or group of users to whom your confirmed studies are assigned.

6.7 Creating or Viewing a Custom Worklist

Use the Custom fields to mark studies of interest or to store additional study information in a worklist folder.

To create a custom worklist:

1. Make sure the Custom Worklist field appears in the Archive.

NOTICE

If the Custom Worklist field does not appear, see Changing Column (Filter) Headings on page 134.

2. Locate the relevant study, then click in the Custom Worklist field of that study.

3. Type a tag that will identify the worklist.
   ⇨ Type a tag that will identify the worklist.
4. Click Enter.
5. Repeat this process for any additional studies you want to mark..

To view a custom worklist:

- Filter the Archive Explorer Custom Worklist column for your custom tag.

NOTICE

We recommend that you use the same Custom Worklist tag for conference purposes. You can then create a personal folder that filters for your tag and access your studies whenever needed by selecting the folder.

See these topics:

About Worklists on page 109

Worklist Folder on page 109

Loading Images in Worklist Mode on page 112

Opening the Worklist Manually on page 112

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7 Loading Images

7.1 About Image Loading

Click on one of the links below for information about loading images.

See these topics:

Loading Images in Worklist Mode on page 112

Loading Images Stored on Your Computer on page 120

Loading Images in Regular Mode on page 120

Loading Key Images on page 121

Loading Images from Non-Worklist Folders on page 126

Working with Global Priors on page 127

7.2 Loading Images in Worklist Mode

When you log on to the Diagnostic Workstation, your customized worklist automatically appears in the left pane of the Archive Explorer. When you load images in worklist mode and finish the study, the images for the next study in your worklist appear. You can load worklists that were previously saved with presentations.

1. From the Archive Explorer, select a worklist folder.

   NOTICE! When you select a worklist folder, the Load tool on the Archive Explorer toolbar changes to Load Worklist.

2. Right-click and select Load Worklist or click Load Worklist  from the drop-down menu of the Load icon  in the toolbar.

NOTICE

You can use a worklist for 'pushed' studies, for a convenient way to see the studies that are stored locally for you or a specific user.

See these topics:

About Worklists on page 109

Opening a Study Saved in Presentation State on page 620

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7.3 Loading Images Stored on Your Computer

7.3.1 DICOM Images

You can load DICOM images from any directory on your computer.

1. Right-click on the Local Drive option in the Archive List, then click Browse.
2. From the Browse window, select the directory that contains the DICOM DIR file.

7.3.2 Transferred Images (Push to Client)

IMPORTANT

A remote connection is a requirement to load images transferred to a local computer.

You can initiate a transfer of studies to a local disk even if you are not using a remote connection, but you can only load images from the local disk if you use a remote connection.

1. Right-click on the Local Drive Option in the Archive List, then click Browse.
2. From the Browse window, select the directory that contains the transferred folder.

When you load studies pushed to your local disk, the loading process will behave as though the images are streamed. For example the image information is taken from the server database for the most current information. The image pixel data is taken from the local disk (lossless). However, if new images are created after the transfer, they will streamed as well.

If you load a study that is still transferring to your local disk, the remaining images or series are streamed.

If you load a study that was transferred to your computer, but the same study is available online and you are not in a remote location, the study is loaded from the fast online server instead of the local disk.

See this topic:

Transferring Studies to a Local Computer (Push to Client) (see About Push to Client on page 445)

7.4 Loading Images in Regular Mode

When you load images in regular mode, then finish with the current study, you must go back to the Archive Explorer to select the next study.

1. From the Archive Explorer, select a study.
2. Right-click and click Load.

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NOTICE

If another user has already opened the selected study, a message notifies you that the study is in use and that it can be opened only in view-only mode.

You can load a study, a series, or individual images. You have the option at each level to select sub-groups of images, such as every second image, every 10th image in a series, and so on, by selecting Sub-Select in the Archive Explorer toolbar.

See this topic:

About Display Protocols on page 594

7.5 Loading Key Images

When you load a study from the Archive Explorer, you can load only images marked as key images, which are the ones that best represent a study. The Has Key Images column indicates if a study has key images belonging to it.

This column has a Y or N value.

1. From the Archive Explorer, select a study.
2. Right-click and select Load Key Images or click Load Key Images  from the drop-down menu of the Load icon  in the toolbar.
   - ⇨ The key images for the selected study appear in the Viewer.
   - ⇨ The key images for the selected study appear in the Viewer.

See this topic:

Manipulating Images on page 495

7.6 Loading SIG Images

When you load only SIG images, the system transfers only the relevant images rather than the whole study.

Whenever you load SIG images, the Key Image Group is loaded as well. If you apply Load Significant Series  on a study that contains Key Images but does not contain SIG images, the Key Images group is loaded into the viewbox application.

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7.6.1 Loading Significant Series from the Archive Explorer

Loading SIG Images at the Study Level

1. Open the Archive Explorer (see Opening the Archive Explorer on page 106).
2. Locate a study which contains SIG images (see Locating Studies with SIG Images on page 530).
3. To load the SIG images:
   - **With an Icon**
     - Select the study.
     - Click Load Sig Series  in the drop-down menu of the Load icon .
   - **With a Right-Click Menu**
     - Select the study.
     - Right-click and select Load Sig Series.
4. Select an appropriate viewbox application such as MPR or PET/CT.

⇨ The entire study loads into the viewbox, including images marked as SIG. The SIG images are organized in the Patient Mini-Archive (PMA).

IMPORTANT

If the study does not contain images marked as Significant Series, the Load Significant Series option is inactive.

Loading SIG Images at the Series Level

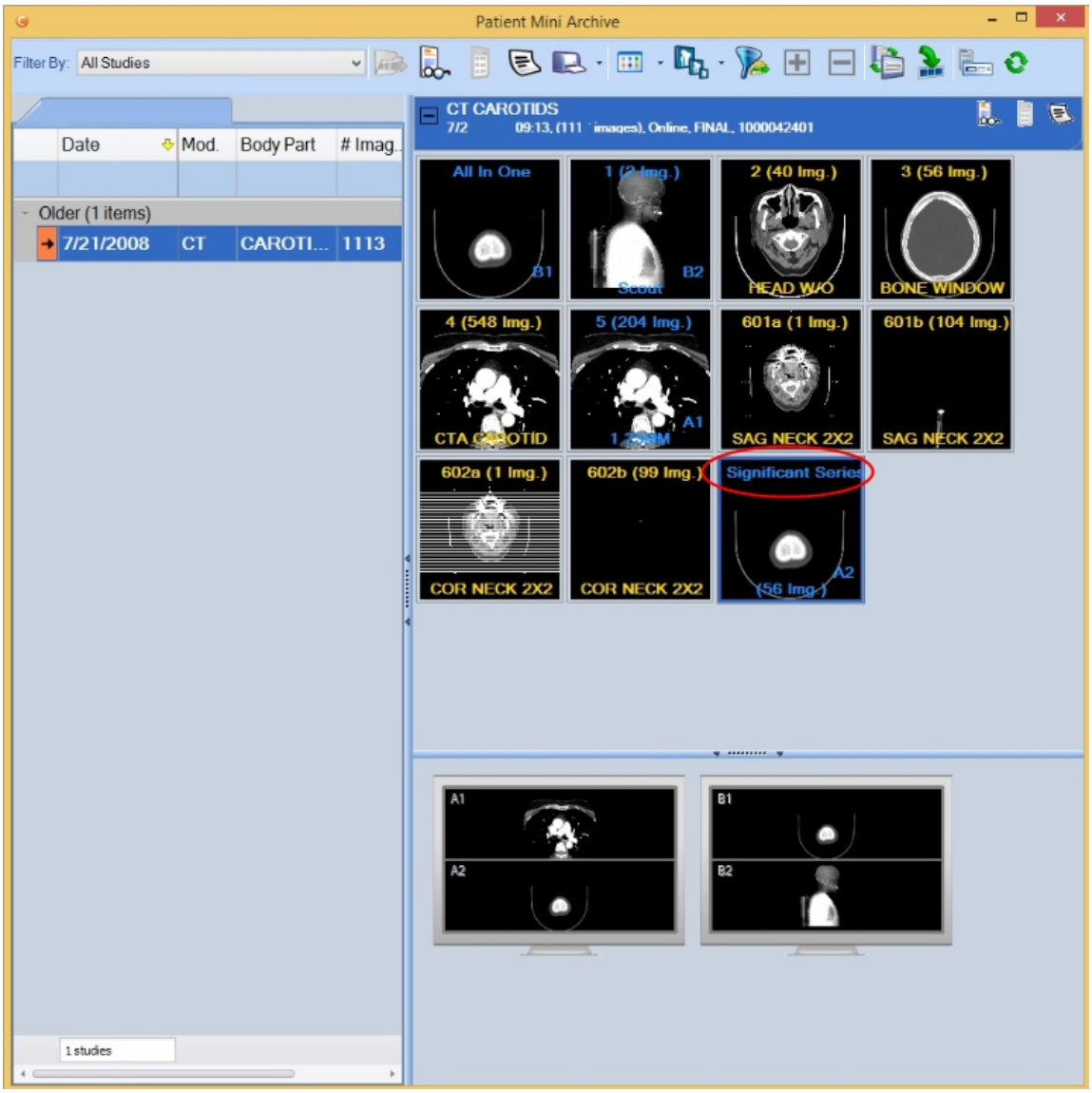
1. Open the Archive Explorer (see Opening the Archive Explorer on page 106).
2. Right-click the column fields area.
3. Select Field Chooser.
4. Drag and drop **Has Significant Series** from Available Fields to Displayed Fields.
5. Click OK. The new column Has Significant Series opens in the Archive Viewer.
   ⇨ The column includes the letter N or Y.
   ⇨ Y—Yes, the study contains SIG images.
   ⇨ N—No, the study does not contain images marked as SIG.
6. Click Has Significant Series to sort and organize the information.
7. Press the CTRL key and click the specific series from the Archive Explorer list.
8. Click Load Significant Series .

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9. Select an appropriate viewbox application such as MPR or PET/CT.

7.6.2 Loading SIG Images from the PMA

Images marked as SIG are visible in the PMA.



When you load a study from the PMA, the study will load SIG images according to the load configuration. If the configuration is set to load only SIG images from the prior study, then only those images from the prior study load to the viewbox.

7.6.3 Loading Significant Series of Prior Studies

You can configure prior studies so that only the SIG images load. You can use the Display Protocol editor tools or the PMA to determine the specific study to load.

You or your system administrator can configure whether the whole study is loaded when the prior study does not contain any SIG images.

Load whole study—default configuration.

Load significant series only from history tag—if this flag is 1, the application will load only significant series in prior studies.

No significant series—if this flag is 0, and the prior study has no significant series, then nothing loads.

Load entire study when no significant series in history tag—if this flag is 1, the application will load the entire study when there are no Significant Series in the prior study.

You or a system administrator can configure these parameters from Administration > System Configuration.

Exceptions and Behavior

Whenever the DP contains a request to Load Key Images Only, only the Key Images will load, even if the configuration is set so that the SIG images are loaded.

7.7 Loading Linked Studies

Linked Studies are studies linked together for reporting purposes, and they share a single report. When loading a study (primary study) that is linked, all studies linked to it are also automatically loaded and displayed together as connected.

These studies are assigned the same color annotation as the primary study.

All linked studies are labeled using the Current annotation followed by a sequential number (e.g. Current 1, Current2…), where Current 1 always represents the most recent study within all linked studies.

7.8 Loading Studies Linked as Display Set

Display sets are sets of studies linked together for display purposes.

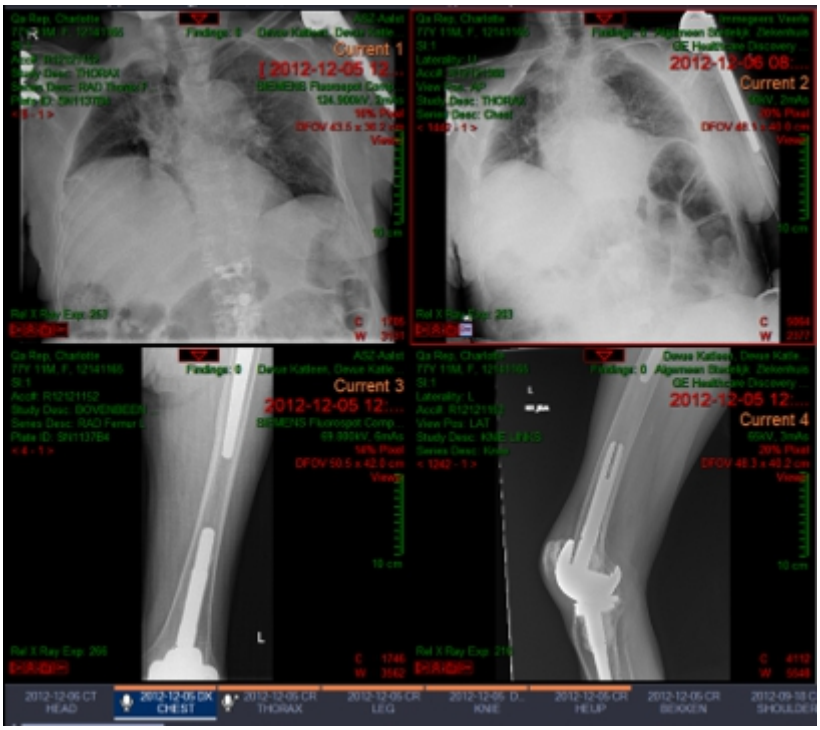
Display sets allow linking multiple studies as clinically relevant — meaning they should be viewed together — while still allowing to create either a single combined report for all of them or separate reports for each study within the set.

When loading a study (primary study) that is a part of a Display Set, all studies in the same Display Set are automatically loaded and displayed together as connected.

These studies are assigned the same color annotation as the primary study. All studies within a Display Set are labeled using the Current annotation followed by a sequential number (e.g. Current 1, Current2…), where Current 1 always represents the most recent study within all studies in the set.

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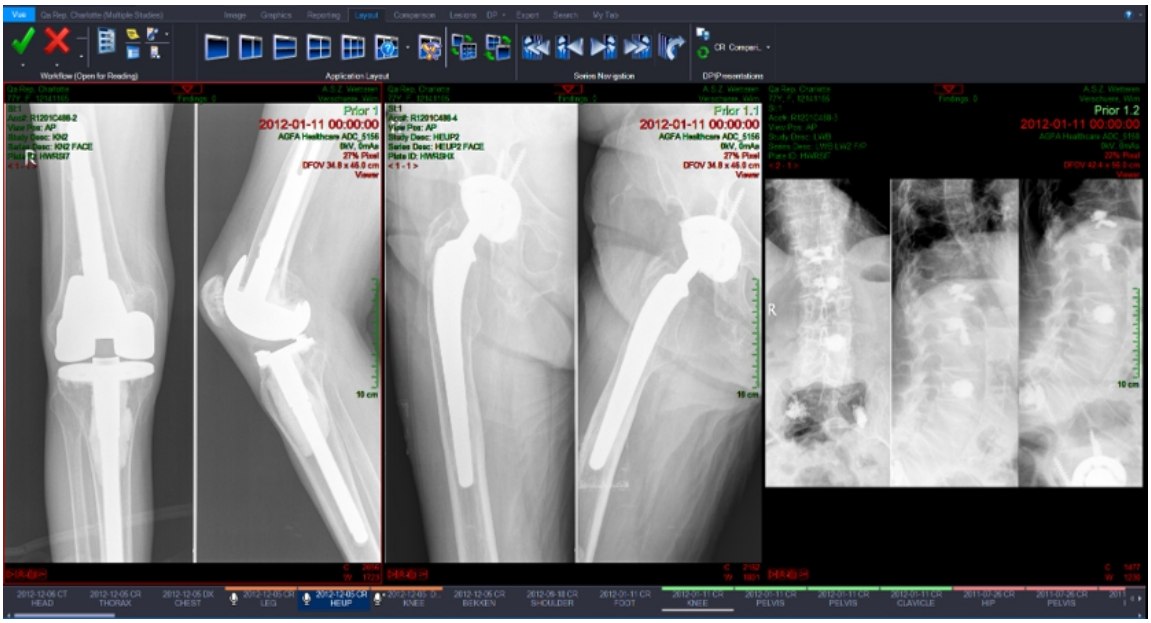
7.8.1 Viewing Linked Priors in Diagnostic Viewer

When working with Display Sets, the system can be configured to load the entire Display Set when any of its studies is requested as a prior study.

When this option is enabled, requesting a study that belongs to a Display Set as Prior N— either automatically via a Display Protocol or manually by the user— also loads all other studies in the same Display Set.

All studies inside the set are assigned the same annotation color and are all labeled using the Prior N annotation followed by a sequential number (e.g., Prior N.1, Prior N.2), where N.1 always represents the most recent study within the Display Set.

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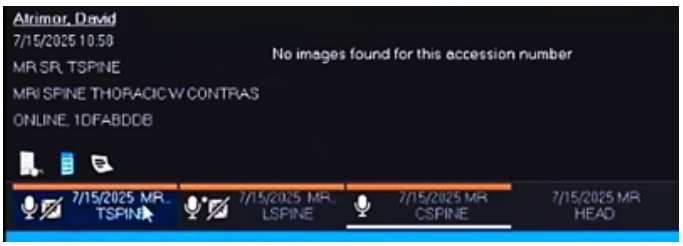
7.9 Loading Studies with No Images (Empty Orders)

Empty orders are studies that contain no images.

A 'no images' icon appears on the study tab in the PMA strip and an indication that no images are found for this study appears in the study's series thumbnails area, in both the PMA strip and Full View PMA.

When an empty order is loaded and it is linked to other studies – either for reporting purposes or as part of a Display Set – it does not contribute to the counter of the linked studies (it is not assigned a “Current X” label) and its modality and body part information are copied from the empty order (if available).

Display Sets can be configured to load together when requested as priors. When enabled, loading an empty order as Prior N, also automatically loads all its linked studies (linked in reporting) and all studies within the same Display Set (linked in display).



7.10 Loading Images from Non-Worklist Folders

When you load images from folders that are not Worklist folders, then finish with the current study, you must select the next study from the Archive Explorer.

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1. From the Archive Explorer, select a folder that is not a Worklist folder.
2. Select the study to load.
3. Right-click and select Load or click Load  in the toolbar.

NOTICE

If another user has already opened the selected study, a message notifies you that the study is in use and that it can be opened only in view-only mode.

You can load a study, a series, or individual images.

7.11 Clearing Images from a Local Computer

The cache size is 5 GB or half the size of free disk space.

You can use Clear Cache in the Push ribbon of the Manage tab in the toolbar to remove the cache of transferred images from your local computer. You can use Remove from Cache to clear specific studies.

See this topic:

Transfer Tools on page 445

7.12 Working with Global Priors

Allows you to work on your regular local worklist and receive the history studies from all other sites through the Data Center (GWL). Global Priors is available in the Archive Explorer.

When enabled by permission, the system queries the history list from both the local machine and the Data Center, displaying a consolidated list in the PMA.

The calling system does not have to specify the global worklist connection parameters to benefit from the complete history list.

	Click the icon once to activate the Global Priors work mode.
	Click the icon again to deactivate Global Priors.
	The feature is disabled.

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7.12.1 Viewing Multiple Patient IDs

In a Enterprise Collaboration Manager (SuperPACS) environment, a single patient might have several different PIDs provided by different issuers. The PID value displayed in the PID column in the Archive Explorer is determined according to the Site ID of the study (default).

The other PIDs are displayed in new, issuer-specific PID columns. You can use the columns to filter search results.

Right-clicking the PID annotation in the Viewer displays all the PIDs of the patient.

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8 Displaying Non-DICOM Data

8.1 Displaying Non-DICOM Exam Data

Vue PACS allows you to display non-DICOM files produced in the course of medical exams in various departments of the medical center and stored in the PACS server.

Supported file formats include:

PDF

MPEG

MPEG-2 (requires installation of a third-party extension)

MPEG-4

Various Image formats (JPEG, TIFF, BMP, PNG etc.)

To display non-DICOM files:

1. In the Archive Explorer, click a study which contains a non-DICOM file.

   NOTICE! Normally, you can identify studies containing Non-DICOM files by their OT (Other) modality.

2. Load the study.

   ⇨ A new application is added, displaying the required content in the same way DICOM images are displayed.

To hide the non-DICOM file, click a different application in the application bar at the top left corner.

To close the application entirely, click Close at the top left corner of the screen.

To re-display any closed document, double-click its icon in the PMA.

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9 Accessing and Managing Images

9.1 About Image Access and Management

See these topics:

Accessing Patient Files and Studies on page 140
Changing Column (Filter) Headings on page 134
Adding and Removing Columns (Fields) on page 136
Managing Studies in the Archive on page 113
Loading Images on page 119

9.2 Working with Folders

Use the Archive Explorer to access and manage images through folders.

9.3 Types of Folders

Folder Type	Description
Worklist	Contains work to be completed (see Worklist Folder on page 109). You can also add additional worklist folders, for example, Hold, Unread, and so on.
Home	Defines the folder that appears in the Archive Explorer when you log in to the Diagnostic Workstation (see Setting the Home Folder (Automatically Opening a Worklist)).
All Studies	Contains a complete list of the contents of the archive.
All Patients	Contains a complete list of the patients and their ID numbers.
Filter	Contains studies extracted from an archive according to a filter you specify (see Filtering Data in the Archive). For example, you can specify that all CR studies be extracted and placed into a folder named CR.
Search	Remains empty until you search based on criteria you specify (see Searching for Data in the Archive).
Teaching	Contains studies designated for teaching purposes. These studies do not include the patient names and IDs (see About the Teaching File and Folder).

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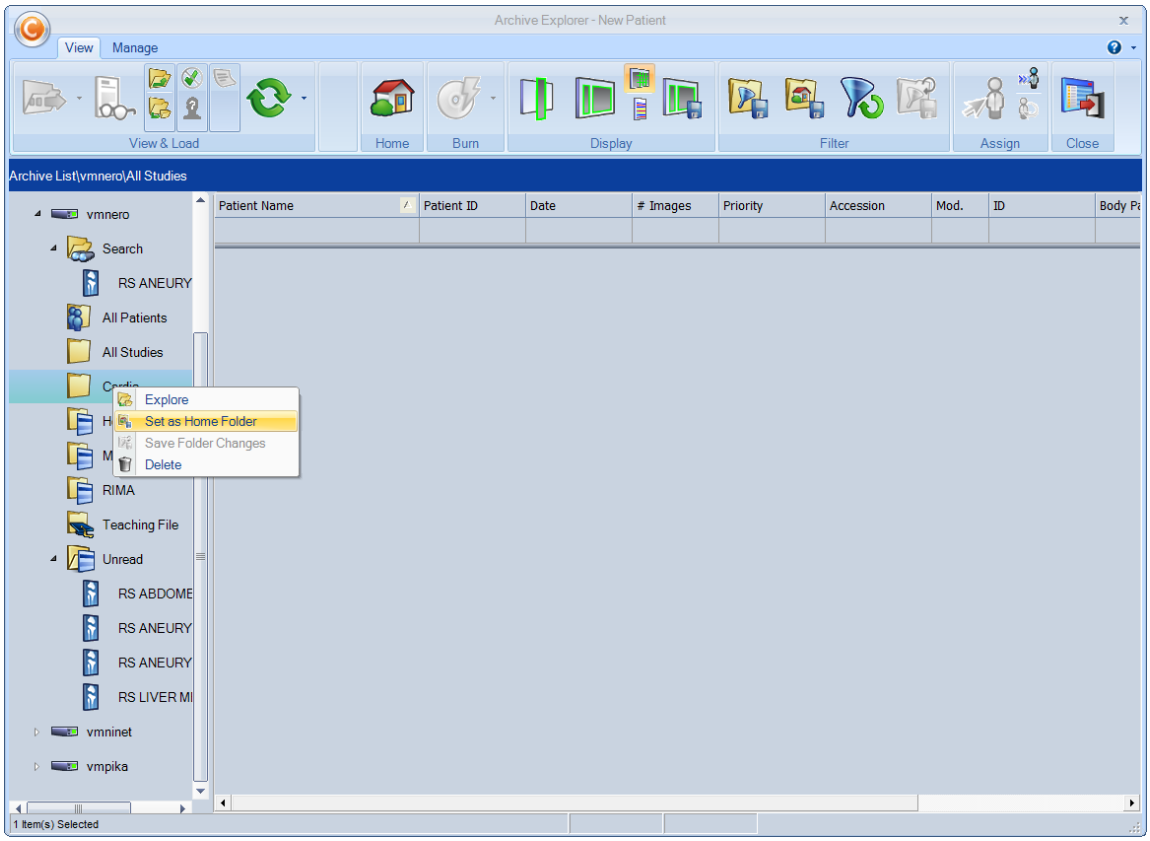
9.4 Setting the Home Folder (Automatically Opening a Worklist)

The home folder designates a particular worklist that appears when you log on to the Diagnostic Workstation. If you specify a home folder, or a home folder has been specified for you, the folder is automatically selected in the left pane after you log in to the Diagnostic Workstation and the Archive Explorer opens. You should designate the folder you use most frequently as your home folder.

9.5 Specifying the Home Folder

Do one of the following:

- From the Archive Explorer left pane, right-click the folder you want as your home folder and select Set As Home Folder.
- Click Set As Home Folder  in the View tab of the toolbar.



9.6 Accessing the Home Folder

From the Archive Explorer toolbar, click Home .

9.7 Loading Prior Studies

The Diagnostic Workstation allows you to load a patient's previous history. Use the Display Protocol editor or hold down the CTRL key, select multiple studies with the same patient ID, and click Load.

NOTICE

Loading multiple studies from different patients can only be done from the Display Protocol Editor (see About the Display Protocol editor on page 597).

The Workstation loads the most recent study as the current study. Other studies are prior studies. This selection overrides the defined Display Protocol editor's prior policy. You can specify which modalities and body parts you would like to load from the patient history. You must determine the layout of these studies on the screen.

9.8 Filtering Data in the Archive

You can filter data in the archive by specifying specific criteria in the Archive Explorer. The column headings in the right pane act as filter fields. You can use all columns for filtering. Depending on the column, you can enter free text for filtering (for example, a patient's last name) or select filter options from a list.

- Click the empty field below the column (filter) heading and enter the appropriate text.
- From the drop-down menu, click the desired option and press Enter.

9.9 Additional Filtering Options

Each field type has a different filter at the top of the window. Double-click the field name (column header) to enable a filter to be entered. One of the following will occur:

- A text box will appear, giving you the option to type in a value. You can type in a character (such as c) and all results that start with that character will be displayed.

  You can also use wildcards (*) instead of letters or numbers. If you enter a suffix, such as *118 in the Patient ID column, the results are all patients with ID numbers ending with 118.
- A drop-down menu appears where relevant. You can select a filter condition from the drop-down menu.

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- A dialog box appears.

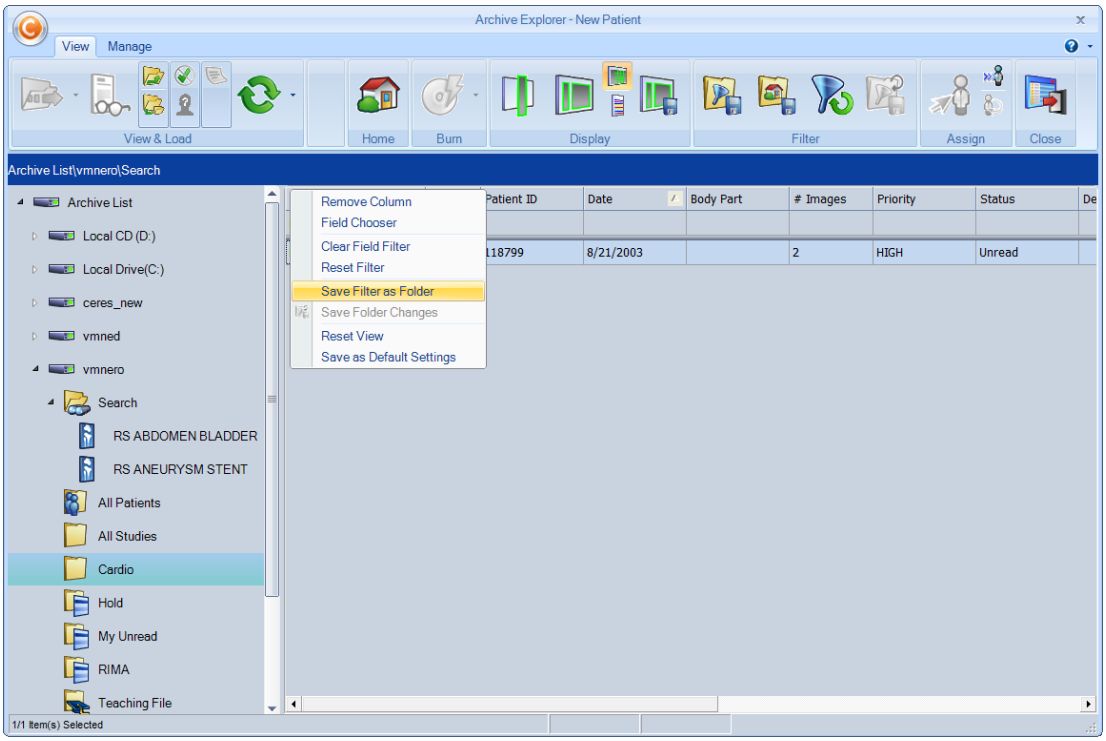
After you define the filtering criteria, click the Refresh icon to display the matching studies. The status bar displays the number of studies found that match the filtering criteria you entered.

If no items are found, nothing appears in the right pane and "0 items" appears in the status bar. To view the list again, select the folder in the left pane.

To save a filter as a folder:

Do one of the following:

- Right-click the window and click Save Filter as Folder.
- Click Save Filter as Folder  in the View tab of the toolbar.



See these topics:

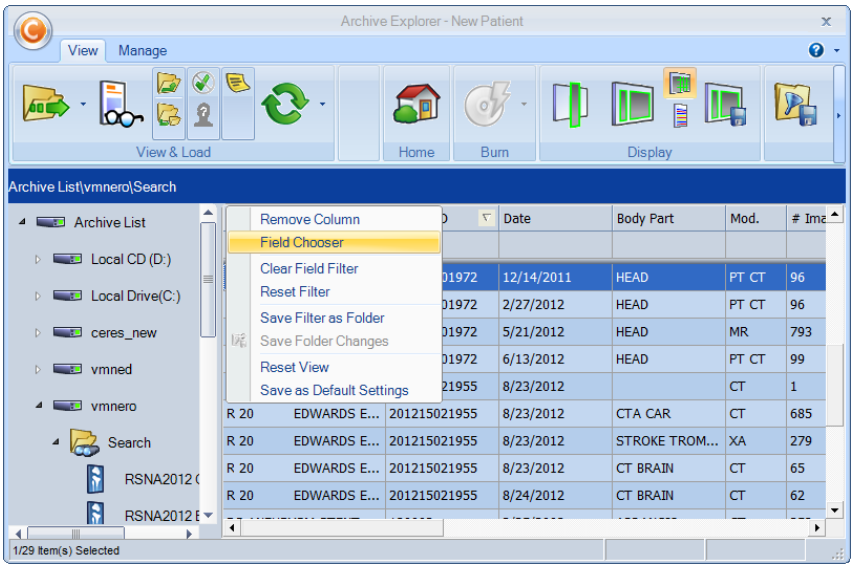
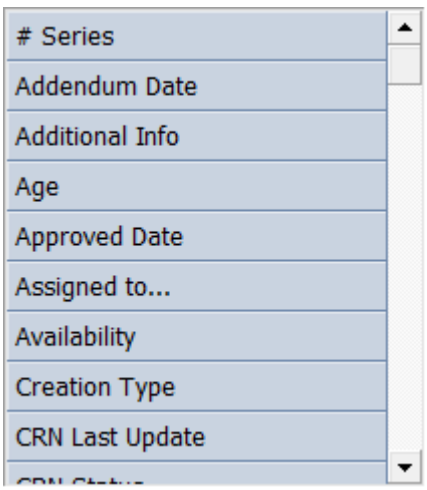
Changing Column (Filter) Headings on page 134.

Adding and Removing Columns (Fields) on page 136.

9.10 Changing Column (Filter) Headings

You can adjust column (filter) headings in the right pane of the Archive Explorer. Changes you make to the columns are saved and used the next time you log in.

To:	Do this:

Move columns	Drag a column to the right or left.
Delete columns	On the column you want to delete, right-click and select Remove Column.
Change the column width	Point to the edge between two adjacent column headings and drag to the position you want.
Reset the filters	Right-click the column heading and click Reset Filter.
Reset the filters	Right-click and select Set Default Settings to save the column settings (the selected fields, sort order, width, and so on) as the default settings to be used for all studies.
Select which fields to display	1. Right-click a column heading and click Field Chooser.  2. Drag the field to be displayed to the desired place. 

See this topic:

Adding and Removing Columns (Fields) on page 136.

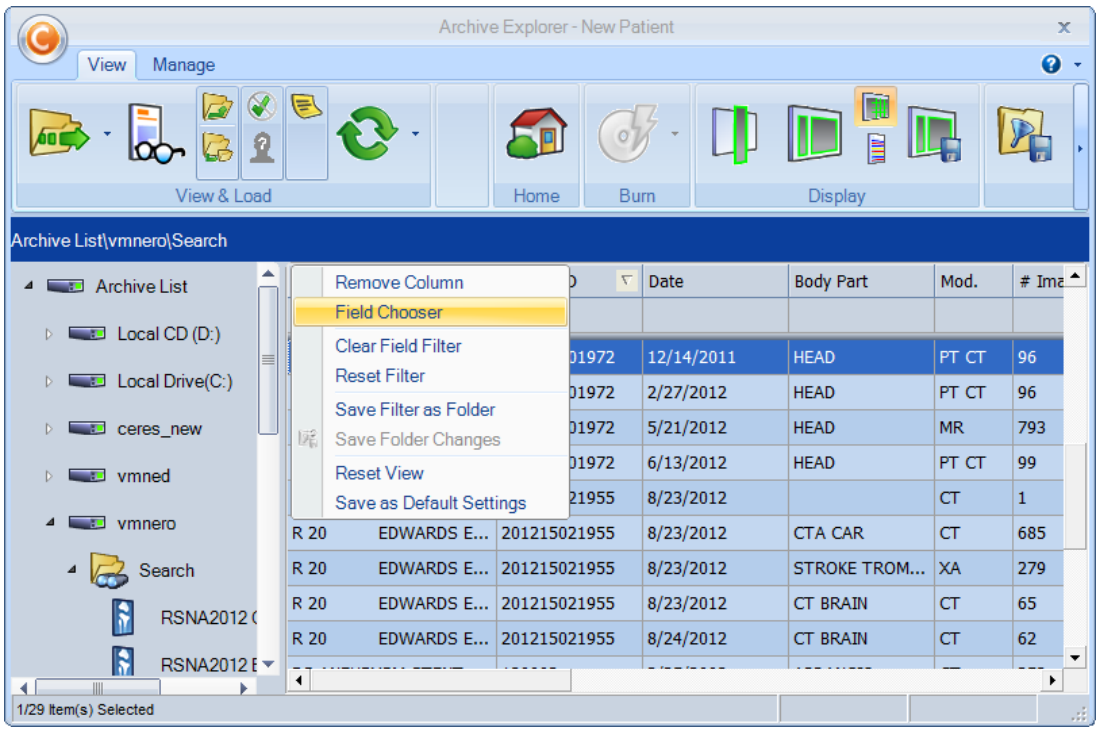
9.11 Adding and Removing Columns (Fields)

You can add and remove columns (fields) to customize the right pane of the Archive Explorer.

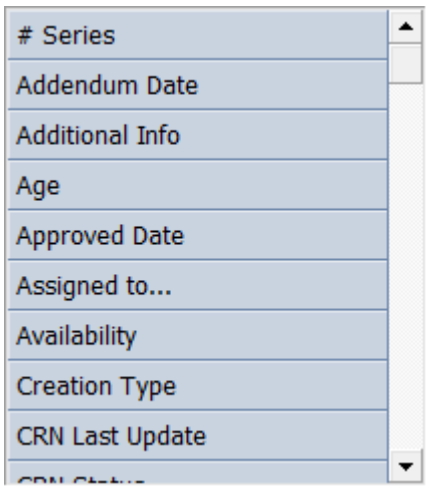
- Right-click any column in the right pane, and select Field Chooser.

To add a column (field):

1. Right-click a column heading and click Field Chooser.



2. Drag the field to be displayed to the desired place.



To remove a column (field):

Right-click a column heading and select Remove Column.

To change the order of the columns:

To change the order in which the columns appear in the Archive Explorer, drag the column headings and place them in the desired order. An arrow appears, showing where the field will be inserted.

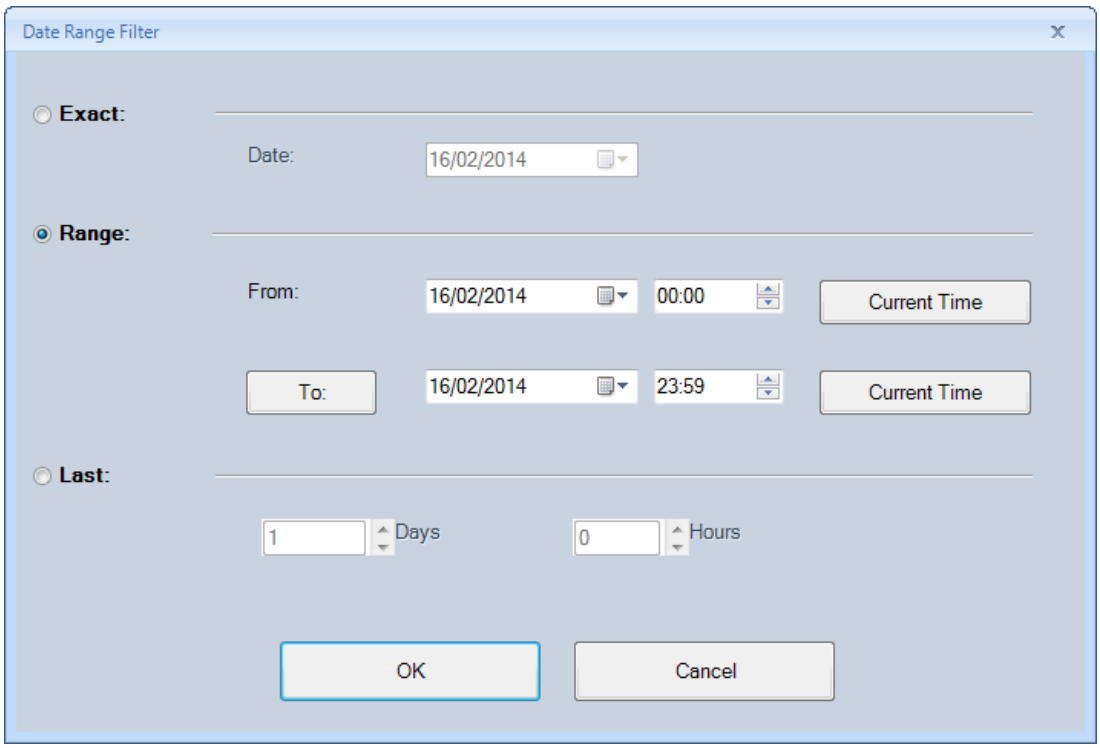
See this topic:

Filtering Studies by Dates on page 137.

9.12 Filtering Studies by Dates

You can filter studies in the Archive Explorer for a specific date range.

1. Click on the Date column, then choose Range.



2. From the Date Range Filter window, select the dates you want to view in the From and To boxes.
3. Click the Current Time button for the exact time of day.

   Or

   Choose the last X days or X hours to filter.
4. Click OK.

9.13 Creating Folders

You can create folders in the Archive Explorer based on one or more filters. A filter selects all studies matching the criteria you specify for a folder's contents. Each time you open the folder or refresh the display, the folder shows the latest studies matching the filter criteria. You must set the filter(s) for a folder before you create the folder.

For example, to create a folder for CT chest images, place a CT filter in the Modality field, then place a chest filter in the Body Part field. To create an Unread MR worklist, place an MR filter in the Modality field, then place an Unread filter in the Status field.

1. Make sure that you have set the folder filters (see Filtering Data in the Archive on page 133).
2. From the Edit menu, select Save Filter as Folder.
   ⇨ The Create Folder dialog box appears.
3. Type a name for the folder (for example, CT Chest or Unread MR).
4. Click one:
   - Regular
   - Worklist
   - Teaching
5. Click one:
   - Private: Only you can access the folder.
   - Public: Everyone can access the folder.
6. Click OK.

⇨ The new folder appears in the left pane of the Archive Explorer.

NOTICE

If you do not have permission to perform specific actions, the options are grayed out. Contact the system administrator.

9.14 Deleting Folders

If you delete a folder, the studies in the folder are not deleted. They remain in the archive.

NOTICE

If you do not have permission to delete public folders, the Delete options are grayed out. Contact the system administrator.

1. Select the folder you want to delete.

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2. Click Delete .
   ⇨ You are asked to confirm the deletion.
3. Click OK.

9.15 Sorting Lists in the Archive

Use the column headings in the right pane to sort lists in the Archive Explorer.

Sort Order	Icon	To Sort:
Sort based on a specific field (primary sort)		• Click the column heading items in ascending alphabetical order (text fields) or reverse chronological order (date/time fields). • Click the column heading again to reverse the sort order.
Sub-sort based on a second field (secondary sort)		• Hold down the Shift key and click the column heading you want to be used for the secondary sort. • Hold down the Shift key and click the same column heading again to reverse the order.
Sub-sort based on a third field (tertiary sort)		• Hold down the CTRL key and click the column heading you want to be used for the tertiary sort. • Hold down the CTRL key and click the same column heading again to reverse the sort order.

9.16 Searching for Data in the Archive

1. From the left pane of the Archive Explorer, click Search .
2. In the field on which you want to base your search, enter the data. For example, patient name or accession number.
3. Press Enter.

   You can also use a comma when you search based on a patient's name. For example, entering A, B, C finds all patients with a last name starting with "A", first name starting with "B," and middle name starting with "C."

   The system administrator can define search settings, such as the maximum number of results to be displayed, the sort order, and so on. If the system administrator has limited the search settings, a message appears in the Status bar informing you that this is not the complete set of results, but is limited according to the system configuration.

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9.17 Canceling a Search

You can cancel a search if it takes too long to provide a response. The extended response time may be a result of too many items in a query. If this is the case, you can add filters to narrow the search. To add filters to a query, you must cancel the current query. See Filtering Data in the Archive on page 133.

- From the Archive Explorer toolbar, click Stop .

  The search stops and only the portion of the list that was queried before canceling appears. The Status bar indicates that only a partial list is displayed.

9.18 Accessing Patient Files and Studies

You can access patient files and studies in several ways in the Archive Explorer. You can also access specific data through filtering and sorting. For more information, see Filtering Data in the Archive on page 133 and Sorting Lists in the Archive on page 139.

To:	Do this:
View several studies at the same time	• Press the CTRL key and click the folders or studies you want to view. The location bar shows the paths of all selected folders. The right pane shows the patient list for the selected folders and the source path. See Loading Prior Studies on page 133 and Using the Editor to Create Display Protocols (see About the Display Protocol editor on page 597).
View all patients in a list	• Click the All Patients folder in the left pane and then click the Refresh button. A list of all Patient Names and their Patient IDs appears.
View all studies of a particular patient	• From the All patients folder, double-click the patient name.

9.19 Exploring the Study Content

You can explore the study content to see the series and image information of the study. You can then load only the series and/or images you want.

1. Do one of the following:
   - Right-click a study and click Explore.
   - Select a study and click Explore  in the toolbar.

   ⇨ All of the series of the selected study are displayed. Each study can comprise a number of series.

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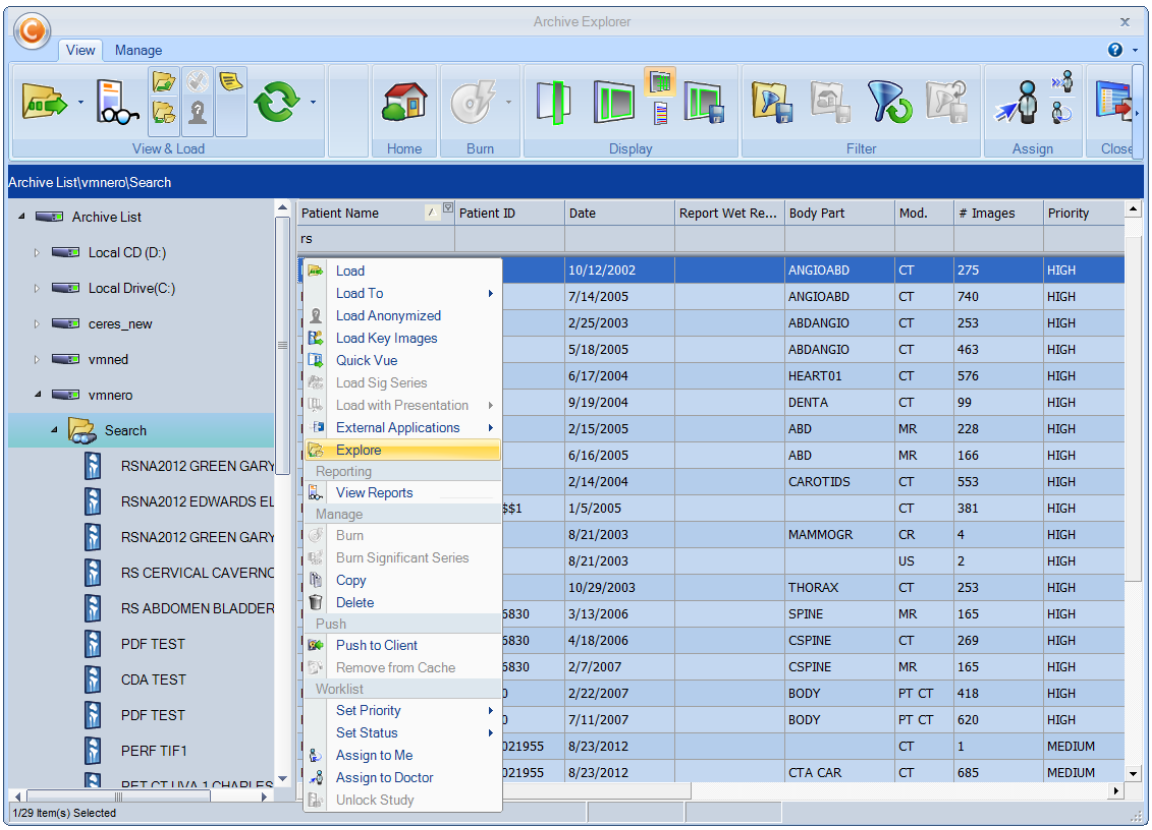
2. Do one of the following:
   - Right-click a specific series and click Explore.
   - Select a series and click Explore  in the toolbar.

   ⇨ All of the images of the selected series appear.

From either the series or image level, you can go back a level by clicking Up One Level .

NOTICE

To select multiple studies/series/images, hold down the CTRL key and click the items you want to explore.



9.20 Viewing DICOM Information

You can view a detailed description of the DICOM data for any image from the Archive Explorer.

1. Explore (see Exploring the Study Content on page 140) the study to the image level.
2. Right-click the image and select D3 Print.
   ⇨ A detailed description of the DICOM data appears.

See this topic:

Viewing Non-DICOM Information on page 142

9.21 Viewing Non-DICOM Information

You can view non-DICOM images and documentation at the study level from the Archive Explorer. The External Document column indicates if a study has non-DICOM information belonging to it. This column has a Y or N value.

External documents also appear in the Patient Mini-Archive and can be loaded from there.

The study is loaded in the same way as a study with DICOM images. See Viewing DICOM Information on page 142.

NOTICE

Non-DICOM images are displayed using MICROSOFT INTERNET EXPLORER, not the Viewer.

9.22 Streaming

You can use the application settings to optimize the system for fast or slow communication lines.

You can configure the system to start automatically on the appropriate line or to prompt you each time you log on. This is useful for users who use laptop computers. You can use this feature both on site and off site.

If slow communication lines are being used, images arrive using streaming. When the system begins to display images, some images have no pixel data and "Loading" appears in the center of the image. Other images appear with lower image quality which will improves as the loading process continues. After all images are loaded, all system functionality is available.

On a slow line, certain images might finish loading with lossy compression. To complete loading with lossless images:

Where the ration annotation appears at the top of the image, right-click it and select the desired option:

- Complete Active Image
- Complete Active Slab (5mm)

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- Complete Active Group

NOTICE

You can also work in lossless mode. To have images arrive without lossy compression, select Lossless Mode  from the Vue PACS icon drop-down menu at the top-left corner. Over a slow line, this might affect the loading performance. Use this option only when necessary.

Until all images are completely loaded and the process is complete, you cannot perform certain functions such as Cine. However, you can use some functions, such as Zoom and Pan.

9.23 Using the Optional Bar Code Scanner to Load a Study

The bar code scanner improves ergonomics and eliminates up to two steps from the process of searching for and loading studies.

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NOTICE

You must scan bar codes in the Archive Explorer. You cannot scan bar codes while viewing images.

- From the Archive Explorer, scan the bar code by pressing the Scan button on the Speech Mike.
  - If only one study is found, it will be loaded automatically.
  - If no studies are found, search for another Accession Number.
  - If multiple studies are found, select the desired study and press Enter to load it.

9.24 Burning Studies to a CD

The Diagnostic Workstation allows you to copy (burn) studies to a CD. This capability requires installation and configuration of the Vue PACS CD Direct Suite. Contact the system administrator for information about your site's capabilities or see the user documentation for the Vue PACS CD Direct Suite.

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NOTICE

If your Diagnostic Workstation is not set up to burn CDs, the Burn tool is inactive (grey and non-functional).

You also have the option to view DICOM DIR standard images on a local CD:

1. Insert the CD into the CD-ROM drive.
2. Navigate to the CD drive.
3. Open the CD.
   ⇨ All studies saved on the CD appear. You can work with these images in View Only mode.

NOTICE

When working with images on a local CD, the Copy and Burn tools are grayed out on the toolbar.

To view the studies burned on the CD, navigate to the required study in the Archive Explorer.

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10 PowerViewer Application Concept

10.1 New Viewer—PowerViewer

The PowerViewer application is the main viewing application for reading image data. You can easily change the rendition type and image parameters. The PowerViewer enhances the reading capabilities of a study, increases usability, and improves the quality of interpretation.

Reference Material	Instructions
PowerViewer Toolbar on page 72 Shortcut Keys on page 67 About the PowerViewer Application on page 151	Using the PowerViewer Application Window on page 152 Creating a PowerViewer View on page 152 Changing the Presentation (see Changing Presentation and Rendition Types on page 153) Saving Presentations in the PowerViewer Application on page 154 Changing Data on page 154 Synchronous Parameters on page 155 Using Shutter on page 156 Completing a Study on page 156 Working with Display Protocols on page 157

PowerViewer provides:

MPR Image Support on page 145

Automatic Registration on page 145

Advanced Comparison Tools on page 146

10.2 MPR Image Support

You can examine original slices and MPR volumetric images directly from the PowerViewer application. You can easily switch between:

- Viewer—default option for original groups.
- MPR, mipPR, and minPR—available for groups with volumetric data, such as CT, MR, and PET.

10.3 Automatic Registration

When the studies are registered, you can easily compare prior and current cases. You can register multiple CT and MR studies with any rendition type, thickness, or orientation.

Automatic registration allows you to:

- Match volume from two or more studies.

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- Map corresponding pixels.
- Obtain full three-dimensional matching.

Reference Material	Instructions
Registration Tools on page 579	Using Register Studies (Automatic Registration) on page 580
About Registration on page 577	Using Guided Registration on page 582
	Using Manual Registration on page 583
	Using Treat Studies As Registered (see Using Treat as Registered on page 584)
	Using Refine Registration on page 585
	Removing Registration on page 586
	Troubleshooting Failed or Unsatisfactory Registration on page 587
	About Automatic Links in Registered Studies on page 588
	Using Realign Link on page 589
	Unlinking Registered Studies on page 590

10.4 Advanced Comparison Tools

When you register current and prior cases, new tools allow you to correlate the relevant location or pathology across the studies.

These comparison tools include:

- Relate (see About Relate Mode on page 590)—Make all the registered studies display the same region simultaneously. The reference point shows on all groups with the same frame of reference (FOR).
- Auto-Reference Lines (see About Reference Lines on page 575)—Automatically set up all the reference lines on all groups with the same FOR and registration, according to the active group.
- Auto-Link (see About Links on page 563)—Automatically link registered groups or link groups sharing frame of reference (FOR).

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11 Enhanced Reading Flow

11.1 About Enhancements to the Reading Flow

The following functionalities have been enhanced:

- Key Images Group (see Key Images Group on page 147)
- Save Presentation (see Enhanced Save Presentation on page 147)
- Significant Series (see Significant Series Images on page 148)

11.2 Key Images Group

Display a new Key Images Group in the PowerViewer application, and link the images to your study. The group is available through:

- Patient Mini-Archive (PMA)
- Replace With dialog

The text annotation (KEY) tells you that the image is part of a Key Images Group.

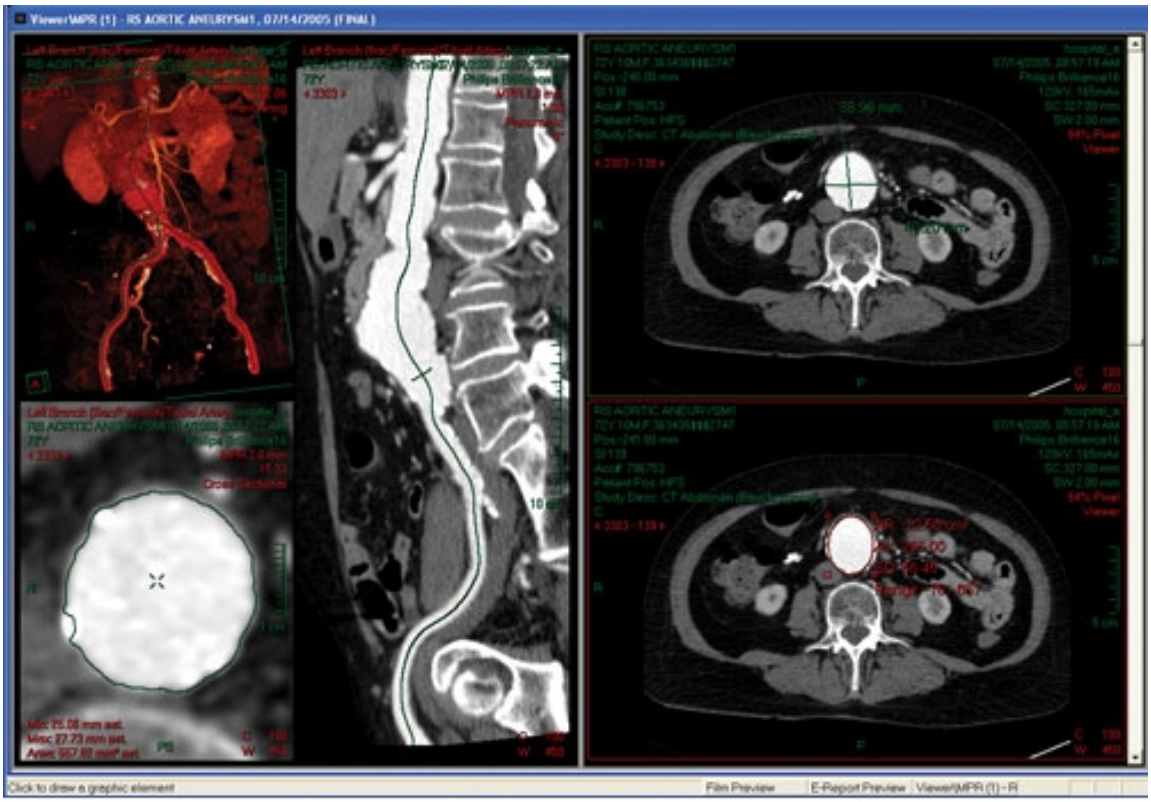


Reference Material	Instructions
About Key Images on page 531	Updating Key Images on page 534
Key Image Tools on page 533	Marking Key Images on page 535
E-Report Preview Toolbar on page 100	Previewing Key Images on page 536
	Scrolling Key Images on page 539
	Clearing Key Images on page 540
	Printing Key Images to Film on page 541

11.3 Enhanced Save Presentation

Save all of your unique information, such as vessel segmentations or 3-D manipulations, from any application. Continue reading the study at a future time from the same display that you saved.

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11.4 Significant Series Images

Significant Series allow you to “scan thin and read thick.” You can save certain series as Significant (SIG) and later read, distribute, or store only these series. You can save the whole series as Significant, or save only a sub-volume out of a series.

Reference Material	Instructions
About Significant Series (SIG) Images on page 516 Workflow for SIG Images on page 517	Marking SIG Images on page 518 Saving SIG Images on page 523 Unmarking SIG Images on page 525 Updating SIG Images on page 526 Loading SIG Images on page 526 Distributing SIG Images on page 529 Locating Studies with SIG Images on page 530 Troubleshooting SIG Images on page 530

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12 Vue Reporting

12.1 Vue Reporting for Vue PACS

The Diagnostic Workstation offers a native reporting solution. For a description see the Vue Reporting User Guide_en-US.

The Vue Reporting provides, among others, tools for improving speech recognition as well as a report comparison tool to review changes in report revisions.

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13 Applications

13.1 PowerViewer Application

13.1.1 About the PowerViewer Application

The PowerViewer application is the central viewbox tool for reading most types of image data. While working with a group in the PowerViewer application, you can change the rendition type and image parameters, and all the changes are retained in the PowerViewer application, even if you open another viewing application, such as the MPR application or 3D Data.

For viewing applications such as the MPR application or 3D Data, the tools integrate into the PowerViewer application toolbar.

When you use the PowerViewer application in the same graphic display application, the group is presented with the updated parameters, including Zoom, Pan and Windowing.

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IMPORTANT

If you change parameters after you open another application, for example in the 3D Analysis Application, and then you return to PowerViewer, the modified parameters are not transferred between applications.

The PowerViewer application allows you to enhance the reading capabilities of a study, improving ease of use as well as quality of interpretation. This is made possible by the following capabilities:

- MPR Image Support .

  You are able to present both original images (slices) and MPR-based (volumetric) images. You can examine the MPR data directly from the PowerViewer. You do not open a separate application to work with MPR images.
- Automatic Registration Capabilities.

  You can automatically register data sets and effectively compare two or more volumes spatially.

  For example, the system can automatically match an MR Head and a CT Head study, even if each image was scanned using different orientations and at different times.

  You are able to scroll and swivel the two registered data sets simultaneously.
- Relating Datasets.

  Using the PowerViewer you can easily localize and examine the same anatomical region within two different data sets. You can use this option for both original slices and MPR-based images.
- Reference Line Enhancements

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You can apply reference lines between different studies (current and prior). Reference lines are not limited to a series of the same study. Reference lines are available for both original slices and MPR images.

See these topics:

About Multi-Planar Reformatting (MPR) on page 159

About Registration on page 577

Correlating Regions of Interest in Registered Studies (Relate Mode-see About Relate Mode on page 590

About Reference Lines on page 575

Synchronous Parameters on page 155

13.1.2 Using the PowerViewer Application Window

After you load images from the Archive Explorer, the images appear in the Diagnostic Workstation PowerViewer application. You can:

- Manipulate and enhance images.
- Perform diagnosis.
- View images.

See these topics:

PowerViewer Toolbar on page 72

About the PowerViewer Application on page 151

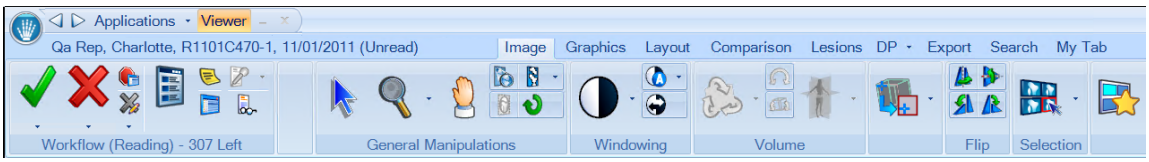
13.1.3 Creating a PowerViewer View

To create a PowerViewer View:	Do This:
From the Archive Explorer	Right-click each current study, select Load To > Viewer.
In the Viewer	Right-click an existing group, select View As, then select Viewer. Or From the Applications menu, select View As and then select Viewer.
From the Patient Mini-Archive	1. Right-click a study group, then drag it to a currently displayed display area. 2. Select Viewer.
To an open application	If the currently open application is PowerViewer, click the study group in the Patient Mini-Archive, then drag it to the display area. The selected group of images appears in the display area in the default PowerViewer view. The reference images and result images appear in the location and layout that was last used. **NOTICE! When you left-click an image in the Patient Mini-Archive and drag it to a display area, the image appears according to the type of application currently open.**

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13.1.4 About the PowerViewer Application Toolbar

The PowerViewer application toolbar comprises tabs, menus and ribbons, each offering tools to facilitate study reading.



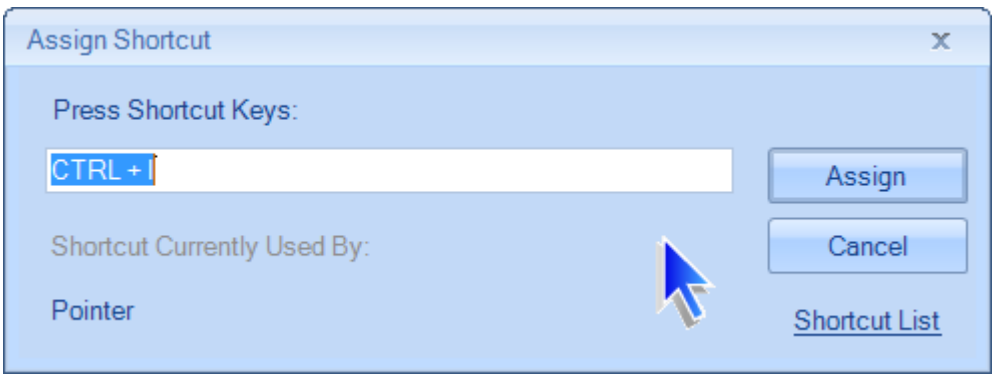
13.1.5 Shortcut Keys

The Diagnostic Workstation provides shortcut keys to many of the actions.

To see a list of the shortcut keys available by default, click Help at the top-right corner, and select Shortcut List.

You can assign your own shortcuts to all actions available via the toolbar icons.

1. To assign a shortcut key, right click the toolbar icon, and select Assign Shortcut or Customize --> Assign Shortcut.
2. Press the keys that are to serve as shortcuts, and click Assign.



13.1.6 Changing Presentation and Rendition Types

You can change the study, group, or data set presented in the PowerViewer application window using:

- Replace With function.
- Patient Mini Archive.

Changing Rendition Types

The rendition type of the selected series is determined according to the rendition type presented in the relevant window. If the window does not contain an image, then the data is presented as if loaded to the PowerViewer application. The same applies to a group that has been dragged or replaced.

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For example, the window presents an MPR type group. You change to a volumetric group (by dragging and dropping the group from the Patient Mini Archive, or by using the Replace With function). The new group is presented in the MPR type.

If you change to a non-volumetric group (CR, DR, localizer), the group is presented as if it is loaded to the PowerViewer application, regardless of the rendition type previously presented.

See these topics:

Viewing Information in the Patient Mini-Archive on page 487

Dragging Groups to a Viewbox (see Dragging Groups to a Group Display Area on page 489)

Changing Data on page 154

13.1.7 Saving Presentations in the PowerViewer Application

The following parameters are saved when using the Save Presentation feature in the PowerViewer application.

- The exact datasets presented in each window
- The exact layout
- All MPR parameters (rendition type)
- Zoom/Pan
- Windowing
- Enhance
- Color Map
- Reference Point
- Reference Lines
- Auto Link

See these topics:

Saving a Study as a Presentation on page 620

Working with Presentations (see About Save Presentation on page 619)

13.1.8 Changing Data

You can change the data presented in the PowerViewer application window or viewbox using the **Replace With** function.

1. Load a study into the PowerViewer application.
2. Hover with the mouse over the Replace With annotation . The cursor changes to a wide right or left arrow.
3. Click to display the previous/next image in the series.
4. To open a list of series and studies, right-click the annotation.
5. Select the desired series, group, or data set from the Replace With list.

See these topics:

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Changing Presentation and Rendition Types

Loading Studies on page 488

Using the Automatic Link Tool on page 569

13.1.9 Synchronous Parameters

The PowerViewer application provides, by default, synchronization of zoom and pan parameters between linked groups.

Zoom and Pan parameters are synchronized in an absolute manner (based on mm-per-pixel information).

NOTICE

In scenarios where the Zoom/Pan operation was performed on an image with mm-per-pixel information, but there are images in the linked groups that do not include mm-per-pixel information, then for these images only, the synchronization is incremental and not absolute.

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NOTICE

The result of the Pan operation will display the same ROI in each window.

NOTICE

Zoom and Pan parameters are synchronized automatically across groups that are linked to one another. These groups can be linked either automatically, using the Link Tool or by the right-drag-link.

NOTICE

You can deactivate the automatic synchronization of the Zoom and Pan in PowerViewer with a specific CFG flag.

IMPORTANT

Contact your System Administrator or Philips Support for further details.

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The default for the above definitions is Group Selection Mode. When you switch to a different selection mode such as Image or All or when the user specifically selects groups using the CTRL + Click mode, then the behavior of the system should comply with these modes and not with the above definitions.

Image Selection Mode

Changing the zoom and pan parameters of one image does not affect any other image either in the same group or across groups.

All Selection Mode

Changing the zoom and pan parameters on one image does affect all other images both in the same group and across groups.

CTRL + Selection Mode

Pressing and holding the CTRL key while selecting several groups, changes the zoom and pan parameters of one image (of the selected group) and affects all other images from the selected groups, regardless if they are linked or not, and should not affect any image not belonging to the selected groups.

13.1.10 Using Shutter

When an image is loaded, it is automatically configured to activate the Shutter option. The Shutter option lets you toggle DICOM-defined shutter areas on and off on selected images.

- Click Shutter  to activate or deactivate the shutter option.

NOTICE

If you are saving an image with the Shutter option, the image will be saved according to the state of the icon (activated or deactivated) at the time of the save.

The area removed by the Shutter option is not affected by the Magnifying Glass option.

13.1.11 Completing a Study

The Diagnostic Workstation supports an automatic workflow configuration in which every study is assigned a status within the system. When you have finished reading the image data, you can proceed in various ways.

► From the PowerViewer application toolbar, click Done .

► Select one of the options in your Workflow dialog box.

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NOTICE

Worklist configuration is dependent upon the workflow of each facility. Contact the system administrator.

See this topic:

About Image Access and Management on page 131

13.1.12 Working with Display Protocols

A Display Protocol lets you customize the display of studies within the PowerViewer application. Display Protocols are user specific. You can build a personal Display Protocol bank that stores all relevant Display Protocols for your viewing. Any time you load a study, it will load according to the Display Protocol that best fits the study parameters.

Use the Display Protocol editor to define Display Protocols. For more information, view the topics listed under Display Protocols (see About Display Protocols on page 594) and Working with Presentations (see About Save Presentation on page 619).

NOTICE

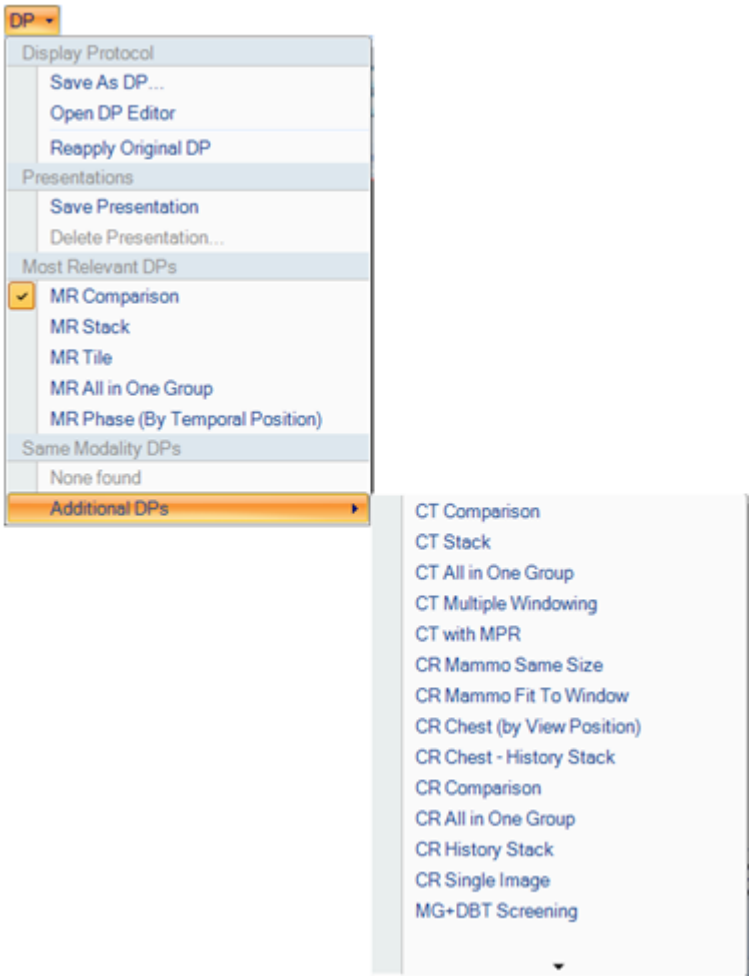
For information about configuring Display Protocols, consult the system administrator or a Philips representative.

To select a different Display Protocol:

From the Viewer toolbar, click DP, then select the display protocol you want to use to display the loaded images.

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Display Protocols that have the same conditions as the current one appear in the Display Protocol menu. All remaining Display Protocols appear in the Additional DPs drop-down menu.

See these topics:

About Display Protocols on page 594

Saving a Study as a Presentation on page 620

13.1.13 Linking MPR Groups

You can create links for Multi-Planar Reformatting (MPR) groups using:

Automatic Link 	Using the Automatic Link Tool (see Using the Vue PACS Viewer on page 477) Linking Groups Automatically on page 570
Link 	Using the Link Tool on page 565 Linking Groups Manually on page 566)
Drag and drop	Linking Groups Manually on page 566)

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When the MPR groups are linked, you can swivel and scroll the images in the group synchronously.

When an MPR group is linked to a PowerViewer group and then you swivel the MPR-based group, the link between these groups is not applied. However, the reference point remains synchronous. If you swivel the MPR group to the original orientation, you also adjust the link so that you can scroll the images in the groups simultaneously.

NOTICE

A reference point (see Working with Reference Points (MPR Images) on page 593) refers to the 'center of swivel' point, which is displayed on MPR groups.

See these topics:

About Links on page 563

Unlinking Groups on page 574

Working with Reference Points (MPR Images) on page 593

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13.2 Multi-Planar Reformatting (MPR) Application

13.2.1 About Multi-Planar Reformatting (MPR)

Multi-Planar Reformatting (MPR) lets you reconstruct data in straight or curved cross-section planes inclined to the original slices. MPR provides better visualization of organs and tissues and the relationship between them.

NOTICE

The MPR application is available only if your profile has a license to use it.

MPR data displays in viewboxes in the MPR view. The basic MPR view is divided into two main parts and displays reference images and result images.

MPR View Type	Description
Reference images	Display as Axial, Sagittal, and Coronal views.
Result images	Display as the reconstructed cross-section images resulting from cutting volumes in a certain plane. You can configure the number of result images that display.

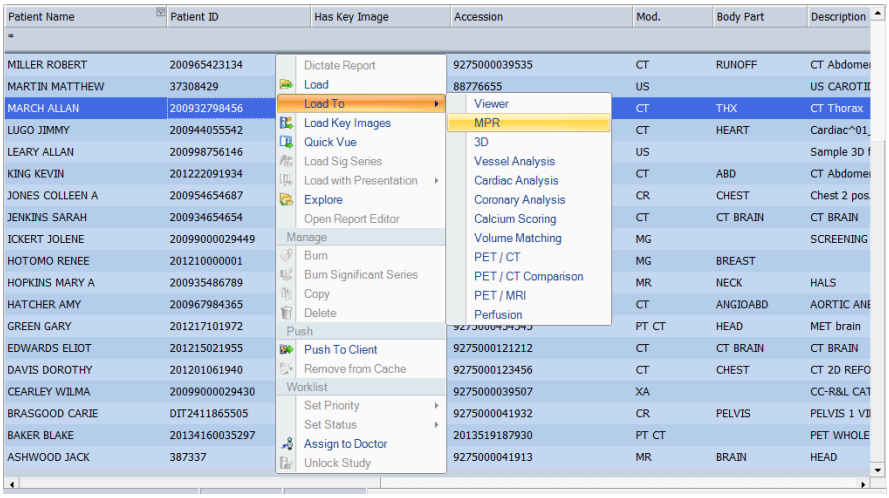
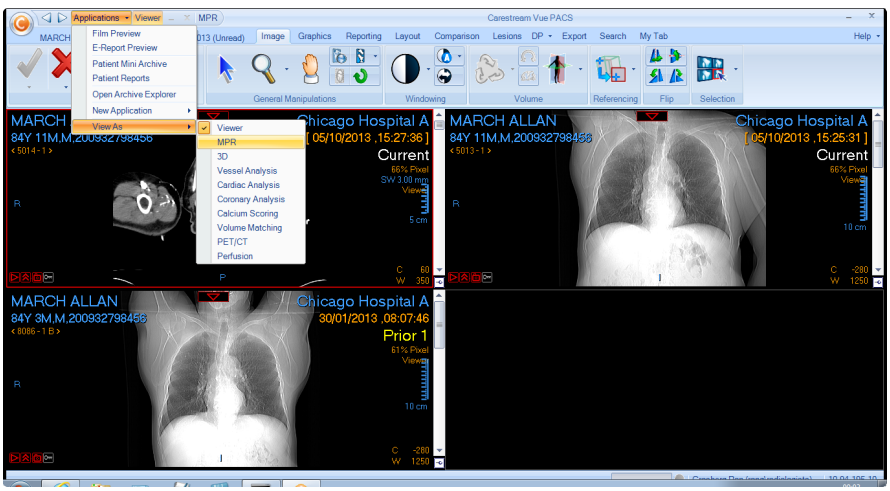
See these topics:

MPR Application Toolbar on page 85

Creating an MPR View on page 160
Viewing an MPR Image on page 163

13.2.2 Creating an MPR View

You can create an MPR view manually, as described in this section. For information about automatically creating an MPR view, view the topics listed under Display Protocols (see About Display Protocols on page 594).

To create an MPR View:	Do this:
From the Archive Explorer	Right-click a study group, select Load To, then select MPR. 
In the PowerViewer	• Right-click an existing group, select View As, then select MPR. Or • From the Applications menu, select View As and then select MPR from the drop-down menu. 

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From the Patient Mini Archive	► Right-click a study group, then drag it to the display area. ► Select MPR.
To an open application	If the currently open application is MPR, click the study group in the Patient mini archive, then drag it to the display area. The selected group of images appears in the application. The reference images and result images appear in the location and layout that was last used.

13.2.3 MPR Application Toolbar

The following tab is added to the toolbar when you open the MPR application.

Icon	Description
Volume	
	Swivel the image.
	Roll the image from side to side around the center of the volume.
	Roll the image to the closest axial, sagittal or coronal plane.
	Click a point of interest to locate the matching point in other registered groups for the same or prior study (see About Relate Mode on page 590).
Application Layout	
	Duplicate a group of result images to manipulate them individually.  None: Duplicates the group.  Vertical: Duplicates the group and displays the duplicate group adjacent to the original group.  Horizontal: Duplicates the group and displays the duplicate group under the original group.

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	Select group layout: • MPR standard Layout (default). Display one result image and reference images showing the scanned volume in axial, sagittal and coronal views with default and additional cross-section lines. In this layout you can select one image, two images, 2x2 images, 2x3 images, or user defined number of images for the result display area. • MPR 2x2 layout. • MPR double oblique layout. Allows you to view the data in a 2x2 layout by retaining a perpendicular relationship between the planes. Press Shift to turn the perpendicular and horizontal cross section lines in the reference images to obliques. You can also apply: • Single-phase mode. • Multi-phase mode.
Rendition Method	
	MPR (average MipPR) - Render the MPR slab using the average pixel value.
	MIP (maximum intensity projection) - Render the MPR slab using the maximum pixel value.
	MinPR (minimum intensity projection)- Render the MPR slab using the minimum pixel value.
	Control rendering parameters. Select rendition type, slice thickness and slice spacing.
Direction	
	Reformat plane and curve: • Axial/Sagittal/Coronal: Lets you define the planar view, or orientation, of the image. • Parallel/Concentric/Sectional/Sectional parallel: Lets you draw and manipulate curved cross-sections on the reference images, as follows: – Parallel: Curved cross-sections that are parallel to one another. – Concentric: Curved cross-sections that decrease in size towards the same central mid-point. – Sectional: Cross-sectional slices that are perpendicular (90°) to a defined curved cross-section. – Sectional Parallel: Parallel cross-sectional slices on a defined curved cross-section.

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13.2.4 Workflow for MPR Images

MPR Image Workflow	Related Topics
1. Create an MPR view.	Creating an MPR View on page 160
2. Change the MPR rendition type.	Changing the MPR Rendition on page 164
3. Change the planar view/orientation.	Changing the Orientation/Planar View on page 166
4. Apply measurements or annotations.	Applying Measurements to MPR Images on page 168 About Annotations and Measurements on page 499
5. Manipulate the images.	About Images on page 495
6. Define MPR parameters.	Defining MPR Parameters on page 614 Changing the Slice Thickness and Spacing on page 170 MPR Application Toolbar on page 85
7. Save, film, or print MPR images.	Saving MPR Images on page 182 Saving Viewing Options as a Display Protocol on page 595 Using Save as DP on page 621 Filming and Printing MPR Images on page 182

13.2.5 Viewing an MPR Image

The MPR view displays in the Viewer window. The viewbox of the MPR view is divided into reference images and result images.

Reference Images

Reference images show the scanned volume in the axial, sagittal, and coronal views. Each reference image contains the following:

- Default MPR Cross-Sections: Each set of crossed horizontal and vertical cross-section lines correlate to the common orientation point in the other two reference images for the currently displayed cross-section slices in the result images. You can manipulate these cross-sections to show different cross-section slices.
- MPR Cross-Sections: These additional cross-sections correspond directly to the data that appears in the result images, depending on the selected layout, as follows:
  - If only one result image displays, only the one relevant cross-section appears in the relevant reference images.
  - If four or more result images display, only the first, active, middle, and last cross-sections appear on the reference images.
  - These cross-sections can be moved or rotated simultaneously to show different cross-section and curved cross-section slices of data in the result images.

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Result Images

Result images show the reconstructed MPR cross-sections that result from cutting volumes in certain planes on the reference images. Result images correspond directly to the cross-sections on the reference images. The number of result images depends on the layout you select.

IMPORTANT

The MPR Double Oblique layout provides specific capabilities for working with result images and reference images. See About the MPR Double Oblique Layout on page 174.

13.2.6 Changing the MPR Rendition

The Viewer rendition is the default.

To change the rendition do the following:

1. Right-click the image and select Change Image to open the drop-down menu.

   Or

   Click on the MPR annotation 

on he right side of the image display area.
2. Select the desired rendition. The renditions include:
   - Viewer (default)
   - MPR
   - MipPR
   - MinPR
   - MPR Parameters

IMPORTANT

MPR, MipPR, and MinPR are available only for groups with volumetric data (CT, MR, PET). Viewer is the default option for all other groups, such as CR, DR, Key Images, and All-in-One.

When you change from Viewer to an MPR rendition (MPR, MipPR, or MinPR), the toolbars update to include the appropriate tools for the rendition.

Tools for Viewer Only	Tools for MPR Renditions Only	Tools for Viewer and MPR Renditions

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• Flip • Rotate **See this topic:** PowerViewer Toolbar on page 72	• Swivel • Roll **See this topic:** MPR Application Toolbar on page 85	• Zoom • Windowing • Pan • Image planar view/ orientation (axial, coronal, or sagittal) **See this topic:** About Images on page 495

The MPR rendition type is set per a specific window, even if the same group is displayed in more than one window. You can view the same group as two rendition types or two windowing levels.

See this topic:

Enabling Dual Windowing on page 181

13.2.7 Using the Orientation Box (Planar Views)

The Orientation Box is located the bottom left-hand corner of an MPR group.

IMPORTANT

You must change the rendition type from Viewer to an MPR rendition to access the Orientation Box.

The Orientation Box shows the position of the slab with respect to the entire volume.

The box represents the entire volume, and the dynamic plane inside represents the position and orientation of the slab.

Right-click on the Orientation Box to select orientations/planar views or to reset the patient axes.

Axial 

Coronal 

Sagital 

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13.2.8 Changing the Orientation/Planar View

NOTICE

The term planar view is synonymous with orientation.

IMPORTANT

The MPR Double Oblique layout provides specific capabilities for working with result images and reference images. See Using MPR Double Oblique (Cardiac and MPR).

You can change the MPR image to any one of the following orientations/planar views:

Axial 

Coronal 

Sagital 

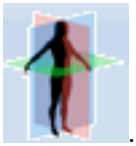
Preparation

1. Load the original MR images to the default Viewer.
2. Change the rendition to an MPR type rendition by doing any of the following:
   - Right-click the Viewer annotation at the right of the image and select the desired rendition:



   - In the toolbar, select the rendition from the Select Image Rendition drop-down.

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- Right-click the Viewer annotation at the right of the image and select the desired rendition .
- Right-click in the image and select the rendition type from the Change Image option.

NOTICE

You can also load the MPR application. See Creating an MPR View on page 160.

To change the orientation/planar view, do one of the following:

Changing the Orientation/Planar View

1. Right-click the Orientation Box .
2. Select Axial, Coronal, or Sagittal.

Or:

► Click Swivel .

► Click on the image and hold the left mouse button as you move the cursor around the screen. The change to the orientation/planar view is shown in the image and in the Orientation Box.

To reset the view:

1. Select Axial, Coronal or Sagittal from the Swivel drop-down menu .

To return to the original view:

► Right-click the Orientation Box .

► Select Reset to Patient Axes.

NOTICE

If you change the rendition from MPR/MipPR/MinPR to Viewer, the slices retain the original orientation/planar view.

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13.2.9 Applying Measurements to MPR Images

1. Load the original MR images to the default Viewer.
2. Change to an MPR rendition.
3. In the Graphics toolbar tab, select the appropriate tool from the Measurements tab.

IMPORTANT

Measurements made in one planar view will not be visible in a different planar view.

If you place a line measurement on slice position X of one planar view, you can scroll through the planar view and the line measurement will display each time you reach the slice position X.

Measurement values are contained in the specific planar view. For example, the measurements marked in the coronal view are not visible in the axial or sagittal views. To see measurements made in the coronal planar view, you must return to the coronal planar view.

When you change the MPR renditions, the measurements are always visible. For example, you apply measurements to images from the MPR rendition. If you change the rendition from MPR to Viewer and then to MinPR, the measurements you made on the MPR images are also visible on the MinPR images.

See this topic:

About Annotations and Measurements on page 499

13.2.10 Working with Cross-Sections

Working with Cross-Sections

Each reference image contains a pair of default MPR cross-section lines (one vertical and one horizontal). You can move these lines individually to show different cross-sections in axial, sagittal, and coronal views. For example, if you move a default MPR cross-section line from side to side, the changing sagittal images appear.

When there are multiple images in one group, four additional cross-section lines appear on the reference images. The four cross-sections represent the following cross-section slices:

- First
- Currently active
- Middle
- Last

You can move or rotate a cross-section to a different angle to change the data shown in the result images. You can also change the cross-section slice thickness and spacing.

See these topics:

Moving a Cross-Section on page 169

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Rotating a Cross-Section on page 169
Changing the Slice Thickness and Spacing on page 170
Viewing Result Images in MipPR Mode on page 171
Viewing Result Images in MinPR Mode on page 171

Moving a Cross-Section

When you move a cross-section on a reference image, the relevant cross-section slices automatically update in the result images. You can also manipulate the result image directly to show the different cross-sections of the image. The result image displays a reference point that serves as the center point for the cross-section manipulations.

To manipulate the result image:

1. From the MPR toolbar, click Swivel .
2. Select the result image.
3. Drag the mouse to create a new cross-section.
   - When in Swivel mode, click Shift to activate the Relate mode.
   - When in Relate mode, click Shift to activate the Swivel mode.

To change the reference point:

- Select the reference point of the result image and drag it.

Or

- From the toolbar, click Relate , then click the image where you want to move the reference point.
  - When in Swivel mode, click Shift to activate the Relate mode.
  - When in Relate mode, click Shift to activate the Swivel mode.

To move a cross-section manually:

1. In the reference image, click a vertical or horizontal MPR cross-section.
2. Drag the cross-section to a different location (up and down or left and right).

To move a cross-section dynamically:

Right-click on a result image and move the cursor up and down.

Rotating a Cross-Section

To display an angle of the volume, you can swivel a cross-section (other than the default cross-sections) on one or more of the reference images.

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NOTICE

You can view multiple slices in the result images depending on the selected result view layout. However, only four MPR cross-sections display on the reference images (first, currently active, middle, and last).

1. In the appropriate reference image, click the end of a cross-section.
2. Move the mouse left or right to rotate the cross-section to the angle you want.
   ⇨ All cross-sections move simultaneously and the resulting cross-section slices display in the result images.

Changing the Slice Thickness and Spacing

You can change the width and spacing of the cross-section slices on the result images. When you change the slice spacing, the change appears in the result images and in the cross-sections on the reference images.

To change the slice thickness and spacing manually:

1. From the MPR toolbar, click MPR Options .
2. Select Parameters from the drop-down menu.
   ⇨ The MPR Parameters dialog box appears.
3. Choose the rendition type.
4. Click the arrows to select the thickness for each of the rendition types.
5. To save the thickness of the MipPR and MinPR rendition types as defaults, select the Save these values as defaults check box.
6. In the Spacing field, click the arrows to select the value for the spacing.
7. Click OK.
   ⇨ The calculation in the SW (Slice Width) annotation for each image changes to reflect the current slice thickness.
   ⇨ The change appears in the result images and the cross-sections on the reference images.

To change the slice thickness dynamically:

1. On the result image, place the cursor over the SW (Slice Width) annotation.
   ⇨ The cursor changes to a box with the word Thick.
2. Click and drag the cursor up or down to increase or decrease the slice thickness.
   ⇨ The calculation in the SW (Slice Width) annotation for each image changes to reflect the current slice thickness.

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To change the slice spacing dynamically:

1. On any of the reference images, click on the edge of a cross-section line and hold down the Shift key.
2. Click and drag the cursor up or down to increase or decrease the spacing of the slices.
   ⇨ The change appears in the result images and the cross-sections on the reference images.

NOTICE

You can adjust the line spacing by dragging the cross-section line to the required position with the mouse. This is relevant for increasing and decreasing and also for rotating the cross-section line.

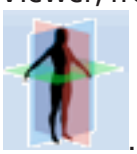
Viewing Result Images in MipPR Mode

You can view slabs of data in a MIP viewing mode, which is used, amongst others, for blood vessels pulmonary nodules etc.

1. Set the result images to show the anatomy you want.
2. Right-click the image and select Change Image.

   Or

   Click the MPR annotation at the right of the image display area.

   Or, in PowerViewer, from the toolbar click the Change Image Renditions drop-down menu .
3. Select MipPR from the drop-down menu.
   ⇨ The result image view changes from a regular MPR view to a MIP view. Also, the slab thickness and spacing changes. The dynamic annotation of slab thickness shows the thickness of the slab, as well as the rendition type being used. For example, a 10 mm annotation will show MipPR 10.0 mm.
   ⇨ You can edit the MipPR slab thickness and spacing in the same manner as regular MPR images. See Changing the Slice Thickness and Spacing on page 170.
4. To return to regular MPR view, select MPVR from the drop-down menu.

Viewing Result Images in MinPR Mode

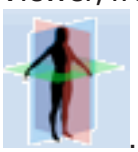
You can view slabs of data in a MIN viewing mode, which is used mainly for airways.

1. Set the result images to show the anatomy you want.
2. Right-click the image and select Change Image.

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Or

Click the MPR annotation at the right of the image display area.

Or, in PowerViewer, from the toolbar click the Change Image Renditions drop-down menu .

3. Select MinPR from the drop-down menu.
   ⇨ The result image view changes from a regular MPR view to a MIN view. Also, the slab thickness and spacing changes. The dynamic annotation of slab thickness shows the thickness of the slab, as well as the rendition type being used. For example, a 10 mm annotation will show MinPR 10.0 mm.
   ⇨ You can edit the MinPR slab thickness and spacing in the same manner as regular MPR images. See Changing the Slice Thickness and Spacing on page 170.
4. To return to regular MPR view, select MPVR from the drop-down menu.

13.2.11 Working with Curved Cross-Sections

Working with Curved Cross-Sections

The MPR view lets you draw and manipulate curved cross-sections on the reference images. The resulting cross-section slices appear in the result images.

You can use the following types of curved cross-sections in an MPR view:

- Parallel: Curved cross-sections that are parallel to one another.
- Concentric: Curved cross-sections that decrease in size towards the same central mid-point.
- Sectional: Cross-sectional slices that are perpendicular (90°) to a defined curved cross-section.
- Sectional Parallel: Parallel cross-sectional slices on a defined curved cross-section.

NOTICE

You can move and rotate curved cross-sections the same way you move and rotate regular cross-sections. You can also change their slice thickness and spacing. See Working with Cross-Sections on page 168.

See these topics:

Creating a Curved Cross-Section on page 173

Changing a Curved Cross-Section on page 173

Moving a Curved Cross-Section on page 173

Changing the Curved Cross-Section Type on page 174

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Deleting a Curved Cross-Section on page 174

Creating a Curved Cross-Section

You can draw a curved cross-section for a specific region of interest on a result image.

You can change the spacing by right-clicking and moving the mouse. There are also sensitive squares on the result lines that you can detect with the mouse that let you change the spacing.

1. From the MPR toolbar, click Plane Reformatting .
2. Select an option.
3. On the reference image, click the location for the starting point of the curved cross-section.
   ⇨ A vertex (handle) appears where you click.
4. Click additional points to draw the curve.
   ⇨ You can remove the last point you created by using the Backspace key.
5. Double-click the last point to finish drawing the curved cross-section.

Changing a Curved Cross-Section

1. Click an existing vertex (handle).
2. Drag the vertex to the location you want.
   ⇨ The curved cross-section displays with the change you made.
3. To add a new vertex, click the curved cross-section. then press Shift.
4. Drag the new vertex to the new location to modify the curved cross-section.
5. To delete an existing vertex, click the vertex, then press Delete.

Moving a Curved Cross-Section

You can move a curved cross-section to another location on an image without affecting the shape of the original curved cross-section.

- Click the curved cross-section, then drag it to the desired location on the image.

Moving Cross-Sectional Slices

You can move the location of the cross-sectional slices along the defined curved cross-section to display different data in the result images.

- Click one of the cross-sectional slices, then move the slices along the curve (all cross-sectional slices move simultaneously).

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NOTICE

Scrolling beyond the edge of the defined curve causes the result images in the viewbox to become blank.

Changing the Curved Cross-Section Type

After you draw a curved cross-section, you can change between four types: Parallel, Concentric, Sectional, or Sectional Parallel.

1. From the toolbar, click Plane Reformatting .
2. Select a curved cross-section type.

Deleting a Curved Cross-Section

You can delete a curved cross-section by either deleting it from the image or by changing to a different result image view that does not contain a curved cross-section.

1. Click the curved cross-section on the reference image.
2. Click Delete.

Switching to a Different Result Image View

See Selecting/Changing the Result Image on page 180.

13.2.12 Using MPR Double Oblique (Cardiac and MPR)

About the MPR Double Oblique Layout

MPR Double Oblique layout allows you to view one volumetric dataset in several oblique (usually perpendicular) planes. You can swivel the reformatted planes to any orientation synchronously. MPR Double Oblique layout retains the perpendicular relationship between the planes.

MPR Double Oblique layout is appropriate to use in the Cardiac and the MPR applications.

Reset Reference Images is a new option available in the MPR menu for the MPR application. Reset Reference Images allows you to reset the images to the original axial/sagittal/coronal views.

NOTICE

Double Oblique View refers to three perpendicular views. In many reading scenarios, the three oblique views are the main images, called reference images.

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See these topics:

Understanding the MPR Double Oblique Layout Capabilities on page 175

Using the MPR Double Oblique Layout on page 177

Applying Phase Modes to the MPR Double Oblique Layout on page 179

Toggling Group Layouts (MPR) on page 180

Understanding the MPR Double Oblique Layout Capabilities

When you select the MPR Double Oblique layout, you can use the capabilities explained here.

Resetting Reference Images

After you manipulate an image, you can reset the reference images.

In the toolbar menu, click MPR --> Reset Reference Images.

The selection resets the orientation of each axes. The reference point, however, remains unchanged.

IMPORTANT

The Reset Reference Images option is only available in the MPR Double Oblique layout.

Resetting Result Images

You can reset the orientation of the Result Image.

MPR	In the toolbar menu, click MPR --> Axial / Coronal / or Sagittal.
Cardiac CT	In the toolbar menu, click MPR --> Reset Heart Axis.

Resetting the result image does not change the axis or the orientation of none of the reference images. The only change in the reference windows is the position of the reference line.

Resetting the Patient Orientation (Result Images, MPR or Cardiac Analysis)

In the MPR and Cardiac CT applications, you can reset the patient orientation for the result image in the MPR Double Oblique layout. The other two images automatically reset. There are three possible combinations.

Combination 1

Result Image	Axial
Coronal	Sagittal

Combination 2

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Result Image	Coronal
Sagittal	Axial

Combination 3

Result Image	Sagittal
Axial	Coronal

Example

If you reset the top-right window to show the axial orientation, then the bottom-left window shows the coronal orientation and the bottom-right window shows the sagittal orientation.

Result Image	**Axial**
Coronal	Sagittal

If you reset the bottom-right window to show the sagittal orientation, then the top-right window shows the axial orientation and the bottom-left window shows the coronal orientation.

Result Image	Axial
Coronal	**Sagittal**

IMPORTANT

Resetting the result image does not change the axis or the orientation of the reference images. Resetting the result image only changes the position of the reference line in the Reference windows.

Resetting the Heart Axes (Reference Images, Cardiac Analysis Only)

In the Cardiac CT application, you can reset the heart axes of the reference image. The heart axes include short, long, and four chambers. When you reset one of the images to a specific heart axes, the other images reset to the relevant perpendicular views. There are three possible combinations.

Combination 1

Result Image	Short
Long	Four Chamber

Combination 2

Result Image	Long
Four Chamber	Short

Combination 3

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Result Image	Four Chamber
Short	Long

You can change the orientation of the axes.

1. Use the mouse to select an axes on one of the reference views.
2. Press Shift on the keyboard and drag the axes.

The perpendicular axis appearing in the same window rotates, keeping 90° between the two axes. The third perpendicular axis (not seen in the window) and the image shown in the window do not change. Changing the orientation of the axes does not affect the result image.

Manipulating Images

In the MPR Double Oblique layout, you can pan, scroll, swivel, roll and automatic roll all three reference views. You can apply windowing, measurements, and rendering (MipPR or MinPR).

Exceptions

Dual windowing is not available in MPR Double Oblique layout.

The MPR Double Oblique capabilities are only available when the MPR Double Oblique layout is active. If you apply another layout, the MPR Double Oblique capabilities are not available.

Synchronizing Views

All image parameters are synchronized in the MPR Double Oblique layout.

Example

If you apply windowing to the reference image or result image, the windowing is automatically applied to the other three images. Scrolling one of the four images causes the other three images to scroll, according to the new position of the reference point.

When you swivel one of the reference images, the other two reference images swivel and retain a perpendicular relationship between the images. The result image orientation does not change as a result of swiveling a reference image.

IMPORTANT

When you swivel the result image, the reference images are not synchronized.

See this topic:

About Images on page 495

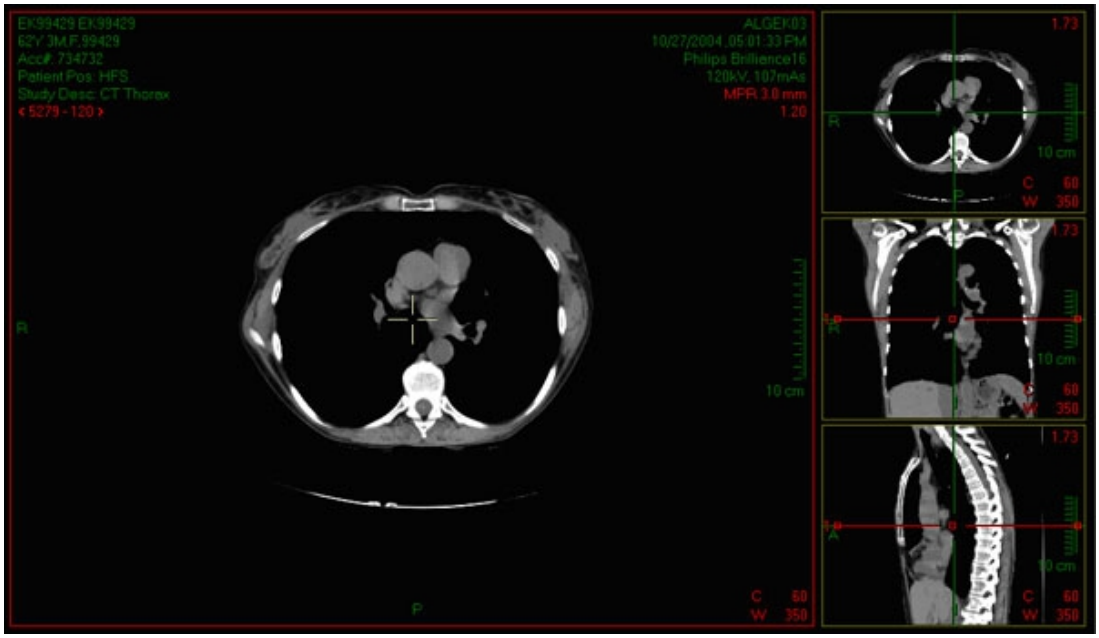
Using the MPR Double Oblique Layout

The MPR Double Oblique layout is available in Cardiac CT and MPR.

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1. Load a study to MPR or Cardiac CT.
2. The study is presented in the default layout. The result image is in the left pane and the axial, sagittal, and coronal reference images appear in the right panes.

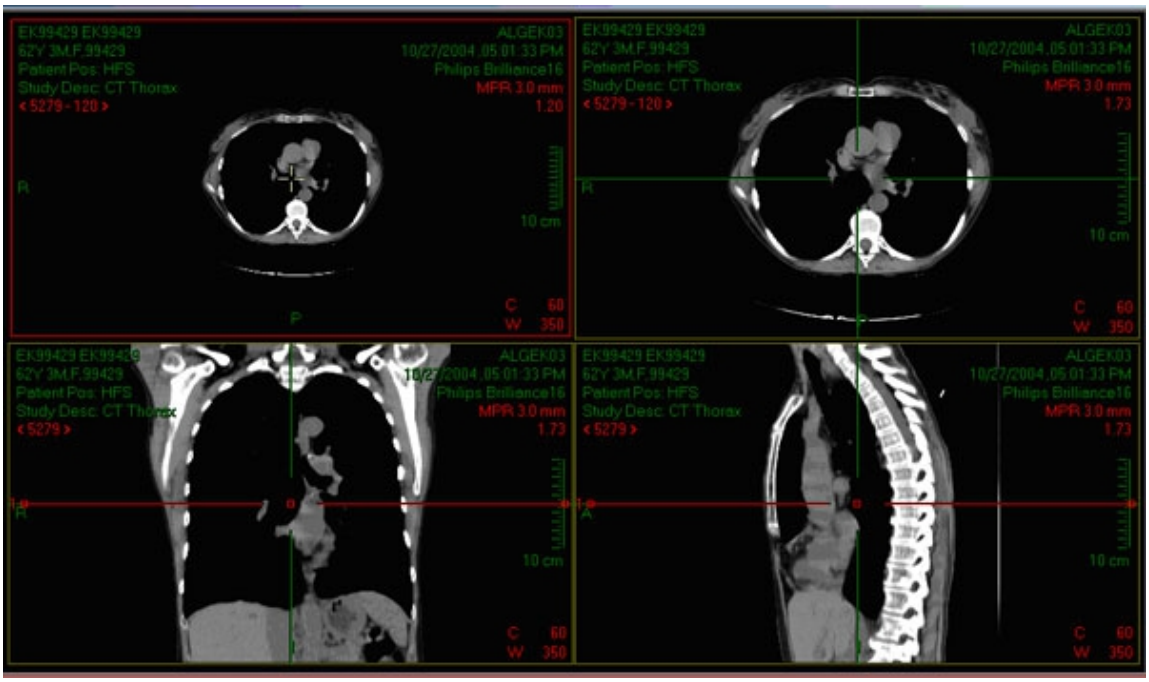


3. In the toolbar menu, click Determine Group Layout  --> MPR Double Oblique.
   ⇨ The view changes to a 2x2 double oblique layout: axial (right top), sagittal (right bottom) and coronal (left bottom).

NOTICE

There are several ways to access the Group Layout (see Configuring a Group Layout on page 561) menu, which contains the MPR Double Oblique layout.

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NOTICE

To change the position of the reference images, select and drag the desired image to a different position.

See this topic:

About the MPR Double Oblique Layout on page 174

Understanding the MPR Double Oblique Layout Capabilities on page 175

Applying Phase Modes to the MPR Double Oblique Layout

The MPR Double Oblique layout is available in Cardiac CT and MPR.

If the study includes phase data, you can apply one of two phase modes to the MPR Double Oblique layout. The two options are:

- Viewing Images in Single Phase Mode on page 245
- Viewing Images in Multi-Phase Mode on page 246

General Step	Reference Topic
1. Load a study containing study phase data to MPR or Cardiac CT.	Creating a Cardiac CT View on page 239 Creating an MPR View on page 160
2. Apply the MPR Double Oblique layout.	Configuring a Group Layout on page 561 Using the MPR Double Oblique Layout on page 177

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3. The phase modes are listed below the MPR Double Oblique layout option. Select Multi-Phase Mode or Single-Phase Mode.	Working with Phases in Cardiac CT on page 244 Viewing Images in Single Phase Mode on page 245 Viewing Images in Multi-Phase Mode on page 246

If you:

- Apply Multi-Phase Mode, the layout changes automatically to Standard MPR Layout.
- Select the MPR Double Oblique layout while in Multi-Phase Mode, the application automatically changes to Single-Phase Mode and restricts the Multi-Phase Mode.

See this topic:

About the MPR Double Oblique Layout on page 174

Toggling Group Layouts (MPR)

When you change the MPR Group Layouts, such as changing from MPR Double Oblique to Standard MPR Layout or 2x2 MPR Layout, you can expect the following behavior:

- The same study or dataset is shown in the selected layout. If you apply one of the phase modes, the phase is shown in the layout you selected.
- The orientation is reset for the reference image and the axes.
- The image parameters, such as zoom, windowing, and MPR parameters, stay the same for the reference images.

To Toggle MPR Group Layouts

Click Determine Group Layout  and select:

- Standard MPR Layout
- 2x2 MPR Layout
- MPR Double Oblique View (see About the MPR Double Oblique Layout on page 174)
- User-defined Layout

See this topic:

Viewing Cardiac CT Images on page 243

Configuring a Group Layout on page 561

13.2.13 Selecting/Changing the Result Image

You can set the initial default result image view or change the existing default to the Axial, Sagittal, or Coronal view. When you change the result image view, the new view appears the next time you create an MPR view.

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To select/change the result image:

1. In the viewbox, right-click the upper left corner of the reference image.
2. Drag the image to the center of the viewbox.
   ⇨ The pointer icon changes according to the orientation (axial, coronal, or sagittal) of the reference image you selected.
3. Release the mouse button to display the selected view.

To select/change the result image view:

1. From the toolbar, click MPR Options .
2. Select the view you want (Axial, Coronal, or Sagittal).
3. Right-click the top left corner of the reference image.
4. Drag the image to the center of the viewbox.
5. Right-click, then select the option you want (Axial, Coronal, or Sagittal).

To view in MPR and choose a 2x2 layout:

1. From the View > Group Layout drop-down menu, select MPR 2x2 Layout.
2. To return to the original layout, select MPR Standard Layout.

13.2.14 Enabling Dual Windowing

Dual windowing in MPR view lets you duplicate a group of result images. Dual windowing lets you manipulate the original group and the duplicated group independently with different values, such as zooming, panning, and performing window level changes. Dual windowing options are:

-  **None**: The images return to the original result image view.
-  **Horizontal**: The original images display horizontally, and the duplicate images appear below.
-  **Vertical**: The original images display vertically, and the duplicate images appear on the side.

1. From the PowerViewer toolbar, click Dual Windowing .
2. Select an option.
   ⇨ You can set different values for the duplicated images, such as different windowing or zoom values.

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13.2.15 Moving a Reference Image

In the MPR view, you can display reference images at the top, bottom, left, or right of the screen.

1. Right-click the top left corner of a reference image.
2. Drag the image to the location you want.

13.2.16 Filming and Printing MPR Images

Filming MPR images consists of setting parameters and exporting the series of MPR images and then viewing and printing the images from Film Preview.

To film MPR images:

1. From the toolbar, click Film Series .
2. Select the number of images you want in the Export a series dialog box.
3. Select a spacing value.

   NOTICE! The images are selected from the center outwards. The maximum number of images available depends on the spacing value defined for the slices.
4. Select the thickness value.
5. In the Localizer area, select the reference images you want to include, if any.
6. Select the High Resolution check box to print the images in high resolution.
7. In the Image Label field, type a name for the new series.
8. Click OK to export the new series.

To preview and print the new series:

1. From the toolbar, click Film Preview .
2. Preview the new series and print images as desired from the new series.

See this topic:

Printing Images to Film on page 545

13.2.17 Saving MPR Images

Saving MPR Rendition Types

You can use Display Protocol (DP) to save the rendition type and the orientation/planar view for MPR images.

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1. Click the DP menu.
2. Select Save As DP.

Saving a Series to the Server

After filming images, you can save the series of MPR images to the server.

1. Follow the procedures in Filming and Printing MPR Images on page 182.
2. From the toolbar, click Save .
3. In the Images Label field in the Save to dialog box, type a name for the MPR images.
4. In the Localizer area, select the reference images you want to include, if any.
5. Select one or more DICOM archives where you want to save the MPR images.
6. Click Add.

   NOTICE! You can modify the selected archives by clicking Remove, Add All, or Remove All.
7. OPTIONAL: If desired, add a text description of the series.
8. Click OK.

   ⇨ The images are saved in the selected archive(s). Selections applied to the images, annotations, or measurements are saved. The original images are not affected.

See these topics:

Saving Viewing Options as a Display Protocol on page 595

Using Save as DP on page 621

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13.3 3D Data

13.3.1 About 3D Data

The 3D analysis application enables you to view and manipulate 3D images. You can view 3D images in any of the viewers except the general viewer. Once you have loaded your images to one of these viewers, you can select whether to view the 3D image as an Angiography MIP image or as a Volume Rendered image. The 3D analysis application also includes tissue definition and bone removal capabilities.

See these topics:

Creating a 3D View on page 184

3D Analysis Application Toolbar on page 87

Angiography Display Window on page 188

Changing the Group Layout on page 188

Manipulating 3D Images on page 188

Drawing a Clipping Plane on page 189

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Manipulating Clipping Planes on page 190
Working with Slabs on page 190
Manipulating Slabs on page 190
Working with Volumes of Interest on page 191
Working with Tissue Definition on page 192
Using Bone Removal on page 192

13.3.2 Enhanced 3D

The enhanced 3-D functions include:

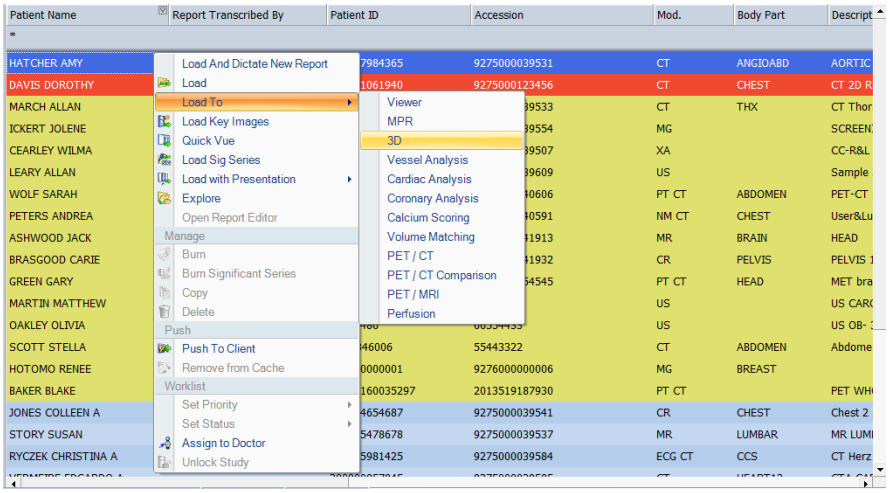
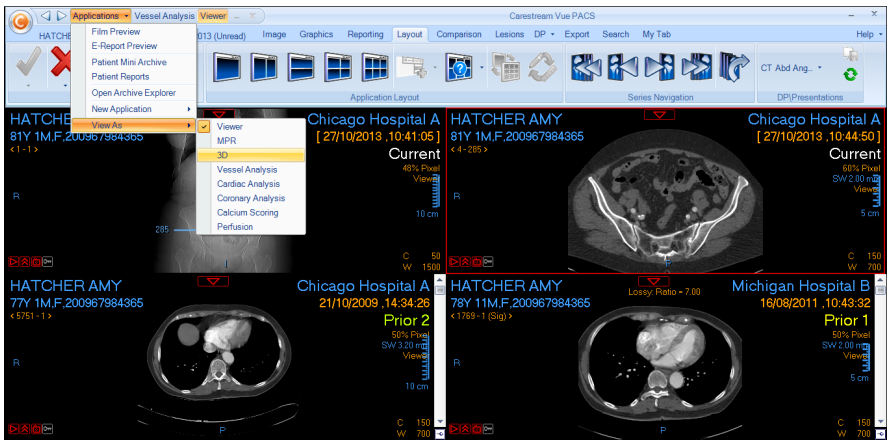
- Volume Rendering Quality (see Adjusting the Quality for Volume Rendered Images on page 633)—applies a special algorithm for high resolution 3-D images.
- Object and Anatomy Removal (see Removing Objects and Anatomy on page 207)
  - Automatic Bone Removal (see Using Bone Removal on page 192)—creates a boneless VolR (below the shoulders). A menu provides new correction tools which you can use to automatically remove additional bone fragments or restore vessel segments (see Adjusting the Results of Bone Removal on page 194).
  - Automatic Scanner Bed Removal (see Removing the Scanner Bed on page 211)—removes the scanner bed from 3-D images (VolR or MIP).
- MPR Double Oblique (see About the MPR Double Oblique Layout on page 174)—allows you to freely swivel the reference images in the MPR and Cardiac applications, and view the same anatomical region from three perpendicular orientations.
- Aneurysm Measurement (see Defining Points of Interest for Aneurysm Measurement (Stent Planning) on page 231)—enables stent planning, such as a stent for an aortic aneurysm.

13.3.3 Creating a 3D View

You can create a 3D view manually. For information about automatically creating a 3D view, go to About Display Protocols on page 594.

To create a 3D View:	Do this:

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From the Archive Explorer	Right-click a study group, select Load To, then select 3D.  **NOTICE! If several phases are selected, the application opens only one viewer window with all the phases.**
In the PowerViewer Application	• Right-click an existing group, select View As, then select 3D. Or • From the Applications menu select View As, and then select 3D from the drop-down menu. 
From the Patient Mini Archive	► Right-click a study group, then drag it to the display area. ► Select 3D.
To an open application	If the currently open application is 3D, click the study group in the Patient mini archive, then drag it to the display area. The selected group of images appears in the application. The reference images and result images appear in the location and layout that was last used.

Using a Display Protocol

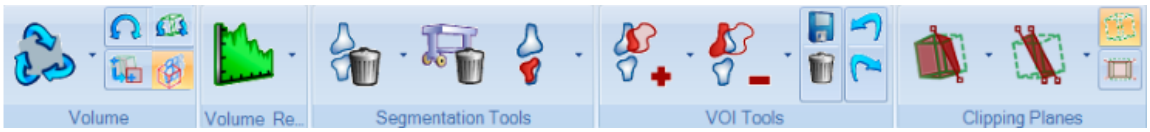
You can define Display Protocols that let you customize the display of studies in the Viewer, including viewing a group of images in Angiography or Volume Rendered mode.

See this topic:

About Display Protocols on page 594

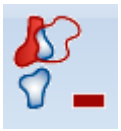
13.3.4 3D Analysis Application Toolbar

The following tab is added to the PowerViewer application (see About the PowerViewer Application on page 151) toolbar when you open the 3D analysis application.



Icon	Description
Volume	
	Swivel the image.
	Roll the image from side to side.
	Roll the image to the closest axial, sagittal or coronal plane.
	Relate a point on the MIP image to its relevant location on the MPR reference images (see About Relate Mode on page 590).
	Weighted MIP On/Off.
Volume Rendering	
	Edit Volume Rendering (VOLR) protocols, use enhanced VOLR to obtain high 3D image quality, and determine responsiveness during 3D volume manipulation by selecting image quality. See About Volume Rendering Protocols on page 636.
Segmentation Tools	
	Using Bone Removal on page 192
	Removing the Scanner Bed on page 211
	Define 3D tissues (see Building and Applying Tissues on page 205 and Tissue Definition Toolbar on page 102).
VOI Tools	

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	Define volume of interest plus. See Working with Volumes of Interest on page 191.
	Free VOI Plus. Lets you define a freehand region of the volume that you want to keep and discard the rest of the volume.
	Oval VOI Plus. Lets you define an oval region of the volume that you want to keep and discard the rest of the volume.
	Rectangular VOI Plus. Lets you define a rectangle region of the volume that you want to keep and discard the rest of the volume.
	Define volume of interest minus. See Working with Volumes of Interest on page 191.
	Free VOI Minus. Lets you draw a freehand shape on the image and then remove the shape from the image.
	Oval VOI Minus. Lets you draw an oval shape on the image and then remove the shape from the image.
	Rectangular VOI Minus. Lets you draw a rectangle shape on the image and then remove the shape from the image.
	Save VOI
	Reset VOI
	Undo Last VOI
	Redo Last VOI
Clipping Planes	
	Add a clipping pane.
	Add a slab.
	Show or hide frames.

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	Create clipping plane that is perpendicular to the plane of the display.

13.3.5 Angiography Display Window

The top left of the Angiography Display window shows the MIP image. You can use tools such as Swivel and Roll to manipulate the image. The other three images show MPR reference images in axial, coronal, and sagittal views. You can manipulate MPR images in the same manner as MPR reference images in the MPR application.

MIP Image	Axial View
Coronal View	Sagittal View

13.3.6 Changing the Group Layout

See these topics:

About Groups on page 560

About Image Layouts on page 511

13.3.7 Manipulating 3D Images

You can use the 3D tab tools to perform different manipulations to provide a more precise and accurate view of the acquired volume.

To:	Do this:
Swivel (rotate)	You can swivel (rotate) the image in any direction so you can view the image from different angles.  ► From the toolbar, click Swivel . ► Drag the mouse to swivel the image. Use the drop-down menu to the right of the Swivel icon to reset the image to an Inferior, Superior, Anterior, Posterior, left or right view and to flip the display.
Roll	You can roll the image from side to side.  ► From the toolbar, click Roll . ► Drag the mouse to roll the image from side to side.

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Relate	You can cross-reference a particular point on a MIP (result) image with its relevant location on the MPR reference image.  ► From the toolbar, click Relate . ► Click the MIP image where you want to place the reference point. **NOTICE! This option is only available when all four images are displayed on screen at the same time.**
Reset the orientation	You can reset the image to its original orientation. Right-click the orientation box on the lower-left, then select the option you want (Inferior, Superior, Anterior, Posterior), or use the drop-down of the Swivel tool.
Show hidden frames	You can show or hide specific frames.  ► From the toolbar, click Show or Hide Frames . ► Click the frames to be shown/hidden.

NOTICE

You can toggle between swiveling and rolling by holding down the Shift key while dragging the mouse.

13.3.8 Drawing a Clipping Plane

The clipping planes option lets you view a specific area of an image by clipping the parts of the image that you do not want to view.

1. Click Clipping Planes icon  in the 3D tab of the toolbar.
2. Click to mark the starting point of the clipping plane, move the cursor to the end point and click again.

   ⇨ The part of the volume from the line outward is deleted. You can draw more than one clipping plane and delete them separately.

Using a Screen Clipping Pane

Use the Screen Clipping Plane tool  in the 3D tab of the toolbar to create a clipping plane that is always perpendicular to the current view.

See this topic:

Manipulating Clipping Planes on page 190

13.3.9 Manipulating Clipping Planes

After the clipping plane is placed on the image, you can use these tools to manipulate the clipping plane.

To:	Do this:
Move	• Click on the clipping plane (but not on any of the vertices [handles]) you want to move, then drag it to the location you want.
Swivel	• Click on one of the four corner vertices, then drag it to the location you want.
Roll	• Click on one of the central vertices, then drag it to the location you want.
Flip	• Click the arrow next to the Clip toolbar button, then select Flip.
Hide	► Click the arrow next to the Clip toolbar button, then select Hide. ► Click Hide again to make the clipping plane reappear. **NOTICE! Hide also removes the clipping plane handles.**
Delete	► Click on the line of the clipping plane you want to delete. ► Press Delete.

13.3.10 Working with Slabs

The Slab option consists of two parallel clipping planes that let you see a portion of the acquired volume.

To draw a slab:

1. Click Slab .
2. Draw a line across the image.
   ⇨ Once one line is drawn, the system automatically draws the second line at the same measurement from the center and deletes everything outside of the lines.

See this topic:

Manipulating Slabs on page 190

13.3.11 Manipulating Slabs

You can use these procedures to manipulate the slab.

To:	Do this:
Move the slab	• Click on the slab and drag the cross-haired cursor to move the slab. • Click on a vertex and drag the double-sided cursor to swivel the slab.

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Scroll the slab	• Use the middle mouse button to scroll a slab.
Swivel the slab	• Click Swivel  and drag the mouse to swivel the slab.
Roll the slab	• Click Roll  and drag the mouse from left to right, or right to left, to roll the slab. Rolling can be done clockwise or counterclockwise.
Remove the slab	• Click the arrow next to the Slab toolbar button, then select Clear.
Increase/decrease the slab	• Point to the edge of the slab, then press Shift to increase/decrease the slab size.

13.3.12 Working with Volumes of Interest

The Volume of Interest (VOI) option lets you remove unnecessary areas of a volume to get a clearer view of pathology.

To:	Do this:
Create a VOI	► Click Define Volume of Interest  and select an option from the VOI Tools list. ► Click the left mouse button and draw the VOI.
Draw a plus VOI	The plus VOI lets you define a region of the volume you want to keep and discards the rest of the volume. ► Click Define Volume of Interest  and select a shape (Free , Oval , Rectangle ). ► Click the mouse and draw the shape. ► When you are finished drawing, double-click to discard the volume outside the shape.
Draw a minus VOI	The minus VOI lets you draw a shape on the image and then remove the shape from the image. ► Click Define Volume of Interest  and select a shape (Free , Oval , Rectangle ). ► Click the mouse and draw the shape. ► When you are finished drawing, double-click to discard the volume inside the shape.

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Undo the last VOI	• Click Define Volume of Interest  and select Undo Last VOI.
Redo the last VOI	• Click Define Volume of Interest  and select Redo Last VOI.
Reset the MIP image	• Click Define Volume of Interest  and select Reset VOI.
Save the defined VOI	• Click Define Volume of Interest  and select Save VOI. **NOTICE! The image saved will be added to the Patient mini archive and saved to disk when the Diagnostic Workstation is closed.**

13.3.13 Working with Tissue Definition

Click the Define New Tissue icon  in the 3D tab to display the Tissue Definition toolbar (see Tissue Definition Toolbar on page 102).

See these topics:

About Tissue Definition on page 196

Creating a VOI for Tissue Definition on page 204

Interpolating a VOI for Tissue Definition on page 204

Restricting a VOI for Tissue Definition on page 205

Building and Applying Tissues on page 205

13.3.14 Using Bone Removal

The Automatically Remove Bone tool lets you remove all bone tissue with a single mouse click.

NOTICE

When you apply Automatically Remove Bone, the Automatic Scanner Bed Removal tool is also applied in tandem. See Removing the Scanner Bed on page 211.

13.3.15 Recommendations

For best results, use the Automatically Remove Bone  on CT scans that are:

- high resolution
- full-body

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- include body parts other than the shoulder, neck, or skull regions
- standard bone structures

IMPORTANT

Atypical bone structures such as bone spurs (osteophyte), bone fractures, or fragments might not be completely removed.

13.3.16 Using the Automatically Remove Bone Tool

1. From the viewing application (viewbox), select the image from which you would like to remove the bone.
2. Click Automatically Remove Bone .
   ⇨ The bone removal calculation might require some additional time. During the calculation process, you will see the following message:
   ⇨ **The Bone Removal calculation is currently taking place, you may continue working. A second message will appear once the calculation has been completed.**
   ⇨ When the bone removal is complete, you will see the following confirmation message:
   ⇨ **The Bone Removal calculation has now been completed.**
   ⇨ **Warning: The Bone Removal function may have extracted additional tissues. In such a case, access Tissue Definition to reapply the extracted tissue.**

13.3.17 Understanding the Clipping Pane

Automatically Remove Bone applies to all bones below the shoulders. You can remove bones above the shoulders using manual segmentation.

Automatically Remove Bone does not remove bones in the shoulder, neck, and skull regions. Automatically Remove Bone places a clipping plane from the shoulder region up to the skull region. The clipping plane hides the shoulder, neck, and skull regions. You can modify and move the clipping plane as required.

13.3.18 Making Adjustments

When the bones are removed, fragments of vessels in the foot, ankle, tibial, intercostal, and gluteal arteries can also be removed from the image. Conversely, small bone fragments can remain in the image. You can use correction tools to adjust the results. You can select the correction tools from the drop-down menu of the Automatically Remove Bone icon.

See these topics:

Adjusting the Results of Bone Removal on page 194

Removing Objects and Anatomy on page 207

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13.3.19 Adjusting the Results of Bone Removal

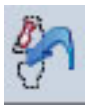
Using Tools to Adjust the Bone Removal Results Manually

After you apply Automatically Remove Bone , the icon changes to .

A drop-down menu contains correction tools.

The correction tools automate the process of removing additional bone fragments or restoring vessel segments.

1. Apply Automatically Remove Bone .
2. Click the drop-down area on . The drop-down menu includes:

	Remove Bone Fragments
	Restore Removed Vessel
	Undo Latest Bone Correction

⇨ Select the correction mode you require. The mouse cursor changes to indicate the correction mode.

Removing Bone Fragments

1. Apply the Automatically Remove Bone tool (see Using Bone Removal on page 192).
2. From the Automatically Remove Bone drop-down menu, click Remove Bone Fragments .
3. Click on each bone fragment that you want to remove from the image.
4. To hide or show the current bone tissue, click Tissue --> Show Tissue --> Bone Tissue.

Exceptions and Behaviors

- If you use VOI tools or Tissue Definition tools to manually remove bone fragments, the bone fragments do not appear in the Tissue menu list.

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- If you click Tissue --> Show Tissue --> Bone Tissue to toggle the entire bone tissue on or off. This will toggle the entire bone tissue, with both the automatically-defined bone and all corrections made to it up to this point.
- If you apply the Automatically Remove Bone tool and then edit the Bone Tissue to remove the bone fragments, the fragments are saved as part of the Bone Tissue.

Restoring Vessel Segments

1. Apply the Automatically Remove Bone tool (see Using Bone Removal on page 192).
2. From the Automatically Remove Bone drop-down menu, click Restore Removed Vessels .

NOTICE

In Restore Removed Vessels mode, you must click in two locations to define a start point and an end point for the vessel.

3. The Status Bar prompts you to place the start point on the image. When the mouse cursor changes to (1), click on the image to define the first point.
4. The Status Bar prompts you to place the end point on the image. When the mouse cursor changes to (2), click on the image to define the second point.

⇨ The tool tracks and generates the vessel segment between the two points. The Status Bar indicates when:

- The vessel segmentation is in process.
- The vessel restoration is complete (successful).
- The vessel restoration is incomplete (failed).

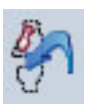
⇨ The mouse cursor returns to the previous mode, such as Swivel or Zoom.

Exceptions and Behavior

When you click on the three-dimensional image, the two-dimensional images indicate the clicking point.

If you select a different mode before you finish defining two points for the vessel, you cancel the Restore Removed Vessels mode.

Using the Undo Function

Click Undo Latest Bone Correction  to restore the bone fragment that you most recently removed from the image, or remove the vessel which you most recently added to the image.

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Using Tools to Adjust the Bone Removal Results Manually

You can manually remove bone fragments or restore vessel segments using VOI tools or the Tissue Definition tools.

See these topics:

Building and Applying Tissues on page 205

Tissue Definition Toolbar on page 102

Creating a VOI for Tissue Definition on page 204

13.3.20 Saving Presentations in 3D Data

When you use the Save Presentation feature in the 3D analysis application the following parameters are saved:

- The exact dataset presented.
- The exact layout.
- All MPR parameters of the MPR images.
- Zoom and Pan of the MPR images
- Windowing.
- Enhance.
- Color Map.
- Reference Point.

For the 3D image, the Save Presentation should retain the 3D rendition type, the VolR protocol including windowing, 3D swivel (orientation), clipping planes and position, VOI, Bone Removal including bone corrections, Bed removal and 3D frame (show and hide).

See these topics:

Saving a Study as a Presentation on page 620

About Save Presentation on page 619

13.4 Using Tissue Definition

13.4.1 About Tissue Definition

Tissue definition is available when viewing images in 3D or when using the Vessel Analysis or Coronary Analysis applications. Tissue definition lets you define 3D tissues to better visualize particular regions or areas of the CT or MR volume. When you view images using one of these applications, you can choose to hide or show tissue definition to better visualize pathology.

1. Right-click the image, select View As, then select Vessel Analysis, Coronary Analysis, or 3D.
2. If required, you can change the type of image. Right-click the image, select Change Image, then select Angiography MIP or Volume Rendering.

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3. From the 3D tab of the toolbar click Tissue Definition .

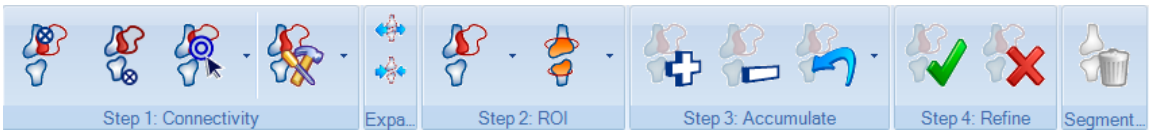
⇨ The Tissue Definition toolbar appears. A default highlight appears on the image. The highlighted area has a center and width calculated according to the range of pixels that are colored.

See these topics:

Changing Highlight Values for Tissue Definition on page 199
Using Balloon on page 200
Placing a Seed Point on page 200
Placing an Outside Point on page 201
Adding and Removing Pixels on page 202
Using Bridge on page 202
Using Minimum Volume on page 203
Using Fill on page 203
Resetting the Images on page 203

13.4.2 Tissue Definition Toolbar

The following tab is added to the toolbar when you define a new tissue using the 3D tools (see 3D Analysis Application Toolbar on page 87).



Icon	Description
Step 1: Connectivity	
	Mark a seed point on the image.
	Mark an outside point on the image.
	Mark a semi-automatic expansion seed and inflate a balloon within it.

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	Define the Tissue Definition parameters.
Expand	
	Add pixels to expand the tissue border.
	Remove pixels to collapse the tissue border.
Step 2: ROI	
	Draw a freehand, oval or square Region of Interest (ROI).
	Draw a freehand, oval or square contour.
Step 3: Accumulate	
	Remove a tissue.
	Add a tissue.
	Reset the changes to the image you are viewing.
Step 4: Refine	
	Accept a tissue.
	Dismiss a tissue.

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Step 5: Segment	
	Automatically remove bone tissue. See: Tissue Definition Toolbar on page 197.

13.4.3 Changing Highlight Values for Tissue Definition

The highlight option lets you indicate which areas of the volume are considered inside or outside a particular tissue. The highlight is an additional color layer superimposed on the Angio and reference MPR or Volume Rendered images. You can control the pixels colored by the highlight using the center and width values.

NOTICE

Colors cannot be seen on black-and-white monitors.

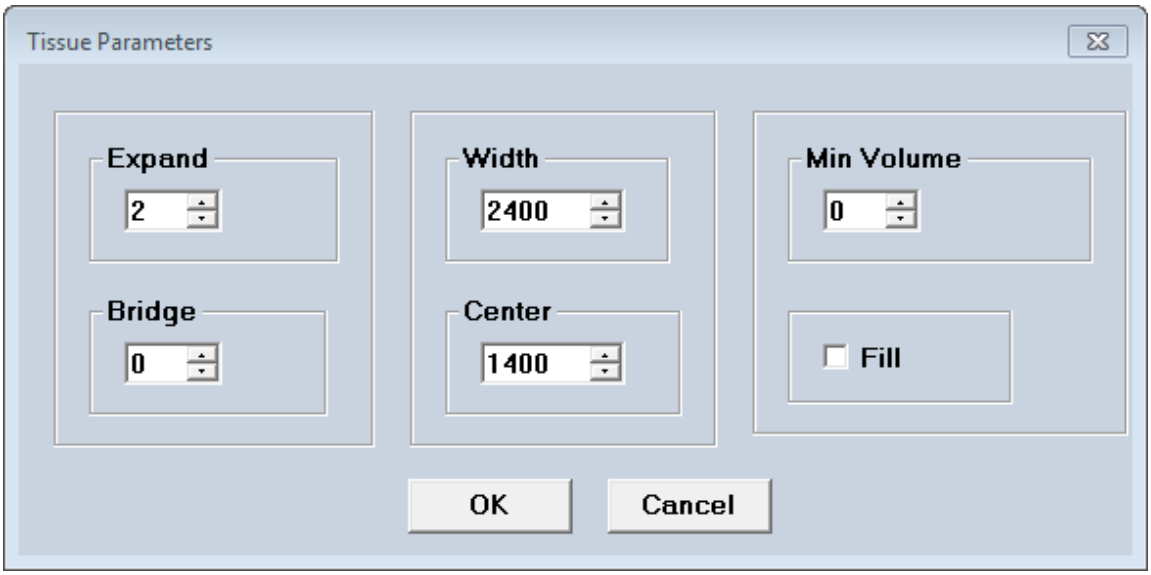
The highlight can appear in three colors:

- Red: Indicates pixels that fall into the highlight center and width values.
- Blue: Indicates pixels that are included in the current tissue. Not all highlighted (red) pixels will actually comprise the final tissue defined. The final tissue is defined by blue pixels that are a subset of the red.
- Green: Indicates areas of the volume that have been removed.

To change the highlight values:

1. Click the drop-down menu to the right of the Tissue Definition icon  in the Tissue tab of the toolbar.
2. Select Tissue Definition Parameters and set the Width and Center.

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13.4.4 Using Balloon

The balloon option lets you choose a particular tissue and highlight it by inflating a balloon within it.

1. Define the tissue to be highlighted.
2. From the Tissue Definition toolbar, click Semi-Automatic Expansion Seed .
3. Click anywhere in the tissue you wish to highlight.
4. Keep the left mouse button pressed to inflate the balloon.
   ⇨ Release the mouse button to stop inflating. To reduce the inflated balloon, click Backspace.

NOTICE

Once the balloon begins inflating, the other toolbar buttons are grayed out and cannot be used.

5. To delete an inflated area, click on it, then press Delete on the keyboard.

13.4.5 Placing a Seed Point

The seed point option lets you separate a particular tissue from other tissues with the same pixel values. A seed point can be placed on the MIP image or any of the MPR or Volume Rendered reference images.

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NOTICE

Only one seed point can be placed on an image. Place the seed point as far as possible from the edges of the tissue. You should look through the slices to gain an idea of the overall tissue structure before picking a point.

1. From the Tissue Definition toolbar, click Mark a Seed Point .
2. Click to place the seed point on the image and location you want.
   ⇨ The connected pixels within the highlight range on all slices are colored blue on the MPR reference images.
3. To place a different seed point, click again on a different location.

⇨ The previous seed point is erased and a new seed point is created where you clicked.

See this topic:

Placing an Outside Point on page 201

13.4.6 Placing an Outside Point

If the seed point is too closely connected to another point, you can make some fine adjustments. You can have multiple outside points on an image.

NOTICE

Place the outside point as far as possible from the edges of the tissue. You should look through the slices to gain an idea of the overall tissue structure before picking a point.

1. From the Tissue Definition toolbar, click Outside .
2. Click the unwanted area of the displayed image.
   ⇨ The point is marked by an X.
3. To add another outside point, click another area.
   ⇨ You can have unlimited outside points, but only one seed point.
4. To delete an outside point, select the point and press Delete.

See this topic:

Placing a Seed Point on page 200

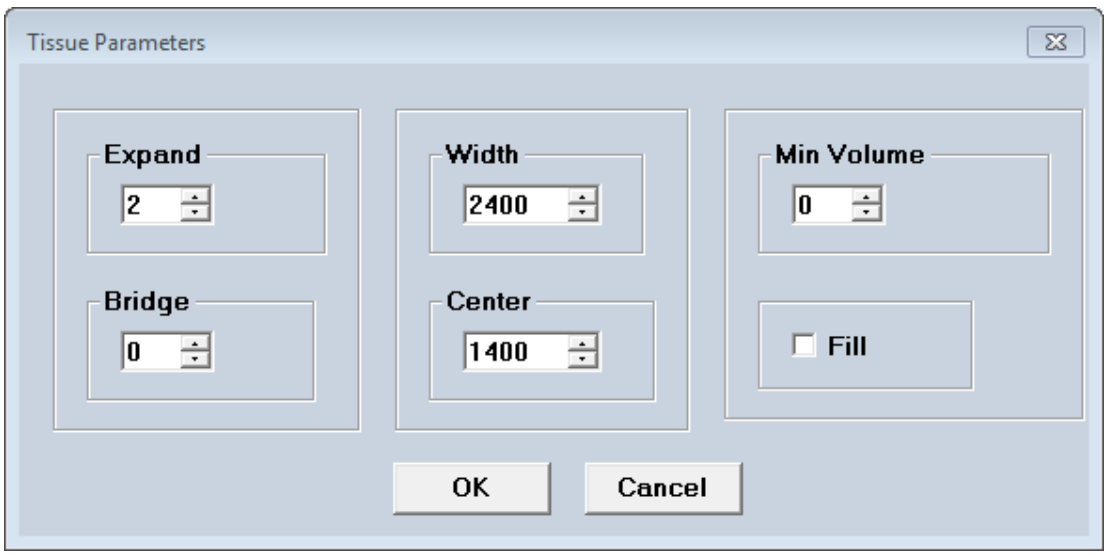
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13.4.7 Adding and Removing Pixels

You can add or remove blue pixels from the tissue to artificially enlarge or decrease the defined tissue. Adding or removing blue pixels lets you cover tissue borders that have different pixel values than the highlight window due to partial volume effects.

From the Tissue Definition toolbar, select one of the following options:

- To add pixels to the tissue border, click Expand  or click the Tissue Definition Parameters icon  and use the Tissue Parameters dialog.



- To Remove pixels from the tissue border, click Collapse .

NOTICE

When you remove bone, we recommend that you use an expand value of 2.

13.4.8 Using Bridge

The bridge option lets you separate small tissue volumes from the main tissue body by specifying the minimum number of pixels that any two bodies need to be connected with. The main tissue body is where the seed point is placed. You can use the bridge option instead of, or in conjunction with, outside points.

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- Outside points: Specify an area within an image that needs to be disconnected from the main tissue body.
- Bridge: Acts on the entire image. For example, a bridge value of 4 means "disconnect any tissue mass that is connected to the main tissue body by less than 4 pixels."

1. From the Tissue Definition toolbar, click Tissue Definition Parameters .
   ⇨ The Tissue Parameters dialog box appears.
2. Enter a bridge value or use the arrows to select a bridge value in the Bridge field.
3. Click OK.

13.4.9 Using Minimum Volume

The minimum volume option is similar to the bridge option in that it lets you separate smaller tissue volumes from the main tissue body. Minimum volume is different from the bridge option because it uses the volume of the tissues, instead of the number of pixels with which they are attached to the main tissue body.

For example, a minimum volume value of 4 means "disconnect any tissue mass that has a volume of less than 4 pixels from the main tissue body."

1. From the Tissue Definition toolbar, click Tissue Definition Parameters .
   ⇨ The Tissue Parameters dialog box appears.
2. Enter a minimum volume or use the arrows to select a minimum volume value in the Min Volume field.
3. Click OK.

13.4.10 Using Fill

The fill option lets you fill cavities that are enclosed in all dimensions. If the regular tissue definition tools leave cavities that need to be part of the defined tissue, you can apply a fill.

1. From the Tissue Definition toolbar, click Tissue Definition Parameters .
   ⇨ The Tissue Parameters dialog box appears.
2. Select the Fill check box.
3. Click OK.

13.4.11 Resetting the Images

You can reset changes that you have made to the image you are viewing.

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1. From the Tissue Definition toolbar, click Reset Images .
2. Select one of the following options:
   - To reset the Bridge, Minimum Volume, and Expand parameters to zero, select Reset Parameters.
   - To reset the MIP image to the original image before the tissue was applied, select Clear Tissue.
   - To undo the last Add or Remove selection, select Undo Last.

13.5 Using Tissue Definition in 3D Images

13.5.1 Creating a VOI for Tissue Definition

You can limit a tissue to a specified region or volume of interest (VOI). The boundaries of the volume define the area in which the tissue can be defined. Even if the highlight values include pixels outside the VOI, those pixels will not be considered when building the tissue.

1. From the 3D tab of the toolbar, click VOI .
2. Select a VOI shape (oval, square, or freehand).
3. Click once to draw the shape you want, then double-click to end drawing.
   ⇨ After you draw the VOI, it is applied through the entire volume.
4. Apply other tissue definition tools to define the desired tissue.

NOTICE

The original VOI that you draw is called the base VOI and is marked in red. As you scroll through the rest of the volume, you will see interpolated VOIs that are marked in green.

Colors cannot be seen on black-and-white monitors.

See these topics:

Adjusting the Results of Bone Removal on page 194

13.5.2 Interpolating a VOI for Tissue Definition

You can define more than one VOI shape in the volume, then have the application interpolate between the shapes drawn.

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1. From the Tissue Definition toolbar, click VOI .
2. Select a VOI shape (oval, square, or freehand).
3. Scroll the reference images to the beginning of the region you want to define.
4. Click once to draw the shape you want, then double-click to end drawing.
5. Select a second region of interest at a different location in the volume.
   ⇨ The regions interpolate from one shape to the other as you scroll through the reference images.

NOTICE

There is no limit to the number of VOIs you can draw.

13.5.3 Restricting a VOI for Tissue Definition

You can specify a beginning and an end to a VOI to restrict it to a certain subset of the volume.

To place an upper limit on the Volume of Interest:

1. Scroll to the location above the Base VOI where you would like to end the VOI.
2. Press Delete.
   ⇨ The VOI is no longer active from that location outwards towards the edge of the volume.

To place a lower limit on the Volume of Interest:

1. Scroll to the location below the Base VOI where you would like to end the VOI.
2. Press Delete.
   ⇨ The VOI is no longer active from that location outwards towards the edge of the volume.

13.5.4 Building and Applying Tissues

Once you have created a tissue by using the various tissue definition tools, you can apply the tissue on the MIP or Volume Rendered image. You can add or remove a specific tissue from the tissue. When you build a tissue, it is possible you will add or remove structures many times until you achieve the results you want.

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Removing and Adding a Tissue

When you remove a tissue, the blue pixels defined on the MPR reference images are removed from the MIP or Volume Rendered image. For example, use this process to remove bone structures.

NOTICE

You must determine if the type of tissue you are going to define will be added or removed.

To:	Do this:
Remove a tissue	• From the Tissue tab of the toolbar, click Remove .
Add a tissue	When you add a tissue , the blue pixels defined on the MPR reference images are added to the MIP or Volume Rendered image. When you define the first tissue, selecting "add" keeps the tissue while removing the rest of the MIP image. For example, use this process to define and keep tissues of blood vessels.

Accepting, Dismissing, and Saving a Tissue

To save a tissue, you must accept it. When you accept a tissue, the tissue definition process is complete.

When a tissue is accepted, the following occurs:

- The application returns to the regular Angio view, with the defined tissue applied on the MIP image.
- The accepted tissue appears in the Patient Mini-Archive, where it can be dragged to the MIP image and applied.
- The accepted tissue appears in the MIP Tissue List under the View menu.

To:	Do this:
Accept a tissue	• From the Tissue tab of the toolbar, click Accept . The tissue is saved in the Patient Mini-Archive, but is not permanently saved until the end of the session.

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Dismiss a tissue	• From the Tissue tab of the toolbar, click Cancel .
Save a tissue	• At the end of the session, click Done  to save the tissue for future reference.

13.5.5 Applying Tissues

You can define several tissues and apply them separately or together on the MIP image.

- Drag the relevant tissue from the Patient Mini-Archive onto the MIP image.

See these topics:

Adjusting the Results of Bone Removal on page 194

13.6 Removing Objects and Anatomy in 3D Images

13.6.1 Removing Objects and Anatomy

You can remove objects and anatomy from three-dimensional images. The object you can remove is the scanner bed. The anatomy includes muscular tissue and supporting connective tissue such as vessels and bone.

Applications

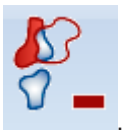
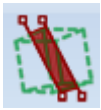
The following viewing applications allow you to remove specific portions of anatomy or objects from a three-dimensional image:

- 3D Data
- Vessel Analysis
- Cardiac CT
- Coronary Analysis

13.6.2 Matrix of Tools for Removing Objects and Anatomy

Anatomy or Object	Related Tools	Topics

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Heart Cage	• Automatically Remove Heart Cage . • Delete All Vessels . • Delete Active Vessel 	Coronary Analysis Toolbar on page 92 Loading Images to the Coronary Analysis Application on page 268 Vessel Analysis Toolbar on page 89 Deleting Vessels on page 236
Bone	• Automatically Remove Bone . • Remove Bone Fragments .	3D Analysis Application Toolbar on page 87 Using Bone Removal on page 192 Vessel Analysis Toolbar on page 89 Tissue Definition Toolbar on page 102 Building and Applying Tissues on page 205 Adding and Removing Pixels on page 202
Scanner Bed	Automatic Scanner Bed Removal .	3D Analysis Application Toolbar on page 87 Removing the Scanner Bed on page 211 Using Bone Removal on page 192 Vessel Analysis Toolbar on page 89 Tissue Definition Toolbar on page 102
VOI	Hide tissue in VOI .	About Tissue Definition on page 196 3D Analysis Application Toolbar on page 87 Tissue Definition Toolbar on page 102 Creating a VOI for Tissue Definition on page 204
Clipping Plane	Add Clipping Plane .	About Tissue Definition on page 196 3D Analysis Application Toolbar on page 87 Tissue Definition Toolbar on page 102 Drawing a Clipping Plane on page 189 Manipulating Clipping Planes on page 190
Create Slab	Add Slab 	About Tissue Definition on page 196 3D Analysis Application Toolbar on page 87 Tissue Definition Toolbar on page 102 Working with Slabs on page 190 Manipulating Slabs on page 190

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Tissue	Remove defined tissue 	About Tissue Definition on page 196 3D Analysis Application Toolbar on page 87 Tissue Definition Toolbar on page 102 Removing Tissue on page 209 Building and Applying Tissues on page 205

13.6.3 Removing Tissue

Use the following tools to remove tissue

- Remove 
- Collapse 

The topic Building and Applying Tissues on page 205contains instructions for removing tissue.

See these topics:

Building and Applying Tissues on page 205

Tissue Definition Toolbar on page 102

About Tissue Definition on page 196

Adding and Removing Pixels on page 202

Removing Objects and Anatomy on page 207

13.6.4 Removing Vessels

To remove vessels, use the following tools:

- Delete All Vessels 
- Delete Active Vessel 

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- Remove 
- Collapse 

See these topics:

Removing Objects and Anatomy on page 207
Deleting Vessels on page 236

Supporting topics:

Vessel Analysis Toolbar on page 89
Tissue Definition Toolbar on page 102
About Tissue Definition on page 196
Building and Applying Tissues on page 205
Adding and Removing Pixels on page 202

13.6.5 Removing Bones

To remove bones, use the following tools:

- Automatically Remove Bone 
- Remove Bone Fragments 

See these topics:

Removing Objects and Anatomy on page 207
Using Bone Removal on page 192
Adjusting the Results of Bone Removal on page 194

Supporting topics:

3D Analysis Application Toolbar on page 87
E-Report Preview Toolbar on page 100
Tissue Definition Toolbar on page 102
Building and Applying Tissues on page 205
Adding and Removing Pixels on page 202
Removing the Scanner Bed on page 211

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13.6.6 Removing the Heart Cage

To remove the heart cage, use the following tools:

- Automatically Remove Heart Cage 
- Delete All Vessels 
- Delete Active Vessel 

See these topics:

Coronary Analysis Toolbar on page 92

Loading Images to the Coronary Analysis Application on page 268

Vessel Analysis Toolbar on page 89

Deleting Vessels (see Deleting Vessels on page 236)

Removing Objects and Anatomy on page 207

13.6.7 Removing the Scanner Bed

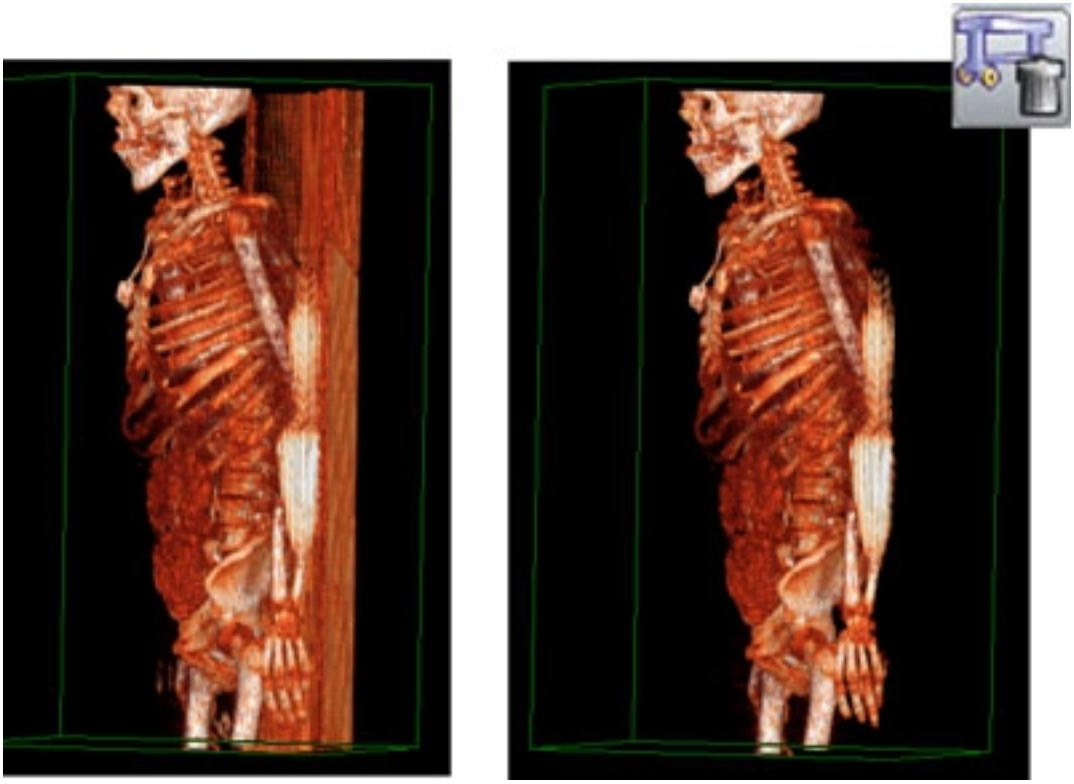
You can automatically remove the scanner bed from three-dimensional images (VolR or MIP).

NOTICE

If the study includes two-dimensional images, the scanner bed remains intact.

1. Load a study with three-dimensional images into a viewbox application such as 3D Data, Vessel Analysis, or Volume Matching.
2. Locate an image that displays the scanner bed.
3. From the toolbar, click Automatic Scanner Bed Removal .
4. The image is processed and displays without the scanner bed.

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NOTICE

The Automatic Scanner Bed Removal tool equates the scanner bed with tissue. After removal, the scanner bed is listed in the Tissue menu. You can select or deselect the scanner bed in the list to show or hide the scanner bed.

Show or Hide the Scanner Bed

1. Apply Automatic Scanner Bed Removal.
2. In the menu toolbar, select Tissue --> Show Tissue --> Scanner Bed. The scanner bed is displayed in the image.
3. To hide the scanner bed, select Tissue --> Hide Tissue --> Scanner Bed. The scanner bed is concealed.

Bone Removal and Automatic Scanner Bed Removal

When you apply Automatically Remove Bone , the Automatic Scanner Bed Removal is also applied in tandem.

See this topic:

Removing Objects and Anatomy on page 207

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13.7 Vessel Analysis

13.7.1 About Vessel Analysis

The Vessel Analysis application lets you track, segment, and analyze vessels to detect stenoses (narrowing) or occlusions (obstruction), and so on, of the arteries. You can use one of the following protocols for segmenting the vessels:

- Aorta Protocol
- General Vessel Protocol
- Neck Protocol
- Manual Protocol

The basic view displays three reference images (Axial, Sagittal, and Coronal views) and a 3D image.

You can fix contours and recalculate vessels. Once the vessel has been segmented, you can toggle between the views of each vessel by right-clicking the vessel name. In the MIP image, you can see the various defined vessels and you can toggle between them by clicking control and the appropriate vessel. You can also mark points of interest in the vessels and create a report.

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NOTICE

The Vessel Analysis and Coronary Analysis applications are available only if your profile has licenses to use them.

The active vessel is indicated by color and a cut line. There are three ways to select which vessel is to be the active vessel. See Switching Between Vessels in Switching Between Vessels on page 236.

See these topics:

Creating a Vessel Analysis View on page 214

Vessel Analysis Toolbar on page 89

Creating a New Vessel on page 216

Using Vessel Tracking on page 217

Tracing Vessels on page 217

Using Automatic Vessel Segmentation on page 225

Viewing Vessel Tissue on page 228

About Vessel Analysis on page 213

Tracing the Aorta and Iliac Arteries on page 220

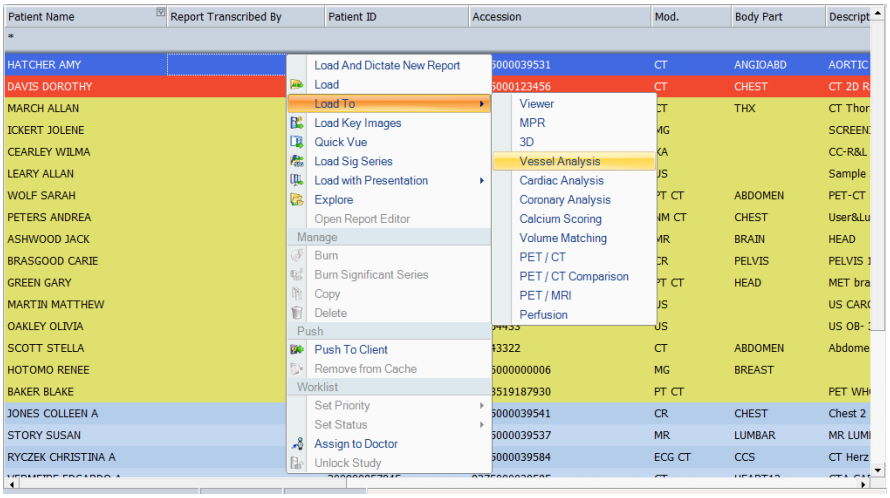
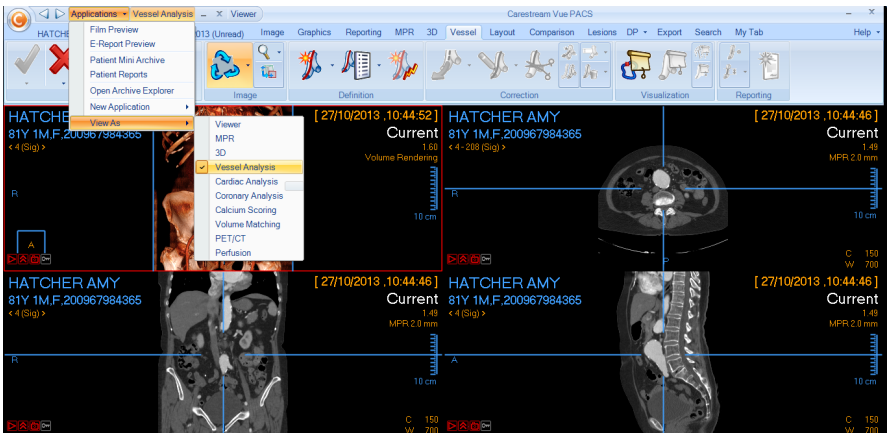
Tracing Carotid Arteries Using the Neck Protocol on page 222

Tracing Arteries Using the General Protocol on page 222

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13.7.2 Creating a Vessel Analysis View

You can create a Vessel Analysis view manually. For information about automatically creating a Vessel Analysis view, go to About Display Protocols on page 594.

To create a Vessel Analysis View:	Do this:
From the Archive Explorer	• Right-click a study group, select Load To, then select Vessel Analysis.  Or • Right-click a study group and, provided that a Vessel Analysis Display Protocol has been pre-defined, select Load.
In the PowerViewerApplication	• Right-click an existing group, click View As, then select Vessel Analysis. Or • From the Applications menu, select View As and then select Vessel Analysis. 
From the Patient Mini Archive	► Right-click a study group, then drag it the display area. ► Select Vessel Analysis.

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To an open Application	If the currently open application is a Vessel Analysis, click the study group in the Patient Mini-Archive, then drag it to the display area. The selected group of images appears in the application. The reference images and result images appear in the location and layout that was last used.

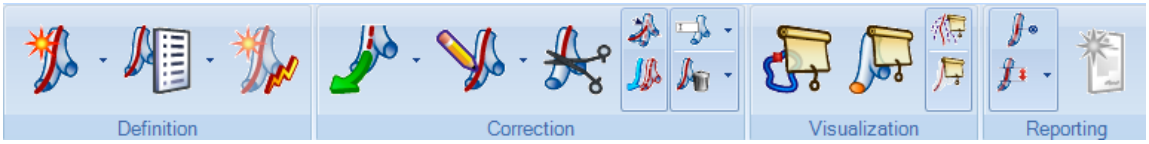
See this topic:

Using Vessel Tracking on page 217

13.7.3 Vessel Analysis Toolbar

The following tab is added to the toolbar when you open the Vessel Analysis application.

See also: 3D Analysis Application Toolbar on page 87.



Icon	Description
Definition	
	Define a new vessel. Select a protocol type that matches the vessel to be segmented.
	Select a vessel from the list for viewing, editing and measuring.
	Mark points on any vessel and segment using the general vessel protocol.
Correction	
	Extend vessel segmentation beyond the existing end point.
	Manually edit segmented vessel center line or contours.
	Truncate the active vessel at a selected point.

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	Create a new vessel by branching from the active vessel at the location of the reference marker.
	Recalculate the vessel based on manual editing.
	Rename the active vessel.
	Delete the active vessel.
Visualization	
	Hide center line and contours of all vessels.
	Hide orange overlay indicating segmented vessels and other vessel-related suggestions in MPR displays.
	Show/hide purple overlay indicating automatic protocol suggestions that have not yet been accepted.
	Hide the rest of the 3D volume to isolate the segmented vessels and tissues.
Reporting	
	Mark a location along the vessel center line as a bookmark.
	Mark a point of interest: • Mark a stenosis type point of interest; • Mark an aneurysm type point of interest.
	Generate a Vessel Analysis report.

13.7.4 Creating a New Vessel

1. On the Vessel Analysis application toolbar, click New Vessel .
   ⇨ The list of protocols is displayed (Aorta, General Vessel, Neck, and Manual).
2. Select the required protocol type.
3. Follow the instructions for how to trace a vessel using each protocol option:
   - Aorta Protocol (see Tracing the Aorta and Iliac Arteries on page 220).
   - General Vessel Protocol (see Tracing Vessels on page 217).

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- Neck Protocol (see Tracing Carotid Arteries Using the Neck Protocol on page 222). This protocol is specifically designed for images of the neck.
- Manual Protocol (see Tracing Vessels Manually on page 219).

In each case, you should define the start, intermediate, and end points for the vessel tracking.

13.7.5 Using Vessel Tracking

The Vessel Tracking feature can be invoked from either the Vessel Analysis or Coronary Analysis applications, according to the type of vessel to be tracked.

You can track a 3D curved path along a vessel and receive a panoramic view and cross-sectional slices of that curve. Once you have defined a path, you can make changes to the path, and then recalculate it (meaning, the vessel path) using the new points.

Each vessel that is created has its own tissue.

See these topics:

Tracing Vessels on page 217

Tracing the Aorta and Iliac Arteries on page 220

Tracing Carotid Arteries Using the Neck Protocol on page 222

Tracing Coronary Arteries Using the Coronary Protocol on page 270

Tracing Coronary Arteries Using the Coronary Tree Protocol on page 271

Tracing Vessels Manually on page 273

Tracing Vessels Manually on page 219

Manipulating Images on a Defined Path on page 233

Defining and Marking Occlusions on page 223

Defining and Marking Extra Points on page 224

Swiveling Panoramic and Scrolling Cross-Sectional Images on page 235

Viewing Vessel Tissue on page 228

Defining Points of Interest as Stenosis Markers on page 231

Defining Points of Interest as Bookmarks on page 232

Choosing Screen Layouts on page 229

13.7.6 Tracing Vessels

To:	Do this:

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Trace a vessel using the General Vessel Protocol	When tracking a vessel other than the aorta, carotid, or coronary, use the general automatic vessel tracking protocol. ► Click Define New Vessel . ► Select General Vessel Protocol. ► Click points along the vessel to trace its path. ► Click Done .
Trace a path manually using the MIP image	► Click Define New Vessel . ► Select Manual Protocol. ► Click points along the vessel to trace the path on the MIP image. ► Click Done . See Tracing Vessels Manually on page 273.
Trace a path manually using the MPR reference images	► Click Define New Vessel . ► Select Manual Protocol. ► Click points on any of the MPR reference images. ► Click Done . ⇨ You can scroll through the MPR image between points, but all points must be placed on the same reference plane.
Cancel the creation of a vessel	• Click Exit  in the Protocol dialog box.
Delete the last point	You can remove the last point you clicked on a vessel path. • Click Delete Last Point  in the Protocol dialog box.

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Reset	You can cancel all points marked on a vessel path and stay in the same dialog box to define a new vessel. • Click  in the Protocol dialog box.

NOTICE

If segmented vessels already exist in the selected phase, the application reverts to the 2x2 layout. The VolR image shows the defined vessel/s as well as the new vessel that is being segmented.

Once you mark the points, they are joined to the vessels that existed previously.

You can view vessels that were segmented in different phases by scrolling to the relevant phase, or by clicking the Vessels menu and then selecting the phase from the Vessels drop-down menu.

13.7.7 Tracing Vessels Manually

You can mark the vessel path (start point, intermediate points, and end point) by placing markers on any of the four displayed images. The system connects the points you marked with lines to show the vessel path.

NOTICE

Marking points on the 3D image is not recommended because you cannot be sure exactly where the point is being placed. If you decide to mark the vessel path point(s) on the 3D image, examine the reference images to check that you marked the point(s) accurately.

1. On the Vessel Analysis toolbar, click New Vessel .
   ⇨ A list of protocols appears.
2. Select Manual Protocol.
3. Enter the Vessel Name in the Manual Protocol window.
4. Mark the vessel start point by placing a marker on one of the images.
5. Mark the vessel path by placing extra points on the same image on which you placed the start point marker.
6. Mark the vessel end point.

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7. Click Done .

13.7.8 Tracing the Aorta and Iliac Arteries

The Aorta Protocol is used for tracing the aorta and iliac arteries. The system provides you with a set of basic points, relating to specific parts of the vessel path, including the start point, bifurcation point, right iliac, left iliac, and end point.

1. In the Archive Explorer, right-click the study you want to view, select Load To, then select Vessel Analysis.
2. In the Vessel Analysis toolbar, click New Vessel .
3. Select Aorta Protocol.
   ⇨ Mark Point  appears on the toolbar. You must select Mark Point each time you want to add new points.
4. Click Aorta Protocol.
   ⇨ The Aorta Protocol dialog box appears.
5. Click the start point on any of the MPR reference images.
   ⇨ Start of Section is checked and Start is marked on the image. If necessary, you can scroll the MPR reference images to view the required location.

NOTICE

You can mark any extra points or occlusions between the start and end points by holding down the Shift key (for extra points) or the Ctrl key (for occlusions) while clicking the image in the required positions.

6. Click on a point to define the Aorta Bifurcation.
   ⇨ The Aorta Bifurcation option is checked and Bifurcation is displayed on the image. You can skip this point and select to mark another point by selecting the point you want to mark in the protocol dialog box. You can mark the skipped arteries at a later stage.

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NOTICE

You can remove the last point you clicked by clicking the Delete Last Point button.

If you reopen the protocol at a later stage, you will be instructed to mark only the sections that were skipped. When the missing points are marked, the new vessels will be joined to the vessels that already existed.

7. Mark a third point at the end of the left iliac artery.
   ⇨ The Left Iliac Artery option is checked. Left Iliac is displayed on the image.
8. Mark a fourth point at the end of the right iliac artery.
   ⇨ The Right Iliac Artery option is checked. Right Iliac is displayed on the image. The Aorta Protocol window appears.

- To mark the intermediate points (the points between the start and end points) in a different order (for example, the left iliac artery before the bifurcation point), select the relevant row in the Aorta Protocol dialog box, then mark the point on the image.
- If you do not want to mark both the left and right iliac arteries, you can mark either one, then mark the other one later. Select New Vessel, then select Aorta Protocol, then mark the other vessel.
- If you do not mark one of the named points, the next time you open the Aorta Protocol dialog box for that vessel, the row of the unmarked point will be selected and ready for marking.

9. Mark a fifth point at the end of the left iliac artery, if desired.
10. Click Done .
    ⇨ A message appears while the vessel is being calculated. Once the vessel has been calculated, additional Vessel menu and toolbar options are displayed.

NOTICE

The end points do not have to be marked at the very end of the arteries. You can decide where to end the vessel tracking.

See these topics:

Defining and Marking Occlusions on page 223

Defining and Marking Extra Points on page 224

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13.7.9 Tracing Carotid Arteries Using the Neck Protocol

The Neck Protocol is specifically designed for tracing images of the carotid arteries in the neck.

NOTICE

The procedure for using the neck protocol is the same as for the General Protocol, though the calculation is different, enabling better segmentation of neck vessels.

1. In the Archive Explorer, right-click the study you want to view, select Load To, then select Vessel Analysis.
   ⇨ By default the study is displayed in a 2x2 layout with an angiography MIP or volume rendering image and three reference images.
2. In the Vessel Analysis toolbar, click New Vessel .
3. Select Neck Protocol.
   ⇨ Mark Point  appears on the toolbar. You must select Mark Point each time you want to add new points.
4. Place the points and the occlusion points on the vessel in the required location.
5. Click Done .
   ⇨ The vessel is calculated and the path is displayed.

See these topics:

Defining and Marking Occlusions on page 223

Defining and Marking Extra Points on page 224

Tracing Arteries Using the General Protocol on page 222

13.7.10 Tracing Arteries Using the General Protocol

The options for using General Protocol are the same as for the Neck Protocol.

1. In the Archive Explorer, right-click the study you want to view, select Load To, then select Vessel Analysis.
2. In the Vessel Analysis toolbar, click New Vessel .

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3. Select General Protocol.

   ⇨ Mark Point  appears on the toolbar. You must select Mark Point each time you want to add new points.

4. Mark extra points or occlusion points along the length of the vessel path:
   - Mark a regular point by holding down the Shift key and clicking the location of the point on the image.
   - Mark an occlusion point by holding down the CTRL key and clicking the location of the point on the image.

NOTICE

A regular point is marked . An occlusion point is marked .

5. Click Done .

   ⇨ The vessel is calculated and the path is displayed. You can proceed to the next vessel.

See these topics:

Defining and Marking Occlusions on page 223

Defining and Marking Extra Points on page 224

Tracing Carotid Arteries Using the Neck Protocol on page 222

13.7.11 Defining and Marking Occlusions

If Vessel Tracking does not find the correct path between two points due to an occlusion, you can mark the occlusion and fix the vessel. You can mark occlusions as part of the process of segmenting the vessel for the first time or as part of the process of fixing the segmented vessel.

Occlusion points are marked on the active line. You must be standing on the correct line in order to define the occlusion. For example, if you mark the bifurcation point as the start of the occlusion, it will be marked on both vessels (left iliac and right iliac).

1. Press CTRL and click a starting point on the reference
2. Select the next protocol or extra point to define the end-point of the occlusion.

   ⇨ When the vessel is calculated or recalculated, a line is drawn along the occluded part of the vessel.

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NOTICE

You can mark two or more occlusion points on an image. The more points you mark, the more accurate the vessel calculation will be.

See these topics:

Defining and Marking Extra Points on page 224

Tracing Arteries Using the General Protocol on page 222

Tracing Carotid Arteries Using the Neck Protocol on page 222

13.7.12 Defining and Marking Extra Points

For each protocol, you can define and mark extra points along the vessel to help segment the vessel between the start and end points. You can enter as many extra points as required.

- Press Shift and click the reference image to mark the point. This point will have the same name as the currently marked line, meaning the one that is checked in the dialog box.
- For tracing a path along the aorta and iliac arteries, press Shift and scroll down to mark additional extra points, until you have finished marking the extra points for a specific section of the vessel. When you release the Shift key, the next row (point) is selected (ready for marking) in the Aorta Protocol dialog box.

NOTICE

All extra points marked between two named points using the Aorta Protocol will have the same name as the named point preceding the extra points.

13.7.13 Deleting Extra Points

To delete the last defined extra point:

- Click Delete Last Point .

To delete all extra points:

1. Uncheck the point check box in the protocol dialog box.

   ⇨ All extra points between the last predefined point and the unchecked point are deleted.

See these topics:

Defining and Marking Occlusions on page 223

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Tracing Arteries Using the General Protocol on page 222

Tracing Carotid Arteries Using the Neck Protocol on page 222

13.7.14 Using Automatic Vessel Segmentation

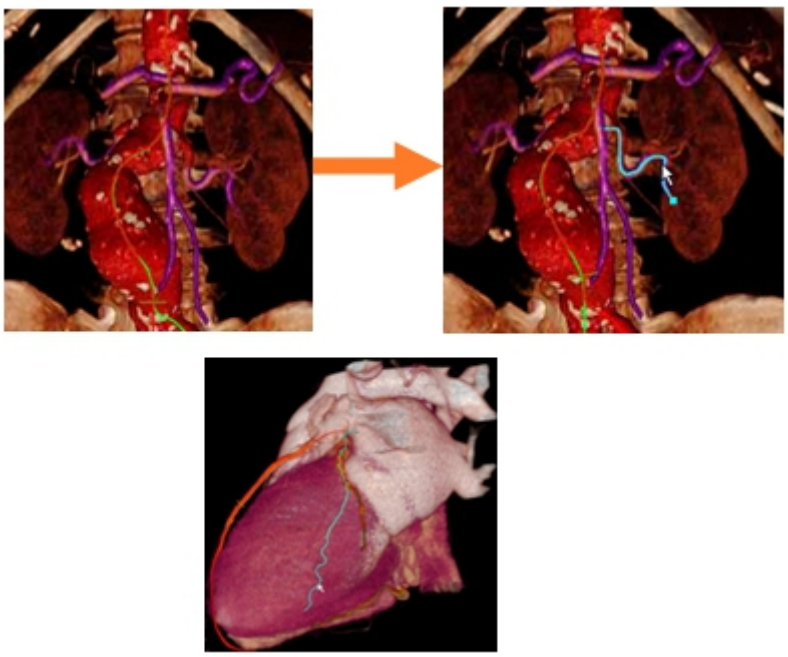
Use the protocol to automatically segment major arteries and generate minor arteries accessible through the reference 2D/3D images.

IMPORTANT

Cage removal is mandatory for cardiac scans. Bone removal is optional but recommended for body scans.

Click New Vessel > Automatic Protocol (Coronary Tree or Torso/Runoff).

The algorithm segments the major vessels and displays the vessels on the 3D image. The layout changes to examine one major vessel. The vessels are purple on the reference images.



Place the mouse cursor over a purple vessel to view the suggested vessel path. The suggested path is cyan (blue).

Right-click the suggested path and select one of the options:

Accept—accepts entire suggested path as a vessel.

Accept As—accepts the entire suggested path with a name from a predefined list.

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NOTICE

You can edit the predefined list through the central configuration.

Accept up to marker—accepts the portion of the suggested path up to the blue marker near the mouse cursor.

NOTICE

Holding the mouse cursor over a defined vessel produces suggestions for vessels branching from the defined vessel, if applicable.

The vessel is made active and shown in the panoramic image. You can edit the vessel with the correction tools in the Vessel tab.

Accessing the vessel menu

Right-clicking a defined vessel in the 3D image opens the menu.

Renaming a vessel

You can rename a defined vessel.

1. Right-click the defined vessel or click the Vessel drop-down menu.
2. Select the name in the predefined list.
3. Edit the name from the central configuration.

Extending a vessel

You can extend a defined vessel distally or proximally. The operation depends on the location of the cursor in the 2D/3D image.

Right-click the vessel and select Extend or click Extend Vessel.

Automatic path suggestions are shown by purple regions. Right-clicking a purple region opens a menu with options for accepting the suggested extensions.

Left-clicking outside the purple regions extends the vessel up to the click point.

NOTICE

This mode of extention is applicable for vessels defined using the other protocols, such as general, aorta, and neck.

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NOTICE

Press the **Shift** key while clicking to maintain the mode for additional seed points.

IMPORTANT

Click Undo extend to cancel the vessel extension results.

Creating a vessel branch

On a defined vessel, move the active vessel cut point to the bifurcation point.

Click Branch to create a copy of the defined vessel up to the bifurcation point.

Click Extend Vessel to track the desired branch.

Recalculating center line/contours

Change the vessel (edit or truncate).

Click Recalculate Contours to update visualization and automatic measurements.

Click Recalculate Vessel to re-center the vessel and update the contours based on the new center line.

Visualization options

Show/Hide vessel graphics—toggles the vessel center lines and contours in all images.

Show/Hide vessel overlays—covers the MPR image with a transparent, color-coded overlay of vessels.

Purple—regions with identified vessels.

Orange—vessels already defined.

NOTICE

Overlay colors and opacity are editable from the central configuration.

Show/Hide vessel suggestions—disable/enable automatic vessel path suggestions and purple regions in 2D/3D images.

NOTICE

Pressing **CTRL** temporarily disables suggestions during operation of other modes.

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Show/Hide data—toggles between vessel-only and full data in VolR image.

13.7.15 Viewing Vessel Tissue

After you have defined one or more vessels, you can select which vessel to view.

1. Click List of Vessels .
2. Choose the required vessel from the list.
   ⇨ When you define a vessel using one of the automatic options, three images appear.

- The original vessel that was defined.
- A panoramic image displaying a graph of minimum diameter along the defined vessel.
- Cross-section image containing three measurements: minimum diameter, maximum diameter, and total area. By default, the diameters are hidden, but you can right-click these measurements and then select Show Diameters or Hide Diameters. The cross-section image is automatically zoomed to display the contour of the vessel.

NOTICE

Click a line on the cross-sectional image you want to move, then drag it to the location you want. The new measurements appear.

3. After you have defined the vessel, you can change the image type.

13.7.16 Working with Tissues

After vessels have been defined, you can use the Tissue menu to:

- View the vessels that have been defined
- Turn tissues on and off, regardless of which vessel you are currently examining
- View tissue information
- Save VOI

See these topics:

About Tissue Definition on page 196

Changing Highlight Values for Tissue Definition on page 199

Using Balloon on page 200

Placing a Seed Point on page 200

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Placing an Outside Point on page 201

Adding and Removing Pixels on page 202

Using Bridge on page 202

Using Minimum Volume on page 203

Using Fill on page 203

Resetting the Images on page 203

13.7.17 Choosing Screen Layouts

The Diagnostic Workstation automatically chooses the most appropriate layout to view the images of the defined vessels. The choice of layout depends on whether the vessel you are defining is horizontal or vertical, or long or short.

The screen layout provides the most accurate and appropriate screen with which to view the image of the defined vessel. If required, you can specify Standard Layout, which is 2 x 2, or Vessel Layout. You generally start with the Standard Layout, define a vessel, then change the vessel layout.

The vessels are arranged according to the way that they were marked on the image.

- If the vessels were marked horizontally on the image, the layout is two images on the top (original and cross-section), and one panoramic image on the bottom.
- If the vessels were marked vertically, the panoramic image is displayed on the right side of the screen, and the original and cross-sectional images are displayed on the left side.

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NOTICE

If you define a number of vessels, the layout will be arranged according to the first vessel defined.

See these topics:

Changing the Vessel Analysis Image Layout on page 230

Changing the Vessel Analysis Image Type on page 229

13.7.18 Changing the Vessel Analysis Image Type

In the Vessel Analysis application, three reference images are displayed (coronal, sagittal, and axial) and a 3D image (angiography MIP or volume rendering). Once the vessel has been segmented, you can toggle between the views of each vessel by selecting the appropriate central line.

- Right-click the image type annotation at the top-left of the image, then select the viewing mode from the shortcut menu.

  Image type options:

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- Angiography MIP: Displays 2D projections of the highest intensity pixels in a 3D volume of interest. These images can demonstrate contrast-enhanced vascular structures and other high-density tissue or respiratory airways. See Angiography Display Window.
- Volume Rendering: Displays the volumetric data, using the assigned color and opacity assigned for each pixel. The effect is that of semitransparent tissues, which partially hide other tissues. The lighting of sources can be used for enhanced 3D sensation. See Using Volume Rendering in Generating Volume Rendered Images (VOLR) on page 632.
- Panoramic: Displays the entire vessel expanded.
- Panoramic Orthogonal: Displays the vessel expanded, but rotated 90 degrees.
- Cross Sectional: Displays the image perpendicular to the curve in the cut point.
- Axial: Displays the axial image at the cut point.

You can select which image type is the default image in the Display Protocol.

NOTICE

If you do not have a default specified in the Display Protocol, contact the system administrator.

In addition, you can change the layout in the layout menu. The standard layout is the default. After defining a vessel, the system automatically changes to vessel layout. (There are different layouts specifically for the examining vessels.) Upon deletion of a vessel, or when defining a new vessel, the system automatically changes back to the standard layout. See Changing the Vessel Analysis Image Layout on page 230.

To hide graphic elements on the vessel:

- From the Vessel menu, select Hide Vessel Graphics.

All contours, central line, and so on are hidden.

13.7.19 Changing the Vessel Analysis Image Layout

You can change the layout of your images using the Layout menu.

► Click Group Layout .

► Select a layout from the list displayed.

See these topics:

Choosing Screen Layouts on page 229

Changing the Vessel Analysis Image Type on page 229

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13.7.20 Defining Points of Interest as Stenosis Markers

You can define points of interest on panoramic images as stenosis location markings or bookmarks. Each stenosis has four points that should be distributed to the correct anatomical places.

To add a stenosis marker:

1. Select a panoramic image.
2. Place the cross-section marker on the desired point.
3. Click Mark Point of Interest .
4. Select Stenosis from the drop-down menu.
   ⇨ Four stenosis markings are displayed on the midline of the vessel at the current cut point, as follows:

- Ref. 1: Reference marking
- Sten St. 1: Stenosis start point
- Stenosis 1: A point between the stenosis
- Sten. End 1: Stenosis end point

5. Select and drag each stenosis marker to the correct position on the midline.
   ⇨ The markers change color.

- You cannot move a marker beyond the next marker, meaning that you cannot move Sten St. 1 past Stenosis 1.
- Make sure that you also move the line connecting the marker to the annotation when dragging the marker.
- Make sure that two annotations do not overwrite each other.
- For each additional stenosis on the same vessel, the point numbering increments by one. For example, the second stenosis on a vessel will be labeled Ref. 2, Sten. St. 2, and so on.

6. If required, add additional stenosis markers on the image.

To delete a stenosis marker (all four points):

1. Select a marker.
2. Press Delete.

To undo all changes made to the vessel:

- Click Reset.

13.7.21 Defining Points of Interest for Aneurysm Measurement (Stent Planning)

You can define points of interest for stent planning, such as a stent for an aortic aneurysm.

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1. Trace the artery using the general protocol (see Tracing Arteries Using the General Protocol on page 222).
2. Click Mark Point of Interest .
3. Select Aneurysm from the drop-down menu. Six markers are placed on the vessel.
4. Move the markers to the necessary position.
5. Measure each segment length correctly for the planned stent.
6. Click Report  to display the report with the measurements.

Aneurysm measurement

In Vessel Analysis:

Segment a vessel.

IMPORTANT

For an abdominal aortic aneurysm, select aneurysm point of interest when the cross-section is located below the origin of the renal arteries.

Six markers are automatically placed on the vessel. Change the locations as needed.

- D1—below the renal arteries
- E2—at the level of bifurcation
- D4—between the end of the aneurysm and E2
- E1—at the end of the aneurysm
- D3—at the maximum diameter of the aneurysm
- D2—at the beginning of the aneurysm

Click Vessel Report to obtain:

- Measurements of the markers
- Measurements of 4 segments:
  - L1—distance between end of renal arteries and neck of aneurysm
  - L2—length of aneurysm
  - L3—distance between end of aneurysm and bifurcation
  - L4—sum of the distances from end of the renal arteries to bifurcation

13.7.22 Defining Points of Interest as Bookmarks

You can bookmark points of interest along vessels in panoramic images.

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To add a bookmark:

1. Select a panoramic image.
2. Place the cross-section marker on the desired point.
3. Click Mark Point of Interest .
4. Select Bookmark from the drop-down menu.
   ⇨ A bookmark marking is displayed on the current position of the cut point, and has the label P1, P2, . . . If you move your cut point, the bookmark stays where it is.
5. If required, add additional bookmarks on the image.
   ⇨ Each bookmark has a sequential number.

To move a bookmark:

- Click the bookmark and drag it to the required position.

To delete a bookmark:

1. Select the bookmark.
2. Press Delete.

To delete all bookmarks:

1. Select the panoramic image.
2. Click Reset.
   ⇨ All changes you made to the vessel in this session are deleted.

13.7.23 Manipulating Images on a Defined Path

After you have defined a path on the vessel, you can manipulate the image.

NOTICE

To perform actions on an existing vessel path, click Edit Vessel  in the New Vessel toolbar to switch to edit mode.

To:	Do this:
Move along the vessel path	► Place the cursor on the cut-line of the vessel path displayed on the panoramic image. ► Drag the mouse to move along the vessel path.

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Change the vessel path	► Click Edit Vessel . ► Drag the cursor to change the path of the vessel.
Change/fix the vessel contour	► Click Edit Vessel . ► Do one of the following: • Click the existing contour on the cross-sectional image, then drag to draw the correct path. • Draw a new contour on the cross-sectional image. • Draw a new central line on the panoramic image. **NOTICE! The segmented tissue does not change. If none of the segmentation parameters were changed, recalculating the vessel does not take this change into account.**
Recalculate the vessel	You can recalculate the vessel after you make changes (for example, after moving the central line). • Click Recalculate Vessel . **NOTICE! If a vessel has been truncated, only the remaining part of the vessel will be recalculated.**
Create a new path	• Click New Vessel . Click Display Vessels  to view a list of previously defined vessels.
Truncate the vessel path	• Move the cut-line to where you want the vessel to end and click .
Move the central line	Drag the  in the cross-sectional image to the required position.
Reset	• Click Reset  to undo all changes.

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13.7.24 Viewing Vessel Measurements

On cross-sectional images, three automatic measurements are displayed in the bottom left corner of the image:

- Minimum diameter
- Maximum diameter
- Total area of the vessel cross-section

1. To display the diameters on the image to see where they occur, or to approve them, right-click the measurement annotation, then select Show Diameters.

   The cross-sectional image is automatically zoomed to display the contour of the vessel. If you change the contour, the area will change.

2. You can move a diameter line on the cross-sectional image by clicking on it and dragging it to the required location.

   The measurements displayed are automatically updated.

NOTICE

If you make any changes (such as diameters, contour, and so on), and then you change the central line in that area, then all your changes will be lost, including points of interest marked on the image.

13.7.25 Swiveling Panoramic and Scrolling Cross-Sectional Images

The panoramic image that displays is a perpendicular view to the MIP image displayed. This means that if the image is showing a coronal view, the panoramic image shows a sagittal cross-section of the traced path.

To swivel the panoramic image:

1. Place the cursor on the MIP image and click Swivel .
2. Drag the mouse in the direction you want to swivel.

   or

   Change the offset.

   ⇨ The offset determines the difference between the 3D image and the panoramic image. To change the offset, hover over the offset annotation (in the top right corner of the image). The cursor changes to an offset button. Click the offset, then move up or down to change it.

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NOTICE

Hovering over any red annotation displayed on the image changes the cursor to a button that lets you change certain properties of the image.

To scroll the cut line on the cross-sectional image:

- Click on the cut line, then use the mouse wheel to drag up or down or right drag.

13.7.26 Switching Between Vessels

You can switch between the defined vessels, meaning that you can select which vessel is displayed in the reference images.

Do one of the following:

- Right-click the vessel name, then select the vessel to display from the shortcut menu.
- Click List of Vessels .
- Press CTRL and simultaneously click the required vessel in the 3D image.

13.7.27 Deleting Vessels

You can delete a selected vessel or all previously defined vessels.

To delete the currently active vessel:

- Click Delete Active Vessel .

NOTICE

If the deleted vessel was the last vessel, the standard layout is displayed.

If a vessel is defined for more than one phase, only the vessel in the current phase will be deleted.

To delete all previously defined vessels:

- Click Delete All Vessels .

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13.7.28 Reporting Vessels

A report can be produced about any vessel that you defined, if the points of interest (bookmarks and/or stenosis) are defined for it.

1. To view the report, click Preview Report  in the toolbar.
   ⇨ The report provides you with the measurements for the points of interest, including:

- Minimum Diameter
- Maximum Diameter
- Mean Diameter
- Area of stenosis/bookmark
- Length of stenosis/bookmark

NOTICE

The contour displayed on the image is calculated automatically. The mean, minimum, and maximum diameters, and the area calculated are estimates, indicated on the image by the suffix est.

These measurements should not be used for diagnosis. To approve the measurements, or to approve the new values after editing the contour, right-click the measurement annotation, then click Approved.

2. Enter comments in the right pane, if desired
3. Select one of the following report options:
   - Preview Report: Displays the Preview Report window in which you can preview the entire report, including your comments and any images in the study that were marked as key images. From the Preview window:
     - Click Save to save the report.
     - Click Print to print the report.
     - Click Cancel to close the Preview Report window.
   - Save Report: Saves the report. A message appears at the bottom of the window to indicate that the report was saved successfully.
   - Close: Closes the report in progress window without saving.

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13.7.29 Using Saving Presentations in Vessel Analysis

The Save Presentation of the Vessel Analysis application takes a real snapshot of the data presented including already segmented vessels. In the Vessel Analysis application, the following parameters are saved:

- The exact datasets presented in each window (including phase information)
- Layout type (standard or vessel layout) and exact layout
- All MPR parameters
- Zoom and Pan
- Windowing
- Enhance
- Color Map
- Reference Point

For the 3D image, the Save Presentation should keep the 3D rendition type, the VolR protocol including windowing, 3D swivel, Clipping planes and position, VOI, Bone removal including bone corrections, bed removal and 3D frame (show/hide).

On studies where you have created vessels, the Save Presentation keeps all relevant information, all created segmentations after editing in the currently displayed vessel, exact view types in each window in the Result layouts all bookmarks, stenosis and aneurism information.

See these topics:

Saving a Study as a Presentation on page 620

About Save Presentation on page 619

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13.8 Cardiac CT Application

13.8.1 About the Cardiac CT Application

The Cardiac CT application lets you view various phases of the heart, view the heart axis images, and prepare images for additional processing.

Cardiac CT launches the Cardiac Phase Viewer, which lets you access the various cardiac analysis tools such as coronary analysis, cardiac cine, and so on. Cardiac Cine lets you create a simulated volume-rendered heartbeat that lets you study the external wall motion of the heart.

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NOTICE

The Cardiac CT application is available only if your profile has a license to use it.

MPR patient analysis uses coronary, axial, and sagittal images. When dealing with the heart, the images use different axes called short axis, long axis, and four chamber view.

By default, Cardiac CT data appears as one group in the Cardiac Phase Viewer. The basic Cardiac CT view has two main parts and displays reference images and result images.

Cardiac CT View Type	Description
Reference Images	• Display as Axial, Sagittal, and Coronal views. or • Display as Four Chamber, Short Axis, and Long Axis views. You can view either the first group or the second group, but they cannot be mixed.
Result Images	Display as the reconstructed cross-section images resulting from cutting volumes in a certain plane. You can configure the number of result images that display.

See these topics:

Creating a Cardiac CT View on page 239
Cardiac CT Application Toolbar on page 90
Viewing Cardiac CT Images on page 243
Working with Phases in Cardiac CT on page 244
Viewing Images in Single Phase Mode on page 245
Viewing Images in Multi-Phase Mode on page 246
Changing the Group Layout in the Phase Viewer Window on page 246
Loading Cardiac Cases on page 247
Printing Cardiac CT Images on page 248
Saving Cardiac CT Images on page 249
Displaying Volume Rendered Images in the Cardiac CT Window on page 249

13.8.2 Creating a Cardiac CT View

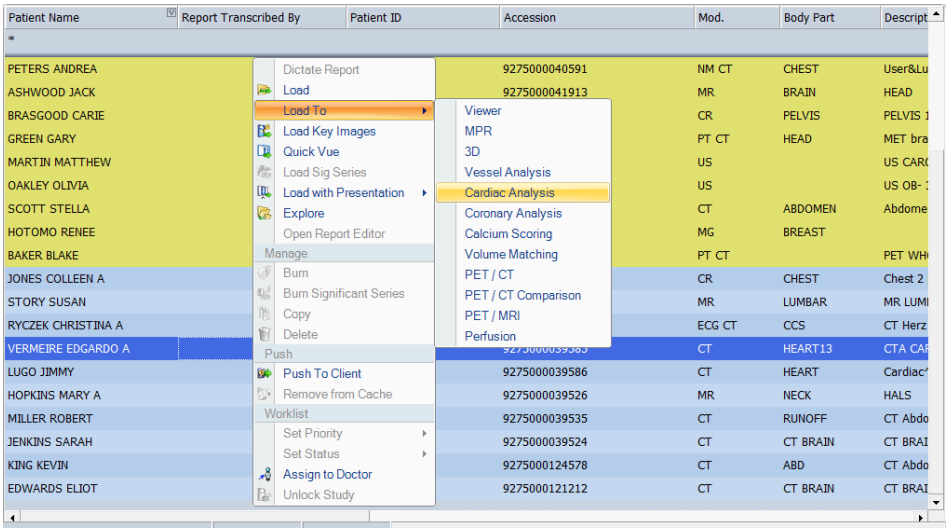
You can create a Cardiac CT view manually. For information about automatically creating a Cardiac CT view, go to Display Protocols (see About Display Protocols on page 594).

To create a Cardiac CT View:	Do this:

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From the Archive Explorer

Right-click a study group, select Load To, then select Cardiac Analysis.



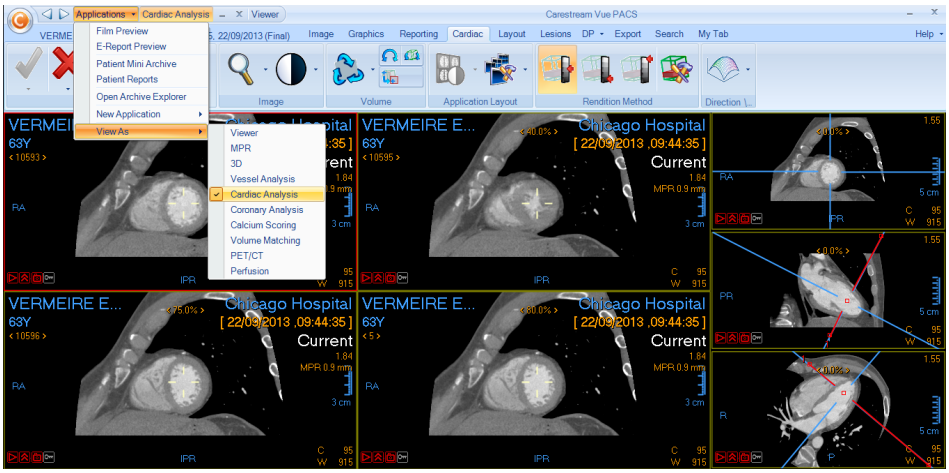
NOTICE! If several phases are selected, the application opens only one viewer window with all the phases. When you load Cardiac Analysis from the Archive Explorer, a dialog box appears that lets you select which phases to load. Only phases that are available in the study appear.

In the PowerViewer Application

- Right-click an existing group, click View As, then select Cardiac Analysis.

Or

- From the Applications menu, select View As, then select Cardiac Analysis.



From the Patient Mini Archive

- ► Right-click a study group, then drag it to the displayed area.
- ► Select Cardiac Analysis.

To an open application

If the currently open application is Cardiac CT, click the study group in the Patient mini archive, then drag it to the display area.

The selected group of images appears in the viewbox in the default Cardiac Analysis view. The reference images and result images appear in the location and layout that was last used.

The Cardiac CT application can be launched and shows full reading functionality even if only a few phases of a study are selected. You can open the Archive Explorer during a Cardiac CT session and add additional phases.

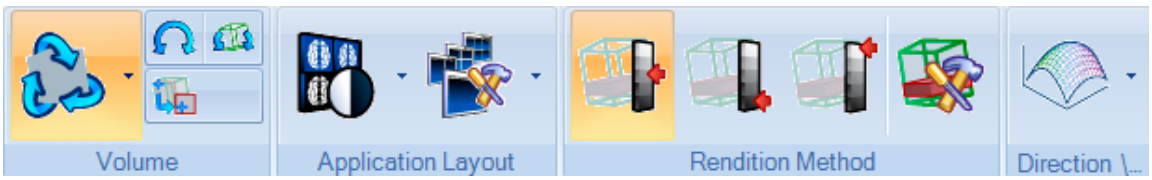
- Drag a group to drag all the phases.

NOTICE

Cardiac CT application auto retrieves all relevant phases, so you cannot add anything from the Patient mini archive to it.

13.8.3 Cardiac CT Application Toolbar

The following tab is added to the About the PowerViewer Application Toolbar on page 72 application toolbar when you open the Cardiac CT application.



Icon	Description
Volume	
	Swivel the image.
	Roll the image from side to side around the center of the volume.
	Roll the image to the closest axial, sagittal or coronal plane.
	About Relate Mode on page 590.
Application Layout	
	Duplicate a group of result images to manipulate them individually. •  None: Duplicates the group. •  Vertical: Duplicates the group and displays the duplicate group adjacent to the original group. •  Horizontal: Duplicates the group and displays the duplicate group under the original group.

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Select group layout:

- MPR standard Layout (default), displaying a result image and reference images showing the scanned volume in axial, sagittal and coronal views with default and additional cross-section lines. In this layout you can select one image, two images, 2x2 images, 2x3 images, or user defined number of images.
- MPR 2x2 layout
- MPR double oblique layout. Allows you to view volumetric data in a 2x2 layout by retaining a perpendicular relationship between the planes. Press Shift to use the perpendicular and horizontal cross section lines in the reference images as obliques.

You can also apply:

- Single-phase mode
- Multi-phase mode

Rendition Method



MPR (average MipPR) - Render the MPR slab using the average pixel value.



MIP (maximum intensity projection) - Render the MPR slab using the maximum pixel value.



MinPR (minimum intensity projection)- Render the MPR slab using the minimum pixel value.



Control rendering parameters. Select rendition type, slice thickness and slice spacing.

Direction



Reformat plane and curve:

- Axial/Sagittal/Coronal: Lets you define the planar view, or orientation, of the image.
- Parallel/Concentric/Sectional/Sectional parallel: Lets you draw and manipulate curved cross-sections on the reference images, as follows:
  - Parallel: Curved cross-sections that are parallel to one another.
  - Concentric: Curved cross-sections that decrease in size towards the same central mid-point.
  - Sectional: Cross-sectional slices that are perpendicular (90°) to a defined curved cross-section.
  - Sectional Parallel: Parallel cross-sectional slices on a defined curved cross-section.

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13.8.4 Viewing Cardiac CT Images

The Cardiac CT application view displays in the Cardiac Phase Viewer window. The Cardiac Phase Viewer viewbox is divided into reference images and result images.

13.8.5 Reference Images

Reference images show the scanned volume in one of the following formats:

- Heart Axes: Four Chamber, Short Axis, and Long Axis views.
- Patient Axes: Axial, Sagittal, and Coronal views.

To change the reference image view:

- From the MPR menu, click Patient Axes or Heart Axes.

You can reset the heart axis view to the suggested view by clicking Reset Heart Axes.

Each reference image contains the following:

- Default MPR Cross-Sections: Each set of crossed horizontal and vertical cross-section lines correlate to the common orientation point in the other two reference images for the currently displayed cross-section slices in the result images. You can manipulate these cross-sections to show different cross-section slices.
- MPR Cross-Sections: These additional cross-sections correspond directly to the data that appears in the result images, depending on the selected layout:
  - If one result image displays, one relevant cross-section appears in the relevant reference images.
  - If four or more result images display, only the first, active, middle, and last cross-sections appear on the reference images.
  - These cross-sections can be moved or rotated simultaneously to show different cross-section and curved cross-section slices of data in the result images.

13.8.6 Result Images

Result images show the reconstructed MPR cross-sections that result from cutting volumes in certain planes on the reference images. Result images correspond directly to the cross-sections on the reference images. The number of result images depends on the layout you select.

IMPORTANT

The MPR Double Oblique layout provides specific capabilities for working with result images and reference images. See About the MPR Double Oblique Layout on page 174.

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13.8.7 About the MPR Double Oblique Layout

MPR Double Oblique layout allows you to view one volumetric dataset in several oblique (usually perpendicular) planes. You can swivel the reformatted planes to any orientation synchronously. MPR Double Oblique layout retains the perpendicular relationship between the planes.

MPR Double Oblique layout is appropriate to use in the Cardiac and the MPR applications.

Reset Reference Images is a new option available in the MPR menu for the MPR application. Reset Reference Images allows you to reset the images to the original axial/sagittal/coronal views.

NOTICE

Double Oblique View refers to three perpendicular views. In many reading scenarios, the three oblique views are the main images, called reference images.

See these topics:

Understanding the MPR Double Oblique Layout Capabilities on page 175

Using the MPR Double Oblique Layout on page 177

Applying Phase Modes to the MPR Double Oblique Layout on page 179

Toggling Group Layouts (MPR) on page 180

13.8.8 Working with Phases in Cardiac CT

The Cardiac CT Application is based on the MPR viewer and can be displayed in the following Group Layouts (see Configuring a Group Layout on page 561):

- Standard MPR Layout
- 2x2 MPR Layout
- MPR Double Oblique View (see About the MPR Double Oblique Layout on page 174)
- User-defined Layout

When you load a study that contains phase information into the Cardiac CT application, the viewer shows the first phase that was loaded. The currently displayed phase is indicated on the top center of the result image, using an interactive annotation.

To view:	Do this:
A lower phase	► On the phase annotation, place the cursor on the back arrow. ⇨ The cursor changes to . ► Click the mouse until you reach the required phase.

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A higher phase	► On the phase annotation, place the cursor on the forward arrow. ⇨ The cursor changes to . ► Click the mouse until you reach the required phase.
A loaded phase	Right-click the phase annotation, then select the phase you want to view.
In Single-Phase mode (see Viewing Images in Single Phase Mode on page 245)	Right-click the phase annotation, then select Single-Phase Mode.
In Multi-Phase mode (see Viewing Images in Multi-Phase Mode on page 246)	Right-click the phase annotation, then select Multi-Phase Mode.

See these topics:

Changing the Group Layout in the Phase Viewer Window on page 246

Configuring a Group Layout on page 561

Using the MPR Double Oblique Layout on page 177

Working with Cross-Sections on page 168

Working with Curved Cross-Sections on page 172

Selecting/Changing the Result Image on page 180

Enabling Dual Windowing on page 181

Moving a Reference Image on page 182

13.8.9 Viewing Images in Single Phase Mode

By default, images in the Phase Viewer are displayed in Multi-Phase mode. In Single-Phase mode, you can view all images belonging to a specific phase.

NOTICE

When moving between the Single-Phase and Multi-Phase modes, the result image corresponds to the active result image in the previous mode.

Moving from Single-Phase mode to Multi-Phase mode before the load process has completed may result in layout changes during the loading process.

See these topics:

Using MPR Double Oblique (Cardiac and MPR) on page 174

Working with Phases in Cardiac CT on page 244

About the Cardiac CT Application on page 238

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13.8.10 Viewing Images in Multi-Phase Mode

The Multi-Phase mode lets you view a specific cross-section across all phases.

When you enter the Multi-Phase mode, the Result section is split according to the number of phases that are loaded. The Reference images are displayed according to the phase you were viewing.

For example, if six phases were loaded (20-70%), and you were viewing phase 30% when you switched to Multi-Phase mode, the Result section splits to show the six images from the six different phases.

The Reference images are displayed according to the 30% phase. If required, you can change the phase displayed in the reference images by right-clicking the phase annotation in the top center of the images.

The reference image always follows the phase of the active image. In Multi-Phase mode, each image has a different phase.

If you select a different image, the reference images are updated to display the same phase as the active image.

If you click on 60%, all reference images will also show 60%.

In Single-Phase mode, the number of images displayed is determined by the layout settings. For example, if the layout setting is 4x4 then 16 images are displayed.

In Multi-Phase mode, the maximum number of images displayed will never be more than the number of phases. If your layout is set to 4x4 and there are 14 phases, only 14 images will be displayed.

NOTICE

You can use the Group Layout (see Changing the Group Layout in the Phase Viewer Window on page 246) feature to change the number of groups that can be displayed. For example, if you change the layout to four groups, then only the first four phases (20-50%) are displayed. In Multi-Phase mode you can never get more groups than the available number of phases.

See these topics:

Applying Phase Modes to the MPR Double Oblique Layout on page 179

Working with Phases in Cardiac CT on page 244

About the Cardiac CT Application on page 238

13.8.11 Changing the Group Layout in the Phase Viewer Window

Phases

- Single-Phase Mode: Changing the group layout lets you define the number of images shown within a selected phase.

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- Multi-Phase Mode: Changing the group layout lets you define the number of phases that can be displayed. For example, if you change the layout to four images, then only the first four phases are displayed.

To Change the Group Layout

See Configuring a Group Layout on page 561.

See this topic:

Working with Phases in Cardiac CT on page 244

13.8.12 Loading Cardiac Cases

A cardiac case can have up to ten phases. Each phase can contain up to 500 images, so a cardiac case can contain up to 5000 images, which may take a long time to load.

- Right-click a study, then click Load or Load to Cardiac Analysis.

If it is a multi-phase study, a dialog box appears that allows you to select which phases you want to load.

NOTICE

Loading All Images (Select All) can be used in cases that have phase images and derived images (not all images have phase information).

If you select Run Automatic Algorithms, all of the phases you loaded are retrieved and starts in Multi-Phase mode. The default layout is always 2x2.

NOTICE

This option is disabled if you are in Coronary CT and have two or fewer phases. If you select three or more phases, this option is enabled (for Coronary CT).

If you load another phase to the system, it is retrieved by the Cardiac CT application and displayed.

For more information about working with Volume Rendered images, see these topics:

Generating Volume Rendered Images (VOLR) on page 632

Viewing a Volume Rendered Image on page 632

Manipulating Volume Rendered Images on page 633

About Volume Rendering Protocols on page 636

Windowing on page 644

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Switching Tissues Between VolR and MIP on page 639

Creating a Relate Point on a Volume Rendered Image on page 636

13.8.13 Printing Cardiac CT Images

Filming Cardiac CT images consists of setting parameters, exporting the series of images, then viewing and printing the images from the Film Previewer.

To film Cardiac CT images:

1. From the Viewer toolbar, click Film Series .
   ⇨ The Export a series dialog box appears.
2. Select the number of images you want to export.
3. Select a spacing value.

NOTICE

The images are selected from the center outwards. The maximum number of images available depends on the spacing value defined for the slices.

4. Select the thickness value.
5. In the Localizer area, select any reference images you want to include.
6. Select the High Resolution check box to save the image in high resolution (1024x1024).
7. In the Image Label field, type a name for the new series.
8. Click OK.
   ⇨ The new series is exported.

To preview and print the new series:

1. From the Viewer toolbar, click Film Previewer .
2. Preview the new series.
3. Print images, if desired.

See this topic:

Printing Images to Film on page 545

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13.8.14 Saving Cardiac CT Images

After filming images, you can save the series of images to the server.

1. From the Viewer toolbar, click Save .
2. In the Images Label field in the Save to dialog box, type a name for the images.
3. In the Localizer area, select any reference images you want to include.
4. Select one or more DICOM archives where you want to save the images.
5. Click Add.

NOTICE

You can modify the selected archives by clicking Remove, Add All, or Remove All.

6. OPTIONAL: If desired, add a text description of the series.
7. Click OK.

The images are saved in the selected archive(s). Changes applied to the images, annotations, or measurements are saved. The original images are not affected.

13.8.15 Displaying Volume Rendered Images in the Cardiac CT Window

1. Right-click and select Change Image.
2. Select Volume Rendering.
   ⇨ The volume rendered image appears.

NOTICE

When an image is changed to a volume rendered image, the system automatically performs cage removal for all phases (regardless of the number of phases), starting with the active phases. Once the system has finished removing the cage from all the phases, the cine is enabled.

3. Click Film .

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4. The Cine toolbar appears with Phase Cine  selected. The cine will switch between phases instead of rotating or scrolling the image. If there are enough phases, a heartbeat is simulated in the volume rendered image.

5. To change to regular cine, click Phase Cine .

⇨ To stop the cine, click Stop .

See these topics:

About Cine on page 555

Cine Toolbar on page 556

Setting Several States for Cine on page 557

Saving a Cine Movie on page 560

Viewing Cine Movies of Cardiac CT Images on page 559

Applying States to Cine Movies on page 558

13.8.16 Saving Presentations in Cardiac CT

When you use the Save Presentation feature in the Cardiac CT application, the following parameters are saved:

- The exact datasets presented
- The exact layout
- The Multi-phase mode
- All MPR parameters of the Result Images
- Zoom and Pan of the Result Images
- Windowing
- Enhance
- Color Map
- Reference Point
- Plane (Swivel and Rotate) in MPR images

In the Double Oblique layout, the axes orientation is saved in addition to the dataset planes.

See these topics:

Saving a Study as a Presentation on page 620

About Save Presentation on page 619

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13.9 Cardiovascular Reading

13.9.1 New Node

13.9.2 About Cardiovascular Reading

Vue PACS offers you a set of tools that facilitate cardiovascular reading. Some of these tools may also be used for reading Ultrasound (US) and X-Ray Angiography (XA) exams.

See these topics:

Automatic Cine Toolbar on page 98

Using Subtraction on page 252

Using Measurements on Doppler Ultrasound Images on page 254

Measuring the Velocity-Time Integral on page 255

Measuring Ejection Fraction on page 256

Cardiothoracic Ratio Measurement on page 258

Synchronizing Heartbeat on page 259

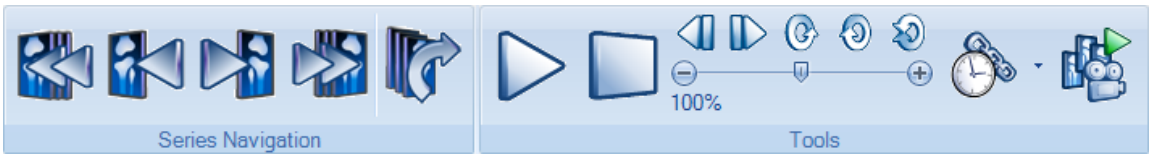
Annotating Cardiac Stress Images on page 260

Cardiac Viewing Display Protocols on page 261

Displaying ECG Lead Waveforms on page 261

13.9.3 Automatic Cine Toolbar

The following tab is added to the PowerViewer (see About the PowerViewer Application Toolbar on page 72) toolbar when you open an Ultrasound or Angio X-ray studies.



Icon	Description
Series Navigation	
	Show previous set of series - All displayed series of the selected study are replaced with the previous set.
	Shift series left - The previous series of the selected study is shown, while shifting the currently displayed series gradually. The series are shifted to the right, taking away the bottom right series in the viewer.

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	Shift series right - The next series of the selected study is shown, while shifting the currently displayed series gradually. The series are shifted to the left, taking away the top left series in the viewer.
	Show next set of series - All displayed series of the selected study are replaced with the previous set.
	Show first set of series - All displayed series are replaced with the first set.
Tools	
	Pause all cine loops - All displayed Auto-Cine groups are paused.
	Stop all cine loops - All displayed Auto-Cine groups are stopped.
	Previous/Next frame -All groups' progress is paused one step at a time (forward or backward, respectively).
	Forward/Backward/Back and Forth - Change the direction of all groups. Play the cine movie from beginning to end/from end to beginning/back and forth.
	Changes the playing rate of all groups. The percentage is applied to the default frame rate.
	Synchronize US or XA linked groups along the scan timeline, relative to the starting point of the scan. Use the Sync Absolute Time option to synchronize all linked groups to the same absolute point in time, regardless of the scan start time. (Used mainly for cases when a number of scanning sources are used). Synchronize heartbeat in linked Stress Ecocardiography US groups.
	Cine All - View all relevant series of a study continuously. The currently applied auto cine stops in all groups, and the selected group starts playing all series of the study in cine mode. When all images of the series have been played, the next series is automatically shown and played in cine mode. The PMA displays the currently playing group.

13.9.4 Using Subtraction

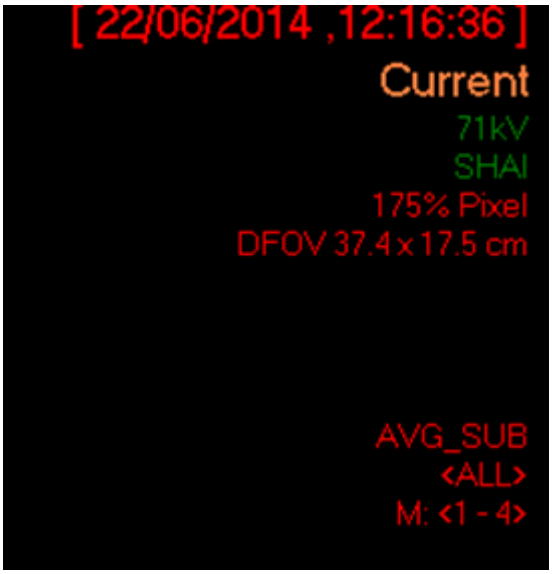
The Subtraction functionality allows you to view subtracted images based either on subtraction information supplied by the modality or on user request.

Subtracted images are shown automatically upon load if the modality adds the relevant subtraction information to the Mask Subtraction Sequence DICOM tag and if the appropriate setting has been configured to show subtraction by default.

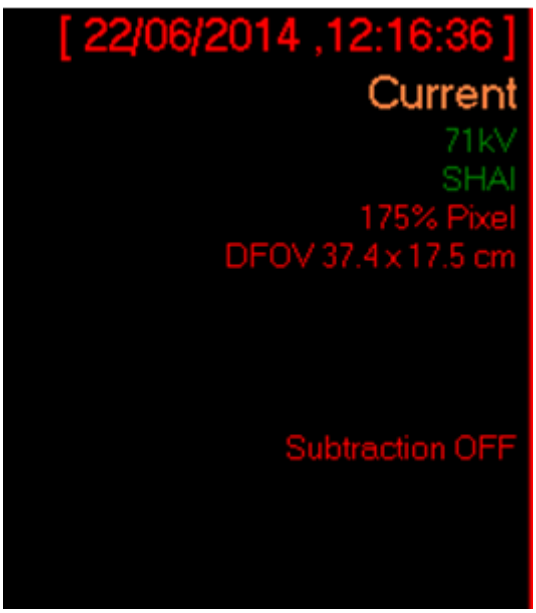
The following subtraction parameters are shown in an active annotation:

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- Subtraction type
  - Average (AVG)
  - Time Interval Difference (TID)
  - Reverse Time Interval Difference (REV TID)
- Applicable frame range - number of images involved in the subtraction.
- Range of mask frames (can be changed by the annotation).

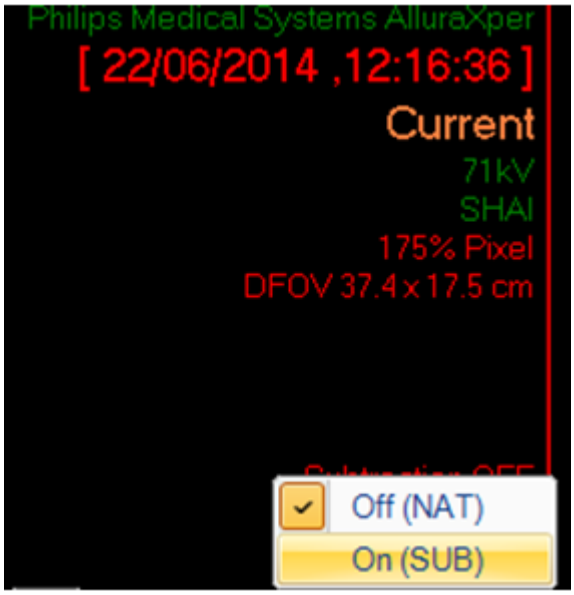


If the subtraction information is not supplied as a DICOM tag or if configuration is not set to show subtraction automatically, an active "Subtraction Off" annotation is displayed.



To activate the "Subtraction Off" subtraction –

1. Right-click the annotation and select **On (SUB)**. (The **Off (NAT)** option signifies native, non-subtracted images).



2. To change the number of mask frames, left-click the subtraction annotation and then drag the mouse up or down to increase or decrease the number of frames.

⇨ As a default, the first frame is used (range 1-1).

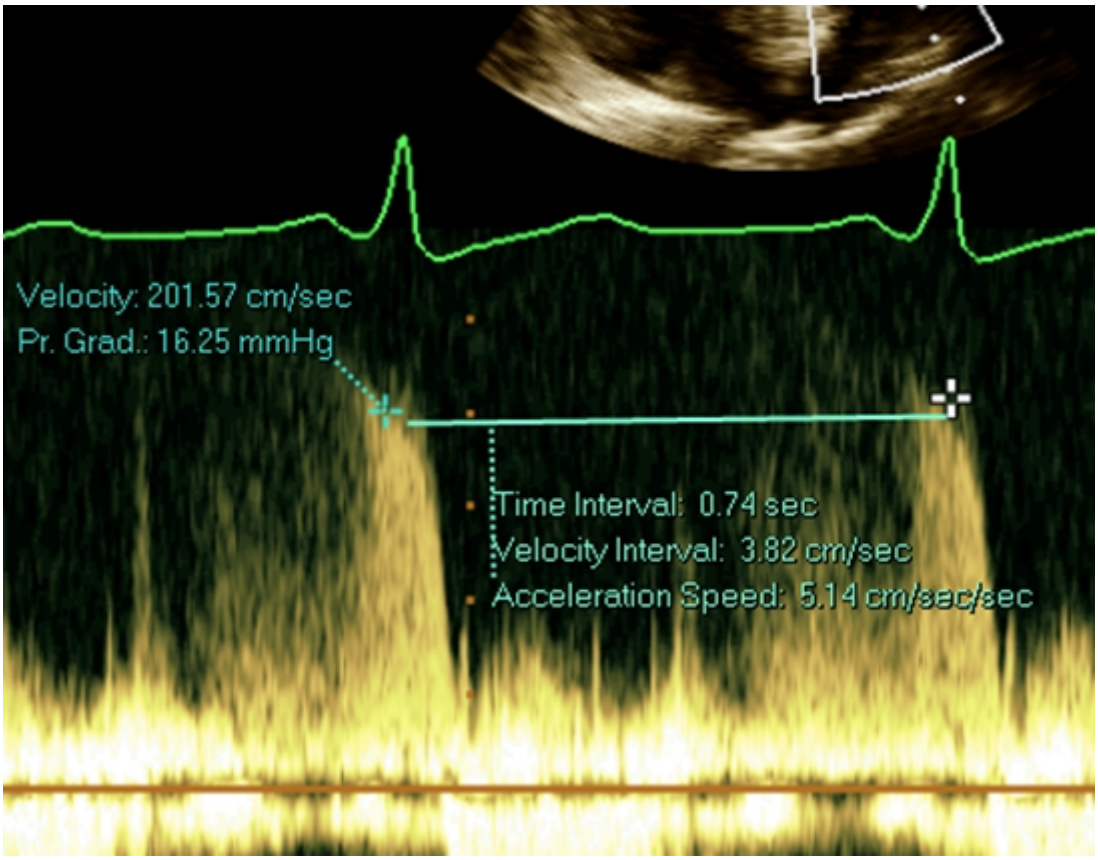
13.9.5 Using Measurements on Doppler Ultrasound Images

Continuous Wave (CW) and Pulsed Wave (PW) Doppler Ultrasound images often contain multiple independent data regions. The data presented in these various regions can represent a multiplicity of physical parameters, for example spatial distance, blood velocity, time, volume, etc.

Cursor and line measurements on various regions of the image yield different measurement values and units in accordance with the specific region on which they are drawn.

The cursor measurement (see Adding a Cursor to Measure Pixel Values on page 504) displays values of specific location, while a line (see Drawing a Line on page 500) measures a difference between the two edges of the line.

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13.9.6 Measuring the Velocity-Time Integral

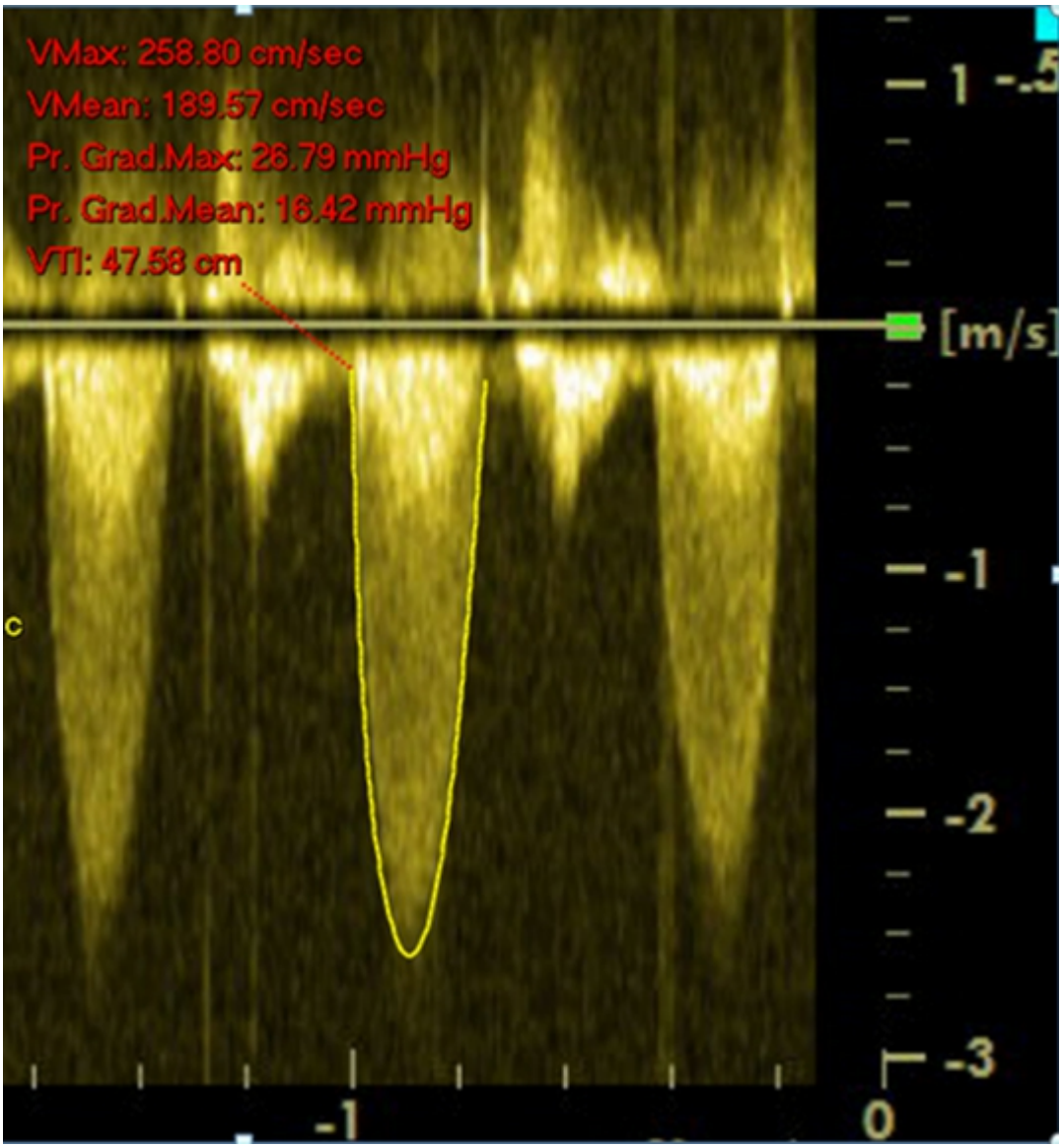
Use the Curve tool to measure the Velocity-Time integral

1. Click the curve icon  in the **Graphics** tab.
2. Trace the desired area to draw a curve. Use either of these methods:
   - Click a starting point and a peak point and then double-click the end point.
   - Multiple points as you trace the area. Double-click at the end point.
3. Adjust the drawn curve using the SHIFT key and the left mouse button.

⇨ The following values are calculated:

- Max velocity
- Max pressure gradient
- Mean velocity
- Mean pressure gradient
- Velocity time integral

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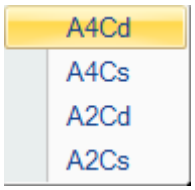
13.9.7 Measuring Ejection Fraction

Use the Cardiology tool  in the Graphics toolbar to measure biplane left ventricular ejection fraction. The complete measurement is accomplished by creating two sets of end diastolic-end systolic volume measurements.

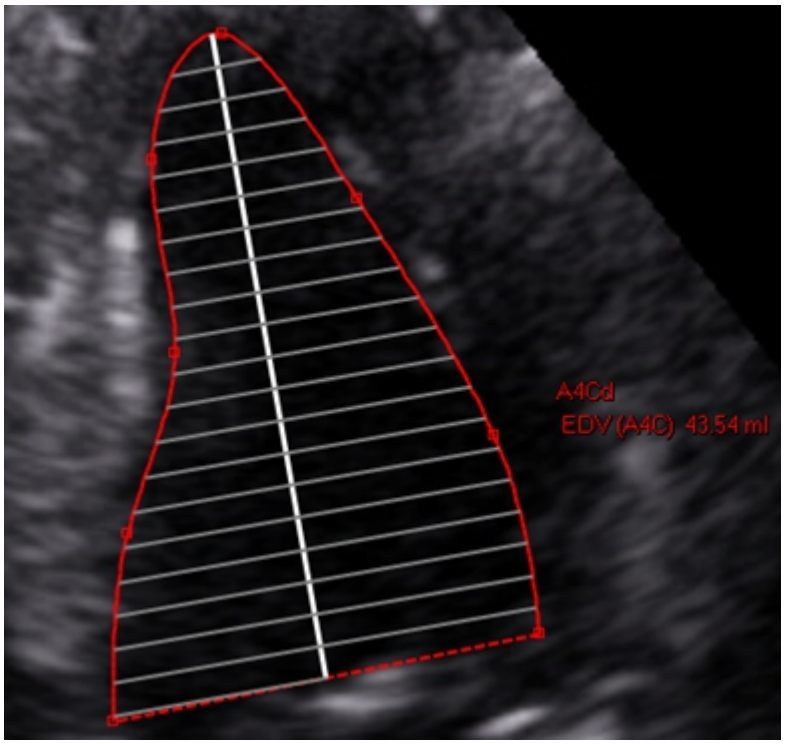
1. Locate the relevant cine loop in the echocardiography exam.
2. From the drop-down list of the Cardiology icon, select the type of volume to be measured.

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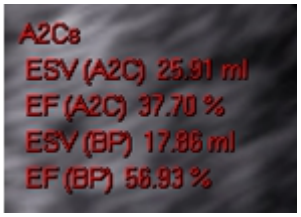
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3. Click the Ejection Fraction tool in the Graphics toolbar and start tracing the endocardial borders to draw their contour. Double click to end the tracing.
   ⇨ A dashed line is automatically drawn, connecting the two edges of the trace along the ventricle valve, and a second, perpendicular line appears, connecting the dashed line with the ventricle apex and marking the long axis of the ventricle. The volume is automatically calculated and displayed beside the curve.
   ⇨



4. Complete the end diastolic-end systolic set on this loop.
   ⇨ When both the end diastolic and end systolic volumes have been measured, the calculated ejection fraction is displayed next to both traced volumes.
5. Measure the second set of volumes.
   ⇨ When you measure the end diastolic or end systolic volumes on both the 4-chamber and 2-chamber views, the biplane volume is shown next to all contours.
   ⇨ If you measure all 4 volumes, the biplane ejection fraction appears as well.
   ⇨



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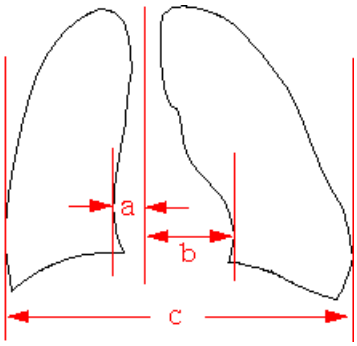
⇨ Measuring a specific volume twice (A4Cd / A4Cs / A2Cd / A2Cs) replaces the old measurement with the new one and the ejection fraction will recalculate.

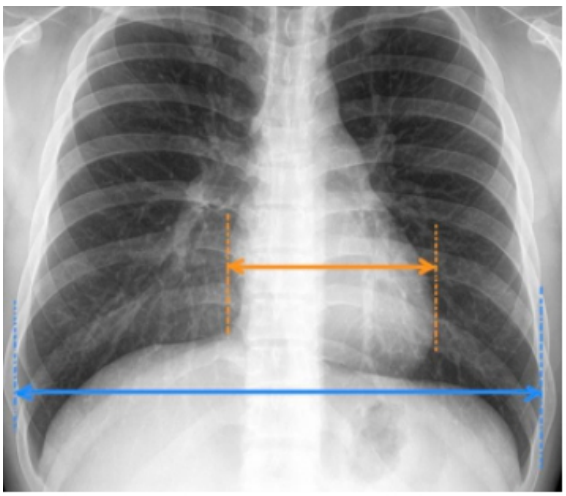
13.9.8 Cardiothoracic Ratio Measurement

The Cardiothoracic Ratio measurement enables measuring the Cardiothoracic Ratio (CTR) in chest X-rays in the PA position. However, the system does not enforce using the measurement only on chest X-rays. This can also be used on any viewer image.

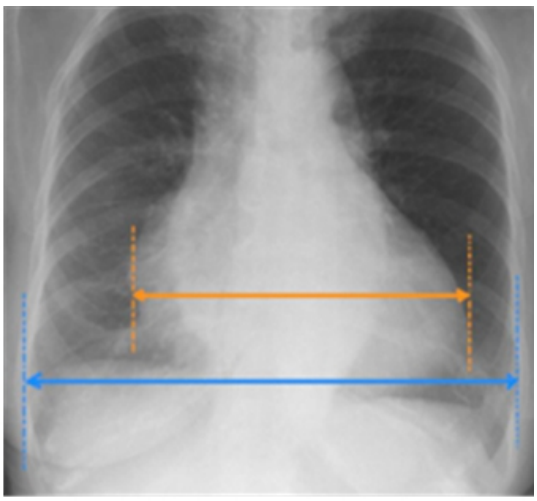
Cardiothoracic Ratio is defined as follows:

CTR = (a + b) / c * 100





Normal Case



Enlarged Case

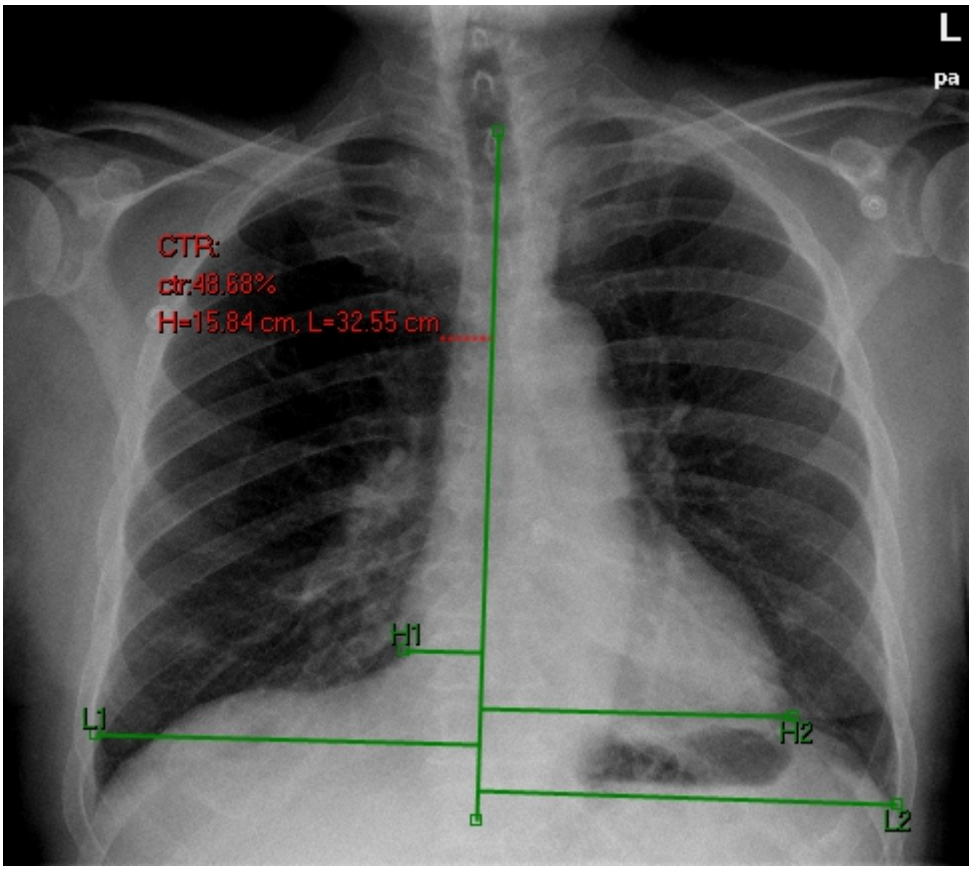
To use the Cardiothoracic Ratio measurement, draw a midline and four points that represent the lung and heart edges, as follows:

1. Click once to start drawing the midline and click again to finish drawing the midline.
2. Click at the edges of the two lungs and the edges of the heart cage, in any clicking order.
3. For each edge point, draw a line that is parallel to the midline and pass through the clicked point so that you can see if this line actually represents the desired edge.

When completed, the lines perpendicular to the midline are displayed and the ratio is displayed on the graphic.

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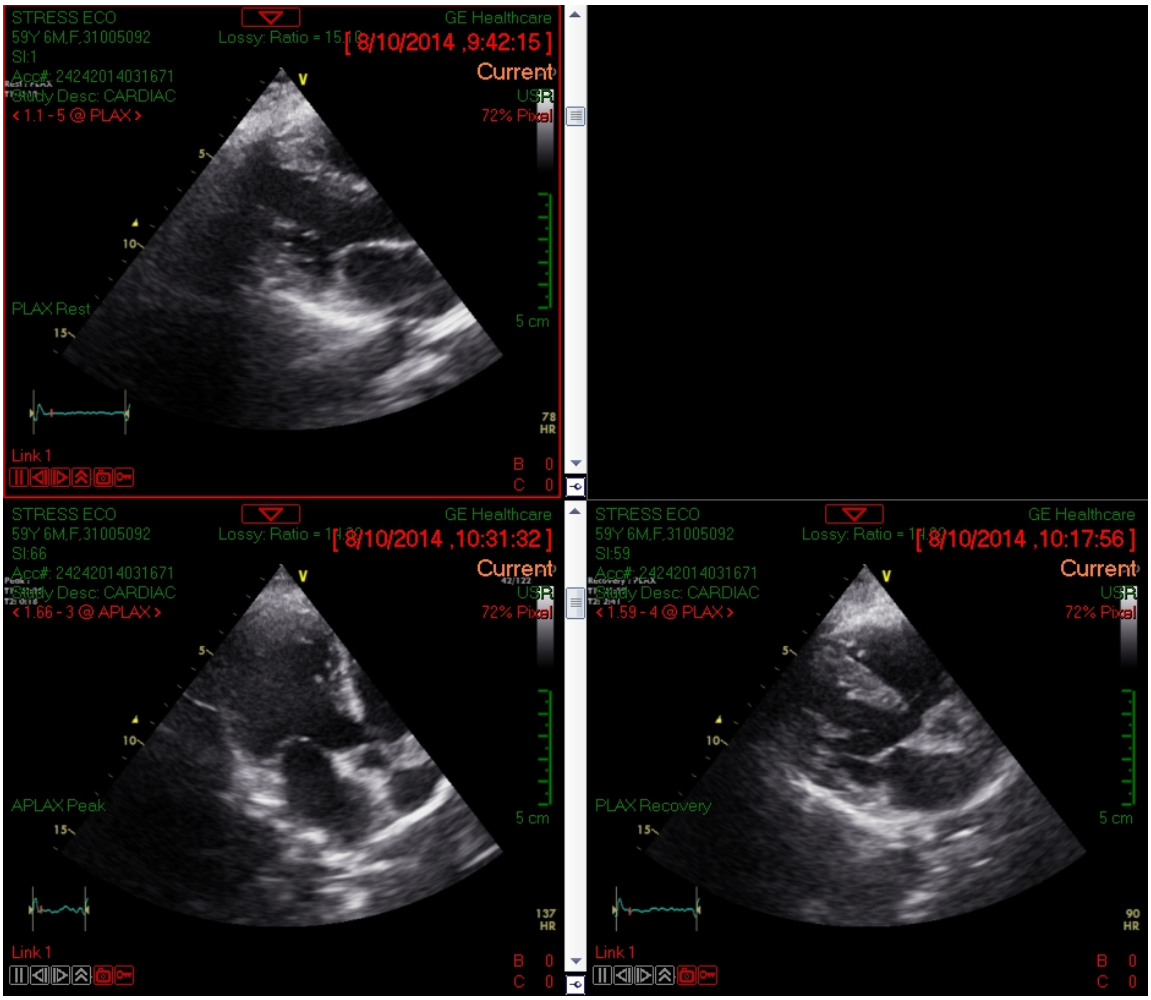
At any stage, it is possible to edit the measurement by moving any one of the input points. Perpendicular lines are adjusted as needed and the calculation is updated to reflect the new ratio.



13.9.9 Synchronizing Heartbeat

You can synchronize the heartbeat of linked Stress Echocardiography (ECHO) Ultrasound study groups, for example of the Rest, Peak, and Recovery Parasternal Long Axis (PLAX) views.

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To activate heartbeat synchronization, click Sync --> Sync Heartbeat in the Cine (see Automatic Cine Toolbar on page 98) toolbar.

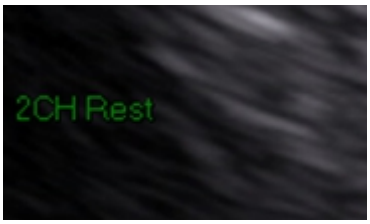
NOTICE

The system may be configured to automatically activate synchronized heartbeat in Stress ECHO studies.

13.9.10 Annotating Cardiac Stress Images

The stress echo view name and stage name are displayed by default on the left side of stress ultrasound images.

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You can remove or change the location of the annotation using Application Settings.

► In Application Settings, go to Annotation Options and select Annotations.

► In the Annotation Placement section, select US from the Modality drop-down list.

► Drag the annotation “view name stage name” to the desired place or select it and delete to remove it completely from the image. If you delete the annotation, it returns to appear in the Default Annotations list.

13.9.11 Cardiac Viewing Display Protocols

You can use Display Protocols (DPs) that support the flow of cardiac viewing. These DPs enhance -

- 4-chamber view
- 2-chamber view
- Long axis view
- Short axis view

You can also add groups using the “stage name” and “view name” tags.

See these topics:

About Display Protocols on page 594

About the Display Protocol editor on page 597

Defining Display Protocol Conditions on page 600

About Viewbox Configuration for Display Protocols on page 602

Defining Groups on page 607

About Group Parameters on page 610

Displaying ECG Lead Waveforms on page 261

13.9.12 Displaying ECG Lead Waveforms

Vue PACS allows you to display Electrocardiogram (ECG) waveforms. You can display a 12-lead ECG view, showing the three bipolar limb leads (annotated I, II, and III), the three unipolar limb leads (annotated aVR, aVL and aVF) and the six unipolar chest leads (annotated V1-6).

Selecting a Screen Layout

You can display ECG lead waveforms of 2 exams simultaneously.

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To select a layout, click the Series Chooser menu and click one of the layouts .

Manipulating ECG Lead Waveforms

Use the Image Manipulation toolbar at the bottom of the exam display to zoom, add measurements, change format, change gain, change speed, and reset the display.

Icon	Description
	Pointer
	Zoom the lead waveform.
	Measurement menu—Lets you measure differences between two points along the lead waveform, assess rhythm (with a caliper), hide grid, hide measurements, and delete measurements.
	Change Format menu —Lets you change the lead display format.
	Change Speed menu—Lets you increase or decrease distance per second (mm/s) representation on the X axis.
	Change Gain menu—Lets you Increase or decrease distance per voltage (mm/mV) representation on the Y axis.
	Reset all changes to the default display.

Zooming

Click the Zoom button  and drag the mouse up and down to zoom in and out in a single lead waveform.

Measuring Time and Voltage Differences

Use the Line tool  to measure time and elevation differences between two points.

1. Hover with the mouse over the Measurement menu  and click Line .
2. Click the lead waveform at the starting point of the measurement line, keep the mouse pressed, and drag to the end point.

   ⇨ A dotted line is drawn and an annotation appears displaying the second (x axis) and millivolt (y axis) values covered by the line.

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Assessing Rhythm

Use the Caliper tool  to assess rhythm normality by defining a time segment and comparing the heart activity during the same duration in other locations along the lead waveform.

1. Hover with the mouse over the Measurement menu , and click Caliper .
2. Click the lead waveform at the starting point of the segment to be defined, keep the mouse pressed, and drag to the end point.
   ⇨ A caliper appears with an annotation of the duration represented by that segment.
3. Click any other location on the lead waveform to move the caliper and compare the rhythm in that duration.

Hiding the Grid, Annotations, and Measurements

Use the Hide Grid tool  in the Measurement menu  to hide the grid in the lead display.

Use the Hide Annotation tool  in the Measurement menu  to hide the block values annotation at the bottom right corner of the display and the Current Study annotation.

Use the Hide Measurements tool in the Measurement menu to hide all measurements you have added to the lead waveform.

Deleting Measurements

Use the Delete Measurements tool  to delete all measurements you have added.

Changing the Format

Use the Change Format menu  to change the format of the lead display. By default the exam opens with a 3 x 4 lead display (each lead representing 2.5 seconds), with a longer rhythm lead (representing 10 seconds) at the bottom (a 3 x 4 + 1 format). You can change the format to 3 x 4 + 3, 3 x 4, 6 x 2, or 12 x 1.

In formats displaying longer rhythm leads at the bottom of the display, you can drag any of the other leads to the bottom part of the display to view the full 10 seconds.

Changing the Speed

Use the Change Speed menu  to change the paper speed representation of the display. The default speed is 25mm/s. You can change the displayed speed to 12.5, 50, 100 or 200 mm/s. The annotation at the bottom left corner changes to reflect the new values per one grid block.

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Changing the Gain

Use the Change Gain menu 

to change gain representation in the display. The default is 10 mm/mV. You can change the displayed gain to 5, 20, or 50 mm/mV. The annotation at the bottom left corner changes to reflect the new values per one grid block.

Interpretation Pane

The right-hand side pane displays information originating from the ECG device used for the exam. The pane displays study-related details (for example accession number, referring physician etc), interpretation values, and the automated interpretation supplied by the device.

13.10 Coronary Analysis

13.10.1 About Coronary Analysis

The Coronary Analysis application lets you define, manipulate, and analyze the coronary tree to detect stenoses (narrowing) or occlusions (obstruction), and so on. This is done by indicating to the system where vessels exist, then running the automatic algorithm that finds them. After that, you can make a diagnosis by looking at these vessels. You can also mark the interesting points in the vessels, and create a report within the application.

You can use one of the following protocols to define and segment the vessels:

- General Vessel Protocol (for general, non-coronary vessels)
- Coronary Protocol (for coronary vessels)
- Coronary Tree Protocol (for a specific, predefined coronary tree)
- Manual Protocol (for defining a curve that cannot be segmented)

The basic view displays three reference images (Axial, Sagittal, and Coronal views) and a 3D image.

You can fix contours and recalculate vessels. Once the vessel has been segmented, you can toggle between the views of each vessel by right-clicking the vessel name. In the MIP image, you can see the different defined vessels and you can toggle between them by clicking Control and the appropriate vessel.

The active vessel is indicated by color and a cut line. There are three ways to select which vessel is to be the active vessel. See Switching Between Vessels on page 236.

NOTICE

The Vessel Analysis and Coronary Analysis applications are available only if your profile has licenses to use them.

Many of the features of the Coronary Analysis application are similar to the features of the Vessel Analysis application. For information about these features, view the topics listed under About Vessel Analysis on page 213.

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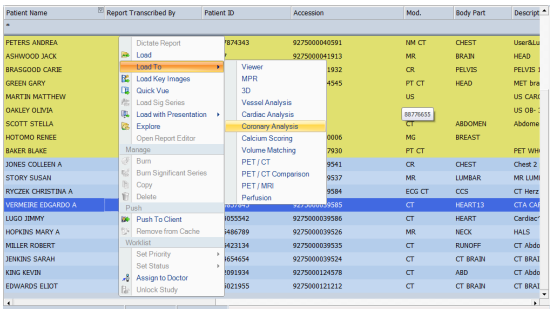
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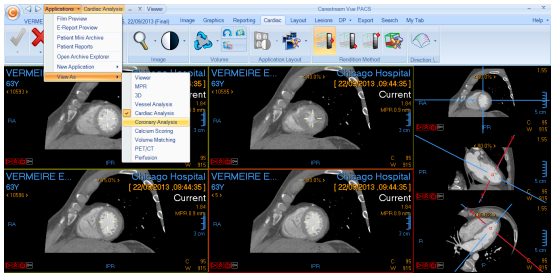
See these topics:

Creating a Coronary Analysis View on page 265
Coronary Analysis Toolbar on page 266
Creating a New Vessel on page 268
Loading Images to the Coronary Analysis Application on page 268
Viewing Different Phases on page 269
Tracing Vessels on page 217
Tracing Vessels Manually on page 273
Using Vessel Tracking on page 217
Tracing Coronary Arteries Using the Coronary Protocol on page 270
Tracing Coronary Arteries Using the Coronary Tree Protocol on page 271
Tracing Arteries Using the General Vessel Protocol on page 270
Viewing Vessel Tissue on page 228
Swiveling Panoramic and Scrolling Cross-Sectional Images on page 235
Reporting Vessels on page 237

13.10.2 Creating a Coronary Analysis View

You can create a Coronary Analysis view manually. For information about automatically creating a Coronary Analysis view, go to About Display Protocols on page 594.

To create a Coronary Analysis View:	Do this:
From the Archive Explorer	Right-click a study group, select Load To, then select Coronary Analysis.  Or Right-click a study group and, provided that a Coronary Analysis Display Protocol has been pre-defined, select Load.**NOTICE! If several phases are selected, the application opens only one window with all the phases.**

In the PowerViewer Application	• Right-click an existing group, click View As, then select Coronary Analysis. Or • From the Applications menu, select View As and then select Coronary Analysis. 
From the Patient Mini Archive	1. Right-click a study group, then drag it to the display area. 2. Select Coronary Analysis.
To an open application	• If the currently open application is Coronary Analysis, click the study group in the Patient Mini-Archive, then drag it to the display area. The selected group of images appears in the application. The reference images and result images appear in the location and layout that was last used.

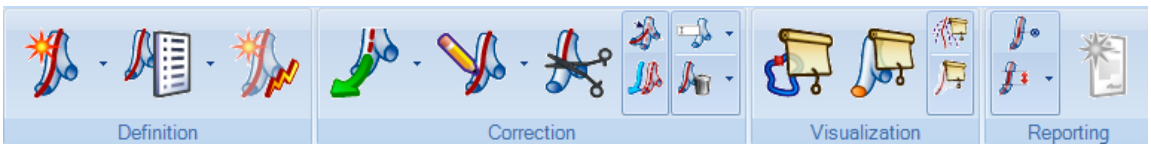
The Coronary Analysis application can be launched and shows full reading functionality even if only a few phases of a study are selected. You can open the Archive Explorer during a Coronary Analysis session, and add additional phases.

You can retrieve the data from the server and decide which phases to review. If you have a phase that is loaded and not viewed, you can drag that phase into the viewer.

1. Drag a group to drag all the phases.
2. Right-click and drag the group to select which phases should be dragged, then click Add Group.

13.10.3 Coronary Analysis Toolbar

The following tab is added to the PowerViewer application toolbar (see PowerViewer Toolbar on page 72) when you open the Coronary Analysis application.



Icon	Description
Definition	

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	Define a new vessel. Select a protocol type that matches the vessel to be segmented.
	Select a vessel from the list for viewing, editing and measuring.
	Mark points on any vessel and segment using the general vessel protocol.
Correction	
	Extend vessel segmentation beyond the existing end point.
	Manually edit segmented vessel center line or contours.
	Truncate the active vessel at a selected point.
	Create a new vessel by branching from the active vessel at the location of the reference marker.
	Recalculate the vessel based on manual editing.
	Rename the active vessel.
	Delete the active vessel.
Visualization	
	Hide center line and contours of all vessels.
	Hide orange overlay indicating segmented vessels and other vessel-related suggestions in MPR displays.
	Show/hide purple overlay indicating automatic protocol suggestions that have not yet been accepted.

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	Hide the rest of the 3D volume to isolate the segmented vessels and tissues.
Reporting	
	Mark a location along the vessel center line as a bookmark.
	Mark a point of interest: Mark a stenosis type point of interest; Mark an aneurysm type point of interest.
	Generate a Vessel Analysis report.

13.10.4 Creating a New Vessel

1. On the Coronary Analysis toolbar, click New Vessel .
   ⇨ The list of protocols is displayed (General Vessel, Manual, Coronary, and Coronary Tree).
2. Select the required protocol type.
3. Follow the instructions for how to trace a vessel using each protocol option:
   - General Vessel Protocol (see Tracing Arteries Using the General Vessel Protocol on page 270).
   - Coronary Protocol (see Tracing Coronary Arteries Using the Coronary Protocol on page 270). This protocol is specifically designed for images of the neck.
   - Coronary Tree Protocol (see Tracing Coronary Arteries Using the Coronary Tree Protocol on page 271).
   - Manual Protocol (see Tracing Vessels Manually on page 273).

In each case, you should define the start, intermediate, and end points for the vessel tracking. Each coronary vessel can be defined more than once, providing that each time it is defined in a different phase.

13.10.5 Loading Images to the Coronary Analysis Application

1. Load the images as described in Creating a Coronary Analysis View on page 265.

   If you load a specific phase of a study, you will be prompted to load the additional patient images suitable for viewing with the Coronary Analysis application.
2. Click Yes to load all the phases of the selected group of images.
   ⇨ The Select Phases for Cage Removal dialog box appears.

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NOTICE

If there are only one or two phases, the cage removal process takes place automatically (meaning that the cage removal algorithm is automatically applied).

3. Select the phase(s) in which the heart cage should be removed.

   You can also select that it should be removed in all phases or not at all.

4. Click OK.
   - ⇨ The cage removal calculation takes place, after which the image is displayed as a Volume Rendered image.
   - ⇨ If the application was invoked from the Archive Explorer, the first phase displayed is the first phase that was loaded.
   - ⇨ If the application was invoked from the Archive Explorer, the first phase displayed is the first phase that was loaded.

⇨ The currently displayed phase is indicated on the top center of the result image.

NOTICE

To perform cage removal, you can also click Cage Removal  on the Coronary Analysis toolbar.

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13.10.6 Viewing Different Phases

Phases are supported by the Coronary Analysis application. The phase annotation appears in the top center of each image indicating which phase is currently displayed.

To view a different phase before defining a vessel:

1. Place your cursor over the backward or forward arrows on the annotation, depending on whether you want to view a lower or higher phase.
   - ⇨ The cursor changes to 

 or 

.
2. Click the mouse until you reach the required phase.

   or

   Right-click the annotation.
   - ⇨ A menu that shows all the stored phases appears.
3. Select the phase you want to view.

To view a different phase after defining a vessel:

1. From the Vessel menu, select Standard Layout.
   - ⇨ The standard 2x2 layout is displayed, enabling you to move between the phases.

2. Click Vessel Layout to return to the panoramic and cross-section images.
   ⇨ The segmented vessel is displayed in its own phase.

NOTICE

You cannot change the phase during the vessel definition process, meaning that all points along a vessel must be in the same phase.

13.10.7 Tracing Arteries Using the General Vessel Protocol

1. In the Archive Explorer, right-click the study you want to view, select Load To, then select Coronary Analysis.
2. On the Coronary Analysis toolbar, click New Vessel .
3. Select General Vessel Protocol.
   ⇨ Mark Point  appears on the toolbar. You must select Mark Point each time you want to add new points.
4. Mark extra points or occlusion points along the length of the vessel path:
   - Mark a regular point by holding down the Shift key and clicking the location of the point on the image.
   - Mark an occlusion point by holding down the CTRL key and clicking the location of the point on the image.

NOTICE

A regular point is marked . An occlusion point is marked .

5. .
   ⇨ The vessel is calculated and the path is displayed. You can proceed to the next vessel.

13.10.8 Tracing Coronary Arteries Using the Coronary Protocol

The Coronary Protocol is designed for tracing images of the coronary arteries.

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NOTICE

The procedure for using the coronary protocol is the same as for the General Vessel Protocol; the calculation is different to enable better segmentation of coronary vessels.

1. In the Archive Explorer, right-click the study you want to view, select Load To, then select Coronary Analysis.

   By default, the study is displayed in a 2x2 layout with an angiography MIP or volume rendering image and three reference images.

2. On the Coronary Analysis toolbar, click New Vessel .
3. Select Coronary Protocol.
4. Place the points and the occlusion points on the vessel in the required location:
   - Mark a regular point by holding down the Shift key and clicking the location of the point on the image.
   - Mark an occlusion point by holding down the CTRL key and clicking the location of the point on the image.
5. Click Done .
   ⇨ The vessel is calculated and the path is displayed.

13.10.9 Tracing Coronary Arteries Using the Coronary Tree Protocol

The Coronary Tree Protocol is used for tracing the coronary tree arteries. The system provides you with a set of basic points, each one relating to a specific vessel location, including the start point, Left Anterior Descending Artery, First Diagonal, and so on.

1. In the Archive Explorer, right-click the study you want to view, select Load To, then select Coronary Analysis.
2. On the Coronary Analysis toolbar, click New Vessel .
3. Select Coronary Tree Protocol.
   ⇨ The Coronary Tree Protocol dialog box appears.
   ⇨ Mark Point  appears on the toolbar. You must select Mark Point each time you want to add new points.

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4. Click the start point on any of the MPR reference images.
   ⇨ Start of Section is checked and Start is marked on the image. If necessary, you can scroll the MPR reference images to view the required location.

NOTICE

You can mark any extra points or occlusions between the start and end points, by holding down the Shift key (for extra points) or the CTRL key (for occlusions) while clicking the image in the required positions.

5. Click on a point to define the Left Anterior Descending Artery.
   ⇨ The Left Anterior Descending Artery option is checked. You can skip this point and mark another point in the protocol dialog box. You can mark the skipped arteries at a later stage.

NOTICE

You can remove the last point you clicked by clicking Delete Last Point .

If you reopen the protocol at a later stage, you will be instructed to mark only the sections that were skipped. When the missing points are marked, the new vessels will be joined to the vessels that already existed.

6. Mark a third point on the First Diagonal.
   ⇨ The First Diagonal option is checked. First Diagonal is displayed on the image.
7. Mark a fourth point at the end of the Second Diagonal.
   ⇨ The Second Diagonal option is checked. Second Diagonal is displayed on the image.
8. Continue to mark points according to the selected row in the Coronary Tree Protocol dialog box until all the rows are checked.

NOTICE

You can mark intermediate points (the points between the start and end points) in a different order. Select the relevant row in the Coronary Tree Protocol dialog box, then mark the point on the image. For example, you can mark the left marginal branch point before the second diagonal point.

If you do not mark one of the named points, the next time you open the Coronary Tree Protocol dialog box for that vessel, the row of the unmarked point will automatically be selected, ready for marking.

If all the named points for a coronary tree are marked, and you uncheck one of the rows in the protocol dialog box, you will be asked to confirm the deletion of the point(s).

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9. Click Done .
   ⇨ A message is displayed while the vessel is being calculated. Once the vessel has been calculated, additional Vessel menu and toolbar options are displayed.

NOTICE

The end points do not have to be marked at the very end of the arteries. You can decide where to end the vessel tracking.

See these topics:

Defining and Marking Occlusions on page 223

Defining and Marking Extra Points on page 224

13.10.10 Tracing Vessels Manually

You can mark the vessel path (start point, intermediate points, and end point) by placing markers on any of the four displayed images. The system connects the points you marked with lines to show the vessel path.

NOTICE

Marking points on the 3D image is not recommended because you cannot be sure exactly where the point is being placed. If you decide to mark the vessel path point(s) on the 3D image, examine the reference images to check that you marked the point(s) accurately.

1. On the Coronary Analysis toolbar, click New Vessel .
   ⇨ A list of protocols appears.
2. Select Manual Protocol.
3. Enter the Vessel Name in the Manual Protocol window.
4. Mark the vessel start point by placing a marker on one of the images.
5. Mark the vessel path by placing extra points on the same image on which you placed the start point marker.
6. Mark the vessel end point.

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7. Click Done .

13.10.11 Manipulating Images on a Defined Path

After you have defined a path on the vessel, you can manipulate the image.

NOTICE

To perform actions on an existing vessel path, click Edit Vessel  in the New Vessel toolbar to switch to edit mode.

To:	Do this:
Move along the vessel path	► Place the cursor on the cut-line of the vessel path displayed on the panoramic image. ► Drag the mouse to move along the vessel path.
Change the vessel path	► Click Edit Vessel . ► Drag the cursor to change the path of the vessel.
Change/fix the vessel contour	► Click Edit Vessel . ► Do one of the following: • Click the existing contour on the cross-sectional image, then drag to draw the correct path. • Draw a new contour on the cross-sectional image. • Draw a new central line on the panoramic image. **NOTICE! The segmented tissue does not change. If none of the segmentation parameters were changed, recalculating the vessel does not take this change into account.**

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Recalculate the vessel	You can recalculate the vessel after you make changes (for example, after moving the central line). • Click Recalculate Vessel . **NOTICE! If a vessel has been truncated, only the remaining part of the vessel will be recalculated.**
Create a new path	• Click New Vessel . Click Display Vessels  to view a list of previously defined vessels.
Truncate the vessel path	• Move the cut-line to where you want the vessel to end and click .
Move the central line	Drag the  in the cross-sectional image to the required position.
Reset	• Click Reset  to undo all changes.

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13.10.12 Deleting Vessels

You can delete a selected vessel or all previously defined vessels.

To delete the currently active vessel:

- Click Delete Active Vessel .

NOTICE

If the deleted vessel was the last vessel, the standard layout is displayed.

If a vessel is defined for more than one phase, only the vessel in the current phase will be deleted.

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To delete all previously defined vessels:

- Click Delete All Vessels .

13.10.13 Reporting Vessels

A report can be produced about any vessel that you defined, if the points of interest (bookmarks and/or stenosis) are defined for it.

1. To view the report, click Preview Report  in the toolbar.

   The report provides you with the measurements for the points of interest, including:

   - Minimum Diameter
   - Maximum Diameter
   - Mean Diameter
   - Area of stenosis/bookmark
   - Length of stenosis/bookmark

NOTICE

The contour displayed on the image is calculated automatically. The mean, minimum, and maximum diameters, and the area calculated are estimates, indicated on the image by the suffix est.

These measurements should not be used for diagnosis. To approve the measurements, or to approve the new values after editing the contour, right-click the measurement annotation, then click Approved.

2. Enter comments in the right pane, if desired
3. Select one of the following report options:

- Preview Report: Displays the Preview Report window in which you can preview the entire report, including your comments and any images in the study that were marked as key images. From the Preview window:
  - Click Save to save the report.
  - Click Print to print the report.
  - Click Cancel to close the Preview Report window.
- Save Report: Saves the report. A message appears at the bottom of the window to indicate that the report was saved successfully.

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- Close: Closes the report in progress window without saving.

13.10.14 Saving Presentations in Coronary Analysis

Close: Closes the report in progress window without saving.

See these topics:

Using Saving Presentations in Vessel Analysis on page 238

Saving a Study as a Presentation on page 620

About Save Presentation on page 619

13.10.15 About Cardiovascular Reading

Vue PACS offers you a set of tools that facilitate cardiovascular reading. Some of these tools may also be used for reading Ultrasound (US) and X-Ray Angiography (XA) exams.

See these topics:

Automatic Cine Toolbar on page 98

Using Subtraction on page 252

Using Measurements on Doppler Ultrasound Images on page 254

Measuring the Velocity-Time Integral on page 255

Measuring Ejection Fraction on page 256

Cardiothoracic Ratio Measurement on page 258

Synchronizing Heartbeat on page 259

Annotating Cardiac Stress Images on page 260

Cardiac Viewing Display Protocols on page 261

Displaying ECG Lead Waveforms on page 261

13.11 Calcium Scoring

13.11.1 About Calcium Scoring

The Calcium Scoring application lets you mark areas in the coronaries that have masses of calcium. Once you mark the areas of calcification, the system calculates a calcium score, indicating whether the patient is in the high-risk sector of the population. The basic view is divided into two main parts:

- The MIP image
- Three MPR views (axial, coronal, and sagittal)

You can only use the axial view for marking calcifications.

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NOTICE

One of the annotations in the axial image is the slice number. In calcium scoring, it is important to know which slice you are examining. For example, 2-1 indicates the first picture in the second series.

Images that are considered important can be marked as key images.

See these topics:

Creating a Calcium Scoring View on page 278

Viewing Calcium Scoring Images on page 280

About Key Images on page 531

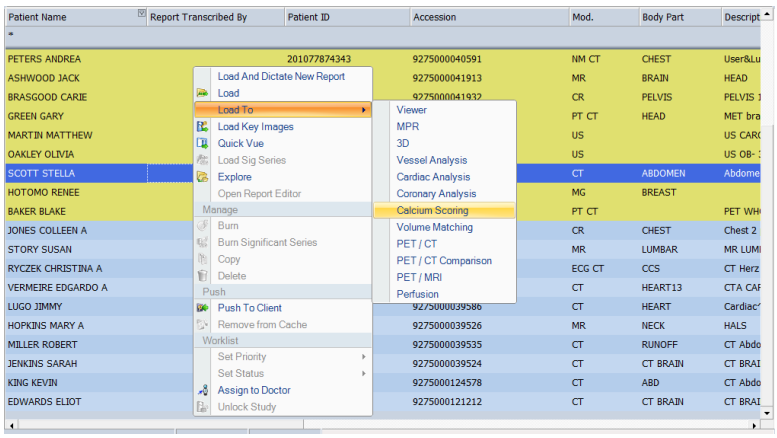
Marking Key Images on page 535

Previewing Key Images on page 536

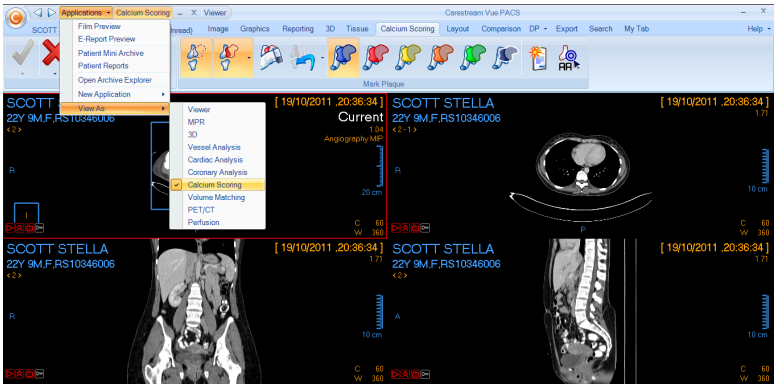
Clearing Key Images on page 540

13.11.2 Creating a Calcium Scoring View

You can create a Calcium Scoring view manually. For information about automatically creating a Calcium Scoring view, go to Display Protocols (see About Display Protocols on page 594).

To create a Calcium Scoring View:	Do this:
From the Archive Explorer	Right-click a study group, select Load To, then select Calcium Scoring. 

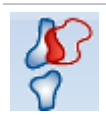
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In the PowerViewer Application	• Right-click a study group, select View As, then select Calcium Scoring. Or • From the Applications menu, select View As and then select Calcium Scoring. 
From the Patient Mini Archive	► Right-click a study group, then drag it to the display area. ► Select Calcium Scoring.
To a default view	If the currently open application is a Calcium Scoring, click the study group in the Patient mini archive, then drag it to the display area. The selected group of images appears in the application in the default Calcium Scoring view. The reference images and result images appear in the location and layout that was last used.

13.11.3 Calcium Scoring Toolbar



The following icons are added to the toolbar when you open the Calcium Scoring application.

Icon	Description
	Hide/Show the markings.
	Draw a Region of Interest (ROI) (freehand, oval, or square).
	Deselect a marked area according to the shape selected for the ROI.

	Reset changes.
	A marker for Left Main Artery (LMA).
	A marker for Left Anterior Descending (LAD)
	A marker for Left Circumflex Artery (LCA)
	A marker for Right Coronary Artery (RCA)
	A marker for Posterior Descending Artery (PDA)
	A marker for Other (this does not belong to a specific coronary)
	Generate a Calcium Scoring report.
	Show/Hide contour.

13.11.4 Viewing Calcium Scoring Images

The Calcium Scoring application covers the entire monitor in a 2x2 layout which shows a MIP result image. The Calcium Scoring application must be used on a color monitor.

To toggle between the MIP and VolR viewing modes:

- Right-click the image, select Change Image, then select the viewing mode from the shortcut menu.

See this topic:

About Calcium Scoring on page 277

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13.11.5 Defining and Marking Calcifications

You can search for and mark the calcifications in the axial slices of the coronary vessels.

1. Scroll through the axial slices and search for the coronary vessels that have calcium (indicated by white patches).
2. Select the artery on which the calcium deposits are to be marked by clicking one of the color-coded buttons (see on page 281) on the toolbar.

NOTICE

You can see the acronym of each artery name by hovering the mouse pointer over the color-coded button.

3. Select the method of area selection (Oval ROI, Square ROI, or Freehand ROI), then mark the calcification areas (on the selected artery) in the axial view.

   You mark a two-dimensional area in each slice, which can be spread over several slices.
4. Repeat this process for each of the arteries.
5. Repeat the process for each calcium deposit in each slice.

   Each area may be marked as a different coronary. Several artery types can be marked in a single slice.

NOTICE

Each calcification marked is also a tissue. The tissue is automatically deleted from the 3D image so that you can see if there are any unmarked calcifications (white spots that are still visible) in the 3D image. In this case, you can go to the appropriate slice and add another marking.

When you mark an area for calcium scoring, only the pixels with a CT value of over 130 HU will be marked.

Icon	Description
	Left Main Artery (LMA)
	Left Anterior Descending (LAD)

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	Left Circumflex Artery (LCA)
	Right Coronary Artery (RCA)
	Posterior Descending Artery (PDA)
	Other (This is for the doctor's use and does not belong to a specific coronary)

13.11.6 Changing Calcification Markings

The following options are available for changing calcification markings:

- Fine-tune the selection by clicking Deselect  and selecting an area to be deselected.
  NOTICE! The shape of the deselection area is determined by the defined region of interest.
- Undo the last marking (area) or clear tissue (remove all markings) by clicking Reset .
- Hide/show the markings (not delete) by clicking Highlight .

See these topics:

Creating a Calcium Scoring View on page 278
Viewing the Calcium Scoring Report on page 282
Drawing an Oval (for a Region of Interest) on page 501
Drawing a Square (for a Region of Interest) on page 502
Drawing a Freehand ROI on page 502

13.11.7 Viewing the Calcium Scoring Report

The Calcium Scoring Report lets you view a report in progress in the lower part of the window.

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1. Click Report In Progress .

   Each time a calcification is marked, the values are automatically updated in the report. If you clear the tissue, the values return to zero.

   - **Coronary**: The artery names (color-coded as per the toolbar buttons).
   - **Agatston Score**: The calcium score (the more calcium that exists in the coronaries, the higher the score and the higher the risk).
   - **Calcium Volume**: The volume of calcium marked in mm3 (the height of the slice x the area marked).
   - **Calcium Mass**: The mass of calcium marked (mg).
   - **Number of Regions**: The number of ROIs marked in the images where the CT value is above 130 HU.
2. Enter comments in the right pane, if desired.
   ⇨ These comments will appear in the detailed report.
3. Select one of the following report options:
   - Preview Report: Displays the Preview Report window in which you can preview the entire report, including your comments and any images in the study that were marked as key images. From the Preview window:
     - Click Save to save the report.
     - Click Print to print the report.
     - Click Cancel to close the Preview Report window.
   - Save Report: Saves the report. A message is displayed at the bottom of the window to indicate that the report was saved successfully.• Save Report: Saves the report. A message is displayed at the bottom of the window to indicate that the report was saved successfully.
   - Close: Closes the Report in Progress window without saving.

See these topics:

Creating a Calcium Scoring View on page 278

About Calcium Scoring on page 277

Defining and Marking Calcifications on page 281

13.12 Volume Matching

13.12.1 About Volume Matching

The Volume Matching applications allows three-dimensional registration of studies taken at different times or by different modalities (CT and MRI).

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The volumetric data sets are synchronized. The synchronization allows you to view reformatted series side by side, and superimposed images (see About Fusion Images on page 287).

IMPORTANT

Most features of the Volume Matching application are identical to those of the PET/CTs.

13.12.2 Volume Matching Application Overview

With this new application, you can accurately compare different volumetric studies from any modality.

The Volume matching application provides:

- A set of predefined Fusion Image Layouts on page 289.
- Image synchronization (see Volume Matching Synchronization and Image Manipulation on page 287) and manipulation capabilities.
- Image fusion (see About Fusion Images on page 287).

You can use Volume matching to:

- Swap (see About Fusion Images on page 287) between primary and secondary images.
- Adjust opacity (see About Fusion Images on page 287).
- Apply a color map (see Using Color Maps on Fusion Images on page 290) to show potential pathology.

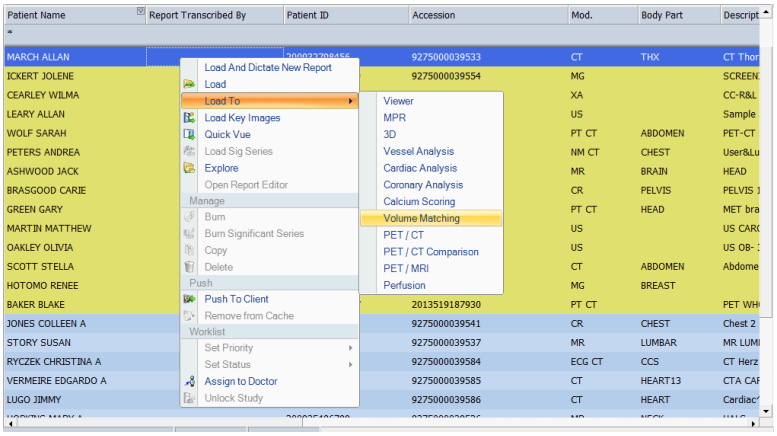
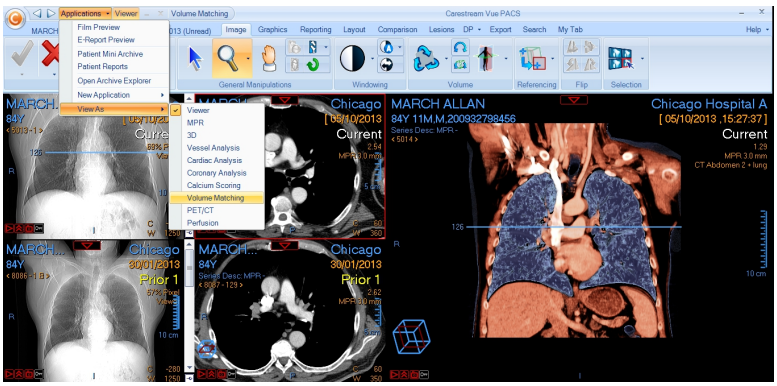
Reference Material	Instructions
About Volume Matching on page 283	Creating a Volume Matching View on page 284
	Volume Matching Synchronization and Image Manipulation on page 287
	About Fusion Images on page 287
	Fusion Image Layouts on page 289
	Using Color Maps on Fusion Images on page 290
	Saving Presentations in Volume Matching on page 291

13.12.3 Creating a Volume Matching View

You can create a Volume matching view manually.

To Create a Volume Matching View:	Do this:

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From the Archive Explorer	Right-click a study group, select Load To, then select Volume Matching. 
In the PowerViewer Application	For current studies: • Right-click a study group, select View As, then select Volume Matching. or • From the Applications menu, select View As and then select Volume Matching.  Or • From the Applications menu, select New Application and then select Volume Matching.
From the Patient Mini Archive	1. Right-click a study group, then drag it to the display area. 2. Select Volume Matching.
To an open application	If the currently open application is Volume Matching, click the study group in the Patient mini archive, then drag it to the display area. The selected group of images appears in the application. The reference images and result images appear in the location and layout that was last used.

13.12.4 Volume Matching Application Toolbar

The following icons are added to the About the PowerViewer Application on page 151 application toolbar when you open the Volume Matching application.

Icon	Description
	Swivel the image.
	Roll the image from side to side.
	Relate a point on the MIP image to its relevant location on the MPR reference images (see About Relate Mode on page 590).
	Select the MPR type: •  MPR (average MipPR)3 •  MIP (maximum intensity projection) •  MinPR (minimum intensity projection)
	Show or hide frames.
	Add a clipping pane.
	Add a slab.
	Define a volume of interest (see Working with Volumes of Interest on page 191). See VOI Toolbar.
	Define 3D tissues (see Building and Applying Tissues on page 205). See Tissue Definition Toolbar on page 102.
	Automatically remove bone tissue (see Using Bone Removal on page 192).
	Automatically remove scanner bed (see Removing the Scanner Bed on page 211).

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	Edit the VolR parameters (see About Volume Rendering Protocols on page 636).
	Toggle the VolR quality (see Adjusting the Quality for Volume Rendered Images on page 633).
	Generate a report.

13.12.5 Volume Matching Synchronization and Image Manipulation

After loading a study to the Volume matching application:

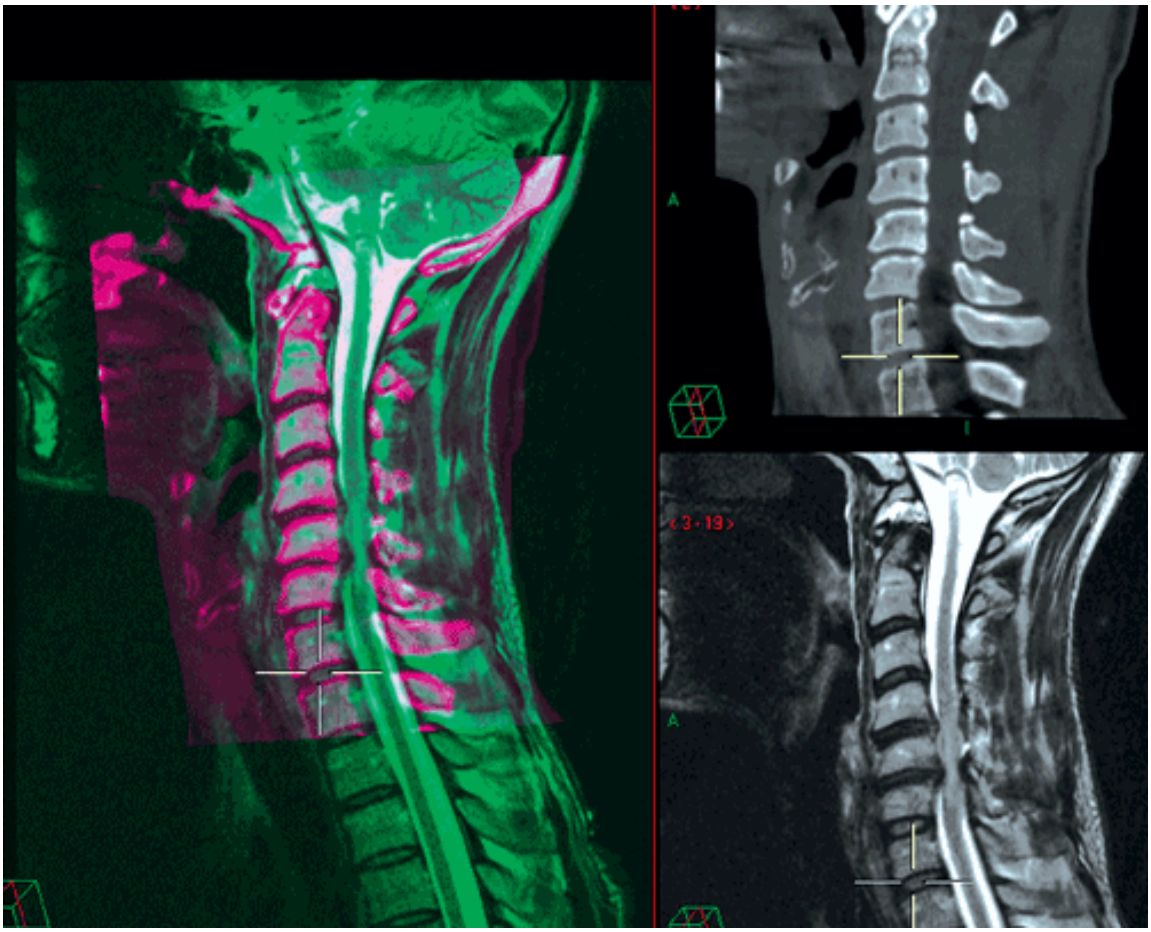
- Registration is available.
- Scroll, Swivel, Roll, Cine, Zoom and Pan are synchronized between studies in all views.
- Click Group Layouts  to make a selection from a set of Display Options, such as VOLR and VOLR plus MPR 2x2.
- Click Zoom , open the drop-down menu, and select Zoom Synch to control zoom synchronization.
- Click Relate  and then click on any interesting point of interest (POI) for pixel-level matching.

13.12.6 About Fusion Images

For the Hybrid NM and Volume Matching applications, a fusion image is the result of superimposing one series over another. The PET/CT superimposes the PET AC series over the CT series of a given study. The fusion image is shown in the layout, and the user can apply coloring to the series within.

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13.12.7 Exceptions and Behavior

Fusion images are not supported by other applications such as PowerViewer, MPR, and 3D. When the Display Option includes a Fusion series, the Fusion series will appear automatically in the relevant window/s.

Fusion image are not shown in the PMA.

You cannot apply a three-dimensional rendition on a fusion image.

You can export a fusion image or the entire fusion group.

13.12.8 Swap

You can use Swap to select assign a dataset as primary or secondary. To swap between Primary and Secondary studies:

- Right-click the Opacity annotation, then select Swap Data.
- Right-click the Replace With annotation, then select Swap Data.

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13.12.9 Adjusting Opacity

1. Right-click on the Opacity annotation.
2. Select the opacity from the drop-down menu.

Or

1. Left-click and drag upwards to increase opacity.
2. Left-click and drag downwards to decrease opacity.

You can also use the shortcut ALT+Shift+O to toggle the opacity between 0%, 50% and 100%.

13.12.10 Adjusting Blending

By default, the superimposed PET and CT datasets are based on a 50%-50% ratio of linear blending (Alpha Blending). Two types of blending create the fused image:

- Alpha Blending—the linear merging of the two datasets is determined only by the blending ratio.
- Highlighted— the two datasets will not be merged evenly (non-linear).

1. Right-click the Blending annotation.
2. Select one of the pre-defined values of 0%, 25%, 50%, 75% and 100%.

13.12.11 Using Film Preview and Parameters

You can film fusion images.

However, when you place the fusion images in the Film Preview, you cannot manipulate the images.

You can perform Zoom, apply the Magnifying Glass, and apply Measurements for length and area only.

13.12.12 Marking Fused Images

You can mark fusion images as Key Images or as Significant Series.

All the image parameters are captured just as they were displayed when the image was saved as Key or SIG. The parameters include Windowing, Alpha blending ratio, and the Color Pallet.

Once saved, the fusion image becomes a static RGB image.

13.12.13 Fusion Image Layouts

Click Group Layouts  to choose a Display Option presenting a Fusion Image, such as Two Datasets + Fusion 3x3 or Two Datasets + Fusion 1x3.

In a Fusion Image, the two displayed data sets are superimposed (or fused) to create the fusion content. To change the fusion content, replace one of the data sets.

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One study in the Fusion Image is considered the Primary and the other as Secondary. You can separately control each study in the fusion image. For example, you can apply windowing or measurements.

See this topic:

About Fusion Images on page 287

13.12.14 Using Color Maps on Fusion Images

From the Image Tab in Toolbar	From the Viewbox
Click Windowing drop-down --> Color Maps.	Right-click the windowing annotation in the group display area --> Color Maps.

When you apply a color map, the colors affect only the PET data of the fused image.

Changing the color map of the CT and/or PET (original) data does not affect the fused image.

If more than one study is displayed (in a Compare layout, for example), changing the color map of the PET or the fused image affects both the prior and current studies.

Color Maps

Color maps are schemes of pre-set color shades you can apply to the fused image.

To apply a color shade, right-click the windowing annotation and click a color shade in the Color Maps section of the menu.

Note that different modalities may offer different coloring schemes. By default, the menu displays the color scheme suitable for the PET. Selecting a shade from the menu applies the coloring to the PET image. To change the default, right-click the Opacity or Replace With annotation and click Swap Data. The menu will display the coloring schemes of the CT.

Industry Standard Color Maps

For PET images, the Color Maps section of the Windowing menu offers you options that are standard in the industry, such as Grayscale, Hot Iron, and others.

PET/CT Color Maps

The Color Maps section of the windowing menu also provides an SUV color map and an Inversed Grayscale color map.

The SUV color map applies a non-gradient color to the images. As a result, pixels with similar values are displayed with the same color, providing you with the ability to quickly note higher SUV value areas.

NOTICE

You can use the Application Settings (see PET/CT Settings on page 328) window to set the minimum and maximum SUV values for the lesion highlight color map.

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The Inversed Grayscale color map creates an inverse display of a grayscale image. When you use this color mode, you do not need to apply Inverse Windowing.

Inversed Grayscale is the default color map for the PET images in all display options.

Inverse Windowing

When you apply inverse windowing to:

- Fusion images—depending on the current active data, the operation affects the CT image or the PET and MIP images.
- CT images—the operation affects the fusion images.
- PET images—the operation affects the MIP and the fusion images.

13.12.15 Saving Presentations in Volume Matching

Saving a presentation in the Volume matching application saves the same parameters as the PET/CT.

See these topics:

Saving Presentations in Hybrid NM on page 328

Saving a Study as a Presentation on page 620

About Save Presentation on page 619

13.13 PET/CT

13.13.1 About the Hybrid Nuclear Medicine (NM) Application

The PET/CT, displaying Positron Emission Tomography/Computed Tomography (PET/CT) images, is an image viewer, a registration tool, and an analysis workstation.

The PET/CT can:

- Fuse together images. See About Fusion Images on page 287.
- Provide on-screen visual illustration of the match between the images. Current and prior (history) images are combined to easily show progress in areas of pathology (whether a tumor has increased or decreased).
- Help clinicians to localize diagnostic information, and more confidently assess potential pathology.
- Provide a variety of defined layout options. See About Hybrid NM Display Options on page 308.

Hybrid NM images combine two scanning technologies. Physicians can use Hybrid NM images to diagnose cancer, tumors, heart disease, and neurological disorders with greater accuracy. To read Hybrid NM images, a clinician or physician requires an application that provides:

- Image-manipulation capabilities, such as applying color maps to show potential pathology.

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- Specific workflow-related capabilities, such as layouts to synchronize and correlate PET and CT image data sets.

Hybrid NM Default Display

After a study is loaded to the PET/CT, the application identifies an anatomical and a functional series for on-screen display. The fusion series is constructed by correctly superimposing the functional series over the anatomical series.

Simple Hybrid NM studies include three series – A Computerized Tomography (CT) series, a Positron Emission Tomography Attenuation Corrected (PET AC) series, and a Positron Emission Tomography Non Attenuation Corrected (PET NAC) series. In these series, the CT is the anatomical series and the PET AC - the functional series.

Some Hybrid NM studies, however, include multiple CT or PET series. In such studies, the application applies a set of rules to identify the CT series that is to be used as the anatomical series and the matching PET series that is to be used as the functional series. By default, the Vue PACS PET/CT includes a basic set of rules to enable this process. It is possible to configure the system in order to apply additional rules for identification and prioritization of the anatomical and functional series. Contact the System administrator.

NOTICE! Studies with PET/MRI, CT/NM and other modality combinations of anatomical and functional images can also be viewed with the Vue PACS PET/CT provided that the system is properly configured to identify the series. Contact the System administrator.

NOTICE! In Nuclear Medicine, the orientation annotation that accompanies an image is only presented if the orientation data is correct. In the event that the orientation data is incorrect, the annotation is not displayed.

Hybrid NM Algorithm

Hybrid NM applies a unique algorithm to different data sets. The algorithm:

- Uses rigid space transformation.
- Synchronizes different data sets with the same frame of reference or enables registration of data sets with different frames of reference.
- Matches two different volumes without distortion.

Hybrid NM Feature Summary

- Matches two different volumes without distortion.
- Calculates PET Standard Uptake Value (SUV).
- Applies color maps to highlight SUV.
- Provides special layouts to support different views.
- Synchronizes the Hybrid NM views and image manipulation, such as link, zoom, pan, swivel, measurements, and relate.
- Provides Volume Matching comparison for current and prior cases.
- Launches the PET/CT directly to a desired study of interest.

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- Stores fusion image results for distribution throughout the health care enterprise.

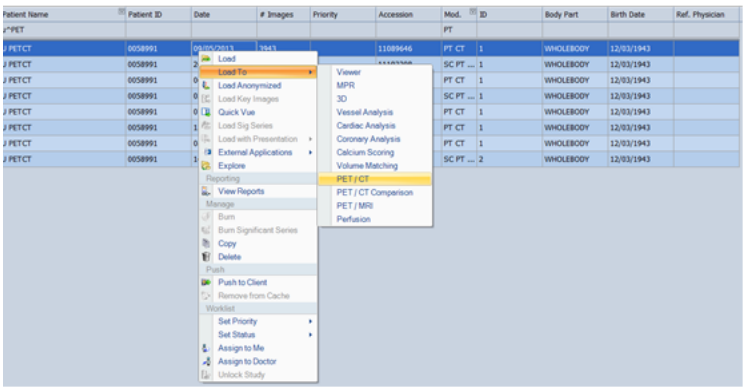
PET/CT Configuration

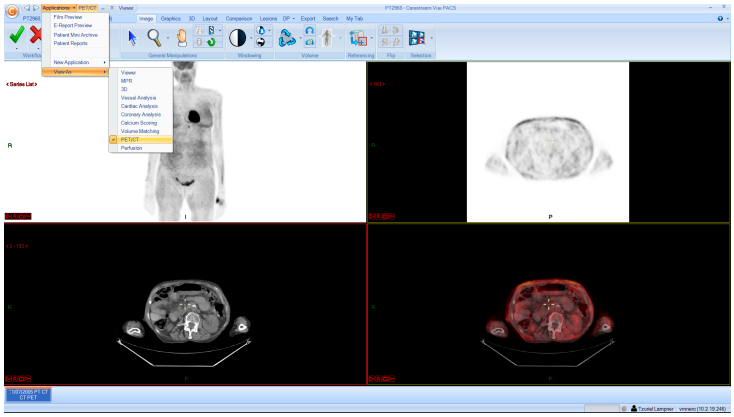
See related topic:

PET/CT Settings on page 328

13.13.2 Creating a Hybrid NM View

You can create a Hybrid NM view manually. For information about automatically creating a Hybrid NM view, view the topics listed under Display Protocols.

To create a Hybrid NM View:	Do this:
From the Archive Explorer	• For current studies, right-click each study and select Load To --> PET/CT.  • For loading current and prior studies, select a study, press the CTRL key and select the other study, then right-click any of these studies and select Load To --> PET/CT Comparison.

In the PowerViewer Application	For current studies: • Right-click an existing group, click View As, then select PET/CT. Or • From the Applications menu, select View As, then select PET/CT.  For current and prior studies: • Right-click an existing group, click View As, then select PET/CT Comparison. Or • In the Applications menu, select View As, then select PET/CT Comparison. Or • In the Applications menu, select New Application then select PET/CT Comparison.
From the Patient Mini Archive	► Right-click a study group and keep the right mouse button clicked, then drag it to a group display area. ► Select PET/CT.
To an open application	• If the current default application is a Hybrid NM view, click the study group in the Patient mini archive, then drag it to the display area. The selected group of images appears in the application. The reference images and result images appear in the location and layout that was last used.

13.13.3 PET/CT Workflow

Workflow	Related Topics
1. Load a current or comparison study that contains PET/CT images. **NOTICE! To see the studies with Hybrid NM, use the Field Chooser to add the Mod field to the Archive Explorer.**	Creating a Hybrid NM View on page 293

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 2. Click Group Layout , and select the appropriate display option. **NOTICE! The layouts for Hybrid NM are unique and specifically defined for the application.**	About Hybrid NM Display Options on page 308
3. Right-click Pixel (above the windowing levels) and select the desired SUV calculation method.	About Standard Uptake Value (SUV) on page 301
4. Apply a color map, such as the SUV color map. From the menu toolbar, click Windowing --> Color Maps --> SUV.	
5. Register the studies. With comparison studies, first click on a current study and then click on a prior study.	About Registration on page 577
6. From the menu toolbar, click Windowing --> Min Max Scale.	
7. For MPR images, adjust MPR renditions or parameters.	About Multi-Planar Reformatting (MPR) on page 159

Use assorted tools to:

- Marking Key Images on page 535
- Mark SIG Images (see About SIG Image Marking on page 518)
- Configure Image Layouts (see About Image Layouts on page 511)
- Manipulate Images (see About Images on page 495)
- Manipulate the 3D Images (see Manipulating 3D Images on page 188)
- Panning Images on page 496
- Create Movies (see About Cine on page 555)
- Annotate the Image or Mark Areas of Interest (see Configuring Graphics Properties on page 466)
- Create a Report (see Dictating a Report on page 626)

13.13.4 PET/CT Toolbar

The following icons are added to the Image toolbar (see Image Tab on page 74) when you open the PET/CT.

Icon	Description

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	Swivel the image.
	Roll the image from side to side.
	Roll the image automatically to the closest axial, coronal, or sagittal plane.
	Relate a point on the MIP image to its relevant location on the MPR reference images (see About Relate Mode on page 590).
	Select the MPR type: •  MPR (average MipPR) •  MIP (maximum intensity projection) •  MinPR (minimum intensity projection)
The 3D toolbar (see 3D Analysis Application Toolbar on page 87) includes tools for facilitating reading of volumetric images, including the following:	
	Show or hide frames.
	Add a clipping pane.

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	Add a slab.
	Define a volume of interest (see Working with Volumes of Interest on page 191). See VOI Toolbar.

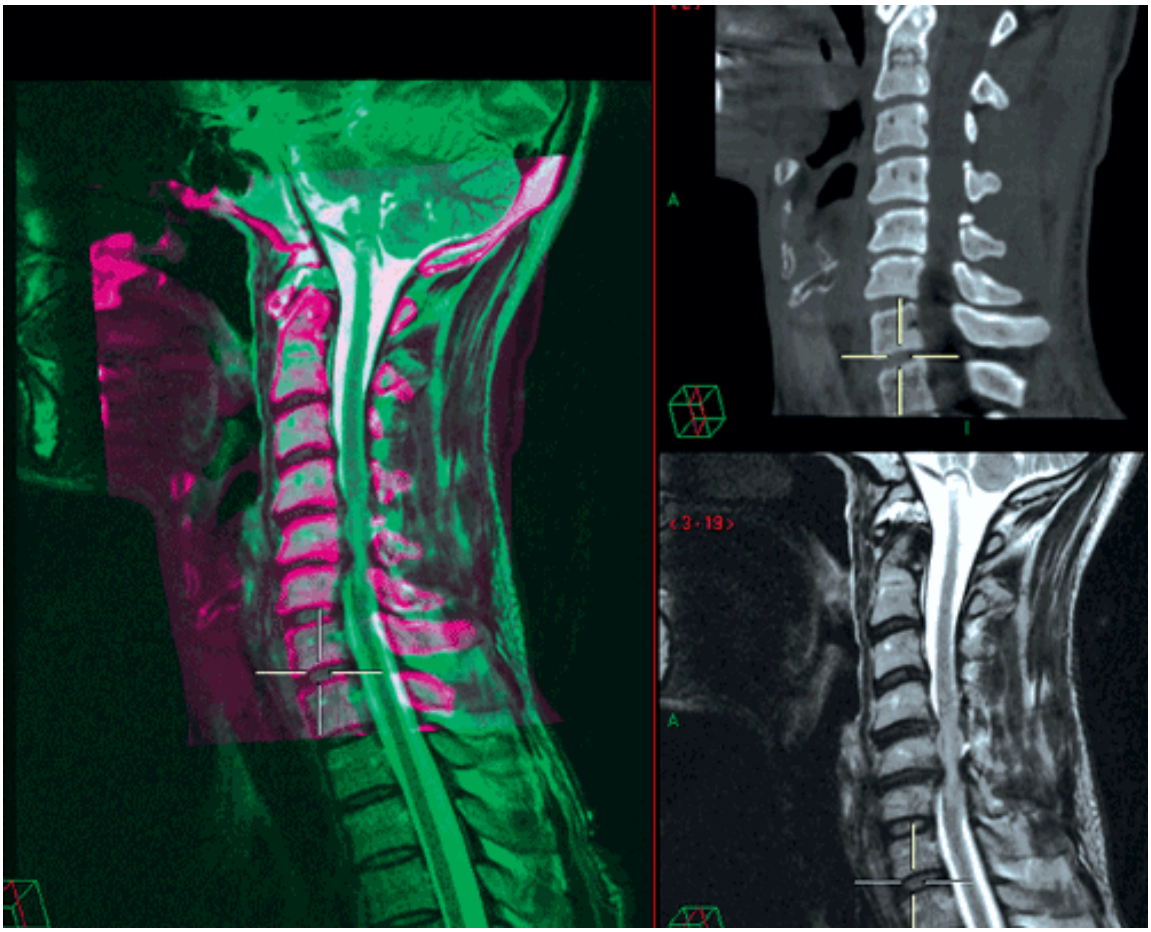
The following icons are added to the PowerViewer (see) toolbar when you click the Define a Volume of Interest button.

Icon	Description
	Free VOI Minus. Lets you draw a freehand shape on the image and then remove the shape from the image.
	Free VOI Plus. Lets you define a freehand region of the volume that you want to keep and discard the rest of the volume.
	Oval VOI Minus. Lets you draw an oval shape on the image and then remove the shape from the image.
	Oval VOI Plus. Lets you define an oval region of the volume that you want to keep and discard the rest of the volume.
	Rect VOI Minus. Lets you draw a rectangle shape on the image and then remove the shape from the image.

13.13.5 About Fusion Images

For the Hybrid NM and Volume Matching applications, a fusion image is the result of superimposing one series over another. The PET/CT superimposes the PET AC series over the CT series of a given study. The fusion image is shown in the layout, and the user can apply coloring to the series within.

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13.13.6 Exceptions and Behavior

Fusion images are not supported by other applications such as PowerViewer, MPR, and 3D.

Fusion images are not supported by other applications such as PowerViewer, MPR, and 3D.

Fusion image are not shown in the PMA.

You cannot apply a three-dimensional rendition on a fusion image.

You can export a fusion image or the entire fusion group.

13.13.7 Swap

You can use Swap to select assign a dataset as primary or secondary. To swap between Primary and Secondary studies:

- Right-click the Opacity annotation, then select Swap Data.
- Right-click the Replace With annotation, then select Swap Data.

13.13.8 Adjusting Opacity

1. Right-click on the Opacity annotation.

2. Select the opacity from the drop-down menu.

Or

1. Left-click and drag upwards to increase opacity.
2. Left-click and drag downwards to decrease opacity.

You can also use the shortcut ALT+Shift+O to toggle the opacity between 0%, 50% and 100%.

13.13.9 Adjusting Blending

By default, the superimposed PET and CT datasets are based on a 50%-50% ratio of linear blending (Alpha Blending).

Two types of blending create the fused image:

- Alpha Blending—the linear merging of the two datasets is determined only by the blending ratio.
- Highlighted— the two datasets will not be merged evenly (non-linear).

1. Right-click the Blending annotation.
2. Select one of the pre-defined values of 0%, 25%, 50%, 75% and 100%.

13.13.10 Using Film Preview and Parameters

You can film fusion images.

However, when you place the fusion images in the Film Preview, you cannot manipulate the images.

You can perform Zoom, apply the Magnifying Glass, and apply Measurements for length and area only.

13.13.11 Marking Fused Images

You can mark fusion images as Key Images or as Significant Series.

All the image parameters are captured just as they were displayed when the image was saved as Key or SIG. The parameters include Windowing, Alpha blending ratio, and the Color Pallet.

Once saved, the fusion image becomes a static RGB image.

13.13.12 Windowing Images

By default, the PET/CT starts up with a default windowing level for PET images and for CT images. For PET series, the windowing preset value Normal is automatically applied, while for CT series the windowing value is read from its DICOM tags. You can change the PET windowing value in Application Settings (see Opening the Application Settings Window on page 453) --> Windowing Presets.

Synchronization:

- Changing the PET image windowing level affects the PET component in the fusion image and the MIP image.

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- Changing the CT image windowing level affects the CT component in the fusion image.

If prior studies are displayed, all registered series are windowed together.

NOTICE! It is possible to configure the PET and Fusion groups to display a bar with a slider allowing you to change the minimum and maximum windowing values. Contact your system administrator.

13.13.13 Using Color Maps on Fusion Images

From the Image Tab in Toolbar	From the Viewbox
Click Windowing drop-down --> Color Maps.	Right-click the windowing annotation in the group display area --> Color Maps.

When you apply a color map, the colors affect only the PET data of the fused image.

Changing the color map of the CT and/or PET (original) data does not affect the fused image.

If more than one study is displayed (in a Compare layout, for example), changing the color map of the PET or the fused image affects both the prior and current studies.

Color Maps

Color maps are schemes of pre-set color shades you can apply to the fused image.

To apply a color shade, right-click the windowing annotation and click a color shade in the Color Maps section of the menu.

Note that different modalities may offer different coloring schemes. By default, the menu displays the color scheme suitable for the PET. Selecting a shade from the menu applies the coloring to the PET image. To change the default, right-click the Opacity or Replace With annotation and click Swap Data. The menu will display the coloring schemes of the CT.

Industry Standard Color Maps

For PET images, the Color Maps section of the Windowing menu offers you options that are standard in the industry, such as Grayscale, Hot Iron, and others.

PET/CT Color Maps

The Color Maps section of the windowing menu also provides an SUV color map and an Inversed Grayscale color map.

The SUV color map applies a non-gradient color to the images. As a result, pixels with similar values are displayed with the same color, providing you with the ability to quickly note higher SUV value areas.

NOTICE! You can use the Application Settings window to set the minimum and maximum SUV values for the lesion highlight color map.

See related topic:

PET/CT Settings on page 328

The Inversed Grayscale color map creates an inverse display of a grayscale image. When you use this color mode, you do not need to apply Inverse Windowing.

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Inversed Grayscale is the default color map for the PET images in all display options.

Inverse Windowing

When you apply inverse windowing to:

- Fusion images—depending on the current active data, the operation affects the CT image or the PET and MIP images.
- CT images—the operation affects the fusion images.
- PET images—the operation affects the MIP and the fusion images.

13.13.14 Adjusting Standard Uptake Values (SUV)

About Standard Uptake Value (SUV)

Malignant cancer cells require large amounts of glucose to grow and multiply.

Malignant cancer cells have a high concentration of glucose transporter proteins, and exhibit a rapid metabolic rate (glycolysis). Glycolysis causes tumors to appear hot on PET scans.

The radioactive molecule fluorodeoxyglucose (FDG) is similar to glucose. FDG is a radiotracer commonly used for PET scans. FDG accumulates in malignant cells because of the high rate of glucose metabolism. The dose of FDG is relative to the patient's weight, height and gender.

PET measures FDG retention per volume of tissue. Tumors and cancer cells in specific areas retain large amounts of FDG, such as in the lungs, breasts, head, and neck. Tumors and cancer cells in other areas can retain variable amounts of FDG, such as in the prostate and liver.

The standardized uptake value (SUV) is:

- A semi-quantitative index for FDG accumulation in tissue relative to the injected dose of FDG.
- The ratio of activity in tissue per millimeter to the activity in the injected radiotracer dose per patient body weight.
- (µCi/gram in tissue)/{(total µCi injected)/(body weight)}

IMPORTANT

The ability to accurately reproduce the SUV measurement depends on the consistency of the clinical protocols during each study. Protocols that can vary include dose infiltration, time of imaging after the FDG administration, type of attenuation maps, size of the region of interest, changes in uptake by organs other than the tumor, and methods of analysis (maximum and mean).

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WARNING

Attention should be given to performing volumetric measurements on the PET/CT images for the placement of ROI. Adjust the threshold setting to be in the minimum range area (2.5 to 3 mm of minimum value) to exclude unwanted tissues within the Lesion.

For a precise volumetric measurement on the PET image, place the ROI in an appropriate area of the lesion and estimate the lesion size by scrolling through the entire volume of the ROI and confirm the lesion is fully contained inside this volume.

Adjust the threshold setting range to an approximate minimum range of 2.5 to 3.0 minimum value to exclude unwanted tissues within the volumetric area.

Enable the “Segment only a single component around the max pixel” in the application settings to avoid inclusion of unwanted lesions/tissues within the region of interest.

Important Information About SUV

When using SUV calculation during PET assessment, assumptions are made about the reference time for acquiring the data series. It is possible to interpret the requirements outlined in the DICOM Standard for determining the start reference time during acquisition and the time that the radiotracer is injected with some variability. This in turn may cause variability in the SUV values calculated by different vendors.

Due to inconsistencies throughout the industry, the acquisition time used in SUV calculation may be any of the acquisition times presented in the DICOM data. SUV is affected by several physiological factors which cause variability.

SUV can be applied as a simplified measure of radiopharmaceutical uptake. SUV has a complimentary role rather than directive role in the assessment, treatment, and staging of disease.

WARNING

Disease Specific guidelines are required when calculated SUV parameters are used for diagnostic purposes.

WARNING

Anatomy (organ) specific measurement interference is to be taken into consideration while using SUV parameters for diagnostic purposes. For example, patients with diabetes can display interference with measured brain PET SUV parameters.

WARNING

Measuring very small lesions may result in partial volume effect, caused by limited partial resolution of the PET scanner, resulting in underestimation of the SUV.

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Formulas to Calculate SUV

The dose of FDG is relative to the patient's weight, height and gender. The types of SUV include:

- SUV-Body Weight (default)
- SUV-Body Surface Area
- SUV-Lean Body Mass (also known as SUL)

PET/CT Standard Uptake Value Formulas

There are three common formulas for calculating SUV. These formulas are based on:

- Body weight (the most commonly used method)
- An approximation of the body surface area
- Lean body mass, according to the patient's gender

SUV Formula - Body Weight

$$\mathrm{SUV_{BW}\ (g/ml)} = \frac{\text{average activity in ROI (Bql/ml)}}{\text{injected dose(Bql)}} * \text{patient body weight(g)}$$

SUV Formula - Body Surface Area

$$\mathrm{SUV_{BSA}(cm^2/ml)} = \frac{\text{average activity in ROI (Bql/ml)}}{\text{injected dose(Bql)}} * BSA(\mathrm{cm^2})$$

Where BSA (Body Surface Area) is calculated by the following formula:

$$BSA(cm^2) = [\text{patient we ight } (kg)]^{0.425} * [\text{patient height } (cm)]^{0.725} * 71.84$$

SUV Formula - Lean Body Mass

$$SUV_{LBM}\ (\mathrm{g/ml}) = \frac{\text{average activity in ROI (Bql/ml)}}{\text{injected dose(Bql)}} * LBM\ (\mathrm{g})$$

Where LBM (Lean Body Mass) is calculated by the following formula:

$$\mathrm{LBM_{MALE}(kg)} = 1.10 * [\text{patient w eight (kg)}] - 128 * \left[\frac{\text{patient we ight (kg)}}{\text{patient height (cm)}}\right]^2$$

$$\mathrm{LBM_{FEMALE}(kg)} = 1.07 * [\text{patient w eight (kg)}] - 148 * \left[\frac{\text{patient we ight (kg)}}{\text{patient height (cm)}}\right]^2$$

NOTICE! LBM should be divided / multiplied by 1000 to get the result in Kg. / g.

SUV Formula - Total Lesion Glycolysis

$$TLG = SUVmean \times MTV$$

See this topic:

Adjusting Patient Data for Standard Uptake Value (SUV) on page 305

Selecting Standard Uptake Values (SUVs)

NOTICE! An SUV of 1 indicates uniform distribution of the radiotracer in the tissue. An SUV greater than 2.5 can be associated with cancer. Many factors can affect the reliability of SUVs. The values are often used as a guide to interpretation rather than as absolute values.

IMPORTANT

The default value in the image view is SUV Body Weight.

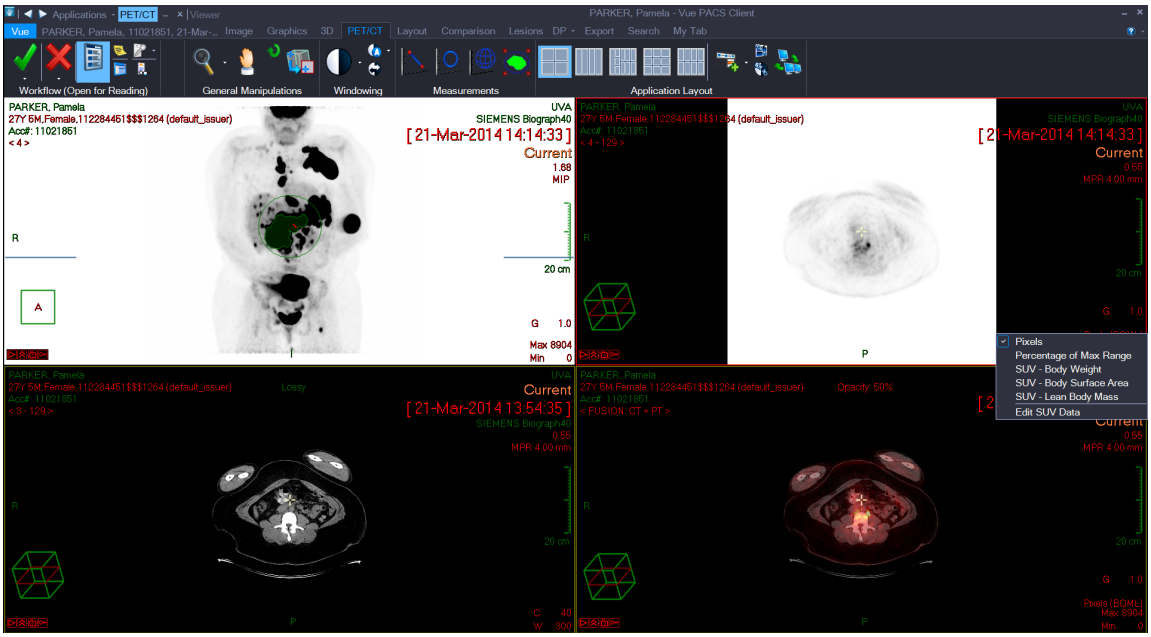
To select SUV:

1. Right-click the dynamic annotation in the bottom right corner. The default text for the annotation is SUV-BW.
2. Select the desired SUV from the drop-down menu.

The options are:

- Pixels
- Percentage of Max Range
- SUV-Body Weight
- SUV-Body Surface Area
- SUV-Lean Body Mass (also known as SUL)

NOTICE! SUV - Body Weight is the most commonly used SUV.



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Adjusting Patient Data for Standard Uptake Value (SUV)

The SUV calculation depends on variable patient data which can change from study to study. This data includes the height, weight, and gender of the patient, as well as the amount of radiotracer injected into the patient.

In addition, the SUV calculation depends on the Decay Correction method.

When Decay Correction = Start, the uptake time used for the SUV calculation is the difference between injection time and the series start time. This uptake time is shown as seen in the patient data dialog.

When Decay Correction = Admin, the uptake time used for the SUV calculation is zero because images were decay corrected to the injected time. Therefore, no additional factor is required.

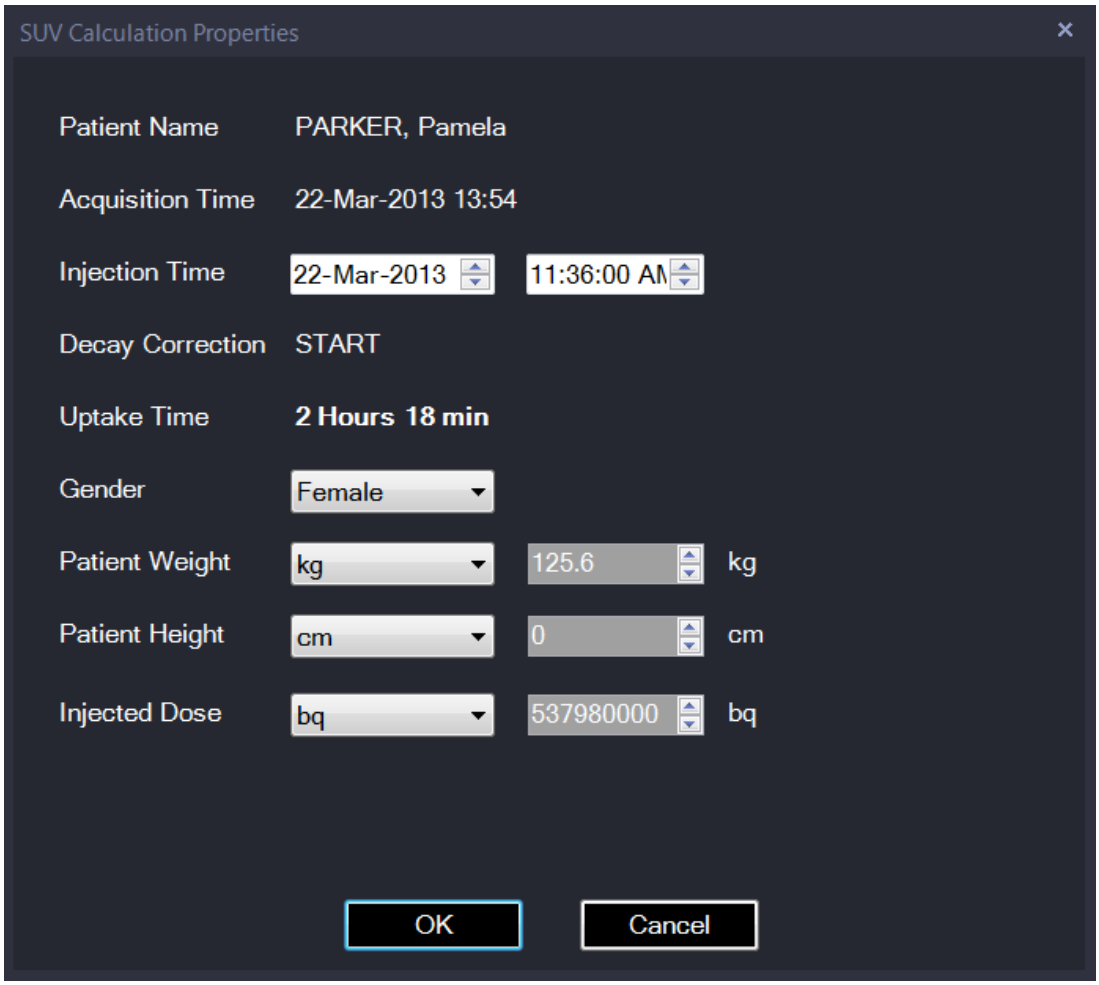
I this case, the uptake time shown in the patient data dialog depends on a new configuration flag (show_uptake_time_as_injection_to_scan_time_diff_for_decay_admin):

- When set to 0, the uptake time displays 0.
- When set to 1, the uptake time displays the difference as with Decay Correction = Start, but the SUV calculation still assumes a zero uptake time, as images were decay corrected to the injection time.

You can adjust the patient data in the PET/CT application.

1. Right-click the dynamic annotation at the bottom of the corner. The default annotation text is SUV-BW.
2. Select Edit SUV Data.
3. In the SUV Calculation Properties window, adjust any of the following data fields:

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- Injection Time
- Patient Weight
- Patient Height
- Injected Dose
- Gender

4. Click OK.

NOTICE! The data values are shown in both metric and imperial values, and converted automatically. For example, when you enter data in metric values and click OK, the metric data is saved and simultaneously converted in the imperial fields.

See this topic:

About Standard Uptake Value (SUV) on page 301

Using the Percentage of Maximum Range Type

The percentage of max range is used for studies with a very low count that need to be scaled rapidly to view the images such as studies with low radioactivity.

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When switching to this active unit, the system determines the maximum voxel value within the PET volume then calculates a percentage of the maximum value for each voxel and colors it accordingly.

This option is available in the active units annotation, called Percentage of max range, below the Pixels option.

When clicking this option, the active unit annotation changes to % max range and the system changes the color-bar scale to 0-100%. The percentage unit is calculated with a one floating point digit.

The graphic calculations do not change as a result of switching to this active unit. Unit calculations such as maximum and average of a region of interest are displayed in pixel values when switching to this mode.

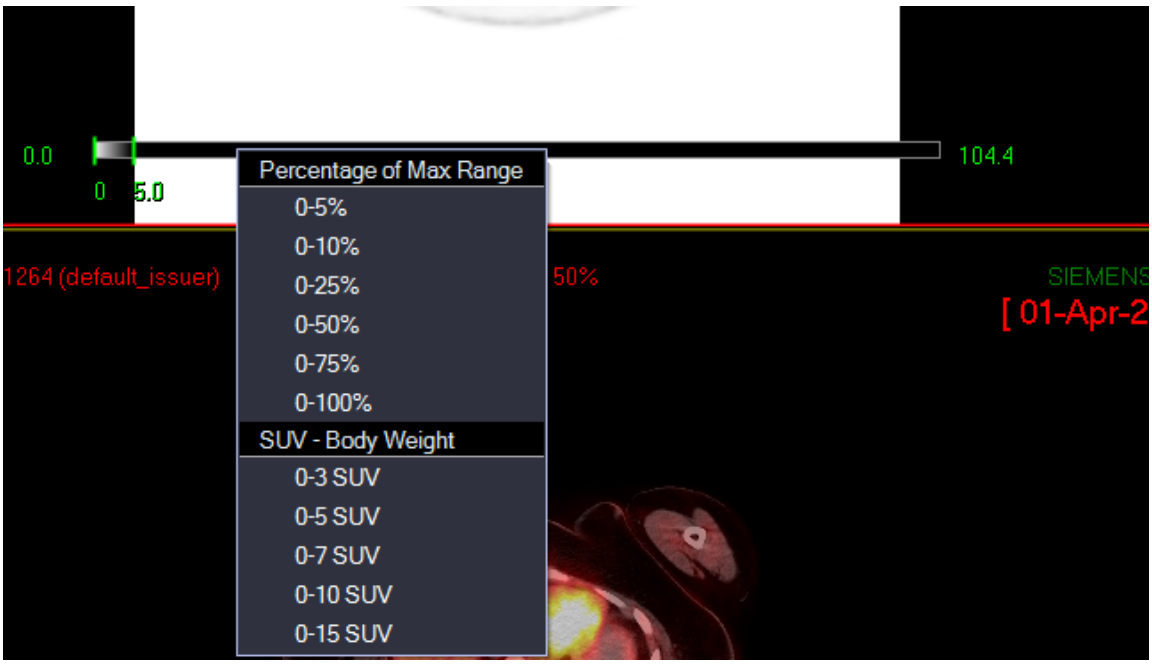
The windowing annotation displays percentages, which correlates to the minimum or maximum markers of the color-bar.

Selecting this option affects all PET or fused images displayed in the same application.

The percentage of max range type is also available in the viewer application.

Using the Color Bar to Set the SUV and Percentage of Max Ranges

The Hybrid NM color bar improves and accelerates the workflow of reading nuclear medicine exams,by providing predefined range presets. The color bar enables you to quickly navigate between predefined ranges within different unit types, based on nominal values or on percentile ranges.



When right-clicking over the color bar, a dynamic menu is opened. The menu has a predefined set of presets.

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When one of the presets is selected, the range is modified accordingly and the image is windowed.

When clicking in between the minimum and maximum markers and dragging the mouse cursor, the range shifts accordingly. When hovering above this range, the mouse cursor changes to range drag.

When hovering above the color bar, the cursor changes to range.

The color bar always displays the range in the selected active units, even if a percentage preset was selected.

Additionally, the color bar can be switched to a zoomed range mode. In certain cases, windowing by percentage may require delicate setting in a narrower range, for example, 0.5% - 0.6%. Switching to the zoomed range enables fine tuning of the range.

Press Ctrl+Click on the left (minimum) marker to reset its value to 0%.

13.13.15 Adjusting Gamma Levels

The PET/CT provides the ability to change the gamma level of areas in a PET scan that have been targeted by radioactive materials. This helps to enhance small changes in the contour of the affected area.

1. Open a PET study in the PET/CT application.
2. Do one of the following:

   - In the bottom right corner of the screen, right-click 

. Select one of the default options: 0.5, 1.0, or 2.0. By default, a gamma value of 1.0 is displayed.
   - Hover your cursor over the gamma indicator, and click and drag upwards (to increase) or downwards (to decrease) the gamma level.

NOTICE! When you change the gamma level of a fusion PET/CT scan, only the PET portion of the image is affected.

13.13.16 Using Display Options

About Hybrid NM Display Options

The PET/CT contains unique pre-defined layout options. There are specific dependencies and relationships required for each layout. The pre-defined layout options for PET/CT are robust, and are referred to as Display Options.

In layouts that include a MIP image, a reference line indicates the exact location of the PET image.

Monitor Configurations

The following monitor configurations are relevant for working with Hybrid NM:

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Configuration	Number of Monitors
Portrait	1 (single) 2 (dual)
Landscape	1 (single) 2 (dual)

Registration Requirements

Some of the Display Options include synchronization between datasets. The datasets must be registered in order to activate the synchronization capabilities.

Register your studies before manipulating the images in the PET/CT.

See this topic:

Using Display Options on page 309

Using Display Options



Open the drop-down menu of the Determine Group Layout icon in the Layout tab.

The display options include:

- Single Dataset 2x2
- Single Dataset 1x4
- Multi Dataset 2x2
- Multi Dataset 1x4
- Multi Dataset no PET
- All
- Compare 1x3
- Compare 2x3
- Compare 3x3
- Compare with NAC (No Attenuation Correction)
- Tile
- Compare with Prior 2x4
- Compare with Prior 2x3
- Compare with Two Priors
- Compare with Three Priors
- Compare with Four Priors
- Compare with Prior no PET
- Multiple Fuse

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- Multiple MIP
- Common View 1x2
- Common View 2x1
- Common View 1x3

Select the display option you require.

NOTICE! The list of layouts in the drop-down list, as well as the layout names, are configurable. See the system administrator to change the displayed layout names.

NOTICE

The list of layouts in the drop-down list, as well as the layout names, are configurable. See the system administrator to change the displayed layout names.

Saving layouts as key images

Click Mark Layout as Key  in the Export toolbar to save the current layout as a key image.

See these topics:

Display Option: Multi Datasets on page 310

Display Option: Single Datasets on page 313

Display Option: All on page 315

Display Option: Compare with Prior on page 322

Display Option: Tile on page 321

Display Option: Compare with Prior on page 322

Display Option: Common View on page 325

Display Option: Multi Datasets

The Multi Dataset display options are available in 2x2 and 1x4 layouts. You can view multiple datasets showing a single axis (MPR images) and a three-dimensional representation.

The default display is an axial orientation of PET, CT and Fusion series (MPR images) and a 3D MIP image of the PET series. The Oblique orientation refers to the ability to freely swivel the default plane.

See the following topics:

Example of Multi Dataset 2x2 on page 311

Example of Multi Dataset 1x4 on page 311

Example of Multi Dataset No PET on page 311

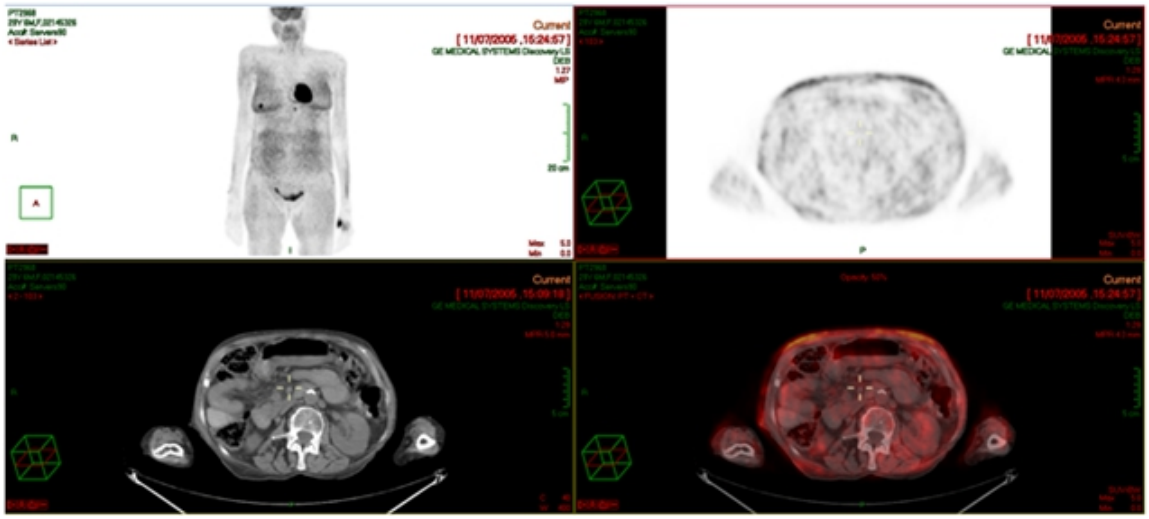
Common Scenarios for Using the Multi Dataset Layout on page 312

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Exceptions and Behavior on page 312

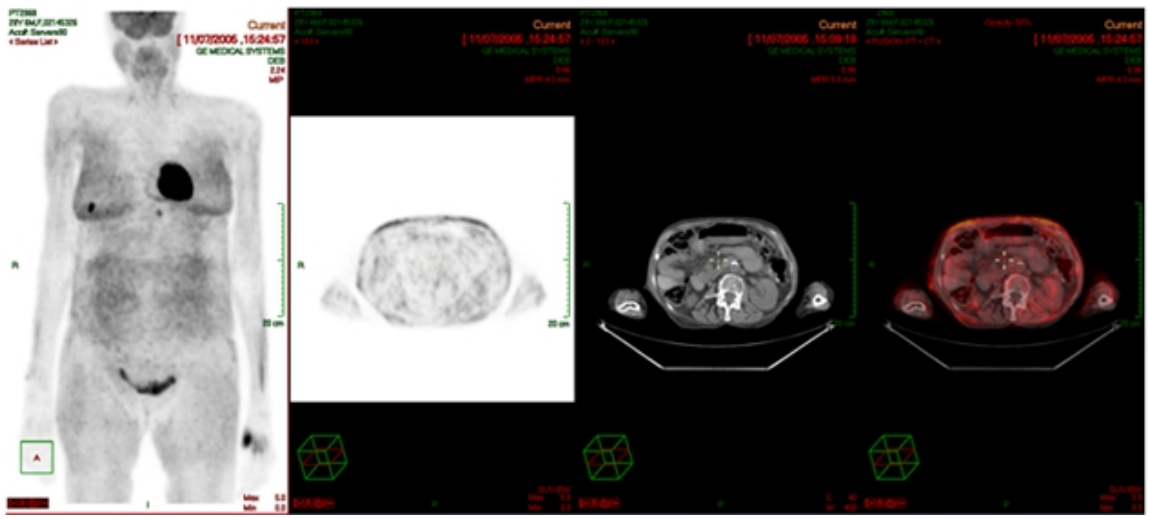
Example of Multi Dataset 2x2

Three-dimensional, PET	Oblique, PET
Oblique, CT	Oblique, Fused



Example of Multi Dataset 1x4

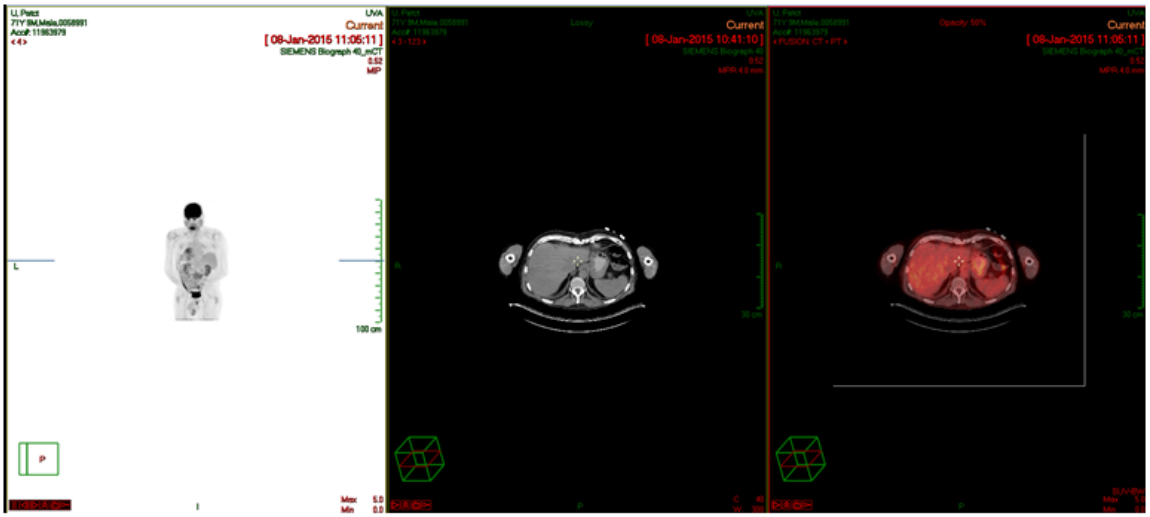
Three-dimensional, PET	Oblique, PET	Oblique, CT	Oblique, Fused



Example of Multi Dataset No PET

Three-dimensional, PET	Oblique, CT	Oblique, Fused

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Common Scenarios for Using the Multi Dataset Layout

Use the PET MIP image in relation to the CT-PET-Fusion images (single plain).

Use the PET MIP image in relation to a single dataset, such as PET, using different windowing.

Exceptions and Behavior

Orientation

The MPR windows must show the same orientation, either of the same or of different datasets. The default is different datasets.

You cannot view registered datasets in different orientations simultaneously. For example, you cannot control the orientation of an MPR window independently from the other MPR windows. If you change the axial axis to a coronal axis in one window, then the orientation in the other images is also affected.

You can view unregistered datasets in different orientations simultaneously. Because the MPR windows are not synchronized, you can control the orientation in each window separately.

Parameters

The dataset displayed in each MPR window is independent from the other windows. The two unfused MPR windows can show the same data. In this situation, you can apply different windowing to each window. The MPR fused windows always show the predefined PET/CT fusion image.

The three MPR windows are linked by default. You can scroll the images simultaneously.

The Zoom and Pan parameters are synchronized between the MPR windows.

The Windowing parameter is not synchronized between the MPR windows.

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The data displayed in the three-dimensional window is not synchronized with the data displayed in the MPR windows. All parameters, such as Zoom, Pan, Scrolling, Orientation, Swiveling, are independent from data displayed in the MPR windows.

Renditions

The three-dimensional window shows by default a MIP rendition of the PET series, and supports following additional rendition types: MIP, MPR Slab, and MIP Slab.

You can select the dataset in the three-dimensional window through the Replace With annotation or through the PMA. The content of the fusion image can not be replaced by another series. However, you can present the pre-defined fused image in any of the window-sets using the Replace With annotation.

If you view a specific rendition type and then change the dataset displayed in the three-dimensional window, the rendition type does not change. For example, if you view a PET MIP image in the three-dimensional window, and used the Replace With annotation to switch to the CT series, the three-dimensional window would show a MIP image of the CT series.

NOTICE

A fusion MIP image is not supported. The three-dimensional window will display the fusion image, but the MIP image option is unavailable.

Relate Mode

You can use Relate Mode  to relate 3D-to-MPR, MPR-to-MPR, and MPR-to-3D images. See About Relate Mode on page 590.

See this topic:

Using Display Options on page 309

Display Option: Single Datasets

The Single Dataset display options are available in 2x2 and 1x4 layouts. You can view a single dataset showing all three standard axes and a 3D representation. The default dataset type is PET series; three MPR images and one 3D MIP image.

See the following topics:

Example of Single Dataset 2x2 on page 314

Example of Single Dataset 1x4 on page 314

Common Scenarios for Using the Single Dataset Layout on page 314

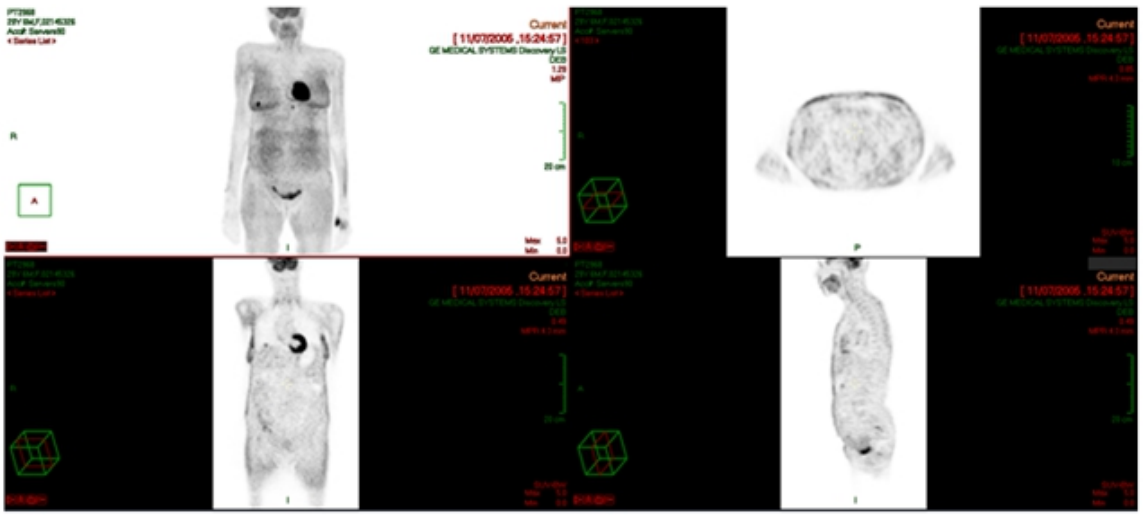
Exceptions and Behavior on page 315

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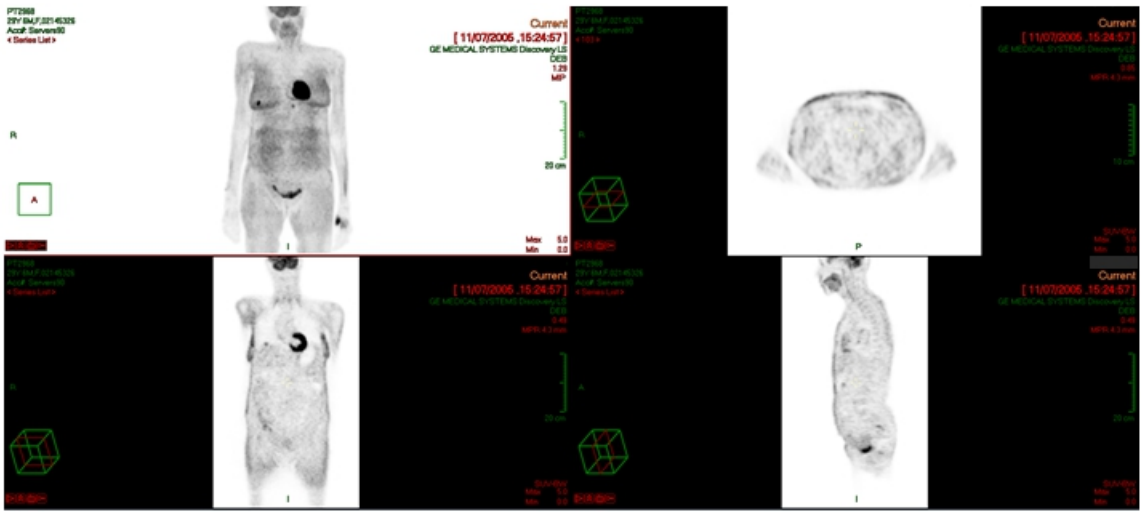
Example of Single Dataset 2x2

Three-dimensional, PET	Axial, PET
Coronal, PET	Sagittal, PET



Example of Single Dataset 1x4

Three-dimensional, PET	Axial, PET	Coronal, PET	Sagittal, PET



Common Scenarios for Using the Single Dataset Layout

- Review single PET series, with MIP image serving as an index.
- Review any other series.

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Exceptions and Behavior

Orientation

The MPR windows show the same dataset, and each window has a pre-defined view (axial, coronal and sagittal).

Changing the Orientation/Planar View on page 166

You cannot control the image in an MPR window independently from the other images.

Parameters

The Zoom, Pan, and Windowing parameters are synchronized between the MPR windows.

Renditions

The three-dimensional window supports by default a MIP rendition of the PET series.

The dataset displayed in the three-dimensional window is the same dataset that is displayed in the MPR windows. If you apply the Replace With annotation, the dataset is switched in all windows. You can also use PMA to switch the dataset.

NOTICE

A fusion MIP is not supported. The three-dimensional window will display a fused dataset as a MIP PET image.

Relate Mode

You can use Relate Mode  to relate 3D-to-MPR, MPR-to-MPR, and MPR-to-3D images. See Correlating Regions of Interest in Registered Studies (Relate Mode) in About Relate Mode on page 590.

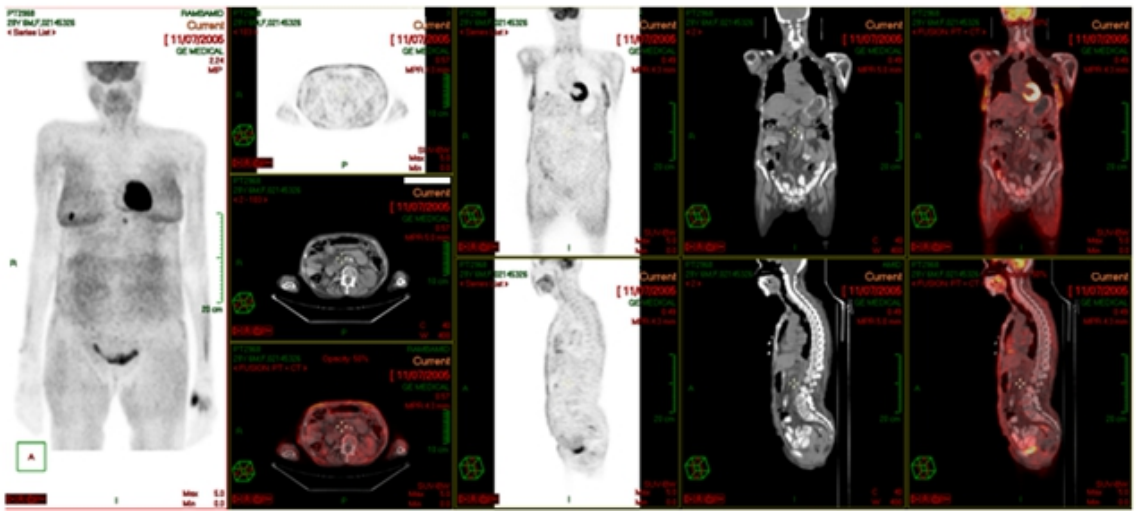
Display Option: All

The All display option shows all three datasets on all three standard axes simultaneously, including a three-dimensional image on the PET series. You can choose to present the fusion image in each of the windows, but you can not control the content of the fusion image. The fusion images present the Hybrid NM fusion image.

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Example of All

Axial, PET	Coronal, PET	Coronal, CT	Coronal, Fused	MIP
Axial, CT				
Axial, Fused	Sagittal, PET	Sagittal, CT	Sagittal, Fused	Three-dimensional



Common Scenario for Using All

Observe all related PET-CT views, including MIP.

Exceptions and Behaviors

Orientation

Each row of MPR images shows a single dataset. The same row cannot mix different datasets. The first two rows in the 3x3 layout could show the exact same data, which you can view with different windowing. The third row in the 3x3 layout window will always show the PET-CT fusion image.

Each column of MPR images shows a single orientation. The same column cannot mix different orientations.

Changing the Orientation/Planar View on page 166

You cannot view registered datasets in different orientations simultaneously. Each dataset is synchronized when you change the orientation.

You can view unregistered datasets in different orientations simultaneously. Because the datasets are not synchronized, you can control the orientation in each window separately.

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Parameters

The Zoom and Pan parameters are synchronized between all MPR images.

Scrolling is synchronized between similar orientations.

Windowing is synchronized for images from the same dataset. Changing the windowing of PET or CT images can affect the Fused images.

You cannot scroll across an orientation or window across a dataset individually. The parameters are synchronized.

You can change the dataset by using the Replace With annotation or the PMA. Each dataset replacement affects the windows belonging to the row that you selected. The other rows are not affected.

Renditions

The upper three-dimensional window shows by default the PET MIP image. You can use the window to show any other dataset or change the rendition type using the applicable annotation.

If you change the data to a fusion image when the MIP rendition is displayed, the rendition changes to MPR Slab, in a coronal orientation.

The bottom three-dimensional window remains empty by default. You can use the window to show any other dataset or change the rendition type using the applicable annotation.

Relate Mode

You can use Relate Mode  to relate 3D-to-MPR, MPR-to-MPR, and MPR-to-3D images. See About Relate Mode on page 590.

Display Option: Compare

The Compare display option is available in 3x3, 2x3, and 1x3 layouts. You can compare datasets using all three standard axes (MPR images).

The composition of the fusion image is predefined. You might see a pair of datasets superimposed on the fusion image that are different from the datasets presented in the other windows.

IMPORTANT

A three-dimensional image is not supported in the Compare Display Option.

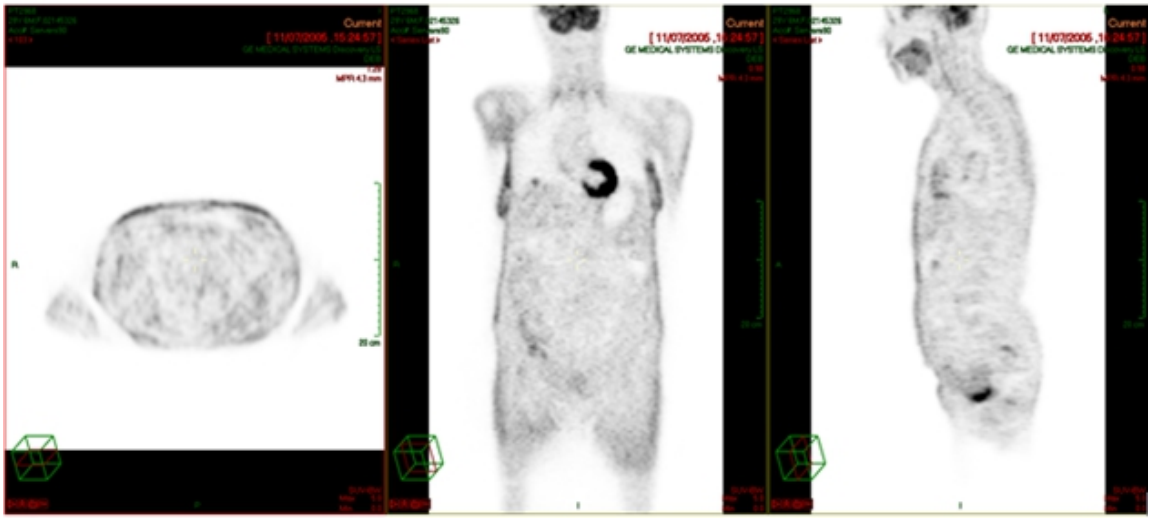
The default display is:

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- First row—MPR axial, coronal and sagittal images of PET.
- Second row—axial, coronal and sagittal images of CT.
- Third row—axial, coronal and sagittal images of fused.

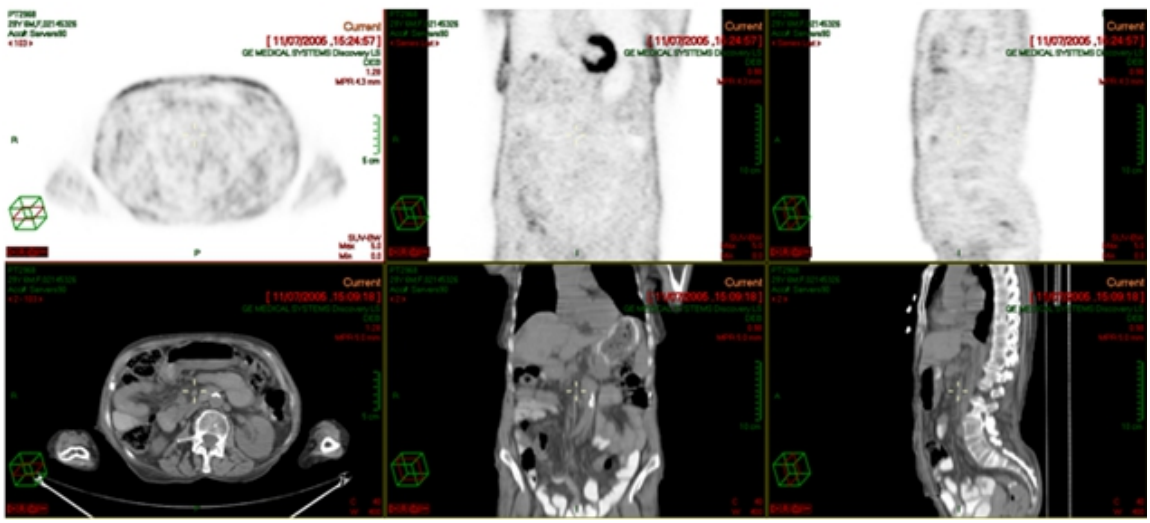
Example of Compare 1x3

Axial, PET	Coronal, PET	Sagittal, PET



Example of Compare 2x3

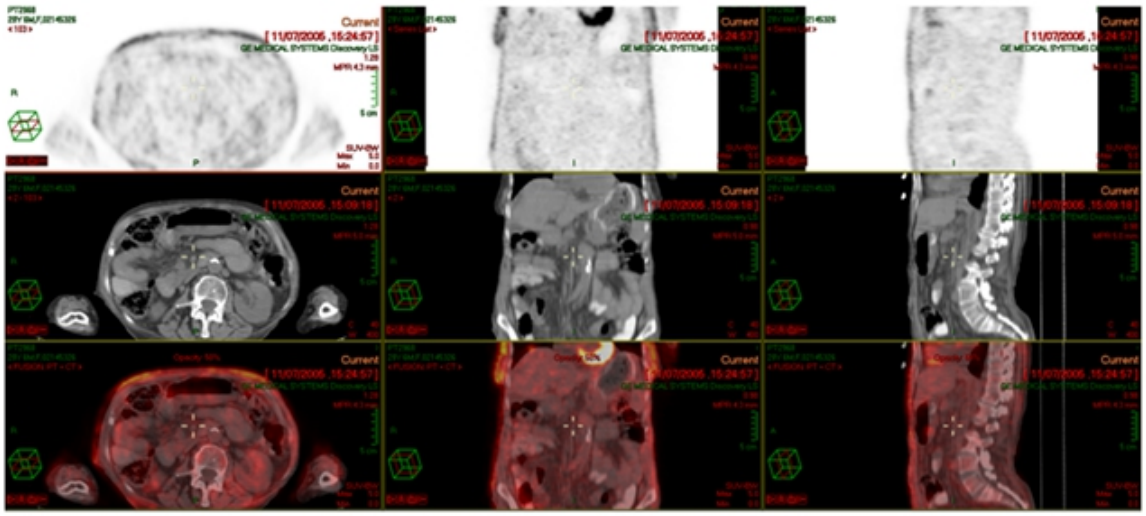
Axial, PET	Coronal, PET	Sagittal, PET
Axial, CT	Coronal, CT	Sagittal, CT



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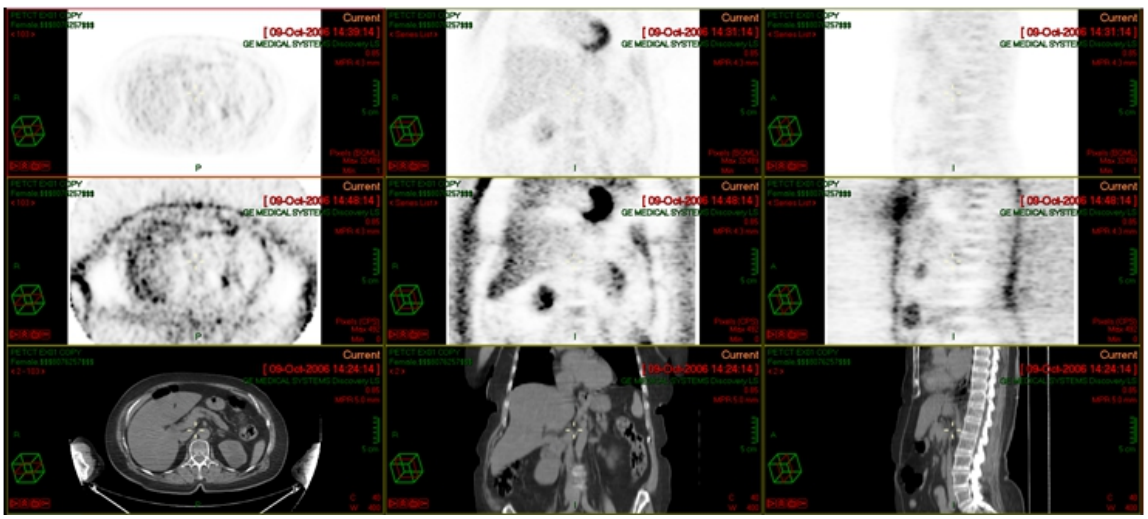
Example of Compare 3x3

Axial, PET	Coronal, PET	Sagittal, PET
Axial, CT	Coronal, CT	Sagittal, CT
Axial, Fusion	Coronal, Fusion	Sagittal, Fusion



Example of Compare with No Attenuation Correction (NAC)

Axial, PET	Coronal, PET	Sagittal, PET
Axial, NAC	Coronal, NAC	Sagittal, NAC
Axial, CT	Coronal, CT	Sagittal, CT



Common Scenarios for Using Compare

- Compare PET/CT, PET/Fusion, or CT/Fusion pairs, or compare a CT/PET/Fusion triplet.

- Compare a current CT/PET/Fusion dataset with a prior dataset.
- Compare different windowing for the same set; for example, CT with different windowing.
- Compare any two datasets; for example, CT with MR.
- Compare original data in the Volume Matching viewbox with secondary or tertiary data.

Exceptions and Behaviors

Orientation

Each row of MPR images shows a single dataset. The same row cannot mix different datasets. The first two rows in the 3x3 layout could show the exact same data, which you can view with different windowing. The third row in the 3x3 layout window will always show the PET/CT fusion image.

Each column of MPR images shows a single orientation. The same column cannot mix different orientations.

Changing the Orientation/Planar View on page 166

You cannot view registered datasets in different orientations simultaneously. Each column of registered MPR images is synchronized when you change the orientation.

You can view unregistered datasets in different orientations simultaneously. Because the MPR windows are not synchronized, you can control the orientation in each window separately.

Parameters

The Zoom, Pan, and Windowing parameters are synchronized between each row of windows. For example, changing the zoom and windowing of the axial PET image also affects the coronal PET and sagittal PET images.

The Zoom, Pan, and Windowing parameters are synchronized between each column of windows. For example, changing the windowing of PET or CT images also affects the Fusion image.

You cannot scroll across an orientation or window across a dataset individually. The parameters are synchronized.

You can change the dataset by using the Replace With annotation or the PMA. Each dataset replacement affects the windows belonging to the row that you selected. The other rows are not affected.

Relate Mode

You can use Relate Mode  to relate all datasets. See Correlating Regions of Interest in Registered Studies (Relate Mode) on page 590.

See this topic:

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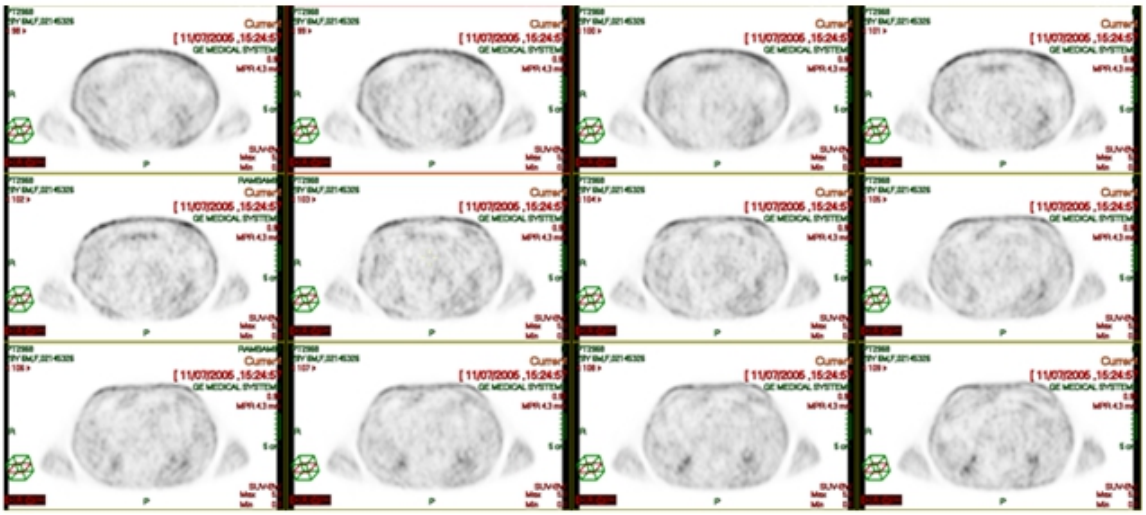
Using Display Options on page 309

Display Option: Tile

The Tile display option provides a 1x1 tile layout. You can view a single dataset in a single plane, including oblique. The default dataset is an axial PET series.

Example of Tile

Oblique, PET	Oblique, PET	Oblique, PET
Oblique, PET	Oblique, PET	Oblique, PET
Oblique, PET	Oblique, PET	Oblique, PET



Common Scenario for Using Tile

Observing a series in stack or tile mode.

Exceptions and Behavior

Tile provides a single MPR window that you can swiveled freely in stack mode.

NOTICE

All current limitations that apply to MPR images in tile mode remain valid. For example, in tile mode the reference point will appear only on the middle image. The Swivel model is inactive in this scenario.

Changing the Orientation/Planar View on page 166

You can change the dataset by using the Replace With annotation or the PMA.

See this topic:

Using Display Options on page 309

Display Option: Compare with Prior

The Compare with Prior display option provides 2x3 and 2x4 layouts. You can view three datasets of two studies. All the datasets are shown in the same orientation. The default display includes an axial PET, an axial CT, and an Axial Fusion image.

NOTICE

The three-dimensional image is not supported in the Compare with Prior display option.

Example of Compare with Prior 2x3

Current Axial, PET	Current Axial, CT	Current Axial, Fusion
Prior Axial, PET	Prior Axial, CT	Prior Axial, Fusion

Example of Compare with Prior 2x4

Three-dimensional, PET	Current Axial, PET	Current Axial, CT	Current Axial, Fusion
	Prior Axial, PET	Prior Axial, CT	Prior Axial, Fusion

Example of Compare with Two Priors

Current Three-dimensional, PET	Current Axial, PET	Current Axial, CT	Current Axial, Fusion
Prior 1 Three-dimensional, PET	Prior 1 Axial, PET	Prior 1 Axial, CT	Prior 1 Axial, Fusion
Prior 2 Three-dimensional, PET	Prior 2 Axial, PET	Prior 2 Axial, CT	Prior 2 Axial, Fusion

Example of Compare with Three Priors

Current Three-dimensional, PET	Current Axial, PET	Current Axial, CT	Current Axial, Fusion
Prior 1 Three-dimensional, PET	Prior 1 Axial, PET	Prior 1 Axial, CT	Prior 1 Axial, Fusion

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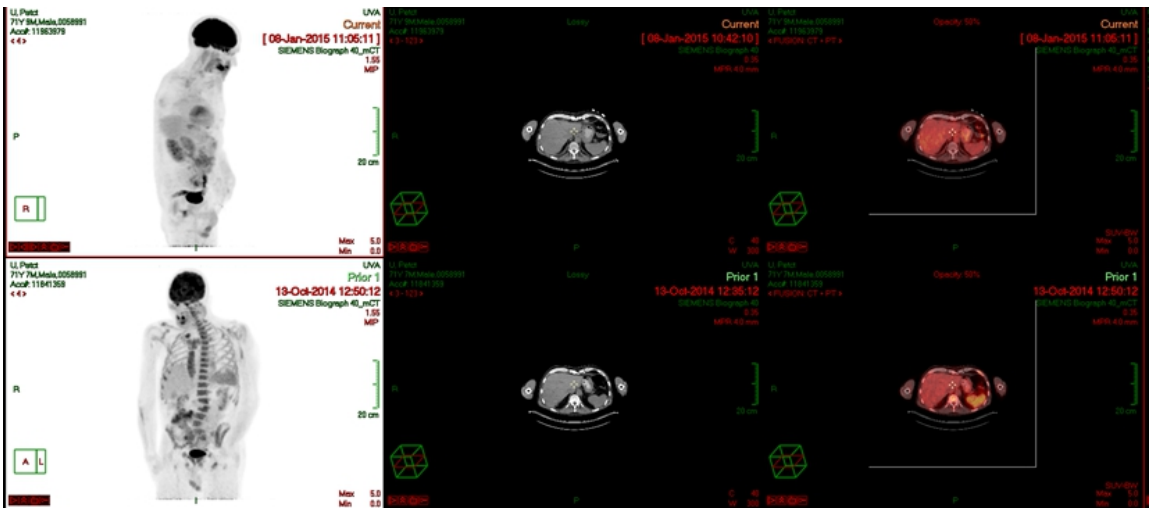
Prior 2 Three-dimensional, PET	Prior 2 Axial, PET	Prior 2 Axial, CT	Prior 2 Axial, Fusion
Prior 3 Three-dimensional, PET	Prior 3 Axial, PET	Prior 3 Axial, CT	Prior 3 Axial, Fusion

Example of Compare with Four Priors

Current Three-dimensional, PET	Current Axial, PET	Current Axial, CT	Current Axial, Fusion
Prior 1 Three-dimensional, PET	Prior 1 Axial, PET	Prior 1 Axial, CT	Prior 1 Axial, Fusion
Prior 2 Three-dimensional, PET	Prior 2 Axial, PET	Prior 2 Axial, CT	Prior 2 Axial, Fusion
Prior 3 Three-dimensional, PET	Prior 3 Axial, PET	Prior 3 Axial, CT	Prior 3 Axial, Fusion
Prior 4 Three-dimensional, PET	Prior 4 Axial, PET	Prior 4 Axial, CT	Prior 4 Axial, Fusion

Example of Compare with Prior no PET

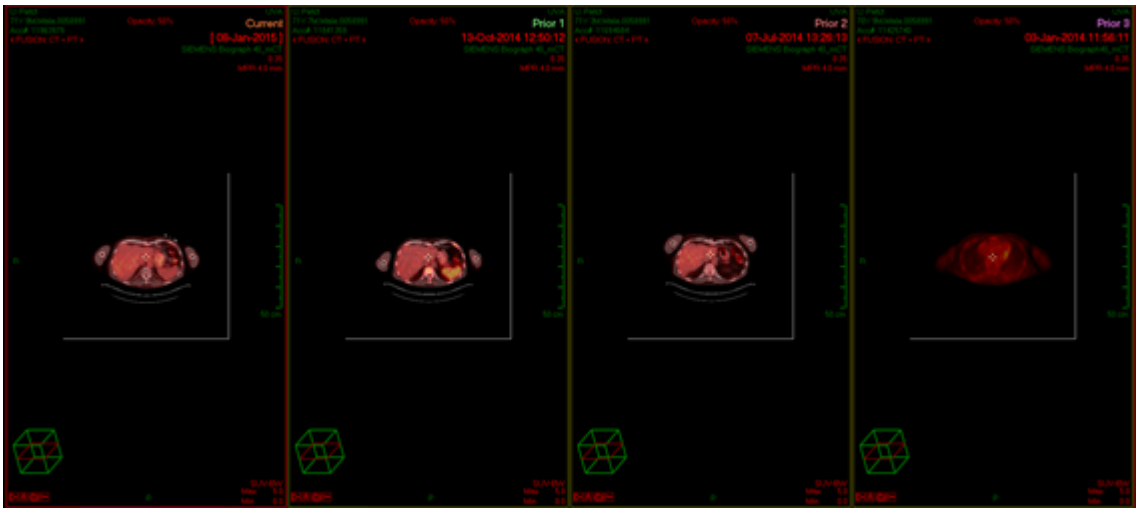
Current Three-dimensional, PET	Current Axial, CT	Current Axial, Fusion
Prior Three-dimensional, PET	Prior Axial, CT	Prior Axial, Fusion



Example of Multiple Fuse

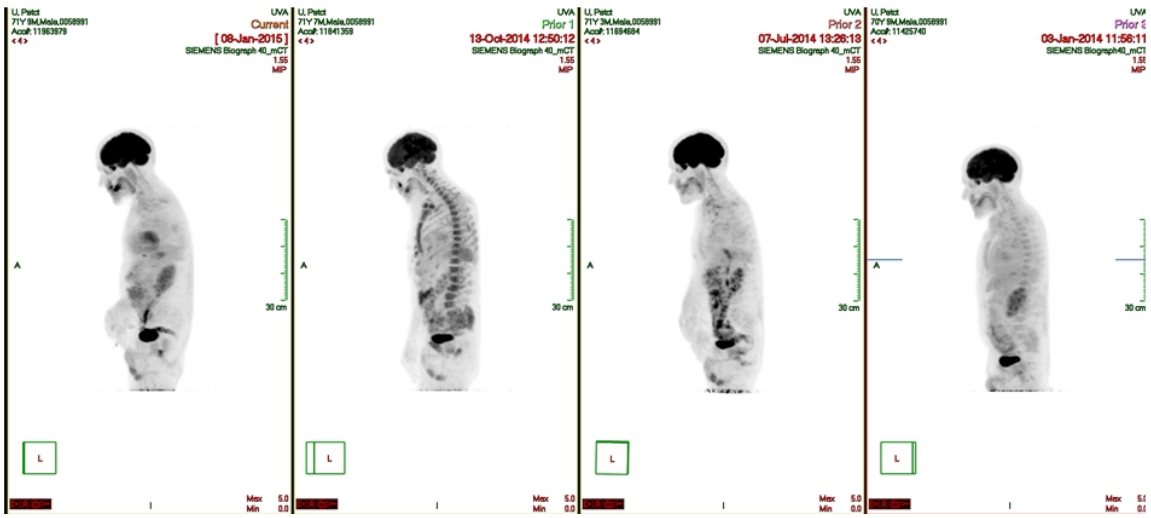
Current Axial, Fusion	Prior 1 Axial, Fusion	Prior 2 Axial, Fusion	Prior 3 Axial, Fusion

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Example of Multiple MIP

Current Three-dimensional, PET	Prior 1 Three-dimensional, PET	Prior 2 Three-dimensional, PET	Prior 2 Three-dimensional, PET



Common Scenarios for Using Compare with Prior

- Compare PET/CT Current and PET/CT Prior in all three datasets.
- Compare the three datasets of same study in two windowing levels or two color maps.
- Compare any set of two/three series of one study with another study.

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Exceptions and Behaviors

Orientation

Each column of MPR images shows a single orientation. The same column cannot mix different orientations.

You cannot view registered datasets in different orientations simultaneously. Each column of registered MPR images is synchronized when you change the orientation.

You can view unregistered datasets in different orientations simultaneously. Because the MPR windows are not synchronized, you can control the orientation in each window separately.

Parameters

The three MPR windows are linked by default. You can scroll the images simultaneously.

The Zoom and Pan parameters are synchronized between the MPR windows.

The Windowing parameter is not synchronized between the MPR windows; however, the fusion image is affected by PET/CT windowing changes.

You cannot scroll across an orientation for a registered dataset individually. The parameters are synchronized.

The three-dimension image is not supported.

You can change the dataset by using the Replace With annotation or the PMA. Each dataset replacement affects the windows belonging to the row that you selected. The other rows are not affected.

Relate Mode

You can use Relate Mode  to relate all datasets. See About Relate Mode on page 590.

See this topic:

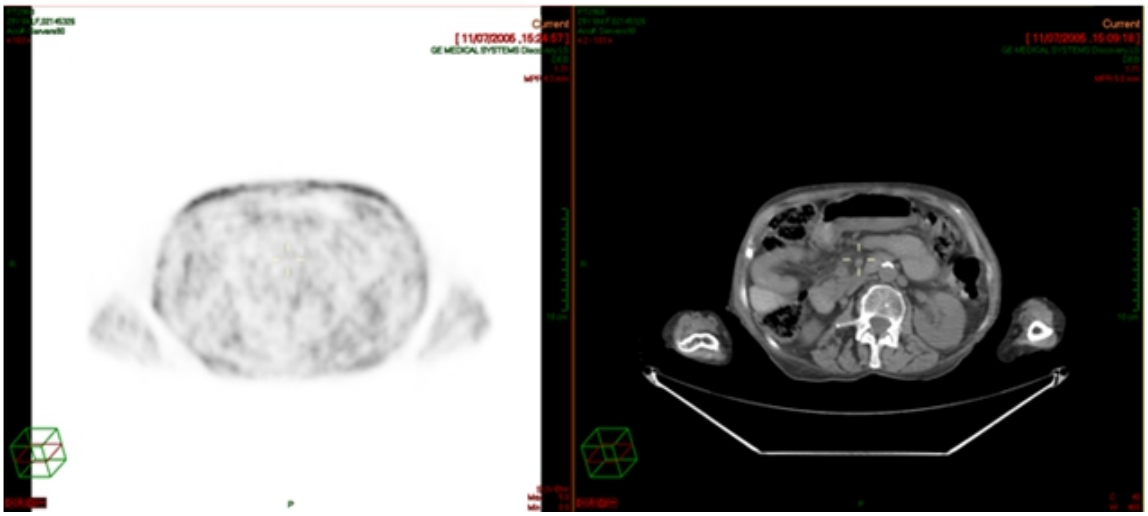
Using Display Options on page 309

Display Option: Common View

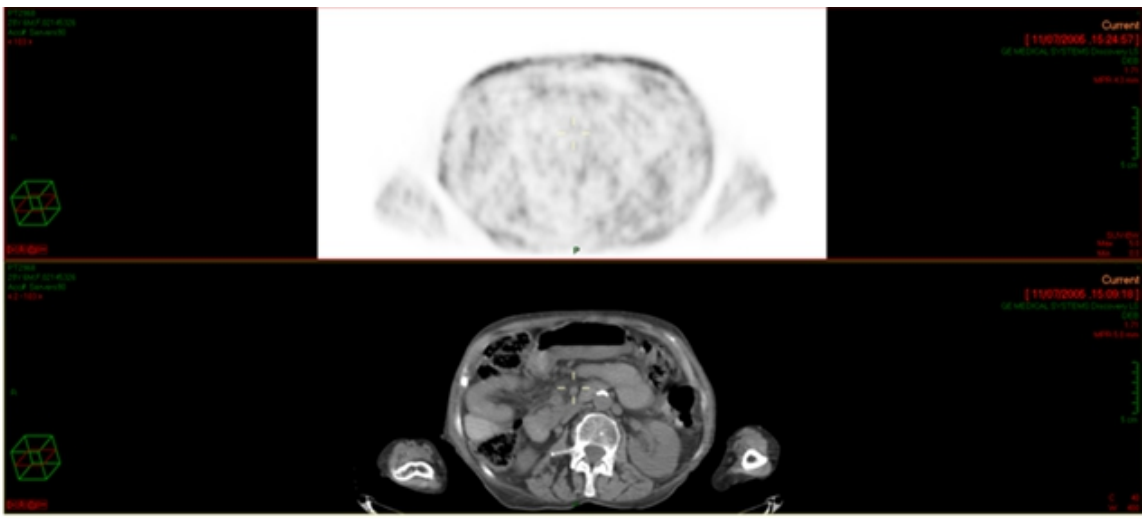
The Common View display options are available in 1x2, 2x1, and 1x3 layouts.

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Example of Common View 1x2

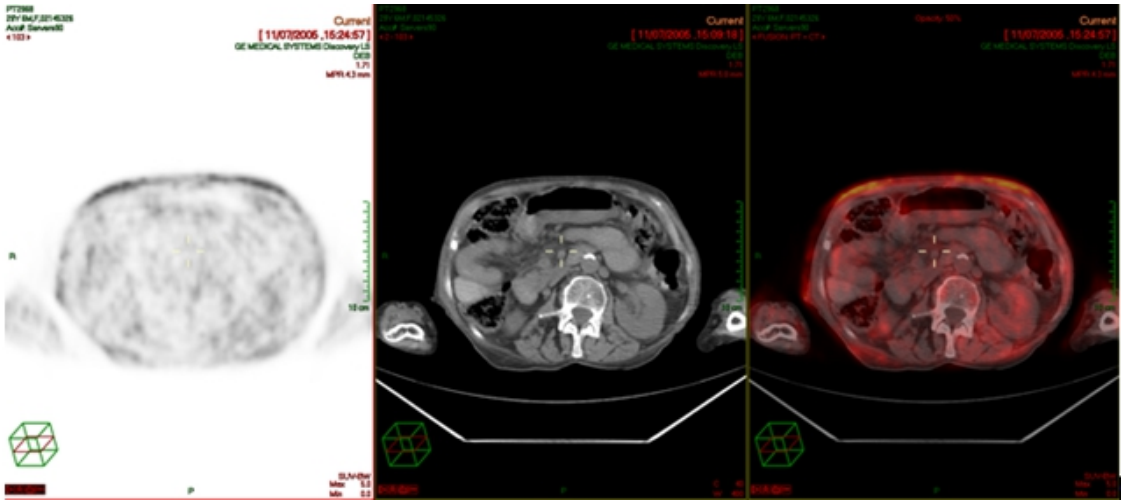


Example of Common View 2x1



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Example of Common View 1x3



See this topic:

Using Display Options on page 309

13.13.17 Defining MPR Parameters for Hybrid NM

You can change the rendition type by right-clicking the image and selecting Change Image, or by right-clicking the MPR annotation.

- In MPR windows, the options are MPR, MipPR, and MinPR.
- In three-dimensional windows, the options are Angiography MIP, MPR, MipPR, and MinPR.

IMPORTANT

The MPR annotation is deactivated for fused images.

The MPR sub-menu includes the MPR Parameters option. See Defining MPR Parameters on page 614.

Use the MPR Parameters tools to change:

- Rendition type
- Thickness
- Spacing

Changing the thickness and/or rendition type only affects the dataset on which the operation was performed. When the updated dataset appears in the fused image, the fused image is updated appropriately. For example, if the Hybrid NM rendition type or thickness changes, the fused image containing the specific CT or PET image also updates to show the change.

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NOTICE

Changing the thickness of MPR images in areas where you placed graphic elements can hide the graphic elements. Scroll to the applicable location to show the graphic elements.

IMPORTANT

Changing the spacing affects all datasets.

The following MPR capabilities are unavailable in the PET/CT:

- Enabling Dual Windowing on page 181

If you need to compare the same dataset with different windowing, drag the dataset so that the same data is displayed in different windows.

- Working with Curved Cross-Sections on page 172(parallel, concentric, sectional and sectional parallel curve)
- About Volume Rendering on page 632

13.13.18 Saving Presentations in Hybrid NM

When you use the Save Presentation feature in the PET/CT the following parameters are saved:

- The displayed Display Option and exact layout.
- The exact datasets presented in each window.
- All MPR parameters.
- Zoom and Pan.
- Windowing.
- Enhance.
- Reference Point.
- Plane in MPR images.

The datasets composing the fused image are retained, even if they are different from other displayed datasets. The opacity and blending type of the fusion image are also saved.

See these topics:

Saving a Study as a Presentation on page 620

About Save Presentation on page 619

13.13.19 PET/CT Settings

Several PET/CT parameters can be configured in Application Settings.

1. Opening the Application Settings Window on page 453 window.
2. Do one of the following:

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- In the left-pane tree, click the plus sign next to Clinical Applications and select PET-CT Application.
- Click Clinical Applications and in the right pane click Configure PET-CT Settings.

3. You can set the following:
   - Determine which tool will be active upon loading of the PET/CT study – Zoom, Windowing, Pointer, Swivel, or Relate.
   - Set the minimum and maximum Standard Uptake Values (SUV) for lesion highlighting.
   - Set the following options:
     - Display a Wireframe Around the MIP Image. By default the wire frame is hidden for all users.
     - Enable automatic swivel of the MIP image upon loading of the study.
     - Default Merge Method. By default, the merge method for fusion images is Alpha Blending. You can change it to Highlight. See About Fusion Images on page 287.

The shown MIP in the PET/CT application is a weighted MIP that better illustrates the depth of the data.

To disable the weighting and thus show a regular un-weighted image click the MIP On/Off button  in the 3D bar.

13.13.20 PET/CT Comparison

About Hybrid NM Comparison

Hybrid NM Comparison is a display option that automatically loads two studies. Whenever you select a current study and load it to the PET/CT, Hybrid NM Comparison loads the prior Hybrid NM study automatically. The two studies show as current and prior in this comparison display option and are automatically registered.

You can load studies to Hybrid NM Comparison either from the Archive Explorer or by using a layout option from the Layout tab once the PET/CT is launched. When you load studies to Hybrid NM Comparison from the Archive Explorer, the default layout is a 2 x 4 layout (one current and one prior study). To use other layouts or display more than one prior, load a study to Hybrid NM and select one of the layout options from the Layout tab.

Selecting a comparison option of more than one prior automatically loads all the relevant priors and displays them in the layout.

PET/CT Overview

The PET/CT is an image viewer, a registration tool, and an analysis workstation. The application supports all features required for PET/CT reading, including the ability to:

- Fuse (see About Fusion Images on page 287) together PET and CT images.

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- View combined current and prior images (see About Hybrid NM Comparison on page 329) to see the progress of an area of pathology.

You can use Hybrid NM to:

- Select a pre-defined Display Option (see Using Display Options on page 309) to present PET, CT, and Fusion images.
- Apply a color map (see Using Color Maps on Fusion Images on page 290) to show potential pathology.
- Apply measurements in Standard Uptake Values (SUV) (see Selecting Standard Uptake Values (SUVs) on page 304).
- Apply layouts (see About Hybrid NM Display Options on page 308) to synchronize PET and CT data sets.
- Register (see About Registration on page 577) and compare (see Creating a Hybrid NM Comparison View on page 330) studies.

Reference Material	Instructions
About the Hybrid Nuclear Medicine (NM) Application on page 291 PET/CT Workflow on page 294 About Hybrid NM Comparison on page 329	Creating a Hybrid NM View on page 293 Creating a Hybrid NM Comparison View on page 330 About Fusion Images on page 287 Windowing Images on page 299 Using Color Maps on Fusion Images on page 290 About Standard Uptake Value (SUV) on page 301 About Hybrid NM Display Options on page 308 Defining MPR Parameters for Hybrid NM on page 327 Saving Presentations in Hybrid NM on page 328

Hybrid NM Comparison Toolbar

Hybrid NM Comparison is a display option for the PET/CT.

See PET/CT Toolbar on page 295.

Creating a Hybrid NM Comparison View

Hybrid NM Comparison is a display option for the Hybrid NM viewbox application.

See Creating a Hybrid NM View on page 293.

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13.14 Lesion Management Application

13.14.1 Lesion Management Application Overview

The Lesion Management application offers tools for the evaluation and monitoring of cancerous and other lesions identified in Computed Tomography (CT) and Magnetic Resonance Imaging (MRI) images.

Lesion Management volumetrically measures and segments lung lesions, liver lesions (or other types of masses), lymph nodes, and other lesions and Regions of Interest (ROIs) based on input such as a drawn line or a drawn contour. It allows pairing of lesions from prior and subsequent studies and performs follow-up calculations to assess size and volume changes over time. Drawing tools are available for measuring lesions two-dimensionally by their diameters.

Lesion Management also includes bookmarking tools designed to assist with navigation through segmentations and other marked findings and to facilitate the monitoring of changes over time.

Various correction tools allow further input and segmentations in order to better measure lesions and observe changes.

13.14.2 Lesion Segmentation

Using the Lesion Segmentation Tools

The Lesion Management segmentation tools let you volumetrically segment lesions found in various tissues. Some of the tools are optimized for lesion identification and segmentation in specific tissues and modalities. For example, the algorithm activated by the Lung Segmentation tool is optimized for identifying lung lesions in CT scans, while the algorithm activated by the Liver Segmentation tool is designed to identify liver lesions in CT scans.

You can also use a two-dimensional drawing tool, a semi-automatic contour-drawing tool, and a lesion tracking tool that identifies lesions in a new study based on the existence of lesions in a prior study.

Segmentation Ribbon



#	Description

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1	**Lung Lesion Segmentation** Volumetrically segment a lung lesion based on your drawn line (long diameter).
2	**Lung Lesion Segmentation** Volumetrically segment a liver lesion based on your drawn line (long diameter).
3	**Lymph Node Segmentation** Volumetrically segment a lymph node based on your drawn line (short diameter).
4	**Threshold Segmentation** Volumetrically segment a lesion located inside your drawn sphere (or spheroid). The segmentation threshold is based on the maximum value point inside the volume boundaries (when the threshold type option is set to Percentage) or on a fixed value (when the threshold type option is set to Fixed). Set threshold type options in Application Settings. See Section Determining Threshold Segmentation Options.
5	**Generic Lesion Segmentation** Volumetrically segment any lesion based on your drawn line (long diameter).
6	**Two Diameters Measurement** Activate a drawing mode that allows you to draw the long and short lesion diameters for a two-dimensional Response Evaluation Criteria in Solid Tumors (RECIST) measurement.
7	**Livewire Mode Segmentation** Define a lesion's contour in a semi-automatic manner in order to volumetrically measure the lesion.
8	**Add Segmentation** Create a new segmentation from scratch using the disk tool. The disk's diameter can be changed by pressing the shift key along with the arrow keys. The SHIFT+LEFT ARROW decreases its size and SHIFT+RIGHT ARROW increases its size. A single mouse click starts the segmentation creation and another click stops the segmentation, to allow moving to a new location and continue the segmentation from there. The ESC key or double-clicking the image finishes the segmentation.

Segmenting Lung Lesions

1. Click the Lung Lesion Segmentation icon 
   ⇨ The cursor changes its shape to signify segmentation mode.
2. Draw a line across the lesion along the lesion's long diameter. To draw the line, click at the line's starting point and then at its end point.

The application draws a contour around the lesion boundaries in all relevant slices (images) and measures the lesion's volume. The calculated volume appears next to the lesion (as well as in the bookmark list).

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The application draws a contour around the lesion boundaries in all relevant slices (images) and measures the lesion's volume. The calculated volume appears next to the lesion (as well as in the bookmark list).

The lung tool is intended for marking small nodules (< 2 cm). When measuring larger lesions other lesion tools may yield better results.

Segmenting Liver Lesions

1. Click the Liver Lesion Segmentation icon .
   ⇨ The cursor changes its shape to signify segmentation mode.
2. Draw a line across the lesion along the lesion's long diameter. To draw the line, click at the line's starting point and then at its end point.

The application draws a contour around the lesion boundaries in all relevant slices (images), and measures the lesion's volume. The calculated volume appears next to the lesion (as well as in the bookmark list).

The application also draws lines reflecting the longest axial diameter and longest perpendicular diameter of the lesion. The diameters are displayed when you hover with the mouse over the segmented lesion in the slice that was calculated to have the longest diameter.

Segmenting Lymph Lesions

1. Click the Lymph Lesion Segmentation icon .
   ⇨ The cursor changes its shape to signify segmentation mode.
2. The cursor changes its shape to signify segmentation mode.

The application draws a contour around the lesion boundaries in all relevant slices (images) and measures the lesion's volume. The calculated volume appears next to the lesion (as well as in the bookmark list).

The application also draws lines reflecting the longest axial diameter and longest perpendicular diameter of the lesion. The diameters are displayed when you hover with the mouse over the segmented lesion in the slice that was calculated to have the longest diameter.

Threshold Segmentation

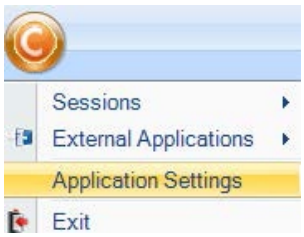
Using the Threshold Segmentation Tool

1. Click the Threshold Segmentation icon .
   ⇨ The cursor changes its shape to signify circle drawing.

Determining Threshold Segmentation Options

Use Application Settings to determine the threshold type, threshold units, display mode and threshold values.

1. Click the round icon at the top left corner of the screen and click **Application Settings**.



2. Expand the **Clinical Applications** node in the left pane and click **Lesion Management**.

   You can set the following options:

Option	Description
Threshold Type	Select a threshold type. Possible values are: • **Fixed** Segmentation is based on fixed values. In PET studies, set the value in the **Fixed SUV Threshold** option. In CT studies, set the maximum and minimum values in the **Fixed HU Maximum Threshold** and **Fixed HU Minimum Threshold** option. • **Percentage** The system looks for the maximum value point inside the spheroid. All voxels with values above the set percentage (of the maximum value point) is included in the segmentation.
Threshold Units	Select threshold units. Possible values are: • **SUV BW** SUV Body Weight • **SUV LBM** SUV Lean Body Mass • **SUV BSA** SUV Body Surface Area
Display Mode	Select a display mode. Possible values are: • **Overlay** The segmented area is marked by a contour and an overlay. • **Contour** The segmented area is marked by a contour only.
Fixed SUV Threshold	Select a value for the fixed threshold type in PET studies.
Fixed HU Maximum Threshold	Select a maximum value for the fixed threshold type for CT studies.
Fixed HU Minimum Threshold	Select a minimum value for the fixed threshold type for CT studies.

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SUV Marker	Select a method to enable the SUV Peak or the SUV Max calculation and marker.
PET Segmentation Measurements	Select one or more threshold segmentation enhanced annotations.
Segment only single component around the max pixel	Segment only the component that contains the maximum pixel within the threshold

Segmenting Generic Lesions

1. Click the **Generic Lesion Segmentation** icon .
   ⇨ The cursor changes its shape to signify segmentation mode.
2. Draw a line across the lesion along the lesion's long diameter. To draw the line, click at the line's starting point, and then at the end point of the line.
   ⇨ The application draws a contour around the lesion boundaries in all relevant slices (images), and measures the lesion's volume. The calculated volume appears next to the lesion (as well as in the bookmark list).
   ⇨ The application also draws lines reflecting the longest axial diameter and longest perpendicular diameter of the lesion. The diameters are displayed when you hover with the mouse over the segmented lesion in the slice that was calculated to have the longest diameter.

Measuring Diameters

The **Diameter Measurement** tool allows you to draw two diameters for a lesion (normally the longest axial diameter and longest perpendicular diameter).

1. Click the **Two Diameters Measurements** icon .
   ⇨ The cursor changes its shape to signify the two-dimensional line-drawing mode.
2. Draw a line across the lesion. To draw the line, click the line's starting point and then the end point of the line. Then draw a second line. The lengths of the lines (in mm) appear next to the lines (as well as in the bookmark list).

⇨ When you have drawn the lines, you may move them around or drag their vertices, the same way you change any line measurement. Bring the mouse over to the line and when the cursor changes to a four-headed arrow, press the left mouse button and while pressed move the line to the desired place.

Defining Livewire Lesion Contours

The **Livewire Mode Segmentation** tool is designed to measure a lesion volumetrically based on semi-automatic contour drawing.

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1. Click the Livewire Mode Segmentation icon .

   The Livewire Contour ribbon appears.



   - 1. **Livewire Mode Segmentation**: Define a lesion's contour in a semi-automatic manner in order to volumetrically measure the lesion.
   - 2. **Livewire Windowing Parameters**: Take into account the image's windowing features.
   - 3. **Delete Current Contour**: Delete the currently displayed user contour.
   - 4. **Accept Lesion Segmentation**: Accept the lesion segmentation and calculated measurements.
   - 5. **Cancel Lesion Segmentation**: Cancel all of the operations performed with the livewire tool.

2. While the **Livewire Mode Segmentation** icon is selected, click the Livewire Windowing Parameters icon if you want the segmentation operation to take into consideration the windowing attributes of the image. If this icon is not chosen, the segmentation tools ignore windowing information and looks at the entire range of intensity values.
3. Click once on the lesion boundary and then hover with the mouse cursor around the lesion (no clicking). The contour is drawn as you progress while changing to follow the lesion boundaries.

   You can click several points along the lesion's boundaries. The clicks serve as control points that determine the contour's route.

   You can also draw the contour by pressing the mouse continuously along the lesion's boundaries. In this method, the application does not change the line to follow the lesion's boundaries, but rather bases the contours on your drawing.

   When you draw the contour by hovering with the mouse or by adding control points, the application suggests an automatic closure of the contour when the drawing is near completion.

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While defining a lesion's contour for the first time, you may use correction actions by using the livewire correction tools. See Section Correcting Contours in Livewire Mode on page 340.

4. Double-click to complete the contour drawing. If an automatic completion of the contour has been suggested by the application, you can complete the contour by a single click as well.

   The lesion's volume (in cc) appears next to the segmented lesion.

   You may repeat the drawing on several slices along the lesion.

   The application interpolates the missing contours between every two consecutive user-defined contours and draws interpolated contours on those images. User contours appear as a thicker line compared with the interpolated contours, which are marked with a thinner line.

5. Click the **Accept Lesion Segmentation** icon to accept all segmentations and calculations and have the diameters of the lesion displayed next to the lesion.

Volume and diameters for the completed lesion are calculated and displayed as for the other lesion segmentation tools.

NOTICE

You can change the orientation of the image after you have drawn contours. If you then draw a contour in a new orientation, the application accepts the segmentation and treats the new contour and any following contours as correction to that segmentation. Clicking **Cancel** dismisses the whole process, including the contours drawn in the original orientation.

Moving the segmentation contour text

The segmentation contour text can be moved from one point to another. Moving the segmentation contour text on one slice moves the segmentation text to that point in all slices.

When the text is moved from its default location, a dotted line is drawn connecting the text to the segmentation.

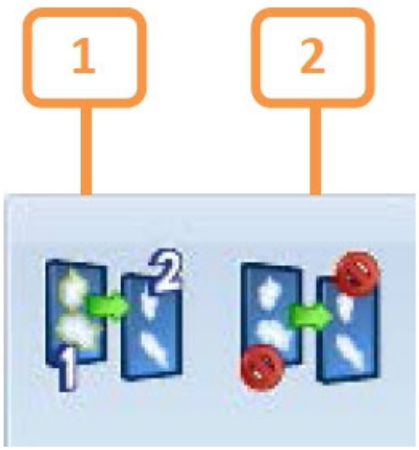
This is the same behavior as 2D measurements, including resetting to the default location.

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13.14.3 Tracking Lesions

Lesion Tracking Ribbon



#	Description
1	**Lesion Tracking Tool** Locate and segment lesions in a destination study based on the location of existing lesions in a source study.
2	**Stop Lesion Tracking** Stop lesions in the destination group from being segmented based on the existence of source group lesions.

Using the Lesion Tracking Tool

The **Lesion Tracking** tool locates lesions in a destination group, based on existing lesions in a source group. Typically, the destination group belongs to the current study while the source group is of a prior study. For each lesion in the source group, the tool searches for a corresponding lesion in the destination group. It then segments the new lesion and creates a Follow-Up set from the source and destination lesions.

To use the tool when the source study is the prior study and the destination study is the current study –

1. Click the Lesion Tracking tool icon.
   ⇨ The cursor changes its shape, displaying the digit 1.
2. Click anywhere on the image group that is to be the source group.
   ⇨ The cursor changes its shape, displaying the digit 2.
3. Click the image group that is to be the destination group.

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⇨ If these groups are not already registered, the application registers (volumetrically matches) them and, based on the registration and on the location of each lesion in the source group, looks for lesions in the destination group. The algorithm then segments the newly found lesions and associates between the source and destination lesions, creating Follow-Up sets.

4. Click the **Stop Lesion Tracking** tool to stop lesions in the destination group from being segmented based on the existence of source group lesions.

NOTICE

Once the Lesion Tracking tool has been activated, any new lesion that is marked at a later stage on the source study is located, segmented, and associated with a lesion in the destination study. This mode is retained until Stop Lesion Tracking is activated, or until Lesion Tracking is activated on a new group.

In cases when an already segmented lesion exists in the destination group in a location corresponding to a lesion in the source group, the existing segmentation is retained.

If the two lesions were not associated in a Follow-Up set, the application creates a Follow-Up set containing the two lesions. However, in cases when the newly located lesion in the destination group overlaps an existing segmented lesion, the following occurs:

- If the overlap covers 90 % (configurable) or more of the existing lesion, the application retains the already existing segmentation and defines a new Follow-Up set if one did not exist. No new segmentation is created and a dialog box alerts the user that no new lesion has been created.
- If the overlap covers less than 90 %, both segmentations (the existing one and the newly located one) are retained. The Follow-Up set is created with the newly segmented lesion.

At the end of the run a dialog box lets you know how many lesions have been successfully transferred from the source group to the destination group.

NOTICE

The lesion tracking tool only tracks lesions of type lung or liver.

13.14.4 Using the Correction Tools

About the Lesion Management Correction Tool

The Lesion Management application offers you tools for correcting already existing segmentations. Correction tools are available in a right-click context-sensitive menu, as well as in the **Correction** ribbon.

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#	Description
1	**Livewire Correction** Correct a drawn contour using the livewire mode.
2	**Merge Lesions** Treat two different lesions as a single one.
3	**Crop Lesion Using Line** Crop a lesion based on a drawn line representing a plane perpendicular to the displayed plane.
4	**Edit Segmentation** Edits an existing segmentation by adding or removing part of the segmentation using a brush tool, similar to the one used in the Add Segmentation tool.

Correcting Contours in Livewire Mode

The **Livewire Correction** tool allows you to correct segmentation contours of volumetric lesions using a livewire-mode correction tool.

1. Click on the **Livewire Correction**  icon in the Correction ribbon or right-click on a contour and select Correct with Livewire.
2. The **Livewire Correction** ribbon appears.



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- 1. **Livewire Mode Segmentation** Define a lesion's contour in a semi-automatic manner in order to volumetrically measure the lesion.
- 2. **Livewire Windowing Parameters** Take into account the image's windowing features.
- 3. **Delete Current Contour** Delete the currently displayed contour.
- 4. **Accept Lesion Segmentation** Accept the lesion segmentation and calculated measurements.
- 5. **Cancel Lesion Segmentation** Cancel all of the operations performed with the livewire tool.

3. While the Livewire Contour Drawing icon is selected, click the Livewire Windowing Parameters icon if you want the segmentation correction operation to take into consideration the windowing attributes of the image.
4. If you have started the process by clicking the Livewire Correction icon rather than by right-clicking a contour, click the image.
5. Start correcting the contour. You may choose any of the following methods:
   - Click a point on the image. The contour changes to accommodate the new point. This method changes the shape and size of the contour based on your clicks.
   - Click the line of the contour and draw the correction to the existing contour. The contour changes its shape to include the new part you draw.
   - Double-click the image and draw a new contour. The newly drawn contour replaces the existing contour.

For methods of drawing, see Section Defining Livewire Lesion Contours on page 335.

Merging Two Lesions

Use this capability to have the application treat two lesions as a single one. This is useful, for example, in cases when two separate lesions have grown and have been merged into a single lesion.

Or in cases when a lesion has decreased over time and has been split into two separate ones. To follow-up the lesions' change in size over time by creating a Follow-Up set, you may want to treat the two lesions as a single one.

This capability is also useful in cases when the lesion has an idiosyncratic shape as often happens in brain lesions. Because it is difficult to segment such lesions in a single segmentation, it is customary to "split" the segmentation to several individual ones but treat the split lesions as a single one.

1. Click the **Merge Lesions**  icon in the **Correction** ribbon and hover with the mouse over the first of the two lesions you wish to combine.
   ⇨ The cursor changes its shape, displaying the digit 1.
2. Click the first lesion and hover over the second lesion.
   ⇨ The cursor changes its shape, displaying the digit 2.

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⇨ Alternatively, you can right-click the first of the two lesions to be combined and select **Merge Lesion With Another**. The cursor changes its shape, displaying the digit 2.

3. Click the second lesion.
   ⇨ The size of the two lesions is calculated as a single lesion. If the two lesions overlap, the segmentation also changes to a single segmentation.

NOTICE

If each of the merged lesions belonged to a Follow-Up set before the merging operation, then this set is removed after the merging has taken place. If only one of the pre-merged lesions belonged to a Follow-Up set, then the follow-up attribute is retained for the merged lesion.

NOTICE

If the lesion is composed of several disconnected components, each of the components has two diameters associated with it. The reported value for the two diameters of the merged lesion is the sum of respective long and perpendicular diameters.

Cropping a Lesion Using a Line

Use the **Crop Lesion Using Line** tool to crop a lesion based on a line you draw.

1. Click the **Crop Lesion Using Line** icon in the Correction ribbon.
2. Draw a line on the lesion to be cropped. The line represents a plane perpendicular to the displayed plane.

The lesion is cropped, retaining the part containing the point where you clicked to mark the lesion. If such a point does not exist, the larger part of the lesion remains. If the segmentation is a line, the midpoint of the line serves as the determining factor.

Cropping a Lesion from the Current Plane

Use the **Crop Lesion from This Plane** feature to crop a lesion from the displayed plane onwards or backwards.

Right-click the segmented lesion and select **Crop Lesion from This Plane.**

In axial images, the cropping removes the part of the lesion either above or below the displayed image. In coronal images, the cropping removes the part that is either in front or behind the currently displayed image.

The lesion is cropped, retaining the part containing the point where you clicked to mark the lesion. If such a point does not exist, the larger part of the lesion remains. If the segmentation is a line, the midpoint of the line serves as the determining factor.

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Correcting a Single Diameter

Use this correction tool to correct the long diameter calculated and drawn by the application.

1. Right-click a segmented lesion and select **Correct Single Diameter**.
   ⇨ You may click on any image containing segmentation, not necessarily on the image showing the long and short diameters calculated by the application.
2. Draw the long diameter. To draw the line, click at the line's starting point and then at the end point of the line.
   ⇨ The diameters calculated and drawn by the application disappear and are replaced by your manually drawn long diameter.

Correcting Both Diameters

Use this correction tool to correct the long and short diameters calculated and drawn by the application.

1. Right-click a segmented lesion and select Correct Both Diameters. You may click any image containing segmentation, not necessarily on the image showing the long and short diameters calculated by the application.
2. Right-click a segmented lesion and select Correct Both Diameters. You may click any image containing segmentation, not necessarily on the image showing the long and short diameters calculated by the application.

Editing a Segmentation

You can edit an existing segmentation, which can be applied to all segmentations even created by another tool such as the liver segmentation. This tool enables you to add or remove part of the segmentation using a brush tool, similar to the one used in the Add Segmentation tool.

To edit a segmentation:

1. Click the drop-down arrow on the **Edit Segmentation** button.



2. Click **Add** to add part of a segmentation or click **Remove** to remove part of a segmentation.
3. Left-click to enter the drawing mode to create a new segmentation. Moving the mouse continues adding disk-like elements to the segmentation. A second mouse click pauses the segmentation allowing you to move to a new location or to a new slice.

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4. Left-click to enter the drawing mode to create a new segmentation. Moving the mouse continues adding disk-like elements to the segmentation. A second mouse click pauses the segmentation allowing you to move to a new location or to a new slice.
5. Press the ESC key or double-click the image to complete the segmentation.

13.15 Bookmarks

13.15.1 Using Bookmarks

Use bookmarks to mark measurement graphics that are of interest for easy retrieval at a later stage.

Lesion segmentations as well as other measurement graphics such as line, ROI, square, rectangle, oval, freehand, curve measurement and arrow are marked as bookmarks.

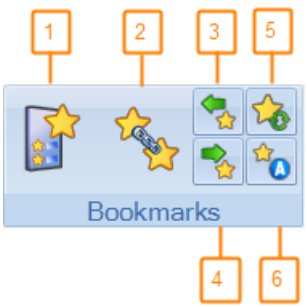
NOTICE

In Lesion Segmentation, you typically mark graphics that serve to measure a lesion in both the prior and the current study. It is recommended to register the two studies before you perform the bookmarking, so that when you view a bookmark in one study, the other study displays the matching image and bookmark.

All bookmarks created in a study are stored when the study is dismissed and will be available when the study is loaded again in the future.

To change bookmark-related settings, click Graphics and Measurements in Applications Settings (see Opening the Application Settings Window on page 453) and then click Configure Bookmarks Settings.

Bookmark Ribbon



#	Description

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1	**Bookmark List** Show and hide the Bookmark List window.
2	**Define Follow-Up Set** Define an association between two bookmarks marking two occurrences of the same lesion or general finding in two different studies.
3	**Previous Bookmark** Navigate to the previous bookmark on the bookmark list. The viewer focuses on the previous bookmark of the selected study.
4	**Next Bookmark** Navigate to the next bookmark on the bookmark list. The viewer focuses on the next bookmark of the selected study.
5	**Synchronize Bookmarks** Use Synchronize Bookmarks to synchronize the study bookmarks in the database without the need to dismiss and reload the study.
6	**Automatically Mark as Bookmark** Automatically mark graphic as bookmark. When this icon is activated (highlighted yellow), graphics you draw, including line, ROI, square, rectangle, oval, freehand, curve measurement and arrow, are automatically marked as bookmarks.

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NOTICE

The Bookmark ribbon also appears in the Graphics tab.

Defining a Follow-Up Set

You can associate bookmarked occurrences of the same lesion in different studies to create a Follow-Up set. Follow-Up sets allow you to follow and accurately assess changes in a lesion's size and volume over time.

NOTICE

The number of studies participating in a Follow-Up set is not limited.

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1. Display the two studies with the two occurrences of the bookmarked lesion.
2. Click the **Define Follow-Up Set** icon . The cursor changes its shape, displaying the digit 1.
3. Bring the mouse over to the bookmark of the first study. The cursor changes its shape.
4. Click once on the bookmark. The cursor indicates FII.

5. Bring the mouse over to the second bookmark in the second study. The cursor changes its shape, displaying the digit 2.
6. Click the bookmark.

An annotation appears next to the bookmarks indicating the Follow-Up set name.

Alternatively, you can right-click on a bookmark, select Define Follow-Up Set and select a bookmark in another study.

NOTICE

Bookmarks of different types may be associated in a Follow-Up set (for example, graphic line and a liver lesion). The graphic line type is changed to Lesion and the line's length is considered as the lesion's long diameter.

NOTICE

It is not possible to create Follow-Up sets of bookmarks that are part of the same study

NOTICE

It is possible to merge two Follow-Up sets provided that the sets do not contain common studies.

After the bookmarked lesions are associated, the **Follow-Up** column in the **Bookmark List** window is populated with the name of the Follow-Up set.

When the bookmarks in the Bookmark List window are displayed in a follow-up layout, the bookmarks are arranged by Follow-Up set. Bookmarks that are not part of any Follow-Up set do not appear in that layout).

NOTICE

Clicking on a bookmark in a Follow-Up Set navigates to the bookmark location in the linked groups, and not to the physical location.

NOTICE

Similar to bookmarks, Follow-Up sets are also stored for later use.

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NOTICE

If Follow-Up sets exist between the current study and prior studies, loading only the current study to the viewer will also retrieve all bookmarks from prior studies that participate in these Follow-Up sets.

Automatic Follow-Up Set Creation

When you add a measurement (bookmark) to one of two registered groups and then add another measurement in the same anatomical area in the other registered group, the system creates an automatic follow-up set. The first time you perform this action, a message appears, allowing you to enable or disable this automatic linking feature. Subsequently, messages appear every time an automatic follow-up set is created to inform you that the system has created the set. You may then view the follow-up set details in the Bookmark List.

Detaching a bookmark from a Follow-Up Set

To break a Follow-Up set by detaching a bookmark from it, right-click a bookmark and select Detach from Follow-Up. The bookmark itself is not deleted and the graphic/lesion change does not change in any way.

Synchronizing Bookmarks

Click the Synchronize Bookmarks  icon to synchronize the study bookmarks in the database without the need to dismiss and reload the study.

When synchronizing bookmarks, the system:

- Saves new or modified bookmarks to the database
- Loads and displays any bookmark added or changed since the study was loaded

This feature is useful when more than one user is working on a study and one user wants to see changes made by the other user.

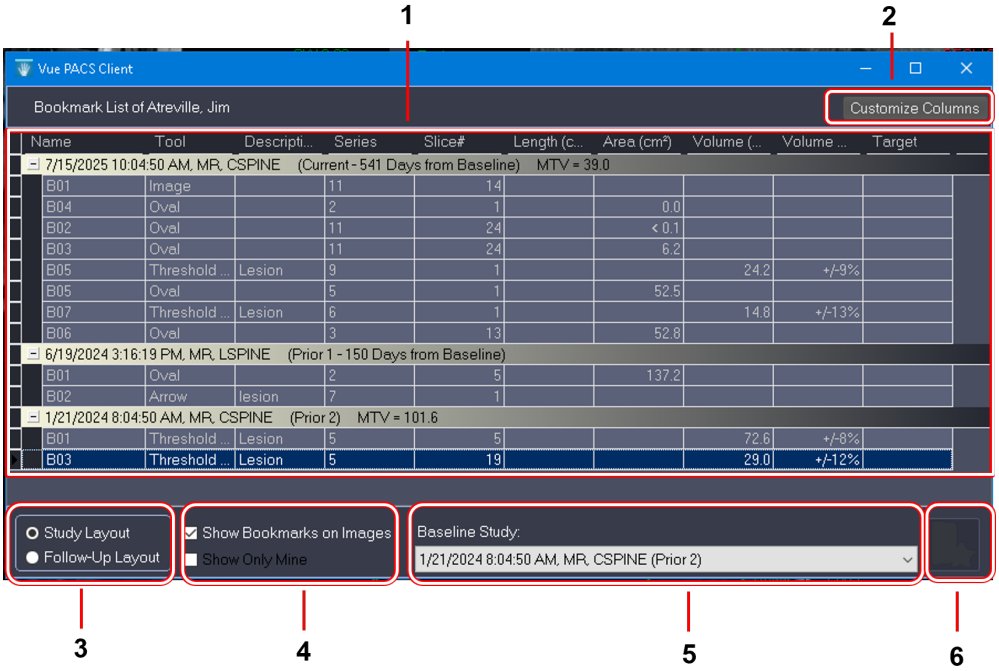
Foe example, an attending doctor adds bookmarks to a study from their station and has the resident see these changes to create hyperlinks to the new bookmarks in the report without closing the study.

Bookmark List

All bookmarks you create are listed in the bookmark list. Clicking on a bookmark in the bookmark list displays the image that contains that bookmark in the viewer.

To open the bookmark list, click the **Bookmark List** icon . The **Bookmark List** window displays a list of all bookmarks created in the current session or in the past in the loaded studies (current and prior):

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#	Description
1	List of bookmarks created in the loaded studies. In case of linked studies, the name of the study contains also an indication of whether the study is "Current" or "Prior" and the numbering annotation that shows if the study is primary or linked to the primary. Click a column header to sort the list by that column (in ascending or descending order). Drag a column to a different location in the window to change the columns' order. Drag a column above the table to hide it.
2	**Customize Columns** Click Customize Columns to display a list of possible column headers you may add to the bookmark list.
3	**Layout** Select the **Study** Layout option to arrange the bookmarks in the list by study. The yellow title row displays information about the study, including study date, study description, time from baseline, and total Metabolic Tumor Volume (MTV) of the study. Select the Follow-up option to arrange the bookmarks in the list by **Follow-Up** sets. Expand the Follow-Up set (click the minus sign near the Follow-Up set name) to display the bookmarks constituting that set.
4	Select **Show Bookmarks on Images** to display all bookmarks created in the study on the viewer images. Select **Show Only Mine** to show only those bookmarks created by you. This option is configurable. For more details, see chapter "Bookmark Display Options" on page 352.

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5	**Baseline Study** The study with which length and volume measurements are compared. By default, the earliest study serves as the baseline and the bookmarks are compared with bookmarks in that study. Click the drop-down menu to change the baseline study, that is, determine a later study as the study with which measurements are compared.
6	**Bookmark Report** Click the Bookmark Report icon to open the bookmark report, which presents summary information about all bookmarked findings, including size, volume and changes over time compared with the baseline study.

Bookmark List Columns

The following fields display as columns in the Bookmark List window:

Field	Description and Additional Information
Creator	Name of physician who created the bookmark.
Type	An indication of whether the bookmark marks a lesion or another type of graphic. Categories can be either General or Lesion.
Sub-type	Bookmarks belonging to the Lesion type can be sub-classified to Liver, Lung, Lymph or Other (that is, lesions that are not tissue-specific). You may change the sub-type to a different one. For example, you may change Other to Liver.
Tool	The tool that was used to create the bookmark (for example, line, oval, segmentation).
Date	The date on which the bookmark was created or modified.
Bookmark Name	The name given by the system to the bookmark.
Slice #	The number of the slice on which the bookmark was created.
Series	The series containing the slice with the bookmark.
Long diameter	The length of the lesion's long diameter.
Short diameter	The length of the lesion's short diameter. The short diameter is the axis drawn perpendicularly to the long axis at the point of the longest possible short diameter.
RECIST Diameter	The reported diameter (either the long or the short diameter).
Volume	The lesion's volume.
Volume Error	The percentage of error, based on inclusion or exclusion of the lesion surface volume.
SUV Max	The maximal Standardized Uptake Value (SUV) in the ROI/VOI.
SUV Mean	The mean Standardized Uptake Value (SUV) in the ROI/VOI.
SUV Peak	The SUV Peak found in the ROI/VOI.

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HU Mean	The mean Hounsfied value in the ROI/VOI.
Pixel Max	The maximal pixel value in the ROI/VOI.
Pixel Mean	The mean pixel value in the ROI/VOI.
Pixel Sum	The sum of the pixel values in the ROI/VOI.
Days from Baseline	For bookmarks that are part of a follow-up, this column shows the number of days elapsed from the date of the baseline study and the date of the study containing this bookmark.
TLG	Shows the Total Lesion Glycolysis (TLG) value of the lesion (mean SUV multiplied by the Volume). **NOTICE! For TLG calculation, SUV is calculated using the Lean Body Mass (LBM) method (SUV-LBM is also known as SUL).**
MTV	Indication of whether or not this bookmark should be included in the MTV value.
DT (days)	The calculated doubling time of the lesion's volume.
Target	RECIST classification of lesions signifies lesions as Target (a measured lesion to be examined in the study), Non-Target (lesions whose presence has been noted but are not included in the clinical study), Non-Target Non-Measureable (lesions that cannot or are not measured), New Lesion, and Unspecified.
Area	Calculated two-dimensional area of a lesion.
Bookmark Description	A general free description. (A default is given by the system.)
Length	The length of a line bookmark.
Report	Indication of whether or not this bookmark should be included in the report.
Reviewed	An indication of whether or not this bookmark has been reviewed by the user. Manually created bookmarks are marked as Reviewed. Lesions created by the Lesion Tracking tool are initially marked as Non-reviewed. Editing a non-reviewed lesion marks it as Reviewed.
Study Date	Date of study creation.

Customizing the Bookmark List Columns

You may change the order of the columns or add columns to those displayed in the list window by default.

1. Click Customize Columns at the top right corner of the window. The Customization window appears.
2. From the Customization window, drag the desired column to the column header area of the Bookmark List window.

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Sorting the Bookmark List

By default, the list of bookmarks within each study is sorted by series number and then by the number of the slice (image) carrying the bookmark in the series. However, you may change this default by clicking any of the column headers. The list is sorted by that column.

Deleting a Bookmark from the List

Right-click a bookmark in the Bookmark List window and select Delete Bookmark, or select the bookmark itself in the viewer, right-click and select Delete. You can also select more than one bookmark, right-click and select Delete Selected Bookmarks.

Marking a Graphic as a Bookmark

1. Draw a graphic on the image.
2. Right-click the graphic and select **Mark Graphic as Bookmark**.

Or

Click **Automatically Mark as Bookmark**  in the toolbar.

An annotation with the bookmark name appears next to the graphic.

NOTICE

Graphics drawn with the Automatically Mark as Bookmark icon activated (highlighted yellow) are always marked automatically as bookmarks.

Cancelling Changes

If you are not interested in saving changes you have made to bookmarks (for example, you have moved a graphic inadvertently), you may dismiss the study without saving the changes.

To unmark a specific bookmark, right-click the graphic and select Unmark graphic as bookmark.

To unmark the bookmark and delete the graphic, right-click the graphic and select Delete and Remove Bookmark.

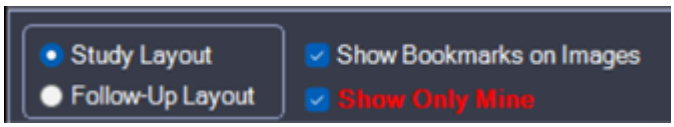
To dismiss the study without saving changes to bookmarks, clear the **Save Bookmarks** option in the **Dismiss Study** menu in the **Workflow** tab.

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Bookmark Display Options

The bookmark display options allow you to control which bookmarks are visible and where they are shown while reviewing studies. Both options can be adjusted by the user during reading and can also be governed by central configuration, which determines how user changes persist across study loads. Whenever an option that hides bookmarks is enabled, this state is visually indicated in red in the bookmark table.



Show Bookmarks on Images

Use the **Show Bookmarks on Images** option to control whether bookmarks are displayed directly on the viewer images.

- When this option is selected, all bookmarks are shown on the images.
- When this option is deselected, bookmarks are hidden from the images, but remain visible in the bookmark list.

The default behavior for this option is defined by a central configuration and the option is enabled by default.

By default, any change made by the user is applied immediately and becomes the default for subsequently loaded studies during the same session.

If a central setting is enabled to enforce the default at each study load, user changes apply only to the currently loaded study, and the configured default is restored when a new study is loaded.

NOTE

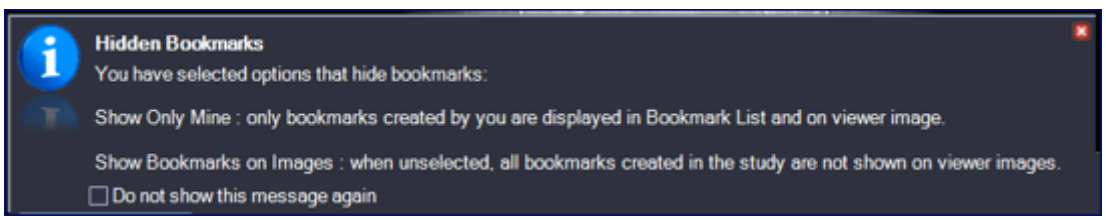
If bookmarks are hidden on images and a new bookmark is created, the newly created bookmark is always shown on the images.

Show Only Mine

Use the **Show Only Mine** option to control whether only bookmarks created by the current user are displayed.

- When the option is enabled, only bookmarks created by the current user are shown in the bookmark list and on the viewer images. Bookmarks created by other users are hidden.

  In this case, the following notification message appears, when loading a study:



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Select the **Do not show this message again** checkbox to hide this notification for any additional study loaded during the current session.

- When the option is disabled, all bookmarks for the study are displayed, regardless of who created them.

The default behavior for this option is defined by a central configuration and is disabled by default.

By default, any change made by the user is applied immediately and becomes the default for subsequently loaded studies during the same session. If a central setting is enabled to enforce the default at each study load, user changes apply only to the currently loaded study, and the configured default is restored when a new study is loaded.

Reports

Reports provide summarized information regarding all bookmarked findings in the currently loaded studies.

1. To display the report, click the **Bookmark Report**  icon in the **Bookmarks List** window. The Bookmark report window displays in preview form, showing the report data.
2. To see a preview of the final report, click **Preview Report**.
3. To save the report to the server, click **Save Report**. You can then access the report via the Archive Explorer.

To save the report to the server, click Save Report. You can then access the report via the Archive Explorer.

Patient and Study Details

Following the patient details, the report displays study information (for example, study date).

Underneath the study date and name, the report displays the following figures:

- Number of days that have passed since the date of the study that was designated as the baseline study.
- Number of days that have passed since the previous exam.

Target Lesions

The Target Lesions section presents summarized information of all bookmarked lesions designated as Target in the current study.

The Sum of Target lesions figure is a summation of all lengths of all long diameters in these lesions.

Other Lesions

The Other Lesions section presents summarized information of all bookmarked lesions that were not designated as Target lesions.

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Findings

The Findings section displays summarized information of bookmarked findings that are not lesions (that is, bookmarked findings created by a graphic tool such as line or oval and not by the Lesions tools).

Graphic Summary – Target Lesions (Sum)

The graphical presentation of the Target lesions shows the sums of all long diameters in the current and prior studies. The Y axis displays the diameters' lengths sum and the X axis displays the prior and study dates.

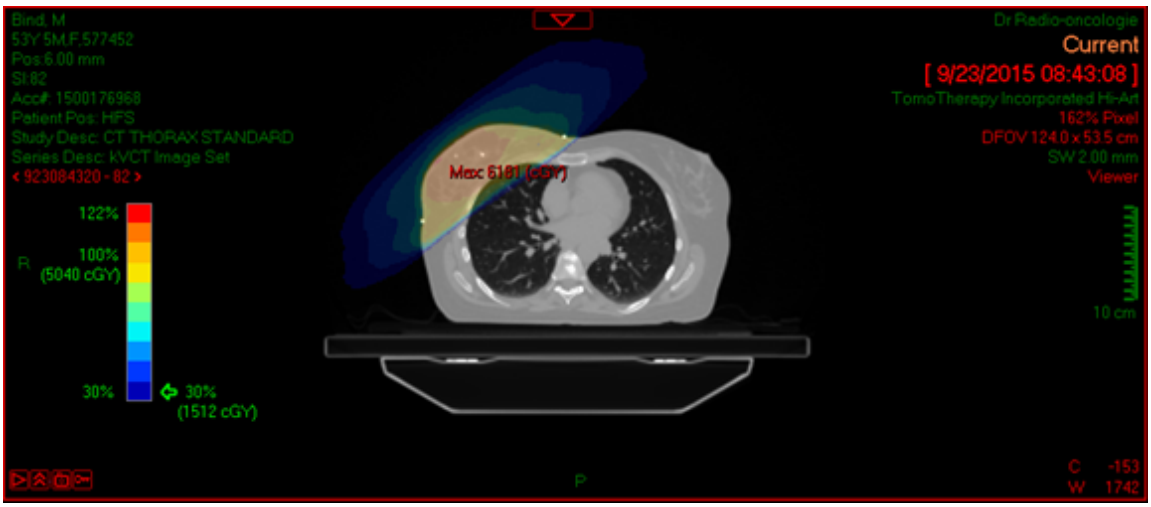
13.16 Radiation Therapy

13.16.1 Viewing Radiation Therapy Information

In Radiation Therapy (RT), a Computerized Tomography (CT) study is used for determining the RT treatment plan for the target organ. Images of RT studies display the amount of radiation received by each part of the body in the radiated area.

To view an RT CT study, load a study with RT modality to the viewer.

Color overlays and annotations displayed on the active image show the levels of radiation for the radiated area.



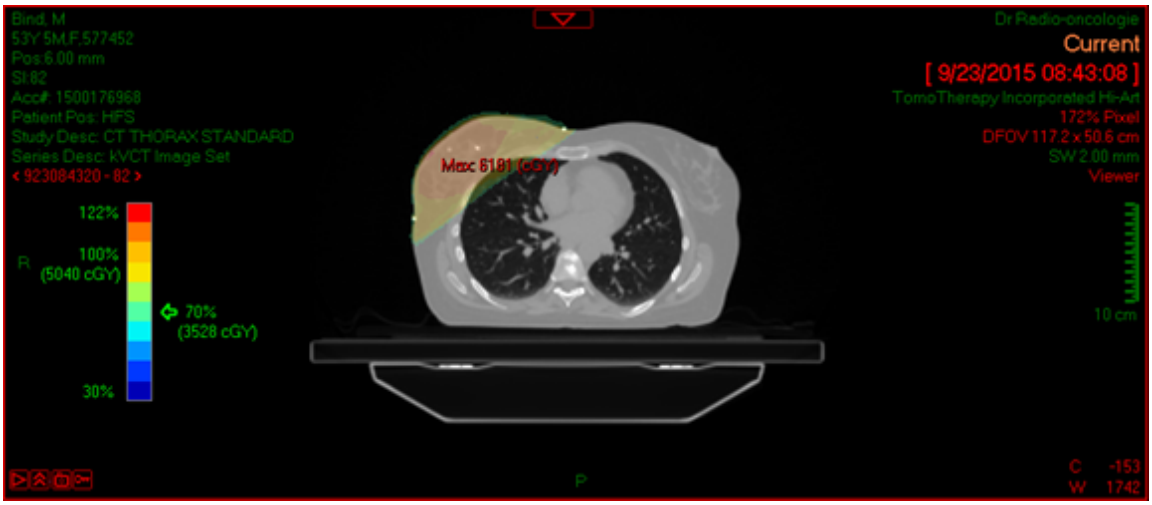
The color bar at the left-hand side presents the radiation dosages as percentages of the prescribed dose for the target organ.

The annotation on the image indicates the maximal dose received in centigray (cGy) units.

To view only radiation levels above a certain value, move the slider on the color bar upwards.

The image does not show areas whose level of radiation is lower than the value indicated by the slider.

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A 100% radiation dose reflects the prescribed dose for the target organ. Values higher than this dose represent areas radiated with doses surpassing the prescribed dose.

Click the RT icon in the Lesions toolbar to show or hide the radiation dosage information on the active image.

If the RT study lacks the target prescribed dose, radiation dosage information is not displayed.

Clicking the RT icon displays a dialog where you can enter the dose manually.

The dialog also mentions the maximum dose value indicated in the study.

The radiation dosage information is then be displayed.

13.17 Vue Mammo Workstation

13.17.1 Worklist Indicators

Study Type

- You can configure a worklist with a custom column indicating if the study type is Screening or Diagnostic, based upon its originating Procedure Code.
- You must map the Procedure Code from the Radiology Information System, Mammography Information System through the Vue PACS HL7 Manager Software. Contact your system administrator.

CAD Available

- You can configure a worklist with a column indicating if the study has a CAD report associated with it.
- You must configure the Has CAD column through the Field Chooser.

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Breast Tomosynthesis Series

- You can configure a worklist to indicate if a study contains a Breast Tomosynthesis series.
- You must configure the 'Additional Info' column through the Field Chooser.

13.17.2 Intended Users

The Vue Mammo Workstation is intended for use by radiologists as an interactive tool for analyzing radiological data.

NOTICE

The images and tools provided by the Vue PACS Mammography Workstation are intended as aids for experienced users only.

13.17.3 Logging on to Vue Mammo

You need a unique user name and password as well as a Mammography license to log on to the Mammography Workstation. Contact the system administrator for assistance.

For a Vue PACS Client Workstation:

1. Click the INTERNET EXPLORER icon. Enter the URL address of your application.

   NOTICE! If you do not know your Vue PACS IP address, contact your system administrator.

   ⇨ The Vue PACS window appears.
2. Click Diagnostic Workstation.

   ⇨ The Vue PACS Login window appears.**NOTICE! The Vue PACS Login window appears.**
3. Type your user name and password.
4. Click OK.

⇨ The Archive Explorer window appears, displaying the list of configured archives on the left, and the studies in the selected archive on the right.

For a Standalone Workstation:

1. Select the Desktop Diagnostic Workstation icon.

   ⇨ The Vue PACS Login window appears.**NOTICE! The hardware that you use can affect how quickly you will see the login window during the first login. When you access the Diagnostic Workstation for the first time, the login window might take several minutes to appear.**
2. The hardware that you use can affect how quickly you will see the login window during the first login. When you access the Diagnostic Workstation for the first time, the login window might take several minutes to appear.
3. Click OK.

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⇨ The Archive Explorer window appears, displaying the list of configured archives on the left, and the studies in the selected archive on the right.

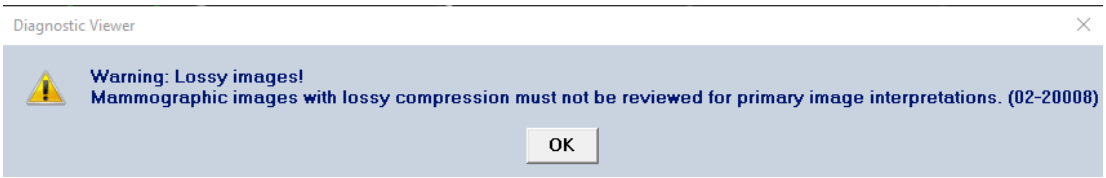
13.17.4 Using Vue Mammo

NOTICE

Integration with a RIS, HIS, or voice dictation system requires installation of special software and proper configuration. Contact the system administrator.

To review cases in the Vue Mammo Workstation:

1. Log on (see Logging on to Vue Mammo on page 356) to the Vue Mammo Workstation.**NOTICE! The Vue Mammo Workstation is available only if your profile has a license to use it.**
   ⇨ A worklist or the Archive Explorer appears. Select and load a case or a worklist of cases.
2. Review images in the Viewer window.



3. Add annotations and graphic elements. Save as needed (see About Images on page 495 and About Annotations and Measurements on page 499).
4. Optional: Dictate a report (see Dictating a Report on page 626).
5. Confirm (mark read) or dismiss the case (see Completing a Study on page 156).
   - If you loaded the studies as a worklist, your next case may automatically load.
   - If you did not load the studies as a worklist, the Archive Explorer or a worklist appears. Select and load a case.

13.17.5 Annotation Mirroring

Annotation Mirroring lets you view annotations on the outside corners (opposite the chest wall) of mammography images, so that annotations do not obstruct the tissue area of the image during display or print.

Annotation Mirroring is automatically applied to Conventional Mammography and Breast Tomosynthesis views when:

- Loaded through Load To from the Archive Explorer
- Loaded through a Display Protocol
- Loaded through Reapply DP

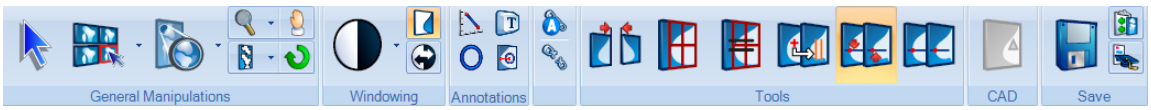
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- Scrolled to when stacked
- Dragged and dropped from the Limited View PMA or Full View PMA to the PowerViewer application
- Dragged and dropped between groups of the PowerViewer application
- The magnification mode – such as True Size, Fit to Window, or Same Size – was manually changed
- Study Replacement or Insertion has occurred

NOTICE! Annotation Mirroring is available only if the user's profile has a license to use it.

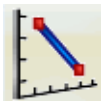
13.17.6 Vue Mammo Workstation Toolbar

The following icons are added to the PowerViewer (see PowerViewer Toolbar on page 72) application toolbar when you load a mammography study. The list also presents shortcuts you can use to perform the various activities.



Icon	Shortcut Keys	Description
	**Ctrl + I**	Put the cursor in neutral mode.
	**Alt + Shift + S** **Alt + Shift + A**	Select single image for actions to be applied. Select all images in current viewbox for actions to be applied.
	**Ctrl + M**	Use the magnifying glass and select its mode.
	**Z**	Use the zoom tool.
	**P**	Use the pan tool.
	Q	A shortcut that toggles between 2D and DBT mammography views when available
	Shift + Q	Shifts between the various suggested groups. To display a list of the suggested groups, right-click the laterality and view position annotation.
		Choose a filter to enhance the selected images.

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	**Alt + Shift + R**	Resets selected mammography images with chest wall justification, nipple alignment, last applied zoom mode, originally applied windowing and VOI LUT.
	**W**	Apply the windowing mode.
	**Alt + Shift + I**	Mask breast tissue of selected mammography images only.
	**Alt + I**	Apply inverse windowing to the selected image.
	**Alt + L**	Select Line Measurement graphic tool.
	**Alt + Ctrl + O**	Select Oval Shape graphic tool.
	**Alt + Shift + O**	Select Oval Shape with Line graphic tool. The tool draws an oval and a line measuring the distance between an oval center and nipple.
	**Alt + T**	Select Text graphic tool.
		Auto link–When Auto link is turned on, all prior studies are linked allowing simultaneous scrolling.
		Unlink–Breaks the links between linked groups.
	**Alt + U**	Justify the chest wall of mammography images against the side of the image window.
	**Alt + Q**	View segments of the mammography image at original resolution, or configured zoom, in a sequence of steps.
	**Alt + Shift + Q**	View segments of the mammography image at same size and original resolution, or configured factor of original resolution, in a sequence of steps.
	**Alt + Shift + R**	Identify a corresponding region on opposing mammography views for a selected point of interest. **NOTICE! This tool is not applicable to Breast Tomosynthesis exams at this time.**
	**Alt + Ctrl + N**	Apply or remove nipple alignment to mammography images.

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	**Alt + Shift + N**	Display nipple reference lines on mammography images for identification of the nipple or for correction.
	**Alt + C**	Display CAD Marks on mammography images. **NOTICE! This tool is not applicable to Breast Tomosynthesis exam at this time.**
	**Ctrl + S**	Save the selected (modified) image(s).
		Export selected images for viewing and printing in the Film Previewer. See the Film Preview Toolbar on page 99.
	**Ctrl + T**	Mark study as a teaching study.

13.17.7 Cine Toolbar

The following icons are added to the PowerViewer application toolbar when you load a multi-image Ultrasound, Angiography, or Breast Tomosynthesis exam.

Icon	Shortcut Keys	Description
	**Alt + Shift + P**	Pause all cine loops in the current application.
	**Alt + Shift + L**	Play all cine loops in the current application.
		Stop all cine loops in the current application.
		Display previous image (or frame) for all cine loops in the current application.
		Display next image (or frame) for all cine loops in the current application.
		Play cine in reverse mode.
		Play cine in forward mode.
		Play cine in back and forth mode.
		Slider to adjust the frame rate.

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13.17.8 Image Level Toolbar



Icon	Shortcut Keys	Description
1	**Ctrl+Up Arrow Ctrl+Down Arrow**	Pause or Play cine loop.
2	**Up Arrow**	Display previous image (or frame) in the stack.
3	**Down Arrow**	Display next image (or frame) in the stack.
4		Display cine tools.
5		Film active image.
6	**Alt + Space**	Mark active image as a Key Image (for desktop diagnostic viewer clients only).
	`(single quote key)	Mark active image as a Key Image (for clients that have both desktop and Web environments).
	Ctrl+Alt+Space	Unmark Key Image (for desktop diagnostic viewer clients only).
	Shift +` (~)	Unmark Key Image (for clients that have both desktop and Web environments).

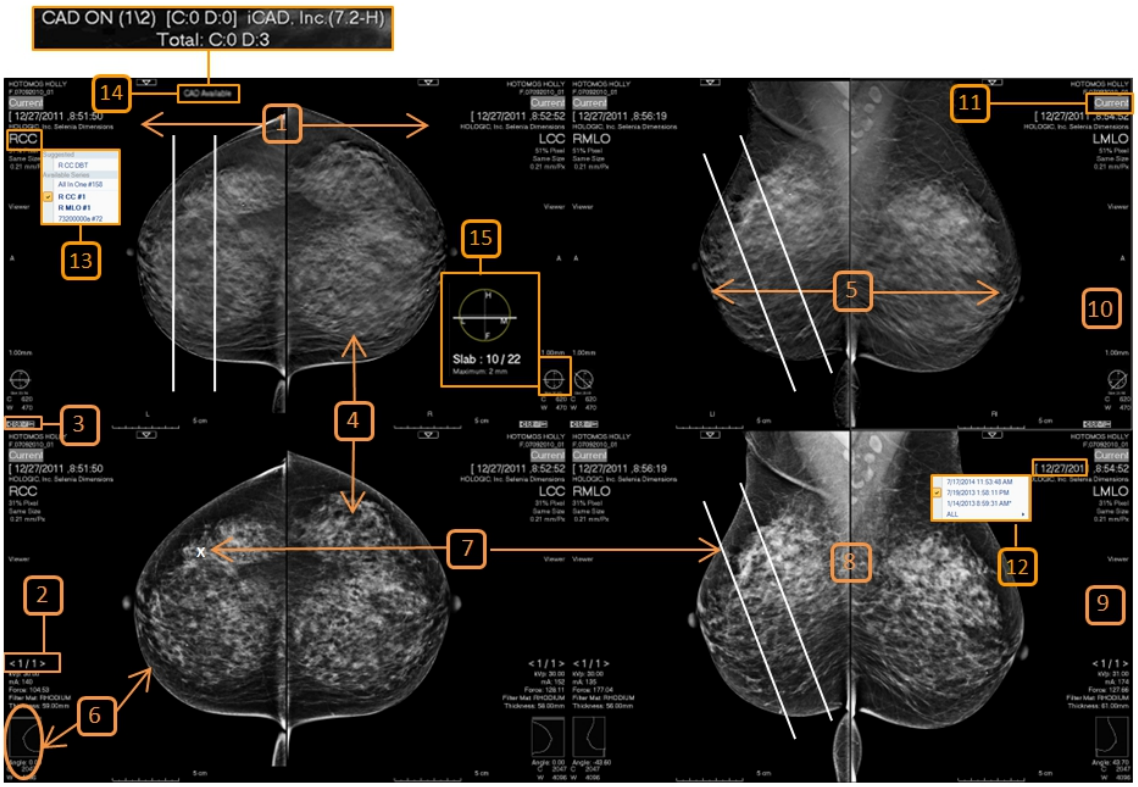
13.17.9 Breast Tomosynthesis Series

- You can configure a worklist to indicate if a study contains a Breast Tomosynthesis series.
- You must configure the 'Additional Info' column through the Field Chooser.

13.17.10 Mammogram Display in PowerViewer

The following figure illustrates an overview of a Conventional Mammogram and Breast Tomosynthesis series along with a number of key capabilities pointed out.

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Items:

1. Annotation Mirroring.
2. Number of images, slices, or planes.
3. Image Level Toolbar.
4. Automatic Same Size between views
5. Automatic Nipple Alignment.
6. Automatic Skin Line Detection and Image Map.
7. Mammography Cross Reference Lines.
8. Chest wall Justification.
9. 2D Mammography Views (bottom row of images).
10. 2D Mammography Views (bottom row of images).
11. Current or Prior exam indication.
12. Study Insertion/Replacement selection.
13. View Replacement. Right-click the annotation to replace the displayed view with an alternative view of the same breast.
14. CAD status appears on the image in the Viewer window. If the mammography CAD markers/outlines are toggled on, total calcification clusters and densities per image and study, CAD vendor, and CAD product version are displayed.
15. Image Map of tomosynthesis series. Reference line indicates location of displayed slice. Slabbing annotation allows adjustment of slab mode and thickness.

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13.17.11 Chest Wall Justification

Chest Wall Justification automatically pans mammography images so that the chest wall is against the side of the image window.

Chest wall justification is automatically applied to Conventional Mammography and Breast Tomosynthesis views when:

- Loaded through Load To from the Archive Explorer
- Loaded through a Display Protocol
- Loaded through Reapply DP
- Scrolled to when stacked
- Dragged and dropped from the Limited View PMA or Full View PMA to the PowerViewer application
- Dragged and dropped between groups of the PowerViewer application
- The magnification mode – such as True Size, Fit to Window, or Same Size – was manually changed
- Study Replacement or Insertion has occurred

NOTICE! Chest Wall Justification is available only if the user's profile has a license to use it.

Removing or reapplying Chest Wall Justification

Select the Chest Wall Justification shortcut key or toolbar icon .

13.17.12 Nipple Justification

Nipple Justification automatically pans mammography images so that the nipple is aligned to the side of the image window.

Nipple justification is automatically applied to Conventional Mammography and Breast Tomosynthesis views when:

- Loaded through Load To from the Archive Explorer
- Loaded through a specifically configured Display Protocol
- Loaded through Reapply DP
- Scrolled to when stacked
- Dragged and dropped from the Limited View PMA or Full View PMA to the PowerViewer application
- Dragged and dropped between groups of the PowerViewer application
- The magnification mode – such as True Size, Fit to Window, or Same Size – was manually changed
- Study Replacement or Insertion has occurred

NOTICE! Nipple Justification is available only if the user's profile has a license to use it.

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13.17.13 Nipple Alignment

Nipple Alignment automatically aligns similar Conventional Mammography and Breast Tomosynthesis views based on the view's nipple location. By default, magnification, spot compression, and cleavage views are not aligned.

The nipple location can be corrected through the Nipple Correction tool. Once the nipple is corrected on a view, any additional stages of the display protocol the same view is displayed are also corrected.

13.17.14 Applying Nipple Alignment

Nipple Alignment is automatically applied when:

- Loaded through Load To from the Archive Explorer
- Loaded through a Display Protocol
- Loaded through Reapply DP
- Scrolled to when stacked
- Dragged and dropped from the Limited View PMA or Full View PMA to the PowerViewer application
- Dragged and dropped between groups of the PowerViewer application
- The magnification mode – such as True Size, Fit to Window, or Same Size – was manually changed
- Study Replacement or Insertion has occurred

13.17.15 Removing or reapplying Nipple Alignment

Select the Nipple Alignment shortcut key or toolbar icon .

13.17.16 Correcting the Nipple Alignment

1. Invoke Nipple Correction mode through its shortcut key or toolbar icon .
2. Left-click the correct nipple location for a specified view.
3. Repeat step 2 for other views needing correction.
4. Toggle off Nipple Correction mode.

NOTICE! Nipple Alignment and Correction are available only if the user's profile has a license to use them.

13.17.17 Absolute Alignment

Absolute Alignment is available only if your profile has a license to use it.

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Absolute alignment of the image to the right or left side of the display area is set by the Display Protocol. Depending on the protocol, images may load to the right or left of the display area. The protocol applies whenever an image is:

- Loaded through Reapply Original DP
- Scrolled to when stacked
- Dragged and dropped from the to the PowerViewer application
- Dragged and dropped between groups of the PowerViewer application
- Manually altered using the magnification mode – such as True Size, Fit to Window, or Same Size

13.17.18 To modify the default Display Protocol:

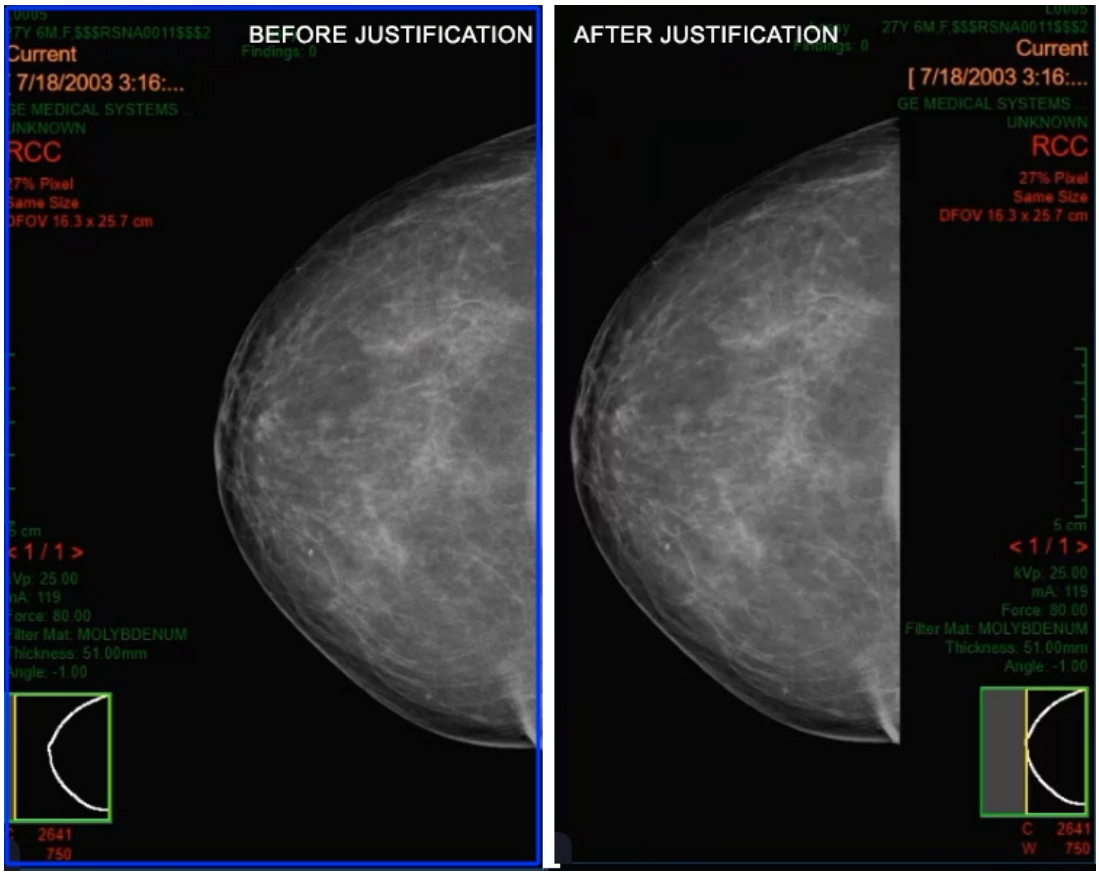
You can only locally realign an image and your settings cannot be saved. The default Display Protocol is reapplied when you exit.

1. Click inside the display area of the image you want to realign.
2. Click the **Mammography** tab.



3. Click the **Toggle Absolute Alignment**  icon.

   In this example, the breast tissue has been realigned to the left side of the image area from its default setting against the chest wall on the right.



4. Click the **Chest Wall Justification** icon in the Mammography tab or repeat the procedure to return the breast tissue to its original orientation.

Invoke Nipple Correction mode through its shortcut key or toolbar icon .

- ► Left-click the correct nipple location for a specified view.
- ► Repeat step 2 for other views needing correction.
- ► Toggle off Nipple Correction mode.

NOTICE! Nipple Alignment and Correction are available only if the user's profile has a license to use them.

13.17.19 Magnifying Mammography Images

Magnify a region of a single image or independent regions of multiple images. If a magnifying glass is placed on a Breast Tomosynthesis view that is playing in cine mode, the magnified region will play in cine mode until paused.

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Magnifying Glass Mode

1. Click the arrow to the right of the Magnifying Glass icon 

and select Multi Mag Glass to toggle the mode between a single magnifying glass and multiple magnifying glasses. The Multi Mag Glass menu item will have a check mark preceding it if the current mode allows multiple magnifying glasses.
2. The default magnifying glass mode can be set in your user preferences.

Magnifying a Single Image

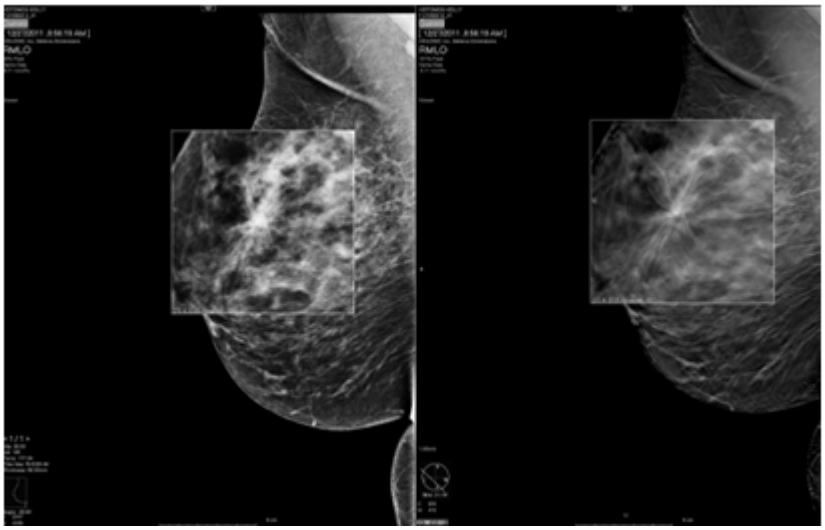
1. Before you begin, verify Multi Mag Glass is not the selected magnifying glass mode.
2. Click **Magnifying Glass**  and hold down the mouse button while over the image region to be magnified.
   - Drag the cursor to move the magnifying glass.
   - Press Alt and move the cursor to adjust the default size of the magnifying glass area.
   - Press CTRL and move the cursor to increase the zoom level while leaving the area of the magnifying glass the same.
   - Press Shift to change the windowing within the area of the magnifying glass.
   - Press I to invert the magnifying glass area.
3. Release the mouse button to close the magnifying glass.

Magnifying Multiple Images Concurrently

1. Before you begin, verify Multi Mag Glass is the selected magnifying glass mode.
2. Click **Magnifying Glass**  and hold down the mouse button while over the image region to be magnified.
   - Drag the cursor to move the magnifying glass.
   - Press Alt and move the cursor to adjust the default size of the magnifying glass area.
   - Press Alt and move the cursor to adjust the default size of the magnifying glass area.
   - Press Shift to change the windowing within the area of the magnifying glass.
   - Press I to invert the magnifying glass area.
3. Release the mouse button to allow the magnified region to remain displayed.
4. Repeat steps 2 and 3 to magnify additional images.
5. Click inside a magnifying glass and release the mouse button to close it.
6. Click another tool to close all magnifying glasses.

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13.17.20 Breast Tissue Inverse Windowing

Breast Tissue Inverse Windowing inverts the breast tissue pixels of mammography images and leaves the background pixels unchanged. Only the tissue image data is affected. You can automatically apply Breast Tissue Inverse Windowing to selected images as part of a display protocol or manually apply it. Breast Tissue Inverse Windowing can be applied to Conventional Mammography and Breast Tomosynthesis views.

NOTICE! Breast Tissue Invert is available only if the user's profile has a license to use it.

Click Inverse Windowing  to invert the tissue pixel data.

Breast Tissue Windowing

Breast Tissue Window Level lets you adjust the window and level of the breast tissue within a mammography image without adjusting the window and level of the background. Only the tissue data is affected. You can automatically apply Breast Tissue Window Level to selected images as part of a display protocol, or manually apply it. Breast Tissue Windowing can be applied to Conventional Mammography and Breast Tomosynthesis views.

NOTICE! Breast Tissue Windowing is available only if the user's profile has a license to use it.

Click Windowing  to window and level the tissue pixel data.

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13.17.21 Intelli Zoom

Intelli Zoom lets you view a full resolution (1:1) image that may not fit entirely on the display in a structured sequence of segments at full resolution. Each segment of the image can be viewed at full resolution (or at a configured factor of full resolution) until the entire image has been read.

When left/right comparison views are being read, the structured sequence of segments is displayed in a mirrored fashion.

The Image Map on page 370 depicts the part of the breast that is visible on the screen.

- Click Intelli Zoom  to view segment 1 at full resolution.
- Click Intelli Zoom again to display the next segment at full resolution.
- Click Reset  to reset to the beginning of the sequence.

Intelli Zoom is available for Conventional Mammography and Breast Tomosynthesis views.

NOTICE! Intelli Zoom is available only if the user's profile has a license to use it.

13.17.22 Intelli Zoom (Same Size)

Intelli Zoom (Same Size) lets you view a full resolution (1:1) image that may not fit entirely on the display in a structured sequence of segments at a minimum of full resolution (or at a configured factor of full resolution). If images with different pixel pitches and/or resolution are compared, each segment will be displayed at the same physical size allowing an abnormality size to be properly assessed.

When left/right comparison views are being read, the structured sequence of segments is displayed in a mirrored fashion.

The Image Map on page 370 depicts the part of the breast that is visible on the screen.

- Click Intelli Zoom (Same Size)  to view segment 1 at full resolution or higher.
- Click Intelli Zoom (Same Size) again to display the next segment at full resolution or higher.
- Click Reset  to reset to the beginning of the sequence.

Intelli Zoom (Same Size) can be configured to apply a specific zoom other than full resolution based upon image manufacturer.

Intelli Zoom (Same Size) is available for Conventional Mammography and Breast Tomosynthesis views.

NOTICE! Intelli Zoom (Same Size) is available only if the user's profile has a license to use it.

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13.17.23 Image Map

Image Map for Conventional Mammography Image

An Image Map is automatically displayed for a Conventional Mammography image to identify what part of the image is visible on the screen. The Image Map is dynamically updated as an image is panned on the display.



The shaded area of the Image Map identifies the portion of the image that is not visible on the display. The non-shaded area of the Image Map identifies the portion of the image that is visible on the display.

NOTICE! Image Map is available only if the user's profile has a license to use it.

Image Map for Breast Tomosynthesis

An Image Map is automatically displayed for a breast tomosynthesis series to identify the orientation, slice/plane of the breast visible on the screen, and slabbing details (if applied). The reference line depicts the location in the breast of the displayed slice/plane and a visual indication of the slab size (if slabbing is applied). The lower annotation identifies the current slice/plane displayed, followed by the total number of slices/planes in the series when slabbing is off. The Image Map is dynamically updated as the series is scrolled through.



NOTICE! Image Map is available only if the user's profile has a license to use it.

Breast Tomosynthesis Slabbing

Slabbing allows a user to combine breast tomosynthesis slices/planes for improved visibility of low and high density objects, along with the potential of reducing the time to read the exam.

A breast tomosynthesis series can be displayed in an Average mode, Maximum mode, or with Slabbing Off. Average mode allows for improved visibility of lower density objects by displaying the average value for each pixel in the slab. Maximum mode allows for improved

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visibility of high density objects by displaying the highest intensity value for each pixel in the slab. Slabbing Off displays the series as provided by the modality without additional slabbing applied.

When slabbing is applied, the lower annotation of the Image Map identifies if the series is slabbed, the current slab displayed, the total number of slabs in the series, slab mode and slab thickness.



NOTICE! Image Map is available only if the user's profile has a license to use it.

Manual Slabbing

The Slab Mode is manually selected by right-clicking the slab mode active annotation and selecting the mode to apply.



The Slab Thickness is manually changed once in Average or Maximum mode by right-clicking on the slab thickness active annotation, and choosing the thickness from the Slab Thickness window. Selecting OK will apply the slab thickness chosen or Cancel will not apply the change. The breast tomosynthesis Image Map reference line will change in thickness to visually indicate the applied slab thickness.

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Automatic Slabbing

A Display Protocol can be configured to automatically apply a slab mode and thickness. This can be configured independently for each stage of the display protocol.

NOTICE! Some modalities can send breast tomosynthesis series with slabbing already applied. Any slabbing applied by the workstation is in addition to what is provided by the modality vendor.

Slabbing Shortcut Preset

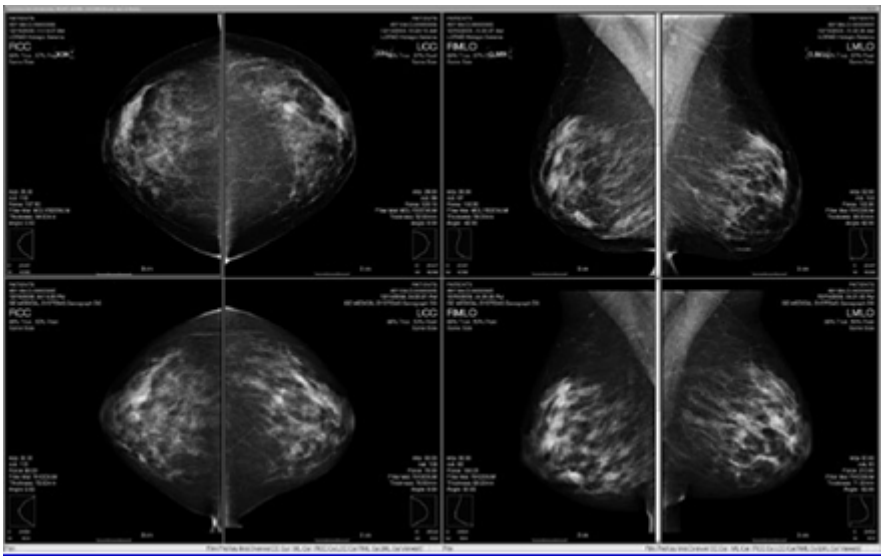
A Shortcut Preset can be configured in Application Settings to apply a pre-configured slab mode and thickness. The Slabbing Shortcut Preset acts as a toggle control what will toggle on the pre-configured slab mode and thickness with one press and toggle back to the prior settings with another press.

13.17.24 Same Size Display

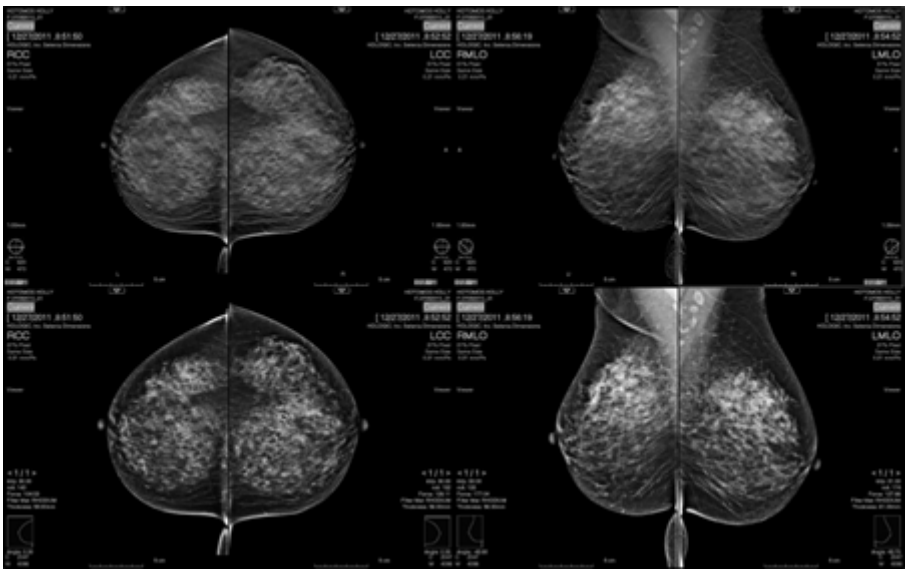
Same Size displays mammography images that were acquired from capture devices with a different pixel pitch and/or resolutions at the same physical size while fitting the tissue to the image window. This applies to Conventional Mammography and Breast Tomosynthesis views that may have been acquired from the same or different vendor acquisition devices. Applying Same Size allows areas of interest to be optimally assessed for a change in size.

In the example shown below, the bottom row of images was acquired on a GE FFDM and the top row of images on a Hologic FFDM.

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In the example shown below, the bottom row of images are Conventional Mammography views that were acquired on a Hologic Selenia Dimensions and the top row of images are Breast Tomosynthesis views from the same device.



In both examples, the two studies being compared were acquired at a different pixel pitch and/or resolution, but the images are displayed at the same physical size when Same Size is applied. Additionally, all images are scaled up/down the same amount to best fit the tissue area of the image to the image window.

NOTICE! Same Size is available only if the user's profile has a license to use it.

13.17.25 Projection View Cross-Reference Lines

Displays parallel lines in all opposing mammography views to indicate the correlated area for a selected point of interest.

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Projection View Cross-Reference Lines applies to Conventional Mammography and Breast Tomosynthesis views.

Using Projection View Cross-Reference Lines

1. Select the **Projection View Cross-Reference Lines** shortcut key or toolbar control .
2. Left-click a point of interest in a selected view. Parallel lines display automatically on all opposing reference views, indicating the correlated area of interest.
3. Toggle off the cross-reference lines using the same method in step 1.

NOTICE! Projection View Cross-Reference Lines is available only if the user's profile has a license to use it.

13.17.26 Identifying the Number of Stacked Images

Identifies the number of images currently displayed and total number of images in a stack of Conventional Mammography views.

- The annotation is in the format <X/Y>, where (X) is the image index in the stack and (Y) is the total number of images in the stack.
- The annotation includes PR (Grayscale Softcopy Presentation State) images in its count.
- The annotation is located on the bottom corner opposite the chest wall for mammography images by default.



Using the Number of Images Annotation

► Place the mouse over the annotation.

► Scroll through the images using the mouse scroll wheel or by clicking on the arrow of the active annotation for the direction to scroll.

► Alternatively, scroll through the images by manually scrolling over the group of interest will the mouse scroll wheel.

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NOTICE! To change the visibility, location, or size, click the Vue PACS icon > Application Settings > Annotation Options > Annotations configuration settings.

13.17.27 Vue Mammo Breast Tomosynthesis Cine Tools

A Breast Tomosynthesis series is displayed as a stack of images/slices/planes that can be automatically played in a cine loop or manually scrolled through.

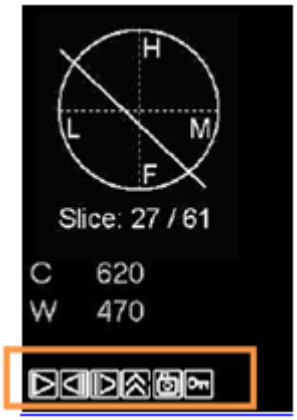
Displaying a Breast Tomosynthesis Series in a Cine Loop

Each Breast Tomosynthesis series is automatically displayed in a cine loop at a pre-configured frame rate by default. The Cine Toolbar (see Vue Mammo Breast Tomosynthesis Cine Tools on page 375) in the PowerViewer application toolbar allows one to pause, play, move through individual images/slices/planes, or change the frame rate for all Breast Tomosynthesis series simultaneously.

- Click Pause  to pause all cine loops in the current application.
- Click Play  to play all cine loops in the current application.
- Click Stop  to stop all cine loops in the current application.
- With the Cine paused, click  to display the previous image/slice/plane of all Breast Tomosynthesis series in the current application.
- With the Cine paused, click  to display the next image/slice/plane of all Breast Tomosynthesis series in the current application.
- While playing in cine mode, click  to play the cine in a reverse direction (for example, higher image/slice/plane number to lower image/slice/plane number).
- While playing in cine mode, click  to play the cine in a forward direction (for example, lower image/slice/plane number to higher image/slice/plane number).
- While playing in cine mode, click  to play the cine in a back and forth direction (for example, lower image/slice/plane number to higher image/slice/plane number to lower image/slice/plane number).
- Move the frame rate slider to change the frame rate.

The Image Level Toolbar (see Mammography Application Workstation Toolbar on page 94) includes the same functionality, but controls each Breast Tomosynthesis series independently. Additionally, the Image Level Toolbar contains controls for filming the active image and marking the active image a Key Image.

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Manually Scrolling through a Breast Tomosynthesis Series

A selected Breast Tomosynthesis series can be manually scrolled when not playing in cine mode using the mouse scroll wheel or similar device.

Mouse or Navigational Device

A selected Breast Tomosynthesis series can be manually scrolled when not playing in cine mode using the mouse scroll wheel or similar navigational device. If the series was playing in autocine mode, the scroll operation will automatically stop the cine and allow the user to manually scroll the series.

Right-Click and Drag

A selected Breast Tomosynthesis series can be manually scrolled by right-clicking on the Breast Tomosynthesis series and dragging the mouse. If the series was playing in autocine mode, this operation will automatically stop the cine and allow the user to manually scroll the series.

DBT Image Map Reference Line

A selected Breast Tomosynthesis series can be manually scrolled by selecting the DBT Image Map Reference Line and dragging it to the desired location. If the series was playing in autocine mode, this operation will automatically stop the cine and allow the user to manually navigate the series.

13.17.28 Saving and Viewing Annotations

Annotations or markups added to an image can be saved for later viewing. By default, annotations are saved as a Grayscale Softcopy Presentation State that references the original image. Depending upon the configuration, markups may be saved automatically (with or without a confirmation prompt) or manually.

Automatically Saving Annotations

If configured to automatically save annotations with confirmation upon closing the case, click OK to continue with the saving or Cancel to cancel the operation.

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Manually Saving Annotations

► Select the image with annotations to save.

► Click the Save Active Image shortcut key or toolbar icon .

Viewing Annotations

Reload a case with saved annotations to view them. When reloaded, annotations can be:

- Displayed on a duplicate image (in memory only) and stacked behind the original image. These additional images with annotations are counted in the Number of Images Annotation (see Identifying the Number of Stacked Images on page 374).
- Dragged and dropped as needed from the Patient Mini Archive (PMA) to the PowerViewer application as needed. Thumbnails representing saved annotations in the PMA are identified with the text (PR).

NOTICE! To learn more about Annotations, see the Diagnostic Workstation Online Help.

13.17.29 Marking and Viewing Key Images

Key Images are images that you select as best representing a study. Individual images of a Conventional Mammogram or individual images/slices/planes of a Breast Tomosynthesis series can be selected as Key Images and saved for later viewing with or independent from the rest of the study.

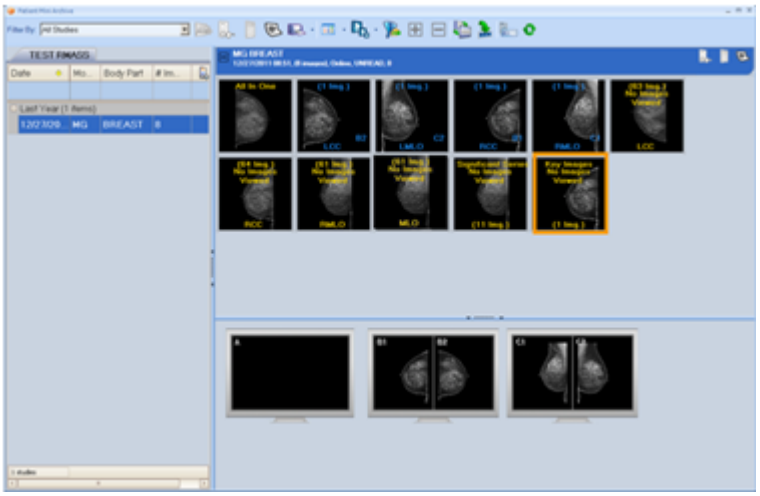
Key Image Groups are always available and include all marked Key Images. The group is saved in the Patient Mini-Archive (PMA), regardless of reading or locking status. The group is also displayed in the PowerViewer regardless of status.

NOTICE! When you close the study, the key images are saved in a new series. The next time the study is loaded, you can choose to load either the entire study or only the key images.

Marking Key Images

1. From the PowerViewer, select an image.
2. Click the Key Image icon  in the Export tab. Alternatively, click the Key Image icon  from the Image Level toolbar. A key annotation appears on the bottom corner of the image and the image appears in the E-Report Preview/Key Image Previewer.

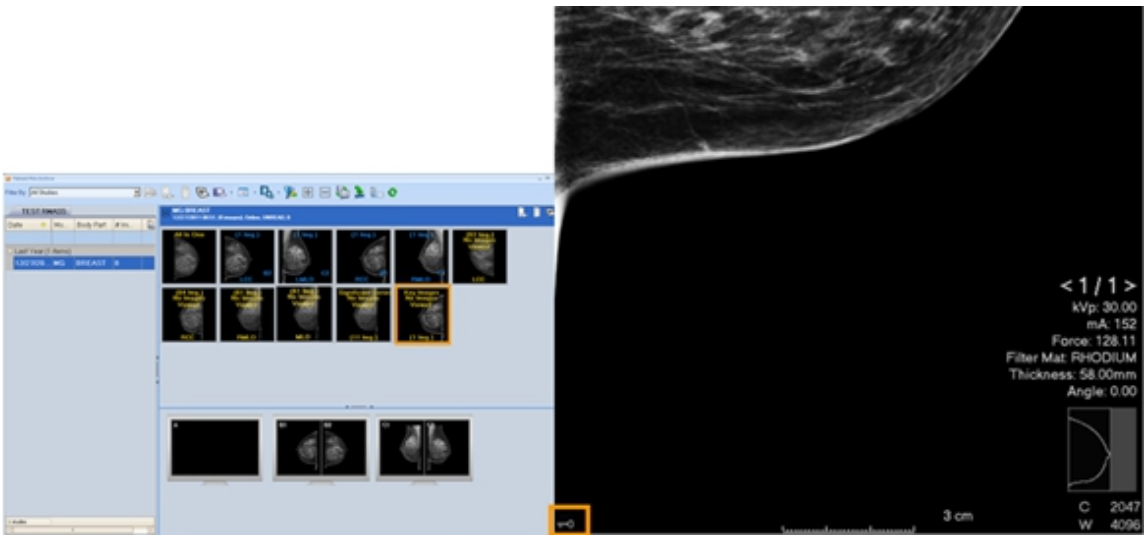
   
3. Repeat Steps 1 and 2 to mark additional key images.
4. Once completed, the key images are saved in the archive, along with their annotations, in a new series labeled with the text (Key Images).



Viewing Key Images

When reloaded, Key Images can be:

- Navigated to in the original series using Scrolling Key Images on page 379 or Keyboard Shortcut on page 379.
- Displayed automatically and independent of the original series by the Display Protocol.
- Displayed in the Key Image Previewer.
- Dragged and dropped from the Patient Mini Archive (PMA) to the PowerViewer application as needed. Thumbnail groups representing Key Images in the PMA are identified with the text (Key Images). Key Images in the PowerViewer application are identified with a key annotation in the bottom corner of the image.



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Scrolling Key Images

You can scroll specifically through Key Images using the Scroll to Next Key Image function. To use the function, press and hold the CTRL key on the keyboard as you use the mouse to scroll (use the middle scrolling wheel on the mouse).

The Scroll to Next Key Image function advances you to the next original image marked as a Key Image.

NOTICE! If there are several instances where the same image is marked as a Key Image, you will advance to the next image, because the original image only shows one instance.

You can toggle dynamically between two scrolling modes. While you press and hold the CTRL key and use the mouse to scroll simultaneously, you will scroll through Key Images only. While you use the mouse only to scroll, you will scroll up or down to further explore proximate slices.

Keyboard Shortcut

Press K on the keyboard to automatically scroll through the series to the next Key Image.

Unmarking Key Images

You can unmark images that were previously marked as key images.

NOTICE! Unmarking removes the Key Image marker. Unmarking does not delete original images in the PowerViewer application.

1. From the PowerViewer, select an image.
2. Click on the Key Image icon  from the Image Level toolbar for a Breast Tomosynthesis series or press Alt + CTRL + space from the keyboard.

   If there are Key Images originating from the image you want to unmark, the following message appears:

   There are a few Key Images originating from this image. Clicking 'OK' will clear them all. If you want to remove a single Key Image, please use the Key Image group or the E-Report Preview.
3. Click OK to unmark the images, or click Cancel to stop the unmark process.

NOTICE! To learn more about Key Images, see the Diagnostic Workstation Online Help.

13.17.30 Marking and Viewing Significant Series

A Significant (SIG) series of images saves selected sequential images/slices/planes of a Breast Tomosynthesis exam as a new single series. A whole series, or only a sub-volume out of a series, can be marked as a SIG series.

The PMA lists studies with SIG images so they easily identified.

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Marking a Significant Series

A whole series or sub-volume can be marked as a SIG series as detailed below.

Type of SIG Marking	Description	Instructions
Mark Whole Series	Mark an entire series within a study.	Marking an Entire Group on page 380
Mark Slab by Borders	Mark the first and last image of the volume you want.	Marking a Slab by Borders on page 380
Mark Slab by Center	Choose the middle image and use dialog box to determine the thickness in millimeters or total number of images.	Marking a Slab by Center on page 381

Marking an Entire Group

You can manually save a full series/group as a SIG, without selecting sub-volume.

From Archive Explorer (CTRL + N)

1. Right-click on a series.
2. Select Mark as Significant Series.

From PowerViewer

1. Right-click on a series.
2. Select Mark Entire Group from the drop-down of the Mark Significant Series icon  in the Export Toolbar. Alternatively, select Significant Series > Mark Entire Group from the right-click menu.

Marking a Slab by Borders

You can mark two images within the same group to create a "border." The SIG contains the border images, plus the range of images between the first and last image.

From PowerViewer

1. Select Mark Slab By Border from the drop-down of the Mark Significant Series icon  in the Export Toolbar. Alternatively, select Significant Series > Mark Slab by Border from the right-click menu.
2. The cursor changes to a square.
3. Scroll through the images and click the image you want to define as a border and include as the first image in the range of images.

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4. Scroll through the images and click the image you want to define as a border and include as the final image in the range.

IMPORTANT

Finish the marking process before you apply annotations or measurements, or manipulate the image. If you change the cursor mode before you mark the final image, you will cancel the marking process prematurely.

Marking a Slab by Center

You can mark one central image, and the system expands the selection to several mm or images in each side.

NOTICE

The system creates a slab with a symmetric number of images or equal thickness from each side of the middle slab image. The system automatically adjusts the calculation to create a symmetric sub-volume around the center image as needed.

From PowerViewer

1. Select Mark Slab By Center from the drop-down of the Mark Significant Series icon  in the Export Toolbar. Alternatively, select Significant Series > Mark Slab by Center from the right-click menu.
2. Click the center (middle) of the image. A window opens.
3. In the window, select one of the following options and input the values requested:
   - Total length of slab in millimeters
   - Total number of images in slab
4. Click OK.

IMPORTANT

Finish the marking process before you apply annotations or measurements, or manipulate the image. If you change the cursor mode before you mark the final image, you will cancel the marking process prematurely.

Saving SIG Images

When you mark a SIG, the system automatically retains the marker.

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The system saves SIG images when you confirm the case.

Most of the image parameters, such as pan or enhance, are saved as part of the SIG image. The zoom image parameter is not saved.

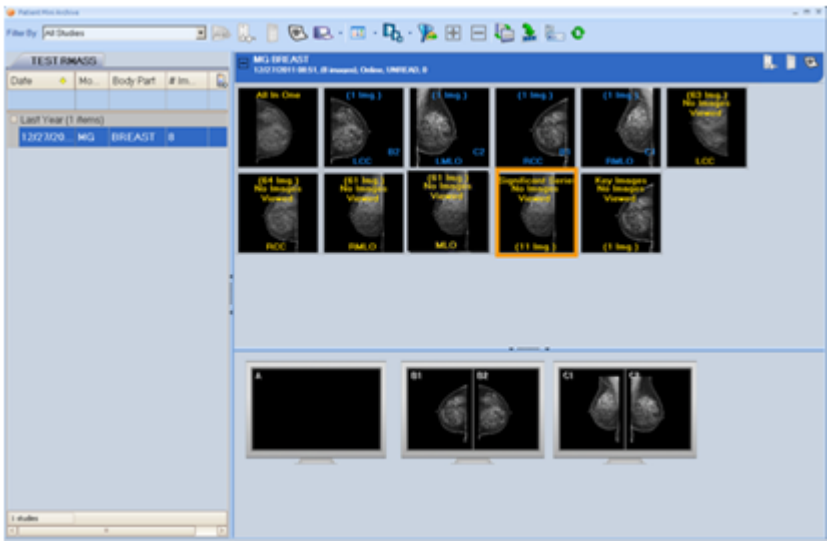
1. Apply annotations or measurements, or manipulate the image as needed.
2. Click Done  or its keyboard shortcut.

When marking full group/series, the same group/series will appear twice, once without Significant Series indication and once with Significant Series.

Use the Has Significant Series column in the Archive Explorer to view and organize series containing SIG images.

Viewing and Annotating SIG Series

After you mark a series, you can see the identity of the new Significant series in the PMA identified with the text (Significant Series).



When you drag a SIG image from PMA into the viewbox, you will see a SIG annotation in the upper left of the group.

When you use the arrow keys to navigate between series, the navigation includes Significant Series.

All Significant Series are part of the All-in-one series. SIG images may appear twice.

Unmarking SIG Images

You must use Archive Explorer to unmark the SIG images from studies.

Important: You cannot use PowerViewer to clear SIG images.

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IMPORTANT

If you do not have permission to clear SIG images, the Unmark Significant Series option is inactive. contact the system administrator.

1. Open Archive Explorer.
2. Select the study containing SIG images.
3. Click Explore , or use keyboard shortcut Ctrl + E.
4. Locate the desired group.
5. Look for Y in the Has Significant Series column. Right-click the group with the SIG images.
6. From the right-click menu, select Unmark Significant Series. The data in the Has Significant Series column changes from Y to N.
   - N—No, the study does not contain images marked as SIG.
   - Y—Yes, the study contains SIG images.

13.17.31 Study and Image Manipulations

Studies and images can be dynamically replaced in the PowerViewer application as needed to make the necessary comparisons. This is particularly useful when additional views exist or when a different prior needs to be quickly compared.

Study Replacement

The Study Replacement feature can be used to replace all images in a selected study across all stages of the applied Display Protocol in one action. The replacement occurs without reloading the entire case. If the study is not already loaded by the Display Protocol, the study is loaded on demand.

Attempting to replace the current study or a study that is already displayed will present a warning to the user.

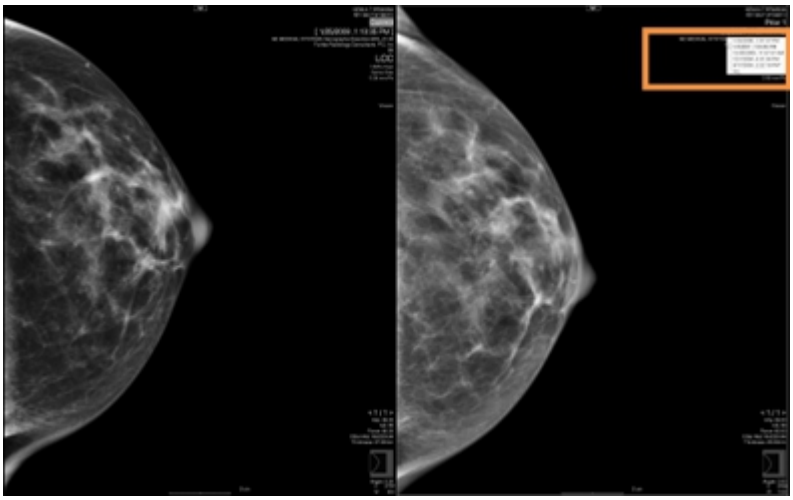
From Active Annotation:

Right-click the date/time annotation of the target study in the PowerViewer application and select the source study that replaces it.

- Target study—the existing study to be replaced.
- Source study—the study that replaces the target study.
- The study currently displayed in the PowerViewer is indicated with a check mark preceding it.
- The baseline study is indicated with an asterisk.

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From the PMA:

Drag and drop the study header (name) from the PMA in either Limited View or Full View over the study to be replaced in the PowerViewer application or Mini-Monitor.

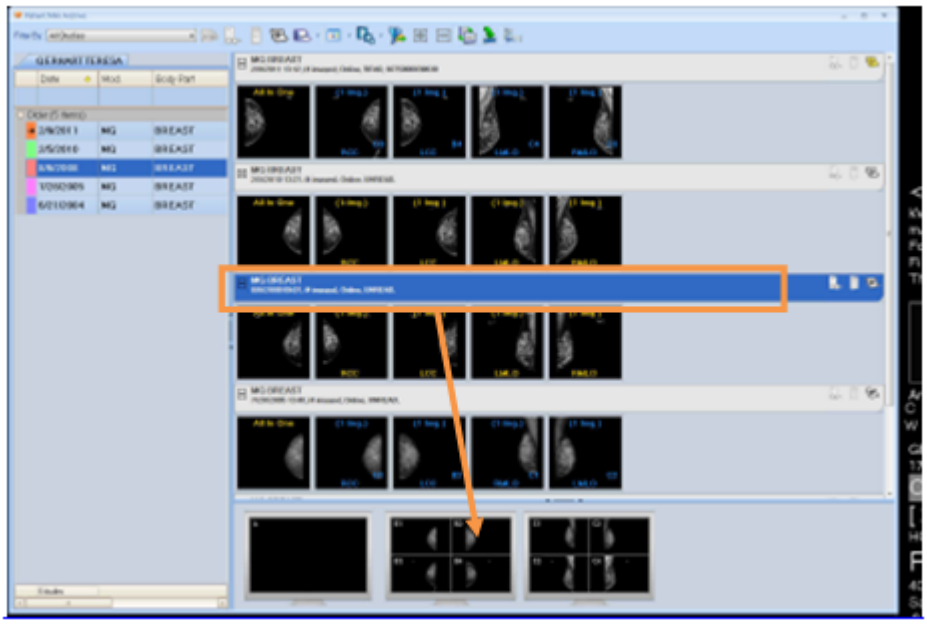


Image Manipulations

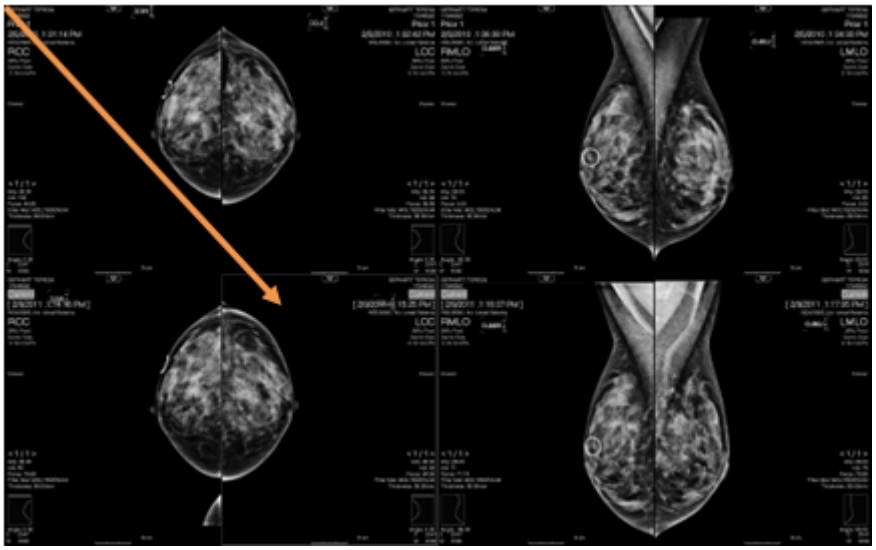
Images can be replaced or swapped in the PowerViewer application as needed to provide the necessary comparison.

From the PowerViewer Application:

Hover the cursor over the top-left corner of the image that you want to move until the cursor changes shape, click on the image, and drag the image to the desired destination.

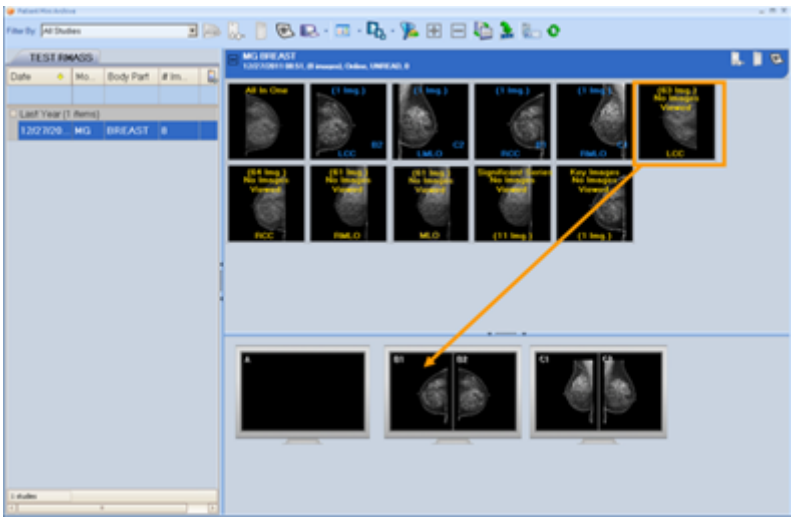
The source and target images will be swapped in the PowerViewer application.

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From the PMA:

Drag and drop a thumbnail group from the PMA in either Limited View or Full View over the image group to be replaced in the PowerViewer application or Mini-Monitor.

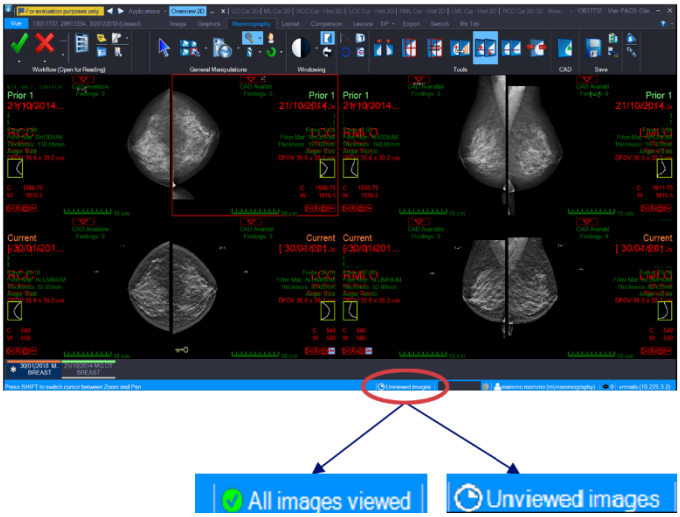


13.17.32 Viewed / Unviewed Images Real-Time Indication and Alert

Real-time study level indication

An indicator in the main viewer shows, in real time, whether all images in the study have been viewed or if any remain unviewed. One of the following notifications is displayed on the bottom bar :

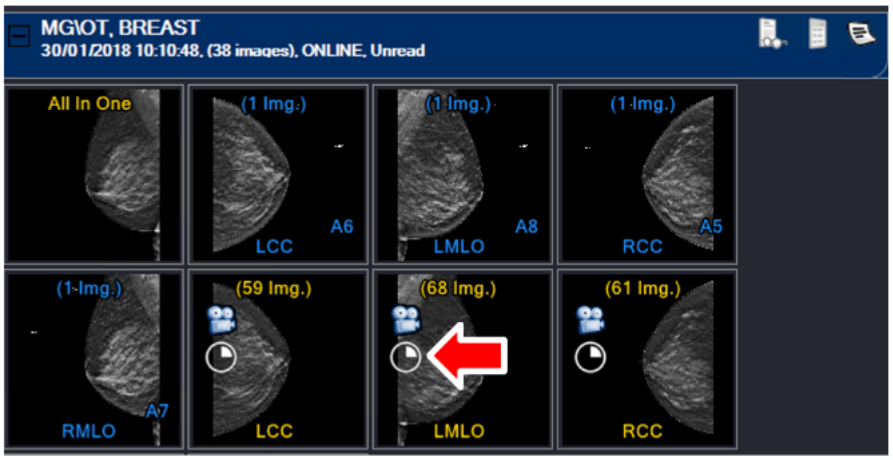
- All images viewed
- Unviewed images

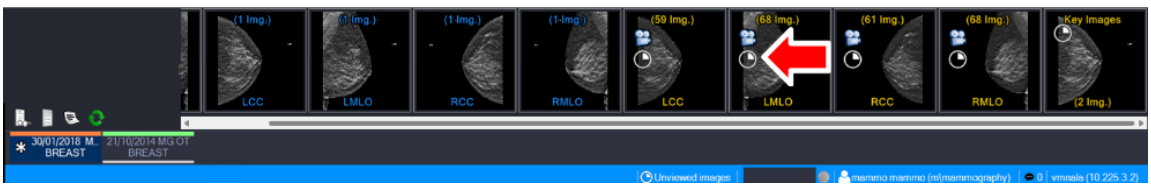


Series-level indication in the PMA and Strip PMA

The viewed/unviewed images on the series-level are indicated in the PMA and Strip PMA by one of the following icons:

- Viewed images
- Unviewed images





Unviewed image alert

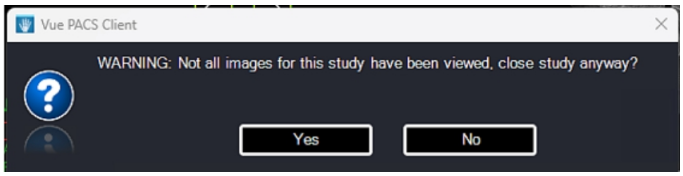
The Unread Image Alert is displayed when you attempt to dismiss a case and all Conventional Mammography and/or Breast Tomosynthesis views in the most recent study have not been viewed, based upon configurable parameters. By default, the alert applies to unviewed images only.

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The alert reads:

WARNING: Not all images for this study have been viewed, close study anyway?

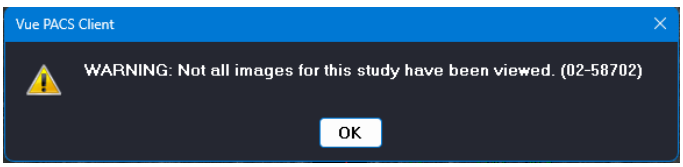
- Click **No** to identify the unread images in the PMA, and proceed to view the images.
- Click **Yes** to dismiss the case without viewing the images.



NOTE

If the Diagnostic Viewer is integrated with an external reporting system (such as PowerScribe) and the session was closed from that system, the same warning message only allows acknowledgment (OK button), without an option to cancel.

You can view the message and close the alert window.



NOTE

If unviewed images are not original, but were created or marked as key images by another user, or if prior study images were loaded, they are not mandatory for review by the current user.

In these cases:

- **The series-level icon will still indicate that the image is unviewed.**
- **The study-level real-time indicator will display All images viewed notification.**
- **The system will allow the study to be closed even if these non-mandatory images remain unviewed.**

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13.17.33 Linked Studies

The linking of studies allows study stacks to be scrolled simultaneously while remaining synchronized by study date. This is most useful when displaying an overview of prior studies that are stacked by study date. Studies can be auto linked by selecting . Studies can be unlinked by selecting . By default, only prior study stacks are linked.

Studies can also be automatically linked by the Display Protocol as defined in the Display Protocols section.

13.17.34 Toggle Between Mammography Views

A mammography view can be quickly switched to one of its corresponding views (such as 2D, DBT, or Slabbed) from the view information annotation (the annotation indicating the laterality and view position).

The following default shortcut keys are available:

- **Q** – Toggle between a specific 2D image and its corresponding DBT image.
- **Shift + Q** – Cycle through images in a predefined suggested list.

  This option can be configured to move to next image in the group, before switching groups. For more information, see chapter “Mammography Settings” on page 460.

2D/DBT toggle

Use the **Q** shortcut key as follows:

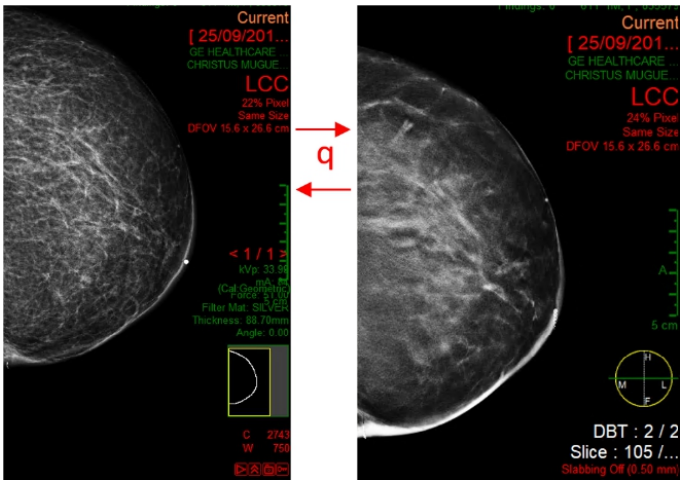
1. **First press**:
   - Toggle a 2D image of a specific laterality → to DBT (Digital Breast Tomosynthesis) image of the same laterality.
   - Toggle a DBT image of a specific laterality → to the 2D image of the same laterality.
2. **Second press**:

   Return to the original source image.

   Example: If toggling began at a 2D image and switched to DBT, pressing Q again returns to the original 2D image.

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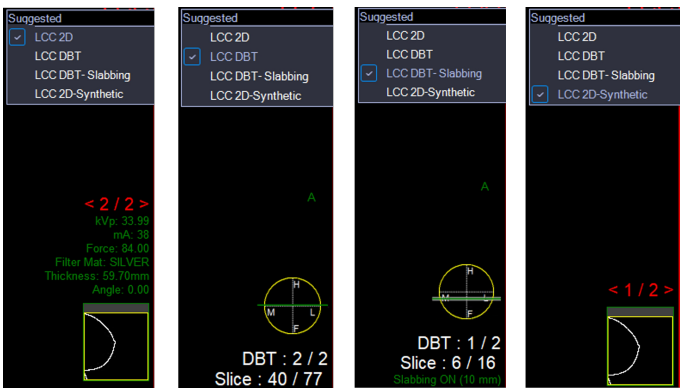
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Cycle through images

Press the **Shift + Q** shortcut key to cycle through images in a predefined suggested list.

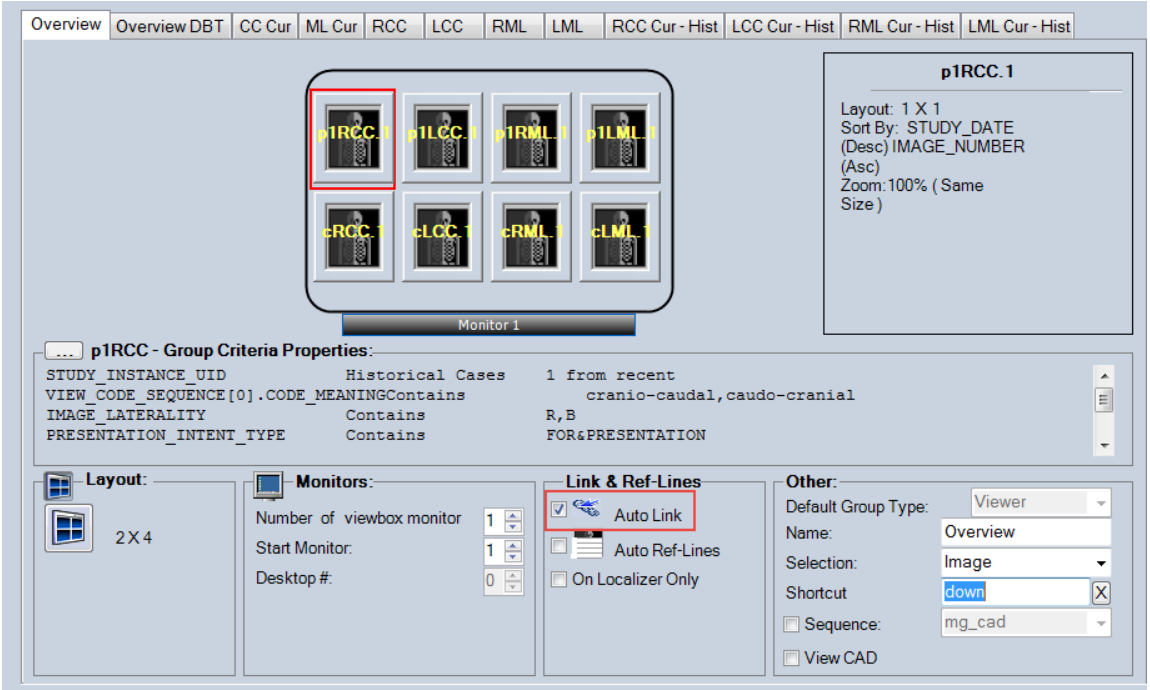
Cycling through images maintains list order unchanged while marking the current image and graying it out.



13.17.35 Display Protocols

Linked Studies

A Display Protocol stage can be configured to link the studies it displays. When linked, the stacks of studies will scroll simultaneously while remaining synchronized by study date.

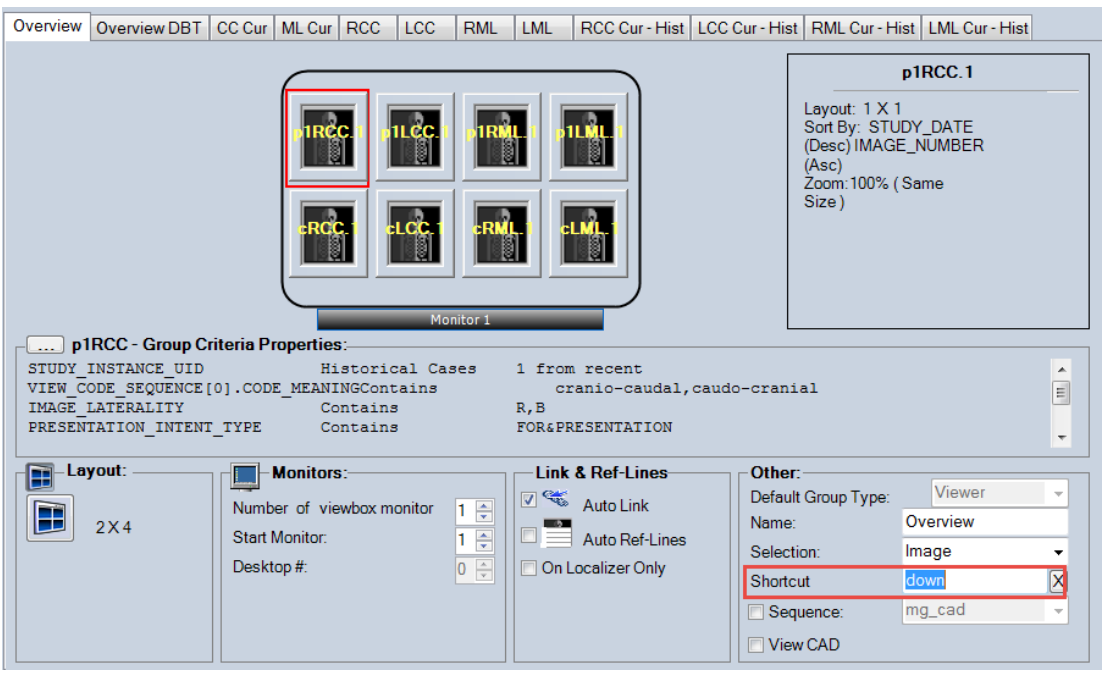


Viewing a Select Stage of Display Protocol

To view a select stage in the Display Protocol, such as a CC or MLO view comparison, select the keypad or shortcut key configured to jump to the selected stage of the Display Protocol.

Configuration:

- A shortcut for Display Protocol stages is configured in the Display Protocol editor.



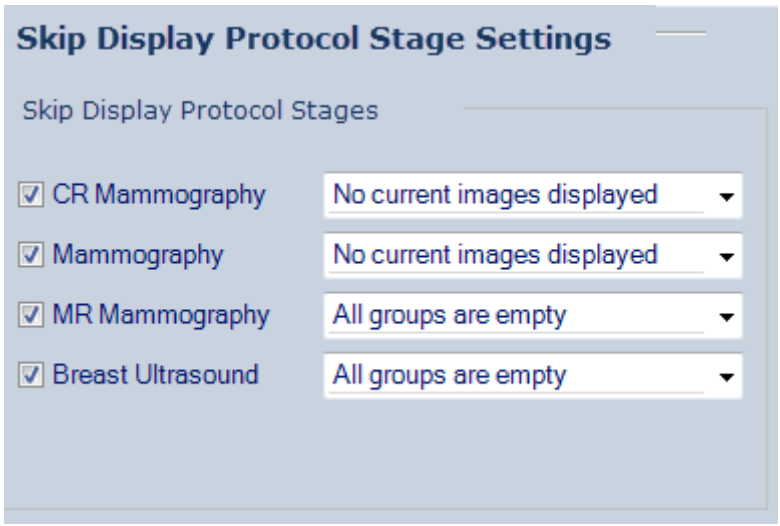
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Auto-Skipping of Display Protocol Stages with Missing Views

The system can be configured to automatically skip Display Protocol stages when views are missing. This configuration is available in Application Settings, where the following selections can be made:

1. Select a modality
2. From the drop-down menu, select the condition that needs to be met in order to skip the Display Protocol stage.



13.17.36 Values of Interest Look Up Table (VOI LUT)

The default Values of Interest Look Up Table (VOI LUT) is applied to an displayed image, if available, to provide optimal image quality.

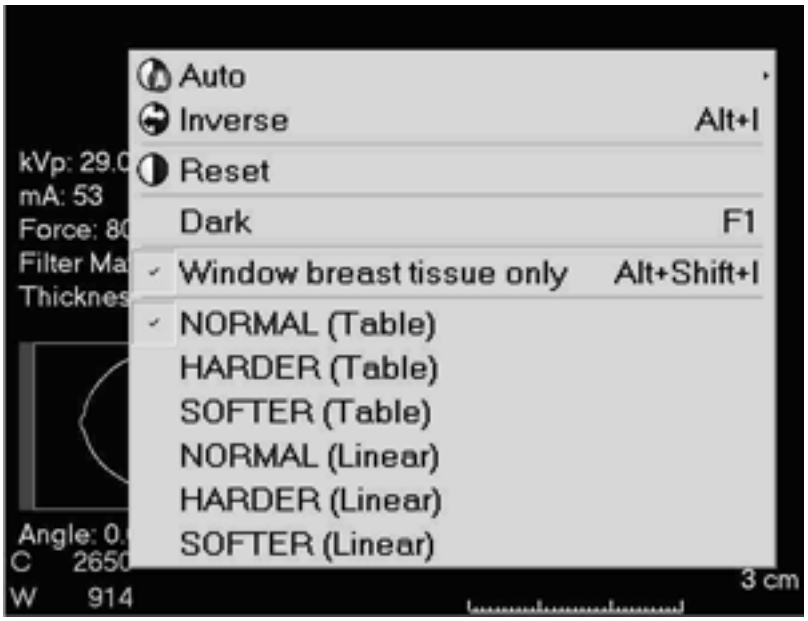
This VOI LUT is used by several DR/FFDM manufacturers including GE Medical Systems, Siemens, and SECTRA.

If multiple tables are available, you can select them from a context menu.

To open the context menu, right-click on the Center and Window annotation.

The example here shows the VOI LUTs available for a particular image.

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The system can be configured to apply a specific VOI LUT by default. Contact your system administrator if this is required.

13.17.37 Digital Mammography CAD Results

Digital Mammography CAD results are received from a CAD system (for example, iCAD, R2, or VuComp) and stored by the Vue PACS as DICOM Mammography CAD Structured Report (SR) Objects.

Each Mammography CAD SR Object contains zero or more CAD findings and their image references. The CAD findings are displayed to the user as graphic overlays, referred to in this description as CAD markers.

The Vue Mammo Workstation displays the total number of densities and calcifications per image and per study. These totals can be configured to be displayed on a single line (CAD ON [C:2, D:1]), or separate lines CAD ON [C:2 D:1] (line 1) Total: C:4 D:2 (line 2).

The Vue Mammo Workstation can display a study level column in the Archive Explorer that indicates if a study contains Mammography CAD results.

CAUTION

It is critical that the radiologist reviews the images in the conventional manner first, before reviewing the CAD results. Reviewing the CAD results before reviewing the images introduces the risk of the so-called satisfaction-of-search error, in which the radiologist fails to examine the unmarked areas of the images with adequate vigilance.

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13.17.38 Displaying CAD Markers

By default, CAD markers are not automatically displayed on loaded images. You can choose whether or not to show all Mammography CAD markers automatically as part of a DP sequence or manually using a GUI control.

View CAD is available only if at least one Mammography CAD SR Object is loaded. View CAD lets you display all CAD markers if any of the images were referenced by a single Mammography CAD SR.

If any images were referenced by more than one Mammography CAD SR, select View CAD from the toolbar again to display the next Mammography CAD SR findings before disabling the CAD markers.

Selecting View CAD one more time will hide the CAD markers off.

1. Click View CAD  to toggle the CAD markers on.
2. Click View CAD to view next CAD report (if it exists).
3. Click View CAD to hide CAD report.

13.17.39 CAD Marker Shape and Size

CAD markers are displayed based upon the center point and outline coordinates defined for each in the Mammography CAD SR.

- If a center point and outline are defined, the CAD marker uses both sets of coordinates, depending on the configuration.
- If only a center point is defined, the shape and its size use configuration settings. The shapes defined by the CAD system manufacturer are represented as closely as possible.

In addition to the CAD markers displayed, the following information is displayed on each image that has at least one CAD finding associated with it:

- Status of CAD (CAD on, available, or failed)
- Number of CAD markers displayed
- CAD manufacturer
- CAD software version
- Number of CAD markers displayed

The following CAD identification markers are supported for R2 CAD basic marker shapes:

CAD Marker	Description
	The asterisk identifies a density, which refers to the projection of a mass lesion.
	The triangle identifies a cluster of calcifications.

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Refer to the CAD System's User Manual for more information about each vendor's CAD markers and their definitions.

13.17.40 Saving and Printing

Images with CAD markers displayed on them can be saved and printed with the CAD markers applied.

13.17.41 Life Cycle Management

The Vue Mammo Workstation and the Diagnostic Workstation allows you to define rules for automatic archiving or deleting Mammography CAD SR Objects after a configured period of time or other specified criteria.

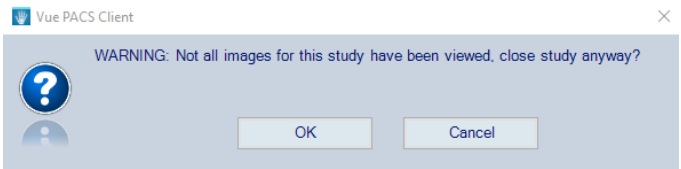
13.17.42 RIS/MIS Integration

The Vue Mammo Workstation supports all RIS Integrations that are currently supported by Vue PACS. In addition, the following Mammography Information/Reporting Systems are supported:

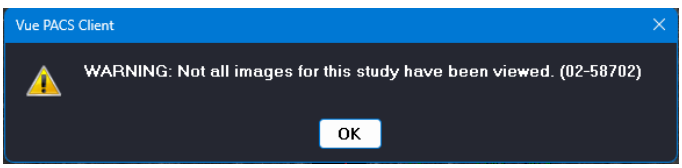
- RIS Mammography Module
- IDX Mammography Module

13.17.43 Exiting the Vue Mammo Workstation

On exiting the Vue Mammo Workstation, a warning message may display in a version of Diagnostic Workstation without integration to third party reporting software which is fully integrated with Philips Diagnostic Workstation (such as PowerScribe). In the event that all images have not been viewed, a warning message appears:



If the Diagnostic Viewer is integrated with an external reporting system (such as PowerScribe) and the session was closed from that system, the same warning message only allows acknowledgment (OK button), without an option to cancel.



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13.18 ORTHOVIEW Orthopaedic Digital Imaging

13.18.1 About ORTHOVIEW Orthopaedic Digital Imaging

ORTHOVIEW Orthopaedic Digital Imaging for Vue PACS is an orthopedic templating software that provides you with a rich feature set for orthopedic surgery planning. ORTHOVIEW is a Meridian Technique Ltd product that is integrated with the Vue PACS system. It features:

- Automated launch of ORTHOVIEW Orthopaedic Digital Imaging directly to a desired exam.
- No manual user login to ORTHOVIEW Orthopaedic Digital Imaging is necessary.
- PACS based storage of templated results for distribution throughout the health care enterprise.

NOTICE! The ORTHOVIEW Orthopaedic Digital Imaging application is available only if your profile has a license to use it.

The topics below cover information related to the integration of ORTHOVIEW Orthopaedic Digital Imaging with the Vue PACS workstation. For information about using ORTHOVIEW Orthopaedic Digital Imaging, refer to the online Help that is accessed from within the ORTHOVIEW Orthopaedic Digital Imaging application.

See these topics:

Launching ORTHOVIEW Orthopaedic Digital Imaging on page 395

Ending a Templating Session on page 396

Resuming a Templating Session on page 396

13.18.2 Launching ORTHOVIEW Orthopaedic Digital Imaging

1. Select the images to be loaded to the workstation display.

   These images may be selected from the study, series, or image level of Archive Explorer.
2. Load the selected images on the Vue PACS workstation display.
3. Select the images you want to use for templating.

   It is most efficient to select only the images to be used while templating. However, more images may be selected and later removed from the templating operation from within ORTHOVIEW Orthopaedic Digital Imaging.
4. To select multiple images for templating, press CTRL and click each desired image.

   Each selected image is outlined with a colored box (red for most recently selected and yellow for previously selected images).
5. From the Vue PACS workstation tools, click the ORTHOVIEW Orthopaedic Digital Imaging Action button. .

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When ORTHOVIEW Orthopaedic Digital Imaging is launched, the selected images will be ready for templating.

13.18.3 Ending a Templating Session

The templated exam must be saved or committed in ORTHOVIEW Orthopaedic Digital Imaging in order for the templating results to be saved to Vue PACS.

- Saving the session lets you continue the templating work later in ORTHOVIEW Orthopaedic Digital Imaging.
- Committing the session saves the session as read-only for later recall and display on a Vue PACS workstation. No further templating work can be done with this templated session. A new templating session would need to be created if further templating work is required.

The templated exam data is stored as a new series in the same Vue PACS study. This series includes images with overlaid templates, as well as an image of a text report. You provide a series description during the save or commit process. This description appears in the Vue PACS worklist for later identification of the templated series.

Completing a templating session results in a modified templated study in the Vue PACS worklist. The Vue PACS Archive Explorer worklist displays a "y" in the OV T field if the study has templating work saved to the Vue PACS.

NOTICE! The field name is OV T by default. However, the field name can be customized during installation.

13.18.4 Resuming a Templating Session

A templating session can be resumed if that session was saved (not committed) in ORTHOVIEW Orthopaedic Digital Imaging. All data related to a previous templating session, including the images, is stored in the ORTHOVIEW Orthopaedic Digital Imaging report image.

1. Load the study on the Vue PACS workstation.

   Only the ORTHOVIEW Orthopaedic Digital Imaging report image is required. More images may be loaded, if desired. Images from the same series as the report may be helpful to identify the appropriate series for further templating work.

   ⇨ The ORTHOVIEW Orthopaedic Digital Imaging user's worklist displays a "y" in the OV T field if the study has templating work saved to the Vue PACS.

   ⇨ The templated series may be identified in the Archive Explorer worklist by the series description. This series contains the text used when the session was saved.

2. Select only the image of the ORTHOVIEW Orthopaedic Digital Imaging report.
3. From the Vue PACS workstation tools, click the ORTHOVIEW Orthopaedic Digital Imaging Action button .

   ⇨ ORTHOVIEW Orthopaedic Digital Imaging launches to the end state of the previous templating session. You can now do more templating work.

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4. After completing your work, save or commit the exam.
   ⇨ Each time a templating session is saved or committed, a new series, including a report and images, is added to the study on the Vue PACS.

See this topic:

Ending a Templating Session on page 396

13.19 CT Perfusion

13.19.1 Overview

CT Perfusion is a clinical tool for evaluating perfusion parameters related to blood flow and blood volume in the brain. These images are obtained by scanning the patient repeatedly during 40-60 seconds with a CT scanner after intravenous injection of contrast material.

13.19.2 Application Specific Intended Use

The system contains interactive tools in order to ease the process of analyzing and comparing three dimensional (3D), CT Perfusion (CTP) images. It is a single system that integrates review, dictation and reporting tools to create a productive work environment for the radiologists and physicians. The system contains a Perfusion module with interactive tools to ease the process of analyzing and comparing Computed Tomography Perfusion (CTP) images of adult patients. The Arterial Input Function (AIF), Venous Output Function (VOF), and Brain Centerline are automatically detected with the ability for manual correction by the user. Blood perfusion parameters are automatically calculated and displayed as a set of user friendly perfusion maps and perfusion tables summarizing the results. The perfusion maps include relative Cerebral Blood Volume (rCBV), relative Cerebral Blood Flow (rCBF), Mean Transit Time (MTT), Time to Peak (TTP), and Time to maximum impulse response function (TMAX). The perfusion tables include the calculation of parameters related to tissue flow (perfusion) and tissue blood volume.

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13.19.3 Application Specific Limitations of Use

WARNING

If the temporal resolution of the scans is greater than 4.0 seconds, quantitative perfusion measurements are not provided. The color maps and numeric values represent relative values only. Specifically, when applying the Summary Maps functionality note that for cases with such poor time resolution there are no standard recommended threshold values for the reduced CBV and increased MTT.

- **When thick-slice Brain images are viewed in the slab mode some partial volume artifacts might occur.**
- **When loading images into CT Perfusion, all images which contain 16 bit data are converted into 12 bit images.**

WARNING

There are no standard recommended threshold values for the Summary Maps calculation in conjunction with the Arrival Time Insensitive method. When using the system default thresholds for the Summary Maps, after applying the Arrival Time Insensitive method, the Summary Maps results may not be optimal.

WARNING

The application results should not be used as a SOLE basis for diagnosis.

13.19.4 Introduction

CT Perfusion is a clinical tool for evaluating perfusion parameters related to blood flow and blood volume in the brain.

The application uses as input a collection of images obtained by scanning the patient repeatedly during 40-60 seconds with a Computed Tomography (CT) scanner after intravenous injection of contrast material.

Based on the input data and on calculation of blood supply parameters, the application assesses the volume of ischemic tissue.

The application provides:

- Automatic selection of reference artery
- Automatic selection of reference vein
- Automatic calculation of the brain symmetry plane
- Automatic motion correction

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- Calculation of perfusion maps based on input data, including:
  - rCBV
  - rCBF
  - TTP
  - MTT
  - TMAX

For further details on the perfusion maps, see Section Analyzing Perfusion Calculation Results on page 403.

- Automatic selection of the affected hemisphere of the brain
- Segmentation of two ischemic regions marked as Lesion and Hypoperfusion. The segmentation of each region is based on thresholds and parameters configurable by the user.

NOTICE! The values for blood volume and blood flow are shown in relative units up to an arbitrary multiplicative constant. Relative units are used because partial volume effects prevent absolute quantification.

The results yielded by the Perfusion application are complementary to the data provided in the original CT scan, and are used in conjunction with the reading of the original CT study to enhance accuracy of the diagnosis and facilitate indication of the desirable course of treatment.

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13.19.5 Perfusion application workflow

When the original CT study is loaded to the CT Perfusion application, the application identifies a reference artery and reference vein, identifies the brain centerline, and marks the results on a standard Temporal Maximum Intensity Projection (TMIP) series.

On the basis of this data, the user can initiate the perfusion calculations, the results of which are displayed in a set of maps. Measurements of parameters for specific Regions of Interest (ROIs) are presented in tables.

Finally, a segmentation of the Lesion and Hypoperfusion areas is marked on the TMIP image.

A typical workflow includes the following automatic and manual steps:

1. Loading of the study to the CT Perfusion application—Executed by the user.
2. AIF Indication—Executed automatically by the application while allowing manual corrections by the user.
3. VOF Indication—Executed automatically by the application while allowing manual corrections by the user.
4. Identification of the brain center line—Executed automatically by the application while allowing manual corrections by the user.
5. Automatic calculation of a brain mask.
6. Automatic calculation of a TMIP series.
7. Motion correction.

8. Calculation of the perfusion parameters—rCBV, rCBF, TTP, MTT, and TMAX.

   The parameters are calculated automatically by the application and displayed as a set of perfusion maps.

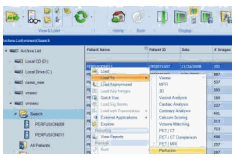
9. Measurement of the above parameters for ROIs drawn manually by the operator. These measurements are displayed in a table.

10. Segmentation of two ischemic regions marked as Lesion and Hypoperfusion The segmentation of each region is based on thresholds and parameters configurable by the user (see Section Determining Perfusion Settings).

13.19.6 Loading the Study

To load a CT perfusion study:

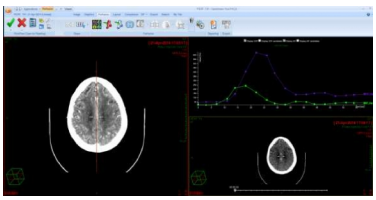
1. In the Diagnostic Workstation, highlight the study in the Archive Explorer.
2. Select **Load To > Perfusion** from the right-click menu.

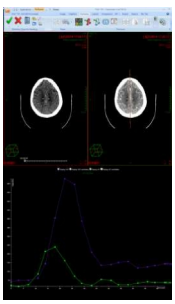


The initial layout includes:

- The calculated TMIP images
- The scanned series
- The AIF and VOF graph
- A temporal slider
- A Perfusion ribbon offering tools for controlling the workflow and for adding manual calculations

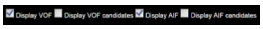
The following illustrations show the initial layout on landscape and portrait monitors.





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By default, the graph shows the AIF and VOF curves. Alternatively, you can choose to display the curves of the default and/or additional candidate VOF and AIF points by using the check boxes at the top of the graph area (see section Adding Arteries and Veins).



Use the temporal slider at the bottom of the screen to view the slices throughout the scan period.



Right-click anywhere in the image display area to select image manipulation activities, such as windowing, zooming, panning and others. For a description of all image manipulation tools available in the Vue PACS application, see the Vue PACS help.



Use the mouse wheel to scroll through the series images.

13.19.7 Calculating Perfusion input values

When you initially load the study, the application automatically calculates values that serve as a basis for the perfusion calculation. You can manually correct the results to improve your reading accuracy.

Identifying the AIF and VOF

The application automatically identifies candidate AIF and VOF points that are to be used for the analysis and marks them as A1 

and V1 

on a TMIP series image.

NOTICE! The artery and vein marks do not necessarily appear on the same slice.

The graph shows the Hounsfield values through the scan period of time for each marked artery (Ai) and vein (Vi), as well as the average graph for the resulting AIF and VOF.

Adding arteries and veins

You can decide to manually add arteries and veins in order to investigate the values of additional voxels.

To add an artery or a vein –

1. Click **Add Artery**  or **Add Vein**  in the Perfusion ribbon.

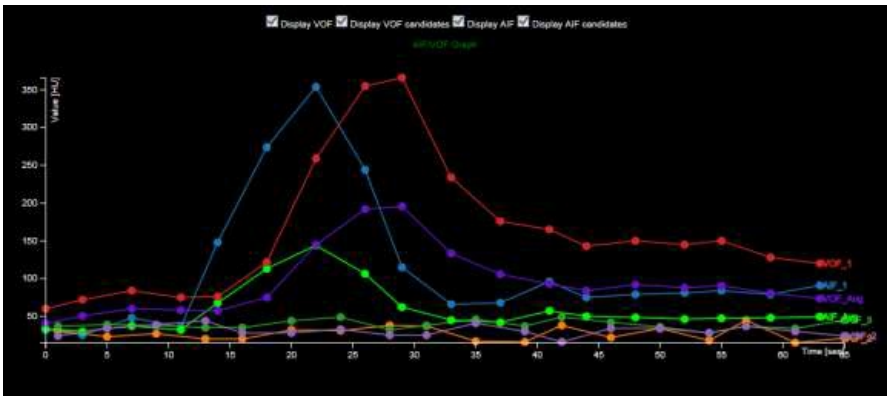
   The cursor changes to .
2. On the TMIP image, click to add the artery or vein. The point is marked as A2 or v2 respectively.

   Additional arteries and veins are marked as A3, A4 or V3, V4, and so on.

   A curve showing the values of the newly marked voxel is added to the graph.

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By default, the VOF and AIF graph displays the curve of average values. When you add arteries and veins, you can choose to display the curve for each vein, each artery and/or the average values. Each curve has a different color, and its label is displayed at the right-hand side.



Using Motion Correction

Use the Motion Correction tool to cancel the effect of patient movement during the scan.

To correct the image, click **Motion Correction** in the Perfusion ribbon.

The correction algorithm is activated and the TMIP image is recalculated.

Using the temporal slider after correction shows a smaller variance of changes in image position along the scan duration.

NOTICE! When motion correction has been carried out, the bed component in the TMIP series becomes less focused.

Click the **Motion Correction** icon again to cancel the correction calculations.

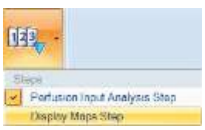
13.19.8 Calculating Perfusion maps

Initiating Map Calculation

When all the required data is available, the application is ready to perform the perfusion calculations and yield the perfusion maps and table data.

To initiate the perfusion calculations, do one of the following:

- Click **Select Step** in the Perfusion ribbon and then click the **Display Maps Step** option in the drop-down menu.

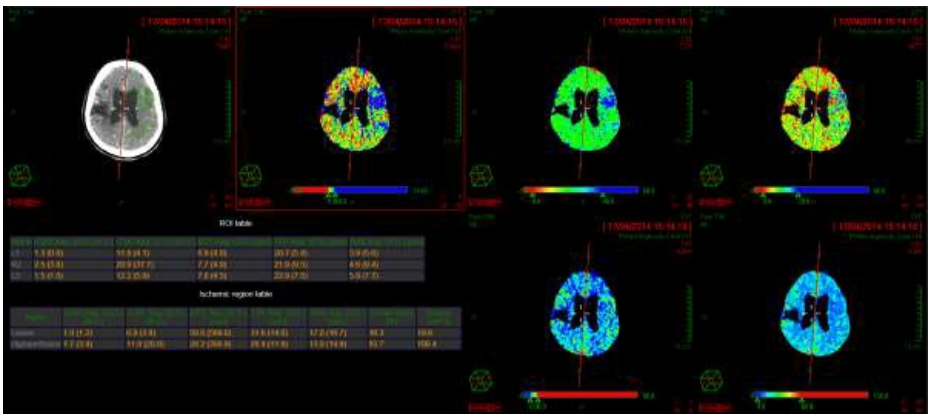


- Click **Next Step** in the Perfusion ribbon.
- Click **Calculate Perfusion Maps** in the Perfusion ribbon.

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Analyzing Perfusion Calculation Results

The system calculates all the blood perfusion parameters and displays a set of maps and tables summarizing the calculated values.



The following is displayed:

A Set of Perfusion Maps

In each of the displayed maps, a color range represents the calculated values of the perfusion parameters.

- rCBV map—Presents the volume of blood in a known volume of tissue, based on the concentration of contrast material present in the tissue over time. The map shows the calculated volume of blood in each voxel throughout the scan in relative units.
- rCBF map—Presents the flow of blood to the affected tissue. The map shows the calculated rate of blood flow in each voxel throughout the scan in relative units.
- MTT map—Presents the period of time during which the contrast material stays in the tissue. The map shows the mean time of blood transit through each voxel.
- TTP map—Presents time to maximum tissue enhancement at each volume of the tissue. The map shows the number of seconds from the scan start to the peak of tissue enhancement in each voxel.
- TMAX map—Shows the residue function time to peak in seconds.

The color bar at the bottom of each map displays the minimum and maximum data values for that specific map. Two sliders represent the current windowing and allow you to change the range of displayed values.

Changing windowing values via the windowing annotation at the bottom right corner allows you to display values that are beyond the values of the color bar. In such cases, the value displayed on the color bar is marked with an asterisk.

You can determine whether the color bar is displayed or not. Right-click the windowing annotation and click **Show Color Bar** to display the bar. If the bar is displayed, click **Show Color Bar** to remove the bar from the display.

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NOTICE! The appearance of the color bar is configurable. Appearance settings include vertical versus horizontal appearance, bar size, bar position, the size of the gradient columns, the display of the minimum and maximum data values, and the display of the sliders. For configuring the color bar appearance, contact your system administrator.

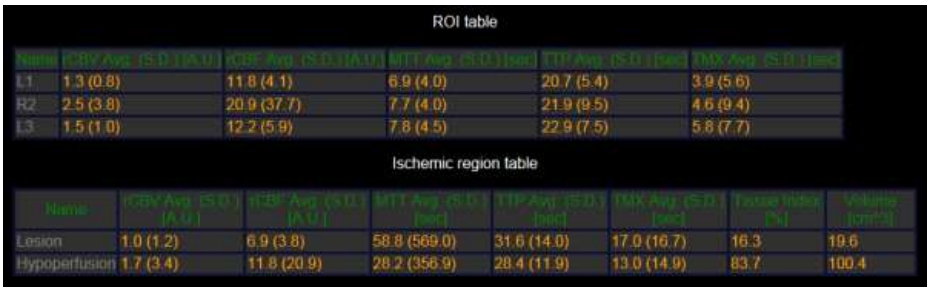
Perfusion Tables

In addition to the perfusion color maps, the calculated values of the perfusion parameters are presented in two tables:

- Ischemic region table—Presents the parameter values in the ischemic areas. The table presents values only if a damaged side is selected (either automatically by the software or manually by the user). If the damaged side is not selected automatically, a message is displayed notifying you that no damaged side was detected.
- ROI table—Presents the parameter values in any ROI you draw. The table is empty until you draw an ROI.

In addition to rCBV, rCBF, MTT, TTP and TMAX, the tables also present the following values in the Ischemic region table:

- Tissue Index—The percentage of Lesion tissue volume and of Hypoperfusion tissue volume out of the entire ischemic region.
- Volume—The volume in cc of the tissue.


ROI table

Name	rCBV Avg (S.D.) [A.U.]	rCBF Avg (S.D.) [A.U.]	MTT Avg (S.D.) [sec]	TTP Avg (S.D.) [sec]	TMX Avg (S.D.) [sec]
L1	1.3 (0.8)	11.8 (4.1)	6.9 (4.0)	20.7 (5.4)	3.9 (5.6)
R2	2.5 (3.8)	20.9 (37.7)	7.7 (4.0)	21.9 (9.5)	4.6 (9.4)
L3	1.5 (1.0)	12.2 (5.9)	7.8 (4.5)	22.9 (7.5)	5.8 (7.7)

Ischemic region table

Name	rCBV Avg (S.D.) [A.U.]	rCBF Avg (S.D.) [A.U.]	MTT Avg (S.D.) [sec]	TTP Avg (S.D.) [sec]	TMX Avg (S.D.) [sec]	Tissue Index [%]	Volume [cm^3]
Lesion	1.0 (1.2)	6.9 (3.8)	58.8 (569.0)	31.6 (14.0)	17.0 (16.7)	16.3	19.6
Hypoperfusion	1.7 (3.4)	11.8 (20.9)	28.2 (356.9)	28.4 (11.9)	13.0 (14.9)	83.7	100.4

TMIP Series

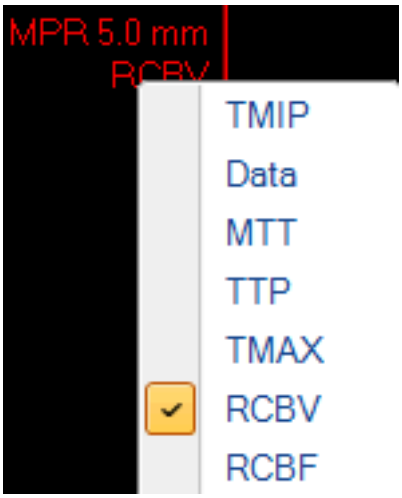
The screen displays the same TMIP series that was displayed in the initial layout with the addition of a color-based segmentation of the Lesion and Hypoperfusion areas. This segmentation is based on thresholds determined for some of the map values.

Determining the Display

You can determine the order of the displayed maps.

Right-click the **Change Data** annotation and click the map you want displayed in each of the display areas.

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Selecting the Damaged Side

Click the drop-down menu of the **Select Damaged Brain Side** icon  to select the damaged hemisphere. Use this tool when you want to override the application's identification of the damaged side or when no damaged hemisphere was detected by the application (in which case a message is displayed informing you that a damaged brain side was not found). The Lesion and Hypoperfusion tissue is segmented and displayed on the side that is indicated as the damaged side.

Adding an ROI

You can add an ROI on any of the maps to further investigate the perfusion parameters in specific areas.

To draw an ROI:

1. Click **Symmetric Operation Toggle**  in the **Perfusion** ribbon if you want the application to duplicate the ROI you draw on the contralateral side.

   NOTICE! You can break the symmetry later by right-clicking one of the ROIs and clicking Detach from Symmetric ROI.

2. Click **Add ROI** .

   ⇨ The cursor changes to .

3. Click the image at the intended place of the ROI and then drag the mouse to draw the ellipse.

   NOTICE! Contact the system administrator for configuration of whether the initial click on the image marks the center of the ROI or a point on its perimeter.

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4. Click to complete the drawing.

The calculated values of the ROI are presented in the ROI table.

Managing Graphic Elements

You can move, copy, delete and determine the graphic properties of any artery, vein, or ROI.

- To move the graphic, drag it to the desired place on the image.
- To copy the graphic, hover over the graphic and when the cursor changes to a 4-arrow cursor, select **Copy** from the right-click menu.
- To delete the graphic, hover over the graphic and when the cursor changes to a 4-arrow cursor, select **Delete** from the right-click menu.
- To change the color and font of the graphic –
  - Hover over the graphic and when the cursor changes to a 4-arrow cursor, select **Properties** from the right-click menu.
  - Select a font and color.



Showing or Hiding Graphic Elements

Click the drop-down menu of the **Hide/Show**  icon to show or hide the segmentation of the ischemic region on the TMIP images (**Show/Hide Ischemic Regions** option), or to hide all graphic elements (**Hide All Graphics** option).

Resetting All Calculations

Click **Reset All Calculations**  to discard all ROIs, tissues, maps, and AIF and VOF corrections and revert to the initial stage at the time of loading.

13.19.9 Selecting a Layout

When the Perfusion application is launched, the Application Layout drop-down in the Layout ribbon lists perfusion-specific layouts.

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For the input display, the menu lists by default a single layout. The layout is adjusted to landscape monitors and to portrait monitors.





For the map display, the menu offers you by default two possible layout types:

- A map-specific layout adjusted to landscape monitors and to portrait monitors.
- A layout for fused images (See Section Displaying a Fused Image on page 407).



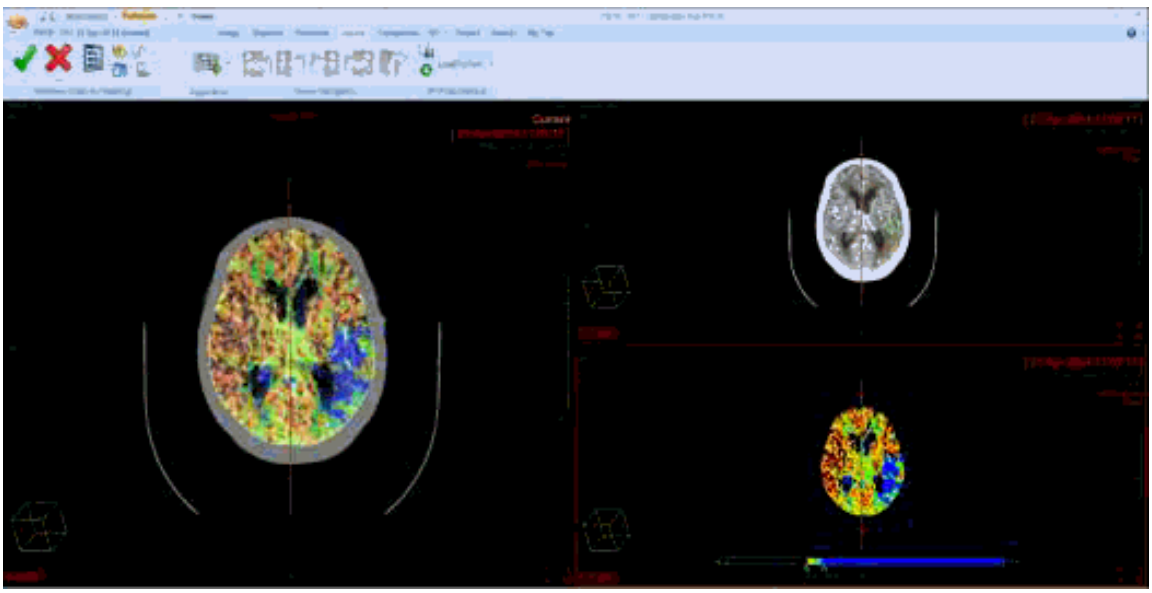


NOTICE! Other layouts can be defined. Contact your system administrator.

13.19.10 Displaying a Fused Image

You can display a fused layout, where the TMIP image and a map image (or two map images) are fused on a single image.

To display a fused image, select **Perfusion Maps** - Fusion from the **Application Layout** drop-down of the **Layout** ribbon.



13.19.11 Determining Perfusion Settings

The **Perfusion Settings** window allows you to change parameters related to the perfusion algorithm, map parameters, clinical parameters, input state, ischemic regions, and tables.

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To change parameters, click **Settings**  in the **Perfusion** ribbon. Use the **Perfusion Settings** window to make your adjustments. You can change the following settings:

Algorithm-Related Settings

Setting	Description
Deconvolution Algorithm	Select a deconvolution algorithm: • **sSVD**—Standard Singular Value Decomposition. • **cSVD**—Circular Singular Value Decomposition. An sSVD algorithm with a circular time curve. This method is stable with respect to delays in the contrast material in the arterial input. • **oSVD**—Oscillating index Singular Value Decomposition. An iterative cSVD method which reduces the Oscillating Index (OI).
sSVD Advanced Settings	Set regularization type and fraction for sSVD. Regularization Type: • **SV cutoff**—Set to zero all Singular Values (SV) smaller than the cutoff value. • **Tikhonov**—Set a threshold for applying the Tikhonov regularization method. Regularization Fraction: Set the fraction of the highest Singular Value (SV) to determine the regularization threshold.
cSVD Advanced Settings	Set regularization type and fraction for cSVD. Regularization Type: • **SV cutoff**—Set to zero all SVs smaller than the cutoff value. • **Tikhonov**—Set a threshold for applying the Tikhonov regularization method. Regularization Fraction: Set the fraction of the highest SV to determine the regularization threshold.
oSVD Advanced Settings	Set a regularization threshold for oSVD. The oSVD method always uses a Wiener filter iteratively until the Oscillating Index (OI) reaches a value lower than the regularization value.

Map-Related Settings

Setting	Description

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rCBV Parameters	Set rCBV parameters. • **Default windowing**—The default windowing range for rCBV maps. • **Acceptance Criteria**—When enabled, only values within the set range are used in the ROI statistics and the segmentation of the ischemic region.
rCBF Parameters	Set rCBF parameters. • **Default windowing**—The default windowing range for rCBF maps. • **Acceptance Criteria**—When enabled, only values within the set range are used in the ROI statistics and the segmentation of the ischemic region.
MTT Parameters	Set MTT parameters. • **Default windowing**—The default windowing range for MTT maps. • **Acceptance Criteria**—When enabled, only values within the set range are used in the ROI statistics and the segmentation of the ischemic region.
TTP Parameters	Set TTP parameters. • **Default windowing**—The default windowing range for TTP maps. • **Acceptance Criteria**—When enabled, only values within the set range are used in the ROI statistics and the segmentation of the ischemic region.
TMAX Parameters	Set TMAX parameters. • **Default windowing**—The default windowing range for TMAX maps. • **Acceptance Criteria**—When enabled, only values within the set range are used in the ROI statistics and the segmentation of the ischemic region.
Ventricle Removal	Disable Ventricle Removal. This setting is enabled by default to allow automatic removal of the ventricles from the maps, ROI statistics and segmentation of the ischemic region. Disable in cases when parts of the brain are mistakenly removed by the ventricle-detection algorithm.

Hematocrit Settings

Setting	Description
Hematocrit	Set the hematocrit values. The ratio between the large and small vessel hematocrit values affects the scaling in the rCBV and rCBF maps.

Input State Settings

Setting	Description

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AIF Candidates Settings	Set the number of automatically detected AIF candidates.
Preprocessing Settings	Enable to preprocess images for noise reduction.

Lesion/Hypoperfusion Settings

Setting	Description
Lesion/Hypoperfusion Morphology Parameters	Set Lesion/Hypoperfusion morphology parameters. • **Consolidate regions (distance)**—Regions separated by a distance smaller than the set value are merged. • **Remove narrow regions**—Regions narrower than the set value are removed. • **Remove small volume regions**—Regions with a volume smaller than the set value are discarded. Use the slider to change the values. The changes are shown immediately on the maps. Morphology calculations are applied in the following order: consolidation of regions, removal of narrow regions and removal of small volumes.
Lesion Threshold Criteria	Set Lesion threshold criteria. Use the drop-down menus to define criteria for the maps. Click **Add** to add the criterion to the criteria list. Click Add to add the criterion to the criteria list. Note that acceptance criteria are applied as well when enabled. Criteria types include: • **Absolute**—The criterion is applied to the actual value. • **Relative**—The criterion is applied to the relative value of the damaged side divided by the opposite side. • **Difference**—The criterion is applied to the relative value of the damaged side minus the opposite side.
Hypoperfusion Threshold Criteria	Set Hypoperfusion threshold criteria: Use the drop-down menus to define criteria for the maps. Click **Add** to add the criterion to the criteria list. A voxel is considered Hypoperfusion if it meets all criteria. Note that acceptance criteria are applied as well when enabled. Criteria types include: • **Absolute**—The criterion is applied to the actual value. • **Relative**—The criterion is applied to the relative value of the damaged side divided by the opposite side. • **Difference**—The criterion is applied to the relative value of the damaged side minus the opposite side.

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Table Settings

Setting	Description
Show Standard Deviation	Enable to show standard deviation values in the ROI and Lesion/Hypoperfusion measurement tables. The changes are shown immediately in the tables.

Default Settings

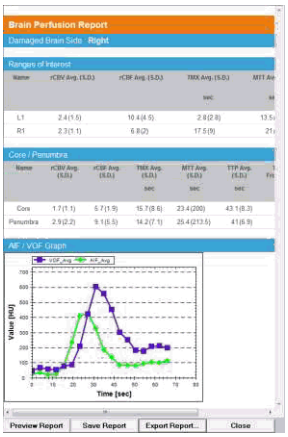
Setting	Description
Save Current Settings as User Defaults	Save to use settings as default.
Restore System Settings	Restore system defaults.

13.19.12 Opening a Report

Click **Reporting**  in the **Perfusion** ribbon to display a perfusion report. The report shows the content of the perfusion tables and graph.

NOTICE! Only the average curves are included in the report graph.

- Click **Preview Report** to display a version of the report that contains the patient details, including patient name, report date, patient ID, accession number, birth date, referring physician, report date, report status and study reason.
- Click **Save Report** to save the report as a Structured Report (SR). The report can then be opened from the Archive Explorer.
- Click **Export Report** to export the report to an MHTML, CSV or Plain Text format.



13.19.13 Exporting the Perfusion Analysis

Click **Export Perfusion Analysis**  in the toolbar to export the calculated maps and TMIP images, including the ischemic regions segmentation, the center line indication and the added ROIs. The maps are exported in their original plane. The exported images are saved with the study, with each map constituting a separate series.

NOTICE! The exported series cannot be reloaded to the Perfusion application.

13.19.14 Accuracy and Limitations

- Image quality—The calculation of perfusion parameters is limited by the scan quality. Excessive noise, patient movement or image artifacts in the original images will ultimately have an impact on the perfusion analysis and the calculated maps. The user should inspect original data and verify that the images are of diagnostic quality and that any patient movement has been corrected using the motion correction algorithm. If image artifacts are present in the original images, the same areas on the maps may not contain valid values.
- Relative units—Some of the values are quoted in relative values (rCBV, rCBF). As such, the values extracted from these maps are valid up to arbitrary constants and therefore should not be confused with absolute measurements. Moreover, the units of these relative values are not normally associated with CBV or CBF measurements.
- Accuracy of values— In places where the standard deviation is given along with the average value, the user is encouraged to examine these values. A large standard deviation compared with acceptable values may indicate noise or artifact in the images.
- Temporal resolution—Preferably, the temporal resolution should not be lower than the resolution of one image per 4 seconds. In general, the better the resolution, the more accurate the deconvolution algorithm.
- Contrast material—The scan duration should allow the contrast material to wash into the different tissues and then wash out of the tissues, with a possible recirculation. This can be verified by visually inspecting the raw images.
- AIF—The CT perfusion application assumes that the AIF describes a well-defined signal originating in the contrast agent injection. The signal should start from a baseline value, climb to a maximum value and show a gradual drop to low values, possibly showing recirculation effects. It is the user's responsibility to review the AIF graph and ascertain that a correct AIF signal is used.
- Spatial resolution—The resolution does not affect the deconvolution algorithm itself. However, a low spatial resolution might introduce partial volume effects. The user is advised to view the TMIP image to assess partial volume effects.
- Scan duration—The scan duration should allow the contrast material to pass through the arteries, into the tissue and out of the veins in order to correctly assess the perfusion parameters. Therefore the user should examine both AIF and VOF and verify that both exhibit a rise and fall of the contrast material.

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13.20 MR Diffusion and MR Perfusion

13.20.1 MR Perfusion

MR Perfusion is a clinical tool for evaluating diffusion parameters related to water flow and perfusion parameters related to blood flow and blood volume in the brain. These images are produced by a MR scanner after intravenous injection of contrast material. DWI MR and DTI MR series are used for calculating the rate and direction of water flow in the brain, while DSC series serve to calculate blood flow, blood volume, and permeability.

13.20.2 Overview

The MR Diffusion and MR Perfusion modules are clinical tools for evaluating water diffusion and blood perfusion parameters in the brain.

The applications use as input a collection of images produced by a Magnetic Resonance (MR) scanner. Diffusion Weighted Imaging (DWI) MR and Diffusion Tensor Imaging (DTI) MR series are used for calculating the rate and direction of water diffusion in the brain, while DSC series serve to calculate blood flow, blood volume, and permeability.

Based on the input data and on the calculation of water and blood supply parameters, the application produces maps that help diagnose the clinical question at hand.

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NOTICE

Footnotes in this section refer to the References on page 444, a detailed list of bibliographic references.

The diffusion module provides[1]:

- Automatic calculation of a brain mask.
- Ability to add or subtract mask areas manually.
- Automatic calculation of DWI maps based on input data, including:
  - ADC
  - eADC
- Automatic calculation of DTI maps based on input data, including:
  - ADC
  - eADC
  - DWI iso
  - Axial diff
  - Rad diff
  - FA
  - VR

  - FA dir
- Ability to add ROIs
- Show calculated information in tabular form

The perfusion module provides[2,3,4,5,6]:

- Automatic calculation of a brain mask
- Ability to add or subtract mask areas manually
- Ability to add or subtract segmented arteries
- Ability to add or subtract segmented veins
- Automatic calculation of the average of all potential AIF points
- Automatic calculation of the average of all potential VOF points
- Automatic calculation of the brain symmetry plane
- Automatic motion correction
- Automatic calculation of DSC perfusion maps based on input data, including:
  - rCBV
  - rCBF
  - TTP
  - MTT
  - TMAX
- Calculation of a k2 permeability map
- Corrected maps based on the k2 maps

For further details on the diffusion and perfusion maps, see Section Viewing Diffusion Series and Section Working with Perfusion Maps.

- Ability to add ROIs.
- Automatic selection of the affected hemisphere of the brain.
- Segmentation of two ischemic regions marked as Lesion and Hypoperfusion. The segmentation of each region is based on thresholds and parameters configurable by the user.
- Show calculated information in tabular form

NOTICE! The values for blood volume and blood flow are shown in relative units up to an arbitrary multiplicative constant. Relative units are used because partial volume effects and other measurement limitations prevent absolute quantification.

13.20.3 Application Workflow

An MR study may include diffusion series, perfusion series, or both diffusion and perfusion series.

For the diffusion series, the following steps are performed:

1. Automatic calculation of the brain mask—Executed automatically by the application while allowing manual corrections by the user.

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2. Displaying of the original image data and calculated maps—executed automatically by the application.

   For DWI series—ADC and eADC maps + the original data.

   For DTI series—ADC, eADC, DWI, Ax diff, Rad diff, FA, VR, and FA dir maps + the original data.

3. Calculation of diffusion parameters for ROIs drawn manually by the operator. These measurements are displayed in a table.

For the perfusion series, the application segments the arteries and veins in order to calculate AIF and VOF signals, identifies the brain centerline, and marks the results on a standard Temporal Minimum Intensity Projection (TMIN) series.

Based on this data, the user can initiate the perfusion calculations, the results of which are displayed in a set of maps. Measurements of parameters for specific Regions of Interest (ROIs) are presented in tables.

Finally, a segmentation of the Lesion and Hypoperfusion areas is marked on the TMIN image.

A typical workflow includes the following automatic and manual steps:

1. Loading of the study to the MR Perfusion application—executed by the user.
2. AIF Indication—Executed automatically by the application while allowing manual corrections by the user.
3. VOF Indication—Executed automatically by the application while allowing manual corrections by the user.
4. Identification of the brain center line—Executed automatically by the application while allowing manual corrections by the user (calculated and shown already for the diffusion series).
5. Identification of the brain center line—Executed automatically by the application while allowing manual corrections by the user (calculated and shown already for the diffusion series).
6. Automatic calculation of a TMIN series.
7. Motion correction.
8. Calculation of the perfusion parameters—rCBV, rCBF, TTP, MTT, TMAX and k2.

   The parameters are calculated automatically by the application and displayed as a set of perfusion maps.

9. Measurement of the above parameters for ROIs drawn manually by the operator. These measurements are displayed in a table.
10. Segmentation of two ischemic regions marked as Lesion and Hypoperfusion. The segmentation of each region is based on thresholds and parameters configurable by the user (see Section Using Settings on page 437).

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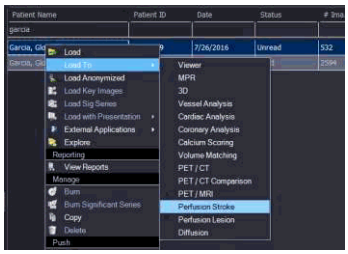
13.20.4 Loading the Study

To load an MR perfusion study –

1. In the Diagnostic Workstation, highlight the study in the Archive Explorer.

2. Select one of the following from the right-click menu:

   – **Load To > Perfusion Stroke**

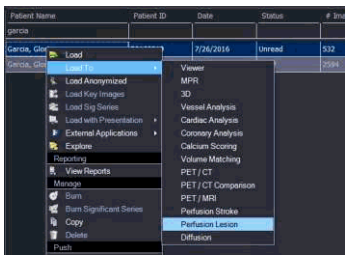
   

   The “Perfusion Stroke” application is the main Perfusion application, which calculates the Core & Penumbra, and compares the two brain sides.

   This application is applicable for Perfusion studies of any modality (CT or MR).

   – **Load To > Perfusion Lesion**

   (Only applicable for MR Perfusion studies)

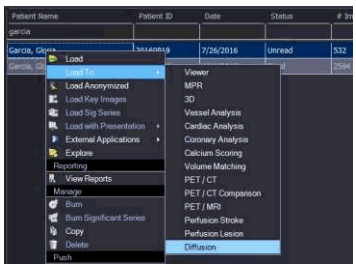
   

   The “Perfusion Lesion” application is intended to measure brain lesions. It does not calculate the Core/Penumbra and the brain center-line is not shown.

   This application is applicable only for MR Perfusion studies.

   – **Load To > Perfusion Lesion**

   (Applicable for any study containing Diffusion groups)

   The “Diffusion” application is intended for any study that contains a Diffusion group, and it loads that group only. Furthermore, only Diffusion maps will be calculated.

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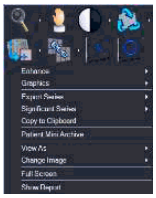
13.20.5 Initial Display

Initial Display

When the study loads, the screen displays the perfusion and/or diffusion data (depending on whether the study contains perfusion series only, diffusion series only, or diffusion and perfusion series) as well as a ribbon with tools to help you control the workflow and add manual calculations.

Basic Image Manipulation

Right-click anywhere in the image display area to select image manipulation activities, such as windowing, zooming, panning, and others. For a description of all image manipulation tools available in the Vue PACS application, see the Vue PACS help.



Use the mouse wheel to scroll through the series images.

Tool Ribbon



#	Description
1	Initiating Map Calculation on page 430—Click to progress to the next step.
2	Initiating Map Calculation on page 430—Select the next step. Steps include display of perfusion input data and display of perfusion maps.
3	Calculate Perfusion Maps (see Initiating Map Calculation on page 430)—Click to initiate the calculation of perfusion maps (perfusion series only).
4	Adding Arteries and Veins on page 427—Click to manually add an artery (perfusion series, in seed mode only).
5	Add New Vein—Click to manually add a vein (perfusion series, in seed mode only).
6	Motion Correction (see Adding Arteries and Veins on page 427)—Click to correct the effect of patient movement (perfusion series only).
7	Selecting the Damaged Side on page 405—Specify the damaged brain side to indicate the side on which the hypoperfusion is assessed and segmented by the application (perfusion series only).

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8	Symmetric Operation Toggle (see Adding an ROI on page 405)—Click to have the application automatically draw an ROI on the contralateral side when you draw an ROI.
9	Showing and Hiding Graphic Elements on page 436—Use the drop-down menu to hide the ischemic regions or to hide all graphics (perfusion series only).
10	Adding an ROI on page 423—Click to manually draw an ROI.
11	Resetting All Calculations on page 406—Delete all ROIs, tissues, maps, AIF and VOF corrections.
12	Settings (see Using Settings on page 437)—Adjust settings related to the algorithm, maps, clinical parameters, input state, ischemic regions, and tables.
13	Opening a Report on page 411—Opens an automatically generated report containing all the measurements and graphs performed by the user.
14	Show/Hide Brain Mask (see Using the Brain Mask Correction Tool on page 429)—Show/hide brain mask. You can also add brain mask manually as well as erase added brain mask coloring.
15	Show/Hide AIF Segmentation (see Displaying Artery and Vein Segmentations on page 428)—Show/hide automatically segmented arteries. You can also add segmentations manually as well as erase the added segmentations (perfusion series only).
16	Show/Hide VOF Segmentation (see Displaying Artery and Vein Segmentations on page 428)— Show/hide automatically segmented veins. You can also add segmentations manually as well as erase the added segmentations (perfusion series only).
17	Exporting the Perfusion Analysis on page 443—Export the calculated maps and TMIN images to the study.

13.20.6 Viewing Diffusion Series

Viewing Diffusion Series

The system calculates water diffusivity and displays a set of maps summarizing the calculated values.

The windowing menu, displayed by right-clicking the windowing annotation, allows you to apply various maps and change the windowing scale to minimum and maximum values.

Use the windowing menu to display values that are beyond the values of the bar. In such cases, the value displayed on the color bar is marked with an asterisk.

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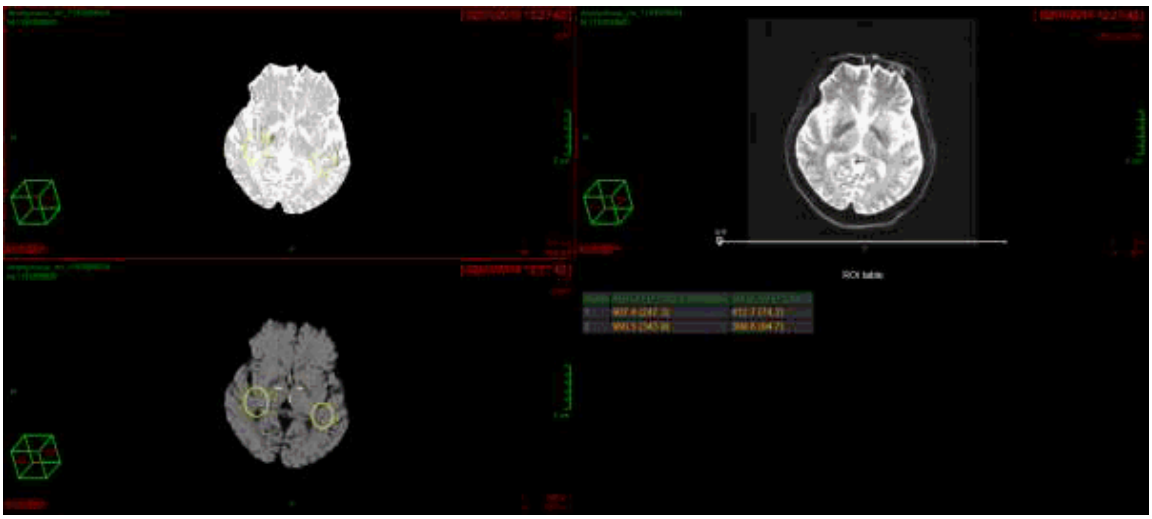
DWI Images

The DWI scan is isotropic and measures the diffusivity in different magnetic field gradients (characterized by different b values).

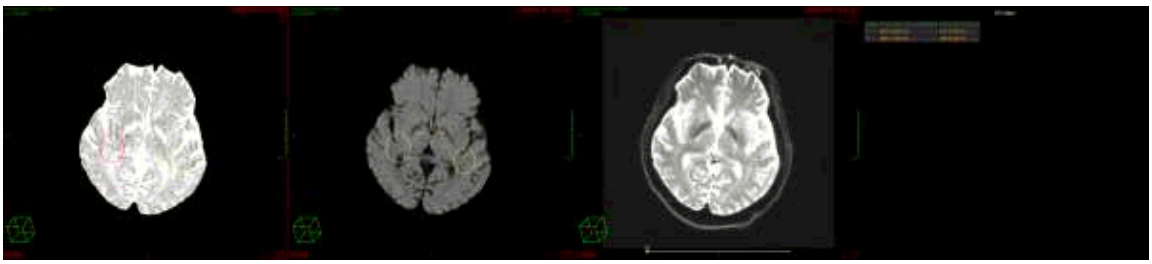
The layout includes:

- The data of the original series with a b-value slider
- Calculated maps

The following illustrations show the initial layout on landscape and portrait monitors.



If you are working with two monitors side by side, you can use a dual-monitor layout. Click **Toggle Dual Monitor**  in the **Layout** ribbon. The display is adapted to the dual-monitor environment.



The slider at the bottom of the original series represents values of gradient factor b (sec/mm2). Use the slider to show the data at the different b-values.



Maps

The following maps are shown:

- ADC—Displays the apparent diffusion coefficient of water molecules calculated based on the different gradient images.
- eADC—Reverses the colors of the ADC map. Because the contrast in the ADC map is the reverse of regular T2 images, the system generates the eADC map based on the formula exp(-b*ADC), b being a configurable constant (1000 by default). This map has a similar contrast to that of regular T2 scans, and reflects the diffusion coefficient ADC.
- DWI iso—Isotropic map that multiplies the eADC by the T2 image (b=0).

Table

If you add an ROI, a table presenting the calculated values in the ROI is displayed on screen.

DTI Images

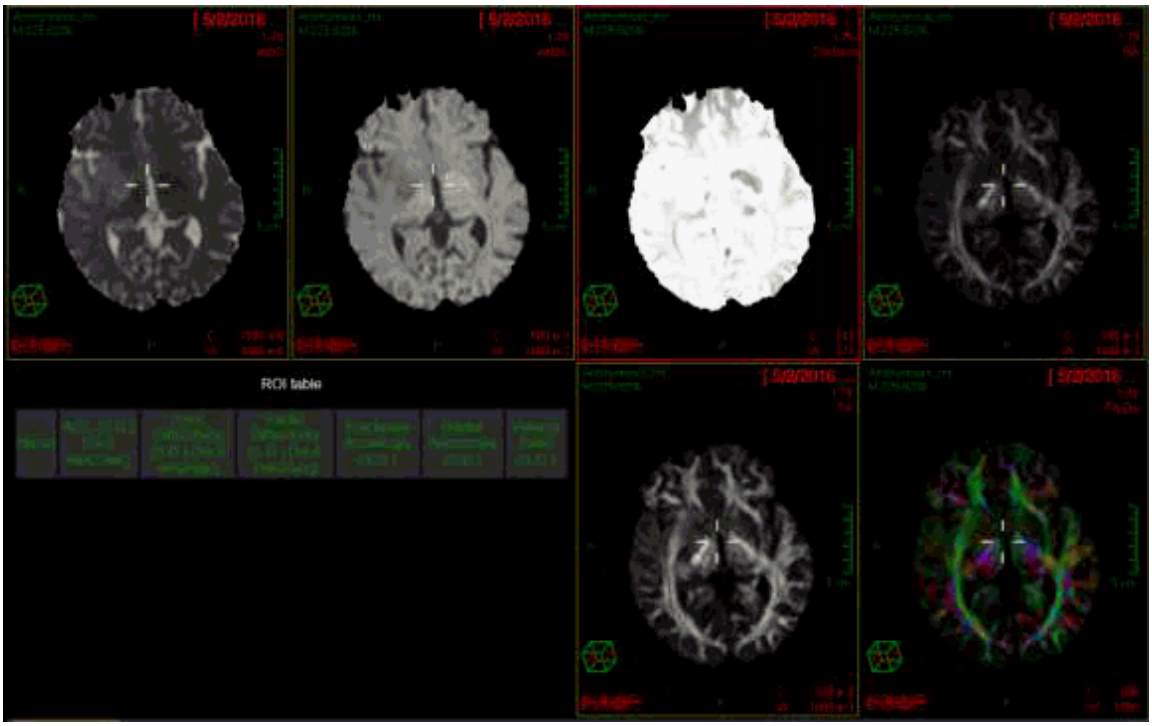
The DTI scan is performed in multiple directions as well as in several gradients (b values). The scan serves to measure the diffusivity in the various directions and to help draw anatomic conclusion based on these measurements[1].

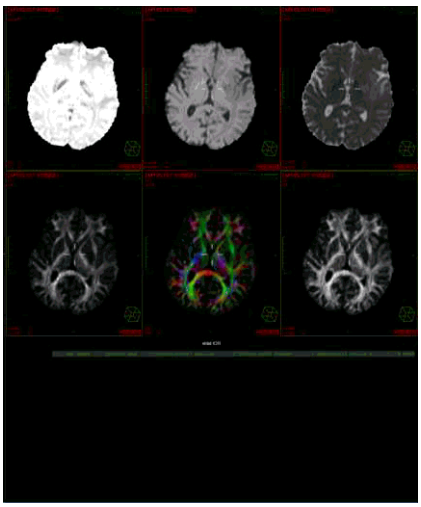
The layout presents the calculated maps.

The following illustrations show the initial layout on landscape and portrait monitors.

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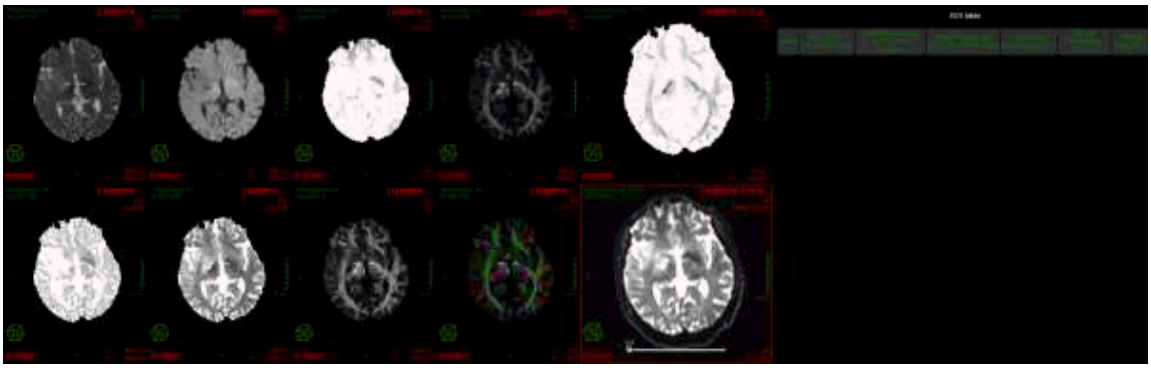
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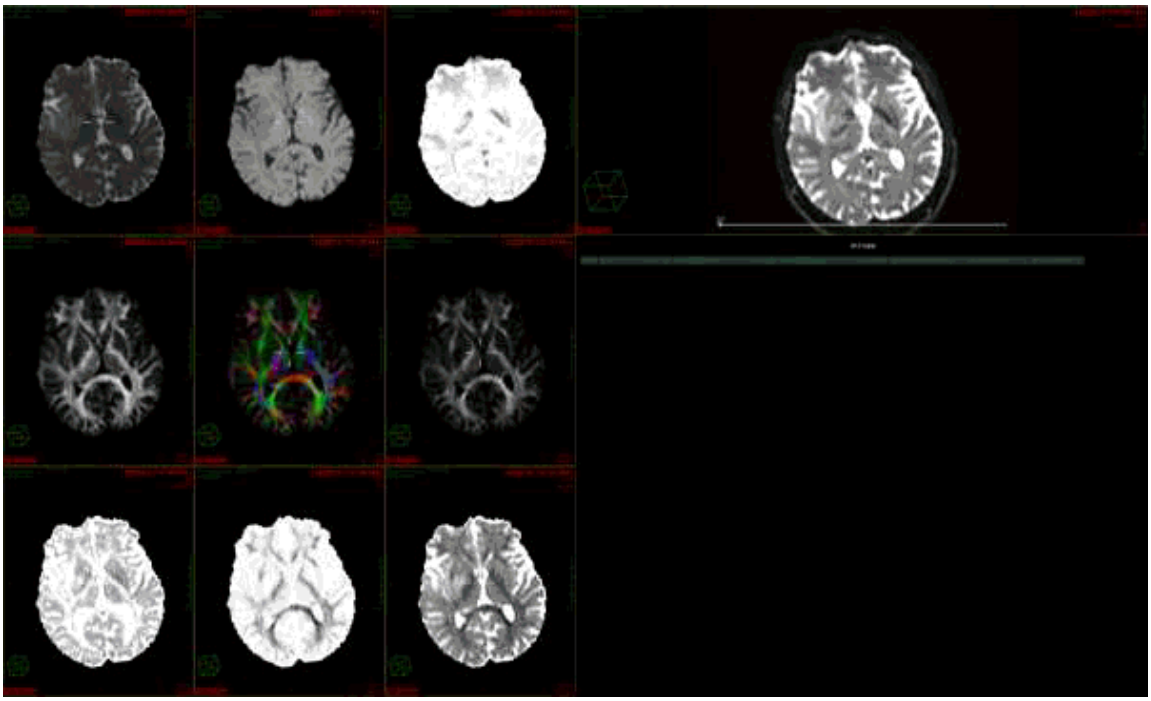




If you are working with two monitors side by side, you can use a dual-monitor layout. Click **Toggle Dual Monitor**  in the **Layout** ribbon. The display is adapted to the dual-monitor environment. Note that the dual-monitor display shows more maps than the single-monitor display. The following illustrations show the dual-monitor layout on landscape and portrait monitors.

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To change the maps that are displayed by default, right-click the map name and change the display (see Section Determining the Display on page 424).The values annotated on the slider at the bottom of the original series signify b values (sec /mm2).



By default, the data of the original series and the slider are not displayed in the single-monitor display. To display this series, right-click the map name and change the display (see Section Determining the Display on page 424).

Maps

Based on the various diffusivity measures, the system generates a diffusion tensor and calculates the tensor's eigenvalues λ1, λ 2, λ 3 (λ 1 > λ 2 > λ 3) and eigenvectors V1, V2, V3 respectively.

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The following maps are shown:

Maps reflecting isotropic diffusivity[1]:

- ADC—Simulates the isotropic scan and is equal to the average of the eigenvalues (λ1+λ2+λ3)/3.
- eADC—Calculated by exp(-b*ADC) for a prefixed b value.
- DWI—Isotropic map that multiplies the eADC by the T2 image (b=0) or by a T2 extrapolation (in cases when there is no b=0 image or when there are several such images).

Maps reflecting anisotropic diffusivity[1]:

- Ax diff—The largest eigenvalue (λ1)
- Rad diff—The average of the two smaller eigenvalues (λ2+λ3))/2
- FA—Measures the difference between the isotropic diffusion measurement and the directional measurement.
- RA—Measures the ratio of the isotropic diffusion measurement to the directional measurement.
- FA dir—A color map, showing the color coding of the main direction of diffusivity (V1) relative to the main axes X, Y, Z. Red indicates the main direction X, green indicates the main direction Y, and blue indicates the main direction Z. At each point, the displayed color may be either a mixture of red, green, and blue, based on the diffusion component, or only red, only green, or only blue, based on the component of the maximal value. The system may be configured to display the colors by one of these coloring options. Contact your system administrator to change the coloring option.

Table

If you add an ROI, a table presenting the calculated values in the ROI is displayed on screen.

Adding an ROI

You can add an ROI on any of the maps to further investigate the diffusion parameters in specific areas. To draw an ROI:

1. Click Add ROI .

   ⇨ The cursor changes to .
2. Click the image at the intended place of the ROI and then drag the mouse to draw the ellipse.

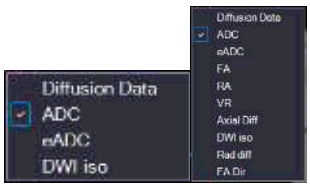
   NOTICE! Contact the system administrator for configuration of whether the initial click on the image marks the center of the ROI or a point on its perimeter.
3. Click to complete the drawing.

   ⇨ The calculated values of the ROI are presented in the ROI table.

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Determining the Display

To change the initial map display, right-click the map name annotation in each display area and select a map from the list of calculated maps.



13.20.7 Perfusion Series

Perfusion Series

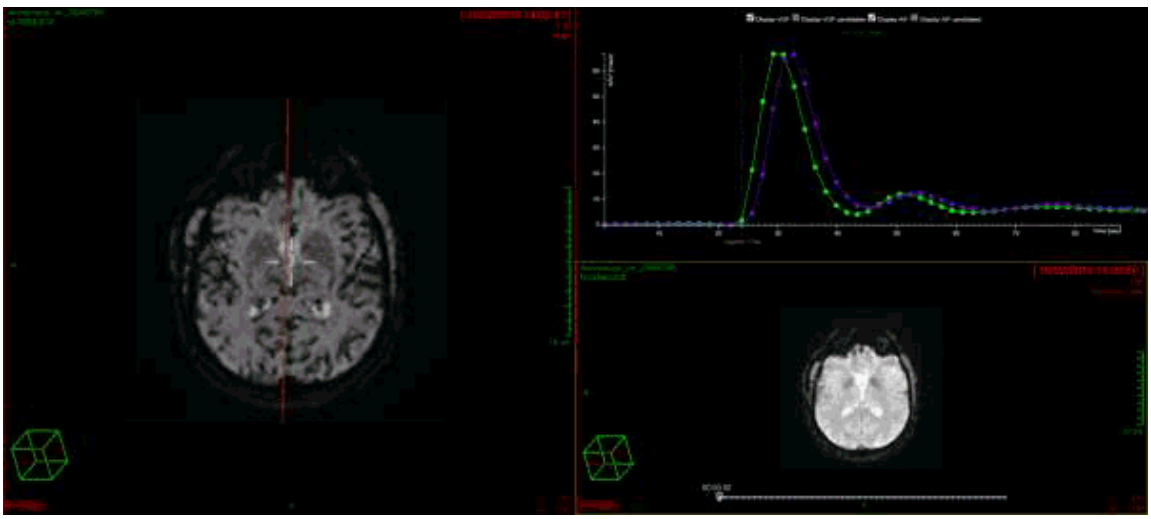
When a perfusion series is loaded, the perfusion input data is displayed first, and then you continue to map calculation.

Initial Layout

The initial layout includes:

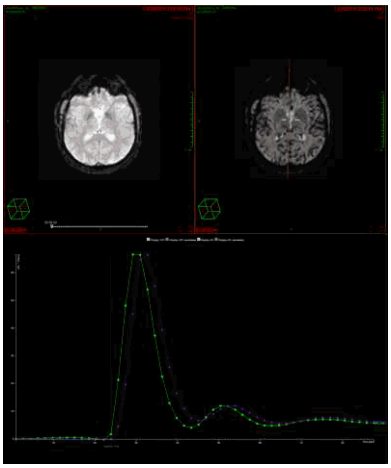
- The calculated TMIN images
- The original series data
- The AIF and VOF graph displaying seed values or segmentation averages
- A temporal slider
- A Perfusion ribbon offering tools for controlling the workflow and for adding manual calculations

The following illustrations display the initial layout on landscape and portrait monitors.



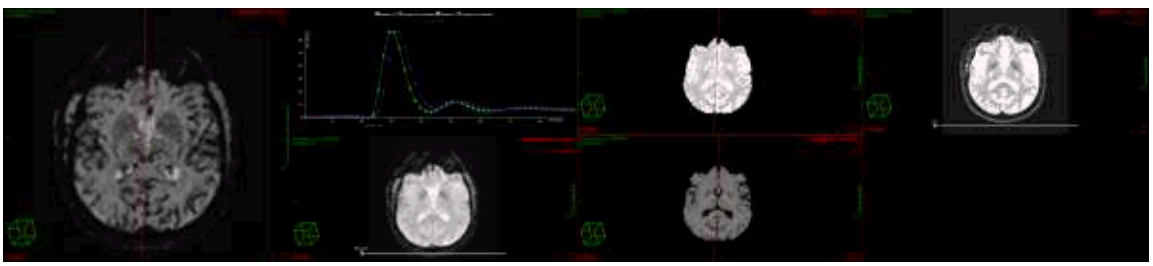
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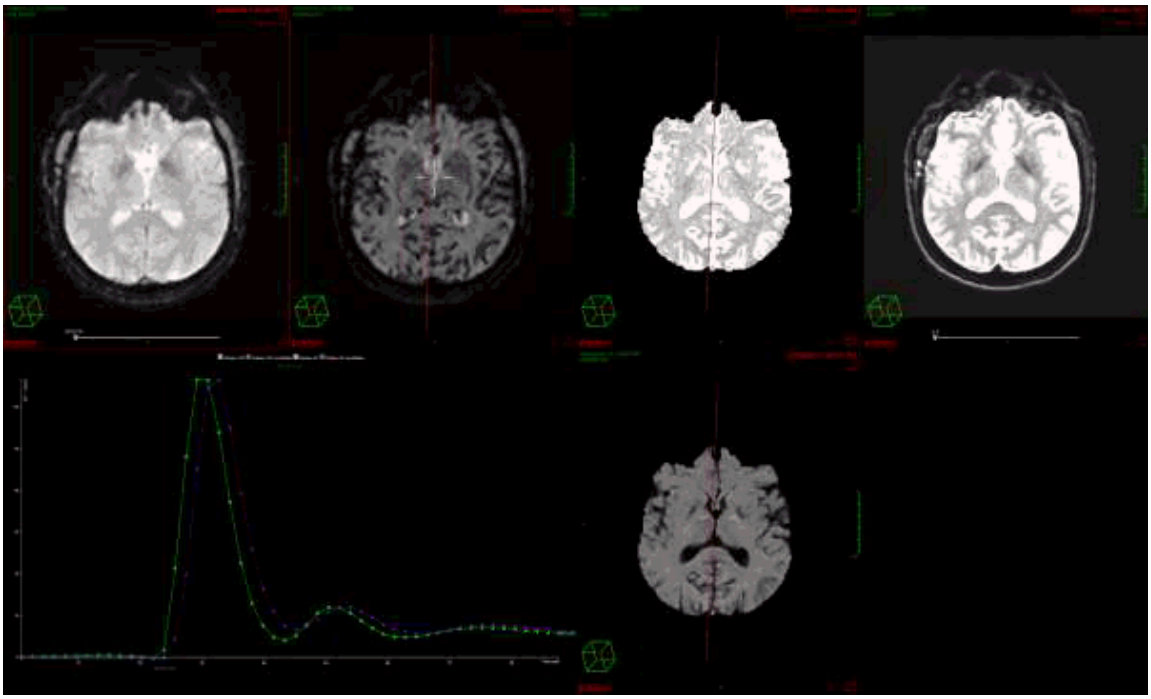


If you are working with two monitors side by side, you can use a dual-monitor layout. Click **Toggle Dual Monitor**  in the **Layout** ribbon. The display is adapted to the dual-monitor environment. Note that the dual-monitor display shows more maps than the single-monitor display. If the study includes both diffusion and perfusion series, the images of the diffusion series are displayed on the monitor on the right-hand side.

The following illustrations display the dual-monitor layout on landscape and portrait monitors.

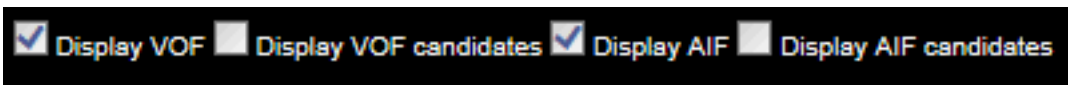


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To change the maps that are displayed by default, right-click the map name and change the display (see Section Determining the Display on page 424).

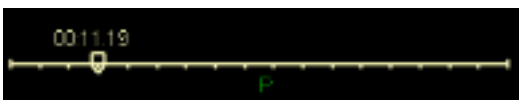
By default, the graph shows the AIF and VOF curves, representing the average values of all found arteries and veins, respectively. Alternatively, you can choose to display the curves of the default and/or additional candidate VOF and AIF points by using the check boxes at the top of the graph area (see Section Adding Arteries and Veins on page 427).



If you choose to display segmented arteries and veins rather than individual candidates (see Section Using the Artery and Vein Segmentation Tool on page 428), the graph presents the average values of all segmented vessels.

The graph also presents a horizontal dotted line signifying the baseline relaxation time and a vertical dotted line signifying the contrast material injection time.

Use the temporal slider at the bottom of the screen to view the slices throughout the scan period.



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Calculating Perfusion Input Values

Calculating Perfusion Input Values

When you initially load the study, the application automatically calculates values that serve as a basis for the perfusion calculation. You can manually correct the results to improve your reading accuracy.

Identifying the AIF and VOF

The application automatically segments arteries and veins to identify candidate AIF and VOF curves that are to be used for the analysis[5].

NOTICE! The artery and vein marks do not necessarily appear on the same slice.

The graph shows the deviation of the spin-spin relaxation rate (ΔR2) from its baseline value throughout the scan for each marked artery (Ai) and vein (Vi), as well as the average graph for the resulting AIF and VOF[2,3,4].

Adding Arteries and Veins

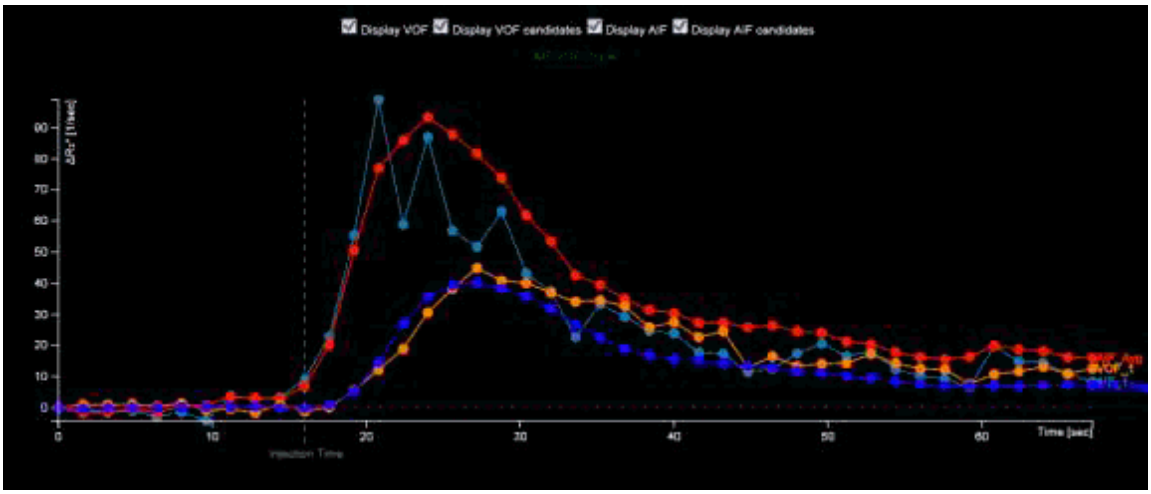
When the Vessel Signal setting is set to Seeds (See Input State Settings in Section Using Settings on page 437), you can decide to manually add arteries and veins in order to investigate the values of additional voxels.

To add an artery or a vein –

1. Click **Add Artery**  or **Add Vein**  in the Perfusion ribbon.
   ⇨ The cursor changes to .
2. On the TMIN image, click to add the artery or vein. The point is marked as A2 or v2 respectively.
   ⇨ Additional arteries and veins are marked as A3, A4 or V3, V4, and so on.
   ⇨ A curve showing the values of the newly marked voxel is added to the graph.

By default, the VOF and AIF graph displays the curve of average values. When you add arteries and veins, you can choose to display the curve for each vein, each artery and/or the average values. Each curve has a different color, and its label is displayed at the right-hand side.

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Using the Artery and Vein Segmentation Tool

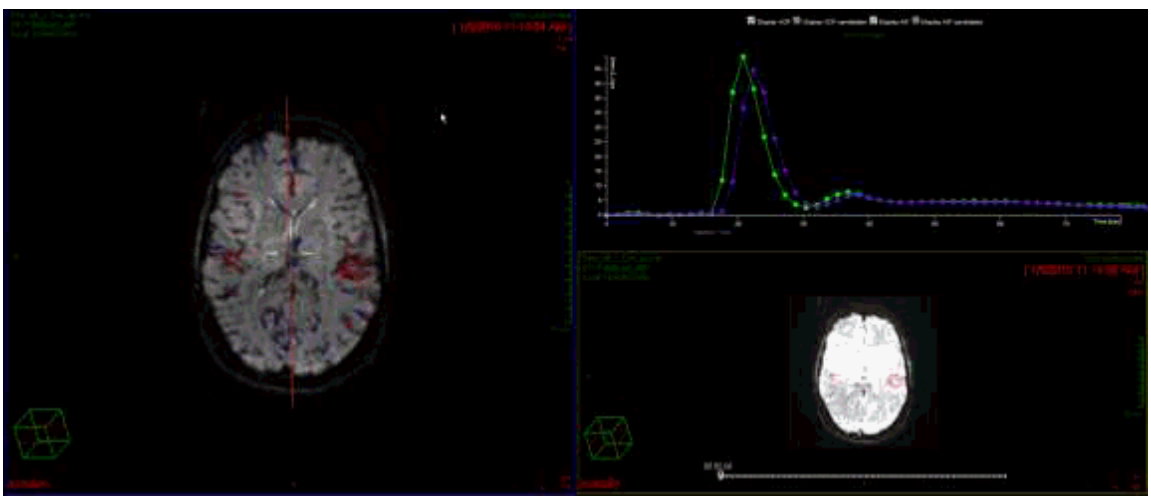
You can use the AIF and VOF Segmentation tools to display automatically segmented veins and arteries rather than display and add AIF and VOF candidate seeds. The **Show/Hide AIF Segmentation** and **Show/Hide VOF Segmentation** icons in the **Perfusion** ribbon are enabled when the **Segmentation** option is selected in the **Input State** settings (See Section Using Settings on page 437).

Displaying Artery and Vein Segmentations

To display all segmented arteries on the images, click **Show/Hide AIF Segmentation** in the **Correction Tools** section of the **Perfusion** ribbon.

To display all segmented veins on the images, click **Show/Hide VOF Segmentation** in the **Correction Tools** section of the **Perfusion** ribbon.

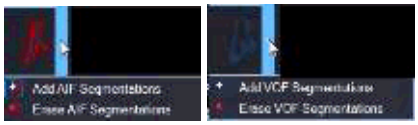
The images display all segmented arteries (red) and veins (blue), while the graph displays average values.



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Adding Artery and Vein Segmentations

1. Click Add AIF Segmentation or Add VOF Segmentation in the Show/Hide AIF Segmentation and Show/Hide VOF Segmentation drop-down menus respectively.



2. Click the left mouse button at the point where you want to start adding artery or vein segmentation in the image.
3. Drag the mouse to add artery or vein segmentation.
4. Left-click the mouse again to end the artery or vein segmentation addition.

Erasing Added Artery and Vein Segmentations

To erase added vein and artery segmentations –

1. Click **Erase AIF Segmentation** and **Erase VOF Segmentation** in the **Show/Hide AIF Segmentation** and **Show/Hide VOF Segmentation** drop-down menus, respectively.
2. Click the left mouse button at the point where you wish to start erasing.
3. Drag the mouse to erase segmentation.
4. Left-click the mouse again to end the erasing.

NOTICE! Artery and vein segmentations can be manually added in all orientations.

Using the Brain Mask Correction Tool

Using the Brain Mask Correction Tool

You can display and hide the brain mask in the displayed input images.

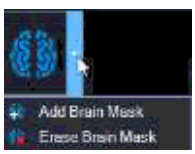
Displaying the Brain Mask

To display the brain mask, click the brain mask icon  in the **Correction Tools** section of the **Perfusion** ribbon. The brain mask is displayed both on the TMIP and the dynamic images.

Adding a Brain Mask

To manually add brain mask on the displayed image –

1. Click **Add Brain Mask** in the drop-down menu of the **Show/Hide Brain Mask** icon.



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2. Click the left mouse button at the point where you want to start adding a brain mask to the image.
3. Drag the mouse to add brain mask.
4. Left-click the mouse again to end the brain mask addition.

Erasing the Brain Mask

To erase an added brain mask marking –

1. Click **Erase Brain Mask** in the drop-down menu of the **Show/Hide Brain Mask** icon.
2. Click the left mouse button at the point where you want to start erasing the brain mask that you added manually.
3. Drag the mouse to erase the brain mask.
4. Left-click the mouse again to end the erasing.

   NOTICE! Brain mask can be manually added in all orientations.

Correcting the Brain Centerline

You can move the drawn centerline to adjust its location.

Hover with the mouse over the handle at the lower or upper part of the line. When the cursor changes to a four-arrow cursor, drag the line to its new location.

Using Motion Correction

Use the Motion Correction tool to cancel the effect of patient movement during the scan.

To correct the image, click **Motion Correction**  in the **Perfusion** ribbon.

The correction algorithm is activated and the TMIN image is recalculated.

Using the temporal slider after correction shows a smaller variance of changes in image position along the scan duration.

NOTICE! When motion correction has been carried out, the bed component in the TMIN series becomes less focused.

Click the **Motion Correction** icon again to cancel the correction calculations.

Working with Perfusion Maps

Initiating Map Calculation

When all the required data is available, the application is ready to perform the perfusion calculations and yield the perfusion maps and table data.

To initiate the perfusion calculations, do one of the following:

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- Click **Select Step** in the **Perfusion** ribbon and then click the **Display Maps** option in the drop-down menu.

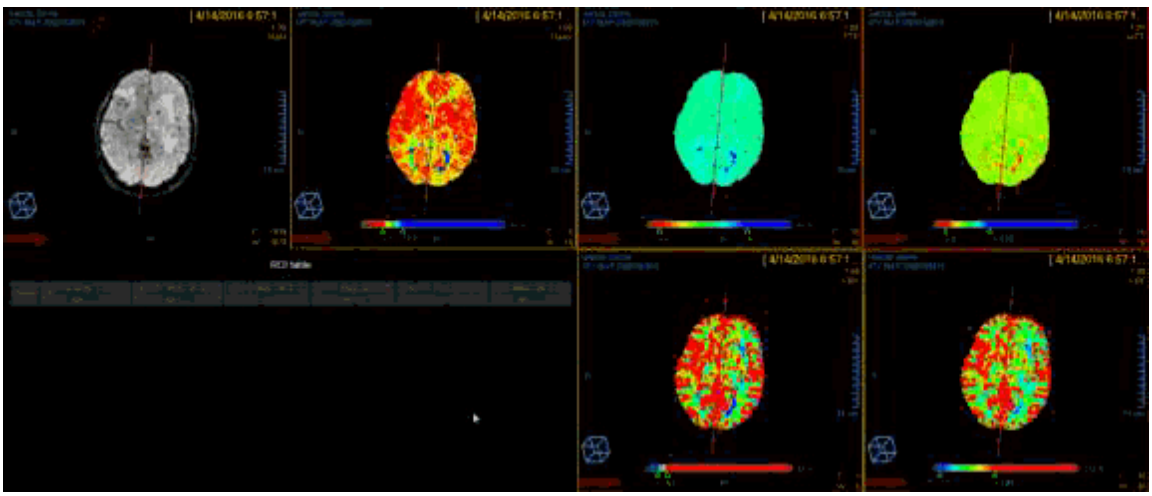


- Click **Next Step**  in the **Perfusion** ribbon.
- Click **Calculate Perfusion Maps**  in the Perfusion ribbon.

Analyzing Perfusion Calculation Results

Analyzing Perfusion Calculation Results

The system calculates all the blood perfusion parameters and displays a set of maps and tables summarizing the calculated values.



The following is displayed:

A Set of Perfusion Maps

In each of the displayed maps, a color range represents the calculated values of the perfusion parameters[2].

- rCBV map—Presents the volume of blood in a known volume of tissue, based on the concentration of contrast material present in the tissue over time. The map shows the calculated volume of blood in each voxel throughout the scan in relative units.
- rCBF map—Presents the flow of blood to the affected tissue. The map shows the calculated rate of blood flow in each voxel throughout the scan in relative units.
- MTT map—Presents the period of time during which the contrast material stays in the tissue. The map shows the mean time of blood transit through each voxel (in seconds).

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- TTP map—Presents time to maximum tissue enhancement at each volume of the tissue. The map shows the number of seconds from the scan start to the peak of tissue enhancement in each voxel.
- TMAX map—Shows the residue function time to peak in seconds.
- k2 map—Shows a measure which is proportional to the rate of contrast material permeability across the capillaries' blood-brain barrier to the extravascular extracellular space (EES). Calculation of the map values is based on the Boxerman-Weisskoff model6. (Calculated k2 values are taken into consideration in the calculation of all other perfusion maps. You can choose to exclude k2 calculations from all perfusion calculations (see Section Using Settings on page 437).

The color bar at the bottom of each map displays the minimum and maximum data values for that specific map. Two sliders represent the current windowing and allow you to change the range of displayed values.

The windowing menu, displayed by right-clicking the windowing annotation, allows you to apply various color maps and change the windowing scale to minimum and maximum values.



Changing windowing values allows you to display values that are beyond the values of the color bar. In such cases, the value displayed on the color bar is marked with an asterisk.

You can determine whether the color bar is displayed or not. Right-click the windowing annotation and click **Show Color Bar** to display the bar. If the bar is displayed, click **Show Color Bar** to remove the bar from the display.

NOTICE! The appearance of the color bar is configurable. Appearance settings include vertical versus horizontal appearance, bar size, bar position, the size of the gradient columns, the display of the minimum and maximum data values, and the display of the sliders. For configuring the color bar appearance, contact your system administrator.

Perfusion Tables

In addition to the perfusion color maps, the calculated values of the perfusion parameters are presented in two tables:

- Ischemic region table—Presents the parameter values in the ischemic areas. The table presents values only if a damaged side is selected (either automatically by the software or manually by the user). If the damaged side is not selected automatically, a message is displayed notifying you that no damaged side was detected.
- ROI table—Presents the parameter values in any ROI you draw. The table is empty until you draw an ROI.

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In addition to rCBV, rCBF, MTT, TTP and TMAX, the tables also present the following values in the Ischemic region table:

- Tissue Index—The percentage of Lesion tissue volume and of Hypoperfusion tissue volume out of the entire ischemic region.
- Volume—The volume in cc of the tissue.

ROI table

L1	5.7 (4.3)	46.0 (34.8)	7.4 (0.9)	26.7 (1.1)	1.7 (1.2)	7.9 (41.4)
R2	8.5 (5.9)	68.2 (44.4)	7.3 (0.7)	26.2 (0.5)	1.1 (0.6)	-15.8 (60.7)
L3	8.8 (11.8)	69.9 (88.3)	7.1 (1.7)	27.7 (4.4)	3.5 (9.6)	-40.4 (123.6)

Ischemic region table

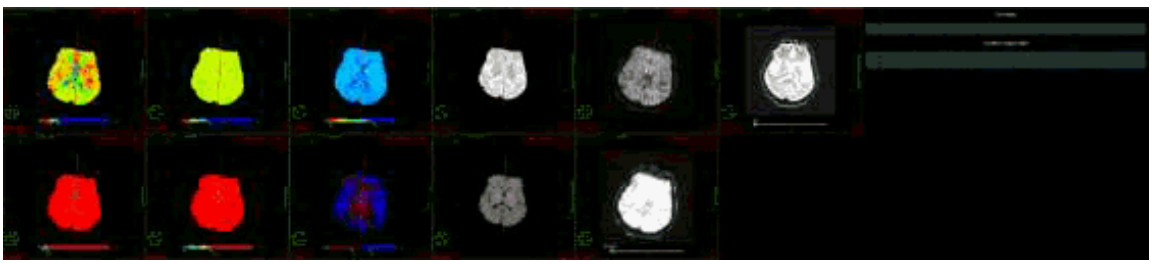
Lesion	1.5 (1.5)	16.3 (9.5)	5.0 (3.7)	30.3 (10.8)	9.7 (19.3)	12.2 (61.2)	75.4	17.8
Hypoperfusion	4.6 (12.6)	56.4 (114.4)	3.6 (4.8)	35.9 (14.5)	18.5 (25.1)	-34.9 (216.1)	24.6	5.8

TMIN Series

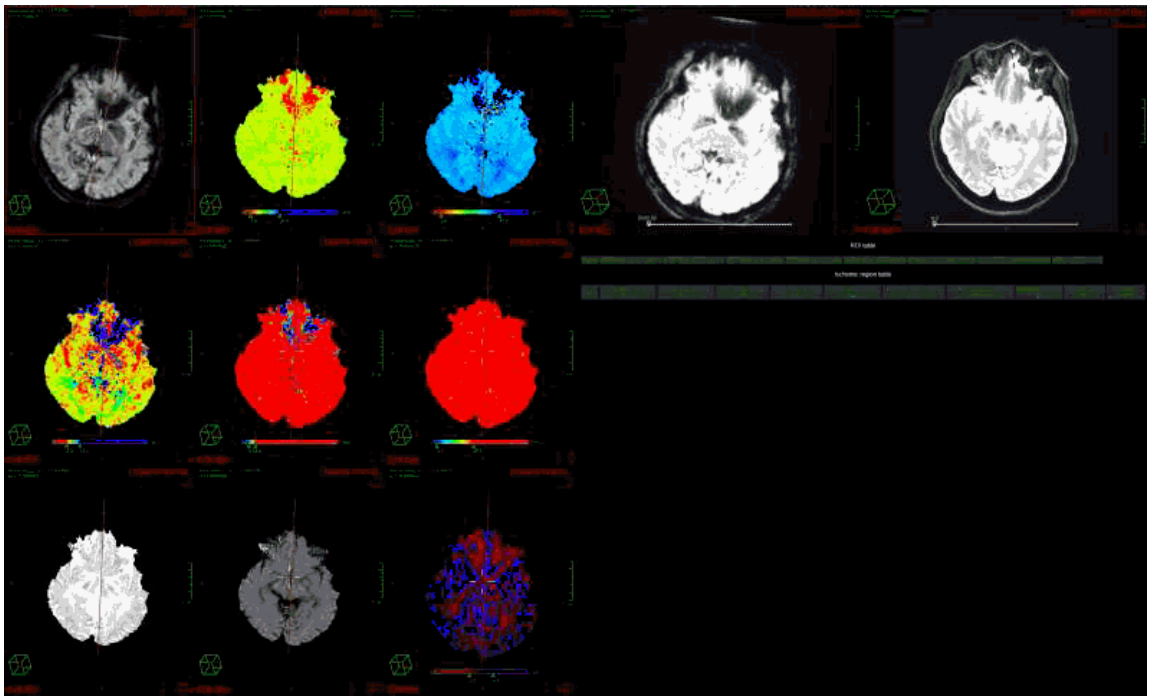
The screen displays the same TMIN series that was displayed in the initial layout with the addition of a color-based segmentation of the Lesion and Hypoperfusion areas. This segmentation is based on thresholds determined for some of the map values.

Perfusion and Diffusion Display

When the study includes both perfusion series and diffusion series, the diffusion data and maps are displayed on the right-hand screen. The following illustrations show the layout on landscape and portrait dual monitors[6].



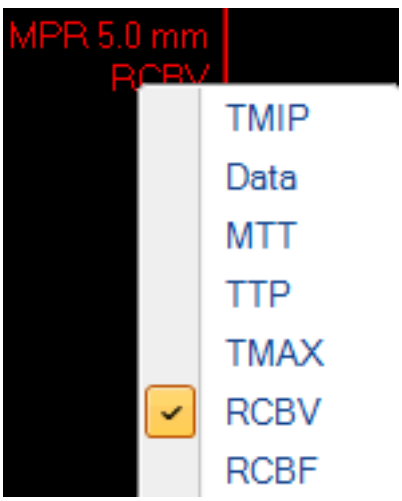
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Determining the Display

You can determine the order of the displayed maps.

Right-click the **Change Data** annotation and click the map you want displayed in each of the display areas.



Selecting the Damaged Side

Click the drop-down menu of the **Select Damaged Brain Side** icon  to select the damaged hemisphere. Use this tool when you want to override the application's identification of the damaged side or when no damaged hemisphere was detected by the application (in

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which case a message is displayed informing you that a damaged brain side was not found). The Lesion and Hypoperfusion tissue is segmented and displayed on the side that is indicated as the damaged side.

Adding an ROI

You can add an ROI on any of the maps to further investigate the perfusion parameters in specific areas.

To draw an ROI:

1. Click **Symmetric Operation Toggle**  in the Perfusion ribbon if you want the application to duplicate the ROI you draw on the contralateral side.

   NOTICE! You can break the symmetry later by right-clicking one of the ROIs and clicking Detach from Symmetric ROI.

2. Click **Add ROI** .

   ⇨ The cursor changes to .

3. Click the image at the intended place of the ROI and then drag the mouse to draw the ellipse.

   NOTICE! Contact the system administrator for configuration of whether the initial click on the image marks the center of the ROI or a point on its perimeter.

4. Click to complete the drawing.

   ⇨ The calculated values of the ROI are presented in the ROI table.

Managing Graphic Elements

You can move, copy, delete and determine the graphic properties of any artery, vein, or ROI.

- To move the graphic, drag it to the desired place on the image.
- To copy the graphic, hover over the graphic and when the cursor changes to a 4-arrow cursor, select Copy from the right-click menu.
- To delete the graphic, hover over the graphic and when the cursor changes to a 4-arrow cursor, select **Delete** from the right-click menu.
- To change the color and font of the graphic –
  - – • Hover over the graphic and when the cursor changes to a 4-arrow cursor, select **Properties** from the right-click menu.
  - – Select a font and color.

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Showing and Hiding Graphic Elements

Click the drop-down menu of the **Hide/Show** icon  to show or hide the segmentation of the ischemic region on the TMIN images (**Show/Hide Ischemic Regions** option), or to hide all graphic elements (**Hide All Graphics** option).

Resetting All Calculations

Click **Reset All Calculations**  to discard all ROIs, tissues, maps, and AIF and VOF corrections and revert to the initial stage at the time of loading.

Displaying a Fused Image

You can display a fused layout, where the TMIN image, The DWI image or a map image (or two map images) are fused on a single image.

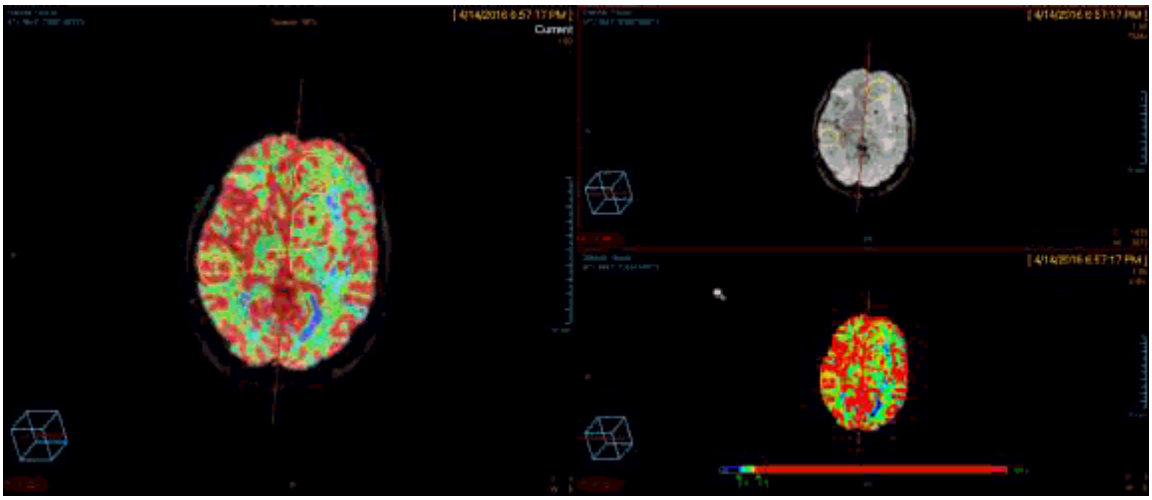
To display a fused image, select **Perfusion Maps - Fusion** from the **Application** Layout drop-down of the **Layout** ribbon.

The displayed fused image (left-hand side image of the screen in the illustration below) is a fusion of the two displayed maps (right-hand side of the screen).

To change the displayed maps, right-click the **Change Data** annotation and click the map you want displayed in each of the display areas.

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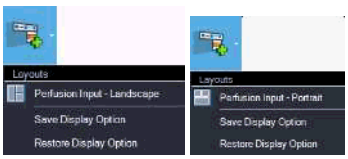
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13.20.8 Selecting a Layout

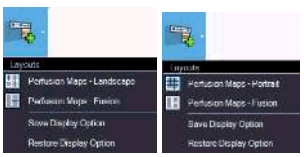
When the Perfusion application is launched, the **Application Layout** drop-down in the **Layout** ribbon lists perfusion-specific layouts.

For the input display, the menu lists by default a single layout. The layout is adjusted to landscape monitors and to portrait monitors.



For the map display, the menu offers you by default two possible layout types:

- A map-specific layout adjusted to landscape monitors and to portrait monitors.
- A layout for fused images (See Section Displaying a Fused Image on page 436).



NOTICE! Other layouts can be defined. Contact your system administrator.

13.20.9 Using Settings

The **Perfusion Settings** window allows you to change parameters related to the perfusion algorithm, map parameters, clinical parameters, input state, ischemic regions, and tables.

To change parameters, click **Settings**  in the **Perfusion** ribbon. Use the **Perfusion Settings** window to make your adjustments. You can change the following settings:

Algorithm-Related Settings

Setting	Description

Deconvolution Algorithm	Select a deconvolution algorithm. • **sSVD**—Standard Singular Value Decomposition. • **cSVD**—Circular Singular Value Decomposition. An sSVD algorithm with a circular time curve. This method is stable with respect to delays in the contrast material in the arterial input. • **oSVD**—Oscillating index Singular Value Decomposition. An iterative cSVD method which reduces the Oscillating Index (OI).
Leakage	Set the Leakage parameter to either Corrected or Uncorrected. Select Uncorrected when you assume no leakage has occurred. When Leakage is set to Uncorrected, the k2 map is not displayed, and all other map calculations take no leakage into account.
Advanced Leakage Correction	When Leakage is set to Corrected, the Advanced Leakage Correction parameter enables you to determine whether the k2 map will be normalized by K1. This option is not selected by default.
sSVD Advanced Settings	Set regularization type and fraction for sSVD. Regularization Type: • **SV cutoff**—Set to zero all Singular Values (SV) smaller than the cutoff value. • **Tikhonov**—Set a threshold for applying the Tikhonov regularization method. Regularization Fraction: Set the fraction of the highest Singular Value (SV) to determine the regularization threshold.
cSVD Advanced Settings	Set regularization type and fraction for cSVD. Regularization Type: • **SV cutoff**—Set to zero all SVs smaller than the cutoff value. • **Tikhonov**—Set a threshold for applying the Tikhonov regularization method. Regularization Fraction: Set the fraction of the highest SV to determine the regularization threshold.
oSVD Advanced Settings	Set a regularization threshold for oSVD. The oSVD method always uses a Wiener filter iteratively until the Oscillating Index (OI) reaches a value lower than the regularization value.

Map-Related Settings

Setting	Description
Map	
Drop-down listing all the available maps. For each map, you can set parameters relating to that map.	

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rCBV Parameters	Set rCBV parameters. • **Default Windowing**—The default windowing range for rCBV maps. • **Default Windowing**—The default windowing range for rCBV maps.
rCBF Parameters	Set rCBF parameters. • **Default Windowing**—The default windowing range for rCBF maps. • **Acceptance Criteria**—When enabled, only values within the set range are used in the ROI statistics and the segmentation of the ischemic region.
MTT Parameters	Set TTP parameters. • **Default Windowing**—The default windowing range for TTP maps. • **Acceptance Criteria**—When enabled, only values within the set range are used in the ROI statistics and the segmentation of the ischemic region.
TMAX Parameters	Set TMAX parameters. • **Default Windowing**—The default windowing range for TMAX maps. • **Acceptance Criteria**—When enabled, only values within the set range are used in the ROI statistics and the segmentation of the ischemic region.
k2	Set k2 parameters. • **Default Windowing**—The default windowing range for k2 maps. • **Acceptance Criteria**—When enabled, only values within the set range are used in the ROI statistics and the segmentation of the ischemic region.
ADC	Set ADC parameters • **Default Windowing**—The default windowing range for TMAX maps. • **Acceptance Criteria**—When enabled, only values within the set range are used in the ROI statistics and the segmentation of the ischemic region.
eADC	Set eADC parameters • **Default Windowing**—The default windowing range for TMAX maps. • **Acceptance Criteria**—When enabled, only values within the set range are used in the ROI statistics and the segmentation of the ischemic region.
Ventricle Removal	Disable Ventricle Removal. This setting is enabled by default for CT studies only to allow automatic removal of the ventricles from the maps, ROI statistics and segmentation of the ischemic region. Disable in cases when parts of the brain are mistakenly removed by the ventricle-detection algorithm.

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Clinical Settings

Setting	Description
Hematocrit	Set the hematocrit values. The ratio between the large and small vessel hematocrit values affects the scaling in the rCBV and rCBF maps.

Input State Settings

Setting	Description
Vessel Settings	• **Number of AIF Candidates**—Set the number of automatically detected AIF candidates. • **Vessel's Signal**—Available options include **Seeds** and **Segmentation**. Set the vessel's signal to **Segmentation** to automatically mark all segmented arteries and veins on the image. Selecting this option hides all AIF and VOF seed marks and enables the AIF and VOF segmentation correction tools. **Segmentation** is the default selected option in MR studies. Set the Vessel's signal to Seeds to show the AIF and VOF candidates and to manually add AIF and VOF points on the image.
Preprocessing Settings	• Split data by slice time or slice number—Use Slice Time to arrange the slices per time stamp. Use the Slice Number option to arrange the slices per slice number rather than slice time (for example, in cases when the original time stamp on the slices is missing or lacking information). The assumed time interval between slices is 1.6 s. Your choice is retained during your entire work session. • **Starting Time** (used mainly in MR studies)—Insert the start time of the study. The start time you insert here affects the start time displayed in the graphic representation of the data. • **Injection Time**—Insert the contrast material injection time to override the injection time calculated automatically by the algorithm. The line signifying the injection time in the graphic representation of the data is repositioned based on your manually inserted time. Use the Reset button to revert to the original time calculated by the algorithm automatically. • **Perform Denoising**—Enable to preprocess images for noise reduction. This setting is turned off by default for MR studies.

Diffusion

Setting	Description
Default B-Value Settings	**Default B-Value**—Set the value that is to be used for calculating the eADC and DWI map.

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B-Value Filter Settings	Set the values that appear in the maps. By default, all values are included. Clicking a value excludes it from the selection. Clicking it again re-includes the value. At least two values must be selected.

Ischemia Settings

Setting	Description
Lesion/Hypoperfusion Morphology Parameters	Set Lesion/Hypoperfusion morphology parameters. • **Consolidate regions (distance)**—Regions separated by a distance smaller than the set value are merged. • **Remove narrow regions**—Regions narrower than the set value are removed. • **Remove small volume regions**—Regions with a volume smaller than the set value are discarded. Use the slider to change the values. The changes are shown immediately on the maps. Use the slider to change the values. The changes are shown immediately on the maps.
Lesion Threshold Criteria	Set Lesion threshold criteria. Use the drop-down menus to define criteria for the maps. Click **Add** to add the criterion to the criteria list. A voxel is considered Lesion if it meets all criteria. Note that acceptance criteria are applied as well when enabled. Criteria types include: • **Absolute**—The criterion is applied to the actual value of the voxel. • **Relative**The criterion is applied to the relative value of the damaged side divided by the opposite side. • **Difference**—The criterion is applied to the value of the damaged side minus the opposite side. • **Relative to Average**—The criterion is applied to the value divided by the average of all voxel values in the map.

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Hypoperfusion Threshold Criteria	Set Hypoperfusion threshold criteria: Use the drop-down menus to define criteria for the maps. Click **Add** to add the criterion to the criteria list. A voxel is considered Hypoperfusion if it meets all criteria. Note that acceptance criteria are applied as well when enabled. Criteria types include: • **Absolute**—The criterion is applied to the actual value. • **Relative**—The criterion is applied to the relative value of the damaged side divided by the opposite side.The criterion is applied to the relative value of the damaged side divided by the opposite side. • **Difference**—The criterion is applied to the value of the damaged side minus the opposite side. • **Relative to Average**—The criterion is applied to the value divided by the average of all voxel values in the map.

Table Settings

Setting	Description
Show Standard Deviation	Enable to show standard deviation values in the ROI and Lesion/Hypoperfusion measurement tables. The changes are shown immediately in the tables.
Setting	**Description**
Save Current Settings as User Defaults	Save to use settings as default.
Restore System Settings	Restore system defaults.

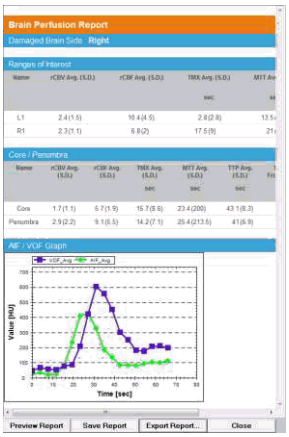
13.20.10 Opening a Report

Click **Reporting**  in the Perfusion ribbon to display a perfusion report. The report shows the content of the perfusion tables and graph.

NOTICE! Only the average curves are included in the report graph.

- Click **Preview Report** to display a version of the report that contains the patient details, including patient name, report date, patient ID, accession number, birth date, referring physician, report date, report status and study reason.
- Click **Save Report** to save the report as a Structured Report (SR). The report can then be opened from the Archive Explorer.
- Click **Export Report** to export the report to an MHTML, CSV or Plain Text format.

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13.20.11 Exporting the Perfusion Analysis

Click **Export**  in the **Perfusion** ribbon to export the calculated maps and TMIN images, including the ischemic regions segmentation, the center line indication and the added ROIs. The maps are exported in their original plane. The exported images are saved with the study, with each map constituting a separate series.

NOTICE! The exported series cannot be reloaded to the Perfusion application.

13.20.12 Accuracy and Limitations

- Image quality—The calculation of perfusion parameters is limited by the scan quality. Excessive noise, patient movement or image artifacts in the original images will ultimately have an impact on the perfusion analysis and the calculated maps. The user should inspect original data and verify that the images are of diagnostic quality and that any patient movement has been corrected using the motion correction algorithm. If image artifacts are present in the original images, the same areas on the maps may not contain valid values.
- Relative units—Some of the values are quoted in relative values (rCBV, rCBF). As such, the values extracted from these maps are valid up to arbitrary constants and therefore should not be confused with absolute measurements. Moreover, the units of these relative values are not normally associated with CBV or CBF measurements.
- Accuracy of values— In places where the standard deviation is given along with the average value, the user is encouraged to examine these values. A large standard deviation compared with acceptable values may indicate noise or artifact in the images.
- Temporal resolution—Preferably, the temporal resolution should not be lower than the resolution of one image per 4 seconds. In general, the better the resolution, the more accurate the deconvolution algorithm.
- Contrast material—The scan duration should allow the contrast material to wash into the different tissues and then wash out of the tissues, with a possible recirculation. This can be verified by visually inspecting the raw images.

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- AIF—The MR perfusion application assumes that the AIF describes a well-defined signal originating in the contrast agent injection. The signal should start from a baseline value, climb to a maximum value and show a gradual drop to low values, possibly showing recirculation effects. It is the user's responsibility to review the AIF graph and ascertain that a correct AIF signal is used.
- Spatial resolution—The resolution does not affect the deconvolution algorithm itself. However, a low spatial resolution might introduce partial volume effects. The user is advised to view the TMIN image to assess partial volume effects.
- Spatial resolution—The resolution does not affect the deconvolution algorithm itself. However, a low spatial resolution might introduce partial volume effects. The user is advised to view the TMIN image to assess partial volume effects.

13.20.13 References

1. *Diffusion MRI.* (n.d.). Retrieved from Wikipedia: https://en.wikipedia.org/wiki/Diffusion_MRI
2. Fieselmann, A., Kowarschik, M., Ganguly, A., Hornegger, J., & Fahrig, R. (2011).

   Deconvolution-Based CT and MR Brain Perfusion Measurements: Theoretical Model Revisited and Practical Implementation Details. *International Journal of Biomedical Imaging, 2011, 20.*
3. Gobbel, G., & Fike, J. (1994). A deconvolution method for evaluating indicator-dilution curves. *Physics in Medicine and Biology, 39*, 1833-1854.
4. Liao, P.-S., Chen, T.-S., & Chung, P.-C. (2001). A Fast Algorithm for Multilevel Thresholding.

   Journal of Information Science and Engineering, 17, 713-727.
5. Perona, P., & Malik, J. (1990). Scale-Space and Edge Detection Using Anisotropic Diffusion.

   IEEE Transactions on Pattern Analysis and Machine Intelligence, 12(7), 629-639.
6. Weisskoff, R., Boxerman, J., Sorensen, A., Kulke, S., Campbell, T., & Rosen, B. (1994).

   Simultaneous blood volume and permeability mapping using a single Gd-based contrast injection. *2nd Annual Meeting of SMRM,* (p. 279). San Francisco.

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14 Push to Local Computer

14.1 About Push to Client

You can use Push to Client  to transfer studies from the network to a local computer.

The studies are stored on the local computer. You can then go to a remote location and conduct a reading session on the studies just as you would from inside the network.

Using Push to Client makes the process of reading studies at a remote location faster and more convenient.

See these topics:

Transfer Tools on page 445

Sending Studies to Your Local Computer (Push to Client) on page 446

Monitoring Transfer Requests (Spooler) on page 448

Transferring Locked Studies on page 449

Receiving Studies on Your Local Computer (Receive Studies) on page 449

Loading Images Stored on Your Computer on page 120

Clearing Images from a Local Computer on page 451

14.1.1 Requirements

You must have a remote connection on the local computer.

You must turn Receive Studies to the On mode  (green traffic light) at the local computer in order to receive transferred studies. The default mode is off  (red traffic light).

14.2 Transfer Tools

14.2.1 From the Archive Explorer

The following tools for transferring studies are available in the Archive Explorer.

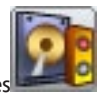
To use:	Do this:

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Push to Client 	• In the toolbar, click Push to Client . • In the menu toolbar, click Push --> Push to Client . • Select a study in the archive, right-click and select Push to Client  in the drop-down menu.
Receive Studies 	• In the toolbar, click Receive Studies . • In the menu toolbar, click Push --> Receive Studies .
Clear Studies 	• In the toolbar, click Clear Studies from Local Drive . • In the menu toolbar, click Push --> Clear Studies --> Clean Cache. • Select a study in the archive, right-click and select Clear Pushed Studies in the drop-down menu .

14.2.2 From the PowerViewer Application

The following tools for receiving studies are available in the PowerViewer application.

To use:	Do this:
Receive Studies 	In the toolbar, click Receive Studies  to the On mode  (green traffic light) at the local computer in order to receive transferred studies. The default mode is off  (red traffic light).

14.3 Sending Studies to Your Local Computer (Push to Client)

1. Open Archive Explorer (Ctrl +N).
2. Select the studies you want to transfer to a local computer.

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IMPORTANT

You must remain at the study level to use Push to Client. The Push to Client is inactive at the series or image level in Archive Explorer.

3. Initiate Push to Client (see Transfer Tools on page 445).
4. In the Push to Client dialog box, select:

   NOTICE! If several studies for the same patient are from the same day, then the system transfers prior studies for the most current case out of the selected studies.

   - **Target Receiver:**
     - **Myself**—Selects your local computer as the destination.
     - **Another User**—Allows you to define another user as the destination.
   - **History Policy:**
     - **Push with Relevant History**—Includes current studies and prior studies for comparison.
     - **Push without History**—Includes current studies only.
5. Click OK to initiate the transfer. The status bar in Archive Explorer shows the message "Selected studies were marked to be pushed."

IMPORTANT

If the studies you select are locked by other users, you will see a warning message. You can click Cancel to deselect studies or select different studies. You can click OK to override the lock status and proceed with the file transfer.

6. Use the Spooler Dialog (see Monitoring Transfer Requests (Spooler) on page 448) to monitor the status of the transfer request.
7. When the Spooler shows that the transfer is successful and complete, the study is available for download on the local computer.

NOTICE! You can use a worklist for 'pushed' studies, for a convenient way to see the studies that are stored locally for you or a specific user.

IMPORTANT

The target receiver must have Receive Studies in the active/on mode  **in order to receive the studies transferred from Push to Client.**

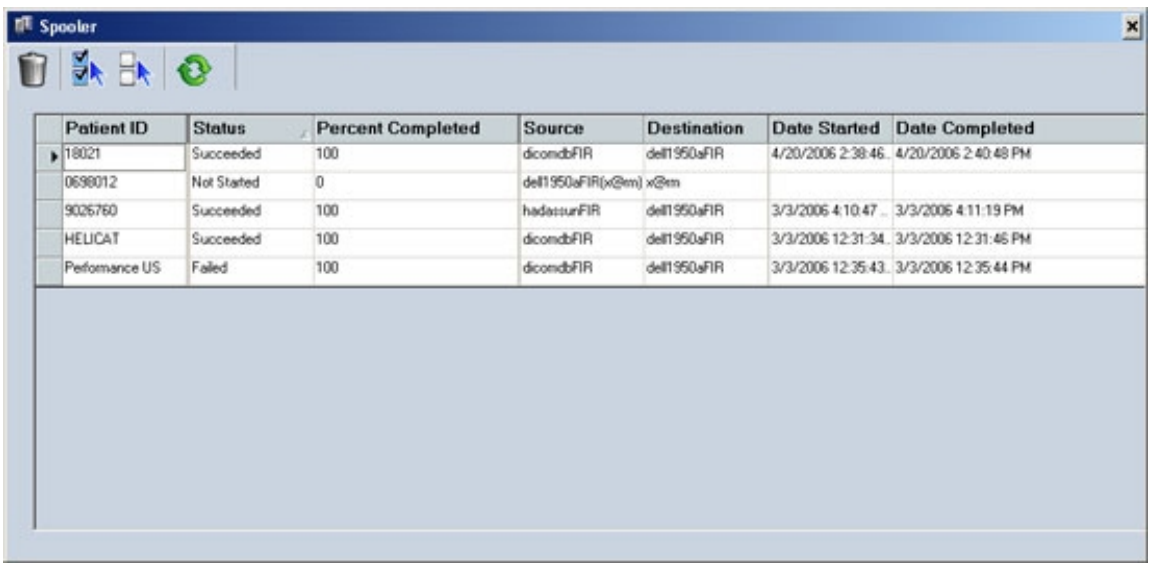
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See this topic:

Opening the Archive Explorer on page 106
Transfer Tools on page 445
Monitoring Transfer Requests (Spooler) on page 448
Loading Images in Worklist Mode on page 112
Receiving Studies on Your Local Computer (Receive Studies) on page 449

14.4 Monitoring Transfer Requests (Spooler)

1. Use Push to Client .
2. Click Open Spooler Dialog .
   ⇨ The Spooler window allows you to monitor the progress of your request to transfer studies to a local client.



You can:

- See the Status of each request, such as: Succeeded, Running, Not Started, or Failed.
- See the Percent Completed for each request to easily track the progress of the transfer
- Click on the column heading to sort and filer the list of studies/requests
- Click Cancel  to immediately cancel and remove any selected request (s)
- Click Select All  to select every request in the list

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- Click Select None  to deselect any selected request
- Click Refresh  to update the list with the newest status information

See these topics:

Loading Images in Worklist Mode on page 112

Sending Studies to Your Local Computer (Push to Client) on page 446

14.5 Transferring Locked Studies

NOTICE

If a lock indicator appears next to a study on the worklist, another user has that study open. You can still load the study for viewing, but you cannot make any modifications. If someone loaded the study since you opened the Archive Explorer, you may not see the lock indicator until you refresh your display.

You can still transfer locked studies to a local client if you have reading permissions, or the targeted user/receiver has reading permissions.

During the transfer process, the study is temporarily locked. If a different user tries to access the study you are transferring, the user can only access the study in view mode (read-only).

14.6 Receiving Studies on Your Local Computer (Receive Studies)

The Receive Studies mode toggles on and off.



The traffic light is green. The mode is on and the Diagnostic Workstation software is ready to accept incoming studies and store the studies locally on your computer.



The traffic light is red. The mode is off. No studies are transferred.

14.6.1 Using Receive Studies

1. Log on to the Diagnostic Workstation from your local computer.

2. If necessary, toggle Receive Studies from off  to on .
3. The requested studies are transferred.

NOTICE

If you toggle Receive Studies to off while a study transfer is in progress, the transfer halts. If you toggle Receive Studies to on, the transfer resumes from the stopping point.

IMPORTANT

The Push to Client operation requires that the target receiver user is logged on to his or her client. While the Receive Studies mode is On, the system uses an automatic screen-lock. The system does not apply an automatic log-out.

See this topic:

Transferring Studies to a Local Computer (Push to Client-see About Push to Client on page 445)

14.7 Loading Images Stored on Your Computer

14.7.1 DICOM Images

You can load DICOM images from any directory on your computer.

1. Right-click on the Local Drive option in the Archive List, then click Browse.
2. From the Browse window, select the directory that contains the DICOM DIR file.

14.7.2 Transferred Images (Push to Client)

IMPORTANT

A remote connection is a requirement to load images transferred to a local computer.

You can initiate a transfer of studies to a local disk even if you are not using a remote connection, but you can only load images from the local disk if you use a remote connection.

1. Right-click on the Local Drive Option in the Archive List, then click Browse.
2. From the Browse window, select the directory that contains the transferred folder.

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When you load studies pushed to your local disk, the loading process will behave as though the images are streamed. For example the image information is taken from the server database for the most current information. The image pixel data is taken from the local disk (lossless). However, if new images are created after the transfer, they will streamed as well.

If you load a study that is still transferring to your local disk, the remaining images or series are streamed.

If you load a study that was transferred to your computer, but the same study is available online and you are not in a remote location, the study is loaded from the fast online server instead of the local disk.

See this topic:

Transferring Studies to a Local Computer (Push to Client) (see About Push to Client on page 445)

14.8 Clearing Images from a Local Computer

The cache size is 5 GB or half the size of free disk space.

You can use Clear Cache in the Push ribbon of the Manage tab in the toolbar to remove the cache of transferred images from your local computer. You can use Remove from Cache to clear specific studies.

See this topic:

Transfer Tools on page 445

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15 GUI Configuration

15.1 About Configuring GUI with Application Settings

The Application Settings window lets you configure the way in which images are viewed.

See these topics:

Opening the Application Settings Window on page 453
Configuring Windowing Presets on page 454
Configuring Annotations on page 455
Configuring Archive Explorer Settings on page 455
Configuring Viewing Settings on page 456
Configuring Clinical Applications on page 460
Configuring Printing Settings on page 464
Configuring Graphics and Measurements on page 465
Configuring Viewer Color and Appearance on page 467
Configuring Report Settings on page 469
Configuring Monitor Settings on page 474
Configuring Action Buttons on page 471
Configuring Network Bandwidth Settings on page 475

NOTICE

You can adjust all configurations manually or at the user, system, or group level, depending on your user profile permissions.

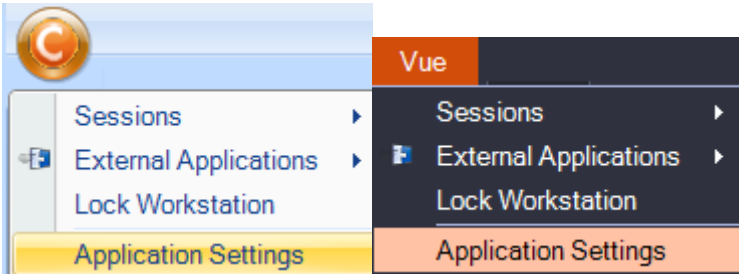
15.2 Opening the Application Settings Window

15.2.1 From Within the Application

1. Open the Archive Explorer or the Diagnostic Workstation.
2. In the upper left corner, click the Vue PACS icon (light color scheme) or the Vue PACS menu (dark color scheme) and select Application Settings.

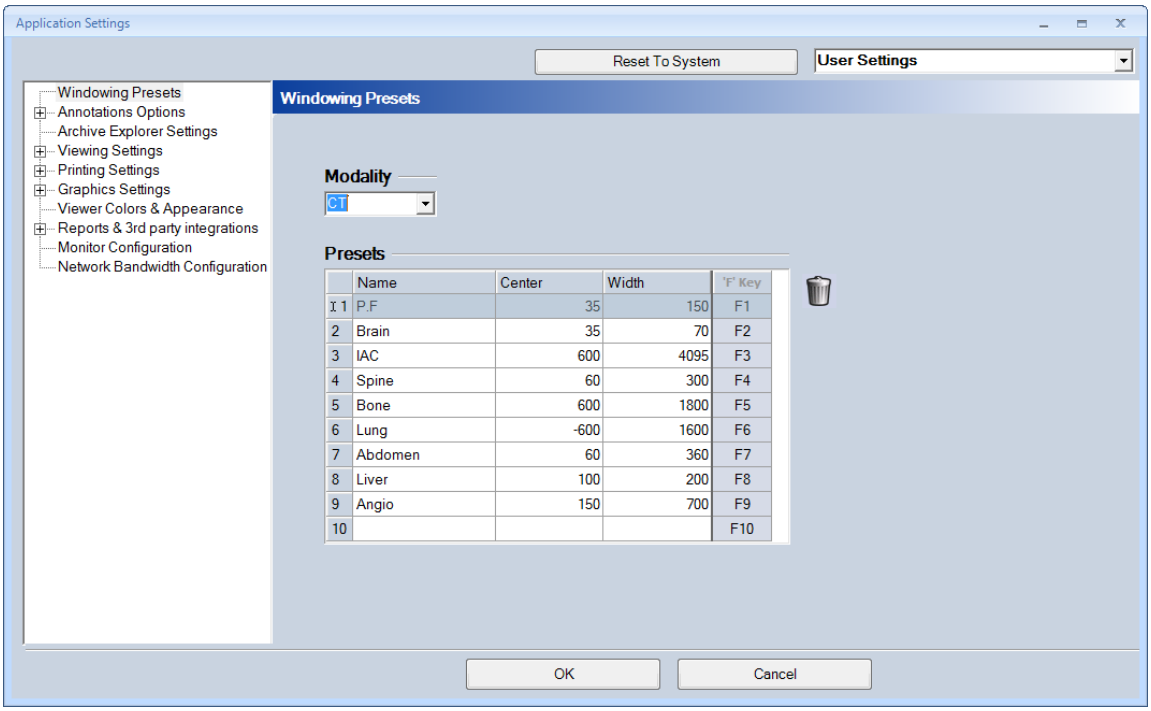
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15.2.2 From the Login Screen

1. In the log-in window, click Administration.
2. Highlight the Client Tools and select the Application Settings option.



15.3 Configuring Windowing Presets

1. Open the Application Settings window (see Opening the Application Settings Window on page 453).
2. In the left pane, select Windowing Presets.
3. In the upper-right corner, select the settings level (user, group, or system) that you want to change.

   CAUTION! Only the system administrator can make system changes.
4. Click the Modality drop-down menu, then select the modality configuration you want to change.

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5. In the Presets table, double-click the field that you want to change.
6. To delete a particular preset, click Delete .
7. To add a preset, insert the preset information in a new row.
8. Click OK.

NOTICE

If the Application Settings window was opened from the PowerViewer, you must restart the application for the changes to take effect.

15.4 Configuring Annotations

1. Open the Application Settings window (see Opening the Application Settings Window on page 453).
2. In the left pane, select Annotations.
3. Click the Modality drop-down menu, then select the modality you want to configure.
4. From the Default Annotations list, click an annotation and drag it into the list on the left side of the displayed image.
5. Click and drag annotations that you do not want to use into the Default Annotations list.
6. From the Additional Tags drop-down menu, you can add a DICOM tag to the image being viewed.
7. Click OK.

15.5 Configuring Archive Explorer Settings

You can configure the system to either load the case or go to the next level (explore) when you double-click a study in the Archive Explorer. You can also select the properties for the automatic filter focus.

1. Open the Application Settings window (see Opening the Application Settings Window on page 453).
2. In the left pane, select Archive Explorer Settings.
3. Set the Archive Explorer properties:
   - Select Enable Automatic Filter Focus, if desired.
   - If the automatic filter focus is enabled, select a field in Default Field Focus to focus on upon opening.
   - Select whether double-clicking a case will load a selected study or explore it.

See this topic:

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Exploring the Study Content on page 140

15.6 Configuring Viewing Settings

15.6.1 About Configuring Viewing Settings

To configure settings, see the topics listed here.

See these topics:

Choosing Viewer/MPR Settings on page 456
Choosing Patient Mini-Archive Settings on page 456
Configuring Layouts on page 456
Configuring Viewer/KP/FP Layouts on page 458
Configuring Image Enhancement Settings on page 458
Configuring Additional Viewing Settings on page 459

15.6.2 Choosing Viewer/MPR Settings

15.6.3 Choosing Patient Mini-Archive Settings

15.6.4 Configuring Layouts

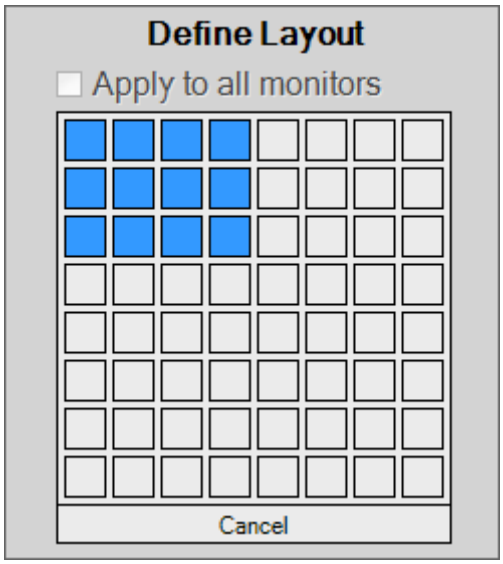
Using the Layout Tab in the Toolbar

Use the Layout tab of the toolbar to define application layouts.

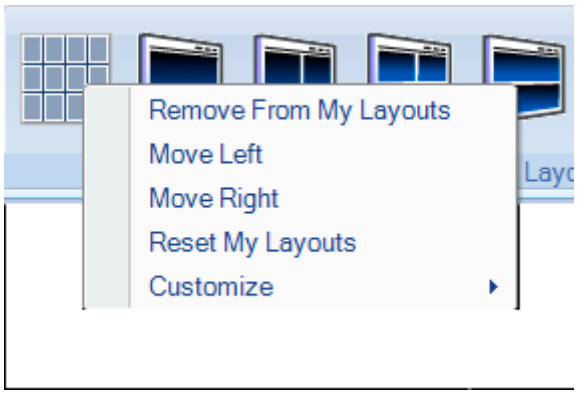
1. In the Layout tab, click the drop-down menu of the Define Layout icon .
2. Select Define Layout. In the Define Layout window, drag the mouse over the grid to highlight the desired layout. Click to complete the selection.

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3. Select the **Apply to all monitors** option if you want the same layout to apply to multiple monitors. Otherwise, the newly defined layout applies only to the active monitor.
4. To save the newly defined layout for future use, select Save as New Layout from the Define Layout drop-down menu.
   ⇨ An icon is added to the Application Layout ribbon in the toolbar to reflect the newly defined layout .
5. Right-click the various layout icons in the Layout tab and use the options of the drop-down menu to organize the Layout tab according to your preferences. You can remove an icon, move icons to left or to the right and reset the layout icons.



Using Application Settings

Use Applications Settings to define which layout will be represented by the different layout icons in the Layout tab of the Layout ribbon.

1. Open the Application Settings window (see Opening the Application Settings Window on page 453).
2. From the left pane, select Viewing Settings.

3. Click Viewer Pre-defined Layout.
   ⇨ The layout buttons appear on the right hand side.
4. Click Edit for each option you want to configure.
   ⇨ The Define Layout window appears.
5. Drag the mouse over the grid to highlight the desired layout. Click to complete the selection.
   ⇨ The new layout is stored and displayed on the main window.
6. Click OK.

15.6.5 Configuring Viewer/KP/FP Layouts

1. Open the Application Settings window (see Opening the Application Settings Window on page 453).
2. From the left pane, select Viewing Settings.
3. Click one of the following:
   - Configure Key Preview, Film Preview, and Viewer Application Layout in the right pane.
   - Viewer/KP/FP Layouts in the Application Settings tree in the left pane.

   ⇨ The Viewer/KP/FP Layouts window appears, allowing you to select viewer, key preview, and film preview layout settings.
4. Click the Modality drop-down menu, then select the modality you want to configure.
5. Do one of the following:
   - To select a predefined body part, select the Body Part from the drop-down list.
   - To add a body part that does not appear in the drop-down list, click New. Enter a body part and click Add. Click  to exit the Add new body part dialog box.
6. For each modality/body part configuration, define the default layout for the Key Preview, Film Preview, and New viewer application (viewbox):
   - To select a predefined body part, click Pre-Defined Layouts.
   - To define a new layout that does not appear in the Pre-Defined Layouts window, click User Defined.

   ⇨ The option appears in the Viewer/KP/FP Layouts window.
7. The option appears in the Viewer/KP/FP Layouts window.
8. Click OK.

15.6.6 Configuring Image Enhancement Settings

You can use the Enhance Settings window to define the values of the image enhancement options, which control image sharpness.

1. Open the Application Settings window (see Opening the Application Settings Window on page 453).
2. In the left pane, select Viewing Settings

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3. Click one of the following:
   - Configure enhance Settings in the right pane.
   - Enhance Settings in the left pane in the left pane.

   ⇨ The Enhance Settings appear in the right pane.
4. Configure these elements to enhance the viewed image:

   NOTICE! You cannot configure Normal. It is always 1.
   - Softer
   - Soft
   - Sharp
   - Sharper
5. Click OK.

15.6.7 Configuring Additional Viewing Settings

1. Open the Application Settings window (see Opening the Application Settings Window on page 453).
2. From the left pane, select Viewing Settings.
3. Click one of the following:
   - Configure Additional Viewing Settings in the right pane
   - Additional Viewing Settings in the left pane

   ⇨ The Additional Viewing Settings window appears, allowing you to select session time out, sticky notes, full screen, study replacement and other settings.
4. Set the following:
   - Enable/disable session time outs. If you enable session time out, do the following:
     - Select the number of minutes to automatic locking of the application.
     - Select the number of minutes to automatic logging out of the application.
   - Settings related to the display of the Sticky Notes window and the monitor on which it appears:
     - Select a display option: Don't show, Show if exists, Always show, or Always show and add new.
     - Select the monitor or the monitor number on which the sticky notes window is to be displayed.

       Available monitors are: The mouse monitor (the monitor to which the mouse is connected), the Admin monitor (the monitor on which the Archive Explorer is displayed), the primary monitor (the monitor on which the application first launches), and the application primary monitor.

     To see the monitor numbers, open the Monitor Configuration Application Settings window.
   - Settings related to full-screen display:

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- Select Start with full screen to have the viewer application open with full screen always. Pressing F11 changes the display to show the toolbar icons and the ribbon tab labels.
- Select Enable 3-state full screen mode to be able to change the display from full screen to a display that includes the ribbon tab labels without the toolbar icons and then to a display that includes the ribbon tab labels as well as the toolbar icons. Press F11 to change from one display to the other.

- Settings related to study replacement:
  - Select Show base study.
  - Select the number of studies in the study replacement list.
- General settings:
  - Enable automatic registration upon loading of the studies.
  - Enable nearline study alert. An alert appears every time a nearline study is being loaded.
  - Enable De-Identifier to obscure patient details originating in the modality.

15.7 Configuring Clinical Applications

15.7.1 About Configuring Clinical Applications

You can configure clinical applications, including Mammography Workstation, Tomosynthesis, PET/CT, and Lesion Management.

See these topics:

Mammography Settings on page 460

Tomosynthesis Settings on page 462

PET/CT Settings on page 328

Lesion Management Application Settings on page 463

15.7.2 Mammography Settings

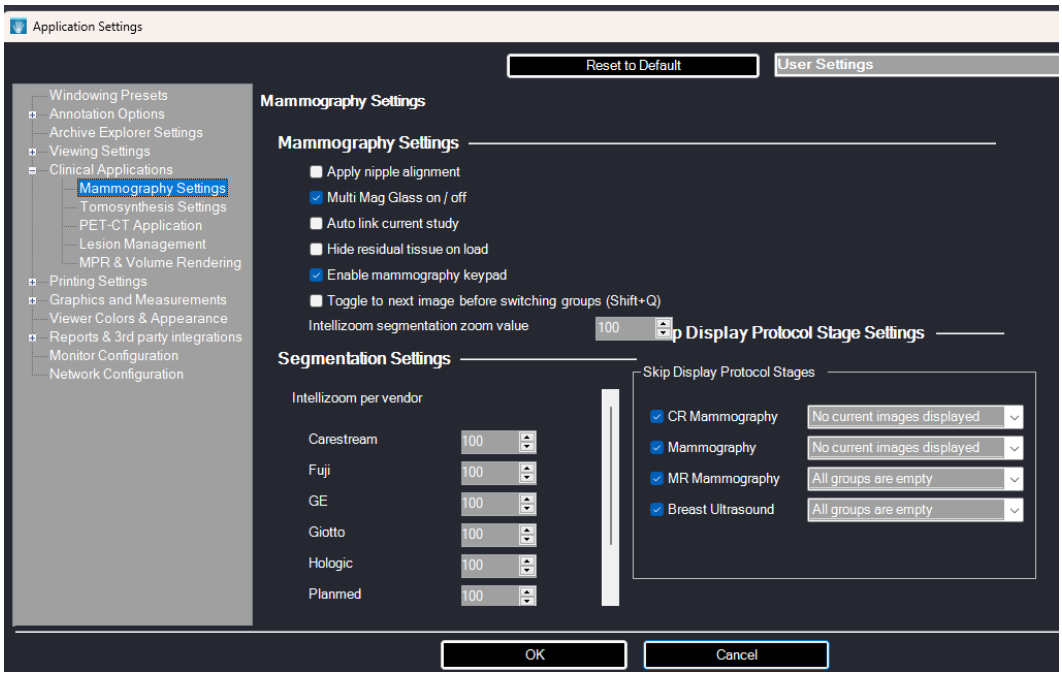
Several Mammography parameters can be configured in Application Settings.

1. Open the **Application Settings** window (see Opening the Application Settings Window on page 453).
2. Do one of the following:
   - In the left-pane tree, click the plus sign next to Clinical Applications and select Mammography Settings.
   - Click Clinical Applications and in the right pane click Configure PET-CT Settings.

   The Mammography Settings page opens.

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3. In the upper right corner, select the level (user, group, or system) that you want to configure.
4. Configure the following settings, and then click **Save**.

Property	Description
General mammography settings	• Enable/disable automatic nipple alignment. • Enable/disable automatic activation of multiple magnifying glasses. • Enable/disable automatic linking of all groups with the same frame of reference and the same orientation/plane. • Enable/disable hiding residual tissue on load. • Enable/disable the mammography keypad. • Enable/disable moving to the next image before changing groups (Shift+Q) • The zoom value of Intellizoom segmentation.
Segmentation Zoom settings	If additional mammography system vendors are set in Central Configuration, the Segmentation Zoom Settings section displays a list of these vendors, allowing you to set the intellizoom value for each of the vendors.

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Property	Description
Skip Display Protocol Stages	For each modality set in Central Configuration, select the condition that should be met in order to skip hanging protocol stages that meet the condition. Possible conditions are: • All groups are empty • No current images displayed • No prior images displayed • No current or prior displayed

15.7.3 Tomosynthesis Settings

You can define shortcuts for pre-set slabbing mode and thickness.

1. From the drop-down menu select Slabbing Off, Average, or Maximum slabbing mode.
2. Select a thickness.
3. Click the Assign Shortcut button located to the left of the drop-down.
4. In the Assign Shortcut dialog, press the shortcut key for the slabbing mode and thickness combination. To see a list of all existing shortcuts, click the Shortcut List link. Click Assign.
5. Repeat the operation in the subsequent rows for each slabbing mode and thickness combination.

The Slabbing Shortcut Preset acts as a toggle control that toggles on the pre-configured slab mode and thickness with one press and toggle back to the prior settings with another press.

15.7.4 PET/CT Settings

Several PET/CT parameters can be configured in Application Settings.

1. Open the Application Settings window (see Opening the Application Settings Window on page 453).
2. Do one of the following:
   - In the left-pane tree, click the plus sign next to Clinical Applications and select PET-CT Application.
   - Click Clinical Applications and in the right pane click Configure PET-CT Settings.
3. You can set the following:
   - Determine which tool will be active upon loading of the PET/CT study – Zoom, Windowing, Pointer, Swivel, or Relate.
   - Set the minimum and maximum Standard Uptake Values (SUV) for lesion highlighting.
   - Set the following options:
     - Display a Wireframe Around the MIP Image. By default the wire frame is hidden for all users.
     - Enable automatic swivel of the MIP image upon loading of the study.

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- Default Merge Method. By default, the merge method for fusion images is Alpha Blending. You can change it to Highlight. See About Fusion Images on page 287.

The shown MIP in the PET/CT application is a weighted MIP that better illustrates the depth of the data.

To disable the weighting and thus show a regular un-weighted image click the MIP On/Off button  in the 3D bar.

15.7.5 Lesion Management Application Settings

Several Lesion Management parameters can be configured in Application Settings.

1. Open the Application Settings window (see Opening the Application Settings Window on page 453).
2. Do one of the following:
   - In the left-pane tree, click the plus sign next to Clinical Applications and select Lesion Management.
   - Click Clinical Applications and in the right pane click Configure Lesion Management Settings.
3. You can set the following:
   - Enable or disable forced perpendicularity when using two diameter measurements. When this option is enabled, the two diameters are always perpendicular.
   - Threshold Type
     - Fixed - Segmentation is based on fixed values. In PET studies, set the value in the Fixed SUV Threshold option. In CT studies, set the maximum and minimum values in the Fixed HU Maximum Threshold and Fixed HU Minimum Threshold option.
     - Percentage - The system looks for the maximum value point inside the spheroid. All voxels with values above the set percentage (of the maximum value point) is included in the segmentation.
   - Threshold units
     - SUV BW - Standard Uptake Value SUV Body Weight
     - SUV LBM - Standard Uptake Value Lean Body Mass (SUV LBM is also known as SUL)
     - SUV BSA - Standard Uptake Value Body Surface Area
   - Display Mode
     - Overlay - The segmented area is marked by a contour and an overlay.
     - Contour - The segmented area is marked by a contour only.
   - Percent Threshold - Percentage of Maximal SUV. Only values above this threshold are considered.
   - Fixed SUV Threshlod - A value for the fixed threshold type in PET studies.

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- Fixed HU Maximum Threshold - A maximum Hounsfield Unit value for the fixed threshold type for CT studies.
- Fixed HU Minimum Threshold - A minimum Hounsfield Unit value for the fixed threshold type for CT studies.
- SUV Markers - Show SUV Peak Marker (MAX), SUV Peak Marker (NCC), SUV Max Value Marker, or do not show any markers.
  - SUV Peak is the mean SUV value of voxels contained in a one cubic centimeter volume around the hottest voxel in the VOI structure. It might extend the VOI boundary if the hottest voxel is at the edge of the VOI for example. This method is referred to as MAX.
  - SUV Peak is the mean SUV value of the hottest one cubic centimeter constrained inside the VOI. It cannot extend the VOI boundary. Search for the 1 cc region within the VOI, which leads to the highest mean value within this 1 cc. The voxel with the highest voxel value might not be included in this 1cc region, but usually it will. This method is referred to as NCC (normalized cross-correlation).
- PET Segmentation Measurements - Select one or more threshold segmentation enhanced annotations.
- Segment only single component around the max pixel - Segment only the component that contains the maximum pixel within the threshold area.

15.8 Configuring Printing Settings

You can configure the header, footer, and printing settings.

See these topics:

Configuring Header/Footer Settings on page 464

Configuring Printing Settings on page 465

15.8.1 Configuring Header/Footer Settings

1. Open the Application Settings window (see Opening the Application Settings Window on page 453).
2. From the left pane, select Printing Settings.
3. Click one of the following:

   The Application Settings window shows the Header/Footer Settings options.
   - Configure Header/Footer Settings in the right pane
   - Header/Footer Settings in the Application Settings tree in the left pane
4. Set the header and footer properties:

   NOTICE! To delete an annotation from the header or footer, you can drag the annotation back to the list of annotations or select the annotation and press Delete.
   - Select the modality (each header/footer is for a specific modality).

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- Drag the required annotations from the Default Annotations list on the left to the Header and Footer fields on the right.
- Select DICOM tags from the Additional Tags list.
- Select the background color for displaying the image on film, paper, and the monitor.
- Select whether to display the header and/or footer.

5. Click OK.

NOTICE! In the Additional Tags and Default Annotation sections, you can select multiple items by holding down the Ctrl key and clicking items.

15.8.2 Configuring Printing Settings

You can specify that for a print job of more than a specific number of pages, a warning message will be triggered. You can also specify if you want printing to start immediately after you click Print, or whether a print dialog will appear.

1. Opening the Application Settings Window on page 453
2. From the left pane, select Printing Settings.
3. Click one of the following:

   The Printing Options window appears.

   - Configure Printing Settings in the right pane
   - Printing Options in the Application Settings tree in the left pane

4. Set the printing options:
   - Select the minimum number of pages in a printing job that will trigger a warning message.
   - Select whether the image(s) should be printed immediately to the default printer from the Film Previewer.
   - Select whether the image(s) should be printed to the default printer from the Patient Mini-Archive.
5. Click OK.

15.9 Configuring Graphics and Measurements

15.9.1 About Configuring Graphics and Measurements

You can configure the graphics settings, including the properties of the graphic elements, of bookmarks, and of the spine labeling settings.

See these topics:

Configuring Graphics Properties on page 466

Configuring Bookmark Settings on page 466

Configuring Spine Labeling Settings on page 467

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15.9.2 Configuring Graphics Properties

The properties defined here determine how graphic elements will be displayed on an image.

1. Open the Application Settings (see Opening the Application Settings Window on page 453) window.
2. From the left pane, select Graphics and Measurements.
3. Click one of the following:

   The Graphics Properties window appears in the right pane.

   - Configure Graphic Elements Settings in the right pane
   - Graphic Properties in the Application Settings tree in the left pane
4. Set the graphics properties:
   - Select whether to display graphics measurements with a black background.
   - Select whether graphic elements work in Single Action Mode, meaning that the tool is only active for one graphic (for example, oval ROI, line measurement) and returns to the default mode. If this is not selected, graphics of the same type can be drawn multiple times without selecting the element each time from the menu.
   - Select whether, when you draw an arrow, the first click marks the head or tail of an arrow.
   - Select whether to allow creation of a spheroid when you change a sphere.
   - Set the measurement units and the radius size for fixed-size spheres and the step size for resizing of fixed-size spheres.
   - Select pre-Defined Text Items.

     Define the text items that can be placed on an image. These are the items that appear on the drop-down menu when the Text graphic element is selected.

     NOTICE! Each text item that you define here has an associated function key.

     You can change the priority of the text items in the list using the up or down arrows.

     Delete a pre-defined text item by selecting it in the list and clicking the Delete icon.
5. Click OK.

NOTICE! To place text on an image, click the Text button on the Graphics toolbar, then click where you want the text to be placed on the image. The Please Enter Text dialog box appears, with the defined text appearing in the drop-down list. If you know the function key tat is associated with the required defined text, you can click that instead.

15.9.3 Configuring Bookmark Settings

1. Open the Application Settings (see Opening the Application Settings Window on page 453) window.
2. Click Graphics and Measurements --> Bookmarks.

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3. You can enable one or more of the following options:
   - Turn the 2D Automatic Follow Up Tool on or off
   - Retain the saved windowing values of bookmarks when you perform bookmark navigation
   - Show the "Delete All Graphics" Warning Message

15.9.4 Configuring Spine Labeling Settings

You can define how disks and vertebrae will be labeled in images of the spine.

1. Open the Application Settings (see Opening the Application Settings Window on page 453) window.
2. From the left pane, select Graphics Settings.
3. Click one of the following:

   These settings determine what appears in the Spine Labeling dialog box.
   - Configuring Spine Labeling Settings in the right pane
   - Spine Labeling Settings in the Application Settings tree in the left pane
4. Set the Spine Labeling properties:
   - Spine Labeling: Select to display either disk annotations or vertebra annotations.
   - Skip Label's Interval: Select the number of disks/vertebra to skip between labels. For example, if you select vertebra c1, then select skip 4, the next vertebra to be marked will be c5.
   - Total Spread Range: Select the total range of disks/vertebrae to be labeled.
   - Reverse Marking sequence: Select the direction to label the disks/vertebrae.
5. Click OK.

See this topic:

Adding a Spine Label on page 506

15.10 Configuring Viewer Color and Appearance

15.10.1 Configuring Viewer Colors and Appearance

Application Style

You can determine whether the general appearance of the user interface would be based on a light or a dark color theme. From the Application style drop-down, select Classic Blue or Metro Dark.

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Fonts and Colors

You can adjust and arrange both the graphics and application fonts (name and size) and colors.

NOTICE! Colors cannot be seen on black-and-white monitors.

1. Open the Application Settings window (see Opening the Application Settings Window on page 453).
2. In the left pane, select Viewer Colors and Appearance.
   ⇨ The Application Settings window shows the Viewer Colors and Appearance options in the right pane.
3. Select a row under Application Font Parameters, then click ....
4. Choose a font or font size in the Font window.
5. Click OK.
6. Repeat steps 3-5 for any other application font parameters you want to change.
7. Select a row under Graphics Font Parameters, then click ....
8. Choose a font or font size in the Font window.
9. Click OK.
10. Repeat steps 7-9 for any other graphics font parameters you want to change.
11. Select a row under Graphics Colors Parameters, then click ....
12. Choose a color in the Color window.
13. Click OK.
14. Repeat steps 11-13 for any other graphics color parameters you want to change.

NOTICE! When you click a parameter, a description of the item is displayed at the bottom of the right pane of the Application Settings window.

15.10.2 Choosing a Color Scheme

You can select a light (blue) or dark color scheme for the Archive Explorer and Viewer windows.

1. Open the Application Settings window (see Opening the Application Settings Window on page 453).
2. From the left pane, select Viewer Colors & Appearance.
3. From the Application Style section at the top of the window, select the required scheme.
4. Click OK.

15.11 Configuring Reports and Third-Party Integrations

You can configure the appearance of reports and third-party integrations in the application.

See these topics:

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Configuring Report Settings on page 469
Configuring Settings for Voice Dictation Integration on page 469
Configuring Settings for RIS Desktop Integration on page 470
Configuring Action Buttons on page 471

15.11.1 Configuring Report Settings

1. Open the Application Settings window (see Opening the Application Settings Window on page 453).
2. From the left pane, click Reports and Third Party Integrations.
3. Click one of the following:

   The Applications Settings window shows the Reports Settings in the right pane.

   - Configure Report Settings in the right pane
   - Report Settings in the Application Settings tree in the left pane
4. Select the Enable check box.

   NOTICE! Report settings are available only at System Level and should be performed by the system administrator.
5. Select the Always display Reports upon Loading check box.
6. Click the drop-down menu to select the monitor on which you would like to display the reports.
7. Click the drop-down menu to configure the report interface.
8. Enter the URL of the site you want to open.
9. Click OK.

15.11.2 Configuring Settings for Voice Dictation Integration

Using a voice dictation system requires installation of special software and proper configuration. See the system administrator.

1. Open the Application Settings window (see Opening the Application Settings Window on page 453).
2. From the left pane, click Reports and Third Party Integrations.
3. Click one of the following:
   - Configure Settings for Voice Dictation Integration from the right pane.
   - Dictation Settings from the Application Settings tree in the left pane.

   ⇨ The Dictation Settings options appear in the right pane.
4. Select the Enable check box.

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NOTICE

Dictation settings are available only at System Level and should be performed by the system administrator.

5. Click the drop-down menu to select the type of Voice Dictation system installed.

NOTICE

The version numbers at the bottom of the screen will change according to the Voice Dictation system chosen.

6. Type the name of the server in the Server Name field.
7. Click the drop-down menu to select the monitor on which you would like to display the reports.
8. Select the correct version of the Voice Dictation system installed.
9. Click OK.

15.11.3 Configuring Settings for RIS Desktop Integration

Integration with a RIS system requires installation of special software and proper configuration. See the system administrator.

1. Open the Application Settings window (seeOpening the Application Settings Window on page 453).
2. From the left pane, click Reports and Third Party Integrations.
3. Click one of the following:
   - Configure Settings for RIS Desktop Integration in the right pane
   - RIS Settings from the Application Settings tree in the left pane

   The RIS Settings options appear in the right pane.
4. Select the Enable check box.

   NOTICE! RIS settings are available only at System Level and should be performed by the system administrator.
5. Click the drop-down menu to select the type of RIS installed.
6. Type the name of the RIS Interface.
7. Click the drop-down menu to select the type of integration.
8. Click OK.

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15.11.4 Configuring Action Buttons

About Configuring Action buttons

See these topics:

Configuring Action Button Settings on page 471

Adding a New Button for Launching an External Application on page 472

Adding a New Button for Integration with COM Interface on page 472

Adding a New Button for Integration with WEB Content on page 473

Using DICOM Tags on page 473

Configuring Action Button Settings

Integration with action buttons requires proper configuration. Contact the system administrator.

1. Open the Application Settings window (see Opening the Application Settings Window on page 453).
2. From the left pane, click Reports and Third Party Integrations.
3. Click one of the following:

   The Action Buttons Settings options appear in the right pane.

   - Configure Action Buttons Settings in the right pane
   - Action Buttons Settings from the Application Settings tree in the left pane
4. The Action Buttons Settings options appear in the right pane.
5. To add a new action button, click Add new button .
6. To delete an action button, click Delete .
7. Click the Type drop-down menu and select the type of action button.

   Three integration mode types are supported.

   - EXECUTE – Enables the PACS to run an external application
   - COM – Enables the PACS to connect to a COM interface
   - WEB – Enables the PACS to interface any with URL while hosting it inside the client
8. Click Browse if you have an icon image stored for the new action button.
9. Add a caption in the Caption field.
10. You must enter a caption. The caption appears next to the icon when you open the External Applications pop menu in the Export tab.

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Adding a New Button for Launching an External Application

1. In the Type drop-down list, click EXECUTE.
2. Click the Browse button to select the icon.
3. In the Caption box, enter the name of the button.
4. In the Command box, enter the third-party application command line. The exact format of the command line depends on the third-party executable being invoked.
5. To use a basic user name (without the substring starting with @), select the Use Basic User check box.
6. To execute the action button only on studies where the site ID matches the local site ID, select the Filter by Site ID check box.
7. Add an optional third-party password in the Password field, if required.
8. To use DICOM parameters of the primary study (not the study of the active image), select the Work on Primary Study check box.
9. For automatic execution of the action button on starting a new session, select the Open on Start Session check box.
10. To close all applications opened by the action button when ending a session, select the Close Before Exit check box.
11. To enable the action button from the Archive Explorer (Application Tools > External Applications), select the Show in AE check box.
12. Check the Save Before Action check box to integrate with a program that needs local access to the images (like ORTHOVIEW). This will save the images to local storage on the workstation before launching the application. Otherwise uncheck this option.
13. Click OK to save your changes and close the dialog box.

Adding a New Button for Integration with COM Interface

1. In the Type drop-down list, click COM.
2. Click the Browse button to select the icon.
3. In the Caption box, enter the name of the button.
4. In the Interface box, add the ProgID of the COM server to be activated.
5. To use a basic user name (without the substring starting with @), select the Use Basic User check box.
6. To execute the action button only on studies where the site ID matches the local site ID, select the Filter by Site ID check box.
7. In the ID box, enter the button ID. This is a numerical value that enables the COM server to differentiate between the different action buttons defined.
8. From the Launch Window list, select the monitor in which the third-party application will appear.

   NOTICE! This parameter is passed to the COM server, which, depending on its implementation, may or may not comply with the window location request.

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9. In the Object Type drop-down list, click the user and password type that is sent to the COM server:
   - No RIS – Sends the Diagnostic Workstation user and a blank password.
   - RIS – Sends the RIS user and password. Action buttons of this type are not visible when RIS integration is not activated.
10. Click OK to save your changes and close the dialog box.

Adding a New Button for Integration with WEB Content

1. In the Type drop-down list, click WEB.
2. Click the Browse button to select the icon.
3. In the Caption box, enter the name of the button.
4. In the URL box, enter the URL, which can include the desired study/user parameters.
5. To use a basic user name (without the substring starting with @), select the Use Basic User check box.
6. To execute the action button only on studies where the site ID matches the local site ID, select the Filter by Site ID check box.
7. Add an optional third-party password in the Password field, if required.
8. To use DICOM parameters of the primary study (not the study of the active image), select the Work on Primary Study check box.
9. For automatic execution of the action button on starting a new session, select the Open on Start Session check box.
10. Click OK to save your changes and close the dialog box.

Using DICOM Tags

Any DICOM tag can be used as a parameter for the action button command line. The tag name must be written in capital letters and surrounded by @. For example: @PATIENTS_NAME@.

A full list of valid DICOM tags can be found in Section 3.6 of the DICOM standard, which is available online. Some useful study level tags are:

@ACCESSION_NUMBER@

@PATIENT_ID@

@STUDY_INSTANCE_UID@

@PATIENTS_NAME@-

NOTICE! The following pseudo-tags provide access to parts of the patient name, including:

- patients_first_name
- patients_middle_name
- patients_last_name

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In a multi-study scenario (for example, a study is that is loaded with its history), the study whose information is sent depends on the currently selected group.

If the application's focus is set on one of the groups, the study to which the group belongs is the study from which the DICOM information is extracted.

If no group is in focus, the DICOM information is extracted from the primary study.

Series and Image Level DICOM Parameters

Series and image level DICOM tags can also be used. The DICOM information is determined by the active (in focus) group/image. If an active group is not set, the series and image level tags are sent empty.

Application Parameters

The following application parameters are supported:

@user_name@—The user name used to log in to the Diagnostic Workstation.

@display_name@—The current user's display name.

15.12 Configuring Monitor Settings

1. Open the Application Settings window (see Opening the Application Settings Window on page 453).
2. In the left pane, select Monitor Configuration.
3. The Application Settings window shows the Monitor Configuration options, which are automatically detected upon installation.

   NOTICE! This screen is not relevant if you have only one monitor.
4. Select the Image Display checkbox to select which monitors should display the Viewstation.
5. Select the Image Display checkbox to select which monitors should display the Viewstation.
6. Click OK.

NOTE

The current system setup accommodates up to 5 monitors. You can arrange these monitors in the following configurations:

4 diagnostic (DX) monitors plus 1 administrative monitor.

or

3 diagnostic (DX) monitors plus 2 horizontal administrative monitors.

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Drawing Method

The system automatically chooses the best-fitting technology for the display of images on screen. Unless otherwise directed, do not change the default settings in this section of the window.

15.13 Configuring Network Bandwidth Settings

1. Open the Application Settings window (see Opening the Application Settings Window on page 453).
2. In the left pane, select Network Bandwidth Configuration.

   The Application Settings window allows you to select a login mode. You can choose to always use the local network to log in, always use the Internet connection to log in, or allow the system to automatically detect which of these modes is optimal for login (at first-time login).

   You can also choose to use compression while saving.

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16 Using the Vue PACS Viewer

16.1 Using Applications

16.1.1 About Applications

An application in Vue PACS allows you to view and manipulate images and define where you can place different groups of images. You can have multiple applications open on the monitor. The open applications appear in the Application Navigation bar at the top right corner of the screen. Only one application can be active at a time. Click the application tab to switch between applications.

Application Name	Description
About the PowerViewer Application on page 151	Displays one or more groups of images as 2D images. See About Groups on page 560.
About Multi-Planar Reformatting (MPR) on page 159	Displays reconstructed cross-sections of data in the Axial, Sagittal, and Coronal views (multi-planar reformatted data).
About 3D Data on page 183	Displays studies in 3D, with bone removal and tissue definition, but without vessel analysis.
About Volume Matching on page 283	Lets you register three-dimensional studies taken at different times or by different modalities (CT and MRI).
About the Hybrid Nuclear Medicine (NM) Application on page 291	Lets you view the combined image data from any two complementary CT, MR, PET, or SPECT examinations. Current and prior (history) images are combined to easily show progress in areas of pathology (whether a tumor has increased or decreased). The PET/CT is an image viewer, a registration tool, and an analysis workstation.
About Vessel Analysis on page 213	Lets you segment a new vessel in addition to already defined vessels. Once the vessel has been segmented, you can toggle between the views of each vessel by selecting the appropriate central line.
About the Cardiac CT Application on page 238	Lets you view the various phases of the heart, view the heart axis images.
About Coronary Analysis on page 264	Lets you perform a full morphological review and quantitative analysis of the coronary arteries. For more information, view the topics listed under Coronary Analysis (see About Cardiovascular Reading on page 251).

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About Calcium Scoring on page 277	Lets you analyze coronary calcified plaque regions in a given set of 2D CT images. It also provides reports to correlate the score to any risk of coronary artery disease. For more information, view the topics listed under Calcium Scoring (see About Calcium Scoring on page 277).

In addition, you can change any of the 3D images to be displayed as one of the following rendition types:

- Angiography MIP: Calculates and displays two-dimensional projections of the highest intensity pixels in a three dimensional volume of interest. These images can demonstrate contrast-enhanced vascular structures and other high-density tissue or respiratory airways. For more information, view the topics listed under About 3D Data on page 183.
- Volume Rendering: Calculates and displays three-dimensional structures and images using acquired CT or MRI images. For more information, view the topics listed under About Volume Rendering on page 632.

See these topics:

Opening a New Application on page 478

Working with Multiple Applications on page 479

Toggling Between Applications on page 479

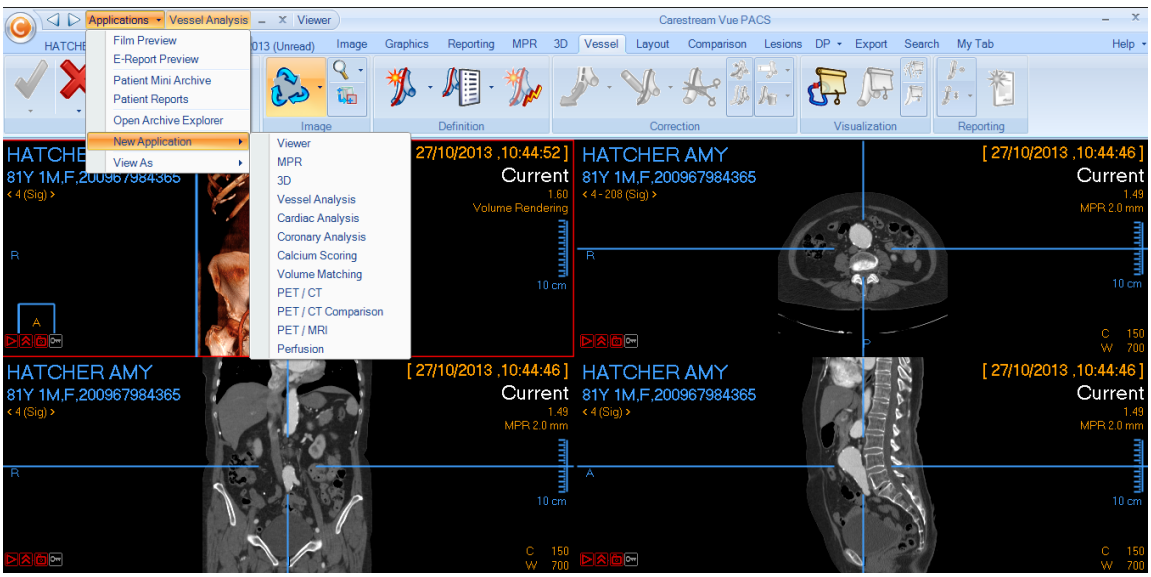
Closing an Application on page 479

Configuring Layouts on page 456

About Viewbox Configuration for Display Protocols on page 602

16.1.2 Opening a New Application

To open a new application, select New Application from the Application menu.



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16.1.3 Working with Multiple Applications

If you have multiple monitors and want to display multiple applications, you can select any single application view to fill the entire Viewer.

- To minimize an application display, click the - in the Application Navigation bar.
- To maximize an application display, click on the application tab in the Application Navigation bar.



16.1.4 Toggling Between Applications

1. To toggle between open applications, click the desired application in the Application Navigation bar at the top left corner of the screen.

   Or

   Click the navigation arrow at the left end of the Application Navigation bar.



To open a new application (see Opening a New Application on page 478), select New Application from the Applications menu in the Application Navigation bar.

16.1.5 Clearing Images from the Active Group

You can clear images from of the active group in the Viewer application.

To clear images from the active group:

1. Hover with the mouse over the group-level toolbar icon  at the top of the group display area.

   ⇨ The dynamic toolbar appears.
2. The dynamic toolbar appears.

16.1.6 Closing an Application

Click x in the Application Navigation bar.



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16.2 Using the Patient Mini-Archive

16.2.1 Opening the Patient Mini-Archive

The Patient Mini-Archive (PMA) provides a complete portfolio of all the studies and reports for the patients that have been loaded into a specific reading session. For each patient, the PMA displays a list of the studies available in the archive, according to the filter selected, as well as an indication of whether each study has a report or order associated with it. The list includes both currently loaded studies and those that are not loaded (for example, previous studies from the patient's history).

See Loading Studies on page 488 for information about loading studies that appear in the PMA, but are not currently loaded in the Diagnostic Workstation.

NOTICE! The specific display protocol in use determines which studies are loaded into the PMA. When the PMA is open, the contents refresh each time you load a new patient.

To open the PMA from a menu:

Click on the Patient Mini Archive icon  in the Workflow toolbar.

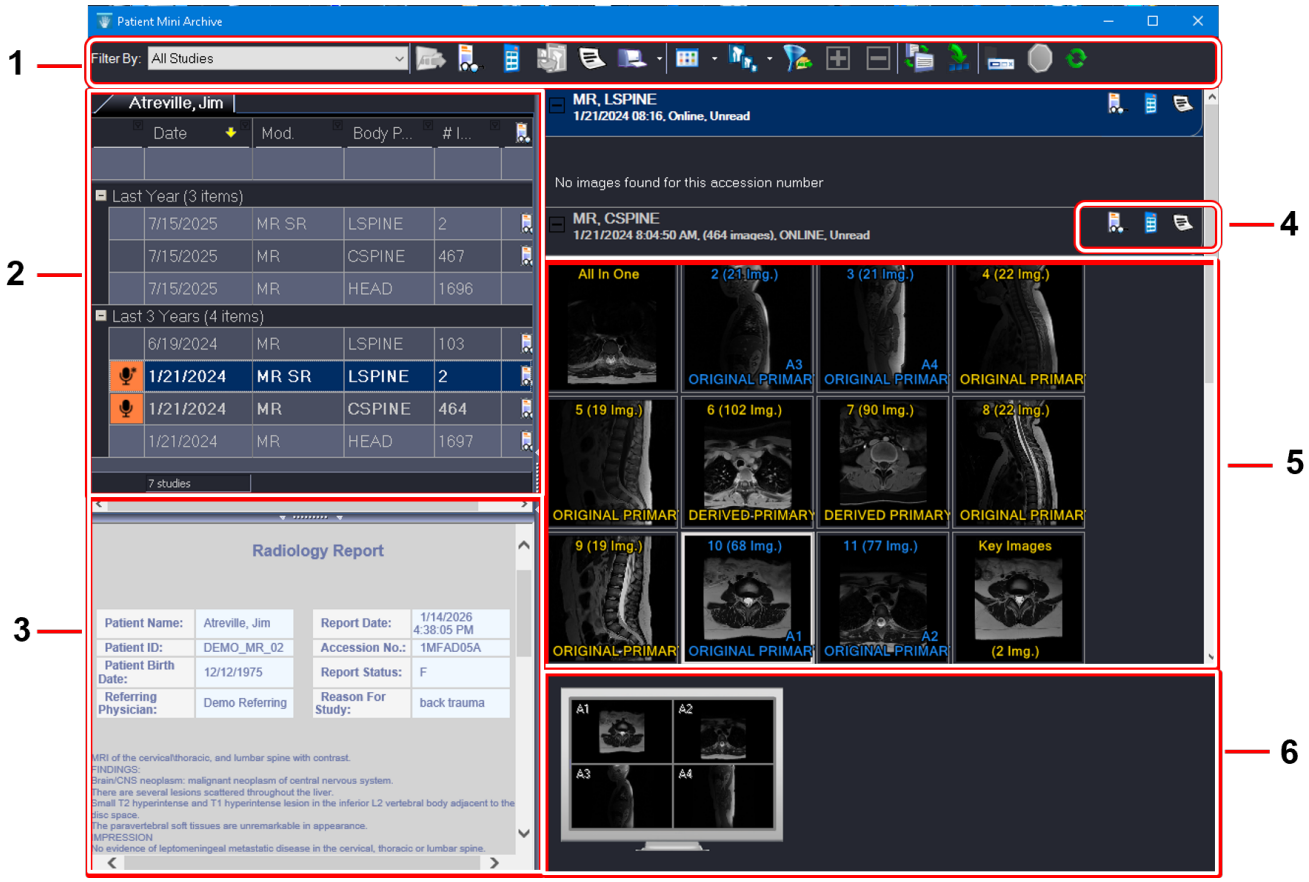
16.2.2 Patient Mini-Archive Overview

Go to the Workflow toolbar and click PMA .

Use the Patient Mini-Archive (PMA) to:

- Filter relevant information in a mini-archive (patient portfolio, prior studies, reports, sticky notes, order information).
- Place additional studies or series on screen.
- Re-arrange existing data.
- Load additional studies or series.

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1	Patient Mini-Archive Toolbar on page 71 The study in context is selected in the **List of Studies** pane.
2	**List of Studies pane** Provides the list of patient studies, allowing you to review the entire patient's portfolio. The List of Studies is grouped per period and contains information icons on each study. **NOTICE! The periods are configurable.**
3	**Report Preview** Displays a preview of the report of the selected study.
4	**Study-level toolbar** Displays information about the study. Indicates if the study has order information, reports, or sticky notes. Queried-only studies can also be loaded.
5	**Series Thumbnails pane** Displays the series thumbnails for each loaded or queried study.

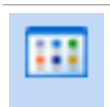
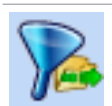
6	**Mini-Monitors pane** Displays the current layout and data for the monitors. You can drag series thumbnails directly to the Mini-Monitors pane to modify and organize data. Monitors are labeled alphabetically. You can also right-click on the mini-monitors to modify the Viewer layout.

Use List of Studies to control which studies are shown in the Series Thumbnail pane. Click the series icon in Series Thumbnails and drag the icon to a location in Mini-Monitors.

Patient Mini-Archive Toolbar



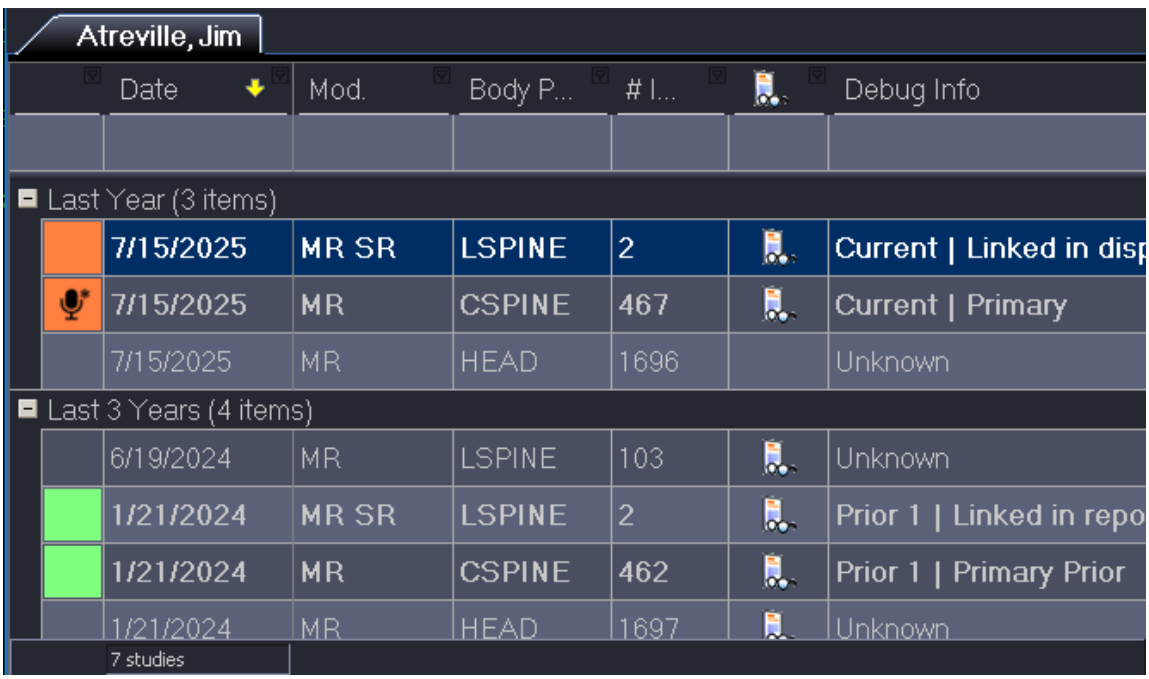
The Patient Mini-Archive toolbar lets you navigate through the displayed information in the Patient Mini-Archive.

Icon	Description
	Load the studies selected in the List of Studies pane.
	Show the report for the selected study.
	Show the order for the selected study.
	Open the Sticky Note dialog for the selected study.
	Print selected studies or groups of images.
	Select thumbnails, text or report view forms.
	Change thumbnails' size.
	Show Loaded studies only.
	Expand all studies.

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Icon	Description
	Collapse all studies.
	Toggle the view between a side-by-side pane view and a view where one pane is on top of the other.
	Switch the Patient Mini-Archive to strip mode.
	Minimize the Patient Mini-Archive
	Stop loading the selected study.
	Update the study with new images.

List of Studies Pane



The List of Studies pane shows the following information about the studies:

- Patient studies are grouped per period and can be sorted according to ascending or descending order.

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- The studies are labeled with colors corresponding to the Current/Prior annotations in the display.
- Linked studies (link in reporting) or studies linked in display (Display Set) are indicated by the same color as primary study.

The following information is indicated by icons for each study in the list:

Icon	Description	When it is shown
	Primary study (reporting context)	Indicates the primary study loaded from the worklist **when the user is in reporting mode**.
	Primary study (view only context)	Indicates the primary study loaded from the worklist **when the user is not in reporting mode** (non-reporting user or view only mode).
	Study linked in reporting (reporting context)	Indicates a study that is **linked to the primary study in reporting**, while the primary study is open in reporting mode.
	Report	Opens the report associated with the selected study (preliminary or final, if available).

Study-level Toolbar

The study-level toolbar lets you perform actions related to the currently loaded study.

Icon	Description
	Opens the Sticky Note dialog for the selected study.
	Shows the report for the selected study.
	Shows the order for the selected study.
	Automatically retrieves the newly acquired images of the current study.

16.2.3 Using Filters and Columns in the PMA

The List of Studies pane provides the following columns: Study Description, Accession Number, Study Time, Study Availability, Study Status, # of Series, Orders, Sticky Notes, Has Key Images, and Has Significant Series. You can filter the displayed studies by entering any value in the line below the table headers.

The patient studies are grouped by periods, which indicate how recently a study was taken.

1. Right-clicking the header area will add a column. Select Field Chooser and select a column from the list. You can drag the column to the List of Studies pane.

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2. Right-clicking the column header and selecting Remove Column removes the column.

16.2.4 Viewing Studies and Reports Together

1. In the Series Thumbnails pane, click View Type  > Report View.
2. Click a study in the List of Studies pane. The most recent applicable report for the study displays in the right pane (Series Thumbnails).

16.2.5 Viewing DICOM Information

1. To view information dynamically, place the cursor on a series. A tool tip shows the title of each DICOM tag and the complete tag value.
2. To view DICOM information constantly click View Type  > Text View.

NOTICE

View Type  > Text View only provides additional DICOM tags, which are configurable.

16.2.6 Changing the Size of Thumbnails

In the Series Thumbnails pane, click Change Icon Size .

Select:

Small—best for studies with many series, such as MR.

Standard—the default size.

Large—best for studies with few series, such as CR or CT.

16.2.7 Changing the Layout of the PMA

1. You can change the PMA layout to show all the panes horizontally or vertically. The PMA layout is saved between sessions/logins.
2. To change the layout, click Change View Layout .
3. Click and drag the pane border to dynamically change the position of the border up/down or left/right.
4. Click the pane border once to move the pane to the edge of the window.

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16.2.8 Using the PMA While an Administration Monitor is Not Available (Strip Mode)

The PMA has another display mode, which is a limited view of the PMA. The PMA Strip Mode presents all the patient studies in separate tabs.

Place the mouse cursor over or click on any tab to show the study's series thumbnails.

Drag any series directly to the Viewer.

Additional series information is available in a tooltip. Place the mouse cursor on the relevant series thumbnail to display the tooltip.

Click the relevant icon on the left pane to open the report, the order information, and the sticky note of the study.

The annotation color of the thumbnails changes to blue while the series is displayed in the Viewer.

NOTICE! By default, the body part DICOM tag is displayed on the study tab. If no body part is available for the study, then the study description tag is displayed. You can configure both tags in Application Settings.

16.2.9 Loading Studies in the PMA

1. You can load an entire study from the List of Studies pane or Series Thumbnails pane:
2. Double-click the study.
3. Select the study and click Load Study .
4. Right-click the study and select Load, Load Key Images, or Load Significant Series.

16.2.10 Querying Studies in the PMA

Click once on the study in the left pane or right-click and select Explore. The study's series shows in the Series Thumbnails pane. To load a queried-only series:

- Use any of the loading methods for an entire study (above).
- Drag the series to the Mini-Monitors pane.
- Drag the series to the Viewer.

16.2.11 Placing a Group in the Display Area

Double-click on a group to place it in the first available group display area. If no spot is available, the group is placed at the top left corner, replacing the currently displayed group.

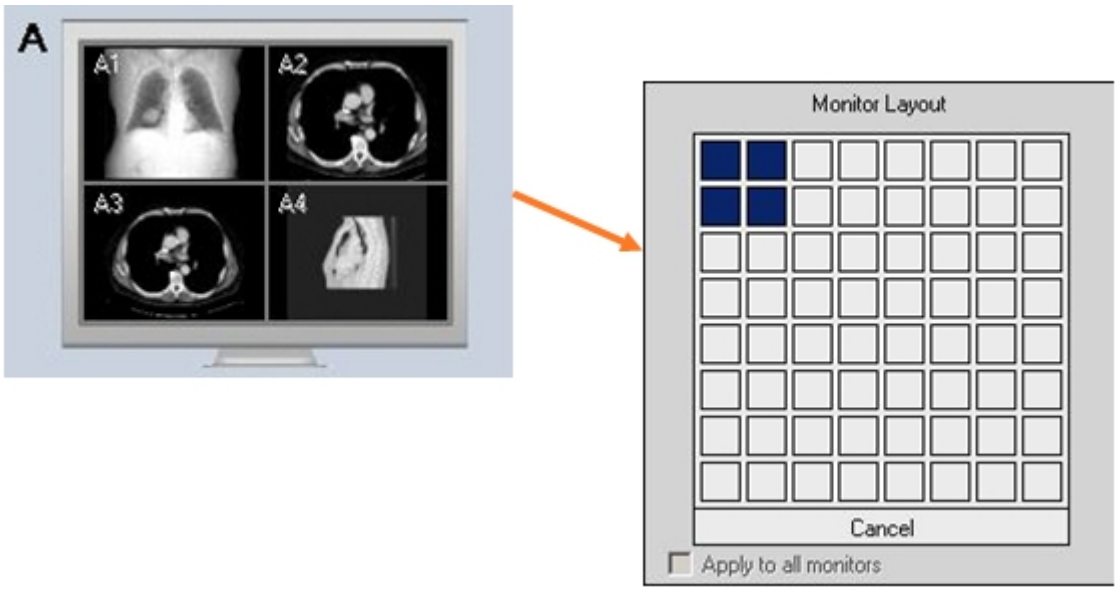
16.2.12 Changing the PMA Mini-Monitors Layout

Right-click the Mini-Monitor pane.

Drag the mouse cursor over the squares to define the layout.

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16.2.13 Viewing Information in the Patient Mini-Archive

The following information is displayed in the Patient Mini-Archive.

Toolbar	Shows the default study filter. By default, the Same Body Part filter is applied.
Patient Name	The name of the selected patient (Last, First, Middle).
Study Header	• The date, time, and the number of images in the study. • A link if the study has an associated report or order. • Studies that are currently loaded in the Diagnostic Workstation appear in bold and show the different groups of images that are loaded. • Studies that are available, but not currently loaded, appear in regular font and are collapsed. (If you click ⊞ next to the name of the study, a dialog box appears, enabling you to load the entire case or only key images.)
Groups Area	• A thumbnail of the first image of the loaded group. If a thumbnail does not appear, contact the system administrator to configure the thumbnail display option. • DICOM information for the group, such as the number of images in the group, the image type, and the series number. A tooltip shows the group rule tags. All available groups appear according to the series number. Groups appearing in white text are currently displayed in the Viewer. Groups appearing in gray text are not currently displayed in the Viewer. Groups that automatically run cine when loaded are marked with a movie icon in the group thumbnail.

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NOTICE

You can click the R, O, or N link in the Study Header only if the Diagnostic Workstation has been properly installed and configured.

You can also click Collapse in the Study Header to collapse the individual study. When all the studies are collapsed, use the toolbar options to scroll through the Study Headers. The study is expanded when you click .

See this topic:

Patient Mini-Archive Toolbar on page 71

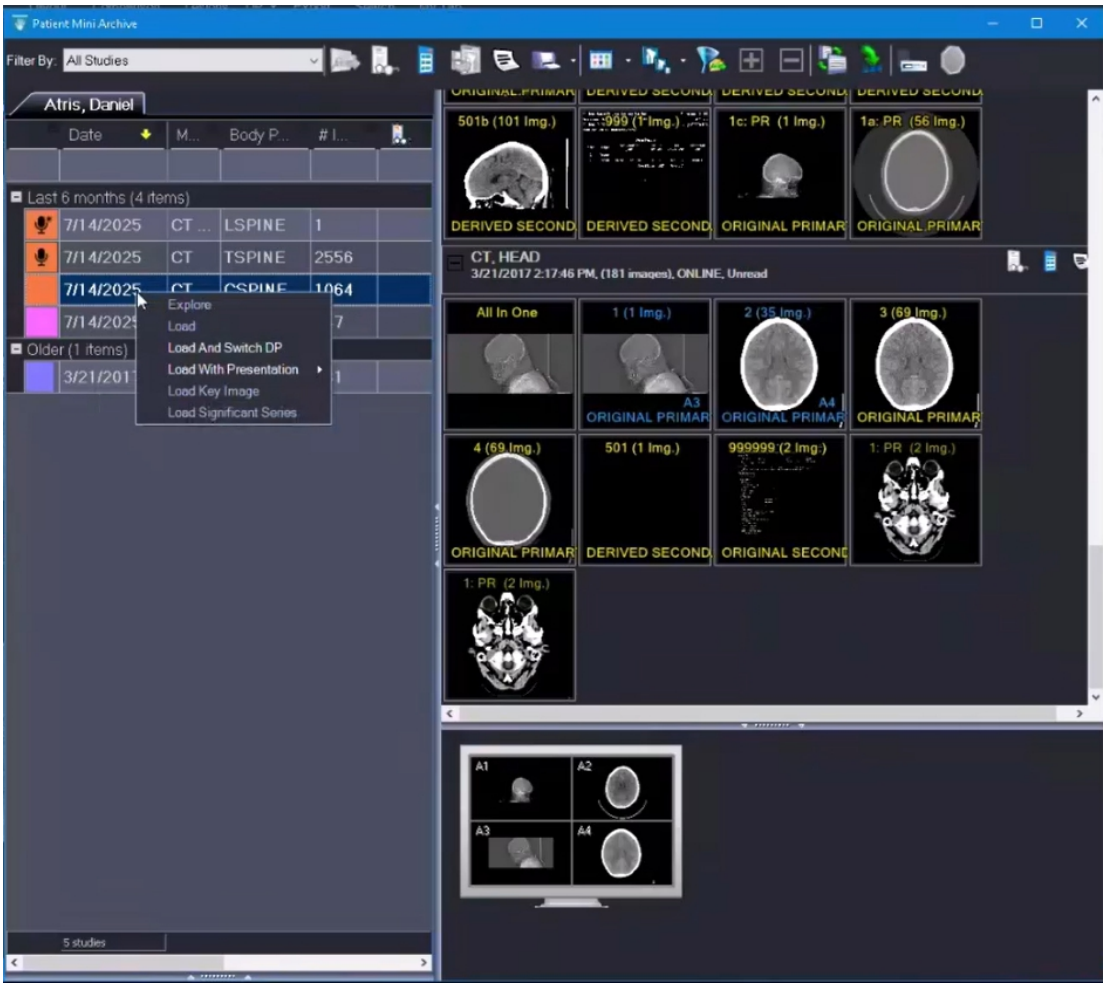
16.2.14 Loading Studies

Studies that are available but not currently loaded are indicated by a Study Header that appears in underlined italics. You can load an entire study, key images or significant series.

1. To load an entire study from the List of Studies pane or Series Thumbnails pane:
2. Double-click the study.
3. Select the study and click Load Study .
4. Right-click the study and select one fo the following options:
   - Explore
   - Load
   - Load and Switch DP
   - Load with Presentation
   - Load Key Image
   - Load Significant Series

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5. You can stop the loading of a study by clicking  in the Patient Mini-Archive toolbar. The partially loaded study will be marked in the Series Thumbnails pane with a dotted border, and an annotation indicating that the study has not fully loaded will appear on the relevant images. To continue the loading, click Complete  in the Patient Mini-Archive toolbar.

16.2.15 Dragging Groups to a Group Display Area

You can drag a group of images from a study loaded in the Patient Mini-Archive to a group display area.

To drag a group to a default view type:

From the Patient Mini-Archive, drag a group to the viewbox. The group displays according to the default view of the display area.

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To drag a group and manually select the group view type:

1. From the Patient Mini-Archive, right-click the group you want to display, then drag it to the viewbox.
2. Select one of the available applications.

   Options include Viewer, MPR, 3D, Vessel Analysis, Cardiac CT, Coronary Analysis, and Calcium Scoring.

In place of dragging a group to the group display area, you can also drag groups to the mini-monitor in the Patient Mini-Archive.

See this topic:

Patient Mini-Archive Overview on page 480

NOTICE! In addition to dragging a group to the display area, you can place a group in the display area by double-clicking it in the Patient Mini-Archive. The group is placed in the first available group display area. If no spot is available, the group is placed at the top left corner, replacing the currently displayed group.

16.2.16 Printing from the Patient Mini-Archive

You can print entire studies or specific groups of images directly from the Patient Mini-Archive.

1. Select the study or a group of images.
2. Click Print  to send the job to the default printer.

   or

   Click Ctrl + , then select the required printer in the Printers dialog box.

   ⇨ The images are displayed in the Film Previewer according to the default layout. When printing is complete, all images are removed from the Film Previewer.

By default, clicking Print  enables you to print immediately, and clicking Ctrl +  displays the images in the Film Previewer and shows the Printers dialog box. You can reverse the configuration option (from Application Settings) so that Ctrl +  enables immediate printing and  opens the Printers dialog box.

By default, you can print as many pages as required when selecting an entire study. You can select that a warning message be displayed when the number of pages to be printed exceeds a configurable number (see Configuring Printing Settings on page 465), which by default is three.

If the study contains unprintable matter (for example, tissue), these images will not be printed and no warning message will appear.

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NOTICE

The layout of the printed page is the default layout for the Film Preview that is configured for the type of images sent. For example, printing the prior MR study for a current CT study will populate the default MR layout. You can configure the default layout in the Application Settings page.

You can change the print layout by clicking the Film Layout icon.

The Print icon  is disabled in the following cases:

- A study is being loaded.
- The selected study has not been loaded. For example, prior studies that were not loaded by default.
- Selecting a group of images that cannot be printed, for example, a tissue group.
- No printers are defined.
- The user profile does not have printing permissions.

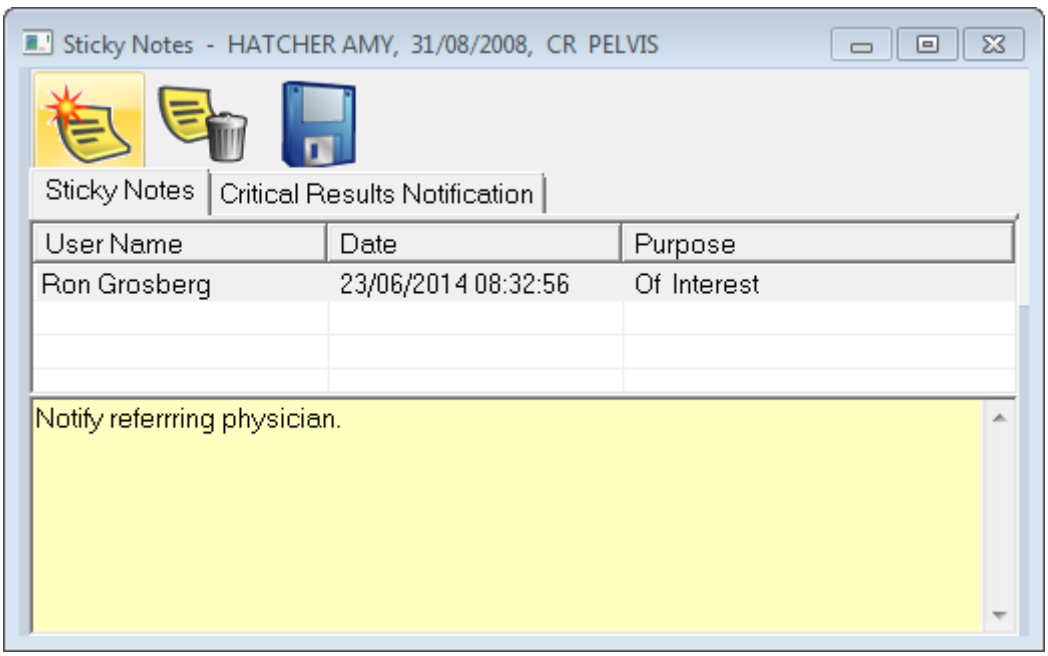
16.2.17 Using Sticky Notes

Sticky Notes are notation files that you attach to studies.

An Open Sticky Notes icon is available in the Patient Mini-Archive toolbar, and in the header of each study.

The icon is yellow if a sticky note is attached to the study.

Click the icon to open the Sticky Notes window.



To add a sticky note:

► Click on the Sticky Notes tab.

► Click on the Sticky Notes icon at the top left.

⇨ Your user name appears at the top part.

► Type the text of the sticky note at the bottom section of the dialog.

16.2.18 Patient Mini-Archive (PMA) Strip

By default, the PMA strip appears as a strip at the bottom of the Diagnostic Viewer screen. It displays the same information as PMA, but in a different layout.



Color annotation

The exam tabs are labeled with colors corresponding to the Current/Prior annotations in the display.

Linked studies (link in reporting) or studies linked in display (Display Set) are indicated in the PMA strip by the same color as primary study.



Exam tabs

The exam tabs in the Strip PMA are displayed in chronological order, with the most recent exam shown first.

The following information can be indicated by icons on each exam tab:

Icon	Description	When it is shown
	Primary study (reporting context)	Indicates the primary study loaded from the worklist **when the user is in reporting mode**.
	Primary study (reporting context)	Indicates the primary study loaded from the worklist **when the user is in reporting mode**. A preliminary or final report exists already for this study.
	Primary study (view only context)	Indicates the primary study loaded from the worklist **when the user is not in reporting mode** (non-reporting user or view only mode).

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Icon	Description	When it is shown
	Primary study (view only context)	Indicates the primary study loaded from the worklist **when the user is not in reporting mode** (non-reporting user or view only mode). A preliminary or final report exists already for this study.
	Study linked in reporting (reporting context)	Indicates a study that is **linked to the primary study in reporting**, while the primary study is open in reporting mode.
	Study linked in reporting (reporting context)	Indicates a study that is **linked to the primary study in reporting**, while the primary study is open in reporting mode. A preliminary or final report already exists for this study.
	No images available	Indicates that the study or order does not contain any images.
	Report	Indicates that a preliminary or final report exists for this study.

Thumbnail images

To view the details and thumbnail images of the exam, hover over the exam tab.

A toolbar is displayed to the left of the thumbnail images:



The toolbar lets you perform actions related to the currently loaded study.

Icon	Description
	Open the Sticky Note dialog for the selected study.
	Show the report for the selected study.
	Show the order for the selected study.
	Automatically retrieve the newly acquired images of the current study.

Drag exams from the PMA strip

You can drag an exam from the PMA strip to a group display area to display it in the viewer. The result depends on where you drop the exam and which option you select.

NOTE

Drag and drop is not available for empty orders.

Exams without images cannot be dragged from the PMA strip.

Drag to an empty GDA (not reserved by a Display Protocol)

- The exam is displayed across all monitors
- All GDAs on all monitors show series from the dragged exam.

This provides a quick way to load and view an exam without applying a specific Display Protocol.

Drag to a GDA that already displays an exam (or to an empty viewbox but reserved by a Display Protocol)

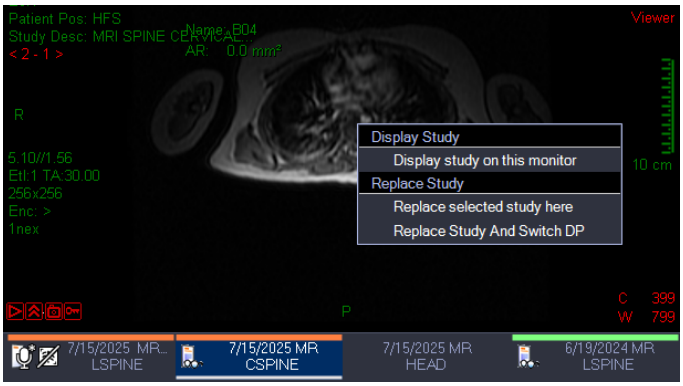
When you drag an exam to a viewbox that already displays an exam, you can select one of the following actions:

- Display the exam on the selected monitor.
  - This fills all GDAs on the selected monitor with series from the dragged exam.
  - Other monitors remain unchanged.
- Display the exam on all monitors.

  This fills all GDAs on all monitors with series from the dragged exam.
- Replace selected study here
  - This replaces the study currently displayed in that GDA with a series from the dragged exam.
  - All GDAs – on all monitors – that belong to the replaced study are also filled with series from the dragged exam.
- Replace study and switch Display Protocol
  - This reloads the viewer using the most relevant Display Protocol for the dragged exam
  - All monitors are updated according to the selected Display Protocol.
  - Additional studies may be loaded automatically, as defined by that Display Protocol.

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NOTE

The following applies to all options described above:

The primary study indication in the PMA strip does not change.

The original study loaded from the worklist remains the primary study, as it is still the study open for reporting.

Current/Prior annotations remain unchanged.

Any additional study loaded through drag and drop is assigned a Newer or Prior annotation based on its acquisition time relative to the primary study.

16.3 Manipulating Images

16.3.1 About Images

You can emphasize important features and analyze and measure images.

See these topics:

Zooming in on Images on page 496

Panning Images on page 496

Flipping Images on page 496

Rotating Images on page 496

Magnifying Images on page 497

Calibrating Images on page 497

Displaying Images in True Size on page 498

Sharpening/Smoothing Images on page 498

Removing Image Artifacts with CR Grid Detection on page 499

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16.3.2 Zooming in on Images

NOTICE! Zoom is the default for the left mouse button.

1. From the Viewer, select the image(s) you want to zoom.
2. In the Image tab of the toolbar, click Zoom .
3. Hold down the left mouse button and do one of the following:
   - Drag the mouse up to increase the zoom factor.
   - Drag the mouse down to decrease the zoom factor.
4. To zoom in on a particular point within the image, press the Alt key, then zoom in.

   The image will be zoomed from the point clicked on the image, not from the center of the image.

   In all cases, the zoom out option will zoom out from the point clicked on the image.

16.3.3 Panning Images

NOTICE! Press the Shift key to toggle between pan and zoom.

1. From the Viewer, select the image(s) you want to pan.
2. In the Image tab of the toolbar, click Pan .
3. Drag the mouse to pan the image.

16.3.4 Flipping Images

1. From the Viewer, select the image(s) you want to flip.
2. From the Image tab of the toolbar, select a flipping option:
   -  Reverses the image display from left to right (flips horizontally).
   -  Reverses the image display from top to bottom (flips vertically).

16.3.5 Rotating Images

1. From the Viewer, select the image(s) you want to rotate.
2. From the Image tab of the toolbar, select a Rotate option:
   -  Rotates the image 90° to the right.

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-  Rotates the image 90° to the left.

16.3.6 Magnifying Images

1. From the Viewer, select the image(s) you want to magnify.
2. In the Image tab of the toolbar, click Magnify .
   - Press Alt and move the cursor to adjust the default size of the magnifying glass area.
   - Press Ctrl and move the cursor to increase the zoom level while leaving the area of the magnifying the area of the magnifying glass the same.
   - Press Shift to change the windowing within the area of the magnifying glass.

16.3.7 Calibrating Images

You can define the mm/pixel settings for images that do not include mm/pixel data, then use these settings to perform accurate measurements.

1. From the Viewer, select the image you want to calibrate.
2. In the Graphics tab of the toolbar, click Scale Calibration .
3. On the image, click once, and then a second time to select the required number of points in a straight line.
   ⇨ When you click on the second point, the Calibration Settings window appears.
   ⇨ **NOTICE! Try selecting points on the distance marker if available. If no marker is available, select points of a well-defined distance. The number of required points depends on the configuration that was defined during installation.**
4. Type the value to be assigned to the distance between the points on the image.
5. Click OK.

16.3.8 Performing True Size Calibration

The Diagnostic Workstation can be calibrated so that images display in True Size (that is, 1 cm on the screen equals 1 cm actual).

True Size calibration is performed whenever it is needed upon the user demand.

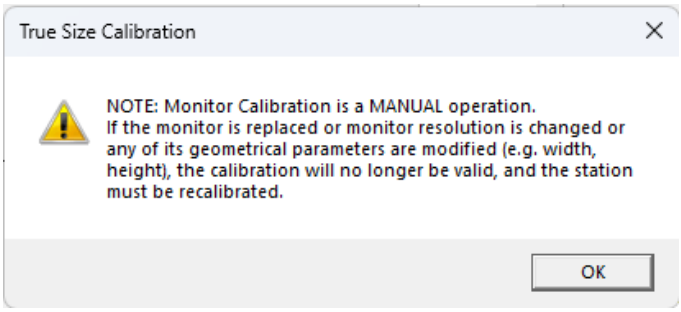
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CAUTION

Recalibration of the True Size tool is required whenever:

- **Monitors are replaced**
- **Screen resolution, scale, or display orientation is changed**
- **Monitor configuration in MP is modified**

The calibration tool must be launched externally. For assistance, contact your System Administrator.



16.3.9 Displaying Images in True Size

NOTICE! The Diagnostic Workstation can be calibrated so that images display in True Size (that is, 1 cm on the screen equals 1 cm actual). See Calibrating Images.

True Size images appear with a zoom annotation indicating the percent of its size relative to its True Size (for example, 46% True).

NOTICE! You cannot perform True Size where the height and width ratio of the image viewbox is greater than 3%.

1. Right-click the zoom annotation on the image.
2. Select one of the following:
   - Fit To Window: Expands the image to fit the entire group area.
   - True Size: Displays the image in True Size (1 cm on the screen = 1 cm actual).
   - Original Resolution: Displays the image in the original resolution at which it was scanned. One data point in the image appears as one pixel on the screen. The actual displayed size of the image in Original Resolution depends on the number of pixels of the display monitor.

16.3.10 Sharpening/Smoothing Images

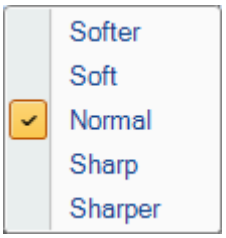
You can sharpen or soften images or a group of images displayed in the Viewer by using predefined values. If you save the images after enhancement, the images are saved as a new copy of the image or as a new group.

NOTICE! The enhancement values are defined when your system is installed and configured. For details about these values, see the system administrator.

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1. From the Viewer, select an image or a group of images.
2. In the Image tab of the toolbar, click Enhance .
3. Select an option from the drop-down menu.



If you want to restore the original image settings, click the Normal option. All other enhancement options are relative to the normal settings for each selection.

16.3.11 Resetting Images

On an active image, you can reset settings to the original values.

1. In the Viewer, select the image(s) to be reset.
2. In the Image tab of the toolbar, click Reset .

The images return to their original zoom, orientation and windowing settings.

16.3.12 Removing Image Artifacts with CR Grid Detection

The CR Grid Detection removes or distorts image artifacts making it easier for the radiologist to view the image.

NOTICE! Contact the system administrator to activate this option.

16.4 Using Annotations and Measurements

16.4.1 About Annotations and Measurements

Annotations and measurements help you to analyze an image.

See these topics:

Drawing a Line on page 500
Drawing a Curve on page 501
Drawing an Oval (for a Region of Interest) on page 501
Drawing a Square (for a Region of Interest) on page 502
Drawing a Freehand ROI on page 502
Drawing a Persistent Oval Region of Interest on page 503

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Drawing a Sphere Volume of Interest on page 503
Adding a Cursor to Measure Pixel Values on page 504
Adding a Shape on page 504
Adding Text on page 505
Adding an Angle on page 505
Adding a Cobb Angle on page 505
Adding Multiple Cobb Angles on page 506
Adding a Spine Label on page 506
Measuring a Midline Shift on page 508

NOTE

When setting a new annotation field that is not part of default annotation fields, especially a DICOM tag, consult Philips representative beforehand, as it might not be saved in Philips database and may have implications when changing DICOM data.

16.4.2 Drawing a Line

NOTICE! This is the default for the left mouse button.

You can draw a line to measure the distance in millimeters between items in images. The graphic is added automatically as a bookmark. Open the Bookmark (see Using Bookmarks on page 344) list to see its details.

1. From the Viewer, select an image.
2. In the Graphics tab of the toolbar, click Line Measurement  in the Measurements ribbon.
3. Click on the image where you want the line to start.
4. Click where you want the line to end.

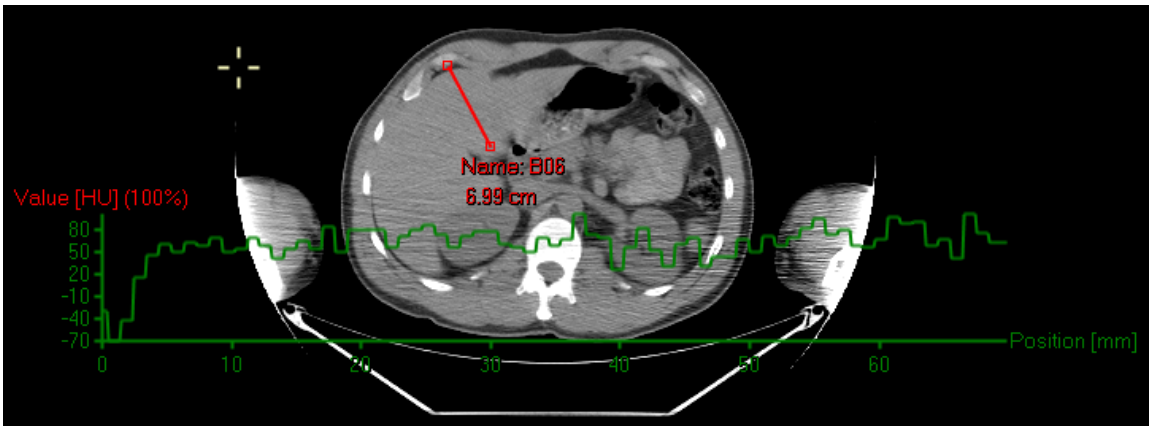
Right-click on the line

NOTICE

An image must have a calibration provided by the original scanner source or by manual calibration. See Calibrating Images on page 497.

Right-click on a drawn line and click Show Profile to display a curve showing the intensity values of the pixels along the line.

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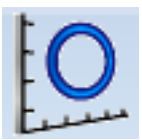
16.4.3 Drawing a Curve

You can draw a curve on an image to measure the length in millimeters of the curve. You can also manipulate a curve by changing one or more of its vertices (handles) without having to draw a new curve. The graphic is added automatically as a bookmark. Open the Bookmark (see Using Bookmarks on page 344) list to see its details.

1. From the Viewer, select an image.
2. In the Graphics tab of the toolbar, click Curve Measurement  in the Measurements ribbon.
3. Click the location where you want to start the point of the curve.
   ⇨ A vertex (handle) appears at the selected point.
4. Click additional points, one after the other, to draw the curve.
   ⇨ Additional vertices appear at each point you click.
5. Double-click the last point to end the curve.

16.4.4 Drawing an Oval (for a Region of Interest)

You can draw a Region of Interest (ROI) to measure the area, average pixel value, and standard deviation of pixel values in an image. The graphic is added automatically as a bookmark. Open the Bookmark (see Using Bookmarks on page 344) list to see its details.

1. From the Viewer, select an image.
2. In the Graphics tab of the toolbar, select Oval ROI  from the ROI drop-down in the Measurements ribbon.
3. Click on the image where you want the ROI to start.
4. Click where you want the ROI to end.

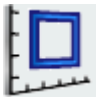
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⇨ The area of the ROI, the radius, and the average digital value and standard deviation of the digital values in the ROI are automatically measured.

To draw a circle, hold down the CTRL key while drawing.

16.4.5 Drawing a Square (for a Region of Interest)

You can draw a Region of Interest (ROI) to measure the area, average pixel value, and standard deviation of pixel values in an image. The graphic is added automatically as a bookmark. Open the Bookmark (see Using Bookmarks on page 344) list to see its details.

1. From the Viewer, select an image.
2. In the Graphics tab of the toolbar, select Square ROI  from the ROI drop-down in the Measurements ribbon.
3. Click on the image where you want the ROI to start.
4. Click where you want the ROI to end.

⇨ The area of the ROI, and the average digital value and standard deviation of the digital values in the ROI are automatically measured.

16.4.6 Drawing a Freehand ROI

You can draw a Region of Interest (ROI) to measure the area, average pixel value, and standard deviation of pixel values in an image. The graphic is added automatically as a bookmark. Open the Bookmark (see Using Bookmarks on page 344) list to see its details.

1. From the Viewer, select an image.
2. In the Graphics tab of the toolbar, select Freehand ROI  from the ROI drop-down in the Measurements ribbon.
3. Click on the image where you want the ROI to start.
4. Draw the area you want as the ROI by moving the mouse.
5. Click where you want the ROI to end.

⇨ The area of the ROI, and the average digital value and standard deviation of the digital values in the ROI are automatically measured. The start and end points will always be connected.

16.4.7 Changing the Freehand ROI Area

To replace a section of the boundary of the ROI:

1. Place the mouse cursor on the line where you want to start the change.

⇨ The cursor changes to a four-way arrow.

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2. Hold down the Shift key and draw the new line, joining to a point on the original freehand shape.
3. Release the mouse button.

⇨ The new line replaces the original line between those points.

To remove a segment while drawing the ROI:

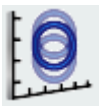
- To remove a small segment of the boundary while you are still drawing, press the Backspace key.

16.4.8 Drawing a Persistent Oval Region of Interest

NOTE

This functionality can be used only in the MPR application.

You can draw an oval Region of Interest (ROI) on a slice, and the ROI will then be shown on all of the images in the group, displaying area measurement, average pixel value, standard deviation and range of pixel value. The graphic cannot be added as a bookmark.

1. From the Viewer, select an image.
2. In the Graphics tab of the toolbar, select Persistent Oval  from the ROI drop-down in the Measurements ribbon.
3. Click on the image where you want the ROI to start.
4. Click again when the ROI is defined.

16.4.9 Drawing a Sphere Volume of Interest

You can draw a sphere Volume of Interest (VOI) on a CT or PET series of images to view the intensities in that volumetric area. The intensity values of the VOI are added automatically as a bookmark. Open the Bookmark (see Using Bookmarks on page 344) list to see the HU mean value for CT images, and SUV mean and max values for PET images.

NOTICE! Depending on configuration, in PET series, the highest intensity value of the sphere can be automatically displayed on the image. Contact your administrator.

1. From the Viewer, select an image.
2. In the Graphics tab of the toolbar, select Sphere VOI  from the ROI drop-down in the Measurements ribbon.
3. Click on the image to start drawing a circle.

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4. Click again when the area is defined.

The sphere (3D) is automatically created around the diameter of the drawn circle. The contours of the sphere (highlighted voxels) are displayed in each of the slices participating in the sphere.

Using a Pre-Set Size

Pressing the Shift key and clicking on the image while the Sphere VOI tool is selected causes the sphere to be drawn in a pre-set size.

Resizing such a sphere is done in pre-set steps.

To determine the pre-set sphere size -

1. Click on the Vue PACS icon at the top left corner and click Applications Settings (see Opening the Application Settings Window on page 453).
2. In the left pane of the Application Settings window, expand the Graphics and Measurements node and click Graphic Properties.
3. In the Constant Sized Sphere section, select the radius and step size.
4. Select the measurement units from the drop-down menus.

16.4.10 Adding a Cursor to Measure Pixel Values

Use a cursor to measure pixel values on an image.

1. From the Viewer, select an image.
2. In the Graphics tab of the toolbar, select Cursor  in the Measurements ribbon.
3. Click a specific point within the image to determine the pixel values.

16.4.11 Adding a Shape

Use an arrow or a shape to point or highlight features of interest on an image and to link features to corresponding text annotations. You can draw an arrow, an oval, a line, a square, a curve or a freehand shape. The graphic is added automatically as a bookmark. Open the Bookmark (see Using Bookmarks on page 344) list to view its details.

1. From the Viewer, select an image.
2. In the Graphics tab of the toolbar, select a shape from the shape drop-down  in the Markers ribbon.
3. Click on the image where you want the shape to start.
4. Click again when the shape is defined.

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16.4.12 Adding Text

Use text to superimpose annotations on images.

1. From the Viewer, select an image.
2. In the Graphics tab of the toolbar, click text  in the Markers ribbon.
3. Click the location in the image where you want the text to appear.
4. Type the text in the dialog box or select a predefined value from the drop-down menu.
5. Click OK.

16.4.13 Adding an Angle

Use angles to measure the angle in degrees between body features in an image.

1. From the Viewer, select an image.
2. In the Graphics tab of the toolbar, click Angle Measurement  in the Measurements ribbon.
3. Click on the image where you want the angle to start.

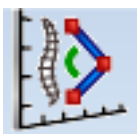
   Place the starting point at the edge of the feature that is farthest from the feature angle that you want to measure.
4. Click a second time at the intended position of the vertex (handle).
5. Click a third time where you want the angle to end.

   ⇨ The ending point should be placed at the edge of the second feature.

NOTICE! Press and hold the Control key to add a 90 degree angle.

16.4.14 Adding a Cobb Angle

You can measure spinal curvature according to the Cobb method. Click on the drop-down menu to choose a single Cobb angle or multiple consecutive angles (see Adding Multiple Cobb Angles on page 506).

1. From the Viewer, select an image.
2. In the Graphics tab of the toolbar, click Cobb Angle Measurement  in the Orthopedic Measurements ribbon.
3. Click on the image where you want the first line to start.
4. Drag the line to the vertebrae.
5. Click the mouse button.

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NOTICE! You can invert the image with the Window tool to get an accurate horizontal line to the vertebrae.

Move the line without affecting its integrity by using the center of the line and dragging, or tilt the line by clicking and dragging either end.

6. Repeat the move with the second line on another vertebra that you want to measure for the curvature.

NOTICE! More than one set of Cobb angles may be needed. These sets are labeled differently so you can distinguish between them.

16.4.15 Adding Multiple Cobb Angles

The Cobb Angle  graphics tool is used for measuring the curvature of the spine; the tool supports consecutive Cobb angles.

1. Click Cobb Angle .
2. Select two points on the image for the first line of the Cobb angle.
3. Select the next two points for the second line that will complete the first Cobb angle. If only a single Cobb angle measurement is needed, end the measurement.
4. Select the next two points for the line that will complete the next consecutive Cobb angle. The two points ending the previous Cobb angle also represent the first two points for this Cobb angle. If this is the final consecutive Cobb angle, end the measurement.
5. Repeat step 4 for additional consecutive Cobb angles measurements.

16.4.16 Adding a Spine Label

You can use predefined spinal markings for Cervical (C1-C7), Thoracic (T1-T12), Sacral (S1-S5) and Lumbar (L1-L5) annotations. You can use the Application Settings window (see Opening the Application Settings Window on page 453) to configure:

- The vertebrae to select (for example, only every second or third vertebra [Skip value]).
- Including vertebra annotations or disk annotations in the Spine Labeling dialog box.
- The first label selected when you launch Spine Labeling.
- The default value for the Spread Range.
- The default direction for spine labeling (top down or bottom up).
- The Apply on all Groups check box default label.

To add a spine label:

1. From the Viewer, select an image.

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2. In the Graphics tab of the toolbar, click Spine Labeling .
   ⇨ The Spine Labeling dialog box appears. It displays disks or vertebrae, depending on how it was configured.

- Mark the middle of the vertebra in the sagittal images so they will be properly displayed in the axial and coronary images.
- You can use other modes, such as zoom or pan, while implementing Spine Labeling.
- You can mark the spine labels on any image in the active group only.
- Axial images can display only one label. If you place a second label on the image, the first label is deleted and only the new label is displayed.
- Sagittal and coronal images can display multiple labels, but each label can be used once only. If you add T2 to an image that already has a T2 label, the first label will be updated and replaced by the new T2 label.

3. Click on the image where the annotations should be placed.
   ⇨ The spinal marking is automatically incremented. After the last marking in the series, the next applicable series starts. For example, the annotation after T12 is L1.
   ⇨ **NOTICE! By default, the spine labeling marked on a specific series is automatically displayed on other applicable series after the labeling process is complete. If required, deselect the Apply on all groups check box.**
4. Click Reverse to mark the vertebrae in reverse (for example when marking the Lumbar spines).
5. If required, change the spread range.
   ⇨ On sagittal and coronal images, spread range determines how far spine annotations marked on one slice should apply to far away slices of the same group. The system copies the markers above and below the set thresholds. On the axial slices, only the nearest slice is marked.
6. Click OK.

   Spine labels can be moved or deleted, and the color can be changed. Any changes affect only the selected label.

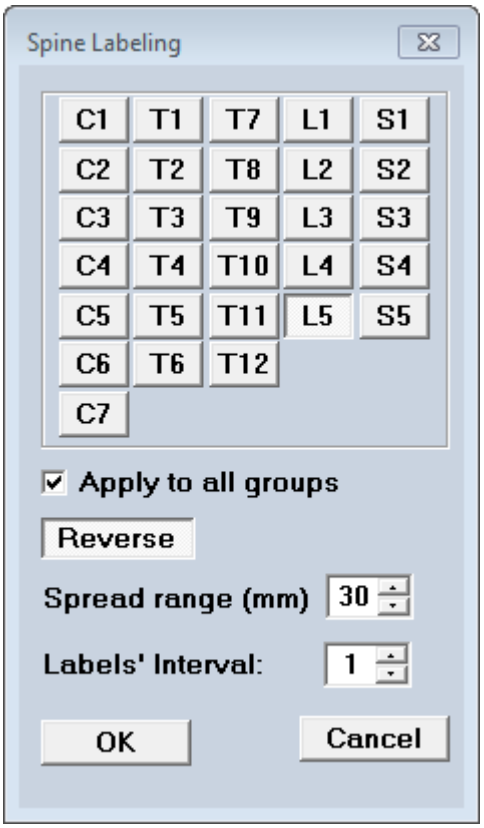
NOTICE! Click Cancel to cancel the current spine labeling session.

16.4.17 Spine Label Intervals

You can determine the deltas between the spine labels displayed on the spinal image.

Click the up and down arrows on the Labels Interval field and select an interval.

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16.4.18 Measuring a Midline Shift

16.4.19 Segmenting the Ventricles and Measuring their Total Volume

You can segment the ventricles on CT brain images.

1. From the Viewer, select an image.
2. In the Graphics tab of the toolbar, click Ventricles Segmentation  in the Neural ribbon.
3. Click on the image at any point inside the ventricles. The 3D segmentation of the ventricles is automatically drawn and the total volume is displayed.
4. Correct the segmentation using the segmentation correction tools.

16.5 Changing Annotations and Measurements

16.5.1 Changing Annotations and Measurements

You can move and change annotations and measurements that have been added to images.

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See these topics:

Changing the Font Size and Color of Annotations and Measurements on page 509
Moving a Measurement or Annotation on page 509
Rotating a Region of Interest (ROI) on page 509
Changing a Curve on page 509
Changing the Shape of a Measurement or Annotation on page 510
Hiding Measurements and Annotations on page 510
Using Graphic Shapes on page 510
Deleting Measurements or Annotations on page 511
Copying and Pasting Measurements or Annotations on page 511

16.5.2 Changing the Font Size and Color of Annotations and Measurements

You can change the font size and color of any graphic or text element that you manually added to an image (measurements, text, and so on). To change the font and color for all elements, refer to Configuring Viewer Colors and Appearance on page 467.

1. Select the element you want to change.
2. From the Graphics menu, select Properties.
   ⇨ The Graphics Properties dialog box appears.
3. In the Text Size field, select the size of the required text (between 8 and 30).
   ⇨ The size of only the selected text items is affected. For example, if you draw an ROI, then change the font size, only the font size of the ROI results (Area, SD, and Ave) change, not the font size of the ROI itself.
4. Select a color from the Color area.
   ⇨ The color of both the text and the graphic is changed.
5. Click OK.

16.5.3 Moving a Measurement or Annotation

1. Click the measurement or annotation you want to move.
2. Drag the measurement or annotation to the location you want.

16.5.4 Rotating a Region of Interest (ROI)

1. Left-click the element vertex (handle) on the ROI that you want to rotate.
2. Drag the vertex to the location you want.

16.5.5 Changing a Curve

1. Click the vertex (handle) that you want to move.
2. Drag the vertex to the location you want.

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16.5.6 Changing the Shape of a Measurement or Annotation

1. Click the vertex (handle) that you want to change.
2. Drag the vertex to the location you want.

16.5.7 Hiding Measurements and Annotations

To hide annotations:

1. Click Show Graphics .
2. Select Hide Annotations.
   ⇨ A check mark indicates that the Hide Annotations option is selected.

To show annotations:

1. Click Show Graphics .
2. Select Hide Annotations.

16.5.8 Using Graphic Shapes

You can add various graphic shapes to images.

1. From the Viewer, select an image.
2. Click Show Graphics .
3. Select Shapes.
4. Select a shape.

You can copy a graphic from one image to another (even if the images have different pixel spacing), within the same group or between groups.

- ► Right-click a graphic and select Copy.
- ► Select the image to which you want to copy the graphic.
- ► Right-click the new image and select Graphics > Paste Graphic.

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16.5.9 Deleting Measurements or Annotations

To delete individual measurements or annotations:

1. Click the measurement or annotation you want to delete.
2. Click Delete.

To delete multiple measurements or annotations:

1. Click Show Graphics .
2. Select Delete All Graphics.

16.5.10 Copying and Pasting Measurements or Annotations

You can copy and paste a measurement or annotation from one image to another, if each image shown in the Viewer has the same millimeter-per-pixel measurements.

1. From the Viewer, select an image.
2. Select the annotation that you want to copy, or add an annotation or measurement.
3. Click Ctrl + C to copy the annotation.
4. Click another image.
5. Click Ctrl + V to paste the annotation.

16.6 Configuring Image Layouts

16.6.1 About Image Layouts

The image layout within a group defines the layout of the images within the viewbox as well as the number of images from a group that display in each viewbox. You can:

Selecting an Image Layout on page 511

Selecting an Image Layout at Group Level on page 513

Changing the Image Layout Order on page 514

Selecting Images on page 514

Scrolling Through Images (Stack and Tile) on page 515

Navigating between Images in the PowerViewer on page 515

16.6.2 Selecting an Image Layout

Use the Layout tab (see Layout Tab on page 78) of the toolbar to select a layout.

Use the Layout tab of the toolbar to select a layout.

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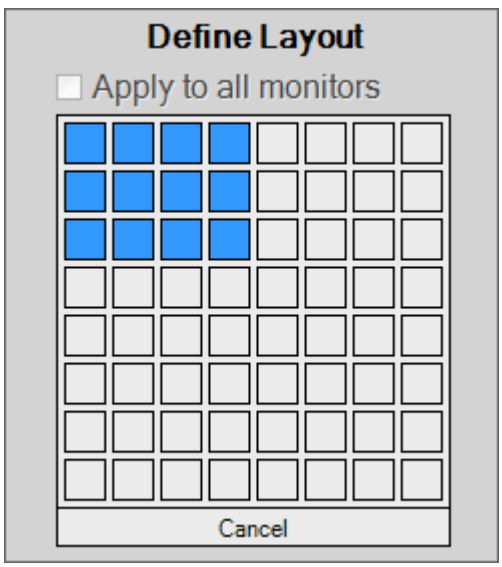
- One Image: Display only one image in the group.
- Two Images: Display one row with two images in the group.
- 2x2 Images: Display two rows with two images each in the group.
- 2x3 Images: Display two rows with three images each in the group.
- User Defined: Create a custom image layout. (See Selecting a User Defined (Custom) Image Layout below.)



Click on any of the icons to change the display option.

To select a user-defined (custom) image layout:

1. In the viewer Layout tab (see Layout Tab on page 78), click the drop-down menu of the Define Layout icon . In applications other than the PowerViewer application, click the Layout icon  to select a layout (display option) and save display option parameters.
2. Select Define Layout. In the Define Layout window, drag the mouse over the grid to highlight the desired layout. click to complete the selection.



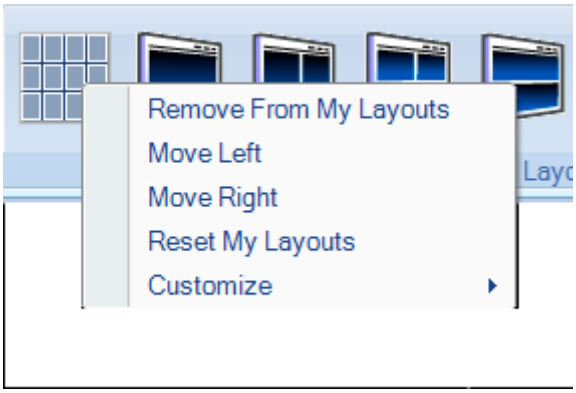
3. Select the **Apply to all monitors** option if you want the same layout to apply to multiple monitors. Otherwise, the newly defined layout applies only to the active monitor.
4. To save the newly defined layout for future use, select Save as New Layout from the Define Layout drop-down menu.

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⇨ An icon is added to the Application Layout ribbon in the toolbar to reflect the newly defined layout .

To organize the pre-defined image layout icons:

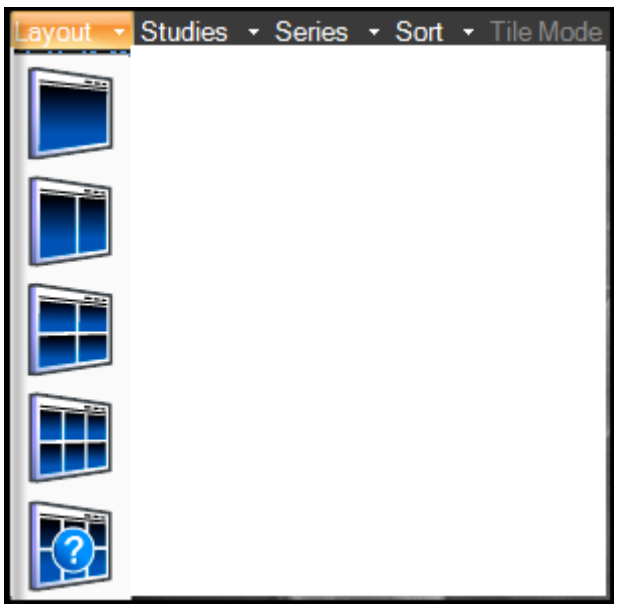
Right-click the various layout icons in the Layout tab and use the options of the drop-down menu to organize the Layout tab according to your preferences. You can remove an icon, move icons to left or to the right and reset the layout icons.



16.6.3 Selecting an Image Layout at Group Level

You can select a display option for each of the group display areas.

1. Click  to disclose the group-level toolbar.
   ⇨ The group-level toolbar appears.
2. From the Display menu at the left hand side of the toolbar, click the display option you prefer.



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For defining custom layouts see this topic:

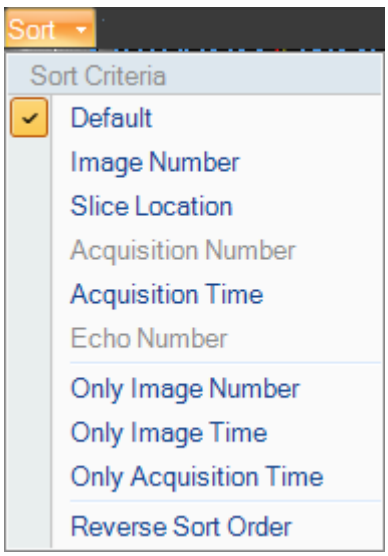
Selecting an Image Layout on page 511

16.6.4 Changing the Image Layout Order

By default, the order of the images in a group is determined in the Display Protocol Editor. The images are displayed from first to the last (top to bottom). However, you can manually sort the groups of images in the Viewer, as well as reverse the sort order to display images from last to first (bottom to top).

To change the sort order:

1. Click  to disclose the group-level toolbar.
2. Click Sort and select a sort option from the drop-down menu.



You can sort the images according to the default sort order determined in the DP Editor, or according to image number, slice location, acquisition number, acquisition time, or echo number. You can also choose to display images in reverse order.

NOTICE! You can sort the images according to the default sort order determined in the DP Editor, or according to image number, slice location, acquisition number, acquisition time, or echo number. You can also choose to display images in reverse order.

To reverse the sort order:

- From the Sort menu, select Reverse Sort Order.

16.6.5 Selecting Images

You can select one or more images, a specific group of images, or all files in the current folder, then work with the selected images.

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1. From the Image tab of the Viewer toolbar, click Selection .
2. Select the desired option:
   - Image: The image is selected.
   - Group: The group is selected.
   - All: All files in the current folder are selected.

16.6.6 Scrolling Through Images (Stack and Tile)

Use Stack mode to view and scroll images one at a time.

Use Tile mode to view and scroll multiple images.

Tile is the default mode.

To Toggle from Tile (Default) Mode to Stack Mode

Use the Tile mode icon  in the Layout tab of the toolbar to tile images across the entire desktop. Click the icon again to revert to Stack mode.

To use tile mode at a group level, click  at the group level and select Tile Mode from the group-level toolbar.

NOTICE! If you double-click a group of tiled images, the images are displayed in stack mode. If you double-click a group of stacked images, the group is enlarged and is displayed on the entire screen. You can toggle between the enlarged group and the stacked group by double-clicking the group.

16.6.7 Navigating between Images in the PowerViewer

You can easily navigate between loaded studies and series in the 2D viewer, without referring to the Patient Mini-Archive. You can replace images, load new studies, delete images, and so on.

To replace the images displayed in the PowerViewer:

1. Right-click the series number.
   ⇨ A menu showing all of the series in the active study appears.
   ⇨ The series are listed in ascending series number order. If a series does not have a series number, it is placed at the bottom of the list. Series that are currently displayed in the active viewbox are checked. The series that is currently selected in the active viewbox is checked.
   ⇨ **NOTICE! If the All In One group is displayed, only the All In One group is checked, and not each individual series.**
2. If the All In One group is displayed, only the All In One group is checked, and not each individual series.

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3. To view a different study, click the Study link, then select a study from the list of studies.
4. To clear the images in a window, click Clear.

16.6.8 Using the Arrow Keys to Navigate between Images

To view:	Do this:
A lower series	► On the series number annotation, place the cursor on the back arrow. ⇨ The cursor changes to . ► Click the mouse until you reach the required series.
A higher series	► On the series number annotation, place the cursor on the forward arrow. ⇨ The cursor changes to . ► Click the mouse until you reach the required series.

16.6.9 Suggested Series

In certain applications, the right-click series menu may list suggested series for replacement. In Echocardiography (ECHO) studies, for example, when you view a Stress ECHO clip, the system suggests other Stress ECHO clips with which you can replace the one you are viewing. In Mammography studies, the suggested series list allows you to replace the displayed series with an equivalent 2D Mammo and Digital Breast Tomosynthesis (DBT) special views (if exist).

16.6.10 Loading a Study to an Empty Group Display Area

1. Right-click the empty viewbox.
   ⇨ A menu showing all loaded studies appears.
2. Select a study to load.

16.7 Using Significant Series (SIG) Images

16.7.1 About Significant Series (SIG) Images

You can save certain series as Significant Series Images (SIG). You can read, distribute, or store only these series. You can save the whole series as Significant, or save only a sub-volume out of a series.

A special menu is available in PowerViewer and in the MPR application to save images with sub-volume.

The PMA lists studies with SIG images.

Significant Series (SIG) images are a set of selected sequential images from a single series. SIG Images provide the same benefits as Key Images, with the added benefit of volumetric data. SIG Images can create a subset of the data, resulting in a faster transfer of smaller files.

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SIG Images can:

- Include all images from the original series
- Include a subset of sequential images from one original series
  - The subset can include sub-volumes of series or a set of slices (by changing spacing/thickness parameters)

SIG Images can be identical to the original images or can have different image parameters, such as zoom, pan, windowing, and measurements.

SIG Images allow you to:

- Separate a group of particular interest out of a study
- Retain only the relevant sub-volume of a specific volumetric series
- Work with thicker slices within the same volumetric series

You can save SIG Images while using the following viewbox applications:

- PowerViewer
- MPR

You can save an entire series (no sub-volume) from the Archive Explorer.

You can:

- View SIG Images using all Diagnostic Workstation applications.
- Apply the SIG function to groups that contain more than one series. The SIG function will collect each set of images into one distinct SIG.

Restrictions

IMPORTANT

You cannot save SIG Images while using applications such as 3D, Cardiac CT, and Vessel Analysis.

IMPORTANT

You cannot use SIG Images based on groups such as Key Images or All in One.

16.7.2 Workflow for SIG Images

SIG Image Workflow	Related Topics
1. Mark SIG images.	Marking SIG Images Manually on page 518 Marking SIG Images Automatically on page 523
2. Load SIG images.	Loading SIG Images on page 121
3. Distribute SIG images.	Distributing SIG Images on page 529

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4. Apply measurements or annotations.	About Annotations and Measurements on page 499
5. Manipulate the images.	About Images on page 495
6. Define MPR parameters.	About Multi-Planar Reformatting (MPR) on page 159
7. Save, film, or print MPR images.	Filming and Printing MPR Images on page 182 Saving MPR Images on page 182

Marking Capabilities

Type of SIG Marking	Description	Instructions
Instructions	Mark the first and last image of the volume you want.	Marking a Slab by Borders on page 521
Mark Slab by Center	Choose the middle slice and use dialog box to determine the thickness in millimeters or total number of images.	Marking a Slab by Center on page 522
Mark Entire Group	To extract one important group from a number of groups within a study.	Marking SIG Images Automatically on page 523

16.7.3 Marking SIG Images

About SIG Image Marking

You can mark SIG images manually using the PowerViewer or Archive Explorer.

The system will also mark SIG images automatically based on specific image criteria.

See these topics:

Marking SIG Images Manually on page 518

Marking SIG Images Automatically on page 523

Marking SIG Images Manually

You can use the PowerViewer or the Archive Explorer to manually mark images as part of a Significant Series (SIG).

PowerViewer allows you to:	Archive Explorer allows you to:

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- Extract one important group from several groups in a study (Mark Entire Group).
- Mark first and last image of the volume you want (Mark Slab by Borders).
- Choose the middle slice and use dialog box to determine the thickness in millimeters or total number of images (Mark Slab by Center).

NOTICE! PowerViewer does not support clearing SIG markers from images.

- Extract one important group from several groups in a study (Mark Entire Group).
- Clear the SIG marker from a series.

NOTICE! The Archive Explorer does not support specific marking options for slabs.

Marking SIG Images from the PowerViewer

IMPORTANT

If you do not have permission to mark SIG images, the options are inactive. See the system administrator.

Marking an Entire Group on page 520
Marking a Slab by Borders on page 521
Marking a Slab by Center on page 522

Marking SIG Images from the Archive Explorer

IMPORTANT

If you do not have permission to mark SIG images, Mark as Significant Series is inactive. See the system administrator.

In Archive Explorer, marking SIG images is based on DICOM tags rather than on pixel data.

1. Open the Archive Explorer.
2. Click the desired study.
3. Select one or more series from the list.
4. From the menu toolbar, click Archive Explorer --> Explore --> Mark as Significant Series.
5. Locate the study with the SIG marker.

See these topics:

Locating Studies with SIG Images on page 530
Marking SIG Images Automatically on page 523

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Marking an Entire Group

You can manually save a full series/group as a SIG, without selecting sub-volume.

If the series spans across several groups, the SIG includes only the active group you marked (saved), and excludes the other related groups.

From Archive Explorer (Ctrl + N)

1. Right-click on a series.
2. Select Mark as Significant Series.

From PowerViewer

In the main menu, click File --> Mark Significant Series --> Mark Entire Group.

From MPR (Application or Rendition)

1. Change to an MPR Rendition (see Changing the MPR Rendition on page 164) or use the MPR viewbox application (see Viewing an MPR Image on page 163).
2. Initiate Export Series:

   Or

   - In the main menu, click File --> Export Series.
   - In the main menu, click File --> Export Series.
3. The Export a Series window opens.
4. Under Export Purpose, choose Create Significant Series.
5. Under Export Parameters, make any necessary to thickness or spacing.
6. In the Series Description field, input a brief and meaningful title for the series.
7. Optional: If desired, select High Resolution.
8. Click OK.

IMPORTANT

Selecting High Resolution will increase the file size of the SIG images.

See these topics:

Marking SIG Images Manually on page 518

Marking a Slab by Borders on page 521

Marking a Slab by Center on page 522

Saving SIG Images on page 523

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Marking a Slab by Borders

You can mark two images within the same group to create a "border." The SIG contains the border images, plus the range of images between the first and last image.

IMPORTANT

Mark Slab by Borders is unavailable for non-volumetric data, such as CR, DR, XR, MG, US or in localizer images.

From PowerViewer	From MPR (Application or Rendition)
1. In the main menu, click File --> Mark Significant Series --> Mark Slab by Borders. 2. The cursor changes to a square.	1. Change to an MPR Rendition (see Changing the MPR Rendition on page 164) or use the MPR viewbox application (see Viewing an MPR Image on page 163). 2. Initiate Export Series: Or • In the main menu, click File --> Export Series. • Right-click the image. From the drop-down menu, select Export Series --> Mark Slab by Borders.

NOTICE! The following steps apply to either the PowerViewer or MPR.

1. Click the image you want to define as a border and include as the first image in the range of images.
2. Scroll through the images and click the image you to define as a border and include as the final image in the range.
3. The Export a Series window opens.
4. Under Export Purpose, choose Create Significant Series.
5. Under Export Parameters, select Slab sub volume (mm), and enter an integer between 2 and 1000.
6. Under Export Parameters, adjust the values for:
   - Number of images
   - Spacing (mm)
   - Thickness (mm)
7. In the Series Description field, input a brief and meaningful title for the series.
8. Optional: If desired, select High Resolution.

NOTICE! Selecting High Resolution will increase the file size of the SIG images.

NOTICE! Finish the marking process before you apply annotations or measurements, or manipulate the image. If you change the cursor mode before you mark the final image, you will cancel the marking process prematurely.

See these topics:

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Marking SIG Images Manually on page 518
Marking an Entire Group on page 520
Marking a Slab by Center on page 522
Saving SIG Images on page 523

Marking a Slab by Center

You can mark one central image, and the system expands the selection to several mm or images in each side.

IMPORTANT

Mark Slab by Center is unavailable for non-volumetric data, such as CR, DR, XR, MG, US or in localizer images.

NOTICE

The system creates a slab with a symmetric number of images or equal thickness from each side of the middle slab image. The system automatically adjusts the calculation to create a symmetric sub-volume around the center image as needed.

IMPORTANT

Finish the marking process before you apply annotations or measurements, or manipulate the image. If you change the cursor mode before you mark the final image, you will cancel the marking process prematurely.

From PowerViewer

1. In the main menu, click File --> Mark Significant Series --> Mark Slab by Center. The cursor changes to a circle.
2. Click the center (middle) of the image. A window opens.
3. In the window, select one of the following options and input a value:
   - Total length of slab in millimeters
   - Total number of images in slab
4. Click OK.

From MPR (Application or Rendition)

1. Change to an MPR Rendition (see Changing the MPR Rendition on page 164) or use the MPR viewbox application (see Viewing an MPR Image on page 163).

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2. Right-click the image. From the drop-down menu, select Export Series --> Mark Slab by Center. The cursor changes to a circle.
3. Click the center (middle) of the image. A window opens.
4. In the window, select one of the following options and input a value:
   - Total length of slab in millimeters
   - Total number of images in slab
5. Click OK.

See these topics:

Marking SIG Images Manually on page 518

Marking an Entire Group on page 520

Marking a Slab by Borders on page 521

Saving SIG Images on page 523

Marking SIG Images Automatically

The system can identify relevant series during the storing process and mark the series as SIG images.

You can define criteria to prompt the system to mark SIG images automatically.

Some examples of the criteria include:

- A volumetric series with a small number of thick images.
- A series with a certain type of derived/secondary images.
- All the series in the study excluding the large volumetric series images. The study includes all non-volumetric series plus compressed volumetric series.
- A series with specific terms in the series description.
- A SIG that was defined in the modality based on a certain DICOM tag.

16.7.4 Saving SIG Images

When you mark a SIG, the system automatically retains the marker.

The system saves SIG images when you confirm the case.

Most of the image parameters, such as pan or enhance, are saved as part of the SIG image. The zoom image parameter is not saved.

1. Create SIG images (see About SIG Image Marking on page 518).
2. Apply annotations or measurements, or manipulate the image as needed.
3. Click Done  or select File --> Done.

The system saves the SIG markers and most of the image parameters, excluding zoom.

The SIG images are now listed in the Archive Explorer.

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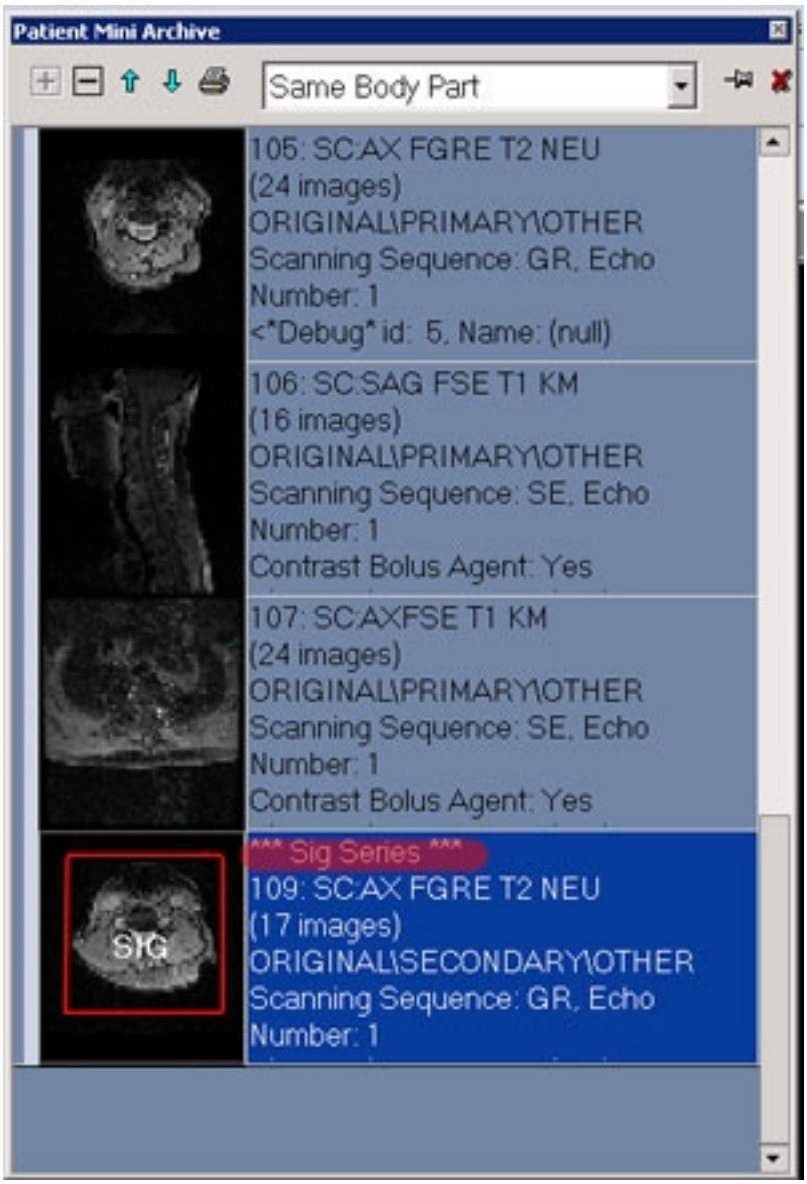
When marking full group/series, the same group/series will appear twice, once without Significant Series indication and once with Significant Series.

Use the Has Significant Series column in the Archive Explorer to view and organize series containing SIG images. See Locating Studies with SIG Images on page 530.

16.7.5 Viewing and Annotating SIG Images

After you mark a series, you can see the identity of the new series in the PMA and the Replace With annotations.

In the PMA, you will see the Significant Series identified with the yellow text SIG sign on the image and a Sig Series note in the details.



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When you drag a SIG image from PMA into the viewbox, you will see a SIG annotation in the upper left of the viewbox.

When you use the arrow keys to navigate between series, the navigation includes Significant Series.

All Significant Series are part of the All-in-one series. SIG images may appear twice.

16.7.6 Unmarking SIG Images

You must use Archive Explorer to unmark the SIG images from studies.

IMPORTANT

You cannot use PowerViewer or MPR (rendition or application) to clear SIG images.

IMPORTANT

If you do not have permission to clear SIG images, the Unmark Significant Series option is inactive. See the system administrator.

1. Open Archive Explorer.
2. Select the study containing SIG images.
3. Click Explore , or use keyboard shortcut **Ctrl + E**.
4. Locate the desired group.
5. Look for Y in the Has Significant Series column. Right-click the group with SIG images.

   Y—Yes, the study contains SIG images.

NOTICE

If you do not see the Has Significant Series column, use the instructions in Locating Studies with SIG Images on page 530 to add the column.

6. From the right-click menu, select Unmark Significant Series. The data in the Has Significant Series column changes from Y to N.

   N—No, the study does not contain images marked as SIG.

   Y—Yes, the study contains SIG images.

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16.7.7 Updating SIG Images

To change the content of an existing series with SIG images:

1. Clear the SIG images from the study.
2. Create new SIG images with the desired changes.

To leverage an existing series with SIG images:

1. Load or select a series with SIG images.
2. Make the desired adjustments and mark SIG images.
3. Save the SIG images.
4. Saving the SIG Images will create an additional series with SIG images and the changes. To conserve disk space, clear the SIG images from the older series.

See these topics:

Unmarking SIG Images on page 525

Marking SIG Images Manually on page 518

Saving SIG Images on page 523

16.7.8 Loading SIG Images

When you load only SIG images, the system transfers only the relevant images rather than the whole study.

Whenever you load SIG images, the Key Image Group is loaded as well. If you apply Load Significant Series  on a study that contains Key Images but does not contain SIG images, the Key Images group is loaded into the viewbox application.

Loading Significant Series from the Archive Explorer

Loading SIG Images at the Study Level

1. Open the Archive Explorer (see Opening the Archive Explorer on page 106).
2. Locate a study which contains SIG images (see Locating Studies with SIG Images on page 530).
3. To load the SIG images:
   - **With an Icon**:
     - Select the study.
     - Click Load Sig Series  in the drop-down menu of the Load icon .
   - **With a Right-Click Menu**:

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- Select the study.
- Right-click and select Load Sig Series.

4. Select an appropriate viewbox application such as MPR or PET/CT.

⇨ The entire study loads into the viewbox, including images marked as SIG. The SIG images are organized in the Patient Mini-Archive (PMA).

IMPORTANT

If the study does not contain images marked as Significant Series, the Load Significant Series option is inactive.

Loading SIG Images at the Series Level

1. Open the Archive Explorer (see Opening the Archive Explorer on page 106).
2. Right-click the column fields area.
3. Select Field Chooser.
4. Drag and drop **Has Significant Series** from Available Fields to Displayed Fields.
5. Click OK. The new column **Has Significant Series** opens in the Archive Viewer.

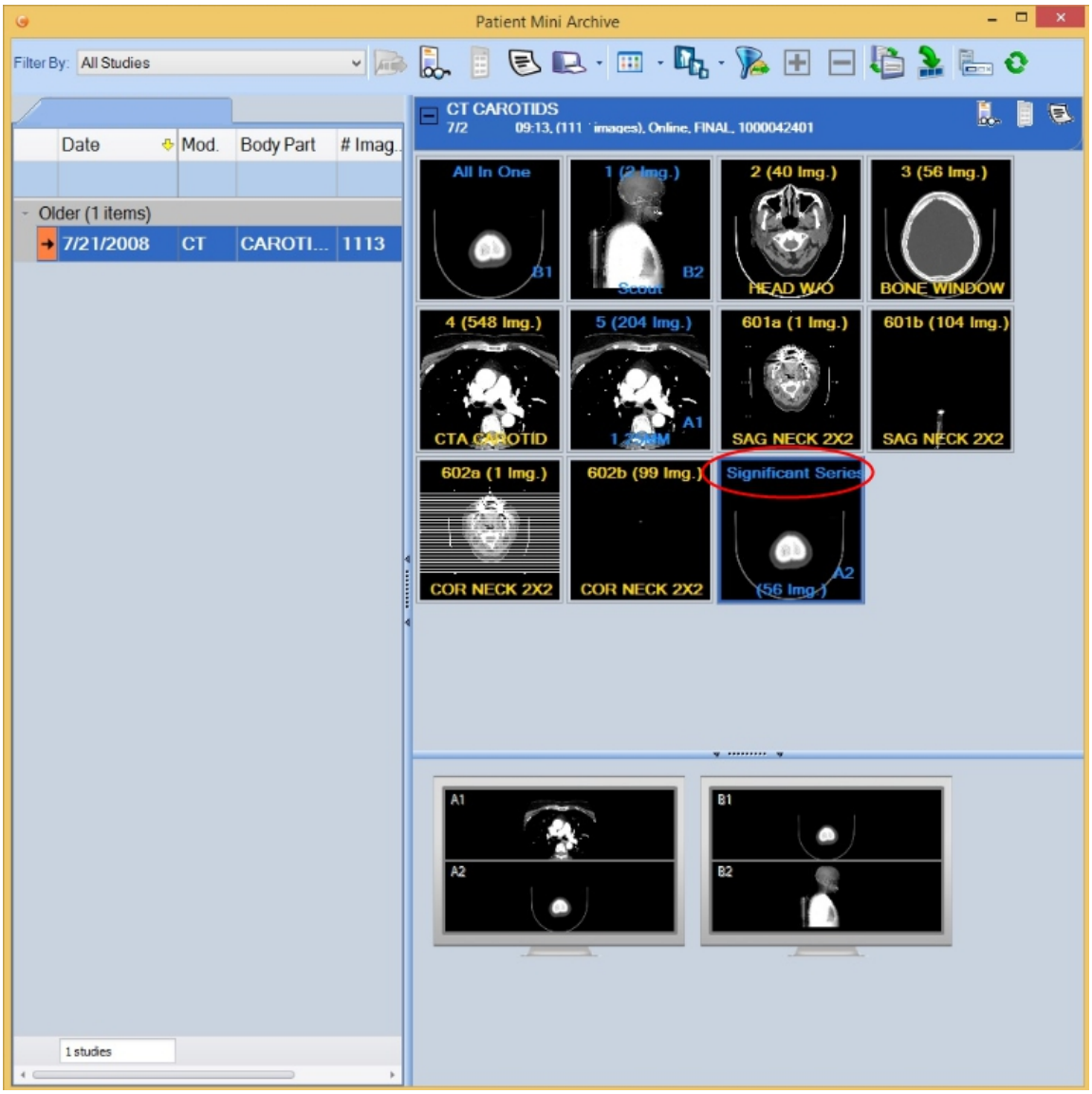
   The column includes the letter N or Y.
   - Y—Yes, the study contains SIG images.
   - N—No, the study does not contain images marked as SIG.
6. Click **Has Significant Series** to sort and organize the information.
7. Press the CTRL key and click the specific series from the Archive Explorer list.
8. Click Load Significant Series 

.
9. Select an appropriate viewbox application such as MPR or PET/CT.

Loading SIG Images from the PMA

Images marked as SIG are visible in the PMA.

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When you load a study from the PMA, the study will load SIG images according to the load configuration. If the configuration is set to load only SIG images from the prior study, then only those images from the prior study load to the viewbox.

Loading Significant Series of Prior Studies

You can configure prior studies so that only the SIG images load. You can use the Display Protocol editor tools or the PMA to determine the specific study to load.

You or your system administrator can configure whether the whole study is loaded when the prior study does not contain any SIG images.

Load whole study—default configuration.

Load significant series only from history tag—if this flag is 1, the application will load only significant series in prior studies.

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No significant series—if this flag is 0, and the prior study has no significant series, then nothing loads.

Load entire study when no significant series in history tag—if this flag is 1, the application will load the entire study when there are no Significant Series in the prior study.

You or a system administrator can configure these parameters from Administration > System Configuration.

Exceptions and Behavior

Whenever the DP contains a request to Load Key Images Only, only the Key Images will load, even if the configuration is set so that the SIG images are loaded.

16.7.9 Distributing SIG Images

1. Open Archive Explorer.
2. Select the desired study containing significant series (SIG) images.
3. Distribute the images. You can:
   - Burn the SIG images to CD

Menu	Icon
1. Right-click the study. 2. Select Burn Significant Series.	

- Send the SIG images to an off-site computer (Push to Client)

Menu	Icon
1. Right-click the study. 2. Select Push to Client. 3. In Push to Client, select the Target Receiver and History Policy. 4. Click OK.	
1. Navigate to the top row of menus in the Archive Explorer toolbar. 2. Select Push --> Push to Client. 3. In Push to Client, select the Target Receiver and History Policy. 4. Click OK.	

NOTICE

You can add a field in Archive Explorer to indicate the studies with SIG images.

See these topics:

About Push to Client on page 445
Locating Studies with SIG Images on page 530
Adding and Removing Columns (Fields) on page 136
Changing Column (Filter) Headings on page 134

16.7.10 Locating Studies with SIG Images

Use the Archive Explorer to locate and sort studies with significant series (SIG) images.

1. Open Archive Explorer.
2. Right-click the column fields area.
3. Select Field Chooser.
4. Drag and drop **Has Significant Series** from Available Fields to Displayed Fields.
5. Click OK. The new column **Has Significant Series** opens in the Archive Viewer.

The column includes the letter N or Y.

Y—Yes, the study contains SIG images.

N—No, the study does not contain images marked as SIG.

6. Click **Has Significant Series** to sort and organize the information.

See these topics:

Adding and Removing Columns (Fields) on page 136
Sorting Lists in the Archive on page 139

16.7.11 Troubleshooting SIG Images

Symptoms

You cannot work with the SIG images in the viewbox.

The Mark Slab by Borders is unavailable.

The Mark Slab by Center is unavailable.

Possible Cause	Suggested Solution
The images do not contain volumetric data.	You cannot use SIG images in a study containing non-volumetric datasets, such as CR, DR, XR, MG, US or localizer images. 1. Verify that you are using volumetric datasets. 2. Load a study with volumetric datasets into the application. 3. Repeat the steps for working with SIG Series. See Workflow for SIG Images on page 517.

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The group does not support SIG images.	You cannot use SIG images based on Key Group or All in One groups.
The viewbox application does not support SIG images.	You cannot use SIG images in viewbox applications such as 3D Data, Cardiac Analysis, and Vessel Analysis. Select New Viewbox --> MPR, or PET/CT, MPR, or Volume Matching.

16.8 Using Key Images

16.8.1 About Key Images

Key Images are images that you select as best representing a study. You can select and view key images and save them independently from the rest of the study.

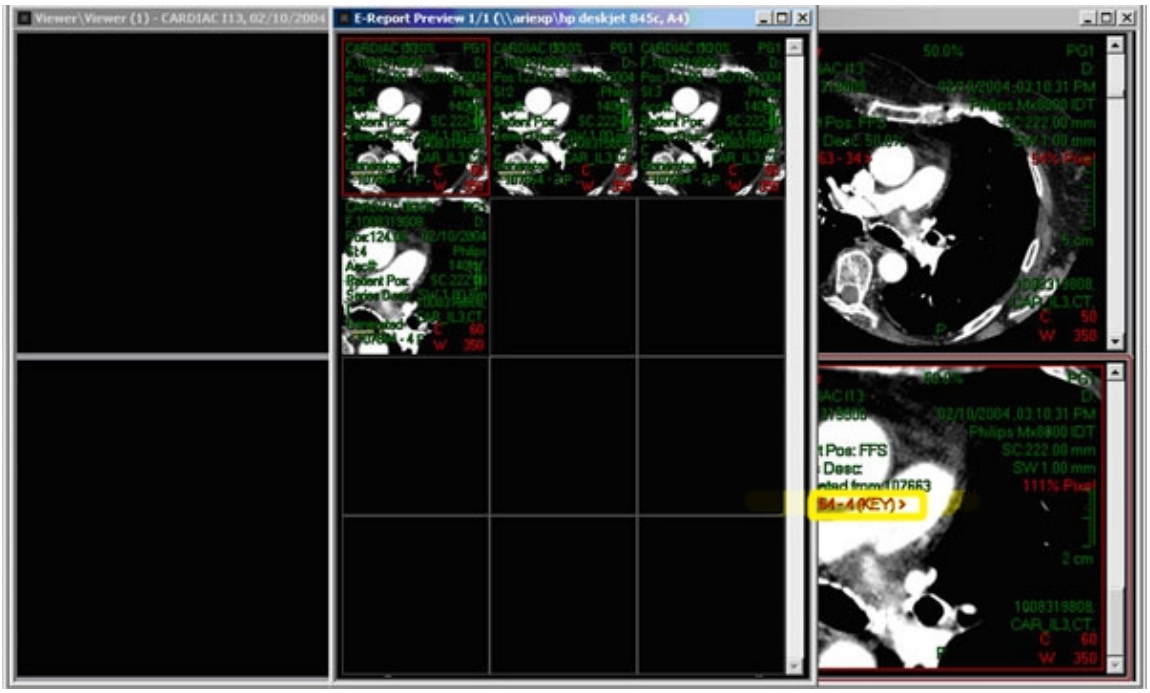
Key Image Groups are always available and include all marked Key Images. The group is saved in the Patient Mini-Archive (PMA) and in the Replace With dialog, regardless of reading or locking status. The group is also displayed in the PowerViewer windows, regardless of status.

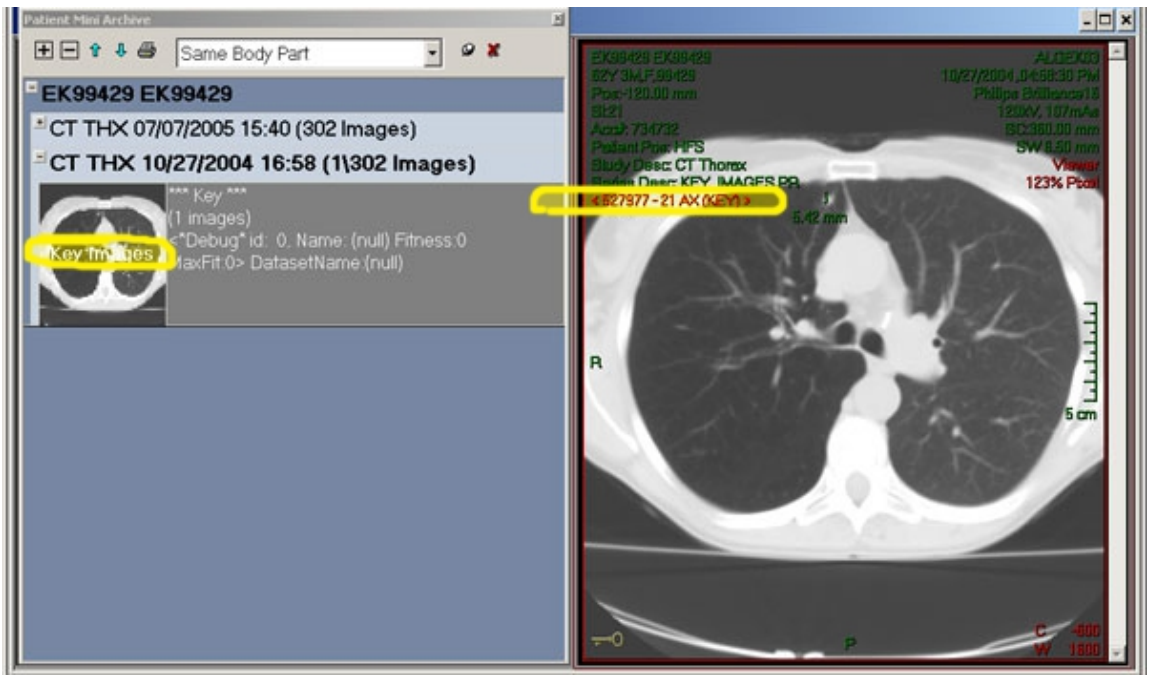
To indicate that the group is a Key image Group, the text (KEY) is visible after the image number.

NOTICE

Press K on the keyboard to make the series automatically scroll through the regular group to the next Key Image. To learn more about scrolling through Key Images, see Scrolling Key Images on page 539.

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The Display Protocol editor (DP) supports the display of the Key Image Group as does the Save Presentation mechanism.

See these topics:

Updating Key Images on page 534

Marking Key Images on page 535

Previewing Key Images on page 536

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Clearing Key Images on page 540
Printing Key Images to Film on page 541
Loading Key Images on page 121

16.8.2 Key Image Tools

To start Mark as Key Image

From a menu:	With a keyboard shortcut:
In the menu toolbar, click **Mark as Key** . Or Right-click on the image and select **Mark as Key**  from the drop-down menu.	Press **Alt + Space** (for desktop diagnostic viewer clients only). Press `(single quote key) (for clients that have both desktop and Web environments).

To start Unmark Key Image

From a menu:	With a keyboard shortcut:
Right-click on the image and select **Unmark Key** from the drop-down menu.	Press **Alt + Ctrl + Space**(for desktop diagnostic viewer clients only) Press **Shift +` (~)** (for clients that have both desktop and Web environments).

To Scroll Through Key Images

With a keyboard shortcut:
Press **K** and the series automatically scrolls through the group to the next Key Image.

16.8.3 E-Report Preview Toolbar

The following icons are added to the E-Report Preview window.



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Icon	Description
Print	
	Open a print dialog box from which you can print the current content. Press the Ctrl key and click the Print icon to print to your default printer.
Film	
	Change the preview window to True-Size mode.
	Enlarge the font size of annotations on the images.
	Reduce the font size of annotations on the images.
	Portrait layout.
	Landscape layout.
Page	
	Insert a new page at the end.
	Clear selected images from the preview window.
	Clear current page from the preview window.
	Clear all images from the preview window.
Key Images	
	Save changes to key images. You can save changes made to the key images, changes made to the layout, or both changes made to the key images and to the layout.

16.8.4 Updating Key Images

Key Image Groups are dynamically updated.

When you mark a new Key Image, the Key Image is immediately available in the Key Image group.

When you clear an existing Key Image, the Key Image is removed from the Key Image group.

You can modify an existing Key Image by changing image parameters such as zoom, pan, windowing, or graphics. Click Save  to retain the changes.

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Example

If a study has no Key Images and you mark an image as a Key Image, a Key Image Group is available in the Patient Min-Archive (PMA) and in the Replace With – Series List. You can display the group on screen.

Any operation performed directly on the images included in the Key Image Group affects the group and the relevant original images.

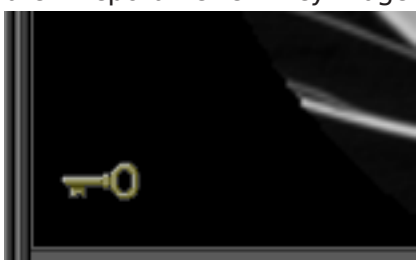
When you clear an image from the Key Image Group, the Key annotation is updated on the original group (from which the key image originated).

16.8.5 Marking Key Images

Key images remain active in the PowerViewer so you can perform image manipulation. When you save the key images, any annotations or changes that you made to the images in the PowerViewer, before and after they were marked as key images, are saved.

NOTICE

When you close the study, the key images are saved in a new series. The next time the study is loaded, you can choose to load either the entire study or only the key images.

1. From the PowerViewer, select an image.
2. Apply the Mark as Key mode (see Key Image Tools on page 533).
   ⇨ A key annotation appears on the bottom left of the image and the image appears in the E-Report Preview/Key Image Previewer.
   ⇨ 
3. Repeat Steps 1 and 2 to mark additional key images.
   ⇨ The key images are saved in the archive, along with their annotations, in a new series labeled Key Images.

NOTICE

To save changes performed on images in the Key Image Group, click Save . You can save changes to the local server (default) or on any remote server.

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16.8.6 Previewing Key Images

You can preview the images using the E-Report Preview window:

- After you mark specific images in a study as Key Image
- Before you confirm the study

In the E-Report Preview, you can perform actions such as adding, moving, or deleting key images. The E-Report Preview window is automatically minimized and resides in the bottom tray of the PowerViewer.

The default order in which key images are sorted is according to the Series Number and Image Number. A Key Image Group is assigned a new series number. However, the system recognizes the series from which each key image originates and allows you to sort the group according to the original series numbers (primary sort) and original image number (secondary sort).

Example

Several key images are marked and generated from the same group. The first portion of images is generated from the PowerViewer. The second portion of images is generated from MPR. The last portion of images is generated from 3D Data.

The images from the PowerViewer are shown first. The 3D images are shown next (sorted by creation order), and the MPR images are shown last (sorted by their creation order).

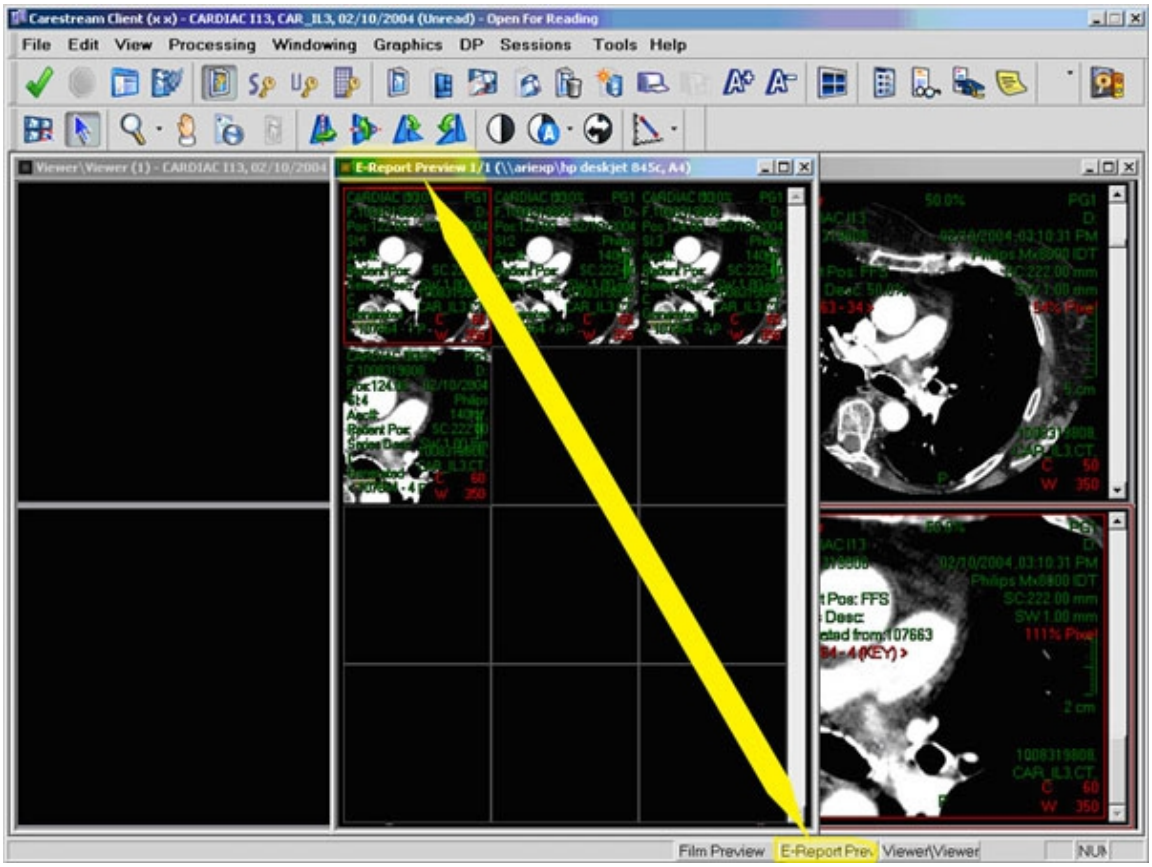
To Open the E-Report Preview Window to the Maximum Size

- From the PowerViewer toolbar, click E-Report Preview .

Or

- Go to the bottom of the screen. In the PowerViewer tray, click E-Report Preview.

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The E-Report Preview window opens and E-Report icons appear in the toolbar.

To Save Changes

- Click Save All Changes .
- Or
- Click Save Changes .

All changes are saved.

To Change the Order of the Images

By default, the order of images in the E-Report Preview follows the order of creation of the Key Images.

From inside the E-Report Preview you can manually change the order of the images. Placing the mouse over the top-left corner of the image in the E-Report Preview.

Drag the image into a different position to re-order the images.

To Minimize the E-Report Preview Window

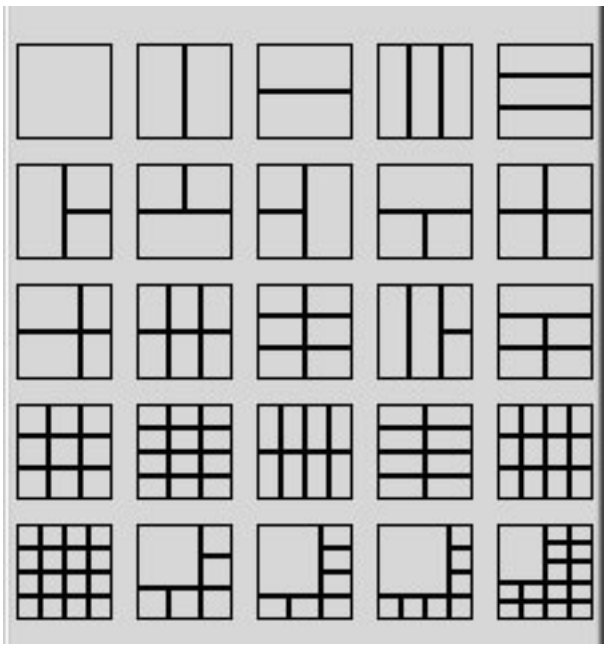
- From the PowerViewer toolbar, click E-Report Preview .

Or

- From the E-Report Preview window, click  or .

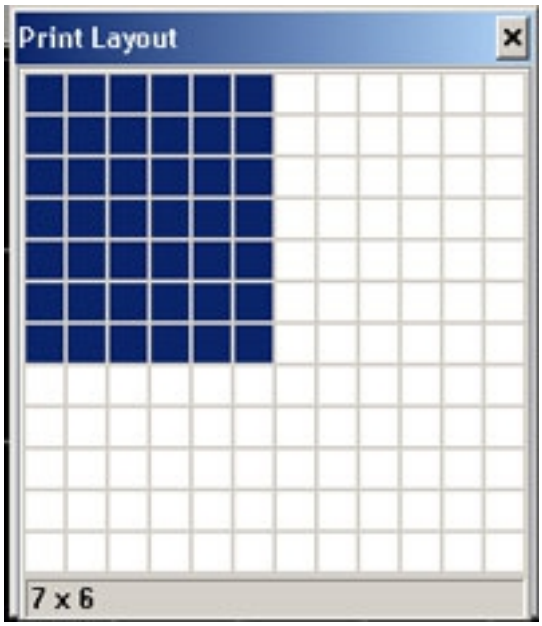
To Change the Layout of the E-Report Preview Window

1. Click Film Layout .
2. Select:
   - Portrait—vertical layout.
   - Landscape—horizontal layout.
   - Assorted—select any of the defined layout options.



   - Custom—click in the window and drag the cursor to create the desired layout.

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3. Click Save Layout Changes .

The new layout is saved. The new layout is available the next time you open the E-Report Preview window.

See this topic:

E-Report Preview Toolbar on page 100

16.8.7 Scrolling Key Images

You can scroll specifically through Key Images using the Scroll to Next Key Image function.

To use the function, press and hold the Ctrl key on the keyboard as you use the mouse to scroll (use the middle scrolling wheel on the mouse).

The Scroll to Next Key Image function advances you to the next original image marked as a Key Image.

NOTICE

If there are several instances where the same image is marked as a Key Image, you will advance to the next image, because the original image only shows one instance.

You can toggle dynamically between two scrolling modes.

While you press and hold the Ctrl key and use the mouse to scroll simultaneously, you will scroll through Key Images only.

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While you use the mouse only to scroll, you will scroll up or down to further explore proximate slices.

Keyboard Shortcut

Press **K** on the keyboard to automatically scroll through the series to the next Key Image.

16.8.8 Unmarking Key Images

You can unmark images that were previously marked as key images.

NOTICE

Unmarking removes the Key Image marker. Unmarking does not delete original images in the PowerViewer.

1. From the PowerViewer, select an image.
2. Apply the Unmark Key mode (seeKey Image Tools on page 533).

If there are Key Images originating from the image you want to unmark, the following message appears:

There are few Key Images originating from this image. Clicking 'OK' will clear them all. If you want to remove a single Key Image, please use the Key Image group or the E-Report Preview.

Click OK to unmark the images, or click Cancel to stop the unmark process.

16.8.9 Clearing Key Images

You can clear images that were previously marked as key images.

1. From the E-Report Preview window, select the key images you want to clear.
2. From the Viewer toolbar, click one of the following:
   - Clear Selected Images  to clear the selected images in the current page.
   - Clear Current Page  to clear all the images in the current page.
   - Clear All Images  to clear all the images in the E-Report Preview window.

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IMPORTANT

If you unmark a Key Image from the Key Images group displayed in the PowerViewer, the actual image is cleared and along with the key indication.

If you are in stack mode, the unmarked image is cleared and the next image is displayed.

If you are in tile mode, the image and its location are deleted, and the tiles are closed so there are no empty spaces.

16.8.10 Printing Key Images to Film

To:	Do this:
Send key images to Film Preview	1. Mark the key images (see Marking Key Images on page 535). 2. Load the key image(s) series (see Loading Key Images on page 121) from the Archive Explorer. 3. From the PowerViewer, select All Images. 4. Click Film .
Open Film Preview	• From the PowerViewer toolbar, click Film Preview . You work with images in the preview window the same way as in the PowerViewer. Scroll through the images in the Film Previewer page by page, where each page is numbered x/y. **NOTICE! The Film Preview is displayed on top of other windows by default.**

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Clear images from Film Preview	1. Click Film Preview  and select the image(s) you want to clear. You can select multiple images by holding down the Ctrl key while selecting. 2. From the PowerViewer toolbar, click one of the following. – Clear Selected Images . – Clear Current Page  to clear all the images in the current page. – Clear All Images  to clear all the images in the Film Previewer.
Adjust the font size	• From the PowerViewer toolbar, click  to increase the font size. • From the PowerViewer toolbar, click  to decrease the font size.

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Determine the film layout and printing issues	1. Click Film Preview . 2. Click Film Layout . A list of default layout options appears. 3. Select Portrait or Landscape. 4. Select a film layout. Images sent to the Film Previewer appear in sequential order (left to right, from top to bottom). If there is more than one page, each page has the same layout. 5. You can move images (see Moving Images on page 547) from one location to another within the Film Previewer. When you send additional images to be printed, images are always added to the last page, even if there are spaces in previous pages. By default, headers and footers are displayed. You can remove headers and/or footers in the Film Previewer by deselecting the Header and Footer option in the View menu. Adding headers and footers (see Printing with Headers and Footers on page 547)- **NOTICE! decreasess the image space on the page. By default, all DICOM tags that are consistent between images appear in the header.** 6. From the PowerViewer toolbar, click Print . 7. Click Settings in the Print dialog box. 8. Select the desired printer settings. 9. Click OK. 10. Select the printer and job priority. 11. Click OK. The images print according to the layout and settings you selected.

16.9 Printing Images

16.9.1 About Printing

The Diagnostic Workstation enables you to work with images in the Film Preview prior to printing them.

When you select the Film option, selected images are sent to the Film Preview. The Film Preview lets you work with the images in the same way as in the PowerViewer, which lets you manipulate the images prior to printing to optimize the reading of the film.

You select a print layout in the Print Layout dialog box. For example, you may prefer to read film in a 3x4 format, while another radiologist may prefer a 4x4 format.

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NOTE: You cannot print tissue images.

See these topics:

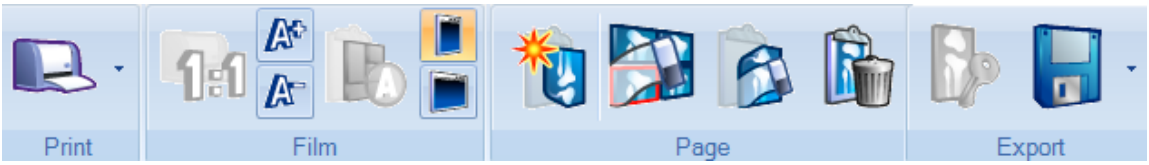
Printing Images to Film on page 545

Printing Images in True Size from Film Preview on page 546

Moving Images on page 547

Printing with Headers and Footers on page 547

16.9.2 Film Preview Toolbar



The following icons are added to the Film Preview window.

Icon	Description
Print	
	Open a print dialog box from which you can print the current content. Press the Ctrl key and click the Print icon to print to your default printer.
Film	
	Change the preview window to True-Size mode.
	Enlarge the font size of annotations on the images.
	Reduce the font size of annotations on the images.
	Use with automatic printing machines to achieve an optimal layout while printing the largest images possible.
	Portrait layout.
	Landscape layout.
Page	
	Insert a new page at the end.
	Clear selected images from the preview window.
	Clear current page from the preview window.

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	Clear all images from the preview window.
Export	
	Mark the active image as key image.
	Save selected images or layout to any available DICOM archive.

16.9.3 Printing Images to Film

To:	Do this:
Send images to the Film Preview	1. From the PowerViewer, select the images (see Selecting Images on page 514) you want to send to the Film Preview. 2. Click Film .
Open Film Preview	• From the PowerViewer toolbar, click Film Preview . You work with images in the Film Preview in the same way as in the PowerViewer. Scroll through the images in the Film Preview page by page, where each page is numbered x/y.
Clear images from Film Previewer	1. Click Film Preview  and select the image(s) you want to clear. You can select multiple images by holding down the Ctrl or Shift key while selecting. 2. From the PowerViewer toolbar, click one of the following. – Clear Selected Images . – Clear Current Page  to clear all the images in the current page. – Clear All Images  to clear all the images in the Film Previewer.

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Adjust the font size	• From the PowerViewer toolbar, click  to increase the font size. • From the PowerViewer toolbar, click  to decrease the font size.
Determine the film layout and printing issues	1. Click Film Preview . 2. Click Film Layout . A list of default layout options appears. 3. Select Portrait or Landscape. 4. Select a film layout. Images sent to the Film Preview appear in sequential order (left to right, from top to bottom). If there is more than one page, each page has the same layout. 5. You can move images (see Moving Images on page 547) from one location to another within the Film Preview. When you send additional images to be printed, images are always added to the last page, even if there are spaces on previous pages. By default, headers and footers are displayed. You can remove headers and/or footers in the Film Preview by deselecting the Header and Footer option in the View menu. Adding headers and footers (see Printing with Headers and Footers on page 547)- **NOTICE! decreases the image space on the page. By default, all DICOM tags that are consistent between images appear in the header.** 6. From the PowerViewer toolbar, click Print . 7. Click Settings in the Print dialog box. 8. Select the desired printer settings. 9. Click OK. 10. Select the printer and job priority. 11. Click OK. The images print according to the layout and settings you selected.

16.9.4 Printing Images in True Size from Film Preview

You can print images in true size, where a given distance on film equals that same distance in reality.

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1. Select the images you want to print and click Film .
2. From the Film Preview toolbar, click True Size Printing .

   The zoom factor of the images changes to the correct factor depending on the calibration settings for the selected printer.
3. Click Print .

   The Print dialog box appears.
4. Click OK.

NOTICE

If the default printer is not the calibrated printer, select a new printer from the list and click True-Size Printing. When True-Size Printing is selected, the zoom option is disabled.

Different media sizes must be calibrated individually for each printer.

16.9.5 Moving Images

In Neutral Mode, you can move images to different locations in the Film Preview.

1. Left-click an image.
2. Drag the image to the location you want.
   - If you drag the image from the center of a layout box, the dragged image switches places with the image currently in that box.
   - If you drag the mouse from the left or right in a layout box, the dragged image moves to the left or right in the box over which the cursor is placed.
   - If there is more than one page, and when you drag the mouse the cursor points to the top/bottom, the Film Preview goes to the next page. Place the image as described above.

16.9.6 Printing with Headers and Footers

You can specify whether headers and footers should be displayed or hidden by default, as well as the details they contain, in the Application Settings window (see Opening the Application Settings Window on page 453).

NOTICE! Adding headers and footers decreases the image space on the page.

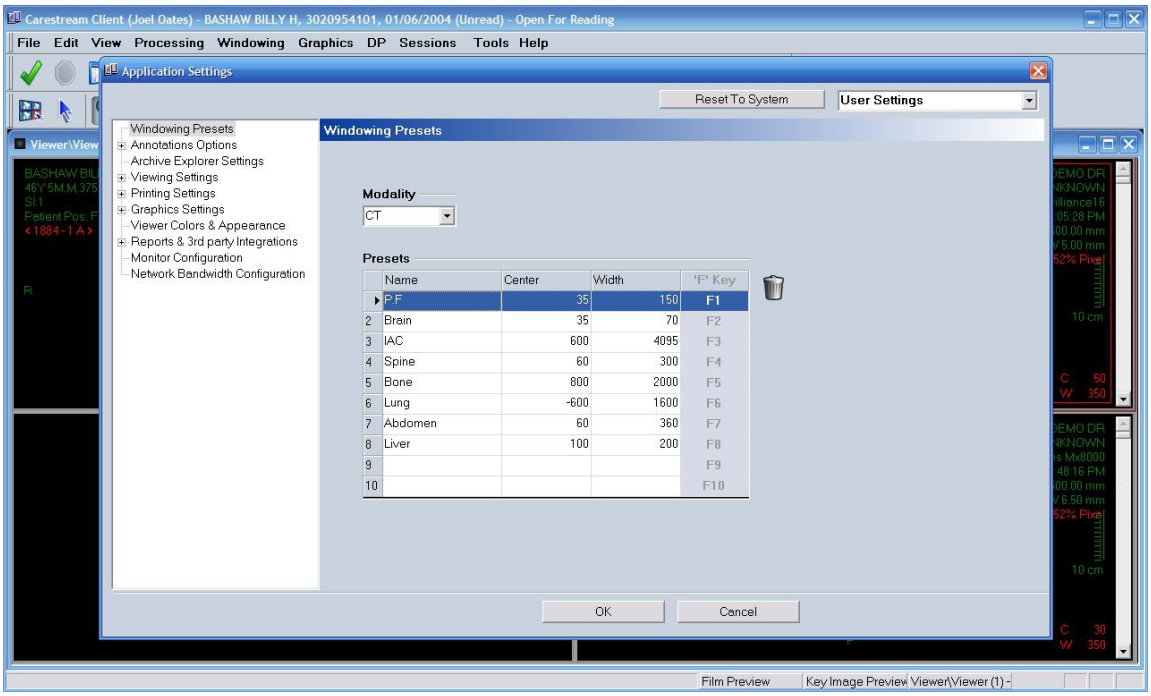
- From the Film Preview View menu, select Header, Footer, or both, to toggle displaying or hiding headers and footers.

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If you select to print headers and footers, they will be displayed on each printed page.

By default, all annotations that are common to all images and that are included in the headers or footers are removed from the image.



16.10 Saving Images

16.10.1 About Saving Images

You can save images in selected DICOM archives or in non-DICOM format.

See these topics:

Saving Images in DICOM Format on page 548

Copying to Studies with Concealed Patient Information on page 550

Saving Images to DICOM DIR on page 551

Saving Images in Non-DICOM Format on page 551

16.10.2 Saving Images in DICOM Format

You can save images in selected DICOM archives. The images can be manipulated and changed by adding graphic elements, annotations, and measurements. The modified image is always saved without overwriting the original image.

If you are saving a 3D image, the image is saved exactly as it appears on the screen. The following values are also saved:

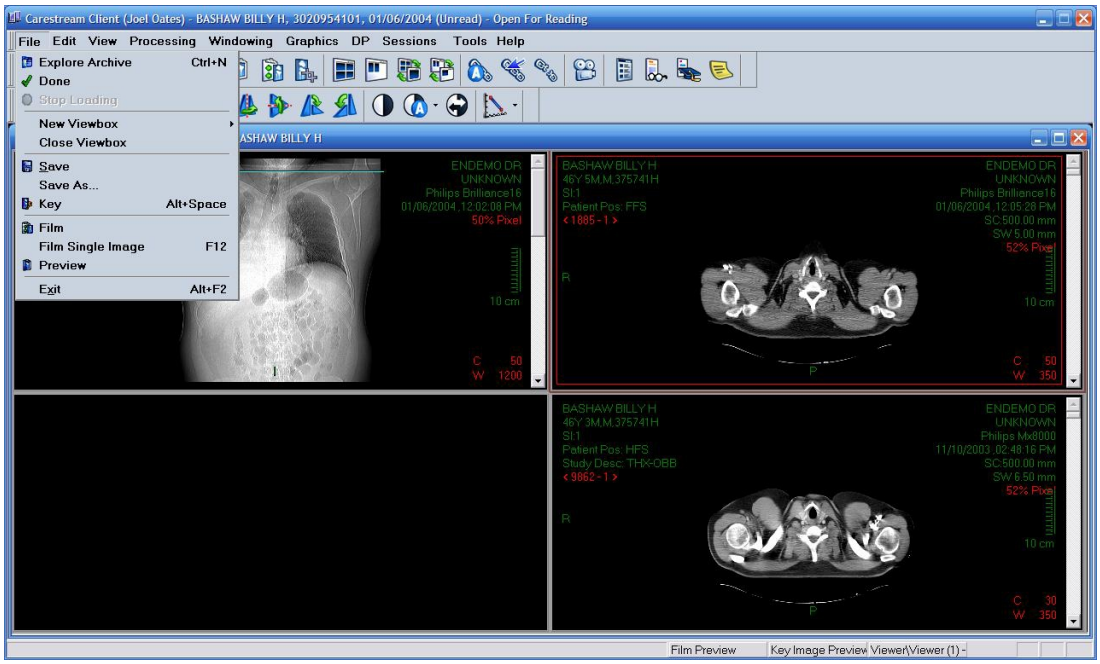
- Windowing values

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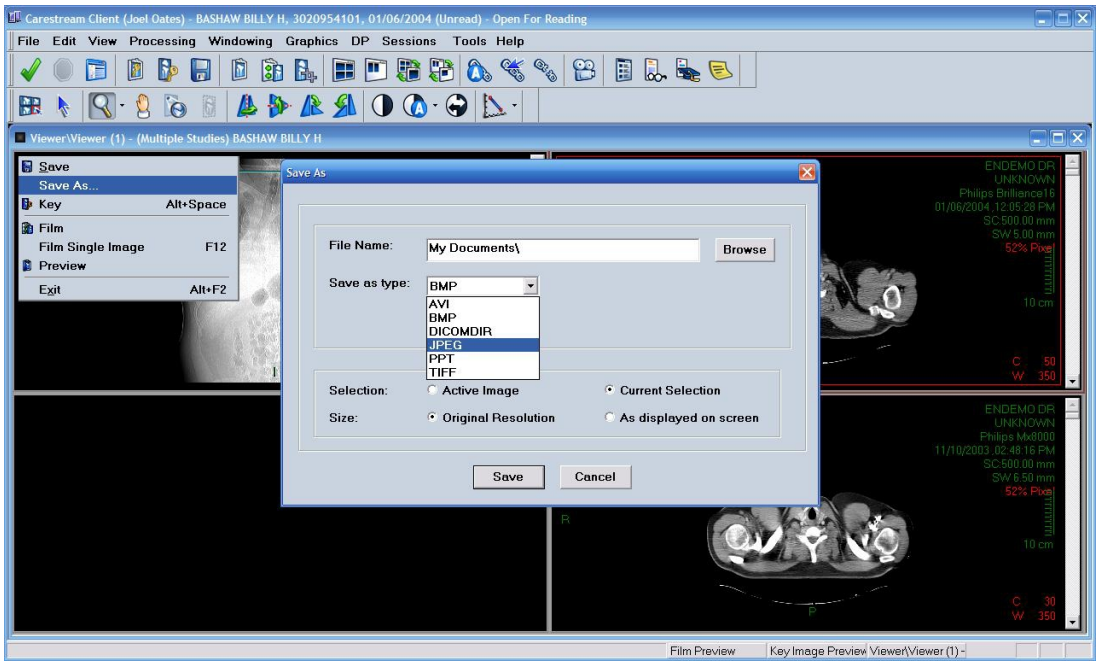
- Swivel and roll angles
- VOIs, tissues, slabs, or clipping panes that are currently activated
- Current protocol, including opacity level and colors
- Vessels that have been tracked and their midline, live panoramic, and cross-sectional images

NOTICE! Only the 3D image is saved, and not the reference images. When loading a saved image that has one or more vessels defined for it, the image automatically opens in the Vessel Tracking layout. You can manipulate these vessels as soon as all of the original images have been loaded.

1. From the Viewer, select the images you want to save.
2. From the File menu, click Save As.



The Save As dialog box appears.



3. In the Images Label field, type a name.
4. Select the Concatenate existing option check box to add the new label to an existing label.
5. In the Archives area, select one or more DICOM archives where you want to save the images and click Add.

   The selected archive name appears on the right side of the window.
6. In the Series Description field, enter a description for the images.
7. Click OK.

   The images are saved in the selected archive(s). Any annotations applied to the images are saved as well. The original images are not overwritten.

16.10.3 Copying to Studies with Concealed Patient Information

The De-identify option lets you save images while removing any identifying marks of the patient, such as Patient Name and Patient ID.

1. From the Archive Explorer, select the study you wish to save.
2. Click Copy .

   The Copy window appears.
3. Select where you want to save the copied study.
4. Select the Conceal Patient Details check box.

   The following fields are activated:

   – Patient ID

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– Patient Field

NOTICE! The Patient ID field always begins with $$$.

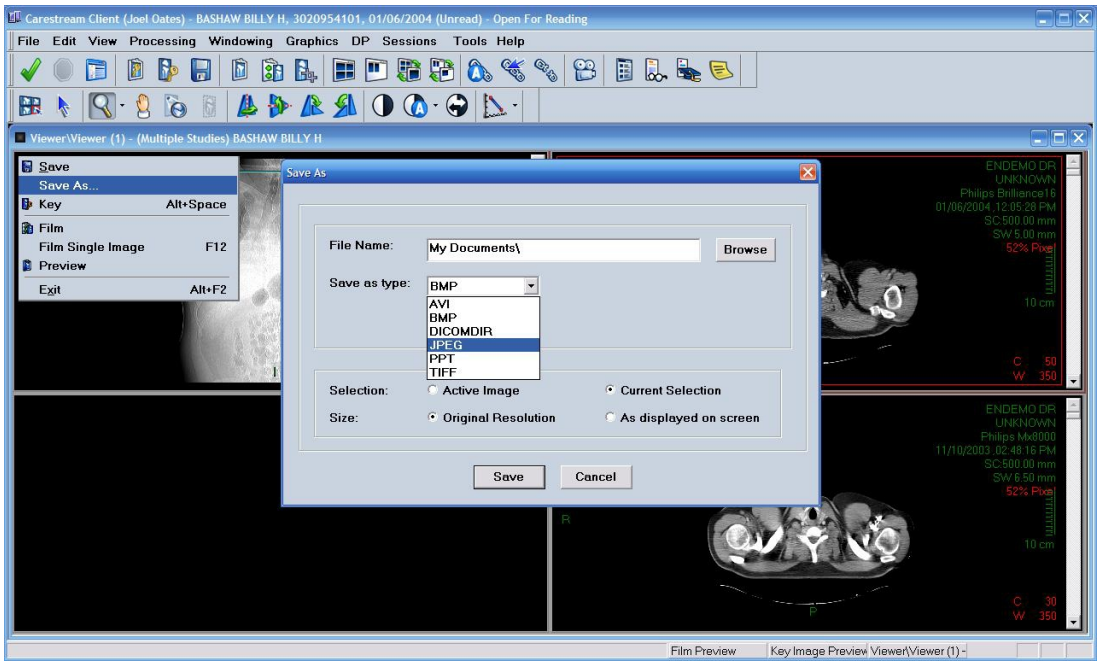
5. Add to or amend the field to de-identify the patient.
6. Click OK.

   The de-identified study is saved to the Archive.

16.10.4 Saving Images to DICOM DIR

1. From the Viewer, select the images you want to save.
2. From the File menu, click Save As.

   The Save As dialog box appears.



3. Add the file name and path of the directory where you wish to save the images.
4. Select DICOMDIR in the Save As Type field.
5. Select Active Image.
6. Click Save.

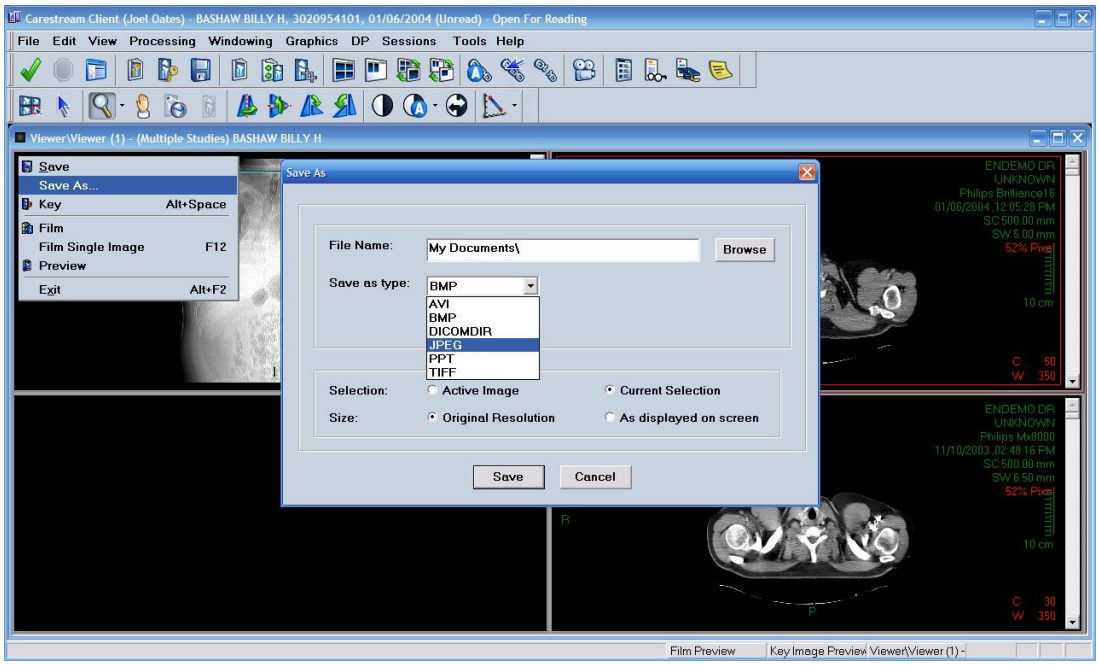
   The image is saved in standard DICOM DIR format for CD on your local drive and can be burned to a CD.

   To add other images, repeat the above procedure.

16.10.5 Saving Images in Non-DICOM Format

1. Select the images you want to save.
2. From the File menu, click Save As.

   The Save As dialog box appears.



3. Add the file name and path of the directory where you wish to save the images.
4. Select an image format in the Save as Type field.
5. Select Active Image or Current Selection.
6. Select whether to save the images in their original resolution or as they appear on screen.
7. Click Save.

NOTICE! Images are saved to the relevant folder in a numbered format (Image01.jpg, Image02.jpg). When you save to PPT format, each image is placed on a separate slide within a MICROSOFT POWERPOINT presentation.

16.10.6 Saving the Exam Link in a Folder

An exam can be saved in multiple folders and in each of them with a different presentation, or it can be saved without a presentation. Folders are available in the Explorer navigation bar.

It is also possible to save the existing layout (e.g., zoom, windowing, measurements, bookmarks, etc.) as a new presentation while saving the case study to a folder. When you next load the exam from that folder, it is loaded using the same settings.

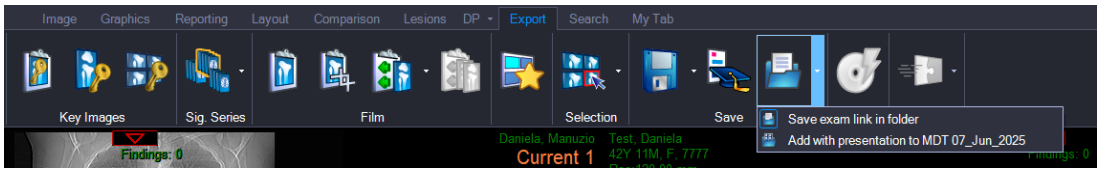
The options to save the exam and the presentation are available through the menu of the **Save exam link** icon.

Saving the exam link in folder

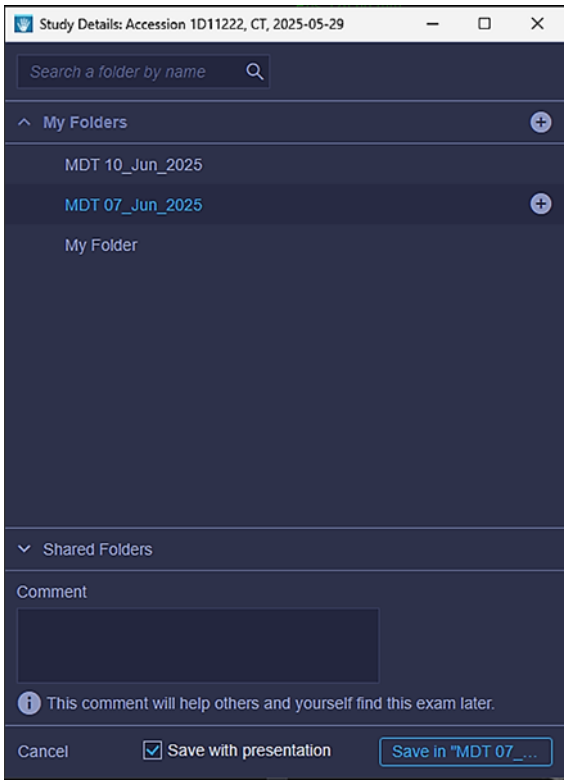
1. Select the study you want to save
2. On the **Export** tab, open the **Save exam link** icon menu and select **Save exam link in folder**.

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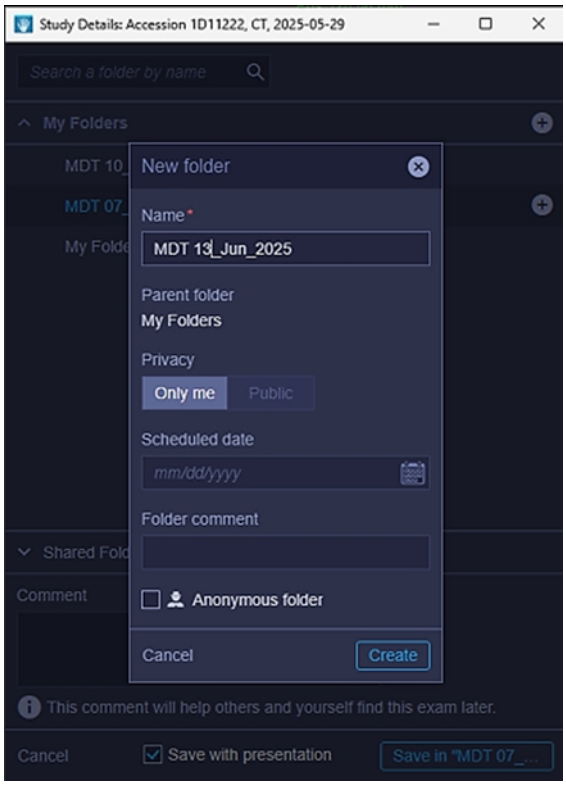


The **Study Details** window appears.



3. Select the destination folder, private or public.
4. Create a new folder, if needed by clicking the '+' button.

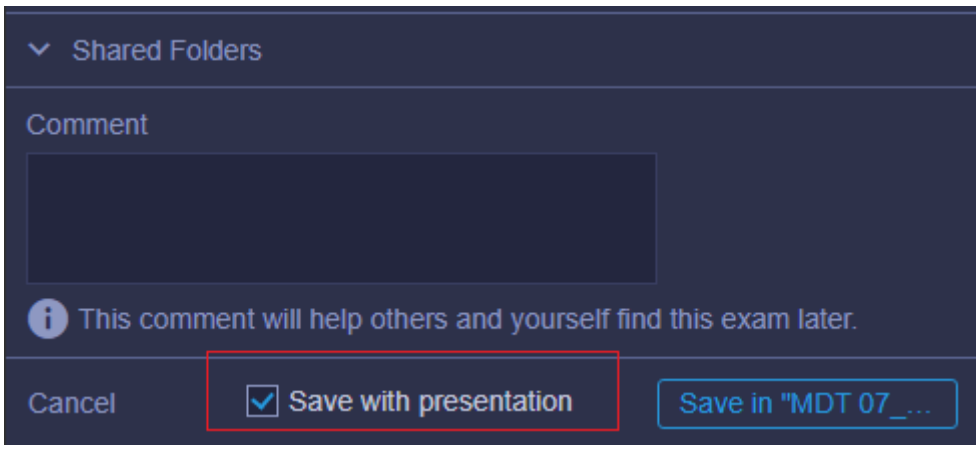
   The **New Folder** window appears.



Fill in the desired information, and click **Create**.

The created folder is added to the **My Folders** list.

5. Add comments, if needed.
6. Select the **Save with presentation** checkbox, if you wish to save the existing layout.



7. Click **Save in <Folder name>** to update the exam with the new presentation.

Add exam link with presentation to the latest folder

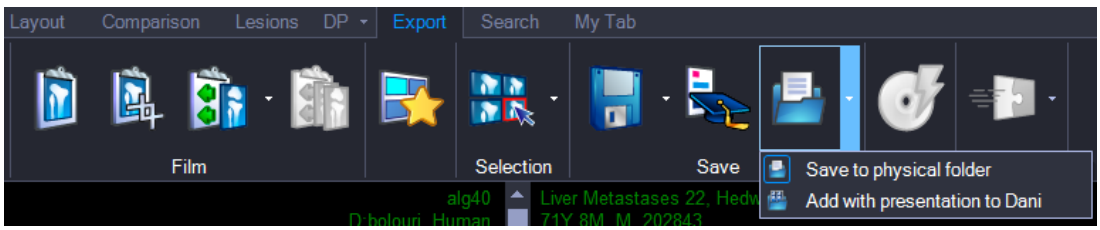
It is possible to automatically add an exam link with presentation to the latest folder.

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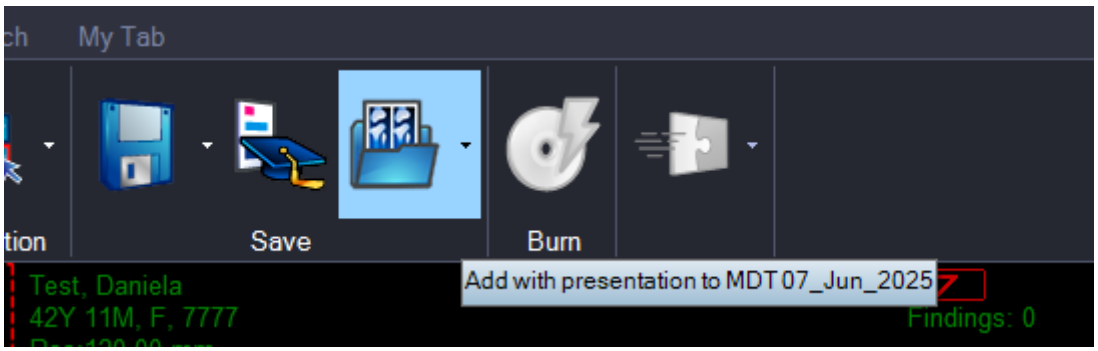
NOTE

The option is enabled only when a folder is selected. If no folder is selected, the option is disabled.

1. Select the study you want to save
2. On the **Export** tab, open the **Save exam link** icon menu and select **Add with presentation to <latest folder>**.



Once selected, the **Save exam link** icon changes and is highlighted to indicate that the option is selected.



A link to the selected exam with the presentation of the current layout is saved to the latest folder.

When you next load the exam from that folder, it is loaded using the same settings and the latest saved layout.

NOTE

When selected, the option becomes the default option during the current viewing session.

16.11 Using Cine

16.11.1 About Cine

The Cine option lets you create movies of regular, MPR, or 3D images.

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- Press Cine  to start the Cine tool.

See these topics:

Setting Several States for Cine on page 557

Viewing Cine Movies on page 557

Applying States to Cine Movies on page 558

Viewing Cine Movies of Cardiac CT Images on page 559

Saving a Cine Movie on page 560 (saving in DICOM or AVI/MPEG formats)

16.11.2 Cine Toolbar

The following cine toolbar controls cine behavior at a group level:



Icon	Description
	Frames per Second - Set the frame rate (frames per second) of the Cine movie.
	Preview - Preview the movie in a low resolution.
	Backwards - Play the Cine movie from end to beginning.
	Forward - Play the Cine movie from beginning to end.
	Move backwards and forwards.
	Set States - Set the range of images to be played in the Cine movie.
	Reset - Create a new Cine movie.
	Stop the cine movie
	Save the Cine movie to a DICOM archive or to a local disk in AVI format.

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16.11.3 Setting Several States for Cine

The Viewer supports a maximum of two states, representing the beginning and end of the Cine movie. When two states are defined, the Cine movie runs only between the first and last image set (and not the entire group), regardless of whether or not the last image set is the last image within the group.

NOTICE! From the Viewer, you can only set two states for a Cine option. When viewing images in MPR and Angiography MIP, you can set more than two states. See Applying States to Cine Movies on page 558 and Viewing Cine Movies on page 557.

1. Select a group of images.

   Make sure you are viewing the first image of the desired Cine movie.

2. Make any necessary changes to the image.

   You can zoom, pan, swivel, rotate, and adjust the window/level.

3. If no Cine movie was previously defined, click Set State  to set the current view of the image to the initial Cine state.

NOTICE

If a previous Cine movie was defined, click New Cine  and set the state of the new Cine.

4. Go to the second presentation of the movie and click Set State  again.
5. Change the zoom, pan, swivel, rotate, and window/level parameters between each state, if desired.
6. After you have defined all states, click Play .
7. Click OK.

   The Cine movie plays. You can change the Frame Rate to increase or reduce the speed of the movie.

16.11.4 Viewing Cine Movies

To view a Cine in:	Do this:

Viewer **MPR** **Coronary Analysis** **Vessel Analysis** **Calcium Scoring** **3D**	To view a regular Cine without specific parameters: 1. Click the relevant group of images. 2. Open the Cine toolbar. 3. Click Play .
Cardiac Analysis	To view a regular Cine, see above. To view a cardiac (Phase) cine: 1. Load the study in the Cardiac analysis application. 2. Click Cine in the Viewer toolbar. The Cine toolbar appears with the additional Phase Cine icon . This icon is already selected by default. 3. Click Play . The cine runs through all the phases.

See this topic:

Setting Several States for Cine on page 557

Applying States to Cine Movies on page 558

16.11.5 Applying States to Cine Movies

To apply states in:	Do this:
Viewer	The Viewer supports a maximum of two states, representing the beginning and end of the Cine movie. When two states are defined, the Cine movie runs only between the first and last image set (and not the entire group), regardless of whether the last image set is the last image from within the group.
MPR	The MPR application lets you define any number of intermediate states when creating a Cine movie. In addition, you can alter the angle and location of the cross sections between states. You must define at least two states to apply a Cine movie to any of the reference images.
Vessel Analysis	The Vessel Analysis application lets you define any number of intermediate states when creating a Cine movie. In addition, you can Swivel and Roll the angio image between states.
Coronary Analysis	The Coronary Analysis application lets you define any number of intermediate states when creating a Cine movie. You must define at least two states to apply a Cine movie to any of the reference images.

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Cardiac CT	The Cardiac CT application lets you define any number of intermediate states when creating a Cine movie. In addition, you can alter the angle and location of the cross sections between states. You must define at least two states to apply a Cine movie to any of the reference images.
3D	The 3D application lets you define any number of intermediate states when creating a Cine movie. In addition, you can Swivel and Roll the angio image between states. You must define at least two states to apply a Cine movie to any of the reference images.

See these topics:

Viewing Cine Movies on page 557

Setting Several States for Cine on page 557

16.11.6 Viewing Cine Movies of Cardiac CT Images

You can view a volume rendered Cine movie of the heart, including all loaded phases.

1. On the Viewer toolbar, click Cine .

   The cage-removal process starts automatically. If the process will take too long, a message appears that lets you choose to wait or to watch the Cine movie with the rib cage in place.

   The Cine toolbar opens at the top left of the image. The result image displays the VolR image in the coronal plane.

2. Click Play .
   - If Cine is invoked while in Single-Phase mode, only the images of the selected mode are displayed. The images swivel by default.
   - If Cine is invoked while in Multi-Phase mode, the result image section is changed to a 1x1 layout, and a cine of the same position between all of the phases is played, representing a heartbeat.

   You can define a different cine behavior using the Cine State mode (see Applying States to Cine Movies on page 558).

3. If required, you can change the frame rate or interact with the image using Swivel, Roll, Clipping Pane, or Slab.

4. Click Stop  to stop the movie.

   If Cine was invoked while in Multi-Phase mode, the layout returns to the format displayed when the function was invoked.

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16.11.7 Saving a Cine Movie

To save a Cine movie in DICOM format:

1. From the Cine toolbar, click Save .
2. Select To Archive.
   The Save To dialog box appears.
3. Type the relevant information,
4. Select the archive where you want to save the Cine movie.
5. Click OK.

To save a Cine movie locally:

1. From the Cine toolbar, click Save .
2. Select To File.
   The Save As dialog box appears.
3. Enter the path and filename.
4. Specify the file type.
5. Select the frames per second (FPS).
6. Specify whether the file should be compressed.
7. Click Save.

16.12 Using Groups

16.12.1 About Groups

A viewbox is divided into groups. Each group is made up of a cluster of images.

See these topics:

Configuring a Group Layout on page 561
Enlarging a Group on page 562
Comparing Groups on page 562
Copying Groups on page 563
Moving Groups on page 563
About Links on page 563
Linking Groups Manually on page 566
Linking Groups in Different Frames of Reference (Semi-automatic Linking) on page 568

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Linking Groups Automatically on page 570

Off Spacing on page 571

Unlinking Groups on page 574

16.12.2 Configuring a Group Layout

You can configure how the groups will be displayed on your monitor. The groups that appear may not be all of the available groups and may not reflect all of the available information.

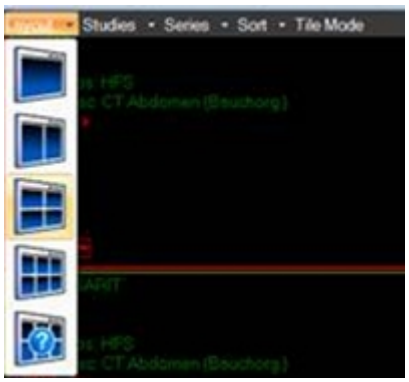
For example, an MRI study may have six series. When the study is loaded, the six series are divided into six groups based on their series number. However, if a display is opened with four groups, you can view only four of them. The other two groups are hidden until you display them. You can also fill the entire display area with one group.

To configure a group layout:

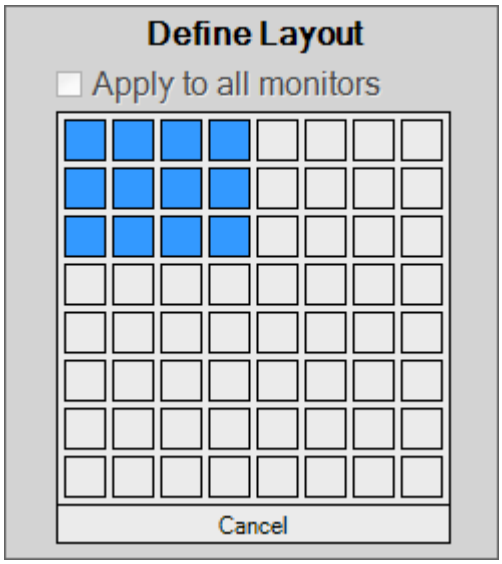
1. Click  to disclose the group-level toolbar.

   The group-level toolbar appears.

2. Click the **Define Layout** icon .



3. In the Define Layout window, drag the mouse over the grid to highlight the desired layout. click to complete the selection.



4. Check the 'Apply to all monitors' option if you want the same layout to apply to multiple monitors. Otherwise, the newly defined layout applies only to the active monitor.

16.12.3 Enlarging a Group

To Fill the Viewbox with One Group (Enlarge a Group)

From a Menu	From the Icon	From the Keyboard
Click View --> Enlarge Group.	Click Enlarge Current Group 	**Ctrl + E**

16.12.4 Comparing Groups

You can duplicate a group in the Viewer and automatically link the original group to the copy so you can compare the images. You can then apply different windowing or zoom values to the linked groups and scroll them simultaneously for comparison.

To duplicate a group and automatically link to the original group:

1. Right-click the upper left corner of the group you want to duplicate and link.

   The pointer changes shape.
2. Drag the group to the location you want.
3. Click Compare Here.

   The original group is duplicated and the groups are automatically linked. You can scroll both groups simultaneously and use different viewing options to compare them.

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16.12.5 Copying Groups

You can copy a group in the Viewer and view it in another location in the same viewbox. For example, you might want to view the group using different windowing values.

1. Right-click the upper-left corner of the group you want to copy.

The pointer changes shape.

2. Drag the group to the location you want.
3. Click Copy Here.

The group is copied to the selected location without affecting the original group.

NOTE: You can also manually link the original group and the duplicated group.

See this topic:

About Links on page 563

16.12.6 Moving Groups

You can move a group from one location to another within the same viewbox.

1. Right-click the upper-left corner of the group you want to move.

The pointer changes shape.

2. Drag the group to the location you want.
3. Click Move Here.

The group moves to the location you select. If a group already existed in the location to which you moved the group, the two groups exchange places.

16.13 Using Links

16.13.1 About Links

Linking allows you to correlate two or more volumes. You can apply links to multiple groups of the same study; the links create a virtual spatial position for each slice. The groups are correlated according to the offset of the slice positions. The offset is usually a measurement in the z axis (head to toe).

You can link two or more of the displayed groups. After you link the groups, you can scroll multiple images synchronously for comparison purposes. When you finish using the linked groups, you can unlink them.

NOTICE! Linked groups are indicated by a link annotation and a link number displayed in the lower-left of each image.

You can also link non-volumetric groups by slice numbers.

See these topics:

Using the Link Tool on page 565

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Linking Groups Manually on page 566
Linking Groups in Different Frames of Reference (Semi-automatic Linking) on page 568
Linking Groups by Slice on page 568
Synchronizing Window Levels on page 568
Using the Automatic Link Tool on page 569
Linking Groups Automatically on page 570
Linking MPR Groups on page 158
Linking Special Groups on page 572
Off Spacing on page 571
Unlinking Groups on page 574
About Reference Lines on page 575
About Registration on page 577

16.13.2 Linking Tools

The PowerViewer provides several tools for linking.

Automatic Link, Link, and Unlink All Tools

The View menu in the PowerViewer menu toolbar provides several options in a drop-down menu. When you click View, you can select any of the following tools:

From the View menu	Shortcut	Description
 Automatic Link	**Ctrl + L**	Use on groups with the same: • orientation/planar view • frame of reference
 Link		Use on groups: • when Automatic Link does not successfully apply the link • where a manual linking process is preferred • without existing links (applied from Register Studies or Automatic Link) • sharing the same orientation/ planar view • sharing the same frame of reference

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 Unlink All	**Ctrl + U**	Removes the links from all the groups in the viewbox.

Link Annotation Tool

When you navigate to the bottom left corner of the group display area, the PowerViewer provides the following tool:

Link Annotation	Description
In the group display area, navigate to the bottom left corner and locate the text Link.	Removes the link from one group.

Link Groups Tool

When you right-click on a group, the PowerViewer provides the following tool:

Link Groups	Description
Right-click, drag, and drop.	Allows groups to scroll together according to the physical location of the image.

Realign Link Tool

When you combine scrolling and the SHIFT key, the PowerViewer provides the following tool:

Realign Link	Description
Press and hold the SHIFT key and scroll on linked groups.	Use on groups: • with different frames of reference • from different studies • that are registered or unregistered Aligns the link between the two registered groups. Realign Link updates the matching between the registered studies. Realignment affects the registration in one axis at a time (the z-axis).

16.13.3 Using the Link Tool

Criteria for the Link tool

You can use the Link tool  on groups with the same:

- frame of reference (where automatic registration - see Using Register Studies (Automatic Registration) on page 580, is not used)
- orientation/planar view

It is not possible to use the Link tool to link groups with different orientations.

NOTICE! You can use the Link tool on groups which do not fulfill the criteria for using the Automatic Link tool.

To Use the Link Tool

1. Verify that your groups comply with the linking criteria.
2. Link the groups. See Linking Groups Manually on page 566.

Criteria for the Drag and Drop Function

You can use a drag and drop function to link groups sharing the same:

- frame of reference (where automatic registration - see Using Register Studies (Automatic Registration) on page 580, is not used)
- orientation/planar
- You can use the drag and drop function to make the orientation the same for MPR groups.

Additional Details

You cannot link groups with different orientations. In some cases, you can force the orientation to match, and then successfully create a link.

You can use the drag and drop function on MPR groups with different orientations/planar views. For example, when you drag and drop Group 1 onto Group 2, the orientation for Group 1 changes to match the orientation for Group 2.

To Use the Drag and Drop Function

1. Verify that your groups comply with the linking criteria.
2. Link the groups. See Linking Groups Manually on page 566.

See these topics:

About Links on page 563

Linking Groups Manually on page 566

Unlinking Groups on page 574

16.13.4 Linking Groups Manually

To allow simultaneous scrolling, you can manually link two or more groups displayed in the same viewbox.

You can use the following tools/methods:

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- The Link tool
- The drag and drop function

NOTICE! Manually linked groups are linked at the image that was active in each group when you made the link. Make sure that the active images in the groups represent the same geometric position in the patient's exam.

To Link Groups Manually Using the Link Tool

1. In the Comparison toolbar, click Link .

   The cursor changes to a chain.
2. Click any of the displayed group(s) .

   The groups are linked. If you click one group after another and the groups are in the same frame of reference, the system links the groups and synchronizes the images.

   – Selected groups that do not have the same frame of reference are assumed to be matching and are linked. See Linking Groups in Different Frames of Reference (Semi-automatic Linking) on page 568.

   – If a selected group does not match any other group (for example, two groups have different angles), the system creates a new link. If a group matching this group is later found, it is added to the link. Otherwise, the link is removed.
3. To stop Link mode, click another tool.

To Link Groups Manually Using the Link Groups Function (Drag and Drop)

1. Select the first group.
2. Place the cursor in the upper left corner of the group.

   The cursor icon changes.
3. Right-drag the cursor to the other group to which this group is to be linked.

   A menu appears.
4. Select Link Groups.

   The groups are linked. The link is indicated by the word Link and a link number that appears in the bottom-left corner of each of the linked groups.
5. Repeat steps 1 - 3 for each additional group that you want to link to the already linked groups.

   You can start the link from any of the already linked groups.

   If you want to make another link that is not linked to the already linked group, repeat steps 1 - 3. Make sure that the groups selected are not already associated with the existing link.

   After the groups have been linked, the groups remain synchronized until they are unlinked. Each time you navigate to another image in one of the linked groups, all other linked groups will move to the matching image.

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NOTICE! When scrolling, if a linked group does not have matching images (meaning, you navigated out of the range of images in the linked group), the link number displayed in the bottom left corner of the window indicates Off Spacing (see Off Spacing on page 571).

See this topic:

Using the Link Tool on page 565

16.13.5 Linking Groups in Different Frames of Reference (Semi-automatic Linking)

When you have two groups of images from different studies (different frames of reference), the patient may have been in a different position. Because of the change in position, even if the group of images shows the same area of the body, the images cannot be automatically synchronized.

To synchronize the images, you can do one of the following:

- Use automatic registration (see Using Register Studies (Automatic Registration) on page 580).
- Link the groups manually

To link the groups manually:

1. Manually scroll to find matching images in the groups being linked.
2. Click Link .

   The cursor changes to a chain icon (Link mode).

   The groups are synchronized according to the images displayed when you clicked Link.
3. To stop Link mode, click another tool.

16.13.6 Linking Groups by Slice

1. In the Comparison toolbar, click Link by Slice in the Link tool  drop-down.
2. Click Link .

   The cursor changes to an chain.
3. Click any of the displayed group(s).

   The groups are linked by slice. Scrolling images by image number in one groups scrolls the images in the linked grouped synchronically.

16.13.7 Synchronizing Window Levels

1. In the Comparison toolbar, click Link .

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The cursor changes to a chain.

2. Click any of the displayed group(s).
3. Click Synchronize Window Level  in the Comparison toolbar to turn on the synchronized window levels mode.

   Window level changes in all linked groups is synchronized. Changing the window level in one group causes the same simultaneous changes in all linked groups.

NOTICE

Changes in window levels is synchronized only if the window level of the linked groups was initially the same.

16.13.8 Using the Automatic Link Tool

Criteria

You can use the Automatic Link  tool on groups with the same:

- frame of reference
- orientation/planar view
- groups registered using Register Studies 

NOTICE

When you use Register Studies, the Automatic Link tool is simultaneously applied to the groups.

Additional Details

- The Automatic Link tool ignores groups with different orientations. As a result, you cannot use Automatic Link to link an axial group to a coronal group.
- Automatic Link is incremental. When Automatic Link is active, any new groups are automatically linked.
- You can scroll PowerViewer groups or MPR groups. You can swivel and scroll linked MPR groups.

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To Use the Automatic Link Tool

1. Verify that your groups comply with the linking criteria.
2. Link the groups. See Linking Groups Automatically on page 570

See these topics:

About Links on page 563

Unlinking Groups on page 574

Linking Groups Automatically on page 570

16.13.9 Linking Groups Automatically

Using automatic linking, the system automatically searches for groups that have a definite match. It removes all previously existing links and creates new links for all matches.

From a menu:	With a keyboard shortcut:
In the Comparison toolbar, click Automatic Link 	Press **Ctrl + L**

1. In the Comparison toolbar, click Automatic Link .

   The cursor changes to automatic link mode.
2. Click any of the displayed group(s) .

   The groups are linked. All relevant series in the selected viewbox are synchronized and linked.

   Repeat the steps for each additional group that you want to link to the already linked groups. You can start the link from any of the already linked groups.

IMPORTANT

When you use Register Studies  **, groups are automatically linked.**

See this topic:

Using the Automatic Link Tool on page 569

Using Register Studies (Automatic Registration) on page 580

About Automatic Links in Registered Studies on page 588

16.13.10 Linking MPR Groups

You can create links for Multi-Planar Reformatting (MPR) groups using:

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Automatic Link	Using the Automatic Link Tool on page 569 Linking Groups Automatically on page 570
Link	Using the Link Tool on page 565 Linking Groups Manually on page 566
Drag and drop	Linking Groups Manually on page 566

When the MPR groups are linked, you can swivel and scroll the images in the group synchronously.

When an MPR group is linked to a PowerViewer group and then you swivel the MPR-based group, the link between these groups is not applied. However, the reference point remains synchronous. If you swivel the MPR group to the original orientation, you also adjust the link so that you can scroll the images in the groups simultaneously.

NOTICE

A reference point (see Working with Reference Points (MPR Images) on page 593) refers to the 'center of swivel' point, which is displayed on MPR groups.

See these topics:

About Links on page 563

Unlinking Groups on page 574

Working with Reference Points (MPR Images) on page 593

16.13.11 Off Spacing

Each group is made up of a series of images. Each series may contain images from a different location or a different size area of the patient's body. When you view two groups, there may be a partial overlap between the groups, and they can be linked.

However, after the groups are linked and synchronized, a location in one group might not have a match in the second group (for example, one group contains only upper body images and the other group contains images of the whole body).

If you are in a linked group and you scroll out of the range of images in the second group, the second group display is either empty (black image) or the best-match-slice (closest) image, unless it is more than x cm from the selected location in the body (x is defined in the system configuration). The link annotation in the lower left corner of the group display changes from Link to Off Spacing. If several groups are linked together, more than one group may be Off Spacing at any particular time.

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NOTICE

For instructions on how to define whether an empty image or the best-match-slice image is displayed, see the system administrator. The default is to display the best-match-slice image.

While you scroll in a linked group, the system searches for a matching image in the group that is out of range. The closest/empty image will be shown until you return to a location that has a match.

16.13.12 Using Realign Link

You can use Realign Link to realign an existing link between:

- two groups with different frames of reference, such as groups from different studies.
- two registered groups.

The link realignment updates the volume matching between the registered studies. Realignment affects the registration in one axis at a time (the z-axis).

To Use Realign Link

1. Press and hold Shift on the keyboard.
2. Scroll the linked group until you achieve the desired alignment.
3. Release Shift.

The realigned link affects all relevant groups. If you realign two groups that are linked to other groups, the link for all the groups is also realigned.

NOTICE

You can apply Realign Link to linked groups with the same original frame of reference. However, the realignment is temporary. As you press Shift and scroll through the groups, you will see the changing offset between the datasets. When you release Shift and stop scrolling, the alignment returns to the original setting.

See this topic:

Registration Tools on page 579

16.13.13 Linking Special Groups

You can create groups with overlapped volumes (both in the same and different orientations). Special groups that contain overlapped volumes can include:

- All-in-one group;
- Groups containing more than one phase;

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- The localizers group in the MR scan;

The Automatic Link and the Link tools do not link these groups to other groups unless the groups are copied. The tools link the copies.

You can use the Link Groups tool to link special groups to similar groups or to regular groups.

To Link Groups Manually Using the Link Groups Function (Drag and Drop)

1. Select the first group.
2. Place the cursor in the upper left corner of the group.

   The cursor icon changes.
3. Right-drag the cursor to the other group to which this group is to be linked.

   A menu appears.
4. Select Link Groups.

   The groups are linked. The link is indicated by the word Link and a link number that appears in the bottom-left corner of each of the linked groups.
5. Repeat steps 1 - 3 for each additional group that you want to link to the already linked groups.

   You can start the link from any of the already linked groups.

   If you want to make another link that is not linked to the already linked group, repeat steps 1 - 3. Make sure that the groups selected are not already associated with the existing link.

   After the groups have been linked, the groups remain synchronized until they are unlinked. Each time you navigate to another image in one of the linked groups, all other linked groups will move to the matching image.

NOTICE

When scrolling, if a linked group does not have matching images (meaning, you navigated out of the range of images in the linked group), the link number displayed in the bottom left corner of the window indicates Off Spacing (see Off Spacing on page 571).

Additional Details

Two groups of images in the same viewbox are linked to scroll together according to the physical location of the image. Groups can be linked either manually or automatically.

For example, if two groups show different anatomical regions and you select Link Groups, the second group selected automatically displays the image showing the anatomical region that is physically closest to the anatomical region displayed in the first group.

After you apply Link Groups, when you scroll through the images in one group, you will see the images in the linked group scroll simultaneously with the same physical distance and in the same direction.

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See this topic:

Copying Groups on page 563

16.13.14 Unlinking Groups

You can unlink individual groups or all linked groups simultaneously, without affecting the original content of the groups.

To unlink one group:

1. Select the group to be unlinked.
2. Place the mouse cursor over the word Link in the bottom left corner of the group display area.

   The cursor changes to a broken chain icon.
3. Click the Link annotation.

   The group unlinks.

A group can link automatically if you:

- navigate to another group and then return to the original group
- register the group

To unlink all groups:

You can unlink groups without affecting the original content of the group.

1. Select the view containing the linked groups.
2. Unlink the groups.

From a toolbar:	With a keyboard shortcut:
In the Comparison toolbar, click Unlink 	Press **Ctrl + U**

All linked sets of groups unlink.

See these topics:

Using the Automatic Link Tool on page 569

Linking Groups Automatically on page 570

About Registration on page 577

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16.14 Using Reference Lines

16.14.1 About Reference Lines

Reference lines display the current location of the slices. The PowerViewer contains options that let you determine how reference lines appear on images. Reference lines for a group of images can be displayed on another group displayed in the same viewbox.

Reference Lines can either be shown or hidden. When Reference Lines are active, the lines show on visible slices for the active group.

For example, if PowerViewer groups and MPR groups are active and you select Show Reference Lines, you can swivel one or more of the MPR groups to a different orientation. The reference lines will display automatically where applicable.

In registered studies, the reference Lines can relate between current and prior studies and further enable comparison capabilities.

IMPORTANT

The results of any registration-related operations affect the reference lines.

See these topics:

Displaying Reference Lines Automatically (Alt + R) on page 575

Displaying Reference Lines Manually on page 576

Relating Reference Lines on page 576

Showing Only Visible Slices on page 576

Showing Mini Reference Lines on page 576

Removing Reference Lines on page 577

About Links on page 563

About Registration on page 577

16.14.2 Displaying Reference Lines Automatically (Alt + R)

When you select Auto Ref-lines Setup  or use the shortcut key Alt+R, the Diagnostic Workstation searches between the groups displayed in a viewbox and automatically sets up all the possible reference lines.

1. Click Auto Ref-Lines  to open a sub-menu.
2. Click Auto Ref-lines Setup.

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The Diagnostic Workstation searches among the groups displayed in a viewbox. All possible reference lines appear on all groups in the viewbox.

16.14.3 Displaying Reference Lines Manually

You can display the reference lines for one or more groups on a single group at the same time in the same viewbox. For example, you can display reference lines for the axial and sagittal groups over a single coronal group.

1. Point to the upper left corner of the group containing reference lines you want to see.
2. Click and drag the group to the group on which you want the reference lines to appear.
3. In the main menu, click View --> Auto Ref-Lines Setup.

   The reference lines of the first (dragged) group appear on the second group.
4. Repeat steps 1 - 3 to display reference lines for additional groups.

16.14.4 Relating Reference Lines

When you use the Relate Mode, you can click an area on the Localizer image to display the relevant slices of the study.

See this topic:

About Relate Mode on page 590

16.14.5 Showing Only Visible Slices

When you select Show Only Visible Slices, only reference lines that relate to the slices on the screen appear on the Localizer image.

- From the main menu, click View --> Ref-lines --> Show On Localizer Only.

Or

- Click  to open the drop-down menu. Select Show On Localizer Only.

16.14.6 Showing Mini Reference Lines

You can display a group of images as if the group is a Localizer image with its own set of reference lines. These reference lines are called mini reference lines. Mini reference lines enable scrolling and viewing of the relevant slices the same way as a Localizer image.

1. Click in the upper left corner of Group B and drag Group B to the top left corner of Group A.
2. Right-click and select Mini Ref-lines.

   Group B appears with mini reference lines that let you view the relevant slices.

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16.14.7 Removing Reference Lines

You can remove reference lines from a group.

1. From the main menu, click View --> Ref-lines.
2. Deselect the group name.

   Or

   Click Auto Ref-lines  and click Auto Ref-lines Setup to toggle the reference lines to "off."

16.14.8 Rotating Reference Lines

1. Press the Shift key.

   The cursor changes to a rounded arrow.
2. Rotate the line using the mouse.

   The slice numbers of the linked series are shown at the edge.

When you swivel the linked series, the reference line rotates automatically to show the location of the slice.

16.15 Using Registration

16.15.1 About Registration

The registration tools allow you to match two or more studies containing volume, even when the studies have:

- a different Frame of Reference
- arrived from different modalities, such as CT or MR
- images in different orientations/planar views

The registration algorithm does not stretch or distort the volumetric image data during the matching process.

You can refine or remove registration as needed.

NOTICE

You can use Register Studies to compare prior and current cases, where the original slices in each case have a different orientation. The registration information presents the same calculated plane and slice automatically in one group, according to the orientation and slice of the other group.

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When you register current and prior cases, you can use the Relate and Reference Line tools. The Relate and Reference Line tools allow you to detect the relevant location or pathology in one study, and correlate the location or pathology to the other study.

When studies are registered, they are automatically linked. You can scroll the linked data sets simultaneously.

When you display the registered, linked studies in the MPR rendition type, you can also swivel the linked data sets simultaneously.

Registration Types

There are 4 registration types:

- **Register Studies**—automatic, global-level registration.
- **Guided Registration**—assisted, local-level registration.
- **Manual Registration**—based on your input.
- **Treat as Registered**—overrides DICOM data and forces registration.

There are 2 registration adjustments:

- **Refine Registration**—allows you to focus registration on the same specific anatomical region and compare the studies.
- **Break Registration**—allows you to remove all registration data on an active study.

Registration Combinations

The following registration combinations are possible:

- You can register studies A and B, and then register studies C and D.
- You can register studies A and B, and then register study C to study A, or study C to study B.
- If you register the pairs A to B and B to C, then studies A and C can be considered registered. However, studies A and C in that case do not have the exact registration information as would occur if you register studies A and C, and then register studies B and C.
- You can register more than 2 studies.
- You can register additional studies to a previously registered set of studies.
- You can register more than one pair of studies.

Registration information is shared across applications. If you applied registration using a non-viewer application, the registration information is also available in the PowerViewer, and tools such as Relate and Reference Line are supported.

Additional Details

- Synchronous actions—such as correlated scroll, correlated swivel, shared reference line, and correlated pan—are supported in special designated display options, and can depend how the different studies are registered.
- If studies are not registered to one another, then most synchronization actions are unavailable.

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- You can apply the following parameters synchronously to registered studies and to unregistered studies:

• **zoom**—based on mm per pixel calculation.

• **initial axis**—if the you use Replace With and switch to a non-registered data set, the initial axis of the dataset is synchronized with the current one.

• **measurements**—any measurements you place on a secondary studies are also applied to a fused image, even if the fused image is composed of unregistered studies.

IMPORTANT

Registration affects links and reference lines.

See these topics:

Registration Tools on page 579

Using Register Studies (Automatic Registration) on page 580

About Automatic Links in Registered Studies on page 588

About Reference Lines on page 575

16.15.2 Registration Tools

IMPORTANT

The registration algorithm is designed for use on volumetric datasets only. For more information about volume rendered images, see About Volume Rendering on page 632.

The Registration tools are available from the PowerViewer for viewbox applications such as PET/CT and Volume Matching.

To start registration, click Register Studies .

Register Studies  provides the following drop-down menu.

Drop-down Menu	Description
 Register Studies	Use for general or global registration. Allows you to click on two or more studies. After you click the specific dataset, group, or series in each study, Register Studies automatically applies an algorithm to the datasets. The algorithm matches any two volumes from two studies, and automatically maps each pixel in one study to the relevant pixel in the other study.

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 Refine Registration	Use for focusing on local regions and comparing the regions. Allows you to focus on a certain region, and then compare the specific region in the two studies. Adjusts the registration algorithm result.
 Guided Registration	Provides global registration that is assisted, precise, and based on manual local matching. Useful to apply when two scans cover a small region of common volume with a small area of overlap. Applies the registration algorithm based on registration points. To create a registration point, you must click the same anatomical region in each study. The points are factored into the registration algorithm to represent similar anatomical locations. The registration points allow Guided Registration to more quickly and more accurately match the volumes and map the relevant pixels in each study.
 Manual Register Studies	Use when the registration results from Register Studies or Guided Registration are unsatisfactory. Matches the two volumes based on the planes of the two studies and on the position of the two points that you create by clicking on each study. You must manually match the orientation and the register points between the groups. Manual Register Studies applies an algorithm based on the input you supply. The results for Manual Register Studies can vary according to the accuracy of the input you supply.
 Treat as Registered	Use for situations where the series are registered in the modality, but the DICOM data does not reflect the registration. For example, you might have a PET series which does not have the same frame of reference but was registered in the modality before the study was copied into the Vue PACS system. After you click on the dataset, group, or series in each study, the studies are considered registered.
 Break Registration	Use to remove the registration points, algorithm calculations, and volume matches from the study. Removes any type of registration for any active datasets, groups, or series in a study.

16.15.3 Using Register Studies (Automatic Registration)

IMPORTANT

Do not apply Register Studies to studies containing non-volumetric datasets. The registration algorithm is designed for use on volumetric datasets only. For more information about volume rendered images, see About Volume Rendering on page 632.

Register Studies is best suited for general registration or global level registration.

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The Register Studies tool applies an algorithm to the datasets in a study. The algorithm matches any two volumes from two studies, and automatically maps each pixel in one study to the relevant pixel in the other study.

1. Display two or more studies containing volumetric datasets.
2. Click Register Studies  to view the drop-down menu.
3. Click Register Studies . The cursor changes to Automatic Registration mode.
4. Click the volumetric groups or series in each study.

If you click on a group more than once, the Register Studies function waits until you click, or choose, another group.

When you click on the same general location in each study, you create a registration point. The registration points are factored into the registration algorithm. The Register Studies tool applies an algorithm to the datasets in a study.

The algorithm matches the volumes from two or more studies, and automatically maps each pixel in one study to the relevant pixel in the other study.

IMPORTANT

If you need to compare specific regions in each study, use Refine Registration (see Using Refine Registration on page 585).

See these topics:

Registration Tools on page 579

Using Refine Registration on page 585

Successful Registration on page 587

Failed Registration on page 587

Unsatisfactory Registration Results on page 587

Troubleshooting Failed or Unsatisfactory Registration on page 587

About Automatic Links in Registered Studies on page 588

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16.15.4 Using Guided Registration

IMPORTANT

Do not apply Guided Registration to studies containing non-volumetric datasets. The registration algorithm is designed for use on volumetric datasets only. For more information about volume rendered images, see About Volume Rendering on page 632.

Guided Registration provides assisted, precise registration. Guided Registration applies global-level registration, based on local registration points that you manually place on a specific region of each study.

Use Guided Registration:

- When two scans cover a small region of common volume with a small area of overlap.
- For large studies, containing hundreds or thousands of images.
- For small studies, containing only a few images.

1. Display two or more studies containing volumetric datasets.
2. Click Register Studies  to view the drop-down menu.
3. Click Register Studies  to apply a global-level registration.
4. Scroll to the same anatomical region in each study.
5. Click Guided Registration . The cursor changes to Guided Registration mode.
6. Click once on the same anatomical region of interest (ROI) in each study, such as the same vertebrae in a pair of MR spine studies.

When you click on the anatomical region in each study, you create a registration point. The registration points are factored into the registration algorithm. The points allow the algorithm to more quickly and more accurately match the volumes in each study, and map the relevant pixels in each study.

See these topics:

Registration Tools on page 579

Successful Registration on page 587

Failed Registration on page 587

Unsatisfactory Registration Results on page 587

Troubleshooting Failed or Unsatisfactory Registration on page 587

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16.15.5 Using Manual Registration

IMPORTANT

Do not apply Manual Registration to studies containing non-volumetric datasets. The registration algorithm is designed for use on volumetric datasets only. For more information about volume rendered images, see About Volume Rendering on page 632.

Manual Registration is appropriate to use when the registration results from Register Studies or Guided Registration are unsatisfactory.

IMPORTANT

You must manually enter the relevant input. The quality of the results depends on the accuracy of the input. If you vary the input, the registration results will also vary.

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You must manually match the studies by adjusting the following input:

- Orientation/planar view—display each study using same orientation.
- Registration points—each registration point must be placed in the same location in each study. The exact clicking point is less important, but the general location must be the same.

When you use Manual Registration, the series/groups/datasets cannot scroll or swivel automatically. You must perform the matching process before you click Manual Registration.

1. Display two or more studies containing volumetric datasets.
2. Manually scroll and swivel each study to present the same orientation in each study.
3. Click Register Studies  to view the drop-down menu.
4. Click Manual Register Studies . The cursor changes to Manual Registration mode.
5. Click once on each study in the same general location of each study.

NOTICE

When you click on the same general location in each study, you create a registration point. The registration points are factored into the registration algorithm, and allow Manual Registration to match the volumes and map the relevant pixels in each study.

See these topics:

Registration Tools on page 579
Successful Registration on page 587
Failed Registration on page 587
Unsatisfactory Registration Results on page 587
Troubleshooting Failed or Unsatisfactory Registration on page 587
About Automatic Links in Registered Studies on page 588

16.15.6 Using Treat as Registered

IMPORTANT

Do not apply Treat as Registered to studies containing non-volumetric datasets. The registration algorithm is designed for use on volumetric datasets only. For more information about volume rendered images, see About Volume Rendering on page 632.

Treat as Registered is most appropriate to use when the studies are correlated but the DICOM data does not reflect the modality registration.

For example, you might have a PET series which does not have the same frame of reference. However, the PET series was registered in the modality before the study was copied into Vue PACS.

1. Display two or more studies containing volumetric datasets.
2. Click Register Studies  to view the drop-down menu.
3. Click Treat as Registered . The cursor changes to Treat as Registered mode.
4. Click once on each group to be treated as registered.

When you click on the same general location in each study, you create a registration point. The registration points are factored into the registration algorithm, and the datasets are registered according to the DICOM information.

You can use all the concurrent actions available for registered studies. See About Registration on page 577.

See these topics:

About Registration on page 577
Registration Tools on page 579
Successful Registration on page 587
Failed Registration on page 587
Unsatisfactory Registration Results on page 587

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Troubleshooting Failed or Unsatisfactory Registration on page 587

16.15.7 Using Refine Registration

IMPORTANT

Do not apply Refine Registration to studies containing non-volumetric datasets. The registration algorithm is designed to use on volumetric datasets only. For more information about volume rendered images, see About Volume Rendering on page 632.

NOTICE

If Refine Registration is inactive, you must perform a global level registration. Perform the steps for Register Studies (see Using Register Studies (Automatic Registration) on page 580) first, and then apply Refine Registration.

- Refine Registration is best for matching two volumes based on local similarities, rather than global similarities. You must apply global registration before you apply Refine Registration.
- Use Refine Registration when you need to focus on specific regions of each study. After you register the studies using Refine Registration, you can better compare the specific regions in the studies.
- Refine Registration adjusts the registration algorithm result. The adjusted values will improve the local registration results, but the global registration results might become worse.

1. Display two or more studies containing volumetric datasets.
2. Use Register Studies (see Using Register Studies (Automatic Registration) on page 580) to apply global level registration.
3. Create a Relate Point for each study. See Creating a Relate Point on a Volume Rendered Image on page 636.
4. Move each relate point to the desired specific location on each study.
5. Initiate Refine Registration.

To initiate Refine Studies using a shortcut:	To initiate Refine Studies from a menu:

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Press the CTRL key on the keyboard when the Relate mode is still active. The cursor changes to Refine Registration mode. Click on the desired location in each study to run the Refine Registration algorithm.	1. Click Register Studies  to view the drop-down menu. 2. Click Refine Registration  to run the algorithm.

The position of the relate points are factored into the registration algorithm.

Refine Registration matches the local volumes and maps the relevant pixels in each study.

See these topics:

Registration Tools on page 579

Successful Registration on page 587

Failed Registration on page 587

Unsatisfactory Registration Results on page 587

Troubleshooting Failed or Unsatisfactory Registration on page 587

16.15.8 Removing Registration

You can remove any type of registration for any active datasets, groups, or series in two or more studies.

IMPORTANT

You can only remove the registration between the active group and the other groups. See the example.

Example

- Groups A, B, and C are registered.
- Group B is active.
- You remove registration on Group B.
- Groups A and C remain registered.

After you remove registration, operations are no longer concurrent between the groups. For example, the scrolling and swiveling actions do not occur simultaneously between the groups.

1. View an active, registered group in a study containing volumetric data.
2. Click Register Studies  to view the drop-down menu.
3. Click Break Registration .

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4. Repeat steps 1 to 3 until you have removed the registration for all the desired studies.

See these topics:

About Registration on page 577

Registration Tools on page 579

16.15.9 Successful Registration

If registration is successful, you will see a Registration Successful status message in the Status Bar.

16.15.10 Failed Registration

If the registration is unsuccessful, you will see a Registration Failed dialog box.

See this topic:

Troubleshooting Failed or Unsatisfactory Registration on page 587

16.15.11 Unsatisfactory Registration Results

Factors such as poor image resolution, significant changes in the patient's condition, or a small overlap between the series can affect the registration results.

If registration results are unsatisfactory, you will see an Unsatisfactory Results message with the option to accept or reject the results.

If you accept the results, the registration is applied.

If you reject the results, the registration is not applied.

See these topics:

Registration Tools on page 579

Troubleshooting Failed or Unsatisfactory Registration on page 587

16.15.12 Troubleshooting Failed or Unsatisfactory Registration

Symptoms

- **You see a dialog box with the message Registration Failed.**
- **You rejected the results for the Registration.**

Possible Cause	Suggested Solution

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The images do not contain volumetric data.	You cannot register a study containing non-volumetric datasets. 1. Verify that you are using volumetric datasets. 2. Load a study with volumetric datasets into the application. 3. Repeat the steps for Register Studies. See Using Register Studies (Automatic Registration) on page 580.
The registration algorithm is not appropriate for the study.	Apply Manual Registration. See Using Manual Registration on page 583.
The study contains hundreds or thousands of images.	Apply Guided Registration. Guided Registration factors in the location that you target when selecting the dataset. Make sure that the targeted location is for the same anatomical area in both datasets. See Using Guided Registration on page 582.
The study requires more precise input.	1. Remove the existing registration. 2. Apply the appropriate registration (global, manual, treat as registered, refine). See Removing Registration on page 586.
The patient scan has changed significantly from the prior scan (due to clinical changes).	
The images in the study have poor resolution.	
Two scans cover a small region of common volume, and have a very small area of overlap.	
The groups are registered already.	

16.15.13 About Automatic Links in Registered Studies

When you register studies with similar orientations, the series, groups, and data sets are automatically linked by default.

NOTICE

Groups with different orientations do not automatically link during registration. For example, if you register an axial group to a coronal group, the groups will not link. If you have two axial groups and one group is from an MR study, the groups will not link if there is a large difference in the angle.

After you register MPR studies, the orientation, position, and reference points will all match together.

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If one registered group is MPR and the other registered group is in the PowerViewer, the MPR group automatically swivels and scrolls to match the orientation and the position of the original slices in the PowerViewer group.

If two or more groups are displayed in PowerViewer mode, the groups do not automatically swivel. The last group in the registration process automatically scrolls to the closest slice. If you change a PowerViewer group to an MPR group, the MPR group automatically swivels and scrolls to match the PowerViewer group.

When you use Manual Registration, the series/groups/datasets cannot scroll or swivel automatically. You must perform the matching process before you click Manual Registration.

The registration algorithm does not run on studies that are already registered. If the orientation is similar for the registered studies, the studies are automatically linked when you apply a registration type, even if the registration algorithm does not run.

See these topics:

Unlinking Registered Studies on page 590

About Registration on page 577

Using the Automatic Link Tool on page 569

Using Register Studies (Automatic Registration) on page 580

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16.15.14 Using Realign Link

You can use Realign Link to realign an existing link between:

- two groups with different frames of reference, such as groups from different studies.
- two registered groups.

The link realignment updates the volume matching between the registered studies. Realignment affects the registration in one axis at a time (the z-axis).

To Use Realign Link

1. Press and hold Shift on the keyboard.
2. Scroll the linked group until you achieve the desired alignment.
3. Release Shift.

The realigned link affects all relevant groups. If you realign two groups that are linked to other groups, the link for all the groups is also realigned.

NOTICE

You can apply Realign Link to linked groups with the same original frame of reference. However, the realignment is temporary. As you press Shift and scroll through the groups, you will see the changing offset between the datasets. When you release Shift and stop scrolling, the alignment returns to the original setting.

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See this topic:

Registration Tools on page 579

16.15.15 Unlinking Registered Studies

You can remove automatic links without affecting the registration. Follow the instructions for Unlinking Groups (see Unlinking Registered Studies on page 590).

When you unlink studies that are registered, you will also remove the ability to use concurrent swivel and scroll on the studies. You can still use the Relate, Swivel, and Scroll functions. However, the swiveling and scrolling action is limited to one active study and does not occur simultaneously for all the registered studies.

You can use the  Automatic Link tool to apply links without applying registration.

See these topics:

About Automatic Links in Registered Studies on page 588

Using the Automatic Link Tool on page 569

Linking Groups Automatically on page 570

Unlinking Groups on page 574

16.16 Correlating Regions of Interest in Registered Studies (Relate Mode)

16.16.1 About Relate Mode

The Relate  mode allows you to correlate a specific region of interest (ROI), point of interest (POI), frame of interest (FOI), or frame of reference (FOR) between registered studies. The registered studies can be current studies or prior studies.

With Relate mode active, you can click on any image to create a relate point. The relate point defines the region of interest. All the groups will scroll to display a correlating region of interest.

Example

A thorax-abdomen scan contains different series covering the two main body parts (thorax and abdomen).

You activate Relate mode. You click a specific area on one of the thorax groups to create a relate point.

The rest of the groups covering the thorax volume automatically scroll to show the correlating area of interest. A relate point marker appears on each of the correlated groups.

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The groups covering the abdomen volume do not scroll or contain any relate point markers.

See these topics:

Using Relate Mode on page 591

Working with Relate Points on page 592

Using Swivel Mode (MPR Images) on page 593

Working with Reference Points (MPR Images) on page 593

16.16.2 Using Relate Mode

IMPORTANT

Relate mode is not appropriate to use on MPR images. If you want to correlate regions of interest for MPR images, use Swivel mode to create reference points. See Using Swivel Mode (MPR Images) on page 593.

1. Register studies.
2. Display the group with the same frame of reference (FOR).
3. Activate Relate mode.
4. Click on the same region of interest (ROI). This process creates a relate point marker in each group.
   ⇨ The groups scroll to display correlating ROI. Each image contains a relate point marker.

⇨ A relate point marker looks like this: +

NOTICE

When you register a study containing a relate point to a new study, the relate point will also appear on the newly registered study.

See these topics:

About Registration on page 577

Using Swivel Mode (MPR Images) on page 593

Working with Relate Points on page 592

16.16.3 Activating Relate Mode

- In the toolbar, click Relate .

- Or
- In the menu toolbar, click Edit --> Relate .

16.16.4 Working with Relate Points

The relate point markers (+) are visible on the group you are currently scrolling on the viewbox.

Repositioning the Correlated Region of Interest:

- Click the relate point marker (+) and drag the marker to a different location

Or

Activate Relate  mode and click the new region of interest to create a new relate point.

A relate point is determined according to a calculation of slice spacing and slice thickness. There is a tolerance, or percentage, for the calculation. The relate point marker is visible when the point is within the tolerance. The relate point marker changes color when the point is within the tolerance but is an inexact match.

Hiding Relate Point Markers

You can show or hide the relate point markers.

- To hide the markers: press ALT + G on the keyboard.
- To view the hidden markers: press ALT + G again.

Deleting Relate Point Markers

You can delete a relate point markers from all groups in the same way as you delete other measurements or annotations. See Deleting Measurements or Annotations on page 511.

NOTICE

The preferred practice is to hide relate point markers instead of deleting the markers.

See these topics:

Creating a Relate Point on a Volume Rendered Image on page 636

Working with Reference Points (MPR Images) on page 593

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16.16.5 Using Swivel Mode (MPR Images)

Activating Swivel Mode

From a toolbar menu:	From a right-click menu:	With a keyboard shortcut:
In the toolbar, click Swivel 	Right-click and select Swivel  .	**Ctrl + W**
In the menu toolbar, click Edit --> Swivel  .		

You can use Swivel  mode to rotate images and apply reference points.

See these topics:

Manipulating 3D Images on page 188

Swiveling Panoramic and Scrolling Cross-Sectional Images on page 235

16.16.6 Working with Reference Points (MPR Images)

The reference point marker (+) is visible on MPR groups when you activate Swivel  mode. The reference point is united with the relate point, even if the relate point is located on a different slice.

When Swivel mode is active, the reference point and relate point move together as you scroll or swivel through an MPR group.

If you activate Swivel mode and then choose and activate a different MPR group, the reference point appears only after you start to manipulate and swivel the group.

Repositioning the Correlated Region of Interest:

- Click the reference point marker (+) and drag the marker to a different location. Repositioning the reference point marker will also affect the relate point marker.

Hiding Reference Point Markers

When you switch to another mode, the reference point marker is hidden.

16.17 Display Protocols

16.17.1 About Display Protocols

The Save as DP Wizard and the Display Protocol editor let you define display protocols used to customize the presentation of studies on the Diagnostic Workstation. You can build a Display Protocol bank, which stores all relevant Display Protocols for a particular user. Anytime you load a study, it loads according to the display protocol that best fits the study parameters.

NOTICE

Additional training is required in order to create the Display Protocols. It is recommended that you use the Save As DP Wizard. For more information about creating display protocols, contact the system administrator.

Display Protocols let you customize the:

- General layout of the application.
- Criteria for determining which groups are displayed and where.
- Criteria for determining if prior studies are to be loaded.
- Default group manipulation such as window level, zoom, orientation, and so on.
- Application types used to display data such as PowerViewer, MPR, 3D, and so on.
- Interactions between groups of images, such as linking groups or showing reference lines.

Considerations for Creating a Display Protocol:

The Total Number of Groups You Expect from the Scan

Different modalities typically contain different formats. For example, a CT abdomen scan usually contains two groups of images: the Localizer image and the axial slices. An MRI might have five or six groups of images, according to the sequence and body position.

Automatic Loading for Prior Studies of a Patient

The Diagnostic Workstation lets you load a patient's previous history. You can specify which modalities and body parts to load from the patient history. You can also specify how these studies are placed on the screen layout.

See these topics:

Understanding the Results for Save as DP on page 595

Saving Viewing Options as a Display Protocol on page 595

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16.17.2 Understanding the Results for Save as DP

When you use Save as DP, the results will retain specific parameters while omitting other parameters. Review the categories of information described here before you apply the Save as DP function.

Saved Information

When you use Save as DP, the Display Protocol retains the following information:

- Image parameters, such as Zoom and Windowing
- Rendition types, such as PowerViewer, MPR, MipPR, MinPR, in each window
- Links
- Reference lines, including Show Reference Only on the Localizer parameter

Excluded Information

When you use Save as DP, the Display Protocol omits the following information:

- Thickness and spacing for MPR images (the information is taken from the DICOM data when applying an DP)
- Orientation in a non-patient plane
- Reference points of the presented datasets

Exceptions

- Thickness and spacing are saved for MipPR and MinPR images.
- Orientation is saved when it is set for one of the patient axis (axial, coronal or sagittal).
- Links created with the Link tool are saved for groups with the same frame of reference.
- If the Automatic Link tool is active, the Save as DP function ignores any other links and saves only the activated mode (automatic link).
-

See this topic:

Saving Viewing Options as a Display Protocol on page 595

16.17.3 Saving Viewing Options as a Display Protocol

IMPORTANT

Review the information in Understanding the Results for Save as DP on page 595 before you perform the procedure for Save as DP.

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You can organize a window as required, then save that layout as a Display Protocol to be used at a later date for other images.

NOTICE

If your user profile has administrative privileges, the locking mechanism is activated while you are saving the viewing options as a Display Protocol, blocking other users from using this feature at the same time.

1. Prepare the screen to be saved as a Display Protocol.
2. From the DP menu, choose Save as DP.
   ⇨ The Save As DP Editor opens.
3. In the Save Changes section, select whether you are making the changes to the current Display Protocol, or saving a new Display Protocol.
   ⇨ If you choose the new Display Protocol option, enter the name of the protocol in the Name field.
   ⇨ **NOTICE! If you are making changes to an existing Display Protocol, its name is displayed next to the To Current DP option. If you do not have permission to make changes to the current Display Protocol, the name is not displayed, and you must enter a new Display Protocol name for it so that you do not overwrite the existing Display Protocol.**
4. If you want to apply the changes to history data, mark the check box accordingly.
5. Define the Display Protocol level.

   NOTICE! This option depends on the permissions of your user profile.
6. Click Next.
7. Choose the studies to apply the Display Protocol.
   - Studies that match initial definition: Applies the Display Protocol to studies that have an identical definition. If you choose this option, the remaining options are grayed out.
   - Studies with: Lets you select more specific options for the condition.
     - Same modality.
     - Contains body part. Enter a value. By default, this field contains the body part defined for the current study.
     - Contains study description. Enter a value. By default, this field contains the study description defined for the current study.
     - Studies that match custom definition: Applies the Display Protocol to studies that match a customized definition, which can be edited in the same way as the Display Protocol editor. See About the Display Protocol editor on page 597.

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NOTICE

When the Display Protocol is applied, the mechanism uses the Body Parts synonym when displaying the images. Contact the system administrator for assistance.

8. Click Next.
9. Identify the groups according to one of the following:
   - Current Criteria: If you are satisfied with the current display. It takes the current layout but uses the existing group.
   - Selected properties: You can indicate which tags are imported when you create groups. The more items you select, the more specific the group displayed.
10. Click Finish to save the Display Protocol.

16.17.4 Using the Display Protocol editor to Create Display Protocols

About the Display Protocol editor

The Display Protocol editor provides an advanced interface for creating and configuring Display Protocols. The modes of use are standalone or from inside the application.

See these topics:

Logging on to the Display Protocol editor on page 597

Creating a New Display Protocol on page 598

Changing a Display Protocol on page 598

Changing the Order of a Display Protocol on page 599

Defining Display Protocol Conditions (see Defining Display Protocol Conditions on page 600)

Exporting a Display Protocol on page 599

Importing a Display Protocol on page 599

Saving Viewing Options as a Display Protocol on page 595

Configuring Viewboxes for Display Protocols on page 602

Logging on to the Display Protocol editor

The Display Protocols defined using the Display Protocol editor are user-specific, group-specific, or system-wide.

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Logging on to the Display Protocol editor in Standalone Mode

Logging on to the Display Protocol editor from the PowerViewer Application

1. From the DP menu in the PowerViewer application, select Open DP Assistant.
   ⇨ The Display Protocol editor window appears showing the current Display Protocol.
2. Go to Creating a New Display Protocol on page 598.

Creating a New Display Protocol

Each new Display Protocol is based on an existing Display Protocol. After you log on (see Logging on to the Display Protocol editor on page 597), the Display Protocol editor window appears.

1. In the DP list, select the Display Protocol you want to use as the base for the new Display Protocol.
2. Click Add .
   ⇨ The New DP dialog box appears.
3. In the DP Name field, type the name for the new Display Protocol.
4. If you want to change the base Display Protocol, select a different base Display Protocol from the Base DP drop-down menu.

   NOTICE! The new Display Protocol has the same viewing settings and conditions as the base Display Protocol until you make modifications.
5. In the DP Level area, select whether the Display Protocol should be Private, Group, or System (depending on User Permissions available).
6. Click OK.
   ⇨ The name of the new Display Protocol appears above the selected Base DP.
7. If required, you can change the order of the new Display Protocol (see Changing the Order of a Display Protocol on page 599) in the DP List.
8. Go to Defining Display Protocol Conditions (see Defining Display Protocol Conditions on page 600) to define the conditions and viewing properties for the new Display Protocol.

Changing a Display Protocol

1. From the DP menu, select Open Display Protocol editor.
2. Make any changes to the Display Protocol.
3. Click Finish.
4. Click OK.

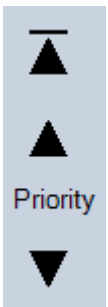
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If you do not have permission to edit Display Protocols, you can view the Display Protocols, but the buttons are disabled and you cannot edit a group Display Protocol.

Changing the Order of a Display Protocol

When you load a study, the system checks the list of Display Protocols sequentially. Make sure that the Display Protocols are listed from the specific (for example, CT Head) to the general (for example, CT).

1. From the DP List in the Conditions dialog box, select the Display Protocol you want to reposition in the list.
2. Click the arrows:



Click  to move the Display Protocol up one position.

Click  to move the Display Protocol down one position.

Click  to move the Display Protocol to the top of the list.

NOTICE! You can move multiple Display Protocols simultaneously. To select more than a single Display Protocol, press the Shift key while clicking the Display Protocols.

Exporting a Display Protocol

You can export a Display Protocol to another location.

1. In the Display Protocol editor, select the Display Protocol you want to export.
2. Click the Export button.
   ⇨ The Save As window appears.
3. Select the location where you want the Display Protocol to reside.

   NOTICE! Make sure that you save the Display Protocol as an XML file.
4. Click Save.

Importing a Display Protocol

You can import a Display Protocol that was saved and exported to another location.

1. In the Display Protocol editor, click the Import button.
   ⇨ The Open window appears.
2. Browse to the Display Protocol XML file you want to import.
3. Click Open.
   ⇨ The imported Display Protocol appears at the bottom of the DP List. It always has a level of Private.

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See this topic:

Changing the Order of a Display Protocol on page 599

16.17.5 Defining Display Protocol Conditions

Defining Display Protocol Conditions

Display Protocol conditions define the conditions that a study must meet to be loaded using a particular Display Protocol. The conditions have an ”and” relationship between them, meaning that all the conditions must be met for the Display Protocol to be activated. Each individual condition can have a number of values. These values have an ”or” relationship between them, meaning that any of the values must be found for that condition to be met.

See these topics:

Adding a New Display Protocol Condition on page 600

Changing a New Display Protocol Condition on page 601

Deleting a Display Protocol Condition on page 602

Adding a New Display Protocol Condition

1. From the DP List in the Display Protocol editor dialog box, select the Display Protocol you want to use as the base for the new Display Protocol.
   ⇨ Any conditions already defined for the existing Display Protocol appear in the area on the right side of the Display Protocol editor dialog box.
2. In the Tag column, click an empty field, then select a DICOM tag from the drop-down menu.
3. In the Operator column, select an operator for the new tag from the drop-down menu:

   Is Equal To: String matches the entered operator value exactly (case sensitive).

   Not Equal To: String is different than the entered operator value (case sensitive).

   Greater or Equal Number: Number is greater or equal to the entered operator value. Only applies to numerical values.

   Less Than: Number is less than the entered operator value. Only applies to numerical values.

   Contains: Whether the entered operator value is included in the string (not case sensitive). You can use one or more of these sub-operators:

Sub-operator	Description
&	x & y in the operator value indicates x value AND y value.

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,	x, y in the operator value indicates x OR y value where x relates to the whole expression before the comma, and y relates to the whole expression after the comma. For example, "contains x & y, z & w" means that the value contains either both x and y or both z and w.
/	x/y in the operator value indicates x OR y value where x and y relate only to the single elements in the expression on either side of the /. For example, "contains x & y/z & w" means that the value contains three values x, y or z, and w.

1. In the Value column, click  to define the value of the tag.
   - • If the tag you selected was MODALITY, the Select Modality dialog box appears.
   - If the tag you selected was any DICOM tag other than MODALITY, the Enter Values dialog box appears.
2. Perform this step according to the dialog box that appears.

   These values have an ”or” relationship between them (any of the values must be found for that condition to be met).

   If you do not select MODALITY, the Enter Values dialog box opens automatically for you to enter the values. You can click  later if you want to change these values.
   - Select Modality: Select the modality you want from the Modality drop-down menu, then click OK.
   - Enter Values: Enter the required value(s) (use a comma to separate multiple values), then click OK.
3. Repeat steps 2 - 5 to define additional conditions for the same Display Protocol.

Examples

- If the tag study description in the list of conditions has the operator Contains and the value head, and a study's description is Head Tumor, then this study will be selected. If the operator is changed to Equals, then the Head Tumor study will not be selected.
- If the tag study description in the list of conditions has the operator Contains and the value head & tumor/bone and a study's description is Head Tumor, then this study will be selected.

Changing a New Display Protocol Condition

You can change the conditions defined for a Display Protocol. The changes only apply to studies you load after you make the modifications.

- In the conditions area of the Display Protocol editor, select the condition field you want to change.

To modify:	Do this:

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Tag conditions	Click the Tag field and select a different DICOM tag from the drop-down menu.
Operator conditions	Click the Operator field and select a different operator from the drop-down menu. See Adding a New Display Protocol Condition on page 600.
Value conditions	Click the Value field and select a new value.

Deleting a Display Protocol Condition

1. From the DP List, select the appropriate Display Protocol.
2. Select the condition you want to delete.
3. Click Delete .

16.17.6 Configuring Viewboxes for Display Protocols

About Viewbox Configuration for Display Protocols

Viewboxes provide the working area for viewing and manipulating images. The following topics describe configuring viewboxes for Display Protocols:

Monitor Configuration on page 603

Adding a New Viewbox on page 604

Defining a Default Viewbox View Type on page 605

Defining the History Mode on page 605

Defining the Layout of a Viewbox on page 606

Linking Groups Automatically in Display Protocols on page 606

Setting Automatic Reference Lines on page 607

Deleting a Viewbox on page 607

Defining Groups on page 607

See these topics:

About Applications on page 477

Configuring Layouts on page 456

Defining Display Protocol History Rules

This window defines which prior studies to load automatically whenever a specific protocol is selected.

1. In the Load section, set the DP Load properties:

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For example, if you load a prior study of the head, the system looks for the most recent x studies of the head, where x is the number you enter in the Priors of the patient with the same body part.

- The quantity of prior studies to load. The studies can have identical modality, body part and/or study description. The most recent prior studies matching these criteria are loaded.

  The base study (oldest matching study) of this patient with this modality.

2. Specify the Additional Prior Studies.

   This option lets you configure up to three rules for selecting additional prior studies. If the check box next to a rule is checked, the rule is active.

   NOTICE! The Body Part and Study Description fields are configured to look at the synonym table in the central configuration and accept the synonyms. For example, if you enter the body part head, the system will also find skull and brain. Contact the system administrator for assistance in defining synonyms.

NOTE:

3. Specify the Custom Rules.

This option lets you select rules that are not in the user interface, but which have been saved by a system administrator in the central configuration tool.

4. Click Next to configure Monitor Settings or click Finish to save the changes and exit DP Editor.

Monitor Configuration

A different layout can be set for each different hardware configuration. For example, the same display protocol can be set up to be displayed differently on two bank and four bank systems.

NOTICE

This option is only available in standalone mode. When you open the Display Protocol editor from the Viewer, only the active monitor configuration can be modified.

The monitor configuration field is disabled unless you work in standalone mode. To access standalone mode, enter from outside the application. In standalone mode, you can configure the number of monitors connected to your system. When defining the desired layout, you must specify the number of monitors to which it applies by selecting the number of monitors from the Monitor Configuration drop-down menu.

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The number refers to the number of monitors on which the Viewer runs. +1 indicates a multiple desktop. For example, 2+1 refers to a multiple-desktop configuration in which the viewer is spread on two black and white monitors and one color monitor. The color monitor serves two purposes: it displays the Archive Explorer; after the study is loaded, the monitor becomes part of the viewer.

NOTICE

After a layout is defined for a specific number of monitors, it only applies to that specific configuration. It is highly recommended that you create a layout for each hardware configuration that is available on your site.

Adding a New Viewbox

You can display multiple viewboxes one behind the other in the Viewer. Click the viewbox tab at the bottom of the Viewer window to switch between viewboxes. The number of viewboxes that appear the first time you access the Display Protocol editor is copied from the system default Display Protocol. From this base, you can add or remove viewboxes.

1. From the DP menu, select Open Display Protocol editor.
2. In the Display Protocol editor dialog box, click Next twice.
3. Click Add .
   ⇨ A new viewbox (represented by an additional viewbox tab) is added to the Display Protocol.
4. In the Monitors section, specify the size and location of the viewbox:

   Number of viewbox monitors: Enter the number of monitors across which the viewbox displays (one or two).

   Start Monitor: Enter the monitor number where the viewbox begins.

   For example, in a two-monitor configuration, 1 indicates the viewbox begins on the left monitor and 2 indicates the viewbox begins on the right monitor.

NOTICE

The viewbox appears across more than one monitor only if you defined the monitor configuration to include two monitors. See Creating a New Display Protocol on page 598.

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Defining a Default Viewbox View Type

A viewbox can have a default view type of any of the applications. This default view type controls how groups of images display when they are left-dragged from the Patient Mini-Archive onto the screen.

NOTICE

If you use the right mouse button to drag the image group from the Patient Mini-Archive, a pop-up menu provides an option to display images in one of the default formats.

1. From the DP menu, select Open Display Protocol editor.
2. In the Display Protocol editor dialog box, click Next twice.

   The Configuration dialog box appears.
3. From the Default Group Type drop-down menu, select an option:
   - Hybrid NM
   - Volume Matching
   - Viewer
   - MPR
   - 3D
   - Cardiac CT
   - Calcium Scoring
   - Vessel Analysis
   - Coronary Analysis

Defining the History Mode

1. From the Settings for studies drop-down menu, select one of the following:
   - With History: The viewbox settings apply to studies for which a patient history is found.
   - No History: The viewbox settings apply to studies for which no patient history is found.
2. You can specify different settings for studies with a history and without a history.

   If the check box is selected, it overrides the setting in the drop-down menu. By default, the check box is always selected. If you do not want your settings to apply to other studies, deselect the check box.
   - When you select With History, the check box name is Apply to studies without history.
   - When you select Without History, the check box name is Apply to studies with history.
   -

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Defining the Layout of a Viewbox

You can define the number of groups displayed in each viewbox, as well as the group layout within the viewbox.

1. Click the tab of the viewbox you want to configure.
2. Double-click the matrix (grid) in the Layout section.
   ⇨ The Define Layout matrix appears.
3. Click the top left square and drag the mouse to define the number and layout of groups you want to display in the viewbox.
4. To define a different layout in each monitor, click Asymmetric Layout.
   ⇨ A note appears in the center of the window.
5. Click on the monitor name to display a window of cells in which you can drag and draw a new layout.

   To return to symmetrical layouts on all monitors, deselect the Asymmetric Layout check box.

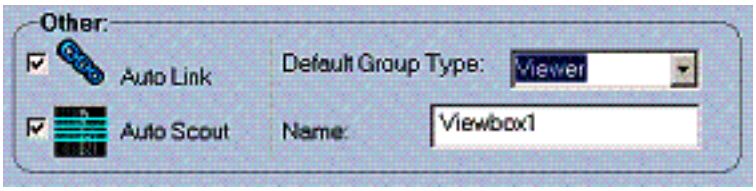
NOTICE

This feature only applies when there are two or more monitors. It does not work for 1 or 1+1 mode.

Linking Groups Automatically in Display Protocols

You can automatically link all groups that display in a viewbox.

1. Click the tab of the viewbox you want to configure.
2. Select an Auto Link option:



   - Auto Link is selected (checked): All groups that display in the viewbox that have the same grid coordinates are automatically linked from the first image of each group.
   - Auto Link is not selected: Groups in the viewbox are not automatically linked.

NOTICE

You can also manually link groups in a viewbox. See Manually Linking Image Groups on page 617.

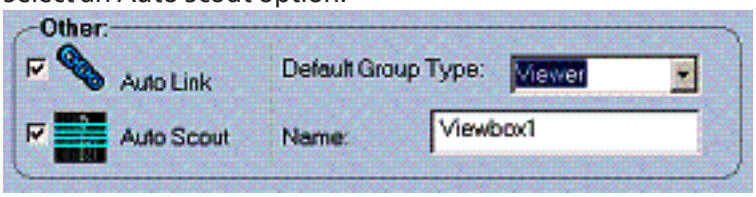
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Setting Automatic Reference Lines

You can automatically show reference lines for all groups that display in a viewbox.

► Click the tab of the viewbox you want to configure.

► Select an Auto Scout option:



- Auto Scout is selected (checked): The Auto Relate Ref. (Reference) Lines option is enabled.
- Auto Scout is not selected: The Auto Relate Ref. (Reference) Lines option is not enabled.

Each of the groups that display in the viewbox will automatically display the reference lines of every other group that can be displayed in the same viewbox.

Deleting a Viewbox

► From the DP menu, select Open Display Protocol editor.

► In the Display Protocol editor dialog box, click the tab of the viewbox you want to delete.

► Click Delete .

16.17.7 Defining Groups

Defining Groups

If you want to place particular groups of images in specified locations in the viewbox, you must define the criteria for each group in a Display Protocol. The criteria are usually a combination of DICOM tags that define what to display in the group. You must also define which study type (history/current) corresponds to each group.

For example, "Place all the ORIGINAL/AXIAL images of the current CT study in one group" uses the DICOM tag IMAGE_TYPE to create a group of images.

See these topics:

Creating a New Group on page 608

Defining/Modifying Group Conditions on page 608

Defining a Group Based on a Prior Study on page 609

Deleting a Group on page 610

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Creating a New Group

You can create a new group based on an existing group. The group conditions are identical to the conditions of the base group until you modify them.

1. From the DP menu, select Open Display Protocol editor.
2. In the Display Protocol editor dialog box, select the Display Protocol for which you want to define a new group.
3. Click Next twice.
   ⇨ The Configuration dialog box appears.
4. Click the tab of the viewbox you want to configure.
5. In the monitor graphic, right-click the group location you want and select Group Properties.
   ⇨ The Expected Group Properties dialog box appears and shows a list of existing groups.
6. Click Add New Expected Group .
   ⇨ The New Expected Group dialog box appears.
7. In the Expected Group Name field, type the name of the new group.
8. If desired, select the group you want to use as a base from the Base Expected Group drop-down menu.
9. Click OK.
   ⇨ The Expected Group Properties dialog box appears.
10. Go to Defining/Modifying Group Conditions on page 608 to define or modify the group conditions.

Defining/Modifying Group Conditions

When you define a group, you must define the criteria for that group using the relevant DICOM tags. The DICOM tags determine the images to display in the group. For example, if you want all original axial CT images to display in one group, create a group based on the MODALITY tag CT and the IMAGE_TYPE tag ORIGINAL AXIAL.

Each group must also have a condition that defines the instance of the study from which the images in the group are taken. This is a mandatory condition and determines whether you want the group conditions to be applied to the current study or to a prior study. See Defining a Group Based on a Prior Study on page 609.

1. From the Expected Group Properties dialog box, select the group whose conditions you want to define or modify.

   Any conditions already defined for the group appear in the Expected Group Conditions area.
2. In the Tag column, click an empty field, then select a DICOM tag from the drop-down menu.

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3. In the Operator column, click the field by the new tag.
4. Select an operator from the drop-down menu.

   This process defines the relationship between the DICOM tag and the value(s).
5. In the Value column, click  to define the value of the tag.
   - If the tag you selected was MODALITY, the Select Modality dialog box appears.
   - If the tag you selected was any DICOM tag other than MODALITY, the Enter Values dialog box appears.
6. Perform this step according to the dialog box that appears:

   These values have an "or" relationship between them (any of the values must be found for that condition to be met). See Adding a New Display Protocol Condition on page 600.
   - Select Modality: Select the modality you want from the Modality drop-down menu, then click OK.
   - Enter Values: Enter the required value(s) (use a comma to separate multiple values), then click OK.
7. Click OK.

Defining a Group Based on a Prior Study

You can specify additional information about a previously defined group. A study has a special condition called STUDY_INSTANCE_UID. The operator for this condition is Historical Cases. It can relate to prior studies that you specifically defined in the second DP Editor window.

1. To edit the criteria, click  on the right of the STUDY_INSTANCE_UID row in the Expected Group Conditions table.

   The additional data window appears.
2. Specify whether this group relates to the current study or to prior (previous) studies.

   If you select Priors, you must also select the Sort order for the studies and the number of prior studies to display:
   - Recent to Past: display the most recent studies first, excluding the current study.
   - Past to Recent: display the oldest study first.
   - Item in priors to display: the number of newest or oldest priors to display (according to whether you selected Recent to Past or Past to Recent).

Each study might have multiple groups for the same patient. For example, each group might be for a different procedure performed on the scanner or you can create a group of images from various procedures.

Each group can be displayed in a different cell in the viewer. If you want to create an expected group, you need to specify where to put it in the layout. After you define a layout, specify the types of group you want to see in each location and the application will try to find the closest match possible among all the studies that are loaded.

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See these topics:

Defining Groups on page 607

Creating a New Group on page 608

Defining/Modifying Group Conditions on page 608

Deleting a Group

You can delete a group that is not required for a specific Display Protocol.

1. From the Expected Group Properties dialog box, select the group you want to delete.
2. Click Delete .

16.17.8 Setting Group Parameters

About Group Parameters

After you define the groups and the relevant criteria, you can set additional parameters that determine which groups are displayed, and how and where the images in the groups display in the viewbox.

See these topics:

Defining Groups Displayed in the Viewbox on page 611

Defining the Image Layout within a Group on page 611

Defining the Image Sort Order on page 612

Defining Image Parameters on page 613

Defining MPR Parameters on page 614

Defining Vessel Analysis Parameters on page 614

Defining Cardiac CT Parameters on page 615

Defining Coronary Analysis Parameters on page 616

Defining 3D Parameters on page 617

Manually Linking Image Groups on page 617

Showing Reference Lines on page 618

Showing Mini Reference Lines on Images in a Group on page 618

Saving the Display Protocol Data on page 618

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Defining Groups Displayed in the Viewbox

You can define which groups you want to display in the viewbox and then define additional parameters for the groups. You can define groups using the Layout, Monitors, and Others options displayed in the Display Protocol editor or using the Group Display Properties dialog box. In the Group Display Properties dialog box, you can also configure the group location to be empty and to edit the group conditions.

1. From the DP List area on the left side of the Conditions dialog box, select a Display Protocol.
2. Click Next twice.

NOTICE

If there is more than one viewbox, you must now select the required viewbox.

3. To define the group using the options displayed in the current window, click the required group and enter the configuration in the layout, monitor, and other options fields.

   Or

   To define the group using the Group Display Properties dialog box, right-click the required group in the monitor graphic and select Group Selection.

   ⇨ The Group Display Properties dialog box appears.
4. Select the group you want to display in the selected location in the viewbox:
   - No Group: Leaves the group location empty.
   - Other Group: Select the required group from the list to display a particular group in the selected location.
5. Click Properties to edit the group conditions.
   ⇨ The Expected Group Properties dialog box appears. See Defining/Modifying Group Conditions on page 608.
6. Select other Group Display Properties dialog box tabs to set additional group parameters.

   or

   Click OK to close the Group Display Properties dialog box.

Defining the Image Layout within a Group

You can define how images within a selected group display in the viewbox.

1. From the DP List area on the left side of the Conditions window, select a Display Protocol.
2. Click Next twice.

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NOTICE

If there is more than one viewbox, you must select the required viewbox.

3. Double-click the required group in the monitor graphic.
   ⇨ The Group Display Properties dialog box appears.
4. Select the Group Layout tab.
5. Double-click the matrix in the middle of the Group Layout tab.
   ⇨ The Define Layout matrix appears.

NOTICE

For 3D applications, coronary analysis, and vessel analysis, there are only three predefined layouts (1x1, 1x4, and 2x2).

6. Click the top left square and drag to define the required number of images to display in the group, and to define the layout of the images.
7. If necessary, select other Group Display Properties dialog box tabs to set additional parameters.
8. Click OK.

Defining the Image Sort Order

You can define the order for how the images within a group are sorted. Each sort is based on a DICOM tag. Up to three sorts can be performed for a single group.

1. From the DP List area on the left side of the Conditions window, select a Display Protocol.
2. Click Next twice.

NOTICE

If there is more than one viewbox, you must select the required viewbox.

3. Double-click the required group in the monitor graphic.
   ⇨ The Group Display Properties dialog box appears.
4. Select the Sort By tab.
5. In the Sort Items By drop-down menu, select the primary sort by selecting the DICOM tag by which you want to sort the group. Select the direction in which you want the results to display (Ascending or Descending).
6. If required, define the secondary and tertiary sorts and the direction of the sort in the Then By areas, in the same way as described in step 7.

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7. If necessary, select one of the other Group Display Properties window tabs to set additional parameters.
8. Click OK to close the Group Display Properties window.

Defining Image Parameters

You can change the default image parameters such as the zoom, orientation, and windowing settings for the images in a group.

1. From the DP List area on the left side of the Conditions window, select a Display Protocol.
2. Click Next twice.

NOTICE

If there is more than one viewbox, you must select the required viewbox.

3. Double-click the required group in the monitor graphic.
   ⇨ The Group Display Properties dialog box appears.
4. Select the Parameters tab.
5. Specify parameters for the Display Protocol:

Parameter	Description
Zooming	Select one of the following zoom options: • True Size: The image is displayed as the same size as the actual scan. • Original Resolution: Lets you adjust the zoom and select what you want to see by moving the Zoom slider. • Fit to Window: An automatic zoom fits the image into the current window.
Rotate and Flip	Click the appropriate Rotate/Flip area.
Pan	Specify to reset the pan by clicking the Reset Pan check box.
Windowing	Do the following in the windowing area: • In the Center field, enter the brightness level of the images. • In the Width field, enter the contrast level of the images. • Select the Auto Windowing check box to apply auto windowing to all other images in the selection. • Select the Inverse Window check box to apply inverse windowing to the images.

► Click OK.

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Defining MPR Parameters

You can define groups as MPR groups by setting the MPR parameters. These parameters define how MPR reference and result images display in the Viewer and how MPR functionality responds. You can also change the defaults defined here during a viewing session.

1. From the DP List area on the left side of the Conditions window, select a Display Protocol.
2. Click Next twice.

   NOTICE! If there is more than one viewbox, you must select the required viewbox.
3. Right-click the MPR group in the monitor graphic, then click Group Selection.

   NOTICE! The MPR Parameters tab appears in the Group Display Properties dialog box only if the selected group is an MPR group. If the group is not defined as MPR, you can define it by right-clicking the group in the monitor graphic and selecting MPR.
4. Select the MPR Parameters tab.
5. In the Set Result Images Parameters area, set the following parameters:
   - Thickness: Lets you define the thickness (in mm) of each cross-section cut made in the image.
   - Spacing: Lets you define the spacing (in mm) between the cross-section cuts.
   - Dual Windowing: Lets you define whether Dual Windowing is enabled and whether it is horizontal or vertical. This option places copies of the images next to each other in the format you select and allows comparisons such as using different windowing values.
   - Result Image Orientation: Lets you define the default orientation of Result images in the Viewer.
   - Sorting: Lets you define the display order of the slices.
6. In the Set Reference Parameters area, set the following parameters:

   NOTICE! To cancel your changes and restore the default values, click Reset to Default.
   - Reference Image Position: Lets you define where Reference images display on the screen. Automatic displays the reference images on the right for a landscape monitor and on the top for a portrait monitor.
   - Resize Reference Images: When selected, Reference images are zoomed automatically to fit the maximum available space.
   - Display Reference Images: Lets you define the Reference image types you want to display.
7. Click OK.

Defining Vessel Analysis Parameters

You can define groups as Vessel Analysis groups by setting the Vessel Analysis parameters. These parameters define how Vessel Analysis reference and result images display in the Viewer and how Vessel Analysis functionality responds. You can also change the defaults defined here during a viewing session.

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1. From the DP List area of the Conditions window, select a Display Protocol.
2. Click Next twice.

   NOTICE! If there is more than one viewbox, you must select the required viewbox.
3. Right-click the Vessel Analysis group in the monitor graphic, then click Group Selection.

   NOTICE! The Vessel Analysis Parameters tab appears in the Group Display Properties dialog box only if the selected group is a Vessel Analysis group. If the group is not defined as Vessel Analysis, you define it by right-clicking the group in the monitor graphic and selecting Vessel Analysis.
4. Select the Vessel Analysis Parameters tab.
5. Select the default image type to be displayed:
   - VOLR: Displays the image as a three-dimensional structure.
   - MIP: Displays the image as Angiography MIP.
6. If you selected VOLR, click Select Protocol, then select the required protocol from the Volume Rendering Parameters window.
7. Click OK.
8. Click OK to close the Group Display Properties window.

Defining Cardiac CT Parameters

You can define groups as Cardiac CT groups by setting the Cardiac CT parameters. These parameters define how Cardiac CT reference and result images display in the Viewer and how Cardiac CT functionality responds. You can also change the defaults defined here during a viewing session.

1. From the DP List area of the Conditions window, select a Display Protocol.
2. Click Next twice.

   NOTICE! If there is more than one viewbox, you must select the required viewbox.
3. Right-click the Cardiac CT group in the monitor graphic, then click Group Selection.

   NOTICE! The Cardiac CT Parameters tab appears in the Group Display Properties dialog box only if the selected group is a Cardiac CT group. If the group is not defined as Cardiac CT, you can define it by right-clicking the group in the monitor graphic and selecting Cardiac CT.
4. Select the Cardiac CT Parameters tab.
5. In the Set Result Images Parameters area, set the following parameters:
   - Thickness: Lets you define the thickness (in mm) of each cross-section cut made in the image.
   - Spacing: Lets you define the spacing (in mm) between the cross-section cuts.
   - Dual Windowing: Lets you define whether Dual Windowing is enabled and whether it is horizontal or vertical. This option places copies of the images next to each other in the format you select and allows comparisons using different windowing values.

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- Result Image Orientation: Lets you define the default orientation of Result images in the Viewer.
- Sorting: Lets you define the display order of the slices.

6. In the Set Reference Parameters area, set the following parameters:

   NOTICE! To cancel your changes and restore the default values, click Reset to Default.

   - Reference Image Position: Lets you define where Reference images display on the screen. Automatic displays the reference images on the right for a landscape monitor and on the top for a portrait monitor.
   - Resize Reference Images: When selected, Reference images are zoomed automatically to fit the maximum available space.
   - Display Reference Images: Lets you define the Reference image types you want to display.

7. Click OK.

Defining Coronary Analysis Parameters

You can define groups as Coronary Analysis groups by setting the Coronary Analysis parameters. These parameters define how Coronary Analysis reference and result images display in the Viewer, and how Coronary Analysis functionality responds. You can also change the defaults defined here during a viewing session.

1. From the DP List area of the Conditions window, select a Display Protocol.
2. Click Next twice.

   NOTICE! If there is more than one view box, you must select the required viewbox.

3. Right-click the Coronary Analysis group in the monitor graphic, then click Group Selection.

   NOTICE! The Coronary Analysis Parameters tab appears only in the Group Display Properties dialog box if the selected group is a Coronary Analysis group. If the group is not defined as Coronary Analysis, you can define it by right-clicking the group in the monitor graphic and selecting Coronary Analysis.

4. Select the Coronary Analysis Parameters tab.
5. From the Select Protocol Name drop-down menu, select a name for the protocol.
6. Select the default image type to be displayed:
   - VOLR: Displays the image as a three-dimensional structure.
   - MIP: Displays the image as Angiography MIP.
7. If you selected VOLR, click Select Protocol, then select the required protocol from the Volume Rendering Parameters window.
8. Click OK.
9. Click OK to close the Group Display Properties window.

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Defining 3D Parameters

You can define groups as 3D groups by setting the 3D parameters. These parameters define how 3D reference and result images display in the Viewer and how 3D functionality responds. You can also change the defaults defined here during a viewing session.

1. From the DP List area of the Conditions window, select a Display Protocol.
2. Click Next twice.

   NOTICE! If there is more than one viewbox, you must select the required viewbox.
3. Right-click the 3D group in the monitor graphic, then click Group Selection.

   NOTICE! The 3D Parameters tab appears in the Group Display Properties dialog box only if the selected group is a 3D group. If the group is not defined as 3D, you can define it by right-clicking the group in the monitor graphic and selecting 3D.
4. Select the 3D Parameters tab.
5. From the Select Protocol Name drop-down menu, select a name for the protocol.
6. Select the default image type to be displayed:
   - VOLR: Displays the image as a three-dimensional structure.
   - MIP: Displays the image as Angiography MIP.
7. If you selected VOLR, click Select Protocol, then select the required protocol from the Volume Rendering Parameters window.
8. Click OK.
9. Click OK to close the Group Display Properties window.

Manually Linking Image Groups

You can link two or more groups in the same viewbox so that you can simultaneously scroll all groups.

NOTICE

You can use the Auto Link option to configure the group layout in a viewbox to automatically link all groups that have the same grid coordinates. See Defining the Layout of a Viewbox on page 606.

1. From the DP List area of the Conditions dialog box, select a Display Protocol.
2. Click Next twice.

   NOTICE! If there is more than one vender, you must select the required viewbox.
3. In the monitor graphic, hold down the CTRL key and select two or more groups.
4. Right-click Link Selected Group.

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NOTICE

To unlink groups, right-click a linked group in the monitor graphic, then click Unlink Selected Groups.

Showing Reference Lines

You can show the reference lines on another group displayed in the same viewbox.

1. From the DP List area of the Conditions dialog box, select a Display Protocol.
2. Click Next twice.

   NOTICE! If there is more than one viewbox, you must select the required viewbox.
3. In the monitor graphic, select the group with the reference lines you want to display, then hold down the CTRL key and select the group on which you want to display the reference lines.
4. Right-click the group on which you want to display the reference lines, then select Show Ref. Lines.

NOTICE

To remove reference lines, right-click a relevant group, then click Remove Ref. Lines.

Showing Mini Reference Lines on Images in a Group

1. From the DP List area of the Conditions dialog box, select a Display Protocol.
2. Click Next twice.

   NOTICE! If there is more than one viewbox, you must select the required viewbox.
3. In the monitor graphic, right-click and select Show Mini Ref. Lines.

   NOTICE! To remove the mini reference lines, right-click a relevant group, then click Remove Mini Ref. Lines.

Saving the Display Protocol Data

After you configure the Display Protocol, you must save it to use it for future reading sessions. You can click Finish at any stage in the Display Protocol configuration.

1. In the Display Protocol editor, click Finish.
   ⇨ The Save DP Changes dialog box appears.
2. Click the appropriate button:
   - Save and Close: Saves the Display Protocol and closes the Display Protocol editor.
   - Close Editor: Closes the Display Protocol editor without saving any changes.

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16.17.9 Deleting a Display Protocol

You can delete Display Protocols from the Diagnostic Workstation. Display Protocols that were created based on the Display Protocol to be deleted are not affected.

NOTICE

You can only delete Display Protocols that you created. Only users with administrator's privileges can delete Group and System Display Protocols.

1. From the DP List area of the Conditions dialog box, select the Display Protocol you want to delete.
2. Click Delete Display Protocol .

16.17.10 Synchronizing the DP Table

16.18 Working with Presentations

16.18.1 About Save Presentation

The Save Presentation feature enables you to take a snapshot of a case during a reading session, this allows you to pause the reading flow and to continue reading the same case again later in the same state. The saved presentation reconstructs the saved display when the presentation is applied.

All parameters including all information created on an image including segmentations, bookmarks and measurements, saved by the Save Presentation command are kept in a way that allows you to resume working on them. When a presentation has been applied and it is edited later, you are asked to choose whether you want to create a new presentation or update the existing presentation.

The Save Presentation feature is available in the following applications:

Using Saving Presentations in Vessel Analysis on page 238

Saving Presentations in Coronary Analysis on page 277

Saving Presentations in the PowerViewer Application on page 154

Saving Presentations in Hybrid NM on page 328

Saving Presentations in Volume Matching on page 291

Saving Presentations in Hybrid NM on page 328

Saving Presentations in 3D Data on page 196

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Saving Presentations in Cardiac CT on page 250

16.18.2 Saving a Study as a Presentation

You can organize images of a particular patient in an arrangement to suit your needs. You can save the layout, graphics, and display settings for future viewing.

⇨ The Save Presentation window appears.



⇨

1. Type the name of the presentation to be saved.
2. Click **OK**.

16.18.3 Opening a Study Saved in Presentation State

1. From the Archive Explorer, right-click a study.
2. Select Load with Presentation.
   ⇨ A list of the presentations saved for that study appears.
3. Select the presentation to be opened.
4. Click OK.

⇨ Changes can be made to the study and resaved by either giving the presentation a new name or overwriting the original presentation name.

16.18.4 Switching Between Saved Presentations

- From the DP Menu, select a presentation from the list of saved presentations.

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NOTICE

If you load all relevant datasets of a certain Presentation but do not use the Load with Presentation option and later revert to the saved Presentation the study is presented as though you have loaded the study with the presentation. If information has already been created, the presentation is presented regardless of the datasets and information presented previously.

NOTE:

NOTICE

If you load part of a relevant dataset or a certain presentation and then change the DP of the saved presentation, the system does not load and display the automatically missing datasets.

16.18.5 Loading a Worklist with a Presentation

► From the Archive Explorer, select a worklist folder.

NOTICE! When you select a worklist folder, the Load option in the File menu and the Load tool on the Archive Explorer toolbar change to Load Worklist.

► Click Load Worklist With Presentation.

⇨ If the selected worklist has a presentation, it will load. If the worklist has more than one presentation, a list of presentations appears. Select a presentation to load.

⇨ The system can be configured to load the most recent presentation configuration automatically. Contact the system administrator.

16.18.6 Using Save as DP

NOTICE

Save as DP will retain specific information in the Display Protocol, and omit other information. For best results, refer to the background information first. Then go to the instructions for Saving Viewing Options as a Display Protocol.

1. Background Information: Understanding the Results for Save As DP (see Understanding the Results for Save as DP on page 595).
2. Instructions: Saving Viewing Options as a Display Protocol (see Saving Viewing Options as a Display Protocol on page 595).

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16.18.7 Deleting a Presentation

1. From the Viewer menu, select DP, then click Delete Presentation.
   ⇨ The Delete Presentation window appears.
2. Select the presentation you want to delete.
3. Click Delete.
4. Click OK.

16.19 Changing/Setting Window Values

16.19.1 About Window Values

Use the windowing options to translate the values of displayed images to a range of gray levels (contrast and brightness) that are suitable for optimal viewing.

16.19.2 Selecting a Preset Window Value

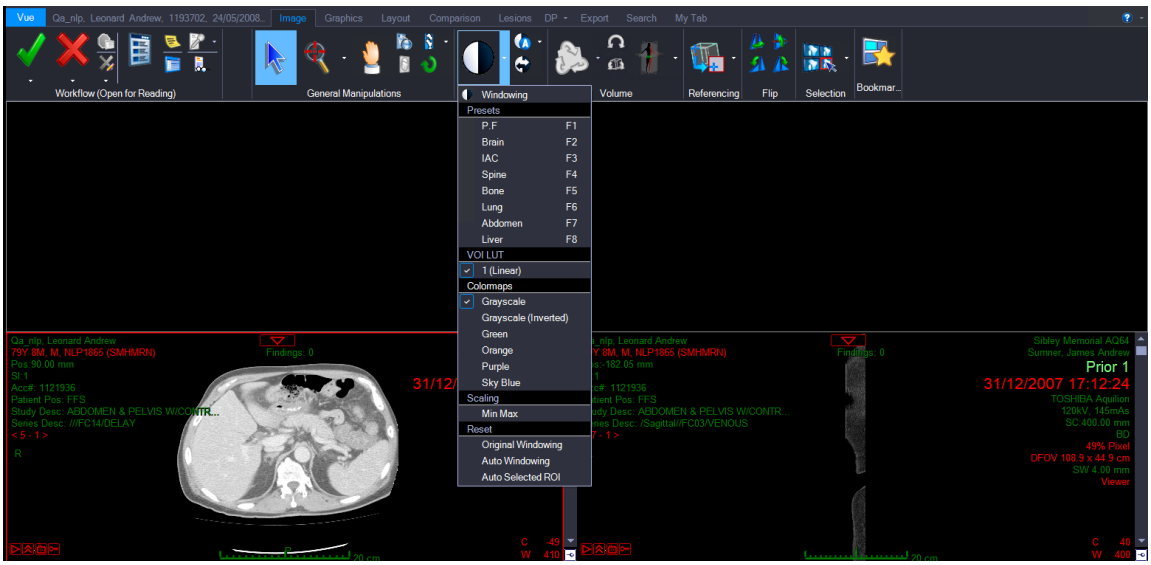
Use preset window level values for optimal viewing.

There are two ways to select a window preset:

Through the Diagnostic Viewer Toolbar

In the Diagnostic Viewer toolbar, click **Windowing** and select the desired window preset option.

Once selected, the option is applied.



Through the Windowing Level Annotation

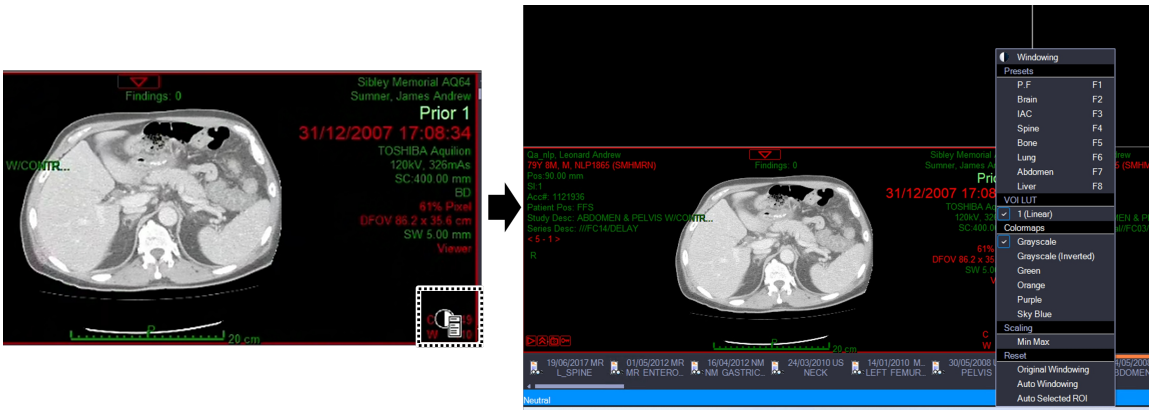
1. Hover over the windowing level annotation located on the lower right of the image.

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2. When the mouse browser changes from arrow to a note sheet, right-click to display a list of windowing presets.
3. Select the desired window preset option.

   Once selected, the option is applied.



16.19.3 Changing the Window Center and Window Width

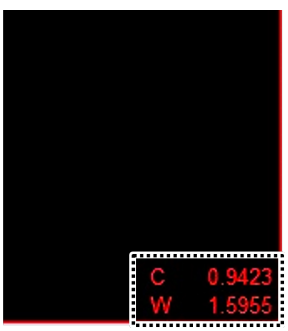
The window center sets the level of the displayed values.

The window width sets the width of the displayed values.

1. From the Viewer, select an image.
2. Click  and drag, or press the middle mouse button and drag:
   - Up to increase the center value.
   - Down to decrease the center value.
   - Right to increase the width value.
   - Left to decrease the width value.
   - Diagonally to change the center and width simultaneously.

The new displayed values that appear in the annotation can be decimal or mathematical.

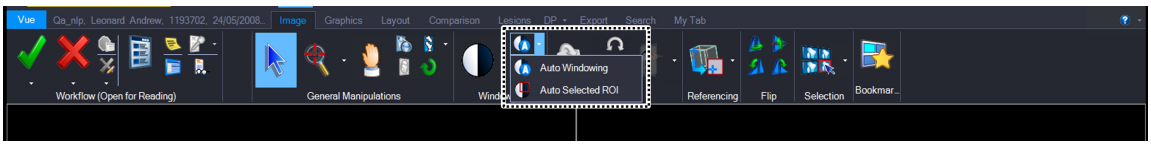




16.19.4 Automatically Windowing Images

Automatic windowing analyzes the digital values in the active image to calculate a reasonable starting point for the image presentation. These values are then copied to all other images in the selection. You can then manually adjust the windowing to visually optimize the presentation.

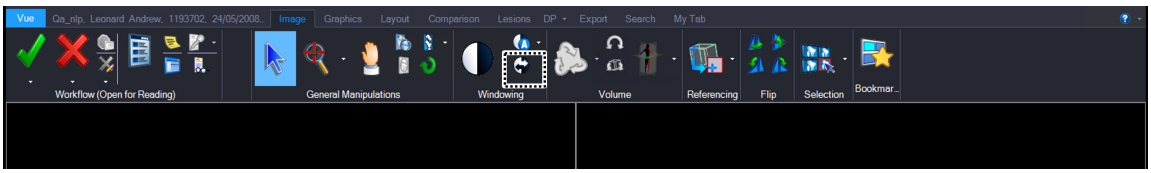
1. From the Viewer, select the image with the values you want to copy.
2. Click **Auto Windowing** .



16.19.5 Inverse Windowing an Image (Display Negative)

Inverse windowing inverts the gray levels of images to display a negative image. For example, white changes to black and vice versa.

1. From the Viewer, select the images you want to invert.
2. Click **Inverse Windowing** .
3. Repeat step 2 to return the image to its original state.



16.19.6 Using VOI LUTs

A VOI LUT is used for performing non-lineal windowing on an image. Instead of lineal windowing, it uses a table or sigmoid that is received from the modality. VOI LUTs only work if the modality manufacturer creates them. A VOI LUT is generally used for mammography images, but is also used for CR, RF, and so on.

1. Right-click on the image windowing value.
2. Select an option from the drop-down menu.

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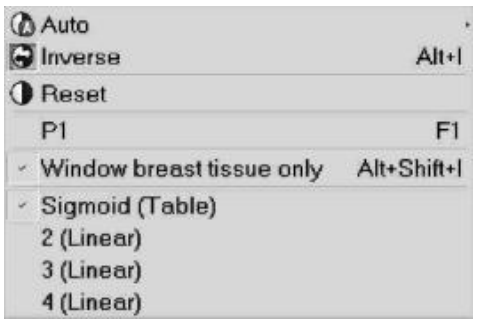
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3. Select Auto to return to regular linear windowing mode.

NOTICE

The display protocol can specify if a VOI LUT is available and if it can be used.

If the loaded image has no VOI LUT name, the Diagnostic Workstation will provide a number (1, 2, 3, and so on) and inserts the VOI LUT type in parentheses.	
One VOI LUT may have a name while another does not (in the example, the image has a VOI LUT where the name is Sigmoid and the type is Table).	

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16.20 Integrating Information Systems and Dictation Systems

16.20.1 Viewing Reports from the RIS/HIS

The Diagnostic Workstation supports integration with information systems (such as a RIS or HIS), so you can view orders and reports that have been generated by the RIS or HIS. In addition, the Diagnostic Workstation supports integration with voice dictation systems to allow integrated report dictation.

The dictation menu options are:

- Dictating a Report
- Multiple Study Dictation (available when more than one study is loaded)

NOTICE

Integration requires installation of special software and proper configuration. See the system administrator for information about your site's capabilities.

To view reports using the Vue PACS HL7 Manager Software:

From the Archive Explorer or PowerViewer toolbar, click Show Reports .

See these topics:

Dictating a Report on page 626

Multiple Study Dictation on page 627

16.20.2 Dictating a Report

NOTICE

Integration requires installation of special software and proper configuration. Contact the system administrator.

The Diagnostic Workstation can be integrated with a voice dictation system, which lets you generate reports. The Diagnostic Workstation can be configured to confirm a study automatically when you sign off the report, or return you to the Viewer when the report is completed.

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► When you have reviewed the study and are ready to dictate your report, click Dictation .

► Follow the dictation procedures according to your type of dictation software.

See these topics:

Multiple Study Dictation on page 627

Viewing Reports from the RIS/HIS on page 626

As an alternative to the integrated solution described above, Vue PACS also includes a native reporting solution. For details about this module, see Vue Reporting User Guide.

16.20.3 Multiple Study Dictation

If a study was loaded with a history (prior studies), and the central configuration has been set up to enable multiple study dictation, you may dictate a single report for multiple studies of the same patient.

1. Click the arrow next to Dictation  and select the Dictate Multiple Studies option.
   ⇨ The dialog box opens with one line for each prior study of the current patient.
2. Select the studies for which you want to dictate by checking the adjacent check boxes.
3. Click OK to start the dictation.

NOTICE

Studies that already have a report cannot be checked. Once the Multiple Study Dictation dialog box is opened, prior studies that have been loaded and that have no report yet are automatically checked.

See these topics:

Dictating a Report on page 626

Viewing Reports from the RIS/HIS on page 626

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16.21 Using the Teaching File (All Viewers)

16.21.1 About the Teaching File and Folder

Teaching File

The teaching file option lets you designate studies to use for teaching. To protect patient confidentiality, all references of patient name and patient ID are removed when you designate a study for teaching.

Teaching File Folder

The Teaching File folder acts much like the other folders in the Archive Explorer, except that patient names and IDs do not appear on studies in the Teaching File folder.

See these topics:

Viewing Studies in the Teaching File on page 628

Loading a Teaching Study on page 628

Designating a Study as a Teaching Study on page 629

Adding Anatomy, Pathology, and Angiography for a Teaching Study on page 629

Customizing the Teaching File Window on page 630

Creating Drop-down Teaching Fields on page 631

16.21.2 Viewing Studies in the Teaching File

1. Select the Teaching File folder .

   You might need to refresh the screen to see the data.
2. To filter the data in the right pane, click the empty field below the column (filter) heading, then enter the filter data you want.
3. If the column has a drop-down menu, click the option you want
4. Press the Enter key.

16.21.3 Loading a Teaching Study

1. Select the teaching study you want to load.
2. Click Load .

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16.21.4 Designating a Study as a Teaching Study

1. From the Archive Explorer, load a study.
2. From the Viewer, click Teaching File .
   ⇨ The Teaching File window appears.
3. Type the information you want to include with the study.
4. Click Submit .
   ⇨ Your name is automatically added as well the date the study was designated as a teaching study.
5. To clear all of the information you entered, click Clear All .
6. To revert to the original data that was entered for the study, click Discard Changes .
7. To close the Teaching File, click Exit .

See these topics:

Adding Anatomy, Pathology, and Angiography for a Teaching Study on page 629

Creating Drop-down Teaching Fields on page 631

16.21.5 Adding Anatomy, Pathology, and Angiography for a Teaching Study

1. From the Teaching File window, click Anatomy and Pathology.
   ⇨ The ACR window appears for the anatomy code and pathology code.
2. Click Anatomy and select the appropriate anatomy designation.
3. Click Pathology and select the appropriate pathology designation.

NOTICE

There are three levels of anatomy and three levels of pathology. To go up a level, click the button at the top right of the window .

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⇨ The anatomy and pathology codes you selected appear in their respective areas in the window.

4. When you have completed the code entry, click OK.
   ⇨ The information you entered appears in the Teaching File window.
5. Click Angiography.
   ⇨ The Angiography Code window appears.
6. Select the appropriate angiography code.

NOTICE

There are four levels of angiography. To go up a level, click the button at the top right of the window .

⇨ The angiography codes you selected appear in their respective areas in the window.

7. Click OK.
   ⇨ The information you entered appears in the Teaching File window.
8. Click Submit .

16.21.6 Customizing the Teaching File Window

You can customize the Teaching File window.

NOTICE

You can only customize the Teaching File window if you have the proper system privileges. See the system administrator.

1. Click Teaching File .
2. Click Design Mode .
   ⇨ The Format dialog box appears.

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3. Select an option:
   - Align Boxes Left: The text box is aligned to the left margin.
   - Align Labels Left: The text box labels are aligned to the left margin.
   - Make Boxes Same Width: All text boxes will be the same width.
4. To rename a label, double-click the label and enter a new name in the Change Label dialog box.
5. Click OK.
6. To change the type of field, right-click the label, then select Drop-down Field or Text Field.

   See Creating Drop-down Teaching Fields on page 631.
7. Click Save Layout .

16.21.7 Creating Drop-down Teaching Fields

You can select whether the fields in the Teaching File window should be regular free-text fields or whether they should contain preset values (drop-down menus). You can create new drop-down menus, as well as edit or delete existing fields in the drop-down menus.

NOTICE

You cannot add new fields to the Teaching File window. You can only add drop-down menus to fields that already exist in the default Teaching File form.

1. Click Teaching File .
2. Click Design Mode .
3. Click List of Values .
   ⇨ The Teaching Form Lists of Values appears, showing the available tables.
4. To add a new table to the Teaching File window, click Add.
   ⇨ The New List of Values window appears.
5. Enter a name for the table in the List Name field.

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6. To add a new drop-down field, click .
   ⇨ The List Value dialog box appears.
7. Enter a value for the field.
8. Click OK.
   ⇨ The values appear in alphabetical order in the drop-down menu.
9. Click OK to close the New List of Values dialog box.
10. To edit the fields, select a table from the list, then click Edit.
    ⇨ You can add new fields, or remove a selected field by clicking .
11. To delete a table, select a table from the list, then click Delete.
12. Click OK to close the Teaching Form List of Values dialog box.

NOTICE

You can create a regular text field or a field with a drop-down menu. To select the field type, right-click the relevant text box, choose Drop-down Field, then select a table from the list or select Text Field.

16.22 Generating Volume Rendered Images (VOLR)

16.22.1 About Volume Rendering

The Volume Rendering option enables visualization of three-dimensional (3D) structures and images using acquired CT or MRI images. Ready-made protocols for various clinical procedures allow for obtaining views of the structures using single-click operations.

Volume rendering is performed by acquiring a set of volumetric data and assigning opacity and color to every pixel in accordance with parameters determined by the user. This assignment can be either predetermined or dependent upon the tissue to which the pixel belongs and on the pixel value.

The application displays the volumetric data, using the color and opacity assigned for each pixel. The effect is that of semitransparent tissues, which partially hide other tissues. The lighting of sources can be used for enhanced three-dimensional sensation.

Volume rendered images may be manipulated in a similar fashion to other 3D images. The original image and the 3D image are both displayed.

16.22.2 Viewing a Volume Rendered Image

Right-click the image, select **Change Image > Volume Rendering**.

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16.22.3 Using a Display Protocol

You can define display protocols that let you customize the display of studies in the PowerViewer or any of the viewing applications, including viewing a group of images in Volume Rendering mode.

See this topic:

About Display Protocols on page 594

16.22.4 Manipulating Volume Rendered Images

You can use the 3D image tools to manipulate images to get a more precise and accurate view of the volume rendered image.

To:	Do this:
Swivel (rotate)	► From the toolbar, click Swivel . ► Drag the mouse to swivel (rotate) the image in any direction.
Roll	► From the toolbar, click Roll . ► Drag the mouse to roll the image from side to side.
Relate	► From the toolbar, click Relate . ► Click the MIP image where you want to place the reference point.
Reset the orientation	• Right-click the orientation box on the bottom left, then select the option you want.

NOTICE

You can toggle between swiveling and rolling by holding down the Shift key while dragging the mouse.

16.22.5 Adjusting the Quality for Volume Rendered Images

When you finish manipulating a VolR image, the Diagnostic Workstation software adjusts the rendition automatically according to your computer's capabilities (power and performance).

Toggle VOLR Quality  mode allows you to manually adjust the quality of the rendition based on the performance capacity of your computer.

The Toggle VOLR Quality  icon is available in toolbars for the following viewing applications:

- 3D Analysis Application Toolbar on page 87

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- Vessel Analysis Toolbar on page 89
- Coronary Analysis Toolbar on page 92

IMPORTANT

Toggle VolR Quality is available only for strong or medium power computers.

Computer Performance Definitions

- **Strong computer**—PC with 4 Cores and above, such as INTEL CORE 2 Quad, 2x INTEL CORE Duo , or 2x INTEL CORE 2 Quad).
- **Low power computer**—any PENTIUM 4 based PC.
- **Medium power computer**—any INTEL CORE DUO PC with two cores only.

Slow Rendition Scenarios

The Diagnostic Workstation software supports two slow rendition modes:

- Standard Slow—default setting.
- Best Slow—superior rendition (compared to Standard Slow).

When you are working in a viewing application that supports VolR images, the default setting is Standard Slow.

Criteria	Rendition Type (Applied Automatically by the Software)
• Strong computer. • The level of performance for the Best Slow rendition is similar to the average performance for the Standard Slow rendition.	Best Slow
• Medium / low power computer. • The level of performance for the Best Slow rendition is significantly different than the average performance for the Standard Slow rendition.	Standard Slow

Manually Adjusting VolR Quality

You can control system behavior during reading sessions using the Toggle VolR Quality mode.

IMPORTANT

Toggle VolR Quality is available only for strong or medium power computers.

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Example

You have a medium power computer. The Toggle VolR Quality mode is off by default. When you activate Toggle VolR Quality mode, the VolR images are rendered based on the Best Slow rendition. While the Toggle VolR Quality mode is active, all the VolR images in slow scenarios are rendered based on Best Slow rendition.

1. Manipulate the VolR image (see Manipulating Volume Rendered Images on page 633) as needed.
2. Click the Toggle VolR Quality  icon to activate the mode.
   ⇨ When activated, the computer renders all VolR images in the slow rendition scenario with Best Slow rendition.
3. Click the Toggle VolR Quality  icon again to deactivate the mode.
   ⇨ When inactive, the computer renders all VolR images in the in slow rendition scenario with Standard Slow rendition.

Fast Rendition

The Diagnostic Workstation software supports four fast rendition quality modes. The fast rendition modes are appropriate for scenarios in which you constantly manipulate VolR images. The fast rendition modes balance the image quality with computer performance.

The four fast rendition modes are:

- Standard Slow
- Standard Fast
- Standard Fast of every second image
- Standard Fast of every fourth image

The Diagnostic Workstation software system applies the rendition type automatically. The system selects the rendition mode that will support the best quality within defined performance restrictions. The restrictions include the maximum time required to draw a single frame (frame-per-second parameter), the complexity of the images, the size of the display area, and the amount of magnification.

NOTICE

Each rendition task is different. The system selects the most appropriate fast rendition mode is selected for each rendition task, rather than for volume, viewing application, or reading session.

See these topics:

Manipulating Volume Rendered Images on page 633

About Volume Rendering on page 632

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About Vessel Analysis on page 213

About Coronary Analysis on page 264

About 3D Data on page 183

16.22.6 Creating a Relate Point on a Volume Rendered Image

The relate option lets you cross-reference a particular point on a Volume Rendered image with its relevant location on the MPR reference images. This option is only available when you look at all four images on screen at the same time.

1. Click Relate .
2. On the Volume Rendered image, click the point you want to relate.
   ⇨ The cross lines on the MPR images move to show the relevant point on the MPR slices.

NOTICE

Since a Volume Rendered image is displayed as a volume rather than a plane, when you use the relate operation in Volume Rendering there is a conceptual issue of where in the 3D space you have clicked. As a result, the final result shown may sometimes be displayed incorrectly.

See this topic:

Using Refine Registration on page 585

16.23 Working with Volume Rendering Protocols

16.23.1 About Volume Rendering Protocols

Protocols are preset configurations that let you obtain views in various cases with a single click. Protocols differentiate between the classes in the image.

A class consists of the class name, opacity, base color, and curve of the volume rendered image. Classes are displayed as graphs, which can be easily altered to suit the needs and requirements of the image being viewed. Each class represents a different object (body part) in the image, such as bones, vessels, and so on.

See these topics:

Opening the Protocol Editor Window on page 637

Enhanced VoIR on page 637

Protocol List Tab on page 638

About Protocol Editor Tab on page 640

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Using Lighting on page 638
Using Grayscale on page 639
Presetting the Tissue Type on page 639
Switching Tissues Between VolR and MIP on page 639

16.23.2 Opening the Protocol Editor Window

From Protocol Editor toolbar, click Edit VolR Protocol .

The Protocol window appears. It contains two tabs: Protocol List Tab on page 638 and Protocol Editor Tab (see About Protocol Editor Tab on page 640).

See: Enhanced VoIR on page 637.

16.23.3 Enhanced VoIR

A new VolR algorithm creates a more realistic image. The system assesses the hardware and applies one of two modes to set the default. The default is the best performance/quality ratio and interactivity level.

Non-enhanced-VolR	Delivers high image rendition performance. You cannot control the level of the Fast or Slow qualities.
Enhanced-VolR	Delivers high image quality. You can control the quality/performance ratio to set the interactivity level to High, Normal, or Low.

You can manually select enhanced-VolR mode or non-enhanced-VolR mode.

1. Click the drop-down menu for Edit VolR Protocol .
2. Select or deselect Enhanced VoIR.
3. If Enhanced VoIR is selected, select High, Normal or Low.
   ⇨ Your selection overrides the system default selection. Choose the mode based on your workstation.

Workstation	Mode
High-end	Enhanced-VolR
Standard	
Low-end	Non-enhanced-VolR

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NOTICE

See the Vue PACS Desktop Diagnostic Workstation Online Help for details about the Protocol Editor (search on Working with Volume Rendering Protocols or About Volume Rendering Protocols).

16.23.4 Protocol List Tab

The Protocol List tab contains a list of all the default protocols available for viewing images using Volume Rendering. The list also contains any new user-defined protocols that are added to suit user requirements.

NOTICE

There are two default protocol settings, one for CT images (called CT Angio 1L) and another for MRI images (called MR Aorta 1L).

To change a protocol for viewing volume rendered images:

1. From the Viewer toolbar, click Edit VolR Protocol .
   ⇨ The Protocol window appears.
2. From the Protocol List tab, click the protocol with which you would like to view the image.
   ⇨ Each time you click a different protocol, the 3D view is changed accordingly.
3. Click OK to display the last selected protocol or click Cancel to return to the original protocol.

See these topics:

About Volume Rendering Protocols on page 636

Opening the Protocol Editor Window on page 637

About Protocol Editor Tab on page 640

16.23.5 Using Lighting

The lighting option for Volume Rendering provides a shadowing effect, which provides improved 3D effects of the image you are viewing. The default setting for the lighting option is "On."

Click Lighting .

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16.23.6 Using Grayscale

The Grayscale option for Volume Rendering lets you see the volume rendered image in black and white.

Click Grayscale .

16.23.7 Presetting the Tissue Type

When you define the same tissue type regularly, you can use the following preset tissue types:

- General (any tissue that does not appear in the remainder of the list)
- Bone
- Vessel
- Lung
- Lesion

16.23.8 Using Placeholders

Placeholders are preset coloring schemes defined in the protocols, depending on the tissue type defined. The significance of the placeholder will change according to the tissue type chosen in the Tissue Type drop-down menu.

16.23.9 Switching Tissues Between VolR and MIP

Tissues can be switched between the MIP and Volume Rendering applications once a particular tissue type is defined. Any changes made in the Volume Rendered image will also appear in the MIP image.

To switch tissue between VolR and MIP:

1. Right-click on the Volume Rendered image.
2. Select Change Image, then select Angiography MIP.

To switch tissue between MIP and VolR:

1. Right-click on the MIP image.
2. Select Change Image, then select Volume Rendering.

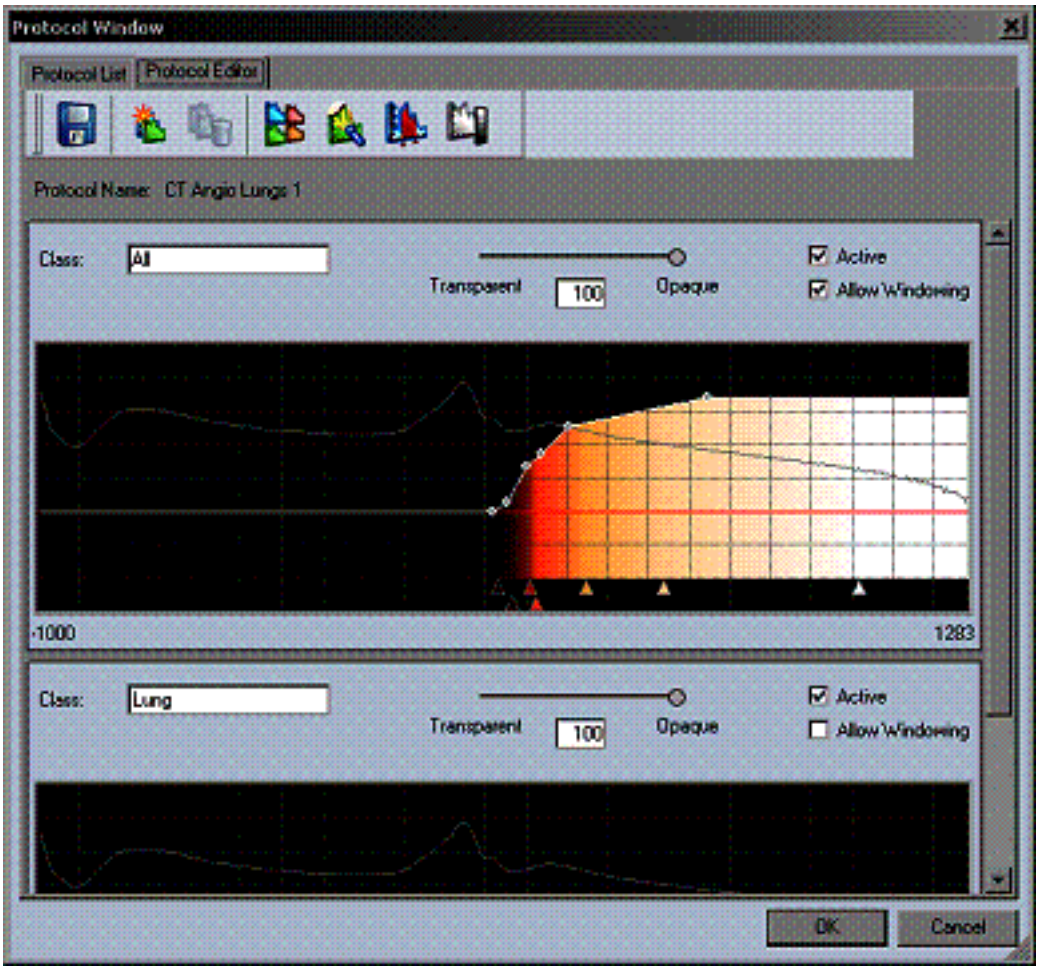
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16.24 Using the Protocol Editor Tab

16.24.1 About Protocol Editor Tab

The protocol describes how you can color the 3D image and the volume rendering of the 3D image by defining classes. The Protocol Editor tab contains details of the classes used in the image that is being displayed in the Viewer.



From this window you can add a new class, delete an existing class, display all classes, change the lighting of the image being viewed, and see the graphs displayed in full view.

NOTICE

In Tissue Class, if Tissue is defined, then it appears automatically as a special class with an additional option to select the Tissue Type.

See these topics:

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About Volume Rendering Protocols on page 636
Adding a New Class on page 641
Changing the Color Display of the Class on page 642
Saving the Protocol on page 643
Opening the Protocol Editor Window on page 637
Protocol List Tab on page 638
Adding/Deleting a Point to an Existing Class on page 643
Showing All Classes on page 644
Displaying a Data Histogram on page 644
Windowing on page 644
Using Full Scale on page 644
Using Lighting on page 638
Using Grayscale on page 639
Presetting the Tissue Type on page 639
Switching Tissues Between VolR and MIP on page 639

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16.24.2 Adding a New Class

1. From Protocol Editor tab, click Add New Class .
   ⇨ A new graph appears with no points on it, indicating zero opacity. The image appears totally black.
2. Type the name of the new class.
3. Click above the line of opacity to determine the level of opacity required for the image.
   ⇨ A point appears on the graph.
4. To adjust the level of opacity, drag the point higher or lower.

   The level of opacity depends on what you want to view in the image. You can add several points to attain the required level of opacity.

   To change the level of opacity of the whole class, slide the Line of Opacity slider left or right.

   The number beneath the line of opacity indicates the percentage opacity.
5. To show the class in the volume rendered image, select the Active check box.

   To hide the class (deactivate), deselect the Active check box.
6. To allow windowing, select the Allow Windowing check box.

⇨ As the colors in the 3D image change, the colors in the graph change.

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16.24.3 Changing the Color Display of the Class

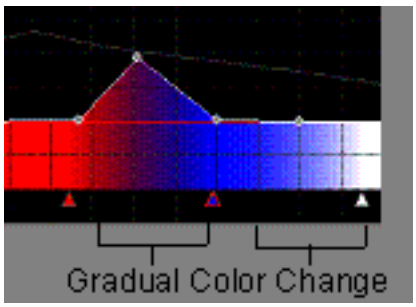
When a new class is created, the color graph appears with a single color area. Move the single color area to change its size. Click and hold on the arrow points to change the color of specific sections.

1. Create a new arrow point by double-clicking on the color line,

   Or

   Double-click an arrow point △ on the graph.

   ⇨ A color menu appears.
2. Choose a color to highlight the opacity on the volume rendered image.



   - When the dot is at the minimum line, the pixel in the image is transparent. When the dot is higher it is opaque (the 3D image turns whiter).
   - You can declare another point (of interest) by single-clicking on the color line. When you move the point up and down, it moves the area of the line between two points. This means that you are making the pixels with this Hounsfield (HU) value (between two values) more or less opaque.
   - Hovering on the point shows the HU value. If you know the HU value of the body part you are trying to emphasize, you can define points in this area and control the opacity.
   - You can define different colors for different areas. Double-click an arrow point △ on the bottom line. These arrows are the specify color. They automatically color the graph between the selected point and the left and right side points. If the selected point has a point to its side, it gradually changes into the next color.
3. Click OK.
4. Repeat the process for each point that you would like to color on the image.

NOTICE

Colors cannot be seen on black-and-white monitors.

The 3D image changes according to the changes made here.

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To delete an arrow point:

► Click the arrow point △.

⇨ A red triangle appears around the arrow point △.

► Press Delete on the keyboard.

16.24.4 Saving the Protocol

1. Click Save .

   ⇨ The Save Protocol window appears.
2. Type the name of the protocol.

   Choose a name that will be associated with the classes in the protocol, such as lungs, spine, ribs, renal arteries, etc.
3. Click OK.

NOTICE

Depending on user permissions, the New Class can be saved at a user or system level.

16.24.5 Adding/Deleting a Point to an Existing Class

To add an arrow or point to an existing class:

Click on the graph.

To delete a point from an existing class:

1. Click on the point you wish to delete.

   ⇨ A small black dot appears inside the point on the graph.
2. Press Delete on the keyboard.

NOTICE

There must always be at least one class and one tissue remaining when deleting.

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16.24.6 Showing All Classes

If a class does not have the Active check box selected, click Show All Classes  to display all inactive classes.

16.24.7 Displaying a Data Histogram

The numerical values displayed in the Volume Rendering application graphs are in Hounsfield Units (HU). The histogram is logarithmic rather than linear. Therefore, the figures are condensed to provide accurate graphs relating to the coloring and shading ratios of the images being displayed in the viewer.

See these topics:

Adding a New Class on page 641

Changing the Color Display of the Class on page 642

16.24.8 Windowing

The windowing option is only available if the class is Active and Allow Windowing is checked. The option allows you to view an image to match the image being viewed (for example, CT or MRI), which may differ from the default settings the system uses to view a particular image.

16.24.9 Windowing Volume Rendered Images

You can change the windowing level dynamically by moving the mouse over the windowing annotation at the bottom right of the image.

1. Move your mouse over the windowing annotation.
   ⇨ The cursor changes to the windowing icon.
2. Drag the mouse up or down to obtain the required windowing level.
3. Release the mouse button.

You can also change the windowing level by clicking the middle mouse button and moving the mouse up and down and side to side to obtain the required windowing level.

16.24.10 Using Full Scale

Use Full Scale when you are editing a class so you can view all points.

Click Full Scale  in the Protocol Editor window.

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16.25 Using Sticky Notes

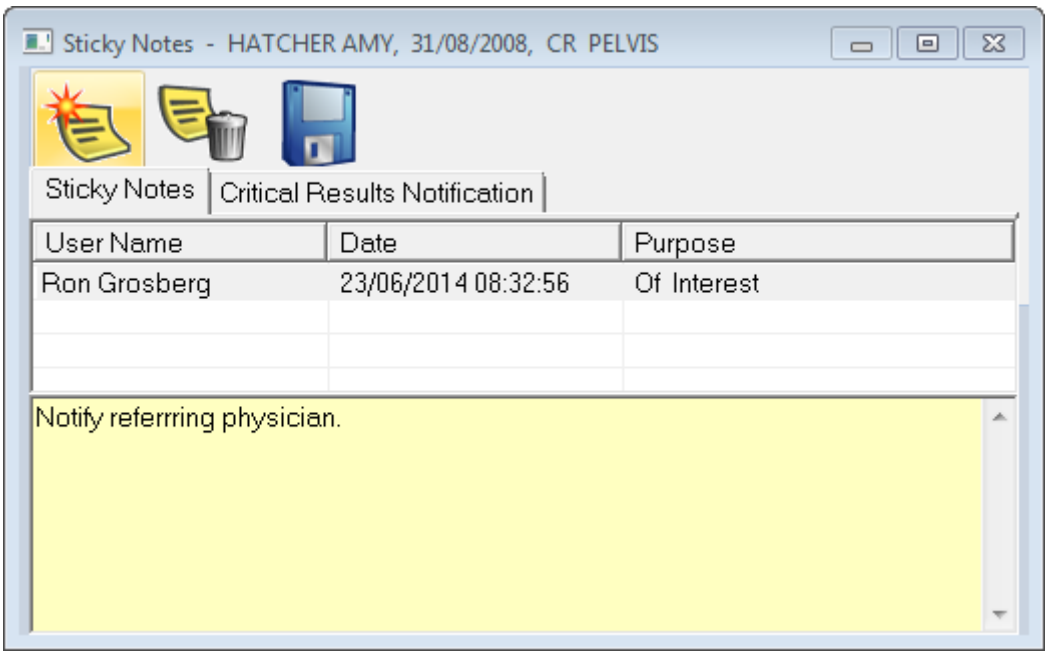
16.25.1 Using Sticky Notes

Sticky Notes are notation files that you attach to studies.

An Open Sticky Notes icon is available in the Patient Mini-Archive toolbar, and in the header of each study.

The icon is yellow if a sticky note is attached to the study.

Click the icon to open the Sticky Notes window.



To add a sticky note:

1. Click on the Sticky Notes tab.
2. Click on the Sticky Notes icon at the top left.
   ⇨ Your user name appears at the top part.
3. Type the text of the sticky note at the bottom section of the dialog.

16.25.2 Adding Sticky Notes

To add a Sticky Note from the Archive Explorer or the Viewer:

1. If you are in the Archive Explorer, select the study for which you would like to add a Sticky Note.

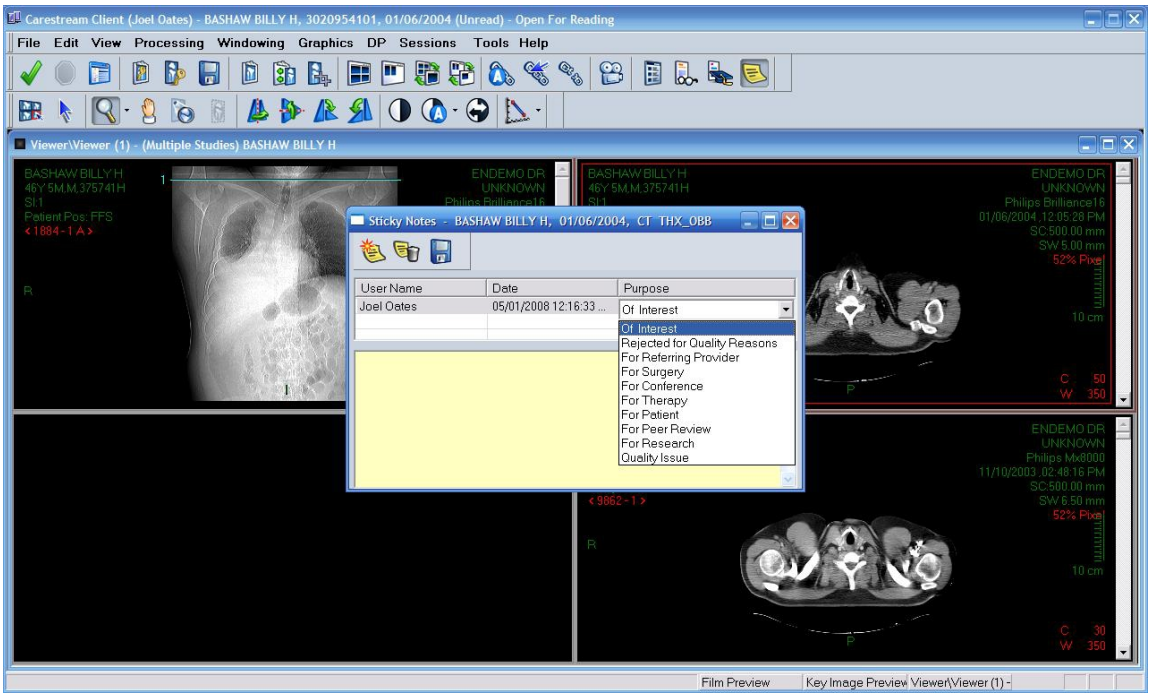
   or

   If you are in the Viewer, go to step 2.

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NOTICE! Cases with Sticky Notes attached are marked with a Sticky Notes icon in the Notes column.

2. Click Sticky Notes .
   ⇨ The Sticky Notes window appears.
3. Click Add New Note .
4. Select the purpose for the note from the Purpose drop-down menu.
   ⇨ If you do not select a purpose, Of Interest appears.
5. Type your comments.
6. Click Save Notes .



To add a Sticky Note from the Patient Mini-Archive:

If an image within a study has a Sticky Note, the Notes icon appears in the corner of the Patient Mini-Archive.

1. Double-click the "N" Notes icon in the Patient Mini-Archive.
   ⇨ The Sticky Notes window appears.

2. Click Add New Note .
3. Select the purpose for the note from the Purpose drop-down menu.
   ⇨ If you do not select a reason, Of Interest appears.
4. Type your comments.
5. Click Save Notes .

See this topic:

Deleting Sticky Notes on page 647

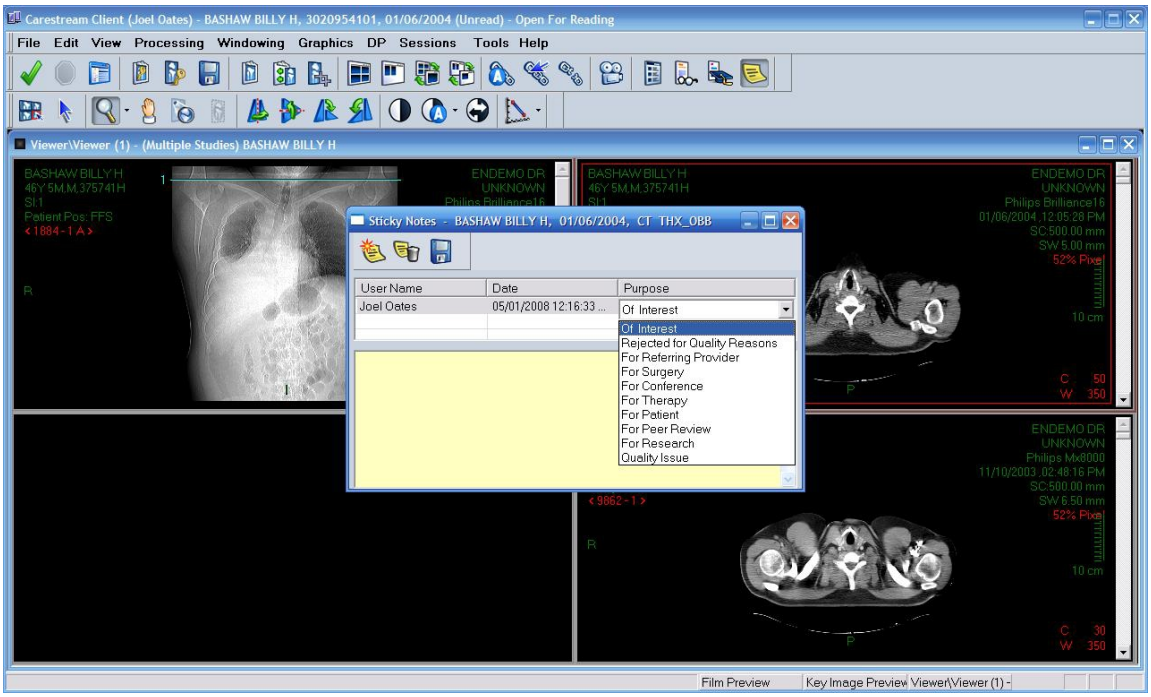
16.25.3 Deleting Sticky Notes

1. From the Sticky Notes window, select the Sticky Note you want to delete.
2. Click Delete Note .

NOTICE

You can delete only the Sticky Notes that you have written, unless your user profile permissions allow you to delete other users' Sticky Notes.

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16.26 Using the Pointer (Neutral Cursor)

The pointer (neutral) option lets you put the cursor in neutral mode (no function is enabled). This enables you to view images in a safe mode without any risk of harming the image, meaning that it will not zoom, pan, move, and so on.

From the PowerViewer toolbar, select Pointer  or press Ctrl + I.

The cursor changes accordingly and remains in neutral mode until you select another option.

16.27 Tissue Definition Tools

To display the Tissue Definition toolbar and use tissue definition tools, click the Tissue Definition icon  in the 3D tab of the toolbar.

See these topics:

About Tissue Definition on page 196

Tissue Definition Toolbar on page 102

Changing Highlight Values for Tissue Definition on page 199

Using Balloon on page 200

Placing a Seed Point on page 200

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Placing an Outside Point on page 201
Adding and Removing Pixels on page 202
Using Bridge on page 202
Using Minimum Volume on page 203
Using Fill on page 203
Resetting the Images on page 203
Creating a VOI for Tissue Definition on page 204
Interpolating a VOI for Tissue Definition on page 204
Restricting a VOI for Tissue Definition on page 205
Building and Applying Tissues on page 205
Removing Objects and Anatomy on page 207
Removing Tissue on page 209
Removing Vessels on page 209
Removing Bones on page 210
Removing the Heart Cage on page 211
Removing the Scanner Bed on page 211

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16.28 About the MPR Double Oblique Layout

MPR Double Oblique layout allows you to view one volumetric dataset in several oblique (usually perpendicular) planes. You can swivel the reformatted planes to any orientation synchronously. MPR Double Oblique layout retains the perpendicular relationship between the planes.

MPR Double Oblique layout is appropriate to use in the Cardiac and the MPR applications.

Reset Reference Images is a new option available in the MPR menu for the MPR application. Reset Reference Images allows you to reset the images to the original axial/sagittal/coronal views.

NOTICE

Double Oblique View refers to three perpendicular views. In many reading scenarios, the three oblique views are the main images, called reference images.

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See these topics:

Resetting Reference Images on page 175
Using the MPR Double Oblique Layout on page 177
Applying Phase Modes to the MPR Double Oblique Layout on page 179

Toggling Group Layouts (MPR) on page 180

16.29 Accuracy of Measurements

This section provides information about the accuracy of Vue PACS viewing application measurements. The accuracy of the measurements relies on a number of factors, particularly the Region of Interest (ROI) being measured.

While the software calculates and displays measurements with a resolution of two decimal places (such as 0.11 mm, 0.11 degree, etc.), several factors limit the accuracy of the measurement.

The image resolution is determined by the size of the area scanned, the matrix size of the captured image and the inter-slice distance for 3D measurements (all three are determined by the modality when the images are created).

For example, the smallest detail in an image acquired with a standard 512 x 512 matrix is 0.5 x 0.5 mm. With a standard 256 x 256 matrix the smallest detail is 1 x 1 mm.

The size of the smallest elements limits the measurement accuracy in the acquisition plane and is the physical minimums. The accuracy in a direction perpendicular to the acquisition plane cannot be better than the distance of the inter-slice.

Other factors including acquisition errors, image artifacts, display settings, and partial volume effects, may affect accuracy for the particular modality and image type. Anatomical features in the images are rarely of a uniform composition or density.

In the Basic Viewer Application regardless of the zoom factor being used to view images, ROI statistics are calculated based on the pixels from the original, unzoomed image data as they arrived at the workstation. Region of interest area statistics are based on the pixels inside the graphic defining the region.

Using the Straight Line Measurement, measurement accuracy for the displayed length is equal to +/– the image pixel size. To minimize errors to the physical minimum, enlarge the image before positioning the measuring tools.

Using Angle Graphics, measurement accuracy depends on the length of the segments and improves as the length of the segments increase. For an angle measured between segments which are 100x the image pixel size, the measurement accuracy of the displayed angle value is equal to +/– one degree.

Using a Region Of Interest Area Graphic (free draw, smooth curve, rectangle or ellipse), measurement accuracy of the displayed area value is equal to +/– the circumference of the region multiplied by (image pixel size) ^2 / 2.

Mean and standard deviation values for the intensity of the pixels in the region are affected by this accuracy.

16.29.1 In Power Viewer and MPR-based Applications

The Line accuracy is one voxel (a volume element, the basic element in a CT or MR data set in 3D) . With high thickness values, accuracy may decrease.

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The ROI statistics are affected by the zoom factor used to view images, ROI measurements and statistics are calculated based on the pixels from the original ZOOMED image data.

16.29.2 3D images (MIP and Volume Rendering) Measurements

Changes in display settings (window W/L) may result in a change to the apparent dimensions of the anatomical features (e.g., the diameter of a blood vessel). The presence of partial volume voxels at the interface between two adjacent anatomical features with different composition or density produces a similar effect.

The automatic algorithms may fail to segment the area the user is analyzing, causing the measurements to be inaccurate. The segmentation and the derived measurements are only an aid for the user. It is the user's responsibility to verify the segmentation. Once the segmentation and measurement positioning is verified, the accuracy of the measurements is one voxel.

Always refer to the Viewer and MPR as baseline to confirm 3D measurements.

Measurements are more accurate when they are performed in the Viewer.

When depositing any measurement tool (Line, Angle, ROI), always check its correct position on reference views.

16.29.3 Tissue Definition

The tissue definition tools have an accuracy of up to two voxels due to the smoothed image data. The accuracy of a tissue volume measurement is given to the user per measurement.

16.29.4 Coronary Vessels

The Coronary definition tools have an accuracy of one voxel.

16.29.5 SUV Calculations on PET-CT Cases

When using an SUV calculation during a PET assessment certain assumptions are made with regard to the reference time for the acquisition of the data series.

It is important to note that SUV is affected by a number of physiological factors which cause changes in the calculated SUV values.

Taking these two factors into account, SUV can be used as a simplified measure of radio pharmaceutical uptake, which has a complimentary rather than directive role in the assessment, treatment, and staging of disease.

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17 Enterprise Collaboration Manager Architecture

17.1 Global Worklist

17.1.1 Multi-Site Querying

The Global Worklist is displayed like any other regular worklist folder in the Archive Explorer. Use the Global Worklist to:

- Read studies from all sites connected to the data center.
- Fetch prior studies from other sites.

Using the Global Worklist

1. Connect directly to the data center or to your local server.
2. Select the Global Worklist to query your studies from all sites.

Multi-Site Loading

Loading speed determines whether streaming is used or not used.

The load speed is chosen automatically, depending on the best study location.

Look at the Expected Rate column to see:

- Availability—Fast (online) or slow (nearline).
- Quality—Best (fast connection) or Progressive (slow connection).

See this topic:

About Worklists on page 109

Working with Global Priors on page 127

17.2 Global Worklist in Archive Explorer

From the Archive Explorer, you can create a global worklist folder which:

- Shows studies from all your sites.
- Supports seamless work planning.
- Eliminates the need to log in to different servers.
- Saves you valuable time.

All studies are synchronized with the original server and are sent to your computer as quickly as possible.

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Reference Material	Instructions
About Worklists on page 109	Worklist Folder on page 109
	Global Worklist on page 110
	Creating or Viewing a Custom Worklist on page 111

17.3 Push to Client

You can read studies faster with Push. The Push capability allows you to transfer studies to your home PC or another remote location. Another person can push studies for you as needed, increasing the potential for collaboration between physicians within the enterprise.

You can transfer, monitor, receive, and clear studies from the Transfer Tools on page 445.

You can receive studies (see Receiving Studies on Your Local Computer (Receive Studies) on page 449) from the New Viewer—PowerViewer on page 145.

Reference Material	Instructions
Transferring Studies to a Local Computer (Push to Client-see About Push to Client on page 445)	Sending Studies to Your Local Computer (Push to Client) on page 446
Transfer Tools on page 445	Monitoring Transfer Requests (Spooler) on page 448
	Transferring Locked Studies on page 449
	Receiving Studies on Your Local Computer (Receive Studies) on page 449
	Loading Images Stored on Your Computer on page 450
	Clearing Images from a Local Computer on page 451

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18 Clinical Applications Additional Features

18.1 Before You Begin

IMPORTANT

The following sections might describe features that are optional and require a special license to run. If these are not available on your system, contact Philips for further details regarding license and feature upgrades.

18.2 General Tools

18.2.1 Cine

Auto-play cine clips groups such as X-ray Angiography (XA) or Ultrasound (US) when loading and dragging from Patient Mini Archive (PMA).

- A new cine toolbar has been added and will be automatically displayed when a group is identified as a cine group.
- The new toolbar also introduces some buttons to centrally control cine loops and change playing speed.
- Not all US/XA groups are cine loops. Some are groups of screen capture images, which will not be played. The user can configure the selection of the group to play.
- Note that auto-cine is not applicable on groups with layouts different from 1x1 (for example, tile).

Automatic cine is triggered upon load, dragging from the PMA, Display Protocol (DP) application and navigation between groups. Use the Cine ribbon to play, pause, stop, step forward and backwards, change direction, and change the playing rate of all groups.

18.2.2 PR Save as Overlays

An option to save images with graphics, instead of as presentations (PRs), is available to support third party systems that do not support PR capabilities. This requires configuration.

18.2.3 Film Screen (2D Only)

When using the 2D viewer, the user can “film” the entire content of the screen, including reference lines so it’s easier to cross-correlate between different views.

From the **Film** menu in the **Export** tab, select the **Film Screen** option.

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18.2.4 Field of View Annotation

The new annotation represents the “field of view”, which is currently presented in the image window. The annotation can be combined with the mm per pixel annotation tomatch object sizes in different images.

This capability requires configuration.

18.2.5 Ultrasound Measurements

Various measurement tools have been extended to be region-aware and to support additional layers of information that exist in US images, including Doppler and M-Mode regions.

- For Doppler regions, the acceleration speed is supplied in addition to time and velocity intervals provided when measuring with the Line tool. The cursor provides the velocity and pressure gradient for a given time point.
- For M-Mode regions, the line measurement provides the time interval, the distance, and the slope. The cursor displays the location for a given time point.

These extended capabilities are provided when the normal measurement tools such as line, oval, and ROI on Ultrasound images are used.

18.2.6 Copy Error Message

An additional button can be configured to allow copying the text of error messages into the clipboard.

18.2.7 Multiple CD Burners

The Diagnostic Workstation now supports multiple CD burners.

- A drop-down list has been added to the **Burn** button in the **Archive Explorer (AE)**, displaying a list of all available CD burners.
- The default burner is automatically selected, but the user can select any other burner on the list.

In the AE, click **Burn** to send the study to the selected burner.

18.3 Image Review and Analysis Tools

18.3.1 PET-CT Registration

This feature is designed for cases in which the PET and CT groups are not from the same study (old modalities) or cases in which the patient moved during the scan and the PET.

From the **Comparison** tab, click **Registration** and then click the groups to be registered.

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18.3.2 Mammography

Nipple/Vertical Alignment

Using either a nipple detection algorithm or information coming from a Computer Aided Detection (CAD) object, the system can automatically align related images vertically by locating both nipples over the same horizontal line.

On the **Mammography** tab, click **Nipple Alignment**.

Study Replacement

Study replacement provides a means of replacing an entire study with a different one either through study date annotation or by dragging a study from the patientmini-archive. The replacement process loads the new study and applies its views to replaced locations as designated by the DP.

To receive a list of available studies for replacement, drag a study from the PMA studies pane or right-click on the **Date and Time** annotation.

Reference Lines and Relate

Reference lines tools provide cross correlation of a given Region of Interest (ROI) between several mammograms based on the distance from the nipple.

The buttons are available in the **Mammography** tab.

Viewbox Shortcuts

The user can now assign keyboard shortcuts through the DP to a designated viewbox. Once clicked, the navigation system is triggered and brings up the designated viewbox.

This is done through the Display Protocol editor, per viewbox.

Stacked Images Support

Advanced mammography tools (same size, nipple alignment, and the quad-zoom) are now fully supported with stacked images. When these tools are applied over a stacked image group, they affect all images, whether they are visible or not.

Study Addition

Study addition provides the means to append an additional study to a stacked images viewbox. Study addition is invoked using the same manner as study replacement. However when a study is “replaced” in the context of a DP defined as stacked history, the study replacement operates as study addition,meaning the new study will be appended rather than replaced.

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Nipple Correction Enhancements

Nipple correction is now applied in a global manner. When the nipple position is corrected on one image, the correction is applied over all image instances, regardless of the viewbox in which they are presented.

Buttons are available in the **Mammography** tab.

Cross Viewbox Reference Lines

When cross-reference lines are applied, the results are available in all viewboxes, so different presentations can be correlated more easily.

Buttons are available in the **Mammography** tab.

Chest Wall Justification in the Film Previewer

The **Film Previewer** (FP) ribbon now includes a **Chest Wall Justification** button, providing support for various mammography printing scenarios.

18.4 Workflow Tools

18.4.1 Worklists

Worklist Highlighting

It is now possible to highlight studies in the **Archive Explorer (AE)** with different colors based on various criteria.

Any study level DICOM tags that are presented by the **AE** can be used as a selection criterion for the highlighting process.

The mechanism supports the definition of multiple criteria as well as colors. For example, the user can highlight in red any study with high priority and in yellow all the "outpatient" studies.

To highlight studies, click the highlight button in the **AE**.

Elapsed Time Virtual Column

The elapsed time virtual column indicates the time passed since the study was acquired. Combined with worklist highlighting, it enables the user to easily locate and highlight studies that may have been forgotten in the worklist over a period of hours.

In **Application Settings**, go to **Annotations Options** and choose the **relative_frame_time** annotation.

Create Group-Level Folders

Save Filter as Folder can now create folders in group level.

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To filter the studies in the **AE**, right-click on the filtered list and select **Save Filter as Folder**. In the **Create Folder** window, check the **Group** option.

Auto Load of Newly Acquired Images of the Current Study

A new **Refresh** button now appears in PMA that lets the user ask for new images to be automatically retrieved.

- This is meant for cases where the radiologist might ask for additional views to be acquired such as in some Mammography (MG) studies or US.
- It can also help in emergency cases in which the doctor might start viewing the images before the study has finished storing (for example, MR studies).
- The newly acquired images will be automatically loaded and placed according to the DP.
- Any updated or newly added group in the PMA will be marked in a different color or by a dashed frame for B&W monitors.
- After the user has clicked the **Refresh** button, auto-refresh is automatically activated until the study is closed so that there is no need to click **Refresh** more than once per study.

To trigger the Automatic Refresh process, click the **Refresh** button in the PMA toolbar or in the PMA strip.

18.4.2 Display Protocols

Auto Load History When Switching DP

Up until now, when applying a different DP or presentation to a study that is already loaded, the system used the same history studies that were loaded with the original DP. If the original DP loaded only one history, but the newly loaded presentation required three priors, users had to manually load the remaining two priors if they wanted to see them. The system now loads any additional prior needed by the presentation or DP.

Control Saved Parameters

An ability to control which parameters (zoom/pan/windowing) will be saved as part of a new DP is now possible when using **Save as DP**.

Use the checkboxes available in the **Save as DP** window.

Save Presentation

- Performance Improvements – Improvements have been made to the load presentation mechanism to reduce the time it takes to fill the screen with the initial presentation view when loading multi-slice data into the 2D viewer.
- Registration – Registration information is now saved as part of the presentation object. In addition, restoring links between current and prior studies as part of the presentation has been improved.

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Ultrasound Multi-Frame DP

A new "sample DP," which separates static and dynamic images based on SOP class grouping rules has been implemented and is available for reference.

This is provided to the user automatically. It replaces the previously existing DP.

All Priors DP

A new System DP places the current study in one **Group Display Area (GDA)** and all loaded prior studies in another, single GDA, stacked together.

The prior groups are sorted by study time with the latest group displayed first.

18.4.3 Assign-To Mechanism

A new mechanism replaces the old assign-to option in **AE**, dramatically enhancing the assigning capabilities:

- An **Assign-To** dialog box is available which lets the user easily select users or groups to which to assign studies.
- The dialog is available both from **AE** and from the **Confirm** button as a drop-down item (similar to the **make stat** option).
- The user can now assign a study to a single user or multiple users/reading groups.
- The user can create reading groups.
- The assign-to dialog shows only users from selected User Manager (UM) groups so that the radiologist will not have to go through the whole list of referring physicians, administrators, and so on.
- A user can filter all studies assigned to them, or any group of which they are part.
- Users can be configured so that in every session, all studies they ready are automatically assigned to a specific user or group. This is good for resident-attending situations.

To access the **Assign To** window, highlight a study in the **AE** and select **Assign To** from the **Edit** menu or from the right-click menu.

To define a Users list, click **Set User List** and select users from the **User List Setup** window. To create a

Reading Team, click **Create Reading Team** and select teams from the **Reading Team Setup** window.

To assign studies to individual users and to reading teams, select a user and/or team in the **Assign Studies** dialog.•

18.4.4 Mark Current Study

The current study is now better marked to enhance visibility on the screen.

A dashed frame makes the current study more prominent on monochrome monitors.

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18.4.5 Configure Decimal Point for Angle Measurement

The number of decimal places for angle measurement is now configurable, affording display of whole numbers only.

18.4.6 Load Study in the Vue Motion from Archive Explorer

It is now possible to load a study in the Vue Motion from the **AE**. The study is loaded in the Vue Motion rather than in the Diagnostic Workstation.

To load a study in the Vue Motion from the Diagnostic Workstation, highlight the study in the **AE**. Right-click and select **Load to Vue Motion**.

- If there are multiple Vue Motion servers, the default node in the configuration determines the server to be selected.
- The loading is secured. The User name and password are not visible in the URL.

18.4.7 Home and End Keys in PowerViewer

Pressing the Home and End keys displays the top (first) and bottom (last) slices, respectively, in the Viewer. This capability is now supported in the PowerViewer as well. Clicking Home and End displays the volume beginning and end, respectively.

18.5 Administrative Tools

18.5.1 "Login As" (Alternative Preferences)

Login As allows service people to log in using another user's preferences, allowing them to modify private behaviors and/or diagnose problems that are specifically related to the user's configuration.

The availability of this tool is controlled by specific permissions and the authorization and access controls are controlled under the primary users' credentials to avoid potential impersonation and access to unauthorized data.

The feature can be used both with the **Application Settings** tool as well as the **Display Protocol editor** and is especially useful when implementing and testing private DPs.

18.5.2 Multi-Monitor Simulator

Using this tool, the user can log in to a system while simulating a different number of monitors than physically supported by the existing hardware (for example, the user can simulate a four-monitor system over a two-monitor system).

Combined with Login As, this tool can enable writing and testing display protocols that cater to specific users regardless of their physical setup.

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Note: This feature is not intended for clinical use and should not be used by physicians. While working in this mode, parts of the user interface may not function properly or fail to adapt for the simulated hardware. This mode was designed and tested for the sole purpose of evaluating display protocols on various platforms.

18.5.3 Display Protocols

DP Usage Statistics

Starting from this version, the Diagnostic Workstation keeps track of the last time an DP was used. Every time an DP is chosen, either automatically by the system or manually by the user, the last used date will be updated.

- The last used date is now shown in the Display Protocol editor.
- In future versions, DPs that haven't been used for a long time will be disabled. This will make the configuration smaller and help the Field Engineer (FE) and Applications Consultant (AC) to distinguish between important and unimportant DPs.

A Synonym Management Tool

The synonym management has been enhanced.

- All synonym tables have been unified to a single table under the configuration.
- A new tool has been introduced to allow the administrator to easily add synonyms to the system. These new synonyms will be used for:
- DP selection
- Selection of prior studies for an DP
- Assignment of groups to be shown

Sort Between Groups

Using this enhancement, you can build Display Protocols, which arrange the groups on screen by a specific order without pre-identifying the groups using specific nominal groups.

The order by which the groups are sent to presentation can be defined by various DICOM tags such as series number, acquisition time, and so on.

Exclude Series Number/UID from Sort Criteria

The ability to remove Series Number/SeriesInstanceUID from the default sort criteria is now available in the **Display Protocol editor** as part of standard DP definitions.

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