VISAGE IMAGING®
Visioneering Science for Life

Online Help

Visage® 7

CE 0197

This software is CE-compliant and is defined as a class IIa medical device in accordance with Medical Devices Directive 93/42/EEC.

All product and company names are trademarks or registered trademarks of the respective companies.

Some of the specifications described herein may not be currently available in all countries. Please contact your local sales representative for the most current information.

Caution

US federal law restricts this device to sale by or on the order of a physician (or properly licensed practitioner).

Information in this manual may be subject to changes without prior announcement.

Manufacturer

Visage Imaging GmbH
Lepsiusstraße 70
12163 Berlin, Germany
Phone: +49 30 700968-0
Email: info@visageimaging.com

US Distributor

Visage Imaging, Inc.
12250 El Camino Real, Suite 230
San Diego, CA 92130, USA
Phone: +1 858 345-4410
Toll-free: +1 888 998-4724

Australian Sponsor

Pro Medicus Limited
450 Swan St
Richmond VIC 3121, Australia
Phone: +61 3 9429 8800

Support and Safety Contact

Phone: +49 30 700968-30
Email: support@visageimaging.com

For contact information and a list of our world-wide office locations visit www.visageimaging.com.

Visage Imaging is a wholly owned subsidiary of Pro Medicus Ltd. www.promedicus.com.

Document Version 11.00

Table of contents

Intended use, data security, and system requirements

Visage 7 is an imaging solution based entirely on efficient thin-client streaming technology. It scales easily from a single radiology practice to large distributed healthcare enterprises and allows efficient viewing, processing, and archiving of very large numbers of images, including thin-slice volumetric data from CT, MR, PET-CT, and other 3D modalities.

Intended use

Visage 7 is a system for distributing, viewing, processing, and archiving medical images in healthcare environments. The Visage 7 server receives image data in DICOM format via network. This provides flexible connections to archives, modalities, and workstations. Modalities supported by Visage 7 are listed in the DICOM Conformance Statement.

Aside from general image interpretation and processing tools, Visage 7 provides specific tool sets for several clinical applications, including:

- CT/MR angiography, for example, for vascular analysis and stent planning
- Cardiac analysis, including calcium scoring and functional assessment of cardiac CT data
- Neuroradiology, including CT and MR brain perfusion analysis
- Oncology, including SUV analysis and lesion marking and analysis

Visage is to be used only by trained and instructed healthcare professionals. It can support physicians and/or their medical staff in providing their own diagnosis for medical cases. The final decision regarding diagnoses, however, resides with the doctors and/or their medical staff in their own area of responsibility. Although the Web and thin-client technologies allow the software to be run on a variety of hardware platforms, for diagnostic purposes the user must ensure that the display hardware used for reading the images complies with state-of-the-art diagnostic requirements and currently valid laws.

Only DICOM for presentation images can be used on an FDA approved monitor for mammography for primary image diagnosis. Only uncompressed or nonlossy compressed images must be used for primary image diagnosis in mammography.

Data protection and data security

Patient data is subject to data protection. Therefore, users have to ensure compliance with all applicable laws and regulations in their country. Visage 7 provides extensive security mechanisms that help you assure data protection and data security. On the administration platform, the system administrator can activate the audit trail option to comply with the strict regulations regarding security and privacy of health data (HIPAA) according to US law.

Caution

For data security reasons, it is not permitted to make changes to the Visage product and its database. Contravention of this will lead to all guarantees being revoked and under some circumstances may violate applicable laws.

System requirements

With Visage 7, all image data is stored on the server at all times. Users access the data directly on the server from any number of radiology workstations, office PCs, laptop computers, or other devices. Image data does not need to be sent to client computers in the process. Instead, Visage 7 employs a technique that is called **thin-client streaming** or **thin-client computing**. All image processing (2D, 3D, or 4D) is performed on the server.

Server hardware consists of standard server platforms, but they must be qualified by Visage Imaging. For a detailed server hardware and software specification, contact customer support.

Client computers neither need to hold large volumes of data nor do they need to perform any of the actual image processing. Therefore, system requirements for Visage 7 Client computers are minimal as far as memory, graphics, or computing power is concerned. As a result, the Visage 7 Client can be installed on virtually any standard computer or standard laptop with a network connection. Visage 7 supports all recent versions of Windows® and Mac OS. With Visage 7, Mac and Windows users can work together in a fully integrated environment and workflow.

Detailed system requirements are documented in the release notes, which are available on your Visage 7 server's download page.

Symbols on the packaging

These symbols on the packaging convey information that is essential for the proper use of the product.

Fragile

Keep dry

Protect from heat and radioactive sources

Temperature limitation

Consult operating instructions

Caution, consult accompanying documents

Date of manufacture (YYYY)

Manufacturer

CE-mark with reference number of VI's Notified Body (TÜV Rheinland LGA Products GmbH)

Serial number

Reference number

System and workflow overview

Visage 7 delivers a fully scalable solution for primary interpretation, advanced visualization, image distribution and archiving. All functionality is provided in a single client software application with native thin-slice access and 3D and 4D postprocessing. Visage 7 is entirely based on client-server streaming technology with all functionality accessible from anywhere in the enterprise network or via the Internet. With the Visage 7 thin-client solution, there is no waiting time for the data to be copied onto your client computer, because all 3D processing and other calculations are performed on the server.

Key features of Visage 7

Visage 7 is an archive-neutral diagnostic and clinical viewing application that provides a comprehensive imaging workflow for all modalities.

- **Universal viewing**

  One thin-client application for reading everything from plain film to cardiac CT.

- **Native thin-slice and 3D processing**

  Seamlessly integrated multiplanar reformatting, volume rendering, and volumetric analysis.

- **Advanced clinical applications**

  Supporting a wide spectrum of modalities, including CT and MR angiography, cardiac CT, neuroradiology, and oncology.

- **Distributed workflow and archiving**

  Instant, unified remote access to multiple locations without replicating data.

- **Native Windows and Mac Client OS**

  Windows and Mac users seamlessly integrated into a single workflow and IT platform.

- **Easy scalability**

  The fully scalable distributed thin-client architecture makes it easy to add more modalities, users, and locations.

- **Features and user levels**

  Most features and tools can be turned on or off for individual user levels. User levels allow the definition of roles, such as the role *referring physician*, who will be presented the **Patient Search** window rather than the **Study Browser**. On a finer level, individual tools can also be enabled or disabled for each user level.

Workflow overview

Visage 7 offers all the benefits of a flexible state-of-the-art PACS with advanced 2D, 3D, and 4D visualization. Efficient image interpretation is central to this solution, in which all data remain on the server at all times and client computers use thin-client technology to access the data.

Image Interpretation

Efficient primary interpretation is facilitated by fast loading times, flexible display protocols, and fully integrated 3D navigation. Prior studies, postprocessing results, and interactive processing tools are instantly available, and the radiologist can easily store and share key images and examination results.

Image Postprocessing

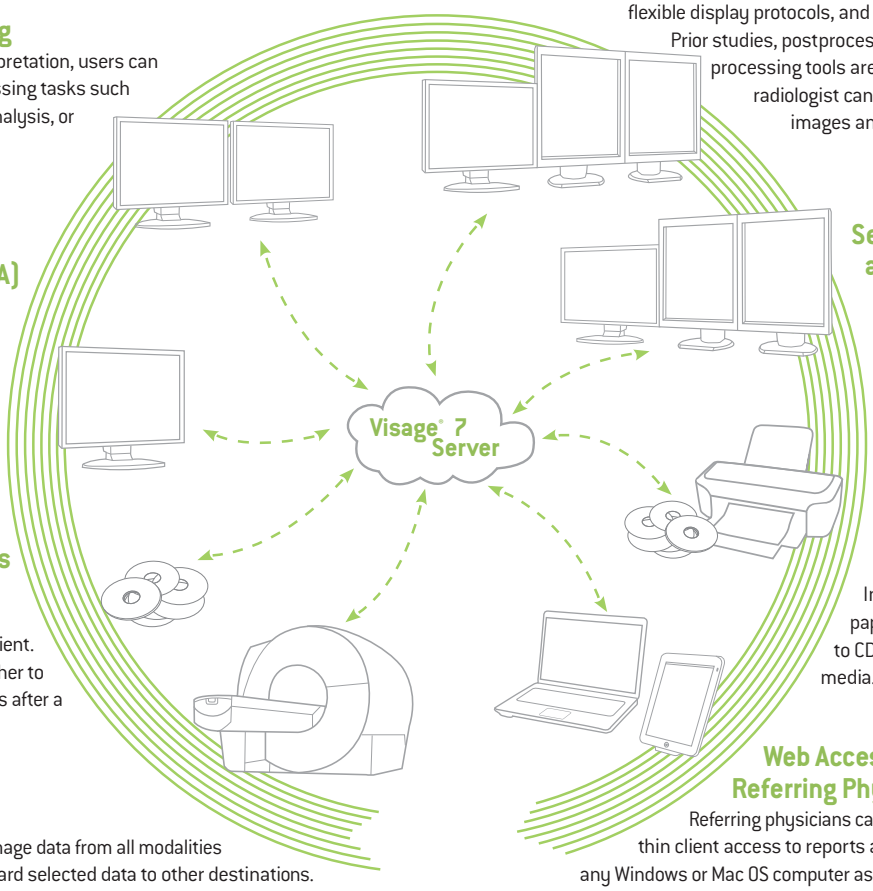
Before or during primary interpretation, users can perform advanced postprocessing tasks such as bone removal, volumetric analysis, or perfusion analysis.

Second Opinion and Demonstrations

Radiologists and clinicians can easily access images and postprocessing results simultaneously or consecutively.

Quality Assurance (QA)

Authorized users (e.g. PACS administrators) can verify or correct the assignment of images to accession numbers and patient IDS, split and merge patients and studies, and delete images.



Media, Paper, Film

Users can export original images as well as key images from any client computer. Images can be printed on paper or film or they can be copied to CD, DVD, or other electronic media.

Importing Prior Studies

Users can import prior studies from any client computer and assign them to the correct patient. Visage 7 can be configured either to archive or to delete prior studies after a period of time.

Web Access for Referring Physicians

Referring physicians can be provided with instant thin client access to reports and images via Internet, from any Windows or Mac OS computer as well as on mobile devices. Display protocols, functionality levels, and access rights can be configured individually per user or user type.

Receiving Image Data

Visage 7 receives and stores image data from all modalities and can be configured to forward selected data to other destinations. Visage 7 can serve as a full archive, or as a cache storage for efficient access to large data volumes on top of an existing archive.

Study Browser

In the **Study Browser**, you search for patient and study data. Here you select the images that you want to read and load them into a **View** window.

Note

If your Visage 7 is integrated in other clinical software, such as a Pro Medicus RIS, the **Study Browser** might not be shown. Instead, you use the worklist of the RIS to select and load data directly into Visage 7.

If the Visage 7 **Study Browser** is shown, remember that the **Study Browser** is not a worklist. A worklist would present and preselect cases and tasks that a user has been scheduled to complete next. By contrast, the **Study Browser** gives an overview of all data that is stored on the Visage 7 server or on connected network nodes. You search these lists for the study or studies that you want to read next.

Find out more about the **Study Browser** and about how to load data and perform data management tasks in the following sections.

- *Query section*
- *Study list*
- *Loading data from the study list*
- *Session management*
- *Data management*

Query section

Before you start defining search criteria for a database query, select the database tab where you want to search. Queries apply only to the database whose tab card is currently shown in the foreground.

Tip

If you do not know a complete name or number, you can use wildcards in your search. For example, type `Mil` in the patient name box to find *Miller, Milford, Miltner,* or `*mil` to find all the above and also *Hamilton*, or `AB??34` in the patient ID box to find *AB1234, AB0034,* and *AB11345678*.

However, even if you use wildcards, always specify your search criteria as precisely as possible. Rather general queries might yield a very long hit list, which requires extensive scrolling.

Filter and search criteria

Use the filter and search criteria in this list to search for study data.

Patient

Enter the name, date of birth, or ID of the patient that you are looking for. If you do not remember the exact name, date, or number, use wildcards.

For names that occur frequently, you might want to include the first name or other components of the patient's name in your search. To define such a search, you need to know how patient names are stored in the database.

```
FamilyName GivenName MiddleName Prefix Suffix
```

The following example shows a search for first name, last name. and title.

```
Doe John*Dr.
```

If you want to search for more than one patient, separate patient names with a semicolon (;) or the pipe character (|). For example, `Anderson|Alexander` or `Miller;Milford`.

Date

Click the **Date** box and select if you want to search by **Study Date** or **Insertion Date**. The **Insertion Date** is the date when the study was transferred to the server from a modality or an archive.

From ... **To** specifies a search period. Type dates in the format YYYY-MMM-DD, or click the button to the right of a date box and select a date in the calendar.

Use the buttons **Today**, **Yesterday**, **1 Week**, **2 Weeks** as a quick way to specify frequently searched periods in the correct format.

You can configure these four search-period buttons. Right-click one of the four buttons and select **Hours > 1 Hour**, for example, if you are frequently looking for studies that were performed within the last 60 minutes.

Modality

Select the check boxes for all modalities for whose studies you want to search:

CT (computed tomography), **MR** (magnetic resonance tomography), **PT** (positron emission tomography, PET), **US** (ultrasound), **CR** (computed radiography), **DX** (digital radiography), **MG** (Mammography), **XA** (X-ray angiography).

-Or-

Enter a modality abbreviation in the **Others** box. Separate multiple modalities by a space, for example, `CT PT MR`.

Fields

Here you can specify three additional criteria from the DICOM information on a study.

Open the lists of available criteria with the double-arrow buttons and select a criterion.

Specify your search string in the input box below the selected criterion. Remember that you can use wildcards in your search.

If you want to search for more than one accession number, for example, separate numbers with a semicolon (;) or the pipe character (|). For example, `12345|67890` or `09876;54321`.

If the search strings themselves contain semicolons, pipe characters, or backslashes, as in `Ward 4; Rm.6` or `Ward 1\Rm.2`, use the following notation: `Ward 4\; Rm.6;Ward 1\\Rm.2` or `Ward 4\; Rm.6|Ward 1\\Rm.2`

-Or-

Click the list button next to an input field.

Select an item.

Study Labels

If you are using labels to organize your studies, you can use these flags to search for data in the **Study Browser**.

Open the list of available labels and select one or several labels.

-Or-

Type the label that you are looking for, or define a combined search.

`Label_A Label_B` - this string searches for all studies with **either** Label_A **or** Label_B.

`Label_A +Label_B` - this string searches for all studies that are marked with **both** Label_A **and** Label_B.

`Label_A -Label_B` - this string searches for all studies that are marked with Label_A **but not** with Label_B.

Note that in the **Study Browser** you can not only search for labels but also assign labels to studies. Use **Study Labels** from the context menu of the study list to assign labels. Proceed in the same way as when you assign labels while reading images. See *Assign and Manage Labels*, page 101.

Study States

Click the **Study States** button and select study states in the **Select State** dialog box.

Note that searching by study state **Interpretation Status** makes sense only if the modalities that send the data to the Visage 7 server set this flag. In Visage 7 you cannot set or edit the interpretation status of a study.

If study states have been defined in your search, the ***Study States*** button label is shown italic and the **Reset** button next to it is available. Click this **Reset** button if you want to reset only study states but none of the other search criteria.

Starting and resetting a search

Use these buttons to start a database search or to reset search criteria.

Click **Query** to start a database search.

Remember that the system queries only the server whose tab card is currently shown in the foreground.

Click **Reset** to return to the default query preset (see *Defining a preset*, page 19). If no default query preset has been defined, **Reset** removes all search criteria.

Query presets

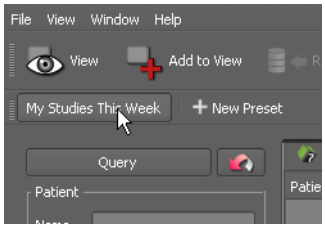
If you frequently use the same combinations of search criteria, you can save them in a preset. Your presets are listed directly above the query section. Any presets that you define are available for your own user account only. You cannot make presets public.

Tip

A preset stores both search criteria and the arrangement of the study list and the preview section.

Quick search with a preset

1. Click a preset button to retrieve its search criteria.



2. Depending on how you defined the preset, you might have to click **Query** to start the search.

Defining a preset

1. In the query section of the **Study Browser**, select and type search criteria.
2. Click **New Preset**.

3. In the **Preset** dialog box, enter a name for your new preset.
4. Select **Default** if you want to make this preset the default query preset.

   See also *Starting and resetting a search*, page 18.
5. Check **Auto Query** if you want the system to reenter your search criteria **and** then run the search immediately. You do not have to click **Query** again.

   -Or-

   Check **Default** plus **Auto Query** to have the system run this search every time you call up the Visage 7 software.
6. Save the preset.

A new preset button appears above the query section.

Tip

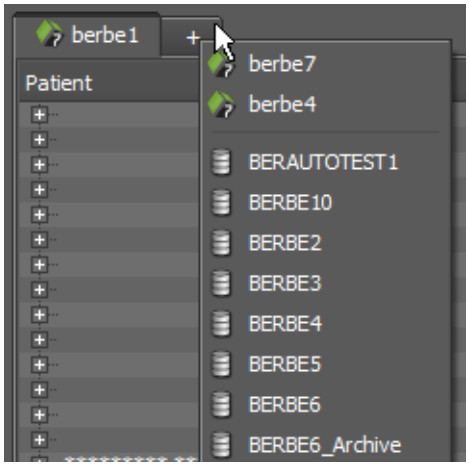
Right-click presets that you have defined earlier. A context menu appears which helps you to manage presets. For example, you can remove preset buttons that you no longer need.

Study list

The study list may comprise one or several tab cards. These tab cards represent Visage 7 servers, connected DICOM network nodes, or external drives.

The leftmost tab card is your Visage 7 server, which is also referred to as the primary server.

1. Click the **+** tab to show a list of available servers, nodes and drives.



Servers with the Visage 7 logo are partner systems. You can load data from partner systems in just the same way as from the primary server. List items without Visage 7 logo are connected DICOM network nodes or external drives. You need to retrieve data from these nodes or drives before you can load the data.

2. Select a server, network node, or drive to add this tab card.

Information in the study list

The study list is arranged in a hierarchical tree view. Use the **+/-** buttons in front of the entries to expand or collapse this list.

For a better overview, you can sort the list by clicking a column header. Clicking a second time reverses the search order.

If a study in the study list appears dimmed, the Visage 7 server has not or not yet received all images and the study is considered incomplete. Whether you can nevertheless load incomplete studies depends on your system configuration.

Patient	The name of the patient.
Date of Birth	The date of birth of the patient.
Issuer	The institution that issued the patient ID.

Patient ID	Patient's identification number.
Accession Number	Job number of the study in the HIS/RIS (hospital or radiology information system).
Modality	Modality or modalities where the patient was examined.
Images	Number of images in a study or series.
3D	This column shows a bullet when a series is a 3D series, which means that it contains at least one continuous 3D volume.
	A green bullet indicates that a volume dataset is available on the primary server or on a partner server.
	A yellow bullet indicates that the system is currently creating a volume dataset from the original slice images.
Study/Series Description	Study or series description.
Study/Series Date	Date and time when the study or series was performed. The format is YYYY-MMM-DD and HH:MM:SS (24 hour clock).
Institution Name	Name of the institution or department where the study was performed.
Insertion Date	Date and time when the study or series was sent to this database. The format is YYYY-MMM-DD and HH:MM:SS (24 hour clock).
Interpretation	This column indicates whether a report exists for a study and shows the report status (new, in progress, draft, preliminary, or final).

Preview section

When you select a series or volume dataset on the primary server (leftmost tab card), a preview image is shown below the study list.

The preview image is the first image of a series, or the central slice of a volume dataset. If you select multiple series, one preview image is shown for each of these series.

Windowing preview images

For a better overview, you can window preview images.

1. Click a preview image.
2. Hold the mouse button down.
3. Drag the mouse up or down or right or left to change brightness or contrast.

Resizing the preview section

You can change the size of the preview section and the study list.

Drag the split bar that separates these screen areas up or down.

You cannot resize individual preview images.

Loading data from the study list

Choose one of the following methods to load data from the study list.

Loading with double-click

To load a single study, series, or volume dataset, double-click it in the study list.

However, be aware that when you double-click a study for which session information exists, the system loads the session and not the original images. See also *Session management*, page 23.

Loading more than one study, series, or dataset into one tab card

1. Select the studies, series, or volume datasets that you want to load.

   Use the **Shift** key or the **Ctrl** (Windows) or **Cmd** (Mac) key for multiselection.

2. Click the **View** button or select **View** from the context menu.

   -Or-

   Use **Add to View** if you do not want to replace the currently loaded data but load additional data.

Tip

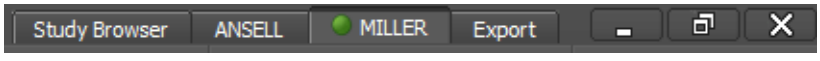
Right-click a patient name and select **Find All Studies For This Patient** as a quick way to find and load prior studies of a patient.

Loading studies into separate tab cards

If you are currently reading images and are interrupted by a request for your opinion on a different case, you can load this new study in a separate tab card.

1. Select the new case in the study list and click the **View In New Tab** button or select **View In New Tab** from the context menu.

   In the title bar, a new tab card appears. The tab of the active tab card is highlighted with a bullet.



2. Use these tabs to switch between cases.

Loading studies into a separate Visage 7 Client

1. Right-click a study in the study list and select **Load in separate window**.

   A new Visage 7 Client opens containing only this case and the **Export** window. A colored bar below the title bar reminds you that this is not the case you worked on originally.

2. Return to your original case with **Alt + Tab** (Windows) or **Cmd + Tab** (Mac), this leaves the second case open.

   -Or-

   Close the new case with the **Close Window** button in the colored bar.

Special loading options

Instead of having the system select a protocol best suited for the selected data, you can preselect data display options when loading the data. You can choose to show all series of a study side by side or, for time series, to show all phases side by side.

1. Select the study you want to load.
2. Right-click and select **View All Series Side-By-Side** or **View All Phases Side-By-Side**.

Viewing reports

If a preliminary or final report exists for a study, you can preview it in **Study Browser**.

Right-click a study for which a preliminary or final report exists and select **View Reports** from the context menu.

Loading data for quality assurance

If your user rights permit you to perform quality assurance tasks, you can load data directly from the study list onto the **Quality Assurance** platform.

1. Select one or several studies, series, or volume datasets.
2. Right-click and select **Quality Assurance** from the context menu.

Session management

Visage 7 supports session management. Session management means that you can save image processing and evaluation results when you have to interrupt your work. When you return later, you can load the session again and resume your work or present your results to colleagues.

Note

Session management requires that your user account is assigned to an appropriate user level. Talk to your system administrator to find out about your user level settings.

Saving a session

Use **File > Save Session** or **File > Save Session As** to save a session. For one study you can save more than one session if you want to document stages or discuss different aspects.

AutoLogoff session

If the system logs you off automatically after an extended period of no user interaction, it saves any changes in an **AutoLogoff** session.

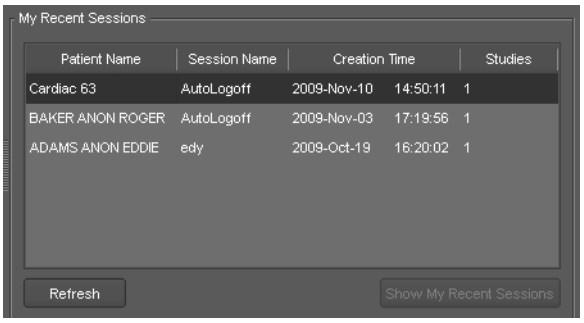
Tip

Open the **AutoLogoff** session immediately after you have logged on again and decide whether to save it in a user-created session. When the system logs you off automatically a second time, a new **AutoLogoff** session is created, which overwrites the previous one.

Session list

If session management has been enabled for your user account, the lower right corner of the **Study Browser** displays a session list.

When no study is selected in the study list, all your recent sessions are shown in the session list.



When a study is selected in the study list, the session list displays only sessions of this particular study. An **AutoLogoff** session is shown in red and in the topmost position of this list.

Loading a session

Double-click a session in the session list.

-Or-

Double-click a study in the study list.

Depending on the configuration of this feature, a double-click either loads the most recent session or starts a new session. See *Properties dialog box*, page 178.

Ignoring session information

You might choose to ignore session information explicitly when you load a study.

1. In the study list of the **Study Browser,** select the study.
2. Then double-click **<New Session>** in the session management box.

The system loads the original data as they were sent from the modality and ignores any intermediate evaluation results.

Sharing sessions

Sessions are usually available only for the user account that created the session. However, you can choose to share sessions with colleagues.

When you save a session, indicate whether you want to make this session available for all users or only for your own user account. Sessions that you made available for all users are marked with the word **(shared)** in the session management box.

You can send shared sessions as session links to colleagues.

1. Select a session in the session management box.
2. Select **File > Email Session Link**.

When your colleagues receive such emails, all they need to do is to double-click the attached link. Visage 7 loads the session, provided, of course, Visage 7 is installed on your colleagues' computers.

More information about sessions

A session saves the following information and image processing results:

- How many and which datasets were loaded at the time the session was saved
- Protocol and display settings
- Key views and snapshots with or without annotations and measurements
- Segmentation results, such as 3D ROIs or vessel segmentation results

- Structures and contours
- Cardiac analysis results

Session information is temporary data. Sessions are stored on the Visage 7 server for as long as the studies they refer to are stored on the server. When a study is deleted from the database, session information is lost. Deletion of study data can be triggered manually or automatically, that is when the hard disk is full. Automatic deletion of study data affects the oldest studies on the server.

To avoid losing sessions that you want to preserve over a longer time, delete-protect these studies. See *Delete-protecting studies*, page 29.

Data management

Aside from the daily tasks of searching and loading study data, you also use the **Study Browser** for less frequent data management tasks.

Importing and exporting studies (external media)

You use these functions when you receive image data on a patient CD or DVD or when you want to create a patient medium.

Note

You need appropriate user rights to be able to import and export studies.

Importing a study from CD, DVD, or USB stick

1. Insert a patient CD, DVD, or connect a USB stick.
2. Select **File > Import DICOM Directory**.
3. Select the drive and browse to the folder or subfolder that contains the data.
4. Click **Choose**. Do **not** select a file.

   In the study list of the **Study Browser**, a new tab card appears.
5. On this new tab card, select the study or studies that you want to import.
6. Click **Import**.

   The **Import DICOM Data** dialog box opens. In this dialog box you can modify certain attributes of the data to be imported.

   For example, if you are importing a study from another institution, you might have to update the patient ID so that it matches the ID used in your own practice. Identical patient IDs is a prerequisite for Visage 7 to identify the imported study as a prior study for a patient who already exists in your system.
7. Select **Create new UIDs** and modify the **Patient ID**, for example.

8. Also select **Don't archive data** (for Visage 7 installations with archive option) if you want to import the data only temporarily and plan to delete it again later.
9. Select **Prevent autorouting** to ensure that your data is not forwarded to other servers, independent of the autorouting rules that are configured in your system.
10. Click **Import Data**.

Tip

If your forgot to select the **Don’t archive data** option during data import, you can select this flag later in the study list. Right-click a study that has not yet been archived and select **Don’t archive data**. Be aware that you cannot reset this flag.

Exporting studies

1. In the Visage 7 database, select the study or studies that you want to export.
2. Right-click and select **Media Export**.
3. Select a **Destination**.

   CD Producer Station - select this option to create a CD or DVD on a CD/DVD producer station that is connected to the Visage 7 server. Also select the storage capacity of your medium.

   Burn Patient CD/DVD - select this option to create a CD or DVD on a CD/DVD writer on your local computer. Also select the storage capacity of your medium.

   Export files to local client folder - select this option to download data onto your local computer or onto a USB stick at your local computer. Also select the drive and folder to where you want to export the data.
4. Select **Include Media Viewer**.

   This allows the recipient of the CD, DVD, or USB stick to read the study data directly from this medium. No other software is required.
5. Click **Export**.

Exporting includes sending the images and creating a DICOM directory. Depending on the data volume that you are exporting, this process might take a while.

Retrieving and sending studies (DICOM network)

You use these functions if you want to fetch a study from a connected DICOM network node or send a study to another DICOM node.

Note

You need appropriate user rights to be able to retrieve and send studies.

Retrieving a study from a DICOM node

You need to retrieve studies from a connected DICOM node before you can load the data. You do not need to retrieve data from partner systems. Partner systems are servers whose tab cards are marked with a Visage 7 logo.

1. Select the tab card of a connected DICOM node.
2. Define search criteria in the query section and click **Query**.

3. In the study list, select the study that you want to retrieve.
4. Click **Retrieve**.

5. Return to the leftmost tab card. That is the tab card of the Visage 7 server.
6. Search for the study that you just retrieved.

Sending data across the network

You can send data either from the primary server, that is your own Visage 7 server, or from partner systems. The tab cards of partner systems are marked with a Visage 7 logo. You cannot send data directly from connected DICOM nodes or external media. If you want to send data from such a node or medium, retrieve the data first.

1. Select the study that you want to send in the study list of the Visage 7 server.
2. Right-click and select **DICOM Send** and select the server or servers that you want to send the data to.

   -Or-

   Select **DICOM Quick Send** to send the selected data off to preconfigured destinations immediately.

Attaching files to studies

You can attach reports, scanned documents, or notes from the referring physician, or other files to a case.

Note

Only pdf files and image files can be imported and attached to a study.

1. In the study list, right-click a study and select **Add Attachment**.
2. In the **Add Attachments To Study** dialog box, click **Browse** and select one or several files in your file system.

   The files will be attached to the study as a new series. The program suggestion for the series number (4000) ensures that the attached series will be added to the end of the study.
3. Modify series information, if necessary.

4. Select **Don't archive data** and **Prevent autorouting** to prevent the attachments from being archived or sent to other network nodes for archiving.

   These settings will affect only attachments and not the study as such.

5. Click **Import**.

Tip

In a **View** window, the attached files will appear as additional thumbnails in the thumbnail section. Here you can double-click an attachment and show the data in a separate window.

Managing access rights to data

When you import a study from an external medium, the study is automatically assigned to your own user account and the user group **Standard**. Change the study assignment to user or user group to make the data available for other users as well.

Note

You need appropriate user rights to be able to grant access rights to individual users or entire user groups.

1. On the primary server (leftmost tab), select one or several studies.
2. Right-click and select **Assign study to groups** or **Assign study to users.**
3. In the **Study Assignment** dialog box, select the user groups or users who will have access to these studies.

Note

In the **Study Assignment** dialog box, you can also revoke access rights to study data. Do not revoke access rights to a study for your own user account or for a user group that you are a member of. If you do, you no longer have access to this study either. You cannot restore your own access rights to study data after you have closed the dialog box. As soon as the study list is updated, the study is no longer listed. You or your user group can only be granted access rights to this study again by another user with appropriate user rights, or by the system administrator.

Delete-protecting studies

Users with advanced user rights can delete studies that are not delete-protected from the Visage 7 server in the **Quality Assurance** window. Manual deletion of studies might become necessary when patient data have been corrected and duplicates of a study exist on the server. Automatic deletion of old data that has already been archived can be configured by the system administrator to free disk space.

When a study is deleted from the server either automatically or manually, session information is irretrievably lost. Therefore, you might want to delete-protect cases whose sessions contain information that you want to preserve over an extended period of time. For example, you might want to save cases that you have marked with labels and that you want to keep for research purposes.

1. Select the study that you want to delete-protect.
2. Right-click and select **Delete Protection**.

Note

You need appropriate user rights to be able to delete-protect studies.

Managing teaching and meeting files

Visage 7 provides mechanisms for creating anonymized teaching and meeting files and for marking studies for presentation or other purposes.

Tip

If you use labels to collect cases for teaching or research purposes, you will probably want to keep these cases in your database for some time. Therefore, consider delete-protecting such cases to avoid that labels and session information being lost when the data is moved to the archive and deleted from the server.

Study labels

You use study labels to mark studies for various purposes.

Three types of study labels exist:

- Public labels for marking teaching files

  You use these labels to mark anonymized cases that you want to discuss with your students. Students who open the Visage 7 Client will see only those studies that have been marked with a teaching file label.

  Teaching file labels start with a configurable prefix, for example, the word `teach`. If `teach` is the configured label prefix, `teach_class2` or `teaching-course2` are considered teaching file labels. However, a public label with the name `class1` or `course2-teaching` would not be identified as a teaching file label but as a public label for other purposes.

- Public labels for other purposes

  You use a label of this type, for example, to mark studies that you want to discuss with your colleagues in your department's weekly meeting.

- Private labels

  Private labels are only visible in your own user account. You use labels of this type, for example, to collect cases for research purposes or simply to find a study again quickly.

Creating and assigning study labels

1. In the study list, right-click a study and select **Study Labels**.
2. Type the new label name.

   Visage 7 now offers you two versions of the new label, *new label (private)* and *new label (public)*.
3. Select the check box in front of the public or private version and click **Apply**.

   Visage 7 creates the new label and assigns the selected study to it.
4. Assign a second label to the study, if required.

Deleting a study label

1. In the study list, right-click a study and select **Study Labels**.
2. Start typing the name of the label that you want to delete.
3. In the list, right-click the study label and select **Delete**.

When you delete a study label you remove the marker from all studies that it had been assigned to. You do not delete the studies.

Creating anonymized teaching files

You can anonymize a study and assign the anonymized copy to a predefined teaching file label in one step.

1. In the study list, right-click a study and select **De-identification and Teaching Files**.

   In the de-identification dialog box, the **De-identify** check box is selected. Do not clear this box.

   Moreover, the system suggests that you replace the patient name with the word *De-identified* and patient ID, study ID, and accession number with random codes. The date of birth is replaced by January 1st of the patient's actual year of birth.
2. Change this random data, and add a study description and study comment, if you want.
3. Select the following options for anonymization:

   Remove other demographic tags and **Remove private tags**: Aside from the data shown in this dialog box, other information might be stored in the DICOM data of this study that also helps to identify the patient. Selecting these two options removes all DICOM tags that might contain information about the patient.

   Don't archive and **Prevent autorouting**: Selecting these options prevents the anonymized study from being archived or sent to another network node for archiving.

4. Select a teaching label for the anonymized copy.

   You can only select predefined teaching labels here. You cannot create a new teaching file label in this dialog box.

5. Click **Apply**.

   When copying is complete, the anonymized study does not appear in the study list immediately.

6. Check your query settings and click **Query** to update the study list.

Tip

Do not forget to delete-protect the anonymized study, particularly if you selected the options that prevent archiving and autorouting. See *When a study is deleted from the server either automatically or manually, session information is irretrievably lost. Therefore, you might want to delete-protect cases whose sessions contain information that you want to preserve over an extended period of time. For example, you might want to save cases that you have marked with labels and that you want to keep for research purposes.* page 29.

Anonymizing cases for other purposes

If you want to create an anonymized copy of a study in order to present it at a conference or to include it in a research project, you proceed in two steps.

Creating an anonymized copy of a case

1. In the study list, right-click a study and select **De-identification and Teaching Files**.
2. Proceed as described in *Creating and assigning study labels*, page 31. However, do not assign a teaching file label.

Marking the anonymized case with a private label

1. In the study list, search for the anonymized case.
2. Right-click the anonymized case and select **Study Label**.
3. Assign a public or private label as described in *Creating and assigning study labels*, page 30.

Patient Search

Patient Search is targeted at referring physicians. Here, referring physicians can search for patients and open reports and images of patients whom they have referred. The list of patients and studies in this window is populated from the RIS (radiology information system) and depends on your access rights that have been defined by your RIS administrator.

Patient Search is subdivided into two sections:

- *Query section*
- *Results list*

Query section

In the query section you can configure your search of accessible studies by selecting one or several of the following criteria.

First Name, Last Name
The patient's last name and first name.

Date of Birth
The patient's date of birth.

The date of birth box allows free text entry in most date formats. For example, for June 3rd, 2009, the system accepts any of the following date entries: 03062009, 3.6.2009, 3.JUN 2009, 3/6/2009, 3/JUN/2009.

The default date format is defined by the property settings of the user interface (date widget, date local settings). For example, the default for the region Germany, Austria, Switzerland, Australia and UK is DD.MM.YYYY.

Patient ID
The patient's identification number.

Location
Name of the location where the study was performed.

Accession Number
Job number of the study in the RIS (radiology information system).

Study Date
Date when the study was performed.

From ... To
Here you can specify a search period. Enter dates in the format YYYY-MMM-DD, or click the button to the right of a date box and select a date in the calendar.

Today, Yesterday, 1 Week, 2 Weeks
Use the buttons **Today**, **Yesterday**, **1 Week**, **2 Weeks** as a quick way to specify frequently searched periods in the correct format.

Modality

Select the check boxes of all modalities whose studies you want to search:

CT (computed tomography), **MR** (magnetic resonance tomography), **PT** (positron emission tomography, PET), **US** (ultrasound), **CR** (computed radiography), **DX** (digital radiography), **MG** (Mammography), **XA** (X-ray angiography).

-Or-

Type the abbreviation of the modality in the text box.

-Or-

Select **All** to search for all studies irrespective of the modality where they were performed.

Only My Patients

Only Patients from my Practice

All Patients

Depending on your access rights in the RIS, you can to search for and open studies of only your own patients, only patients from your practice, or all patients.

If you have access rights to all patients, you have to provide the exact **Patient ID**, **Date of Birth** or **Accession Number** for identification

Only Signed Reports

Limits your search to reports that are finalized, that is signed.

Click this button to start the search.

Results list

In the search results list, you find images and reports for patients that you referred for radiologic examination.

Viewing images

You can open images directly from the results list, where they are shown with the patient name, date of study, examination type, and modality.

Double-click the image symbol to open the images.

Opening reports

When reports are available, a report button is shown next to the images in the results list.

Double-click this button to open the report from the RIS (radiology information system).

-Or-

Double-click this button to open a signed report.

Tip

In the report window, you can view and print reports.

View windows

Once you have loaded images, these are shown in one or several **View** windows which appear as tab cards in the title bar. Tab cards show the name of the patient whose data they contain. The active tab card is highlighted with a bullet.

Use tab cards to switch between cases.

Depending on your selection of data, a **View** window is shown with a specific screen layout. This screen layout is defined in a protocol.

The system preselects a different protocol for data of different modalities and anatomical regions, and depending on the monitor configuration and the number of loaded series. If you prefer a different screen layout, you can select a different protocol, show a different arrangement of viewers, or show and hide toolbars and tool cards.

Find out more about these options and the tools available for reading images in the following sections:

- *Protocols*
- *Viewers and viewer layouts*
- *Tools*
- *Tool cards*

For more information about how to perform complex tasks that combine various tools and tool cards, refer to this section:

- *Complex tools and applications*

Protocols

Protocols define the screen layout and the display parameters for the loaded images.

Protocol assignment

When a user loads one or several studies, series, or volume datasets, the system automatically selects a suitable protocol for the data. The system uses the following matching criteria to make this selection.

- Monitor configuration

  Different protocols exist for different combinations of monitors and for different screen resolutions.

- Study and series criteria

  Protocol matching criteria usually include the modality or a combination of modalities that acquired the data.

  For example, a CT series might be shown with a different screen layout than an MR series or a combination of CT and PET series. Other study and series criteria include the study description, the part of the body, or whether current and prior studies are displayed.

- Protocol availability and protocol ranking

  Protocols might have been defined in such a way that they are available for individual users or individual user levels only. Moreover, users can assign priority ratings to protocols. A protocol with a high priority rating is more likely to be automatically selected than a protocol with a low priority rating.

Protocol definition

Your system comes with a number of predefined protocols. Users with advanced user rights can adapt these protocols and their matching criteria or create protocols of their own.

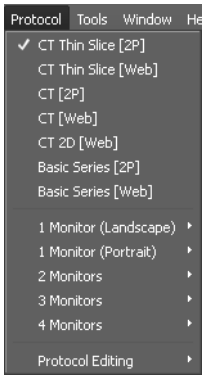
See *Properties and protocols*, page 178.

A protocol typically defines the following layout and display aspects:

- The number and arrangement of image segments (viewers)
- The initial rendering parameters for each viewer
- The linking of viewers for synchronized navigation in multiple viewers
- The availability and location of toolbars
- The availability and location of tool cards

Selecting a different protocol

1. Drop down the protocol menu and select a different protocol.



   Further up in the **Protocol** menu, you find alternative system suggestions for the current dataset. Further down in the list, you find all protocols that exist in your system. These protocols are grouped by monitor configuration and by modality or modalities.

2. Select one of these protocols to change the screen layout.

Viewers and viewer layouts

After you have loaded one or several studies, series, or volume datasets, Visage 7 displays the images in one or several viewers.

Use the following controls and the various tools from the toolbars to optimize and read image data. See also *Tools*, page 48.

Use the mouse if you want to rearrange datasets in viewers: Click any of the four corners of a viewer where the image text is shown. Drag the thumbnail that represents the data in this viewer to another viewer.

Layouts toolbar

With the buttons of this toolbar you can switch between various viewer layouts that are suitable for the loaded data. These layouts have been defined in the active protocol. Different protocols offer different sets of layouts.

You can rearrange the **Layouts** toolbar for frequently used protocols.

1. Drag a layout along the toolbar to show it in a more prominent place.

   -Or-

   Right-click a layout and select **Make default** from the context menu to show this layout right after loading a study.

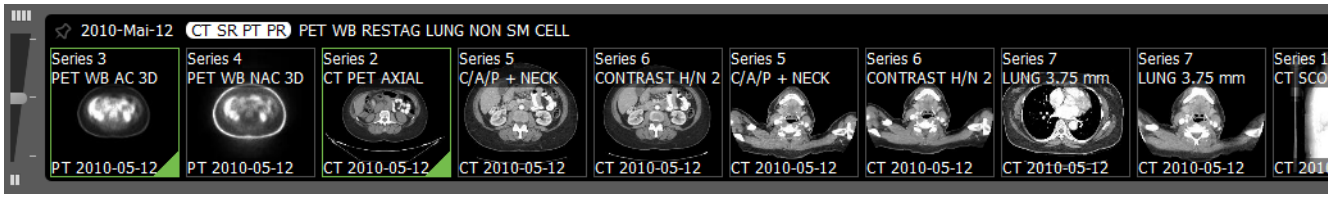
2. Select **Save Layout Preferences** to save these changes for your user account.

Tip

Double-click a viewer in any of the available layouts to show this viewer fullscreen. Double-click again to return to the original layout.

Thumbnail section

At the bottom of the screen the thumbnail section might be shown. If the thumbnail section is currently not shown, click the small arrow that points up at the bottom of the screen.



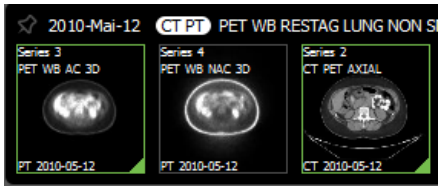
Initially, the thumbnail section shows the study (or studies) that you have loaded into the **View** window as well as any prior studies that were identified by the system as potentially relevant for a case.

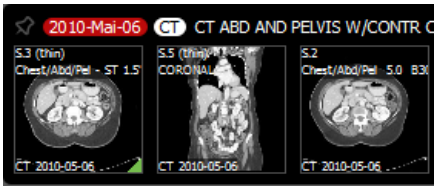
A green border around a thumbnail indicates that this image set is currently shown in the active viewer. Click a thumbnail with a green border to highlights the active viewer briefly.

A green triangle in the lower right corner of a thumbnail indicates that this image set is shown in one of the other viewers on the screen.

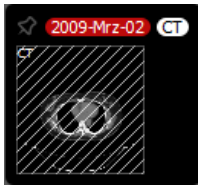
A gray triangle in the lower right corner of a thumbnail indicates that this image set had been displayed in a viewer at some time during the current session but has been unloaded in the meantime.

Studies whose study dates are shown with a black background are current studies. Studies, whose study dates are shown with a red background are prior studies.





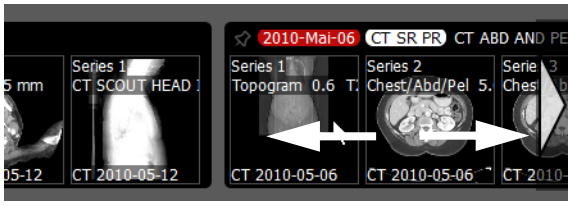
A thumbnail with background hatching represents a prior study that has not been loaded or expanded yet.



Scrolling in the thumbnail section

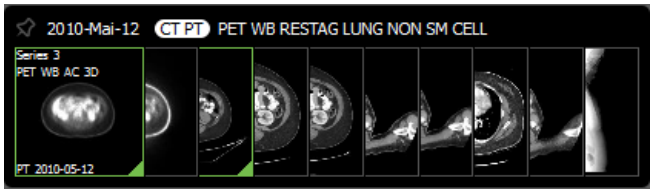
If more studies or image sets have been loaded than can be shown in the thumbnail section at a time, a white triangle is shown at the right edge of the thumbnail section. This triangle indicates that there are more thumbnails further to the right.

Drag any of the shown thumbnails to the left to scroll in the thumbnail section.

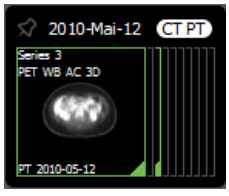


Collapsing or expanding studies

1. Click a study date to collapse the study.



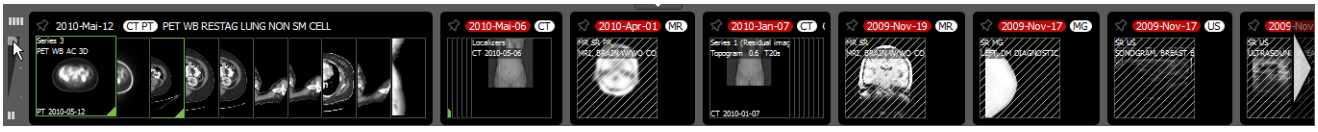
2. Click the study date a second time to collapse the study even further.



3. Click the study date a third time to expand the study again.

Showing all studies of a patient

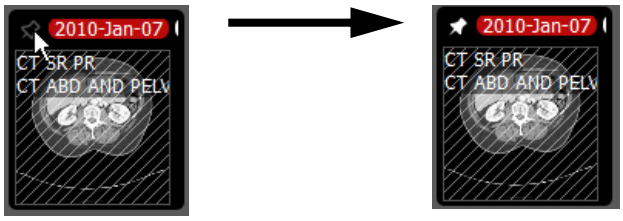
Move the slider to the left of the thumbnail section all the way up to show all studies that exist for this patient on the Visage 7 server.



Selecting more prior studies

If you find more prior studies that you consider relevant for your case, select them.

Click the pin symbol in front of the study date to select a study.



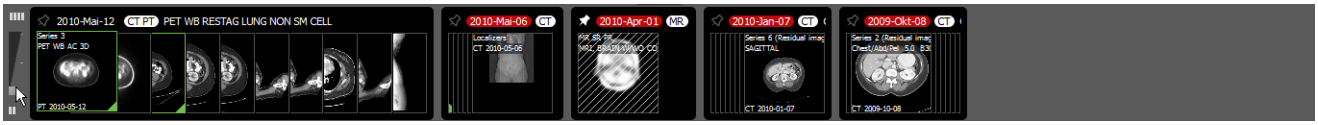
Controlling display of prior studies

If a large number of studies exist for a patient on the Visage 7 server, use the slider to the left of the thumbnail section for a better overview.

Slider position bottom: shows only loaded studies and studies you selected with a pin symbol.

Slider position center: shows all the above studies plus studies preselected as relevant prior studies by the system as a result of auto-prior loading settings.

Slider position top: shows all studies of this patient on the Visage 7 server.



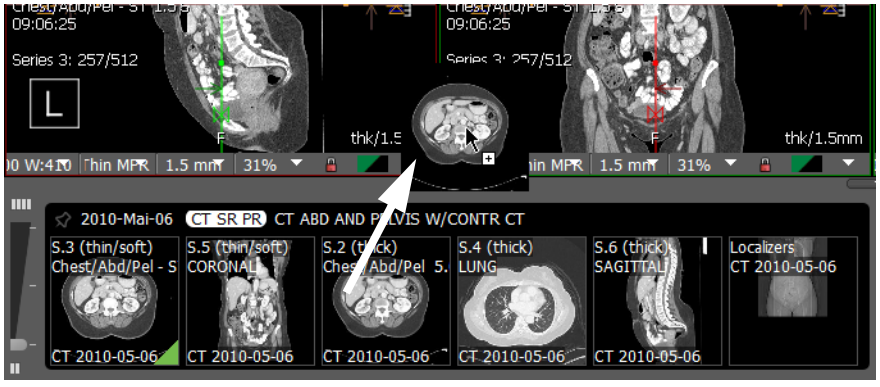
Popup viewer

Double-click a thumbnail to show this image set in a separate floating window.

For example, you can use this window to show a scout image, which can remain open while you read images in the various viewers.

Loading image sets

Drag a thumbnail from the thumbnail section into a viewer to load this image set.



You cannot load entire studies this way.

Note

Not all image sets can be displayed in all viewers. For example, an MPR viewer or a 3D viewer accepts only 3D volumes, but no 2D images. If you cannot show 2D images in a viewer, select a different layout and try again.

Unloading image sets

Click any of the four corners of a viewer and drag the thumbnail back to the thumbnail section to clear a viewer.

-Or-

Right-click and drag the thumbnail back to the thumbnail section to remove only the overlay dataset from the viewer but not the primary dataset.

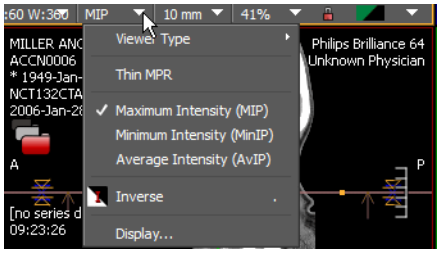
Viewer controls

Below each viewer, a bar with controls can be shown. These controls are within easy reach of each viewer and help to optimize image display. For example, you can use the viewer controls to change the zoom factor or window level for your images.

From the viewer controls, you can select which type of image you want to display in a viewer. The viewer controls bar offers different display options for different image types. For example, if you are currently showing thick slices, you can change the compositing mode here. See also *Compositing modes for thick slices*, page 45.

1. From the viewer context menu or tool palette, select **Viewer Controls** to show this bar.

2. Click the arrow button next to a control to drop down a list of options.



-Or-

Click to select window level, slice thickness, or zoom factor and overwrite these settings.

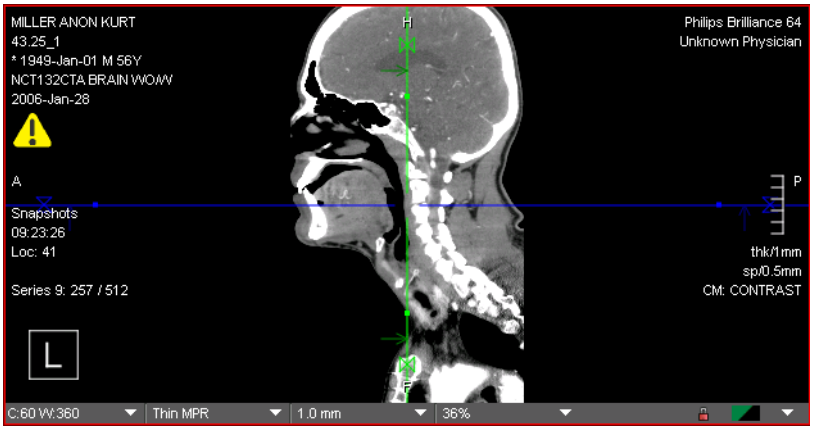
Navigation and display options for volume datasets

These options are available only if you have loaded volume datasets. This means that these options are available in MPR viewers or 3D viewers but not in 2D viewers.

Crosshair navigation in MPR viewers

In MPR viewers, scoutline crosshairs indicate the orientation and position of the slices that are currently shown in other MPR viewers.

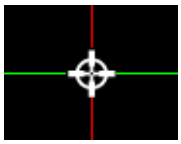
- A blue line represents the image in the MPR segment with the blue viewer frame.
- A green line represents the image in the MPR segment with the green viewer frame.
- A red line represents the image in the MPR segment with the red viewer frame.



Note

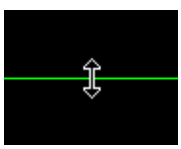
The scoutline crosshair is shown only in viewers that show orthogonal views of the same volume dataset. Crosshair lines are not shown in viewers that display 2D data, or in isolated MPR viewers.

Small arrows that point to the crosshair indicate the viewing direction in the other two MPR viewers.

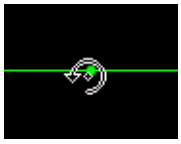


When you move the cursor over the center of the crosshair, the cursor changes its shape. Use the crosshair center to drag the entire crosshair. This moves two view planes simultaneously and shows new slice images in the other two MPR viewers.

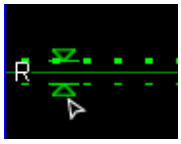
The move cursor is not available for partial crosshair display.



When you move the cursor over a crosshair line, the cursor changes its shape. Drag this line up or down to move through the volume along one of the other two standard axes. Dragging a crosshair line updates one of the other two MPR viewers.



When you move the cursor over the rotation handles (small dots), the cursor changes its shape. Drag the cursor up or down to rotate the crosshair. Crosshair rotation updates the two other MPR viewers and generates images with nonstandard views.



When you click one of the small triangles on the crosshair lines along the edges of the image the crosshair lines appear dotted.

You can now change the slice thickness in the MPR viewers by dragging the handles up or down. When you release the mouse button, the slice thickness indicator and the selected thick slice compositing mode in the viewer controls are updated.

Compositing modes for thick slices

The default slice thickness for reconstructed images in MPR viewers is specified in the active protocol. The default slice thickness is usually the slice thickness of the original scans.

You can change the slice thickness for your loaded images and then choose a different compositing mode for thick slices from the viewer controls.

- Thin MPR

  In this mode, slices are shown in their original slice thickness.

- Maximum intensity (MIP)

  In this mode, data values are computed as the maximum of the values of the original slices.

- Minimum intensity (MinIP)

  In this mode, data values are computed as the minimum of the values of the original slices.

- Average intensity (AvIP)

  In this mode, data values are computed as the average of the values of the original slices.

-Or-

Use this tool or keyboard shortcut **T** to switch from display of thin slices to display of thick slices and vice versa.

Use this tool or keyboard shortcut **Shift + T** to toggle compositing modes (MIP, MiniIP, AVIP).

Display options in 3D viewers

The 3D viewer displays a 2D projection of a volume. In this viewer, you can choose between several volume rendering techniques and volume display modes.

- 3D MIP (maximum intensity projection)

  Visage 7 calculates the maximum of all the voxel values that lie on the virtual viewing ray behind this pixel. 3D MIP requires a grayscale color map.

- VRT (volume rendering technique, also called emission-absorption model)

This technique maps data values to colors and transparencies defined in a 3D color map. The voxels are interpreted as small diffuse light sources that emit and absorb light in the direction of the viewer. Each voxel is interpreted as a local diffuse light source, without additional shading.

- VRT (diffuse)

  This rendering technique is similar to VRT. However, an additional virtual light source and a diffuse lighting model adds shades to the surfaces of the volume. For example, curved surfaces become darker toward the edges, which results in a more natural appearance.

- VRT (specular)

  In addition to diffuse shading, specular shading uses a lighting model that reflects light dependent on the angle between the incoming and reflected light. This means that on smooth surfaces users see highlights, and that shading becomes even more expressive than with diffuse shading. Specular shading is especially good for large surfaces with fine detail.

- Perspective projection

  This projection mode gives a more natural impression. Perspective projection corresponds with the everyday experience of perspective distortion. Objects that are far away appear smaller than objects close by.

  If perspective projection is not selected, orthographic projection is active. Orthographic viewing is like viewing an object through a lens with a very long focal distance, a telelens. The viewing rays are almost parallel to each other and no perspective distortion occurs. In orthographic mode, you can perform measurements in the image plane, for example distance measurements and angle measurements. With perspective projection turned on, measurements are not possible.

  The **Perspective Projection** toggle is available only from the 3D viewer context menu (**Properties > Perspective Projection**) but not from the viewer controls.

- Smart sampling

  This option reduces artifacts in the volume display.

  The **Smart Sampling** toggle is available only from the 3D viewer context menu (**Properties > Smart Sampling**) but not from the viewer controls.

Image text and warning symbols

Aside from image information, viewers contain information about the loaded data in the form of image text and symbols.

Warning symbols

These symbols alert you to the fact that an image is shown with reduced image quality or that warnings exist concerning the displayed images.

Low resolution warning

A red bullet in the lower right corner of a viewer indicates reduced image quality. The low-resolution warning appears while the dataset is still being loaded and the system generates full image quality. The low-resolution warning also appears if a low streaming compression level is selected.

See *Best Image Quality*, page 101, for information on how to load individual images in best image quality but with slower download time.

Image synchronization in progress

A yellow bullet indicates that the image has not yet been updated with your latest image processing step. The previous image is still displayed while image processing is performed in the background. When image processing is complete, the yellow bullet disappears.

Miscellaneous warnings

A yellow warning triangle in the upper left corner of the images indicates that warnings exist for this dataset.

Note

Do not use images that show a red or yellow bullet for primary diagnosis.

Find out more about warnings by clicking the yellow warning triangle if you see it in your viewers.

Scale

In calibrated image types, for example, CT images, a scale can be shown on the right edge of the viewers. The scale looks like a small ruler and indicates centimeters. When you zoom in on an image the scale switches to millimeters.

Showing or hiding image text

If the image text is in your way during image processing, you can hide it.

Use **View > Show in Viewer** to hide or redisplay image information.

-Or-

Use tools from the tool palette to show or hide image information. See *Tools for switching image text and graphics on and off*, page 103.

Tip

When you are working with a small window size and low screen resolution, it is not always possible to show image texts and symbols correctly. Texts are truncated, and symbols, the scale, or a color bar might be shown on top of each other. Maximize the program window and then switch to fullscreen mode for display of all image information.

Showing image text larger or smaller

Position the cursor over image text, hold the **Ctrl** key down, and rotate the mouse wheel to show the image text in all viewers larger or smaller.

Tools

A number of buttons are shown along the edges of your screen after you have loaded data. These buttons represent tools with which you can start functions or select options with a single mouse click. The tools are grouped in toolbars. Which toolbars are shown when you first load data, the position of toolbars, and the assignment of tools to toolbars depends on the selected protocol.

Arrangement of toolbars

Select **View > Show Toolbars** to show more toolbars or to hide toolbars.

-Or-

1. Click the toolbar handle to the left or above a toolbar.
2. Drag the toolbar across the screen and drop it wherever you prefer it to be shown.

When you drag a toolbar to the left, right, or bottom edge of the screen, a new toolbar section appears there. When you drag a toolbar anywhere else on the screen, it turns into a floating window.

If you are working with more than one monitor, use **View > Show Toolbars > Synchronize with other monitors** to synchronize your arrangement of toolbars on all monitors.

Tool palette and viewer context menu

A selection of the most frequently used toolbar buttons is also available from right within a viewer.

1. Right-click a viewer to show the tool palette, viewer context menu, or both.

   In your user profile, you can define whether tool palette, viewer context menu, or both are shown. See *Configure Tool Palette dialog box*, page 177.

2. Click the **Show Context Menu** button on the tool palette to show this menu if it is not displayed when you right-click a viewer.

Keyboard shortcuts

Some of the functions and options that are represented by toolbar buttons can also be selected with keyboard shortcuts. These keyboard shortcuts are active even if a toolbar or button is currently not displayed on the screen.

A number of keyboard shortcuts have been predefined for your system. These shortcuts are indicated in brackets after the tool name in this document.

Tip

Select **Help > Keyboard Shortcuts** in the main menu to show the list of factory-default shortcuts. From this dialog box, you can copy the shortcuts list and print it out with another software program.

On your keyboard, press **Ctrl + A** (Windows) or **Cmd + A** (Mac) to select all shortcuts and then **Ctrl/Cmd + C** (copy).

Open your word-processing program.

Paste the shortcuts list (**Ctrl/Cmd + V**) and then print it (**Ctrl/Cmd + P**).

Note

Users with appropriate user rights can change the assignment of keyboard shortcuts for their own user account or for other users as well. See *Configure Keyboard Shortcuts dialog box*, page 175.

Therefore, the keyboard shortcuts indicated in this document might no longer be correct for your system.

Basic navigation and image display tools

This set of tools is available in almost all protocols. Typically, these tools are part of the **Standard Tools** toolbar.

Default Navigation

This tool is assigned to the function that is most frequently used in the context of an image type and viewer type.

1. Click the **Default Navigation** button to select this tool.
2. Use the left mouse button to perform the function that is assigned to the default navigation tool.

Default Navigation tool assignment is defined in the active protocol. Therefore, the meaning of this tool varies, depending on the active protocol and the viewer type.

Tip

Even if a different tool is selected, you can return to the default navigation tool temporarily. Press and hold the **Ctrl** key on a Windows system, or press and hold the **Cmd** key on a Mac.

Default navigation is active for as long as you hold the **Ctrl** key or **Cmd** key down. When you release the key, you return to the tool that is currently selected.

Zoom

With this tool, you can enlarge or reduce images interactively.

1. Click the **Zoom** button to select this tool.
2. Click a viewer and hold the mouse button down.
3. Drag the cursor up to zoom in.

-Or-

Drag the cursor down to zoom out.

Tip

Use the middle mouse button (or wheel button) to zoom images without selecting the **Zoom** button on the toolbar first.

-Or-

Use the percentage box in the viewer controls to change the image display size.

Pan

With this tool, you can move an image within a viewer.

1. Click the **Pan** button to select this tool.
2. Drag the mouse across a viewer to move the image within the viewer.

You typically use this tool after you have zoomed an image and relevant image information has moved out of the viewer.

Tip

Use the right mouse button to pan images without selecting the **Pan** button on the toolbar first.

Inverse (.)

This tool inverts the image in the active viewer. Inversion means that light areas are displayed dark and dark areas are displayed light.

Inversion is not possible for the 3D viewer.

Tip

The factory-defined keyboard shortcut for the inversion tool is the period key.

Edge enhancement

Use this tool to optimize image quality and to increase contrast between structures in slice images.

1. Click the **Edge Enhancement** button to select this tool.
2. Drag the mouse up or down to adjust image sharpness.

   -Or-

   Use the edge enhancement slider on the **Display** tool card to adjust image sharpness.

Tip

The edge enhancement filter is particularly useful for improving the sharpness or definition of XA images.

Window level tools

With this set of tools, you can change contrast and brightness in images.

Window Level

With this tool, you can change the contrast and brightness in images interactively.

1. Click the **Window Level** button to select this tool.

   -Or-

   Use the left **and** right mouse button to window images without selecting the **Window Level** button on the toolbar first.

2. Click a viewer and hold the mouse button or mouse buttons down.
3. Drag left or right to change the window width (contrast).

   -Or-

   Drag up or down to change the window center (brightness).

Histogram

While the **Window Level** tool is active, a histogram of grayscale values or HU values is shown in the lower left corner of the viewer. In the histogram, a small white bar shows window settings graphically. The bar moves when you move the window center and expands or shrinks when you change the window width.

If the histogram is in your way, you can hide it. See *Toggle Histogram*, page 104.

Windowing in fusion mode

When you window an image in fusion mode, this affects the window level of the primary dataset. To window the image of the overlay dataset, press and hold the **Shift** key while you window the image.

Auto Window Level in ROI

With this tool, you can optimize contrast and brightness in images by focusing on a specific region of interest.

1. Click the **Auto Window Level in ROI** button to select this tool.
2. Click and draw an ellipse around your region of interest.

When you release the mouse button, the system identifies the minimum and maximum pixel intensities in this ROI. The system then applies these window levels to all images in this viewer and in all linked viewers.

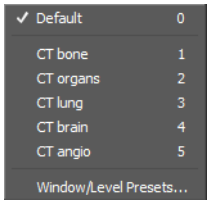
Tip

This tool is particularly useful with image data that is not calibrated. For example, use **Auto Window Level in ROI** in MR images in which the local receive coil sensitivity varies considerably and with it the voxel intensity.

Show Window Level Presets

Use this tool to show a list of all window level presets that exist for an image type.

1. Click the **Show Window Level Presets** button to open a menu.



2. Select a window level preset from the list.

   -Or-

   Select **Window/Level Presets** to define new window level presets. See *Configure Window/Level Presets dialog box*, page 174.

Save Current W/L as Presentation State

Use this tool to save window level adjustments permanently.

Clicking this tool saves window level adjustments in a DICOM presentation state. In **Study Browser**, the presentation state appears as a new series with modality PR. The next time you load this study, images will be displayed with the saved window levels automatically.

Tools for adjusting the display size

In addition to interactive zooming (see *Zoom*, page 49), Visage 7 offers several other tools for optimizing image display size quickly.

Fit Width/Height, Fit Width, Fit Height

Fit Width/Height fits images optimally in their viewers. **Fit Width** makes optimum use of the viewer width, and **Fit Height** makes optimum use of the viewer height.

If an MPR viewer is active when you click one of these buttons, the images in the active viewer and in all linked viewers are resized. If the 3D viewer is currently active, only the volume display is resized, other viewers are not affected.

Zoom 100%

This tool shows images in their original size. This means that one pixel from the image file corresponds to exactly one pixel on the monitor.

If an MPR viewer is active when you click this button, the images in the active viewer and in all linked viewers are resized. If the 3D viewer is currently active, only the volume display is resized, other viewers are not affected.

Tip

Clicking the **Zoom 100%** tool has the same effect as selecting zoom level 100% (**1:1**) from the viewer controls.

Magnifying Glass

Use this tool to be able to see details without having to zoom the entire image.

1. Click the **Magnifying Glass** button to select this tool.
2. Click an image and hold the mouse button down.

   A rectangular area appears, which is magnified by a configurable factor (typically factor 2).
3. Drag to move the rectangle across the image.

   This movement gives you the impression of holding a magnifying glass in your hand.
4. Rotate the mouse wheel while you still hold the left mouse button down to increase or decrease the zoom factor of the magnifying glass.
5. Release the mouse button to turn the magnifying glass off.

   The tool is still selected and you can click again in another viewer and use the magnifying glass there.
6. Click the tool on the toolbar a second time.

   Only now is the **Magnifying Glass** tool turned off again.

Tip

Choose multiple **Magnifying Glasses** rather than a single **Magnifying Glass** whenever you want to inspect and compare magnified sections in more than one viewer. See also *Magnifying Glasses*, page 99.

Tools for rotating and flipping images

With the tools in this section you can rotate or flip images.

Be sure to show the orientation cube or orientation labels in the viewers before you use these tools. Select **View > Show in Viewer > Orientation Cube**, or **View > Show in Viewer > Orientation Labels** to show these orientation aids.

Rotate Clockwise, Rotate Counterclockwise

These tools rotate the image in the active viewer by 90° clockwise or counterclockwise.

Rotation affects only the viewer in which you clicked. Images in linked viewers are not affected.

Flip Horizontally, Flip Vertically

These tools rotate the image in the active viewer around its vertical or horizontal axis. Rotation affects only the viewer in which you clicked. Images in linked viewers are not affected.

Note that you cannot flip the volume in the 3D viewer.

Rotate in Plane

Use this tool to rotate an image with the mouse.

1. Click the **Rotate in Plane** button to select this tool.
2. Click an image and hold the mouse button down.
3. Drag to rotate the image.

Rotation affects only the viewer in which you drag. Images in linked viewers are not affected.

Tip

Use this tool, for example, to straighten up images that were acquired tilted.

Save Flip/Rotate as Presentation State

Use this tool to save flipped or rotated images permanently.

Clicking this tool saves flipped or rotated images in a DICOM presentation state. In **Study Browser**, the presentation state appears as a new series with modality PR. The next time you load this study, affected images will be displayed flipped or rotated automatically.

Tools for scrolling in image stacks

The tools in this section help you to scroll through the images in image stacks.

Browse Slices

With this tool, you can use the left mouse button or the mouse wheel to move through an image stack in a 2D viewer or MPR viewer.

1. Click the **Browse Slices** button to select this tool.
2. Drag up or down or use the mouse wheel to scroll forward or backward through the image stack.

   When you drag quickly, **Browse Slices** skips slices so that you reach your destination as quickly as possible. If you use the mouse wheel for scrolling, whether or not slices will be skipped depends on whether the tool **Skip Slices While Scrolling** is also selected. See also *Skip Slices While Scrolling*, page 57.

Note

When scrolling in an MPR viewer in thick-slice mode, you can define the scrolling increment, that is the overlap between thick slices, with the property **Tools, Slice Browsing, Overlap of Thick Slices**. Refer to section *Properties dialog box*, page 178, to learn how to change properties for your user profile.

Overlap 0 means that each click of the mouse wheel scrolls the distance of the slice thickness of a thick slice. With overlap 1, scrolling is very smooth because one click of the mouse wheel scrolls the distance of an original thin slice. Any value in between 0 and 1 defines an overlap. For example, 0.2 means that when you scroll to the next thick slice, this slice overlaps approximately 20% with the previous slice.

Tip

When you browse slices in MPR viewers, scrolling up with the mouse wheel, arrow keys, or by dragging with the left mouse button scrolls deeper into the respective viewer. By contrast, scrolling down scrolls further out.

Referring to standard orientations, this means that scrolling down results in the following browsing behavior.

- In axial slices and view **F** (feet), you move toward the patient's feet.
- In coronal slices and view **A** (anterior), you move toward the patient's front.
- In sagittal slices and view **L** (left), you move toward the left side of the patient.

Skip Slices While Scrolling

This tool affects the behavior of the arrow keys and the mouse wheel when you use the tool *Browse Slices*.

If the **Skip Slices While Scrolling** tool is selected, scrolling quickly with the mouse wheel or arrow keys results in slices being skipped. Canceling the selection of this tool ensures that you will not skip images when browsing slices with the mouse wheel or arrow keys. Scrolling might become slower if the tool is turned off.

Note

Skip Slices While Scrolling is selected by default.

You need to clear it explicitly if you want to see every single image in an image stack when you browse slices.

-Or-

Use the tool *Browse Continuously* instead of the tool *Browse Slices* when scrolling through an image stack to be sure you see all slices.

Browse Continuously

This tool is an alternative to *Browse Slices*. **Browse Continuously** has a cine-like effect with a steady browsing speed. This tool shows all the images in an image stack, it does not skip slices even if you move the mouse fast.

1. Click the **Browse Continuously** button to select this tool.
2. Start dragging up or down to start scrolling forward or backward through the image stack.

After an initial mouse movement you no longer need to move the mouse. Hold the mouse steady and the left mouse button down. Scrolling continues at a steady speed showing one image in the image stack after the other until you reach the last image in the stack.

Note

When you scroll in an MPR viewer in thick-slice mode, you can control the slice overlap for scrolling with properties settings. See *Browse Slices*, page 56, and *Properties dialog box*, page 178.

Scroll Page by Page (Mouse Wheel Mode)

Some protocols, typically those for ultrasound and plain-film images, present images as so-called tiles rather than in image stacks. Tiled presentation arranges images next to each other, and scrolling causes all viewers in this presentation mode to be updated synchronously.

Two modes exist for scrolling in tiled presentation mode:

- The **Scroll Page by Page** tool is selected.

  Use **Browse Slices** or scroll with the mouse wheel to replace the contents of all viewers with the next page of new images.

- The **Scroll Page by Page** tool is not selected.

  Browse Slices or the mouse wheel causes each viewer to advance by just one image at a time. This gives you the impression of images flowing through your viewers, for example, from the lower right to the upper left.

First Slice (Home), Previous Slice (↑), Next Slice (↓), Last Slice (End)

Use these tools to scroll slices in viewers that show image stacks of either scans or reformats.

Tip

The factory-defined keyboard shortcuts for browsing to the previous or next slice are the up and down arrow keys.

Previous Thick Slice (PgUp), Next Thick Slice (PgDn)

If you have switched to thick-slice display in a volume dataset, use these tools to browse slices.

Play/Pause

With this tool, you can play back images in a stack or time series, or you can rotate around a volume in a 3D viewer. The tool gives you the impression of a movie being played back.

Use the **Cine** tool card to define playback parameters such as playback type, playback range, frame rate and playback speed. See *Cine*, page 113, for details.

Tip

While the movie is being played back, the toolbar button changes its shape. Use the **Pause** button to interrupt or stop the playback.

Synchronized display of pre- and post-stress cardiac echo

If you have loaded appropriate data, Visage 7 synchronizes cine display in two or more viewers based on ECG information embedded in the images.

A typical application for synchronized cine display is a comparison of cardiac ultrasound (cardiac echo) sequences before and after physical exercise (pre- and post-stress). After stress, the heart rate is higher. To allow comparison of the pre-stress and post-stress sequence, the system slows down playback of the post-stress sequence (or speeds up playback of the pre-stress sequence). As a result, images of corresponding heart phases are shown side by side at any time during playback.

Synchronization of cine display based on ECG data is defined in the active protocol.

Show Multiframes in Single Tiles

With this tool, you can switch display of multiframe images:

- Collapsed

  The multiframe objects are shown in single viewers as an image stack.

  Use the tools **Next Frame (Ctrl/Cmd ↑), Previous Frame (Ctrl/Cmd ↓), First Frame (Ctrl/Cmd Home), Last Frame (Ctrl/Cmd End)** to scroll through the image stack of a collapsed multiframe.

  -Or-

  Click a viewer and drag up or down or hold the **Ctrl/Cmd** key down while you turn the mouse wheel to scroll frame by frame.

  -Or-

  Click a viewer and simply turn the mouse wheel (**Ctrl/Cmd** key **not** held down) to scroll on to the next multiframe object.

- Expanded

  Each of the individual images of a multiframe object occupies a separate viewer.

Tools for browsing datasets

The tools in this section help you to browse datasets without having to return to the **Study Browser**.

Choose which of these tools you use or combine tools according to your preferred mode of working.

- Select and load multiple datasets in the **Study Browser**.

  Use the following tools to scroll through the loaded data: *Previous Study, Next Study*, *Previous Volume (Ctrl/Cmd ←), Next Volume (Ctrl/Cmd →)*, *Previous Image Set, Next Image Set*, *Previous Phase (←), Next Phase (→)*.

- Filter and sort the list in the **Study Browser** so that it shows the studies you want to read next. Load the first of these studies.

  Use the following tools to move on to the next study: *Previous Study from Study Browser, Next Study from Study Browser*.

Previous Study, Next Study

These tools expect you to have loaded more than one study.

Use **Previous Study/Next Study** to scroll through the loaded studies.

Previous Volume (Ctrl/Cmd ←), Next Volume (Ctrl/Cmd →)

These tools expect you to have loaded more than one volume dataset.

Use **Previous Volume/Next Volume** to scroll through the loaded datasets.

Previous Image Set, Next Image Set

These tools expect you to have loaded more than one image set.

Use **Previous Image Set/Next Image Set** to scroll through the loaded series.

Previous Phase (←), Next Phase (→)

If you have loaded a time series, use **Previous Phase/Next Phase** to scroll through the phase images.

Previous Study from Study Browser, Next Study from Study Browser

Use these tools to load the study right above or below the one currently selected in the **Study Browser**.

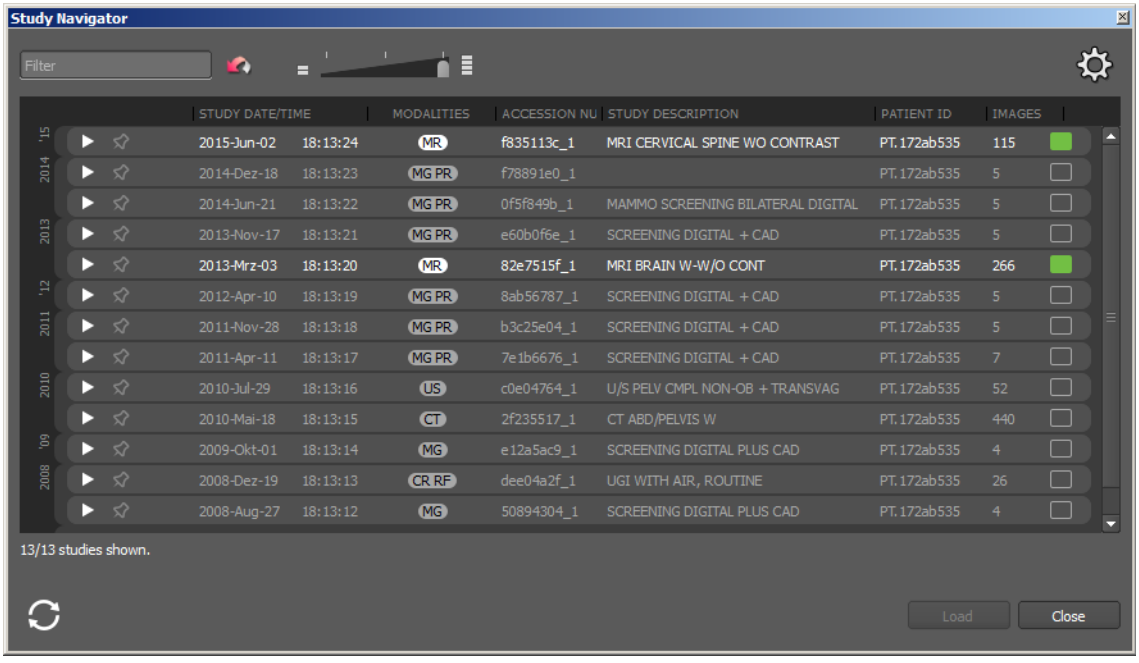
Workflow integration tools

Visage 7 can be integrated in a variety of clinical workflow programs, such as radiology information systems (RIS), hospital information systems (HIS), or picture archiving and communications systems (PACS). The level of workflow integration depends on the particular setup and configuration of systems in your organization. Therefore, some functions described here might not be available in your installation or might be configured to behave slightly differently than described here.

Study Navigator

This tool opens the **Study Navigator** dialog box, from where you can select and load more studies of the current patient. The tool appears gray if the current study is the only study that is stored on the Visage 7 server for the current patient.

When you open the **Study Navigator** for the first time, all studies that are stored on the server for the current patient are shown.

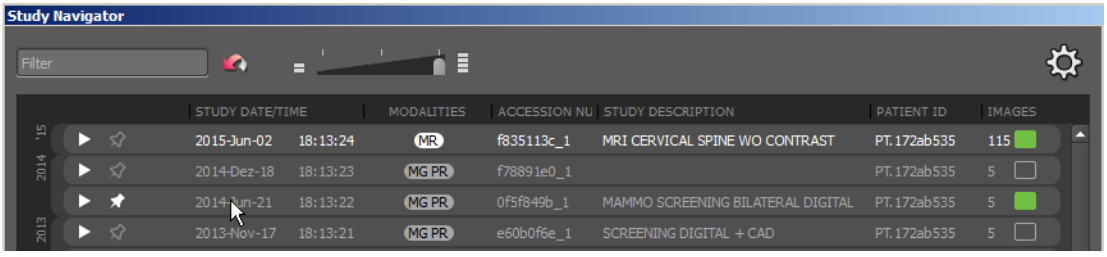


The studies that have already been loaded are marked with a green box along the right edge of the dialog box. Prior studies that are potentially relevant for a case are shown in standard display. Any other studies are slightly grayed out.

Selecting more relevant prior studies

You might consider more prior studies relevant for the case than the ones suggested by the system.

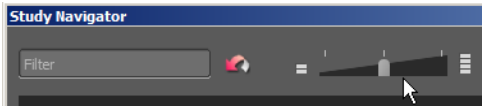
Double-click such a prior study.



The study is now marked with a white pin symbol.

Controlling display of prior studies

If a large number of studies exist for a patient on the Visage 7 server, use the slider for a better overview.



Slider position left: shows only loaded studies and studies you selected with a pin symbol.

Slider position center: shows all the above studies plus studies preselected as relevant prior studies by the system as a result of auto-prior loading settings.

Slider position right: shows all studies of this patient on the Visage 7 server.

Filtering the study list

Type a search string in the **Filter** box.

The study list is updated showing loaded studies, studies you marked with the pin symbol, and studies whose study description or study date/time fields contain this string.

Loading studies from Study Navigator

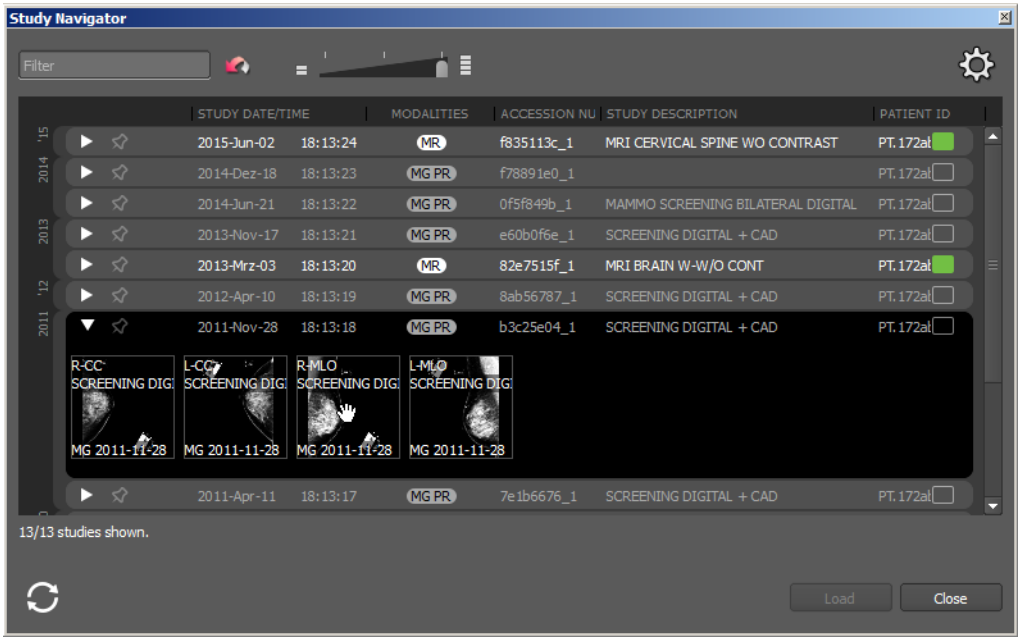
1. Select the box all the way to the right of a study.

   The box turns green.

2. Click **Load**.

Loading individual image sets

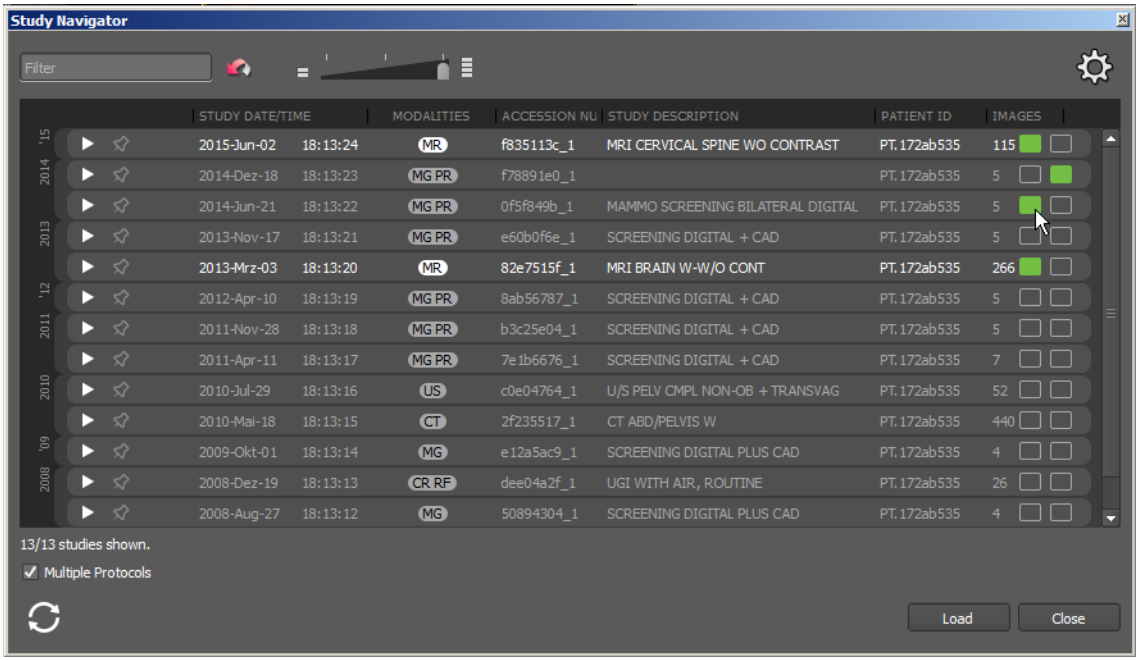
1. Click a study to show thumbnails of the images, series, and volume datasets it contains.
2. Drag a thumbnail from the **Study Navigator** into a viewer.



Multiple Protocols

If you are using more than one monitor for reading images with Visage 7 Client, you can define which study or studies you want to show on which monitor.

1. Select the check box **Multiple Protocols**.
2. Select a monitor column for each study.

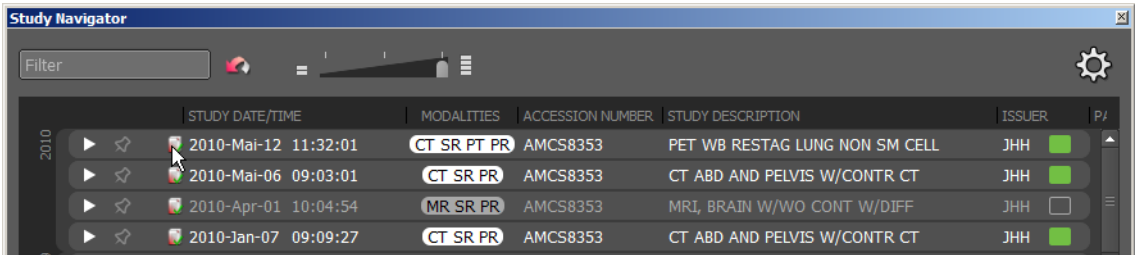


3. Click **Load**.

Viewing a report

If a report exists for a study, a report icon is shown which also indicates the report status.

Click a report icon to show a preliminary or final report.



Close Session

This tool unloads all data from a **View** window. The tool also closes all viewers, toolbars, and tool cards and leaves the **View** window entirely blank.

Switch to the **Study Browser** to select and load new data after you have clicked **Close Session**.

Start/Stop Dictation

Use this tool to start or end dictating a report.

1. Click **Start/Stop Dictation** after you have loaded a study.

   If you have loaded more than one current study, the system will ask you which study the report refers to.
2. Start dictating your report.
3. Click the button again when you have finished the report.

   This marks this study as reported on (dictation status completed).

Depending on your system configuration, ending dictation might load the next case automatically.

Reset Dictation

You cannot create a second report for a study for which a report has already been dictated.

If you want to delete a report and create a new one instead, use this tool to reset the dictation status of the currently loaded study. **Start/Stop Dictation** is available again and you can dictate a new report now.

Go To Next Study

If you have selected more than one study for report dictation in your radiology worklist, use this tool to move on to the next study.

If the **Start/Stop Dictation** tool is still turned on when you click **Go To Next Study**, you are prompted to confirm that the first report is finished.

Skip to Next Study

If your worklist supports skipping, use this button to mark the current study as *to be skipped* in the worklist. You proceed to the next study or item in the worklist.

Reports and Scanned Documents

Click this button to open the reports window of your RIS.

Show Worklist

Click this button to open the worklist window of your RIS (radiology information system), HIS (hospital information system), or PACS (picture archiving and communications system).

Referrer Information

Click this button to open the referrer details window of your RIS (radiology information system), HIS (hospital information system), or PACS (picture archiving and communications system).

Tools for linking viewers

In Visage 7, many image navigation and image processing tasks can be synchronized across viewers, which helps to compare images. For example, synchronized scrolling means that when you scroll an image stack in a viewer, image stacks in linked viewers scroll too. For example, synchronized zooming means that not only the image in the active viewer is enlarged but all images in all linked viewers are.

Viewer linking is defined in the active protocol. After loading image data, the protocol decides which viewers are linked and with respect to which activities. Viewer linking can be modified interactively. You use the tools described in this section to redefine how activities are synchronized across viewers.

When you close a study or load new data, modifications to viewer linking are discarded. To preserve your modifications, save your session or save the protocol. See also *Session management*, page 23, and *Properties and protocols*, page 178.

Toggle Linking

Use this tool to turn viewer linking on or off. **Toggle Linking** affects all viewers that are assigned to any of the linking groups that are defined in the protocol.

Link Current Position

Use this tool to align two 3D datasets based on a common reference point, which are shown in side-by-side MPR viewers. The tool requires that appropriate linking groups are defined in the active protocol.

1. Scroll to corresponding images in viewers that are currently not linked.

   This means, cancel the selection of the tools **Toggle Linking** or **Link Current Position** first.

2. Select the tool **Position Crosshair** and click to position the crosshair in the same reference point in both datasets.

   -Or-

   Press and hold the **Alt** key, and click to position the crosshair.

   Use a landmark that can be identified easily, such as the bifurcation of the trachea or a large calcification.

3. Select **Link Current Position**.

The viewers are now linked for synchronized scrolling. Visage 7 calculates a true 3D registration for the two datasets using the 3D position of the reference point and the orientation of your MPR viewers. You can now scroll in any direction or rotate MPR planes and the two datasets remain linked.

Reset Viewer Linking

Use this tool to reset any dataset alignment made with the **Link Current Position** tool.

Automatically Link Viewers

Use this tool to link scrolling in all corresponding 2D viewers in basic CT or MR protocols. Visage 7 will try to link all currently displayed image stacks that show the same part of the body and that use the same spatial orientation.

For example, select **Automatically Link Viewers** in a layout that shows five axial stacks and three sagittal stacks. Visage 7 links all axial stacks that show the same part of the body, and also all sagittal stacks that show the same part of the body. This creates two linking groups for synchronized scrolling.

Automatically Link Viewers reads DICOM information to identify corresponding images.

Automatic Viewer Registration

Use this tool to link scrolling in viewers that show corresponding images.

Caution

Be aware that automatic registration does not always align images correctly. Please verify registration results and correct registration manually, if necessary.

Technically speaking, **Automatic Viewer Registration** compares grayscale values of pixels to identify corresponding structures and to align images. Therefore, **Automatic Viewer Registration** can even link viewers that show images from a current study and one or several prior studies.

Link Display Properties

Use this tool to synchronize changes to certain display properties such as modification of the slice thickness to all linked viewers.

Link Scrolling

Use this tool as a shortcut to **Edit Viewer Linking** (see below). **Link Scrolling** synchronizes various activities across viewers.

Clicking this tool has a different effect on different viewer types.

Only two viewers shown

Select the **Link Scrolling** tool.

Scrolling, panning, rotating, flipping images and, for MPR groups, also zooming and 3D rotation is now synchronized.

More than two viewers: 2D viewers

1. Select the **Link Scrolling** tool.
2. Select all viewers that show series with a similar orientation and that you want to include in synchronized scrolling.

   Selected viewers are highlighted with a red border.
3. Click **Accept and Exit** in the lower right corner of the last selected viewer.

In a layout with more than two viewers that show 2D images, for example, X-ray images, scrolling, panning, rotating, and flipping images is now synchronized.

More than two viewers: MPR groups

An MPR group is a set of three MPR viewers that show MPR reformats from a 3D dataset side by side, initially in axial, sagittal, and coronal orientation. These three MPR viewers are linked automatically, that is by the protocol.

With the **Link Scrolling** tool you can link several such MPR groups, for example one in a current examination and one in a prior examination. Linking MPR groups in this way will synchronize the following activities in the current and prior examination: scrolling, panning, rotating, flipping, zooming, and 3D rotation.

1. Select the **Link Scrolling** tool.
2. Click an MPR viewer in one MPR group.

   This viewer and the other two MPR viewers in the group are highlighted with a red border.
3. Click an MPR viewer in a second MPR group.

   All six MPR viewers are highlighted now.
4. Click **Accept and Exit** in the lower right corner of the last selected viewer.

-Or-

1. Position the crosshair on the same reference point in both datasets.
2. Select the **Link Scrolling** tool.
3. Click an MPR viewer in one MPR group.

   This viewer and the other two MPR viewers in the group are highlighted with a red border.
4. Click an MPR viewer in a second MPR group.

   All six MPR viewers are highlighted now.

5. Click **Accept with Current Position and Exit** in the lower right corner of the last selected viewer.

Visage 7 calculates 3D registration for the two datasets using the 3D position of the reference point rather than DICOM frame of reference information stored in the datasets.

Linking individual MPR viewers or MIP viewers

In viewers that show individual MPR or MIP slices, **Link Scrolling** synchronizes scrolling but no other activities.

1. Select the **Link Scrolling** tool.
2. Select all viewers in which you want to synchronize scrolling.

   Selected viewers are highlighted with a red border.
3. Click **Accept and Exit** in the lower right corner of the last selected viewer.

Unlinking viewers

1. Select the **Link Scrolling** tool a second time.
2. Click a viewer.

   All viewers that you linked with the **Link Scrolling** tool earlier are now highlighted with a red border.
3. Click linked viewers to remove the red border and to remove them from the linking group.
4. Click **Accept and Exit** in the lower right corner of the last viewer that you remove from the linking group.

Edit Viewer Linking

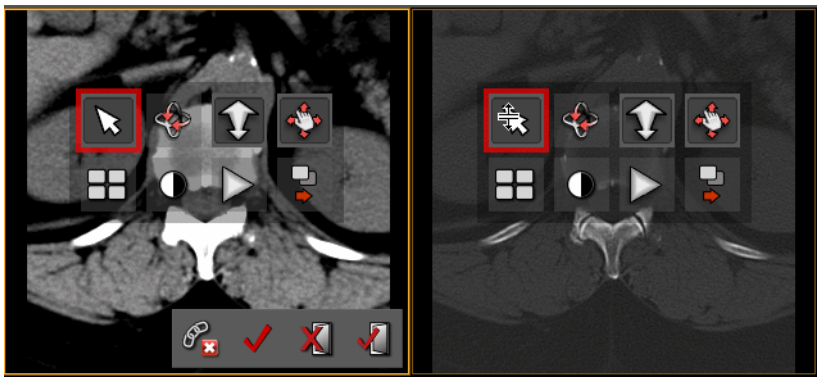
With this tool, you can edit the assignment of viewers to linking groups for synchronized image navigation and image processing.

Editing viewer linking

1. Click the **Edit Viewer Linking** button to select this tool.

   In this mode, graphical buttons appear in all viewers. These buttons represent types of activities that can be synchronized across viewers.
2. Point to one of these buttons in a viewer.

   The button is highlighted in this viewer and all other viewers that belong to a group in which this activity is synchronized.



3. Click this button in more viewers to add them to this group.

   All viewers that belong to this group are now highlighted with a red border.

4. Click a second activity button to synchronize this activity across the viewers of this group, too.

5. Click **Apply** to confirm linking group definition.

   Continue and define more groups now.

   -Or-

   Click **Delete All Viewer Groups** to reset viewer linking and start defining groups again from scratch.

   -Or-

   Click **Accept and Exit** to end linking group definition.

The group concept

The idea of viewer linking is to synchronize certain activities in multiple viewers. Synchronized activities help you to compare images and to optimize image display across linked viewers with a minimum of mouse clicks.

Several linking groups can coexist. For example, if you have loaded CT or MR series and have a screen layout with eight viewers, two groups might exist. Group 1 might comprise the upper left two viewers and group 2 might combine the lower right two viewers.

In group 1, only scrolling is synchronized. This means that when you scroll the image stack in the upper left viewer, images also scroll in the viewer next to it. When you zoom the image in the upper left viewer, only this image is enlarged but the image in the viewer next to it is not.

In group 2, zooming and panning is synchronized but scrolling is not. When you zoom in on the image in the lower right viewer, the image in the viewer next to it is also enlarged. However, when you start scrolling in one of these lower right image stacks, only the active viewer is affected.

However, viewers can only belong to one linking group of a specific type.

Activities that can be linked

The following activities can be linked across viewers.

Cursor Position/Navigation Synchronization

Linking viewers with this button synchronizes **scrolling** in these viewers.

3D Rotation Synchronization

Linking viewers with this button synchronizes **3D rotation** in these viewers.

Zoom Synchronization

Linking viewers with this button synchronizes **zooming** in these viewers.

Pan/Rotate Synchronization

Linking viewers with this button synchronizes the following activities: **rotation clockwise** and **counterclockwise, flipping horizontally** and **vertically**, and **panning**

Tiled Navigation

Linking viewers with this button creates a group of viewers for tiled image display. See also *Scroll Page by Page (Mouse Wheel Mode)*, page 58.

Window/Level Synchronization

Linking viewers with this button synchronizes **windowing** in these viewers.

Time Synchronization

Linking viewers with this button synchronizes playback of time series and browsing in time series.

Dataset Synchronization

Linking viewers with this button synchronizes **loading of data** in these viewers, for example, from the thumbnail section.

Detaching viewers from groups temporarily

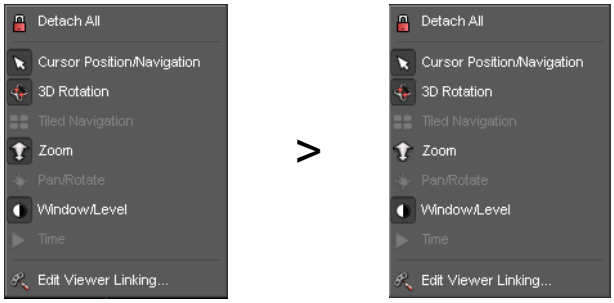
If viewers are linked but you want to apply a particular processing step to one viewer only, you can detach this viewer from its group.

1. Click the lock in the viewer controls.

2. Click the lock again later on to reattach the viewer to its linking groups.

-Or-

1. Right-click the lock and cancel the selection for an activity to detach the viewer from this group.



Right-click the lock again and reattach the viewer to its group later.

Group Editing tools

Use these tools instead of the *Edit Viewer Linking* tool as a quick way of linking viewers with respect to one activity only.

In most protocols you find these tools on a separate toolbar, which is called **Viewer Linking (Group Editing)**.

Quick linking of viewers

1. Select one of these tools, for example, **Modify Window Level Group**.

2. Click all viewers in which you want to synchronize windowing.

   Selected viewers are highlighted with a red border.

3. Click **Accept and Exit** in the lower right corner of the last viewer to confirm.

Overview of group editing tools

The following tools are available for quick and easy group definition:

Modify Translation Navigation Group

Assign viewers to a translation navigation group for **synchronized scrolling**. Datasets in a translation navigation group share the same reference point.

Modify Rotation Navigation Group

Assign viewers to a rotation navigation group for **synchronized 3D rotation**.

Datasets in a rotation navigation group share the same reference point and orientation.

Modify Zoom Group

Assign viewers to a rotation navigation group for **synchronized zooming**.

Synchronized zooming shows structures of the same size in the same size in all linked viewers. This does not necessarily mean that the zoom factor in all linked viewers is identical when you zoom in or out.

Modify Pan/Rotate Group

Assign viewers to a pan/rotate group for **synchronization of** the following activities: **rotation clockwise** and **counterclockwise, flipping horizontally** and **vertically**, and **panning**.

Modify Tile Group

Assign viewers to a group for tiled image display. See also *Scroll Page by Page (Mouse Wheel Mode)*, page 58.

Modify Window Level Group

Assign viewers to a window level group for **synchronized windowing**.

Modify Time Phase Group

Assign viewers to a time phase group for synchronized playback of time series and synchronized browsing in time series.

Modify Dataset Group

Assign viewers to a dataset group to ensure that several viewers show the same dataset. For example, if you load data in one viewer from the thumbnail section, all viewers in a dataset group are updated.

Annotation and measurement tools

With this set of tools you can annotate and evaluate image information

Note

In the 3D viewer, measurements are only possible in orthographic but not in perspective projection. See also *Perspective projection*, page 46.

Every time you add an annotation to an image or perform a measurement, the program creates a snapshot and sends it to the **Export** window. From there you can insert these snapshots in your report.

If annotations or ROI statistics make it hard to read image information that lies underneath, you can hide annotations and measurements. See *Toggle Annotations* and *Toggle Annotation Statistics*, page 104.

Arrow/Text Annotation (N), Arrow Annotation

Use one of these tools to add annotation text or draw arrows to point to observations.

Creating a text annotation

1. Click the **Arrow/Text Annotation** button to select this tool.
2. Click a point in an image.
3. In the **Edit Annotation** dialog box, type your annotation text.

Creating an arrow plus text annotation

1. Click the **Arrow/Text Annotation** button to select this tool.
2. Click where you want to point to.
3. Hold the mouse button down, and drag across the image to create an arrow.
4. Release the mouse button.
5. In the **Edit Annotation** dialog box, type your annotation text.

Drawing only an arrow (no text)

1. Click the **Arrow Annotation** button to select this tool.
2. Click where you want to point to.
3. Hold the mouse button down, and drag across the image to create an arrow.
4. Release the mouse button.

Moving or editing an annotation

1. Click an annotation text to select it.
2. Drag the text to move it.

-Or-

1. Click the arrow head.
2. Drag to move this end of the line until it points to a different observation.

-Or-

1. Right-click an annotation text or an arrow and select **Properties**.
2. In the **Edit Annotation** dialog box, change the way the annotation is displayed.

Showing text at a fixed viewer position

1. Right-click a text annotation.

   Do not right-click an arrow plus text annotation.
2. Select **Fixed Position in Viewer**.
3. Start scrolling slices.

The annotation text remains static. This means the text appears in each slice image and at the same window position.

Circle Annotation

Use this tool to draw a circle around an area of interest and to add annotation text that comments your observation.

Do not confuse the **Circle Annotation** tool with the **Circular ROI** tool. Annotation tools merely highlight an area of interest but do not evaluate image information. See also *Circular ROI*, page 84.

Creating a circle annotation

1. Click the **Circle Annotation** button to select this tool.
2. Click a point in an image to create a circle around this point.
3. Drag in or out to make the circle smaller or larger.
4. Release the mouse button.
5. In the **Edit Annotation** dialog box, type your annotation text.

Moving or editing a circle annotation

1. Click the annotation graphic or the text to select it.

   Four dots appear around the circle and one dot in the middle of the circle.
2. Drag the dots around the circle in or out to resize the circle.

   -Or-

   Drag the dot in the middle to move the entire annotation graphic plus text.

   -Or-

   If the **Move text freely** option in the **Edit Annotation** dialog box is selected, you can select and move the text only.

Distance (D)

Use this tool to measure distances. Distances are indicated in millimeters.

Caution

The accuracy of distance measurements is ± 2 pixels. Larger errors can occur if the image is displayed with reduced matrix size, that is, if not every original pixel is shown on the screen due to zoom-out. For optimum accuracy, we recommend zooming into the structure of interest as much as possible. The accuracy is further limited by the physical resolution of the acquisition itself. If the monitor used for display does not permit exact pixel selection, the inaccuracy can be still greater.

Measuring a distance

1. Click the **Distance** button to select this tool.
2. Click where you want to start your distance measurement.
3. Hold the mouse button down, and drag across the image.
4. Release the mouse button at the endpoint of your distance line.

Showing the measurement in all slices

1. Right-click the distance line.
2. Select **Show on all Slices**.
3. Start scrolling slices.

The measurement graphics and results are shown in all slices.

Perpendicular Distance

Use this tool to perform two distance measurements that are exactly perpendicular. For example, use this tool to measure the dimensions of a lesion.

Caution

The accuracy of distance measurements is ± 2 pixels. Larger errors can occur if the image is displayed with reduced matrix size, that is, if not every original pixel is shown on the screen due to zoom-out. For optimum accuracy, we recommend zooming into the structure of interest as much as possible. The accuracy is further limited by the physical resolution of the acquisition itself. If the monitor used for display does not permit exact pixel selection, the inaccuracy can be still greater.

Measuring a perpendicular distance

1. Click the **Perpendicular Distance** button to select this tool.
2. Click where you want to start your distance measurement.
3. Hold the mouse button down, and drag the mouse across the image.
4. Release the mouse button at the endpoint of your distance line.
5. Draw the second distance line in the same way.

   If the lines are exactly perpendicular, the right angle symbol is shown where the lines intersect.

Tip

Be sure to draw the second line immediately after you have finished the first. If you click elsewhere in the meantime, the system interprets both lines as separate distance measurements.

Showing the measurement in all slices

1. Right-click the measurement.
2. Select **Show on all Slices**.
3. Start scrolling slices.

The measurement graphics and results are shown in all slices.

Calibrate Image

Use the calibration tool if a distance measurement yields only an estimate, which is indicated by an asterisk, or if the measurement yields pixel values.

Caution

The accuracy of distance measurements is ± 2 pixels. Larger errors can occur if the image is displayed with reduced matrix size, that is, if not every original pixel is shown on the screen due to zoom-out. For optimum accuracy, we recommend zooming into the structure of interest as much as possible. The accuracy is further limited by the physical resolution of the acquisition itself. If the monitor used for display does not permit exact pixel selection, the inaccuracy can be still greater.

1. Click the **Calibrate Image** button to select this tool.
2. Measure an object with known dimensions.
3. In the **Calibrate** dialog box, enter the known length.
4. Click **OK**.

The program recalculates any previously measured distances. In the upper right corner of the image the words **manual calibration** indicate that manual calibration has been performed on this image.

Angle

Use this method of measuring angles if the legs of your angle intersect within the image area.

Caution

The accuracy of all angle measurements (2D, Cobb's angle) depends on the length of the shorter of the two angle legs. The longer the angle legs are, the better the accuracy.

For example:

Length of shorter angle leg (measurement error): 10 pixels (± 12°),
20 pixels (± 6°), 50 pixels (± 2.5°), 100 pixels (± 1.1°)

Larger errors can occur if the image is displayed with reduced matrix size, that is, if not every original pixel is shown on the screen due to zoom-out. For optimum accuracy, we recommend that you zoom into the structure of interest as much as possible. The accuracy is further limited by the physical resolution of the acquisition itself. If the monitor used for display does not permit exact pixel selection, the inaccuracy can be still greater.

Measuring an angle

1. Click the **Angle** button to select this tool.
2. Click and drag to draw the first leg of your angle.
3. Release the mouse button at the vertex.
4. Drag to draw the second leg.
5. Click to end drawing the second leg.

Showing the measurement in all slices

1. Right-click the angle.
2. Select **Show on all Slices**.
3. Start scrolling slices.

The measurement graphics and results are shown in all slices.

Angle (Two Lines)

Use this method of measuring angles, for example, if the legs of the angle intersect outside the image area.

Caution

The accuracy of all angle measurements (2D, Cobb's angle) depends on the length of the shorter of the two angle legs. The longer the angle legs are, the better the accuracy.

For example:

Length of shorter angle leg (measurement error): 10 pixels (± 12°),
20 pixels (± 6°), 50 pixels (± 2.5°), 100 pixels (± 1.1°)

Larger errors can occur if the image is displayed with reduced matrix size, that is, if not every original pixel is shown on the screen due to zoom-out. For optimum accuracy, we recommend that you zoom into the structure of interest as much as possible. The accuracy is further limited by the physical resolution of the acquisition itself. If the monitor used for display does not permit exact pixel selection, the inaccuracy can be still greater.

Measuring an angle

1. Click the **Angle (Two Lines)** button to select this tool.
2. Click and drag to draw the first line.
3. Release the mouse button to finish the first line.
4. Click and drag to draw the second line.
5. Release the mouse button to finish the second line.

Of course, you can also use **Angle (Two Lines)** if the lines intersect. For intersecting lines the system calculates both the acute angle and the obtuse angle.

Showing the measurement in all slices

1. Right-click the angle.
2. Select **Show on all Slices**.
3. Start scrolling slices.

The measurement graphics and results are shown in all slices.

Distance Ratio

Use this tool to measure two distance lines and to have the system calculate the ratio between both measurements.

Caution

The accuracy of distance measurements is ± 2 pixels. Larger errors can occur if the image is displayed with reduced matrix size, that is, if not every original pixel is shown on the screen due to zoom-out. For optimum accuracy, we recommend zooming into the structure of interest as much as possible. The accuracy is further limited by the physical resolution of the acquisition itself. If the monitor used for display does not permit exact pixel selection, the inaccuracy can be still greater.

Calculating the distance ratio

1. Click the **Distance Ratio** button to select this tool.
2. Measure the first distance line.

   Click, drag, and release the mouse button at the endpoint.
3. Measure a second distance line.

Tip

You can use this tool to calculate the cardiothoracic ratio in X-ray images, for example.

Showing the measurement in all slices

1. Right-click the measurement.
2. Select **Show on all Slices**.
3. Start scrolling slices.

The measurement graphics and results are shown in all slices.

Vertical Distance

Use this tool to measure the vertical distance between points in your images.

Caution

The accuracy of distance measurements is ± 2 pixels. Larger errors can occur if the image is displayed with reduced matrix size, that is, if not every original pixel is shown on the screen due to zoom-out. For optimum accuracy, we recommend zooming into the structure of interest as much as possible. The accuracy is further limited by the physical resolution of the acquisition itself. If the monitor used for display does not permit exact pixel selection, the inaccuracy can be still greater.

Measuring a vertical distance

1. Click the **Vertical Distance** button to select this tool.
2. Click a point in your image.
3. Click a second point in your image.

The system draws two horizontal lines through both image points and calculates the vertical distance between the two lines.

Tip

You can use this tool to measure the pelvic tilt in an X-ray image of the hip of a standing patient, for example.

Showing the measurement in all slices

1. Right-click the measurement.
2. Select **Show on all Slices**.
3. Start scrolling slices.

The measurement graphics and results are shown in all slices.

Annotate Vertebral Bodies/Disks

Use this tool to label vertebrae and intervertebral disks in images of the spine.

When you click the tool, a new toolbar appears in the lower right corner of the active viewer, and the **Spine Labeling** tool card opens.

Labeling vertebrae or intervertebral disks

1. Select whether you want to label vertebrae or intervertebral disks.

2. Select the direction in which you want to proceed.

3. Select if you want to label vertebrae or intervertebral disk consecutively or if you want to label only every second or third vertebra or intervertebral disk.

4. On the **Spine Labeling** tool card, select the vertebra or intervertebral disk label with which you will begin.
5. Click this vertebra or intervertebral disk in the image to label it.

   -Or-

   Click and drag away from the vertebra or intervertebral disk to create an arrow.

   On the **Spine Labeling** tool card, the **next** vertebra or intervertebral disk label is selected now.
6. Click the next vertebra or intervertebral disk in the image and continue until you have labeled all vertebrae or intervertebral disks.
7. Right-click a label in the image and select **Properties** to change font settings or graphical display settings for a label.

Showing labels in all slices

1. Right-click the label of a vertebra or an intervertebral disk.
2. Select **Show on all Slices**.
3. Start scrolling slices.

The label is shown in all slices.

Cobb's Angle

Use this tool to measure Cobb’s angles in images of the spine.

Caution

The accuracy of all angle measurements (2D, Cobb's angle) depends on the length of the shorter of the two angle legs. The longer the angle legs are, the better the accuracy.

For example:

Length of shorter angle leg (measurement error): 10 pixels (± 12°),
20 pixels (± 6°), 50 pixels (± 2.5°), 100 pixels (± 1.1°)

Larger errors can occur if the image is displayed with reduced matrix size, that is, if not every original pixel is shown on the screen due to zoom-out. For optimum accuracy, we recommend that you zoom into the structure of interest as much as possible. The accuracy is further limited by the physical resolution of the acquisition itself. If the monitor used for display does not permit exact pixel selection, the inaccuracy can be still greater.

Measuring Cobb’s angles

1. Click the **Cobb’s Angle** button to select this tool.
2. Click and draw a first line.
3. Draw a second line. The lines do not have to intersect.

   The acute angle between the two lines is shown.
4. Draw a third line.

   The acute angle between the second and third line is shown.
5. Continue in this way to measure more Cobb’s angles.

Showing the measurement in all slices

1. Right-click the measurement.
2. Select **Show on all Slices**.
3. Start scrolling slices.

The measurement graphics and results shown in all slices.

Elliptic ROI

A 2D ROI evaluates image information in the currently displayed image or slice.

Caution

The relative error of an elliptical ROI measurement is ± 2 pixels/(shorter radius).

For example:

Shorter radius (measurement error): 10 pixels (± 20%), 20 pixels (± 10%), 50 pixels (± 4%), 100 pixels (± 2%).

Larger errors can occur if the image is displayed with reduced matrix size, that is, if not every original pixel is shown on the screen due to zoom-out. For optimum accuracy, we recommend that you zoom into the structure of interest as much as possible. The accuracy is further limited by the physical resolution of the acquisition itself. If the monitor used for display does not permit exact pixel selection, the inaccuracy can be still greater.

1. Click the **Elliptic ROI** button to select this tool.
2. Click the center of your region of interest and drag the mouse out.
3. Release the mouse button when the ellipse is large enough.

Circular ROI

Use this tool to evaluate a 2D region of interest that is exactly circular.

Do not confuse the **Circular ROI** tool with the **Circle Annotation** tool. Annotation tools merely highlight an area of interest but do not evaluate image information. See also *Circle Annotation*, page 75.

Drawing a circular ROI

1. Click the **Circular ROI** button to select this tool.
2. Click the center of your region of interest and drag the mouse out.
3. Release the mouse button when the circle is large enough.

Comparing circular regions of interest

If you want to compare regions of interest, you can predefine the size of your next ROI.

1. Right-click your first circular ROI.
2. Select **Set Size as Default.**
3. Select the **Circular ROI** tool again.
4. Click to create a second circular ROI.

   The new ROI has exactly the same size as the first ROI.

Spherical ROI

Use this tool to evaluate 3D ROIs that are exactly spherical.

1. Click the **Spherical ROI** button to select this tool.
2. Draw a circle in a slice image.

   The program calculates the statistics of a volume of interest (3D ROI) with the size of the circle in all dimensions.
3. Scroll through the image stack to see 2D representations of the selected spherical volume in various slices.

Tip

A 3D ROI evaluates volume information and therefore only makes sense in data of modalities that allow generation of volume datasets.

3D ROIs are also called VOIs (volumes of interest).

Point-Sized ROI, Pixel Value

If you want to evaluate a point rather than an area or volume, use the **Point-Sized ROI** or the **Pixel Value** tool.

Point-sized ROIs

1. Click the **Point-Sized ROI** button to select this tool.
2. Click a pixel in an image.

The grayscale or density value of this pixel is shown and the program creates both a snapshot and a key view.

Pixel Value

1. Click the **Pixel Value** button to select this tool.
2. Move the cursor across an image.

The intensity value of the current cursor position is shown in the lower left corner of the viewer, below the series and image number. The program does not create a snapshot.

Freehand 2D ROI

Use this tool to draw a freehand shape and evaluate image information in this region of interest (ROI).

Freehand 2D ROI tools

When you click the **Freehand 2D ROI** tool, a new toolbar appears in the lower right corner of the active viewer. Here you find the following tools for drawing and refining freehand shapes in 2D.

New Elliptical Contour

Use this button to circle the area of interest with an ellipse or a circle. Click a start point, and drag the mouse out.

New Freehand Contour

Use this button to draw a freehand shape. Click a start point on the contour. Hold the mouse button down, and draw a contour line.

New Balloon Contour

Use this tool to draw a border around a structure or area of interest of a specific brightness. Click in the structure and drag out.

Append mode

With any of the contour tools, use the **Shift** key to start **Append** mode (the cursor turns into an arrow with a plus sign).

Draw a contour or select a contour you have drawn earlier.

Press and hold the **Shift** key down and then draw a second contour.

If the contours overlap, the system merges them into a single ROI. If the contours do not overlap, the system nevertheless interprets them as parts of a single region of interest. Add a third contour to this ROI, if necessary.

Release the **Shift** key to turn **Append** mode off again.

Refine Contour

Use this tool to correct or refine contour lines.

Click anywhere in the image and drag the mouse to show a circle with which you can correct the ROI graphic. The further away from the contour line you click, the larger the circle will be.

Click inside the ROI graphic to enlarge the ROI graphic by pushing the contour out. Click outside the ROI graphic to use the circle to push the contour line in.

Undo

Use **Undo** to retrace your steps.

OK

Click **OK** when you have finished drawing and refining 2D ROIs to close the tool.

Freehand 3D ROI

Use this tool to define a freehand 3D ROI by drawing ROI graphics in various slices of a volume dataset.

Freehand 3D ROI tools

When you click the **Freehand 3D ROI** tool, a new toolbar appears in the lower right corner of the active viewer. Here you find the following tools for drawing and refining freehand shapes in 3D.

New Elliptical Contour

Use this button to enclose the area of interest with an ellipse. Click a start point, and drag the mouse out to draw a circle or ellipse.

New Freehand Contour

Use this button to draw a freehand shape. Click a start point on the contour. Hold the mouse button down, and draw a contour line.

New Balloon Contour

Use this tool to draw a border around a structure or area of interest of a specific brightness. Click in the structure and drag out.

Append mode

With any of the contour tools, use the **Shift** key to start **Append** mode (the cursor turns into an arrow with a plus sign).

Draw a contour or select a contour you have drawn earlier.

Press and hold the **Shift** key down and then draw a second contour.

If the contours overlap, the system merges them into a single ROI. If the contours do not overlap, the system nevertheless interprets them as parts of a single region of interest. Add a third contour to this ROI, if necessary.

Release the **Shift** key to turn **Append** mode off again.

Refine Contour

Use this tool to correct or refine contour lines.

Click anywhere in the image and drag the mouse to show a circle with which you can correct the ROI graphic. The further away from the contour line you click, the larger the circle will be.

Click inside the ROI graphic to enlarge the ROI graphic by pushing the contour out. Click outside the ROI graphic to use the circle to push the contour line in.

When you have finished drawing and refining a ROI graphic in one slice, scroll on to the next slice and also draw a ROI there.

Continue in this way through all slices that show the volume of interest.

Undo

Use **Undo** to retrace your steps.

OK

Click **OK** when you have finished drawing and refining ROI graphics in all slices.

The system calculates ROI statistics and closes the freehand 3D ROI tool

Save Annotations as Presentation State

Use this tool to save annotations and measurements permanently.

Clicking this tool saves annotations and measurements in a DICOM presentation state. In **Study Browser**, the presentation state appears as a new series with modality PR. The next time you load this study, your annotations are shown in the images.

Delete All Measurements/Annotations

Use this tool to delete all measurements and annotations in your dataset.

Note
Clicking this tool removes **all** measurements in **all** images including those that are currently in the background. Moreover, key views and snapshots, which the program created automatically for each measurement or annotation, are also deleted.

Snapshot tools

Snapshots serve the purpose of documenting observations. For example, you create a snapshot to show it in your report.

Every time you add a text or graphical annotation or perform a measurement, the program takes a snapshot. Snapshots are hard copies of the image in the currently selected viewer, complete with annotations, measurements, and image text, if shown. If you want to preserve an image without annotating it, you create a snapshot with one of the snapshot tools. Visage 7 collects all snapshots that you create during a session in the **Export** window. From the **Export** window, you can save these snapshots, send or print them, or include them in your report.

Snapshot Active Viewer (S)

Use this tool to create a snapshot of the currently selected viewer. The snapshot is sent to the **Export** window.

Snapshot All Viewers (Shift + S)

Use this tool to create snapshots of all viewers that are currently shown on the screen. Several snapshots are sent to the **Export** window.

Combined Snapshot All Viewers (Alt + S)

Use this tool to create a combined snapshot that shows all viewers that are currently displayed on the screen in one image. One snapshot is sent to the **Export** window.

Key views tools

When you read images, you make observations that you want to highlight and also save to be able to come back to them later. For cross-sectional images, that is CT, MR, and PET images, Visage 7 offers the concept of key views for this purpose.

Key views help you to come back to an observation in a later session and also to repeat or refine measurements, for example.

A key view is created every time you annotate an image or perform a measurement. In addition to this, you can create a key view for every other slice to which you want to return later.

Note

Key views exist for the duration of the current session. To preserve key views, save your session. See also *Session management*, page 23.

Store Key View (K)

Use this tool to save what is currently shown in the active viewer in a key view. When you save a key view this way, the program also creates a snapshot and sends it to the **Export** window.

Delete Key View

Use this tool to delete a key view. This button is available only if a key view is shown in the active viewer.

When you delete a key view, the corresponding snapshot in the **Export** window is also deleted.

Previous Key View, Next Key View

Use these tools to browse through the key views that are stored in your session.

Tools for 3D navigation

In 3D datasets, you use the tools in this section or the scoutline crosshair to move through the volume. See also *Crosshair navigation in MPR viewers*, page 44.

Tip

For a better overview, show orientation labels and the orientation cube before you start navigating through the volume. Use **View > Show in Viewer** on the menu to display the orientation cube and orientation labels.

3D Rotate

Use this tool to rotate around the volume in the 3D viewer or in the MPR viewers.

3D rotation in the 3D viewer

3D Rotate is the standard navigation tool in the 3D viewer.

1. Click anywhere in the 3D viewer.
2. Hold the mouse button down and drag to rotate the volume in the direction of the mouse movement.

Tip

Use any of the standard orientation buttons or keyboard shortcuts to reset rotation. See *Anterior (A), Posterior (P), Left (L), Right (R), Head (H), Foot (F) View*, page 91.

3D rotation in MPR viewers

1. Click the point in an image that is to be the center of rotation.
2. Hold the mouse button down and drag to rotate the image plane.

New slice images in nonstandard orientations are created in the process. The orientation labels and orientation cube indicate the new image orientation.

Tip

Use *Reset Slice Orientations* to return to the original image orientation

2D rotation

Hold the **V** key down while you drag to rotate a single image or 3D volume.

V + 3D Rotate has the same effect as choosing the tool **Rotate in Plane**. See *Rotate in Plane*, page 55.

Reset Slice Orientations

Use this tool to reset the orientation in all linked MPR viewers to their original orientation. Images are now shown in the orientation in which they were displayed right after loading.

Anterior (A), Posterior (P), Left (L), Right (R), Head (H), Foot (F) View

Use these tools to display the image in the currently active viewer in one of the standard anatomical views.

For example, if you click **H** or **F** in an MPR viewer that shows axial slices, this reverses the viewing direction in this viewer. If you click **H** or **F** in an MPR viewer that shows sagittal or coronal slices, this rearranges viewers.

Clicking a standard orientation button in the 3D viewer affects the 3D viewer only.

Position Crosshair

Use this tool to focus on a particular point in the volume in **linked** viewers.

Note

Position Crosshair affects linked viewers only.

1. Click the **Position Crosshair** button to select this tool.
2. Click a visible (opaque) structure in the 3D viewer.

   -Or-

   Click any point in one of the images in the MPR viewers.

Clicking sets the crosshair of the MPR viewers to this 3D position and updates all MPR viewers that show this dataset.

Tip

Show the 3D crosshair in the 3D viewer before you click **Position Crosshair**.

Triangulation

Use this tool to focus on a particular point in the volume in **all** viewers that show images or volume datasets that contain this point.

Note

Triangulation affects image display in **all** viewers and not only in linked viewers.

1. Click the **Triangulation** button to select this tool.
2. Click a point in any of the viewers.

Tip

The **Triangulation** tool is particularly useful when you are reading multiseries MR datasets.

Center View

Use this tool to move images in linked viewers in such a way that the scoutline crosshair is in the viewer center.

For example, use this tool after you have moved the crosshair. See also *Crosshair navigation in MPR viewers*, page 44.

Cropping tools

Use the cropping tools to cut away portions of the volume that hide more important information that lies underneath.

Tip

Show the bounding box in the 3D viewer before you select one of these tools. The bounding box helps you to identify the portions of the volume that you want to cut away.

Crop Box

Use this tool to cut away the outer parts of the volume.

1. Click the **Crop Box** button to select this tool.

   This tool removes the outer volume parts, a smaller volume box in the center of the volume dataset remains.

2. Click inside the box to move it.

   -Or-

   Drag a border line to resize the box.

   -Or-

   Click a corner of the box and drag to rotate the crop box.

3. Click the **Crop Box** button a second time to show the entire volume again.

Tip

When you click a cropping tool, the **Lock Crop Region** button appears in the lower right corner of the active viewer.

Clicking this button locks the crop region. You can now move or rotate the volume within the crop box.

Crop Slab

Use this tool to cut away portions of the volume so that only a slab remains. A slab is a section of the volume between any two parallel planes with oblique orientation.

1. Click the **Crop Slab** button to select this tool.

   -Or-

   In the 3D viewer use the keyboard shortcut **T** to turn slab display on or off.
2. Drag slab boundaries out or in to change the slab thickness.
3. Click the **Crop Slab** button a second time to show the entire volume again.

Tip

When you click a cropping tool, the **Lock Crop Region** button appears in the lower right corner of the active viewer.

Clicking this button locks the crop region. You can now move or rotate the volume within the slab.

Crop Plane

Use this tool to cut away a corner of the volume along an oblique cutting plane.

1. Click the **Crop Plane** button to select this tool.
2. Drag the orange line, which defines what will be cut away, to move this plane in or out.
3. Click the **Crop Plane** button a second time to show the entire volume again.

Tip

When you click a cropping tool, the **Lock Crop Region** button appears in the lower right corner of the active viewer.

Clicking this button locks the crop region. You can now move or rotate the volume within the remaining volume box.

Crop Corner

Use this tool to cut away a box from the corner of the volume.

1. Click the **Crop Corner** button to select this tool.

   A box is removed from the corner that is pointing toward you in the 3D viewer.
2. In the MPR viewers, drag the orange lines, which define the corner to be cut away, to increase or decrease the box.
3. Click the **Crop Corner** button a second time to show the entire volume again.

Tip

When you click a cropping tool, the **Lock Crop Region** button appears in the lower right corner of the active viewer.

Clicking this button locks the crop region. You can now move or rotate the volume within the remaining volume box.

Fusion registration tools and tools for displaying primary and overlay data

With Visage 7 you can display suitable datasets in fusion mode. Fusion display overlays datasets, for example, a CT and a PET series of the same study.

Fusion display requires that datasets are registered, which means that they are aligned spatially. Even though Visage 7 usually aligns datasets automatically when you load suitable data, always check and confirm alignment manually.

Manual Registration

Use this tool to start manual alignment mode. In this mode, the two datasets are overlaid. The primary dataset is shown pink, and the overlay dataset is shown green in the active viewer. An outlined cross also appears in the viewer.

1. Click the center of the cross.
2. Hold the mouse button down, and drag the green layer.
3. When corresponding structures in the green and pink layer are exactly overlaid, release the mouse button.

-Or-

1. Click one of the ends of the cross.

   The cursor changes its shape and indicates rotation.

2. Hold the mouse button down and drag to rotate the green overlay layer.

Tip

Before you align datasets manually, window the two datasets in such a way that prominent structures, such as bones, are clearly visible. This helps you to overlay the two corresponding images correctly.

Align Centers

Use this button to have Visage 7 align the centers of the bounding boxes of the two datasets.

Automatic Registration

Use this button to have Visage 7 identify and align corresponding structures by comparing pixel intensities.

Caution

Be aware that automatic registration does not always align images correctly. Please verify registration results and correct registration manually, if necessary.

Tip

Automatic Registration of primary and overlay datasets and **Automatic Viewer Registration** for linked scrolling use the same principle of comparing grayscale information in images.

See also *Automatic Viewer Registration*, page 67.

Reset Registration

Click this tool to undo manual alignment, center alignment, or automatic registration. The two datasets are now registered in the same way as they were right after loading.

Accept Registration

Click this tool after you have finished aligning your datasets manually.

Viewer Objects (Primary), Viewer Objects (Overlay)

Multimodality studies can contain more than one series per modality. Multiple series are indicated by these buttons in the MPR viewers and the 3D viewer.

Use these tools to open a menu from which you can select a different primary or overlay dataset.

Tools for time-series analysis

When you load time series, the system selects a protocol that has been optimized for comparison and analysis of images at various phases.

Time-density analysis

Time-density analysis plots the density progression in one or several regions of interest over time in time-resolved 3D datasets.

1. Select the viewer that shows the baseline phase. Typically this is the upper left viewer.
2. Draw a circular, elliptical, freehand, or point-sized ROI.

3. Right-click and select **Time-Density Analysis**.

   The program evaluates the density of the ROI in the various time steps of the series and plots this information in a graph.
4. Draw a second ROI.

5. Right-click and select **Add to Time-Density Analysis**.

The graph of the second ROI is added to the plot. ROIs are numbered both in the plot and in the image.

Subtract Baseline Phase

Use this tool to subtract the baseline phase from the other images of a time series. As a result you see only those structures in which changes occurred over time. In a time-series with contrast medium, subtraction helps to focus on the flow of contrast medium.

Tip

Click **Subtract Baseline Phase** a second time to reset subtraction and show all image information again.

Tools for viewing mammography studies

Protocols for mammography studies feature a specific arrangement of images, which is particularly well-suited for a comparison of the left and right breast.

Moreover, these protocols offer tools for synchronized image navigation in high-resolution images and for comparing magnified sections in corresponding images.

Quadrant Navigation

Use this tool to enlarge the displayed images and to read them quadrant by quadrant.

1. Click the **Quadrant Navigation** button to select this tool.
2. Press the right arrow key to show the upper right quadrant of images of the right breast and the upper left quadrant of images of the left breast enlarged and side by side.
3. Press the right arrow key a second time to move on to the lower right quadrant (right breast) and lower left quadrant (left breast).
4. Press the right arrow key a third time to move on to the lower left quadrant (right breast) and lower right quadrant (left breast).
5. Press the right arrow key a fourth time to move on to the upper left quadrant (right breast) and upper right quadrant (left breast).
6. Press the right arrow key a fifth time to show the entire images again.
7. Continue pressing the right arrow key to return to quadrant display.

Magnifying Glasses

Use this tool rather than **Magnifying Glass** to be able to compare enlarged sections of the left and right breast.

1. Click the **Magnifying Glasses** button to select this tool.
2. Click the image of the left breast and hold the mouse button down.

   A rectangular area appears which shows this section of the image in its original size (100%).
3. Drag to move the rectangle across the image.
4. Release the mouse button and move on to the image that shows the right breast.
5. Also click here and move the magnifier to the area of interest.

   The magnifiers remain visible in both viewers for as long as the **Magnifying Glasses** tool is selected.
6. For layouts that show images in more than one orientation, you can continue applying magnifying glasses to these other viewers as well.
7. Click the tool on the toolbar a second time or click another tool to remove the magnified sections from all viewers.

Tip

The tool **Magnifying Glasses** is not reserved for mammography studies but also available in other protocols, image types and viewers.

Choose multiple **Magnifying Glasses** rather than a single **Magnifying Glass** whenever you want to inspect and compare magnified sections in more than one viewer. See also *Magnifying Glass*, page 54.

Previous Prior Study (Mammo), Next Prior Study (Mammo)

Use these tools to scroll through corresponding images in prior studies.

Data handling tools

These tools help you with various data handling tasks.

Study Info Dialog

Use this tool to show the study information dialog box. The information in this dialog box is read-only, except for the **Comment** box.

In the **Comment** box you can add or edit study comments. Any changes are saved on the Visage 7 server automatically. No further user interaction is required to save comments.

View Structured Reports

Use this tool to show any DICOM structured reports that exist for the currently loaded study, as well as for associated prior studies.

View Reports (RIS)

Use this tool to show reports that exist for the currently loaded studies in the RIS. The reports are shown in a separate report window.

The tool icon indicates the report status (unsigned report, signed report, report for prior study only, no report at all).

Tip

In the report window, you can view and print reports.

View Reports (PACS)

Use this tool to view PACS reports or HL7 reports for the currently loaded studies. This tool opens the **Export** window and displays the reports there.

The tool icon indicates the report status.

Best Image Quality

For users who access the Visage 7 server over the Internet, a red bullet might be permanently shown in the lower right corner of all images. The red bullet indicates low image resolution as a result of high compression rates, which were selected to improve download speed.

Use the **Best Image Quality** tool and select individual images only. These images are downloaded with best image quality but potentially slow download times.

Assign and Manage Labels

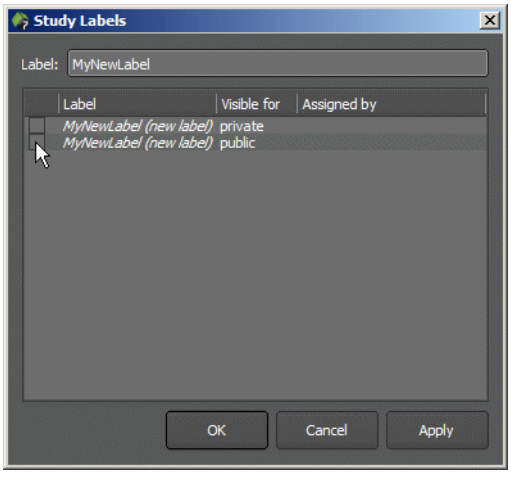
Use this tool to open the **Study Labels** dialog box.

Assigning a label to a study

1. Select one or several of the existing labels that you want to assign this study to.

   -Or-

   Type the name of a new label and select either the public or private version of the new label.

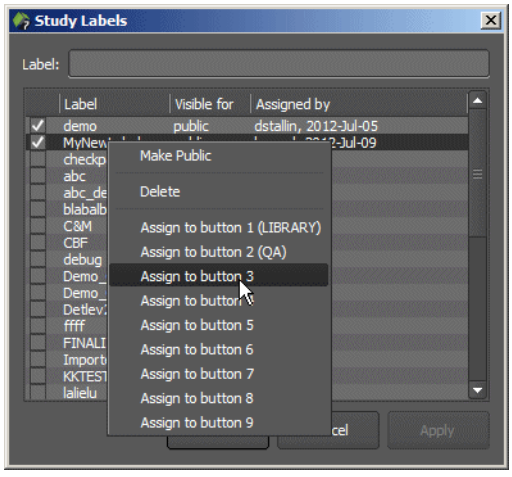


2. Click **Apply**.

Creating a label button

For even easier label assignment in future, you can create label buttons on the **Labels** toolbar.

1. Right-click a label and assign it to a button placeholder.



2. Next time you want to assign this label, click the button on the **Labels** toolbar.

Tip

For more information about study labels, see *Managing teaching and meeting files*, page 29

Tools for DICOM print

With these tools you can send images to a DICOM printer for output on paper or film. DICOM print requires that a DICOM printer is connected to your Visage 7 server.

DICOM print tools

DICOM print tools are available from the viewer context menu.

Print Image

With this tool, you can print the image in the active viewer. Image orientation, zoom and window settings in the printout are the same as in the active viewer when you click the tool. If image texts are currently shown in the image, these texts are printed as well. Measurements or annotation texts are not printed.

Print Image Set

With this tool, you can print all images of the image set currently shown in the active viewer. All images are printed in their original orientation and together with any image texts that are currently displayed on the screen. Measurements or annotation texts are not printed.

Print Visible Image

With this tool, you can print all images that are currently shown on the screen. Image orientation, zoom and window settings in the printout are the same as on the screen when you click the tool.

Print Visible Images is available only if all viewers show original images.

Print Visible Image Set

With this tool, you can print the images of all image sets that are currently displayed in the various viewers of the selected layout. If one image set is shown in more than one viewer, it is printed only once. All images are printed in their original orientation.

DICOM print settings

Clicking one of the DICOM print tools opens the **DICOM Print** dialog box, where you can select the printer or change printer settings.

Device

In the upper part of the dialog box, you can select the DICOM printer and the number of copies.

Layout

Here you can select how many images you want to print on one page or film sheet by specifying the number of **Rows** and **Columns**.

Selecting 1 for rows and also 1 for columns prints exactly one image per page or film sheet. Selecting 2 for rows and also 2 for columns prints exactly four images per page or film sheet.

Also specify the **Fit Mode**:

Image fits the image into the image box on the page or film.

Viewer prints images as shown in the viewer. This option is available only for the tools **Print Image** and **Print Visible Image**.

True Size scales the image up or down so that one centimeter on the printout corresponds to one centimeter in reality. This mode takes image calibration into account. If you select this option for uncalibrated images, a warning appears.

Media Properties

In this section of the dialog box, select medium type, size, orientation, and color mode. Which options are available in this section depends on the DICOM printer that is connected to your Visage 7 server.

Tools for switching image text and graphics on and off

With the tools in this section, you can show or hide texts or graphics that overlay the actual images. Some of these tools show or hide all text or groups of text or graphics, whereas other tools toggle only specific information.

Toggle tools affect all viewers or all viewers of a specific viewer type. For example, you cannot show patient and study data in one viewer but hide this information in all other viewers.

Toggle tools on the tool palette

The toggle tools can be configured to be shown in toolbars or on the tool palette. Show the tool palette by right-clicking a viewer. However, remember that it depends on your system configuration whether right-clicking shows the tool palette, or the viewer context menu, or both (see also *Configure Tool Palette dialog box*, page 177).

Toggle All

Use this tool to show or hide any texts or graphics that are currently selected for display in the **View > Show in Viewer** menu.

Alternatively, use the **Space** key on your keyboard to show or hide text and graphics.

Toggle Patient/Study Data

Use this tool to show or hide patient or study information in all viewers.

Toggle Orientation Labels

Use this tool to show or hide orientation labels in viewers.

Orientation labels indicate the viewing direction: **A** for anterior, **P** for posterior, **L** for left, **R** for right, **H** for head, and **F** for feet.

Toggle Orientation Cube

Use this tool to show or hide the orientation cube in the lower left corner of the viewers.

For DBT (digital breast tomosynthesis) volumes, a slice-position reference graphic is shown instead of the orientation cube.

Toggle Histogram

While the **Window Level** tool is active, a histogram of grayscale values or HU values is shown in the lower left corner of the viewer.

Use this tool to hide or redisplay the window level histogram.

Toggle Scale

In calibrated image types, for example, CT images, a scale can be shown on the right edge of the viewers. The scale looks like a small ruler and indicates centimeters or millimeters when you zoom in.

Use this tool to hide or redisplay the scale.

Toggle Color Scale

In viewers that show color images, a scale that indicates the value range can be shown. For example, in PET (positron emission tomography) images the value range indicates standard uptake values (SUV) and the colors they correspond to.

Use this tool to show or hide the color-map value-range indicator.

Toggle Annotations

Use this tool to show or hide annotation text, annotation arrows, and measurement graphics and results.

-Or-

Toggle Annotation Statistics

Use this tool to hide or redisplay the results of measurements only. With **Toggle Annotation Statistics** turned off, measurement graphics are still visible, only the results of measurements are hidden.

This tool is particularly useful in the context of ROI statistics, which might hide underlying image information.

Note that instead of showing or hiding all ROI statistics you can also hide the results of individual ROI measurements only. Select a ROI measurement and use the context menu and not the **Toggle Annotation Statistics** tool to show or hide this information.

Toggle Viewer Controls

Use this tool to show or hide the viewer control bar at the bottom edge of the viewers. **Toggle Viewer Controls** affects all viewers of the same viewer type.


Toggle 2D Bounding Box, Toggle 3D Bounding Box

Use these tools to show or hide a box or cube that indicates volume borders in MPR viewers or 3D viewers.


Toggle 2D Crosshair, Toggle 3D Crosshair

Use these tools to show or hide scoutline crosshairs in MPR viewers or the 3D crosshair in 3D viewers.

Toggle Partial Crosshair

When the full 2D crosshair is shown the crosshair center becomes a move handle, irrespectively of the tool that is currently selected.

Switch to partial crosshair display to turn the move function off. For example, switch to partial crosshair display before you perform any measurements that start at or near the crosshair center.

Toggle Scoutlines

Use this tool to show or hide scoutlines. Scoutlines are dashed lines in 2D viewers or MPR viewers that indicate the location of a slice shown in one of the other viewers.

Toggle Slice Boundaries

In thick-slice display use this tool to show slice boundaries in MPR viewers of the same dataset.

Toggle Centerline

Use this tool to show or hide the curve definition or vessel centerline during vessel analysis or curved planar reformatting.

Note that in curved view centerline display must be turned on in the context menu. Only then can you use the **Toggle Centerline** button on the toolbar to hide or redisplay the centerline.

Toggle DICOM Overlays, Toggle DICOM Annotations

Toggle DICOM Shutters, Toggle ECG curve

Use these tools to show or hide DICOM overlays, DICOM annotations, DICOM shutters, or the ECG curve.

These tools are available only if images contain this information.

Toggle Localizer Image

Use this tool to hide or redisplay the embedded scout or localizer image in fullscreen mode.

Note that this is possible only if display of the embedded scout or localizer has been defined in the property settings of a viewer type.

Tools for performing quality assurance on images

On some occasions it is necessary to correct images so that these corrections apply even if the images are viewed with a viewer software other than Visage 7 Client.

Such corrections include the following cases:

- Patient information or orientation labels that are burnt into the images need to be replaced.
- 2D images need to be rotated or flipped.
- Window level settings need to be changed in individual 2D images or in a 3D volume dataset.
- The assignment of images to series or studies needs to be corrected.

Note

Visage 7 Client provides two tools to make and save permanent changes to image content. However, these tools are available only if your user account has appropriate user rights.

Permanent Text Label

Use this tool to overwrite patient or study data or orientation labels that are burnt into the images.

1. Click the **Permanent Text Label** button to select this tool.

   The **Edit Permanent Labels** dialog box opens. Text label creation and editing mode is active as long as this dialog box remains open.

2. In the image, click the patient information or orientation label that you want to overwrite.

A black box appears. The box more or less covers the existing patient information or orientation label.

3. Drag to move the box or use the sizing handles (orange dots) so that the box covers the text that you want to overwrite completely.
4. Type the correct information in the **Label properties** box of the **Edit Permanent Labels** dialog box.
5. Use the **Font size** slider to resize the text.
6. Under **Image selection**, select whether to apply the new label to the current image only or to all images in the image set.
7. Save your changes and close the dialog box.

   Closing the dialog box ends label creation and editing mode.

Tip

To change a text label that you just entered, or to delete one of your labels, reenter label editing mode.

Click the **Permanent Text Label** button again and click a label that you entered earlier to select it. You can now change the label text, move or resize the label, or delete it with the **Del** key on the keyboard.

Save Modified Image

Use this tool to save changes to image content permanently.

1. Click **Save Modified Image**.
2. Select which changes you want to save.

   You can only save changes to window level settings, flip or rotate operations, or changes to text labels, but no other modifications to image content.

Select for Quality Assassurance

Use this tool to load a case onto the **Quality Assurance** platform.

1. Select an image.
2. Click **Select for Quality Assurance**.

Here you will find the selected case in the **Performed Procedures** list.

Tool cards

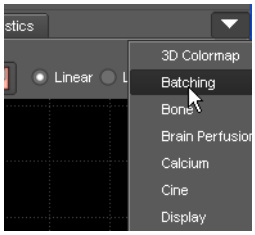
Tool cards can be arranged in one or several stacks, usually along the right edge of the program window. Alternatively, tool cards can be displayed as floating windows.

Your currently active protocol defines how and how many tool cards are shown right after you have loaded data.

Showing or hiding tool cards

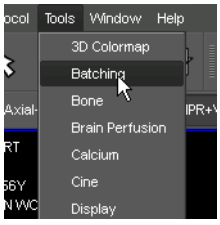
1. Click the arrow button on the right edge of the screen to show tool cards, if these are currently hidden.

2. Select the tool card you need from the drop-down list.



-Or-

Select a tool card from the **Tools** menu.



When you select a tool card from the **Tools** menu, it is shown as a floating window.

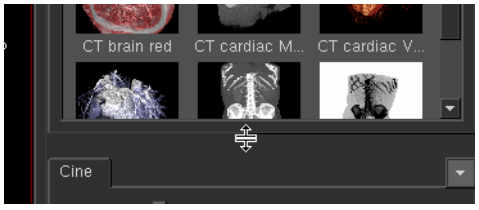
Tips for arranging tool cards

Some tool cards require more space than others. You can therefore resize tool card stacks or the width of the entire tool card area.

1. Point to the line that divides two stacks of tool cards.

   The cursor changes its shape.

2. Drag the line up or down to resize the tool card above and below.

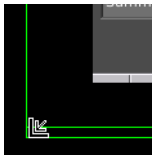


If the tool card area is temporarily in your way, you can hide it.

Clear **View > Show Tool Cards** in the main menu to hide the tool card section.

Floating windows are usually displayed in a size that ensures that they are not in your way while you are reading images. You can enlarge these windows, if necessary.

Click the lower left or lower right corner of the window and drag it out to show the tool card larger.



Templates

Templates offer a quick way to optimize the volume display in the 3D viewer for specific tasks.

A template defines volume rendering and display parameters for volume datasets of a particular modality or a combination of modalities.

A template stores the following information:

- The modality of the primary and overlay dataset
- A color map for the primary and overlay dataset

  See also *3D Color Map*, page 110.
- Rendering and display settings for the volume display in the 3D viewer

User-defined templates

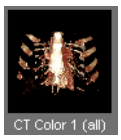
A number of predefined templates came with the system. Advanced users can adjust these to their own requirements or define their own set of 3D templates. When you save a new or adapted template, you can make it available for all users or for your own user account only.

Note

When you edit and save one of the **All users** templates, you change this template permanently and for all Visage 7 users in your network. The factory-defined template version is lost this way.

Controls on this tool card

Use the following buttons and tools to select a template or to manage templates:



Click a template thumbnail on the tool card to select it.

The tool card lists only templates that were defined for the modality or modalities of the data that is currently loaded.

Click **Reset** to return to the original volume display and to revoke your changes.

Click **Save** to save the 3D rendering and display settings currently applied to the volume in the active 3D viewer. A dialog box opens. Enter a template name and decide whether the new template will be available for all users or for your user account only.

Select a thumbnail and click **Delete** to remove it from the list of available templates.

3D Color Map

On the **3D Color Map** tool card, you can select and edit the color map that is used for VRT rendering in the 3D viewer.

A color map assigns colors and transparencies to different tissue types as defined by their window level. By selecting and adjusting a color map, you focus on structures and tissue types that are of particular interest to you. With a suitable color map you can display these structures particularly clearly and hide what would only distract you from the question at hand.

User-defined color maps

A number of predefined color maps came with your system. Advanced users can adjust these or define their own set of 3D color maps. When you save a new or adapted color map, you can make it available for all users or for your own user account only.

Note

Some of the available color maps, for example, gray ramp and temperature, can only be edited to a limited extent. In these color maps you can adjust only the data windows of the tissue types but no color and transparency settings. You cannot save changes to these color maps either.

Controls on this tool card

Use the following controls to select the dataset and color map that you want to change, and to manage color maps.

Primary Dataset, Overlay Dataset

Fusion mode only.

Select which of the two color maps you want to edit, the color map of the primary dataset or the overlay dataset.

Color map selection

Click the arrow button next to the currently selected color map label to drop down a list of all color maps available in your system

Click **Reset** to return to the original 3D color map and to revoke your changes.

Click **Save** to save changes or to create a new color map. A dialog box opens. Enter a color map name and decide whether the new color map will be available for all users or for your user account only.

Click **Delete** to remove the selected color map from the list.

Color map editor

The color map editor shows the histogram of grayscale values or HU values of the selected dataset as a background image. The graphs that overlay the grayscale histogram represent the tissue types and their color and transparency settings for VRT rendering.

You can edit these graphs to change the color map.

- You can change the data window for a tissue type.

  See *Moving or resizing the histogram*

- You can select different colors for each graph or you can change the transparency settings for a tissue type.

  See *Editing a graph*

- You can change the tissue type description.

  See *Editing a graph*

- You can add or delete tissue type graphs.

  See *Adding or removing a graph*

Moving or resizing the histogram

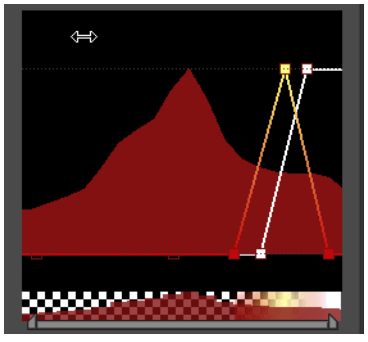
1. Click the black area above or below the grayscale histogram, and hold the mouse button down.

   The cursor changes its shape: it turns into a double-arrow.

2. Drag the mouse to the right or left to move the histogram and to show areas to the right or left that were previously hidden.

   -Or-

   Drag the cursor up or down to condense or expand the histogram.



Editing a graph

1. Click a graph to select it.
2. Drag the boxes along the bottom line of the histogram to change the window center and window width of this tissue type.

   -Or-

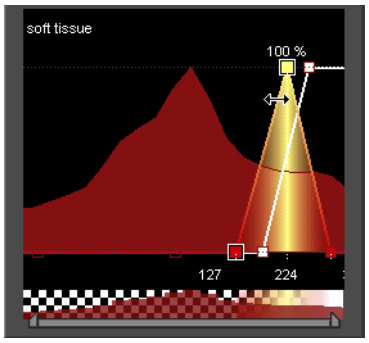
   Double-click the boxes along the bottom line or at the apex or apices to change the color definition of the graph.

   -Or-

   Drag these boxes up or down to change transparency settings.

   -Or-

   Click the tissue description text above the histogram and edit this text.



Renaming a graph

1. Select a tissue graph.

   The name of the selected tissue type appears above the graph section.
2. Select this text to overwrite it.

Adding or removing a graph

1. Right-click next to a graph to open a menu.
2. Select **New Tissue** to add a new graph.

   -Or-

   Select **Delete Tissue** to delete the selected graph.

   -Or-

   Select one of the listed tissue types for editing.

Display

On this tool card you can adapt display settings in the selected viewer. The **Display** tool card offers slightly different controls depending on the selected viewer and whether fusion mode is active or not.

Display tool card in fusion mode

When you have loaded suitable data, you use this tool card to turn fusion mode on and off and to adjust display settings.

Primary Dataset, Overlay Dataset

Use these check boxes to turn fusion mode on and off.

Select which dataset to display on top of the other from the drop-down lists below the **Primary Dataset** and **Overlay Dataset** check boxes.

Fusion display is particularly suitable for studies from combined multimodality scanners, such as CT-PET and CT-SPECT. However, you can also use this feature to overlay two CT series, for example.

Histogram and color map

Use the slider below a histogram to adjust the window settings for this dataset. Or drop down a list of color maps with the arrow button to the right of the histogram and select a suitable color map.

Fusion slider	Use this slider to fade between the primary and the overlay datasets. If you move the slider all the way to the left, only the primary dataset is visible. If you move it all the way to the right, only the overlay dataset is visible. If **Smart Fusion Slider** is configured in the tool properties for fusion mode, image display switches to grayscale inverse for a 100% PET image. See *Properties dialog box*, page 178, for information about how to configure tool properties.
Edge enhancement slider	Use this slider to adjust the sharpness of images. This slider is available only when the **Edge Enhancement** tool is selected.
Display tool card in nonfusion mode	When you have loaded data that is not suitable for fusion display, you use this tool card to adjust window level and image resolution.
Dataset selection	If you have loaded more than one dataset, use the drop-down list of the **Display** tool card to select which dataset to display.
Histogram and color map	Use the slider below the histogram to adjust window settings. Alternatively, drop down a list with the arrow button to the right of the histogram and select a color map.
Always Highest Resolution	This check box is available only if the active viewer is an MPR viewer, the CPR viewer, or the lumen viewer. Select this box to show full resolution images even during image processing. This might slow down system performance. To show a downsampled image during program interaction, clear this check box.

Cine

With the controls on the **Cine** tool card you can animate image display in a viewer. For example, you can scroll through images in an image stack, or play back a time series or a video. In the 3D viewer, you can rotate the volume or move the crop plane through the volume.

You can record these animations for presentation purposes, for example. You can save the resulting images as a new DICOM series (.dcm) on the primary server or send them to another DICOM server. Or save images on your computer as an MPEG movie (.mpg), or as JPEG (.jpg), PNG (.png), or DICOM (.dcm) images.

The **Cine** tool card looks slightly different depending on the loaded data and the selected viewer.

Cine tool card for MPR viewers	The following options are available for MPR viewers with image stacks or time series.
Batching	Select whether you want to scroll through the slice images (**Stack**) or whether you want to show a time series over the acquired time (**Time**).
Position	Select the first and last image of your movie.

Increment	Select an increment for scrolling. The increment can either be the **Same as Slice Thickness** or any other value in millimeters (**Custom**).
Frame Rate	Select **Frame Time**, **Frame Time Vector**, or **Recommended Display Frame Rate** to play back the movie with the frame rate defined in the DICOM data. -Or- Select **User-Defined** to define the frame rate in frames per second (**FPS**) here on the **Cine** tool card. -Or- Select **Default Cine Rate (User Property)** to play back the movie with a preferred frame rate, which you have defined in your user profile.
Play Speed	Use this slider to slow down or speed up playback interactively.
Update All Viewers	Only active for time series. With this check box you decide whether to apply cine mode to all viewers or to play the film in the selected viewer only.

Cine tool card for 3D viewers

The following options are available for 3D viewers.

Batching	Select an animation mode here: **Rotate** - this rotates the entire volume. **Crop** - this has a crop plane move through the volume. This option is shown only if the **Crop Plane** tool is currently turned on. **Time** - this plays the volume back over time. This option is available only if the loaded dataset is a time series.
Parameters	Select the rotation **Angle** (360° is full rotation) and **Increment**.
Axis	Select a rotation axis and decide whether this axis refers to the patient coordinate system (**Object Coordinates**) or to **Screen Coordinates**.
Frame Rate	Select **Frame Time**, **Frame Time Vector**, or **Recommended Display Frame Rate** to play back the movie with the frame rate defined in the DICOM data. -Or- Select **User-Defined** to define the frame rate in frames per second (**FPS**) here on the **Cine** tool card. -Or- Select **Default Cine Rate (User Property)** to play back the movie with a preferred frame rate, which you have defined in your user profile.
Play Speed	Use this slider to slow down or speed up playback interactively.
Best 3D Quality	Select this box for slow playback in best 3D quality.

Update All Viewers	Only active for time series. With this check box you decide whether to apply cine mode to all viewers or to play the film in the selected viewer only.
Cine tool card for CPR or lumen viewer	The following options are available if the active viewer is the CPR viewer or lumen viewer.
Batching	Select whether you want to scroll slice by slice (**Stack**) or whether you want to rotate around the segmented structure or vessel (**Rotation**).
Position, Increment	Only active if you have selected **Stack**. Select the first and last image of your movie. Select an increment for scrolling. The increment can either be the **Same as Slice Thickness** or any other value in millimeters (**Custom**).
Parameters, Axis	Only active if you have selected **Rotation**. Select the rotation **Angle** (360° is full rotation) and **Increment**. Select a rotation axis and decide whether this axis refers to the patient coordinate system (**Object Coordinates**) or to **Screen Coordinates**.
Frame Rate	Select **Frame Time**, **Frame Time Vector**, or **Recommended Display Frame Rate** to play back the movie with the frame rate defined in the DICOM data. -Or- Select **User-Defined** to define the frame rate in frames per second (**FPS**) here on the **Cine** tool card. -Or- Select **Default Cine Rate (User Property)** to play back the movie with a preferred frame rate, which you have defined in your user profile.
Play Speed	Use this slider to slow down or speed up playback interactively.
Best 3D Quality	Select this box for slow playback in best 3D quality.
Update All Viewers	Only active for time series. With this check box you decide whether to apply cine mode to all viewers or to play the film in the selected viewer only.

Cine tool card for videos

The following options are available if the active viewer shows a video.

Batching

Indicates that the active viewer displays a video file (MPEG or H264)

Frame Rate

Select **Frame Time** to play back the movie with the frame rate defined in the video.

-Or-

Select **User-Defined** to define the frame rate in frames per second (**FPS**) here on the **Cine** tool card.

-Or-

Select **Default Cine Rate (User Property)** to play back the movie with a preferred frame rate, which you have defined in your user profile.

Play Speed

Use this slider to slow down or speed up playback interactively.

Playback tools

Use the following tools on the **Cine** tool card to start or halt cine display:

Click **Play** or use the keyboard shortcut **C** to play your film back once.

Click **Pause** or use the keyboard shortcut **C** again to pause the playback.

Select **Loop** to play the film in an endless loop.

Click **Record** to open the **Cine Options** dialog box.
(Not possible if a video is displayed.)

Choose whether to save your film as an MPEG movie or as a slide show. Alternatively, you can save the film as a new DICOM series on your local computer or on a connected DICOM server.

Progress bar slider

Use this slider to fast-forward or rewind the video.

Line Profile

The **Line Profile** tool card shows the grayscale or HU value profile of a selected distance line. If there is only one line in the image, the profile of this line is shown even if you have not selected it.

If you have moved a distance line that was in your way no line profile can be shown. Move the distance line back to its original position to redisplay the line profile.

Controls on this tool card Use the controls on this tool card to save line profile data or to create a snapshot.

Linear/Log Select linear or logarithmic scale.

x/y- axis The x-axis shows the length of the line or lines, the y-axis represents grayscale values, HU (Hounsfield units), or SUV (standard uptake values).

In fusion mode, two profiles are shown, one for the primary image and one for the overlay image. The colors of the lines correspond to the colors of the units shown on the two y-axes.

 Click this button to create a snapshot of your line profile or profiles. The snapshot is sent to the **Export** window. From the **Export** window, you can save it to hard disk, or drag it into your report.

 Click this button to save the data of your line profile onto your hard disk as a comma-separated list (*.csv file).

Complex tools and applications

This section describes complex tasks and applications that involve more than one tool or a combination of tools from toolbars and tool cards.

Batching tools and tool card

Batching is a process that generates new slice images (reformats) from a volume dataset and saves them on the server or on your local computer.

Two types of batching are possible with Visage 7:

- *Stacked batching*
- *Rotational batching*

Stacked batching

Stacked batching is a process in which a new stack of coplanar reformats is created.

Stacked batching tools

When you click the **Stacked Batching** tool, a new toolbar appears in the lower right corner of the active viewer. Here you find tools for creating a new image series.

Toggle Direction

This button reverses the direction in which you will walk through the volume.

Toggle Aspect Ratio

This button plans new images either in the resolution of the viewer or in a standard 512x512 pixel resolution. 512x512 is available for grayscale images only.

Toggle RGB/Grayscale

With this button you select the color scheme for the reformats: grayscale or RGB.

Grayscale creates a new series of medical images. These images can be windowed, resized, or evaluated in future postprocessing sessions, just like any other DICOM series.

RGB images are snapshots and any information that they contain is burnt into the images. This means that you cannot change any of their display parameters or perform measurements in these images in future postprocessing sessions.

Save/Send

With this button you start the batching process and save your new series on the server or on a DICOM node. See *Saving, sending, or exporting images*.

Export

With this button, you start the batching process and export the new images to your local computer or to a folder in your network. See *Saving, sending, or exporting images*.

Open Tool Card

With this button, you open the **Batching** tool card in stacked batching mode. On the tool card, you can specify the number of images to be created, their slice thickness, overlap, and slice distance.

Cancel

With this button, you exit stacked batching mode without creating a new series.

Batching tool card in stacked batching mode

On the **Batching** tool card, you define slice parameters and you lock or unlock parameters.

Unlocking a parameter means that this slice parameter changes when you adjust the range of the new image stack graphically in the scout images.

Locking or unlocking of slice parameters affects only graphical processing steps. You can overwrite slice parameters on the **Batching** tool card irrespectively of whether they are locked or not.

Number of images This parameter defines how many new reformats will be created.

Image thickness This parameter defines the slice thickness of the new reformats.

Overlap This parameter indicates whether and how much images overlap. A positive value creates overlapping slices, a negative value creates gaps between slices.

Direction With these buttons, you define the direction in which you will walk through the volume.

Distance This parameter defines the distance between corresponding slice boundaries.

Properties With this button, you can open the configuration dialog box for stacked batching.

See also *Properties dialog box*, page 178.

Save/Send

With this button, you start the batching process and save your new series on the server or on a DICOM node. See *Saving, sending, or exporting images*.

Export

With this button, you start the batching process and export the new images to your local computer or to a folder in your network. See *Saving, sending, or exporting images*.

Rotational batching

Rotational batching is a process that creates new reformats from a volume dataset by rotating around a center point. In 3D this gives you the impression of walking around the volume. Rotational batching can be started from MPR viewers or from CPR viewers.

Rotational batching tools

When you click **Rotational Batching (Vertical)** or **Rotational Batching (Horizontal)**, a new toolbar appears in the lower right corner of the viewer. Here you will find tools for creating a new image series.

Toggle Direction

This button reverses the direction in which you will walk around the volume.

Center Rotation Axis

This button moves the rotation axis to the center of the preview image. This function is useful if you have panned the image in the viewer that is to become the preview before you started rotational batching.

Toggle Aspect Ratio

This button plans new images either in the resolution of the viewer or in a standard 512x512 pixel resolution. 512x512 is available for grayscale images only.

Toggle RGB/Grayscale

With this button, you select the color scheme for the reformats: grayscale or RGB

Grayscale creates a new series of medical images. These images can be windowed, resized, or evaluated in future postprocessing sessions, just like any other DICOM series.

RGB images are snapshots and any information that they contain is frozen into the images. This means that you cannot change any of their display parameters or perform measurements in these images in future postprocessing sessions.

Save/Send

With this button, you start the batching process and save your new series on the server or to a DICOM node. See *Saving, sending, or exporting images*.

Export

With this button, you start the batching process and export the new images to your local computer or to a folder in your network. See *Saving, sending, or exporting images*.

Open Tool Card

With this button, you open the **Batching** tool card in rotational batching mode. On the tool card, you can specify the number of images to be created, their slice thickness, overlap, and slice distance.

Cancel

With this button, you exit rotational batching mode without creating a new series.

Batching tool card in rotational batching mode

On the **Batching** tool card, you define slice parameters and you lock or unlock parameters.

Unlocking a parameter means that this slice parameter changes when you adjust the range of the new image stack graphically in the scout images.

Locking or unlocking of slice parameters affects only graphical processing steps. You can overwrite slice parameters on the **Batching** tool card irrespectively of whether they are locked or not.

Number of images This parameter defines how many new reformats will be created.

Angular increment This parameter indicates the increments between slices.

Image thickness This parameter defines the slice thickness of the new reformats.

Direction With these buttons, you define the direction in which you will walk around the volume.

Properties With this button, you can open the configuration dialog box for rotational batching.

See also *Properties dialog box*, page 178.

Save/Send

With this button, you start the batching process and save your new series on the server or on a DICOM node. See *Saving, sending, or exporting images*.

Export

With this button, you start the batching process and export the new images to your local computer or to a folder in your network. See *Saving, sending, or exporting images*.

Saving, sending, or exporting images

You can save, send, or export images from all the toolbars of all three batching modes and from the **Batching** tool card.

Save/Send or **Export** starts the actual batching process. It is not until you click one of these buttons that new images are actually created.

Tip

In Visage 7 we make a distinction between the concepts of saving, sending, and exporting data. **Saving** data means storing data on the Visage 7 server in DICOM format. **Sending** data means transferring data to a connected DICOM node. **Exporting** data means downloading data to the file system of your local computer, or to a network drive and folder.

Save/Send

With this button, you save the new series on the server or on a DICOM node. Clicking **Save/Send** opens the **DICOM Send** dialog box. Here you select send options:

Destination - select one or several servers where you want to save the new series.

Scout Images - select whether you want to include the scout images in the series. If you also select **Show Measurements and Annotations** and **Show Orientation Cube** under **Scout Images**, this refers to scout images but not to new reformats.

Series Number and Series Description - enter a series number and series description. For example, enter a high number to append the series to the end of the study.

Make Default - this button saves your settings as program suggestions for subsequent batching jobs.

Save - this button starts the batching process and sends the new series to the selected server or servers.

Export

With this button, you export the new images to your local computer or to any folder in your network. Depending on the color scheme that you selected earlier, clicking **Export** opens the **Export Grayscale** dialog box or the **Export RGB** dialog box.

Export as - select the file format of the new images. Note that the file formats *.jpg, *.mpg, and *.png are available only for RGB images but not for grayscale images. Note also that when you select DICOM for RGB images this creates snapshot images only. Windowing and measurements are only possible in new reformats of the type grayscale plus DICOM format.

Destination - click **Browse** to select a destination folder.

Scout Images - select whether you want to include the scout images in the series. If you also select **Show Measurements and Annotations** and **Show Orientation Cube** under **Scout Images**, this refers to scout images but not to new reformats.

Options - for grayscale DICOM images enter a series number and series description. For RGB images of any file format, select whether patient information and orientation labels are to be shown permanently in the images.

Export - this button starts the batching process and saves the images on your local computer or in a folder of your network.

3D segmentation tools and tool cards

Visage 7 provides various tools and techniques for 3D segmentation. 3D segmentation is the process of identifying objects in 3D and defining their contours. As a result of 3D segmentation, the system has assigned each voxel in the volume either to this object or to surrounding structures.

3D segmentation is relevant in a variety of contexts and for a variety of objects or structures. In all applications, 3D segmentation is the first step before objects can be removed or before structures can be analyzed in greater detail. Visage 7 provides tools for automatic, semiautomatic, or manual 3D segmentation and also permits a combined approach.

Tools for automatic removal of structures

These tools segment and remove specific structures automatically. Both tools are available for CT datasets only.

Caution

Automatic segmentation tools (remove table, remove leg bones, remove chest wall) support the physician by hiding structures that occlude important information in the images.

However, the software cannot guarantee that the detected pixels correspond to the actual anatomical structures for each individual patient and scan. It is the responsibility of the user to check whether any relevant structure has been accidentally removed. In that case, simply click the respective tool again to bring the removed structures back.

Remove Patient Table

Use this tool to remove the patient table from a CT dataset with a single click. Click the button a second time to redisplay the patient table.

Remove Chest Wall

Use this tool to remove the chest wall or rib cage from a CT thorax dataset with a single click. Click a second time to redisplay the chest wall.

Bone removal tool card

For CT angiography datasets, Visage 7 provides a tool for semiautomatic segmentation of the bones of the legs, or of pelvis and spine.

Caution

The **Bone** tool card supports the physician in finding bone structures in the image data.

However, the software cannot guarantee that the detected and displayed structures actually correspond to the bones of the pelvis, spine, and the bones of the legs. It is the responsibility of the user to check the plausibility and accuracy of the presented data.

Bone segmentation tools

The **Bone** tool card guides you through the segmentation process step by step.

Run Segmentation Algorithm

Select **Run Segmentation Algorithm** and also which bones you want to remove.

Next, click **Find Aorta**.

The system attempts to find the aorta and asks you to verify the aorta position before you continue.

If the system cannot identify the aorta, you are prompted to identify it manually. In an MPR viewer, scroll to a slice in which the aorta is clearly visible. Move the scout-line crosshair so that its center points to the aorta.

Next, click **Compute**.

Use these buttons to switch between display of vessels only, bones only, or display of both bones and vessels.

Click **Reset**, if bone segmentation did not yield correct results. Run the algorithm again. However, pay closer attention to the aorta verification step this time.

Load Pre-Computed Segmentation

Bone segmentation with the **Bone** tool card is automatically stored by the system.

The next time you load the same dataset, you do not have to perform bone removal again. Instead, load the results from the last segmentation run.

Select **Load Pre-Computed Segmentation** and click **Load**.

-Or-

Remove Leg Bones

Use this tool on the toolbar to reload bone segmentation.

If no segmentation information exists for this dataset, a message requests you to run the segmentation algorithm on the **Bone** tool card first.

Freehand cropping tool

Use this tool to segment structures manually.

1. Click the **Freehand Crop** button on the toolbar to select this tool.
2. Select the viewer that shows the structure that you want to crop particularly clearly.
3. Drag the mouse around the structure.

   When you release the mouse button the system closes the shape.

Freehand cropping tools

After you have drawn a freehand shape, a new toolbar appears in the lower right corner of the active viewer. Use the tools on this toolbar to remove the volume inside or outside the freehand shape.

Remove Inside

Use this button to remove all that lies inside the shape that you have just drawn.

-Or-

Remove Outside

Use this button to remove all that lies outside the shape that you have just drawn.

The system determines what to remove from the volume by extruding the shape through all slices in the direction orthogonal to the current image plane. These voxels are removed from the volume in the 3D viewer.

Remove Last Contour

Use this button to delete the last shape that you drew in this viewer.

Reset Remove

Use this tool to reset freehand cropping. The complete volume is shown again.

Accept and Exit

Click **Accept and Exit** to accept cropping and to close the **Freehand Crop** tool.

Edit tool card

The **Edit** tool card offers tools for threshold-based segmentation or contour-based segmentation and also for managing segmentation results.

Segmentation principles

Two basic principles exist for identifying a structure within a volume dataset:

- Threshold-based segmentation

  Threshold-based segmentation combines graphical identification of what to segment and definition of a range of grayscale or HU values.

- Contour-based segmentation

  Contour-based segmentation expects you to draw a contour around the structure that you want to segment in two or more slices. The system then connects the contours throughout the volume and identifies all voxels that lie within the 3D contour as belonging to the selection.

Key terms for managing 3D segmentation

To be able to manage 3D segmentation results efficiently, you need to be familiar with the following key terms:

- Selection

  When you identify a structure with threshold-based segmentation tools or contour-based segmentation tools, you create a selection. A selection is shown red until you add it to an object, remove it from an object, or clear the selection.

- Object

  An object is a named 3D segmentation result. You can add selections to an object, remove selections from an object, and show, hide, and fade objects that you have segmented in your volume.

Tools on the Edit tool card

Use these tools on the **Edit** tool card to segment portions of the volume and manage objects.

Connected Voxels in Value Range (3D)

When you select this tool, the system highlights certain structures in the MPR viewers. These structures have a grayscale or HU value that lies within the range that is defined by the **Data Range** slider on the **Edit** tool card. In the 3D viewer, only structures of this data range are visible now.

Now click the structure of interest. This is either a visible structure in the 3D viewer, or a yellow area in an MPR viewer. The system creates a selection now. The selection is shown red.

Encircle Voxels in Value Range (3D)

When you select this tool, the system highlights structures of the range defined by the **Data Range** slider in the same way as for the tool above.

Now draw a freehand shape around the structure of interest. Circle either a yellow structure in an MPR viewer or a visible structure in a 3D viewer. The system creates a selection now. The selection is shown red.

Encircle Voxels in Value Range (2D)

When you select this tool, the system highlights structures of the range defined by the **Data Range** slider, in the same way as for the tools above.

Now draw a freehand shape around a yellow structure of interest in an MPR viewer. This selects all voxels within the freehand shape that lie within the specified data range but only in one slice. If you zoom in on the volume in the 3D viewer you see that only a small ribbon is shown red.

Data Range

Use the data range slider or **Min.** and **Max.** boxes to define or fine-tune the data range of the structure that you want to segment.

Define Contour in 3D

This tool starts contour-based segmentation, which is independent of the data range that is defined by the **Data Range** slider.

When you select this tool, a new toolbar appears in the lower right corner of the active viewer.

Select **New Elliptical Contour** or **New Freehand Contour** and roughly circle the area of interest, or select **New Balloon Contour**, click, and drag out. (See also *Freehand 3D ROI*, page 87)

Use the **Refine Contour** tool to correct and refine contour lines.

Click anywhere in the image and drag the mouse to show a circle with which you can correct the ROI graphic. The further away from the contour line you click, the larger the circle will be.

Click inside the ROI graphic to enlarge the ROI graphic by pushing the contour out. Click outside the ROI graphic to use the circle to push the contour line in.

The precision required in contour definition depends on the clinical task at hand. Use your clinical judgement to determine the required accuracy for this contour definition task.

Scroll to the next slice, and repeat contour definition and refining. You do not have to use the same contour definition tool in all slices. Choose whichever tool is most appropriate from slice to slice. Moreover, you do not have to define a contour in all slices. If the contour of the structure does not change significantly for a few slices you can skip contour definition in these slices.

Proceed in the same way in several slices until you reach the last slice in the image stack that shows the structure.

Click **OK** when you have finished drawing and refining the contour in the last slice. **OK** ends contour-based segmentation. The system interpolates your contours and creates a selection, which is shown red.

Use the **Grow** and **Grow 2x** buttons to expand the selection by a few pixels.

-Or-

Use the **Shrink** and **Shrink 2x** buttons to reduce your selection.

Use **Clear** to undo a selection that you have not yet assigned to an object, and to start again from scratch.

Objects list

By default, this list contains the objects **Exterior** and **Cropped**.

Consider **Cropped** a generic container for any portions of the volume that you want to remove but not name. **Exterior** is a container for all portions of the volume that are not assigned to **Cropped** or any other object.

If you have already performed segmentation with another segmentation tool, such as the **Remove Patient Table** tool, these objects are also listed here.

Right-click the list to create a new object or to manage existing objects in the list.

Click the plus button to the right of an object to add a selection to an object.

-Or-

Click the minus button to the left of an object to remove a selection from this object.

Use the lock button to the right to allow modification of an object (green and open lock) or to protect an object from accidental modification (red and closed lock).

Structures tool card

You use the **Structures** tool card to perform contour-based segmentation of a complex structure, for example, a tumor or an entire organ. You can then evaluate the structure, calculate its area or volume, and move on to the **Statistics** tool card.

Contour-based segmentation

Contour-based 3D segmentation expects you to draw a contour around the structure that you want to segment in several slices. The system connects the contours throughout the volume and identifies all voxels that lie within the 3D contour as belonging to the selection.

2D and 3D structures

On the **Structures** tool card, you can segment both 2D structures and 3D structures.

2D and 3D structures are the same as freehand 2D or 3D ROIs that you draw with the corresponding tools from the toolbar. See also *Freehand 2D ROI*, page 86, and *Freehand 3D ROI*, page 87.

Freehand 2D structure

Click the **New 2D** button on the tool card. A new toolbar appears in the lower right corner of the active viewer.

New Elliptical Contour

Use this button to enclose the area of interest with an ellipse. Click a start point, and drag the mouse out to draw a circle or ellipse.

New Freehand Contour

Use this button to draw a freehand shape. Click a start point on the contour. Hold the mouse button down and draw a contour line.

New Balloon Contour

Use this tool to draw a border around a structure or area of interest of a specific brightness. Click in the structure and drag out.

Append mode

With any of the contour tools, use the **Shift** key to start **Append** mode (the cursor turns into an arrow with a plus sign).

Draw a contour or select a contour you have drawn earlier.

Press and hold the **Shift** key down and then draw a second contour.

If the contours overlap, the system merges them into a single ROI. If the contours do not overlap, the system nevertheless interprets them as parts of a single region of interest. Add a third contour to this ROI, if necessary.

Release the **Shift** key to turn **Append** mode off again.

Refine Contour

Use this tool to correct or refine contour lines.

Click anywhere in the image and drag the mouse to show a circle with which you can correct the ROI graphic. The further away from the contour line you click, the larger the circle will be.

Click inside the ROI graphic to enlarge the ROI graphic by pushing the contour out. Click outside the ROI graphic to use the circle to push the contour line in.

Undo

Use **Undo** to retrace your steps.

OK

Click **OK** when you have finished drawing and refining 2D ROIs to close the tool.

Freehand 3D structure

Click the **New 3D** button on the tool card.

A new tool card appears in the lower right corner of the active viewer.

New Elliptical Contour

Use this button to circle the area of interest with an ellipse. Click a start point, and drag the mouse out to draw a circle or ellipse.

New Freehand Contour

Use this button to draw a freehand shape. Click a start point on the contour. Hold the mouse button down and draw a contour line.

New Balloon Contour

Use this tool to draw a border around a structure or area of interest of a specific brightness. Click in the structure and drag out.

Append mode

With any of the contour tools, use the **Shift** key to start **Append** mode (the cursor turns into an arrow with a plus sign).

Draw a contour or select a contour you have drawn earlier.

Press and hold the **Shift** key down and then draw a second contour.

If the contours overlap, the system merges them into a single ROI. If the contours do not overlap, the system nevertheless interprets them as parts of a single region of interest. Add a third contour to this ROI, if necessary.

Release the **Shift** key to turn **Append** mode off again.

Refine Contour

Use this tool to correct or refine contour lines.

Click anywhere in the image and drag the mouse to show a circle with which you can correct the ROI graphic. The further away from the contour line you click, the larger the circle will be.

Click inside the ROI graphic to enlarge the ROI graphic by pushing the contour out. Click outside the ROI graphic to use the circle to push the contour line in.

When you have finished drawing and refining a ROI graphic in one slice, scroll on to the next slice and also draw a ROI there.

Undo

Use **Undo** to retrace your steps.

OK

Click **OK** when you have finished drawing and refining ROI graphics in all slices.

The system calculates ROI statistics and closes the freehand 3D ROI tool.

Editing structures

Use the structures list on this tool card to select ROIs or contours for editing.

Click a ROI or a contour to show the slice that contains the ROI graphic.

The freehand ROI toolbar opens in the lower right corner of the viewer. You can now refine the ROI or add more contours to a 3D structure.

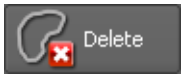
-Or-

Right-click a ROI or a contour to rename it.

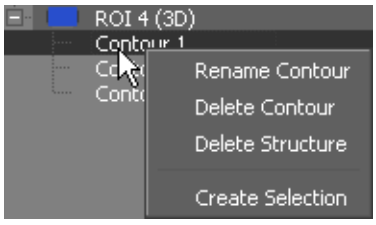
-Or-

Use the **Delete Structure** button or the context menu of the structures list to delete a ROI.

Use the button to delete an entire ROI.



Use the context menu if you want to delete only a single contour in a 3D ROI.



Tip

If ROI graphics are in your way in further image evaluation steps, clear the **MPR** check box in the structures list. This hides ROI graphics in MPR viewers.

ROIs are usually not shown in the 3D viewer. Select the **3D** box for a ROI in the structures list to ensure that this ROI is visible in the 3D viewer.

Converting a ROI into an object

When you create a 3D structure or freehand 3D ROI, the program assumes that you want to perform statistical evaluation of this volume of interest. The program does not automatically assume that you want to turn it into an object too.

To turn a 3D structure or freehand 3D ROI into an object, proceed as follows:

1. Select the 3D ROI on the **Structures** tool card.
2. Right-click and select **Create Selection**.
3. Go to the **Edit** tool card.
4. Create a new object and add the selection to the new object.

See also *Objects list*, page 128.

Statistics tool card

The **Statistics** tool card performs statistical analysis of all ROIs and structures that you have defined in your dataset:

- Volumes of interest that you have cropped with the **Freehand Crop** tools
- The table, if you removed it with the **Remove Patient Table** tool
- Bones that you have segmented with the **Bone** tool card
- The chest wall, if you removed it with the **Remove Chest Wall** tool
- Vessels that you have analyzed with the **Vessel** tool card
- Structures that you have defined on the **Structures** tool card
- Objects that you have segmented and named on the **Edit** tool card
- Lesions that you have segmented with the **Segment Lesion** tool on the **Lesion** toolbar

Tip

For a better overview, show the **Statistics** tool card as a floating window.

Double-click the **Statistics** tab in the tool card section.

Statistics for the report

1. Click **Compute** to update the results table on the **Statistics** tool card.

2. Click the **Snapshot Statistics** button in the upper left corner of the **Statistics** tool card.

This button creates a snapshot of the entire results table and sends it to the **Export** window. You can drag the snapshot into your report from there.

-Or-

Select one or several rows in the results table and click the **Snapshot Selected Statistics** button if only selected measurements are relevant for the report.

Exporting results

If you want to evaluate statistics any further, export the entire results table or only individual lines as comma-separated lists (*.csv). Comma-separated lists can be imported in spreadsheet programs, such as Excel.

Click **Export CSV**.

-Or-

Select one or several rows in the results table and click **Export CSV Selected**.

Vessel analysis tools and tool card

Visage 7 provides tools specifically for the segmentation and analysis of vessels in 3D datasets of CT and MR angiography studies.

These tools are available from the **Vessel** tool card and from toolbar buttons. If you plan to trace more than one vessel in a dataset, start from the **Vessel** tool card.

Caution

Vessel tracing supports physicians in finding vessel-like structures in the image data and in navigating quickly along these structures for efficient review.

However, the software cannot guarantee that the detected and displayed structures correspond to an actual vessel fragment. It is the responsibility of the user to check the plausibility and accuracy of the presented data.

1. Select and name the vessel you are about to trace.

   -Or-

   Right-click the vessels list and insert a new vessel.
2. Define and edit a curve and start vessel tracing.

   See *Curve definition and vessel tracing*.
3. Switch to one of the overview and analysis views for further vessel evaluation.

   See *Curved View*, page 136, or *Lumen View and Cross-Section View*, page 136.

Curve definition and vessel tracing

You use the **Define/Edit Curve** tool on the toolbar or on the **Vessel** tool card to start curve definition.

Defining a new curve

1. Click **Define/Edit Curve** to start curve definition mode.
2. Now click control points along the vessel, either in the 3D viewer, or in MPR viewers, or in a combination of both.
3. End curve definition and have the system trace the vessel.

Semiautomatic versus manual vessel tracing

When you define a curve and trace a vessel be aware that two vessel tracing modes exist, semiautomatic vessel tracing and manual vessel tracing.

- In semiautomatic vessel tracing a user clicks control points and the software searches for the vessel segments between these points. Semiautomatic vessel tracing uses a tracing algorithm that uses information such as pixel value thresholds and gradients to identify vessel segments.

  Click points between which you want the system to trace the vessel. This creates green dots in the images.

- In manual vessel tracing the program assumes that the user-defined control points lie on the centerline of the vessel. The software then connects these points by straight lines instead of performing a search.

  To define manual control points, press and hold the **Shift** key while you click. This creates blue dots in the images.

Tip

You can even combine the two methods to connect critical points where automatic, that is voxel-density-based tracing, would fail.

Image navigation during curve definition

Even while you are defining or editing points, you can return to standard image navigation functions by holding the **Ctrl** (Windows) or **Cmd** (Mac) key down. For example, press and hold the **Ctrl** or **Cmd** key and drag in an MPR viewer to scroll through the stack, or drag in a 3D viewer to rotate the volume.

Switching endpoints

When you define a new control point for a vessel, the software automatically connects it to the closest endpoint of the vessel. This point is shown as a pink box.

In very curved vessels, both endpoints might lie close to the new point and the software might pick the wrong endpoint. If this happens, switch to the correct endpoint manually. Press and hold both the **Shift** and **Ctrl** (Windows) or **Cmd** (Mac) keys when you define a new point.

Editing existing curves or vessels

If you have already defined a curve or vessel, use the **Define/Edit Curve** tool to edit control points and points inserted by the software.

1. On the **Vessel** tool card, select the curve or vessel that you want to modify.
2. Click **Define/Edit Curve** to start curve-editing mode.

   Now you can see points along the curve in your MPR and 3D viewers.
3. Click a point to position the MPR crosshair exactly on this point.

   -Or-

   Click a point and drag the mouse to change its 3D position but without positioning the MPR crosshair on this point. After you have moved a point, the software retraces the segments adjacent to this point and adjusts the curve accordingly.
4. To delete a point, briefly rest the cursor on the point to select it, then press the **Del** or **Backspace** key. Surrounding curve segments are retraced.

   -Or-

   To define new points, position the mouse away from an existing point and click, or press and hold the **Shift** key and click. New points are connected to the closest endpoint of the curve.

   -Or-

   Position the cursor between two existing points to highlight a curve segment. Click the segment and drag the mouse to define an additional control point between two existing points.

Tools in the curve editing toolbar

When you select the **Define/Edit Curve** tool, a new toolbar appears in the lower right corner of the active viewer.

Large Vessel Tracing

Click this button when you have finished clicking points along the length of the relevant vessel section and when you are analyzing a large vessel.

-Or-

Small Vessel Tracing

Click this button if you are analyzing a small vessel, and in particular a coronary vessel.

To start large or small vessel tracing you can use either a tool on the toolbar or a tool card button. Both the tools and buttons start the same function. Both the large and small vessel tracing tools also end curve-editing mode.

Show All Vertices

This button is particularly useful if you are using MPR viewers and not the 3D viewer to define a curve along a vessel.

Show All Vertices projects the curve that you have defined so far onto the currently shown slice. If you switch **Show All Vertices** off, only those points that lie in the currently displayed slice are visible.

Undo

Click this button to undo the last curve editing step.

-Or-

Clear Points

Use the **Clear Points** button on the **Vessel** tool card to delete all points and start curve definition again from scratch.

Accept and Exit

Click **Accept and Exit** to end curve definition without actually tracing a vessel but to create a curved view only.

Curved View

Use this tool to open curved view, which is an additional viewer.

If you have not yet defined a curve, this viewer is empty. After you have defined a curve this viewer shows a projection image of a curved plane defined by the vertices of your curve definition.

See also *Curve definition and vessel tracing*, page 133.

Navigating in curved view

1. If you have traced more than one vessel, use the context menu of the CPR viewer to select which vessel you want to display.
2. Click **Toggle Centerline** for better orientation.

   See also *Toggle Centerline*, page 105.
3. Rotate around the centerline in curved view. Rotation is the standard navigation tool in the CPR viewer.

   
4. Press and hold the **Alt** key, and click a point on the vessel in the CPR viewer.

   The crosshair moves to exactly this point in all MPR viewers.

Curved view other than in vessel analysis

You can use curved view not only in the context of vessel analysis but also to analyze curved structures.

1. For example, use the **Define/Edit Curve** tool to define a curve along the spine.
2. End curve definition with **OK**.

   See also *Curve definition and vessel tracing*, page 133.
3. Open curved view.

Lumen View and Cross-Section View

Lumen view and cross-section view are two views particularly for the analysis of vessels. Both views are not available in any other context. Both views are available only if you have defined a curve and then clicked either the **Large Vessel Tracing** or the **Small Vessel Tracing** tool.

See also *Curve definition and vessel tracing*,page 133.

Navigating along the vessel in lumen view

1. If you have traced more than one vessel, use the context menu of the lumen viewer to select which vessel you want to display.
2. Rotate around the vessel.

   The rotation tool is selected automatically in this viewer. Therefore, you can rotate by dragging the left mouse button.

3. Drag one of the vessel sliders to a point of interest.

   The active vessel slider is highlighted with an orange triangle at its bottom.
4. Click **Switch Active Vessel Slider** to switch between vessel sliders.

   Alternatively, use the keyboard shortcut **E** to switch vessel sliders.

Navigation in cross-section view

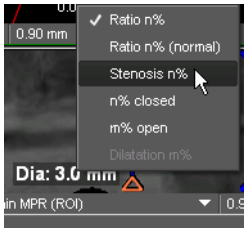
Clicking and dragging a vessel slider in lumen view turns cross-section view on in the upper left viewer.

Scrolling in cross-section view means navigating along the vessel slice by slice. While you scroll, the slice orientation changes so that you always see an exact cross-section of the vessel.

Measuring stenoses

1. Use lumen view, or cross-section view, or a combination of both views to move to points of interest along the vessel.
2. In cross-section view, use the **Distance** tool to measure vessel cross-sections.

   In lumen view, measurement results are shown next to the vessel sliders.
3. Right-click a measurement text and classify the measurement. For example, select **Stenosis n%**.



   If **Stenosis n%** is not available, you might have right-clicked the vessel slider and not the text. Or you have clicked the text of the reference point, which is the higher value.

Measuring vessel segment length

In lumen view, use the **Distance** tool to measure the length of a vessel segment.

The segment length is shown in millimeters in lumen view and the endpoints of the measurements are indicated in curved view. Measurements are color-coded in both views.

Cardiac analysis for CT studies

Cardiac analysis options require that the cardiology option is installed and that your user account has been granted the right to work with this option.

LV Analysis tool card

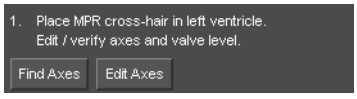
The **LV Analysis** tool card provides tools for LV segmentation and LV analysis. The tool card also guides you through LV analysis step by step.

Caution

The LV tools support the physician in finding the left ventricle in the image data. However, the software cannot guarantee that the detected and displayed structures correspond to the left ventricle. It is the responsibility of the user to check the plausibility and accuracy of the presented data.

Step 1: finding and correcting axes

1. Move the scoutline crosshair to the left ventricle in one MPR viewer.
2. Click **Find Axes** on the **LV Analysis** tool card.

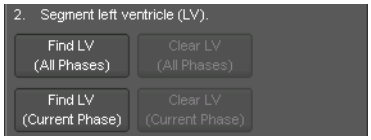


   The system identifies the long and short axes of the left ventricle and selects **Edit Axes** mode. The short and long axes are now shown as orange lines in the MPR viewers.
3. Correct axes by moving or rotating the orange lines in the MPR viewers, if necessary.
4. Next, correct the valve level in one of the long-axis views (pink line).

   The endpoints of the valve line serve as rotation handles.
5. When you have positioned axes correctly, click **Apply**.

Step 2: segmenting the left ventricle

1. Click **Find LV (All Phases)**.



When segmentation is complete, the left ventricle is shown as a yellow shaded area in the MPR viewers.

2. Browse phase images, and check segmentation results in all phases.

If you do not agree with segmentation results in one or several images, click **Clear LV.** Adjust the valve level and the axes as described above.

Click the **Find LV** button again when you have finished your adjustments.

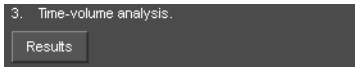
-Or-

Proceed slice by slice and use the **Clear LV (Current Slice)** and **Find LV (Current Slice)** buttons.

When segmentation has been performed correctly, proceed with LV analysis step 3.

Step 3: time-volume analysis

Click **Results** to start time-volume analysis of the left ventricle.



LV Results tool card

The **LV Results** tool card or floating window appears after you have clicked **Results** on the **LV Analysis** tool card.

LV analysis results

When the **LV Results** is a floating window, it consists of three segments:

- Summary section
- Curve display section
- AHA (American Heart Association) bull's-eye view

When you display the **LV Results** card in one of the tool card stacks, only one of these segments can be shown at a time.

Use the drop-down selection box in the lower left corner of the tool card to select a different view of your LV analysis results.

Summary

Enter the heart rate of your patient here. The cardiac output value is updated automatically.

Also adjust the system's selection of the end-diastolic (ED) and end-systolic (ES) phases with the sliders, if necessary.

Global volume Here you find a graph of the total LV volume over one heart cycle.

Bull's-eye view View the results of the calculation of regional ejection fractions (%) in a bull's-eye view. The segments in this bull's-eye display correspond to the AHA classification.

Move the cursor over a segment to show the segment designation as a tooltip. Or right-click anywhere in the bull's-eye view for a context menu with commands for switching between results view and segment ID view.

Regional volume, endocardial distance In this segment you find the stroke volume curves of the LV regions.

Initially the curves of all regions are shown. If you find this view hard to read, right-click anywhere in this section. Select individual region curves.

When you create a report, only those curves that are currently shown will be included.

Wall motion, bull's-eye motion This segment shows the accumulated wall motion in a bull's eye view.

Click **Report** in the lower right corner of the **LV Results** window to send snapshots of all graphs and analysis results to the **Export** window.

Calcium tool card

Visage 7 provides a tool card for identifying the extent of calcified plaque in coronary arteries. The **Calcium** tool card is shown when you load a suitable CT study.

Tools for identifying plaque Use the following tools on the **Calcium** tool card to identify plaque in your images.

Click the **Calcium Scoring** button.

All areas with an intensity of more than 130 HU are highlighted (yellow).

Now start scrolling through the image stack slowly.

When you observe plaque in an image, first select the vessel in which the plaque is observed. Next, either click into the plaque or click and drag the mouse to draw a line around the plaque. This assigns the plaque to the selected vessel.

To select a vessel, click one of the following buttons on the tool card: **LM** (left main artery), **LAD** (left anterior descending artery), **CX** (left circumflex artery), **RCA** (right coronary artery), **PDA** (posterior descending artery), **A1, A2, A3** (placeholders for any other arteries).

Right-click one of the A1 to A3 artery buttons and select **Properties**. Enter a label and select a color for this artery.

In multislice mode, both voxels in the slice in which you click and adjacent voxels of the same density in adjacent slices are assigned to plaque.

With multislice mode turned off, only voxels of the currently displayed slice are assigned to plaque.

Reporting tools At the bottom of the **Calcium** tool card, you find tools and input boxes that help you to prepare your report.

Coronary Artery Age The system calculates this information based on the amount of plaque that you have identified in the images. You cannot overwrite this information.

Sex, Patient Age Correct this information, if necessary.

Ethnicity The information that you select here refers to the study that you want to refer to in your report:

Select **Undefined**, if you want to refer to Hoff, 2001.
(Hoff, Julie Anne et al. Age and Gender Distributions of Coronary Artery Calcium Detected by Electron Beam Tomography in 35,246 Adults. J. Am. Coll. Cardiology 2001, Vol. 87:1335-1339)

Select **White, Black, Chinese, Hispanic**, if you want to refer to MESA, 2006.
(McClelland, Robyn L. et al. Distribution of Coronary Artery Calcium by Race, Gender, and Age: Results from the Multi-Ethnic Study of Atherosclerosis (MESA). Circulation 2006, 113:30-37).

Click **Report** to send your findings to the **Export** window.

-Or-

Click **Export CVS**, to save your results as a comma-separated list on your computer. *.cvs files can be read by spreadsheet programs, such as Excel.

Brain perfusion analysis tools and tool card

Brain perfusion analysis requires that the neurology option is installed and that your user account has been granted the right to work with this option.

Perfusion toolbar

This toolbar comprises all the tools that you need to perform brain perfusion analysis.

Caution

The brain perfusion tool provides calculated results for neurologic diagnosis and supports the physician in correcting patient movement in images.

However, the software cannot guarantee that the identified arterial and venous points are correct. It is the responsibility of the user to check the plausibility and accuracy of the result.

The tools are arranged left to right in the order in which you will need them.

Display tMIP

As a first step in brain perfusion analysis, click this tool to calculate a tMIP image.

In a temporal MIP of a CT dataset, the brightness of each pixel indicates the maximum pixel value in any of the time steps. In MR datasets, tMIP shows the minimum pixel value. tMIP helps to show contrast-filled vessels particularly clearly.

Define Artery

As a second step, click this button and then the main artery of the brain in the tMIP image.

The point where you clicked is marked as a ROI and an uptake curve for this ROI appears in the viewer. The update curve for the artery is displayed red.

Define Vein

As a third step, click this button and then the main vein of the brain in the tMIP image.

The uptake curve of the vein is added to the graph. The uptake curve for the vein is displayed blue.

Identification of the vein is necessary in CT datasets, but usually not in MR datasets.

Calculate Perfusion

Next, click **Calculate Perfusion**.

This calculates the following functional maps: mean transit time (MTT), time to peak (TTP), cerebral blood flow (CBF), cerebral blood volume (CBV).

Mirror Mode

Select the tMIP image (large viewer) and click **Mirror Mode**.

Drag the orange line so that it separates the left and right half of the brain. By clicking and dragging the endpoints you can rotate the line. You might have to move the plot if it is in your way.

Define ROI

Select one of the functional maps, and click **Define ROI**.

A new toolbar appears in the lower right corner of the active viewer. The tools on this toolbar are the same as when you evaluate freehand 2D ROIs in any other type of image. Therefore, refer to this section for details on how to work with these tools: *Freehand 2D ROI*, page 86.

Use this toolbar to draw an elliptical ROI or a freehand ROI around an area of interest and to refine the contour.

Toggle Mirror Line

If the mirror line is in your way while you are analyzing functional images, use this tool to hide and later redisplay it. Hiding the mirror line does not turn mirror mode off, however.

Brain Perfusion tool card

In standard brain perfusion analysis, you might not need to adjust parameter settings on the **Brain Perfusion** tool card.

Adjust these settings only if default settings do not yield good results.

Value Range for Brain

To speed up calculation and to make interpretation of computed maps easier, only brain tissue voxels are processed in brain perfusion analysis. Therefore, a mask is computed from the first phase of the perfusion image series. The mask includes only voxels with values between the **Min** and **Max** values that are defined here. All other voxels are not analyzed during computation.

Default values 0 (**Min**) and 120 HU (**Max**) for CT images and 10% and 100% of the grayscale value range in an MR dataset (indicated as OT for "other type", meaning unspecified).

Images before contrast application

This parameter indicates the number of phases acquired before the contrast medium reaches the brain. The baseline signal is computed by averaging these images. After definition of the artery, the number of baseline images is determined automatically.

With this slider you can adjust these program suggestions and exclude more or fewer precontrast images.

Limit analysis

Use this slider to exclude late images from the analysis.

Use the uptake curve of the main artery to check how many images you exclude when you move the slider.

Hematocrit value small to large vessel

Contrast agent distributes in blood plasma only. The volume of blood plasma varies with the vessel size, which is specified by the hematocrit ratio between small and large vessels. Because the arterial input function is measured in a large vessel but tissue perfusion is mostly supplied by capillaries, a correction has to be applied when quantifying perfusion for brain tissue.

By default, the program suggests a standard value for adults.

Click the **Default (small children)** button if you are analyzing a brain perfusion study of a small child. You find this button at the bottom of the tool card.

-Or-

Move the slider to adjust the value manually.

Hematocrit value large vessel

Hematocrit value for large vessels such as arteries and veins.

Artery radius

When you define an artery in the image, all voxels within a radius specified by this parameter are processed and the best of those voxels are selected for determining the arterial input function.

Vein radius

Same as artery radius for determining voxels for the venous input function. In MR perfusion analysis, calibration with a venous input function is not possible and this parameter has no effect.

Smoothing

To improve the signal-to-noise ratio (SNR), a Gaussian image filter can be applied to all images before the computation. This parameter turns the smoothing filter on or off and also allows the adjustment of the kernel width of the filter. Larger values improve the SNR at the expense of a diminished spatial resolution.

Density Factor

Blood flow and blood volume are calculated per 100 g of brain tissue. This parameter specifies the density of brain tissue. Brain tissue density allows conversion of perfusion values per voxel volume into units of ml/100 g/min for blood flow and ml/100 g for blood volume. In MR perfusion analysis, calibration with a venous input function is not possible and this parameter has no effect.

If you observe motion artifacts in the tMIP image, register your data before you continue.

Use the **2D Registration** and **3D Registration** buttons on the tool card to align images and to recalculate the tMIP image.

Use the **Default (adult)** and **Default (small children)** buttons to switch hematocrit values between program suggestions for adults and small children. You can fine-tune these values with the slider further up on this tool card.

Use the **Calculate Perfusion** button at the bottom of the tool card or toolbar button if you want to recalculate functional maps after parameter adjustments.

Lesion tracking tools and SUV tool card

Lesion tracking requires that the oncology option is installed and that your user account has been granted the right to work with the oncology option.

SUV tool card

Use the **SUV** tool card to check patient data and SUV settings.

Settings on the SUV tool card

Check these settings after you have loaded a CT+PET study and before you start lesion tracking.

Patient's weight, height, and sex

Check this information and add missing information. This information is relevant for the calculation of SUV for lean body mass and SUV for body surface area.

Radionuclide half-life, total dose, tracer injection, scan time

Check this information and add missing information, if necessary.

If you have changed patient or radionuclide information, you can use this button to redisplay the data stored in the DICOM header of the dataset.

Measured Activity, SUV, Counts

With these buttons you can select the units for radionuclide activity in the patient's body. Choose between becquerel or standardized uptake values (SUV), or select **Counts** for data acquired with Philips scanners.

Make Default

This button stores the values for the initial data windows and for the preferred SUV type in the global settings for your user account.

Lesion tool and Lesions tool card

Use the **Lesion** tool and toolbar to mark and measure lesions.

Use the **Lesions** tool card for an overview of all the lesions that you have identified in the loaded datasets.

Lesion tool

Click the **Lesion Tool** button to show a new toolbar in the lower right corner of the active viewer.

This toolbar comprises all the tools that you need for lesion tracking.

Segment Lesion

Click the lesion in the current study and also in the prior study, if the lesion is visible in both studies.

If you have identified the lesion in both studies, the system creates a lesion pair, labels it, and calculates activity.


Measure Lesion, Measure Lesion (2 Diameters)

If automatic lesion segmentation is not possible because of poor image quality or because of artefacts in the images, resort to manual evaluation tools.

Select either the **Measure Lesion** or **Measure Lesion (2 Diameters)** tool, depending on which standard you follow. Drag the mouse across the lesion to measure its diameter. Also measure the second diameter, if you work with the **Measure Lesion (2 Diameters)** tool. Measure lesion dimensions in the prior study as well.

Caution

The accuracy of distance measurements is ± 2 pixels. Larger errors can occur if the image is displayed with reduced matrix size, that is, if not every original pixel is shown on the screen due to zoom-out. For optimum accuracy, we recommend zooming into the structure of interest as much as possible. The accuracy is further limited by the physical resolution of the acquisition itself. If the monitor used for display does not permit exact pixel selection, the inaccuracy can be still greater.

Mark Lesion

If a lesion does not exist in both datasets, use this tool to mark the spot where a lesion exists in the other dataset.

Delete Lesion

Select a lesion by clicking on the lesion text and then use this tool to remove the marker from the dataset.

Classify Lesion

Use this tool or the keyboard shortcuts to classify a lesion or lesion pair.

A **Target Lesion (TL, F1)** or a **Target Lymph Node (LN-TL, F4)** exists in both the current and prior study and is relevant in both studies.

A **Non-Target Lesion (NTL, F2)** or a **Non-Target Lymph Node (LN-NTL, F5)** exists in both studies but is of no relevance in the prior study.

A **New Lesion (NL, F3)** or a **New Lymph node (LN-NL, F6)** exists in the current study only.

An **Unspecified Lesion (F10)** is not considered in the report. Therefore, do not leave lesions unspecified, unless you explicitly want to exclude them from the report.

Previous Lesion, Next Lesion

Use these tools to browse through your lesion segmentations and to review your findings.

Accept and Exit

Click this tool when you have identified and classified all lesions in your current and prior study. This tool closes the lesion tool and creates a report in the **Export** window.

Lesion tool card

Click the **Open Lesion Toolcard** button to show this tool card.

The Lesions tool card displays an overview of the lesions that you identified in the loaded studies.

Tip

If the tool card section along the edge of the screen is too narrow to show all prior studies in the **Lesions** tool card, show the tool card as a floating window.

Double-click the **Lesions** tab and drag the window so that it is not in your way while you are reading the images.

Name

The **Name** column lists all lesions and a summary of lesion diameters in target and non-target lesions.

Click **New Lesion** and measure a lesion in an image to identify a new lesion.

Double-click a lesion name in this column to edit the lesion name.

Right-click a lesion in this column or any of the other columns and select **Delete** to remove a lesion from the list.

Type

Double-click the **Type** column of a lesion and then the double-arrow button that appears when you double-click. Select a different lesion type from the list. See also *Classify Lesion*, page 146.

Cur

P1 ... Pn

The columns of the current and prior studies show the diameters of the lesions that you identified in the images.

Click the column header of the current study or a prior study and drag it into a viewer to show this study in this viewer.

Use the context menu in these columns to split or merge lesions.

Splitting lesions: You have identified areas of activity in corresponding images of the current and prior study and the system has assigned them to one lesion. In retrospect, you realize that both areas of activity belong to different tumors.

Right-click the current or prior study column of this lesion and select **Split into New Lesion**.

Merging lesions: You have identified two areas of activity in the current and prior study and marked them as two separate lesions. In retrospect, you realize that both areas of activity belong to the same tumor.

Select (left-click) the table row of one lesion, and then right-click the table row of the second lesion. Select **Merge With Selected Lesion** from the context menu.

Previous Lesion, Next Lesion

Use these tools to browse through your lesion segmentations and to review your findings.

Select the **Follow** button to browse lesions in the current and prior studies simultaneously, even if viewers are not linked.

Clear the selection of the **Follow** button to browse lesions in one study only.

Selecting or clearing **Follow** makes sense only if viewers are not linked. If corresponding viewers are linked in the current and prior studies, selecting or clearing **Follow** has no effect on browsing.

Click **Report** to send lesion statistics to the **Export** window as snapshots.

-Or-

Click **Save** to create a DICOM structured report of your findings and append it to the current study as a new series (modality SR).

Export window

You use the **Export** window to create reports or to save, send, or print snapshot images.

The **Export** window is subdivided into two sections:

- *Snapshots*

  In this section you find snapshots from the session in the active **View** window. This is the tab card that is highlighted with a bullet.

- *Reports*

  This section presents you with a template for quick and easy report creation. Relevant patient and study information from the case in the active **View** window has already been entered.

Snapshots

Snapshots are bitmap images that you have created or that were created automatically to document observations or evaluation results. Because snapshots are bitmaps, you cannot edit them, even if you send them as a DICOM series, or save them in DICOM format.

Snapshots list

In this list, you find the following types of snapshots:

- Snapshots that were created by the software when you stored a key view.

  These snapshots are labeled **Auto** in the lower right corner. See *Annotation and measurement tools*, page 73, and *Key views tools*, page 89.

- Snapshots that you have created with one of the snapshot tools.

  Snapshots are numbered. All snapshots that you have created with **Snapshot All Viewers** have the same number. See *Snapshot tools*, page 88.

- Line profiles, which you have sent to the **Export** window with the snapshot tool of the **Line Profile** tool card. See *Line Profile*, page 117.

- ROI statistics, which you have sent to the **Export** window with the snapshot tool of the **Statistics** tool card. See *Statistics tool card*, page 131.

- Tables and graphs that result from an LV analysis or a calcium scoring analysis.

  You have sent these analysis results to the **Export** window with the **Report** button on the corresponding tool card. See *LV Results tool card*, page 139, and *Calcium tool card*, page 140.

Displaying snapshots

Double-click a snapshot to show it in a floating window.

If the snapshots list contains more than one snapshot, use the **Previous Snapshot/ Next Snapshot** buttons in this floating window to browse snapshots.

Deleting snapshots

Click a snapshot to select it and click **Delete** to remove snapshots that you do not want to save.

Sending snapshots

Sending snapshots means saving them on the Visage 7 server, on a partner system, or on a connected DICOM node.

1. Select the snapshots that you want to send.

   -Or-

   Press **Ctrl + A** (Windows) or **Cmd + A** (Mac) to select all snapshots in the **Export** window.

2. Click **Send**.

3. In the **DICOM Send** dialog box, select one or several DICOM servers.
4. Enter a **Series Number** and **Series Description**.

   The program suggests 1000 as a series number. This adds the snapshot series to the end of the study.

5. Click **Send**.

   -Or-

   To have the system save your snapshots automatically next time, select **Save Automatically** and **Make Default** before you click **Send**.

The next time you close a study for which snapshots exist, Visage 7 creates a snapshot series and sends it to the server. If you have selected automatic data transfer with confirmation, a message appears when you exit the program or try to load a new study.

Saving snapshots

Saving snapshots means storing them on your local computer or in your network.

1. Select the snapshots that you want to save.

   -Or-

   Press **Ctrl + A** (Windows) or **Cmd + A** (Mac) to select all snapshots in the **Export** window.

2. Click **Save**.

3. Select the drive and folder where you want to save the images.

4. Enter a file name and select a file format.

   Remember that if you select *.dcm the images are saved in DICOM format. You need a DICOM viewer or a graphics program that can read DICOM data to be able to view these images.

5. Click **Save**.

Printing snapshots

If a DICOM printer is connected to your Visage 7 server, use **Print** below the snapshots list to print images on paper or on film.

1. Select the snapshots that you want to print.

   -Or-

   Press **Ctrl + A** (Windows) or **Cmd + A** (Mac) to select all snapshots in the **Export** window.

2. Click **Print.**

3. In the **DICOM Print** dialog box, select the printer and change printer settings, if necessary.

   See *DICOM print settings*, page 103.

Copying snapshots to the clipboard

If you want to show a snapshot in a presentation or in a text file, the easiest way is to copy the snapshot to Clipboard and paste it into your document from there.

1. Select the snapshot that you want to copy.
2. Right-click and select **Copy**, or use the keyboard shortcut **Ctrl + C** (Windows) or **Cmd + C** (Mac).

Tip

You can only copy **one** snapshot at a time.

Reports

Depending on the overall organization of reporting in your hospital you will proceed in a different manner.

Basic reporting

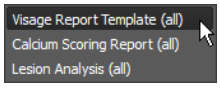
In this mode of working, you use the Visage 7 Client **Export** window to summarize your findings on a study and save it on your computer or in your network. However, the final report on the case will be created in a different system, for example, the reporting platform of the RIS (radiology information system).

To create a summary of findings in the Visage 7 Client **Export** window, you fill out a report template and then save your report.

Filling out a report template

A standard report template is already selected in the **Export** window and basic patient data and study information has been entered in the report header.

1. If necessary, select a different report template.



2. Use the **Insert Placeholders** command on the **Edit** menu to add more study data to the header or to the report text.
3. Add findings or comments by typing them into the report.
4. Use the buttons on the **Text Formatting** and **Paragraph Formatting** toolbars to highlight or align your findings or comments text.
5. Drag snapshots into the report where you want to show them.

Saving a report

Visage 7 offers various alternatives for saving reports, either in your network, on a connected DICOM network node, or in the RIS (radiology information system).

Click **Export Word** or **Export PDF** to save your report as a Word file or pdf file on your local computer or in the network.

Note

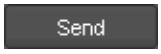
Export Word is available only on Windows PCs and only if Word for Windows is installed on your client PC.

-Or-

1. Create a snapshot of your report pages.

Creation of a snapshot of your report requires that a printer is installed at your client PC.

2. Select all report pages in the **Snapshots** section.
3. Send these report pages as a snapshot series to the Visage 7 database or to a connected DICOM network node.



-Or-

Use the **Send to RIS** button if your Visage 7 is connected to a radiology information system, such as a ProMedicus RIS.

Diagnostic reporting workflow

In this mode of working your Visage 7 has been configured for creation and storage of reports. Visage 7 records a history of changes by creating a new version of the report every time a user edits and saves it again. Draft and preliminary reports are expected to be signed off. Final reports can no longer be edited. Reports are stored on the Visage 7 server and are eventually archived together with the image data of a study.

In a diagnostic reporting workflow users are assigned specific rights regarding creation and review of draft, preliminary and final reports. This means, that your user account might not be permitted to perform all the steps described below. For example, you might have the right to create preliminary reports but not to sign off reports.

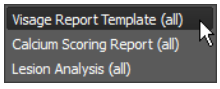
Tip

If you have any questions about your role in the diagnostic reporting workflow, talk to your system administrator.

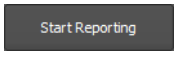
Creating a report

A standard report template is already selected in the **Export** window and basic patient data and study information has been entered in the report header.

1. If necessary, select a different report template.



2. Click **Start Reporting** above the report template.



3. Fill out the report template.

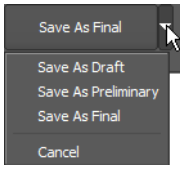
   Use the **Insert Placeholders** command on the **Edit** menu to add more study data to the header or to the report text.

Add findings or comments by typing them into the report.

Use the buttons on the **Text Formatting** and **Paragraph Formatting** toolbars to highlight or align your findings or comments.

Drag snapshots into the report where you want to show them.

4. Save the report.



Editing a report

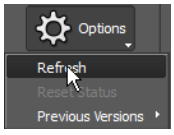
You can edit a draft or preliminary report either you or a colleague created for a study. However, only one user can edit or create reports for a study at any one time.

When you load a study from **Study Browser** and move on to the **Export** window, the most recent version of the study report is shown here.

1. Click **Start Reporting**.

   If you try to edit or create a report another user has worked on since you have loaded the study, a message will ask you to update the report first.

   Click **Options > Refresh** near the right edge of the **Export** window.



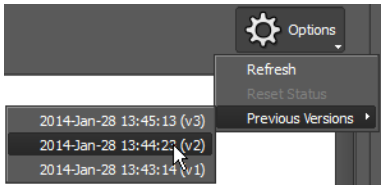
   Click **Start Reporting** again.

2. Add or correct findings and comments.
3. Save the report again.

Viewing previous report versions

Every time you or another user edits a report and saves it again, a new report version is created.

Click **Options > Previous Versions** and an earlier version of this report.

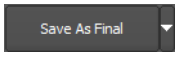


Visage 7 Client opens this earlier version of the report in a separate tab card. You can read but not edit or sign off this report version.

Signing off a report

With appropriate user rights you can sign off a report. Signing off means saving the most recent report version as the final report.

Click **Save as Final**.



A report with report status final can no longer be edited.

Resetting the report status

If your user account has the right to sign off reports, you can also reset the report status of final reports. Resetting the status of a final report to preliminary becomes necessary when you need to add findings to an already signed off report.

Click **Options > Reset Status**.

The report status is reset to preliminary. You can now open it (**Start Reporting**) and add any new findings, comments, or images and save it again.

Creating report templates

Templates contain patient and study data as placeholders and standard text. The software comes with a few sample templates, which help you to understand the basic concept and to create templates of your own. You can base a new template either on a system template or on a typical report that you have just created.

1. Select **Edit > Edit Template**.
2. Add all the required placeholders and standard texts.
3. Format placeholders and standard texts.
4. Click **Save** next to the template selection list.

5. In the **Save** dialog box, enter a template name.
6. Also decide whether you want to make this template available for all users or only for your own user account.

Quality Assurance

Visage 7 provides a platform for performing quality assurance. Quality assurance here means checking the assignment of studies to orders from the RIS (radiology information system) and correcting patient, study, and series information.

Refer to *Tools for performing quality assurance on images*, page 106, for quality assurance regarding image content.

Find out more about the **Quality Assurance** window and how to perform quality assurance in the following sections.

- *Query section*
- *Performed procedures and scheduled procedures lists*
- *Quality assurance tasks*

Note

Only users with appropriate user rights are permitted to perform quality assurance. For users without these user rights, the **Quality Assurance** window is not available in their Visage 7 Client installation.

The right to perform quality assurance is independent of any other user rights. This means that a user whose task it is to perform quality assurance might not have access to any other program windows. Talk to your system administrator to find out how these tasks are assigned in your institution.

Query section

The query section of the **Quality Assurance** window comprises two tab cards.

- **Study** tab card

  Data that you find as a result of a search on the **Study** tab card is listed in the **Performed Procedures** list.

- **Order** tab card

  Data that you find as a result of a search on the **Order** tab card is listed in the **Scheduled Procedures** list.

Tip

If you do not know a complete name or number, you can use wildcards in your search. For example, type `Mil` in the patient name box to find *Miller, Milford, Miltner,* or `*mil` to find all the above and also *Hamilton*, or `AB??34` in the patient ID box to find *AB1234, AB0034,* and *AB11345678*.

However, even if you use wildcards, always specify your search criteria as precisely as possible. Rather general queries might yield a very long hit list, which requires extensive scrolling.

Filter and search criteria

Use the filter and search criteria in this list to search for studies or orders.

Patient

Enter the name, date of birth, or ID of the patient that you are looking for. If you do not remember the exact name, date, or number, use wildcards.

For names that occur frequently, you might want to include the first name or other components of the patient's name in your search. To define such a search, you need to know how patient names are stored in the database.

```
FamilyName GivenName MiddleName Prefix Suffix
```

The following example shows a search string for first name, last name, and title.

```
Doe John*Dr.
```

If you want to search for more than one patient, separate patient names with a semicolon (;) or the pipe character (|). For example, `Anderson|Alexander` or `Miller;Milford`.

Date

Select the **Date** box. Select if you want to search by **Study Date** or **Insertion Date** (**Study** tab card), or by **Modification Date** (**Order** tab card).

The **Insertion Date** is the date when a study was transferred to the server from a modality or an archive. The **Modification Date** is the date when an order was created or modified on the RIS (radiology information system).

From ... **To** specifies a search period. Type dates in the format YYYY-MMM-DD, or click the button to the right of a date entry box and select a date in the calendar.

Use the buttons **Today**, **Yesterday**, **1 Week**, **2 Weeks** as a quick way to specify frequently searched periods in the correct format.

You can configure these four search-period buttons. Right-click one of the four buttons and select **Hours > 1 Hour**, for example, if you are frequently looking for studies that were performed within the last 60 minutes.

Modality

Select the check boxes of all modalities whose studies you want to search:

CT (computed tomography), **MR** (magnetic resonance tomography), **PT** (positron emission tomography, PET), **US** (ultrasound), **CR** (computed radiography), **DX** (digital radiography), **MG** (Mammography), **XA** (X-ray angiography).

-Or-

Enter a modality abbreviation in the **Others** box. Separate multiple modalities by a space, for example, `CT PT MR`.

Fields (Study tab card)

Here you can specify three additional criteria from the DICOM information on a study.

Open the lists of available criteria with the double-arrow buttons and select a criterion.

Specify your search string in the input box below the selected criterion. Remember that you can use wildcards in your search.

If you want to search for more than one accession number, for example, separate numbers with a semicolon (;) or the pipe character (|). For example, `12345|67890` or `09876;54321`.

If the search strings themselves contain semicolons, pipe characters, or backslashes, as in `Ward 4; Rm.6` or `Ward 1\Rm.2`, use the following notation: `Ward 4\; Rm.6;Ward 1\\Rm.2` or `Ward 4\; Rm.6|Ward 1\\Rm.2`

-Or-

Click the list button next to an input field.

Select an item.

Study States (Study tab card)

Click the **Study States** button and select study states in the **Select State** dialog box.

If you want to search by **QA status**, ask your system administrator how these status flags are assigned on your server.

Searching by study state **Interpretation Status** makes sense only if the modalities that send data to the Visage 7 server set this flag. In Visage 7 you cannot set or edit the interpretation status of a study.

If study states are included in your search, the **Study States** button label appears italic and the **Reset** button next to it is available. Click this **Reset** button next to the **Study States** button if you want to reset only study states but none of the other search criteria.

Fields (Order tab card)

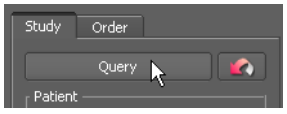
Here you can specify two additional criteria when searching for scheduled procedures. Open the lists of available criteria with the double-arrow buttons and select a criterion. Then specify your search string in the input box below the selected criterion. Remember that you can use wildcards in your search.

Status (Order tab card) Here you can filter the schedules procedures list. Choose whether to display either only those scheduled procedures that are assigned to performed procedures or only those that cannot be assigned.

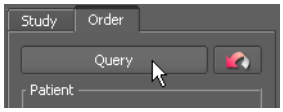
Starting and resetting a search

Use these buttons to start a database search or to reset search criteria.

Click **Query** on the **Study** tab card to update the **Performed Procedures** list.



Click **Query** on the **Order** tab card to update the **Scheduled Procedures** list.



Click **Reset** to return to the default query preset (see *Defining a preset*, page 161). If no default query preset has been defined, **Reset** removes all search criteria.

Query presets

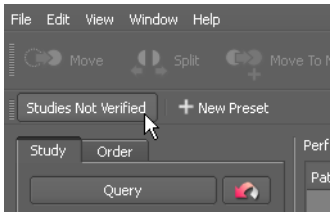
If you frequently use the same combinations of search criteria, you can save them in a preset. Your presets are listed directly above the query section. Any presets that you define are available for your own user account only. You cannot make presets public.

Tip

A preset stores filter and search criteria on both tab cards (**Study** and **Order** tab cards). It also stores the size and arrangement of the **Performed Procedures** and **Scheduled Procedures** lists.

Quick search with a preset

1. Click a preset button to retrieve its search criteria.



2. Depending on how you defined the preset, you might have to click **Query** to start the search.

Defining a preset

1. On the **Study** and **Order** tab cards, select and type search criteria.
2. Click **New Preset**.

3. In the **Preset** dialog box, enter a name for your new preset.
4. Select **Default** if you want to make this preset the default query preset.

   See also *Starting and resetting a search*, page 160.
5. Select **Auto Query** if you want the system to reenter your search criteria **and** then run the search immediately. You do not have to click **Query** again.

   -Or-

   Select **Default** plus **Auto Query** to have the system run this search every time you call up Visage 7 and **Quality Assurance**.
6. Save the preset.

A new preset button appears above the query section.

Tip

Right-click presets that you defined earlier. A context menu appears, which helps you to manage presets. For example, you can remove preset buttons that you no longer need.

Performed procedures and scheduled procedures lists

The **Performed Procedures** and **Scheduled Procedures** lists display the results of the last query that you performed on the **Study** and **Order** tab card.

Information in the performed procedures list

Performed Procedures lists all studies that are currently stored on the Visage 7 server.

Patient Name Name of the patient.

Click the pin symbol in front of a patient name to retain this patient in the performed procedures list before you start a new database query.

This way, you can combine the results of subsequently performed procedures queries (that is queries on the **Study** tab card).

Issuer The institution that issued the patient ID.

Patient ID	The patient's identification number.
Date of Birth	The patient's birth date.
Sex	The patient's sex: **M** (male), **F** (female), **O** (other or unknown).
QA Status	This provides meaningful information only if your Visage 7 is connected to a RIS (radiology information system). In this case, the **QA Status** of a study indicates whether the study (performed procedure) can be matched to a RIS order (scheduled procedure). **COMPLETED**: This QA status indicates that this study has been matched with a RIS order either automatically or manually. **SCHEDULED**: This QA status indicates that the study cannot be matched with a RIS order automatically. You either need to assign this study to an order manually or wait until a new order message arrives from the RIS. **DISCONTINUED**: This QA status indicates that quality assurance for this study was terminated. **NOT SCHEDULED** (column remains empty): This QA status indicates that no matching of performed procedure to scheduled procedure was planned for this study. Use the **Study States** button on the **Study** tab card to search for studies of a specific QA status.
Date/Time	Date and time when the study or series was performed. The format is YYYY-MMM-DD and HH:MM:SS (24 hour clock).
Accession Number	Job number of the study in the RIS (radiology information system).
Study ID	Identification number of the study.
Modality	Modality or modalities where the patient was examined.
Body Part	The part of the body or anatomical region that was examined in this study or series. Use one of the **Fields** boxes on the **Study** tab card if you want to search for studies by DICOM flag *Body Part*.
Images	Number of images in a study or series.
Description	Study or series description.
Comment	A study comment, if such a comment exists for a study. A study comment can either have been sent from the modality or entered in the **Study Info** dialog box of the Visage 7 **View** window.
Performing Physician	Name of the physician who performed a study. Use one of the **Fields** boxes on the **Study** tab card to search for studies by performing physician.
Institution Name	Name of the institution or department where the study was performed.

Information in the scheduled procedures list

Scheduled Procedures lists all orders that have been sent from a connected RIS (radiology information system). If your Visage 7 is not connected to a RIS, the scheduled procedures section is nevertheless shown, however, the list will remain empty.

Patient Name Name of the patient.

Patient ID The patient's identification number.

Birth Date The patient's date of birth.

Sex The patient's sex: **M** (male), **F** (female), **O** (other or unknown).

Assigned This column indicates whether a scheduled procedure (RIS order) has been assigned to a performed procedure.

The corresponding study in the performed procedures list has the QA status *COMPLETED*.

Use the **Status** box on the **Order** tab card to search for scheduled procedures that have already been assigned or that cannot be assigned.

Order Status Status of the RIS order.

Study Date/Time Date and time of the study. The format is YYYY-MMM-DD and HH:MM:SS (24 hour clock).

Accession Number Job number of the study in the RIS (radiology information system).

Modality Modality or modalities where the patient was examined.

Organizing and rearranging procedures lists

You can rearrange the performed procedures and scheduled procedures lists for a better overview.

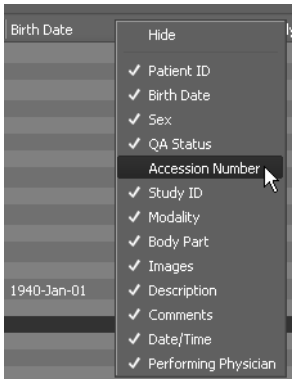
Enlarging or reducing window sections

Drag the split bar above the **Scheduled Procedures** list up or down to enlarge or reduce this window section.

If your Visage 7 is not connected to a RIS, you might choose to hide the scheduled procedures list altogether. Drag the split bar all the way to the bottom of the **Quality Assurance** window in this case.

Rearranging columns

1. Right-click the column header of the performed procedures or scheduled procedures lists.
2. Cancel the selection for any columns that you want to hide or move.



3. Point to a column to the right of which you want to reinsert a hidden column.
4. Right-click and select the column again.

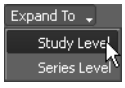
Expanding or collapsing the performed procedures list

The performed procedures list is arranged in a hierarchical tree view.

Use the **+** (plus) button in front of an entry to expand it and show lower levels of information.

-Or-

Click the **Expand To** button below the performed procedures list to show the study level or the study and series level for all performed procedures.



-Or-

Use the **-** (minus) sign in front of an entry to collapse this level, or click **Collapse All** to show only the patient level.

Quality assurance tasks

Quality assurance typically involves different tasks, depending on whether your Visage 7 is connected to a RIS (radiology information system) or not.

Quality assurance with RIS

When your Visage 7 is connected to a RIS, quality assurance is performed automatically and in the background.

Automatic data consolidation

When a RIS connection exists, Visage 7 has been configured in such a way that all incoming studies are automatically matched with orders from the RIS. If study data contain errors, for example, if the patient name was misspelled during patient registration, these errors are automatically corrected with information from the RIS order. Studies that can be matched to RIS orders receive the QA status *COMPLETED*. These studies require no further user interaction.

Assigning studies to orders

When your Visage 7 is connected to a RIS, you need to perform manual quality assurance only if automatic matching of studies and RIS orders fails.

1. In the **Performed Procedures** list, search for studies with **QA Status** *SCHEDULED*.

   Use the **Study States** button on the **Study** tab card to define such a query. Start the search with the **Query** button on the **Study** tab card.

2. In the **Scheduled Procedures** list, search for orders that have not yet been assigned to studies.

   In the **Status** box at the bottom of the **Order** tab card select *NOT ASSIGNED*. Start this search with the **Query** button on the **Order** tab card.

3. Select a study in the **Performed Procedures** list and the corresponding order in the **Scheduled Procedures** list.

   Use **Accession Number** information or patient information (columns **Patient Name**, **Patient ID**, **Birth Date**, and **Sex**) to identify studies and orders that require matching.

4. Click **Assign Order to Study** on the toolbar.

   A message appears that asks you to confirm study to order assignment.

   If patient data for study and order are not identical, a second message appears.

5. Click **Update** to update the patient data of the study.

   -Or-

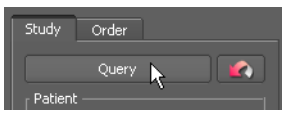
   Click **Create New Patient** to correct the patient information stored in the order.

Quality assurance without RIS

If your system is not connected to a RIS (radiology information system), quality assurance means completing patient information or correcting errors that were made during patient registration.

Completing data of an emergency registration

1. On the **Study** tab card, search by study date and modality, for example.
2. Click **Query**.

3. Select an emergency patient in the **Performed Procedures** list.
4. Click **Edit**.

5. Overwrite any preliminary information with the correct patient information.

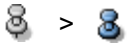
6. Click **OK**.

The **Performed Procedures** list is updated automatically now.

Merging patients

1. Search for an emergency study or a patient whose name is misspelled.
2. Click the gray pin symbol in front of the patient name.

The pin symbol turns blue when you select it.



3. Search for the correct patient name.
4. In the **Performed Procedures** list, select the emergency patient or misspelled patient.
5. Press and hold **Ctrl** or **Cmd** while you also click the correct patient name.
6. Click **Merge Patients**.

7. Select the correct patient name.
8. Click **OK**.

The **Performed Procedures** list is updated. Only the correct patient name is displayed now and the study has been moved. The emergency or misspelled patient entry has been deleted.

Moving studies, series, or images

If studies, series, or images were assigned incorrectly, move the data to another patient, study, or series. You proceed in a similar way in all these operations.

1. Select the study, series, or images that you want to move and the patient, study, or series that you want to move the data to.
2. Click **Move**.

3. Read the message and confirm with **OK**.

-Or-

1. Select a study, series, or image that you want to move to a patient, study, or series that does not yet exist in your database.
2. Click **Split**.

3. Enter the new patient, study, or series information in the **Edit Patient**, **Edit Study**, or **Edit Series** dialog box.
4. Click **OK**.

Tip

For series **Split** means moving the series to a new study of the same patient.

If you want to move the series to a new study of a new patient, use the **Move to New Patient** button instead.

Editing patient, study, series, or image information

1. Select a patient, study, series, or image.
2. Click **Edit**.

3. Overwrite the patient, study, series, or image information in the **Edit Patient**, **Edit Study**, **Edit Series,** or **Edit Image** dialog box.
4. Click **OK** to confirm and close the dialog box.

Deleting patients, studies, series, or images

Deleting a study might become necessary if patient data are corrected at a modality after the patient's data have already been sent to the Visage 7 server. Delete the patient on the server as soon as you learn about this situation and before the corrected study is sent to the Visage 7 server again.

Before deleting data, ensure that the data is no longer required by your users. After you have deleted a study from the server, you cannot restore it again, unless you have access to the long-term archive of the modality.

1. Select one or several patients, studies, series, or images.
2. Click **Delete**.

3. Click **OK** if you are sure you no longer need this data on the server.

Customizing Visage 7 Client

Visage 7 users can customize the Visage 7 Client in various ways. For some of these configuration options advanced user rights are required, others are available for all Visage 7 users.

Tip

If you cannot find some of the configuration options described in this section on your user interface, ask your system administrator about your user rights.

Basic settings

Basic configuration settings can be made by all Visage 7 users. Users do not need advanced user rights to access these commands and dialog boxes.

UI appearance and display size

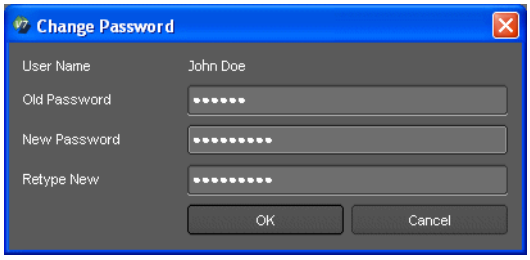
Select **View > UI Appearance** and **Native Style**, **Visage Bright**, **Visage Dark**, or **Visage Medium** to adapt the user interface to the ambient light conditions of your workplace.

Point the cursor to a screen or section of a screen, hold the **Ctrl** key down, and rotate the mouse wheel to display image text larger or smaller.

Change Password dialog box

You should change your password from time to time for data security reasons.

1. Select **File > Preferences > Change Password**.
2. Enter your **Old Password**, the **New Password**, and repeat the new password in the **Retype New** box.



3. Press **Return**.

Use the new password from now on when you log in.

Reset all warnings

If you have selected **Do not show again ...** for any warning that has appeared since you called up Visage 7, **View > Reset All Warnings** revokes this selection. From now on, all warnings are shown again.

Streaming compression

With **View > Streaming Compression** you can select a compression level for image transfer from the server to your computer.

Note

Depending on the system configuration and your user role, you might not see all the compression options listed here. Furthermore, Visage Imaging's customer service can fine-tune the compression settings to optimize performance and network use in your organization. Contact your system administrator if you have further questions on this topic.

Select a compression level depending on the network you are working in and on the image quality you require.

- **Auto** analyzes the current network bandwidth and the latency characteristics and optimizes the compression level.
- **Lossless Only** transfers only losslessly compressed data with full image quality. Select this option only for fast networks, for example, in local area networks (LANs). Your server needs to be configured to support this function.
- **High Quality** applies a low compression level that ensures high image quality. Select this option in fast networks.
- **Medium** applies a medium compression level. Select this option, for example, in a slow local area network (LAN) or in a wide area network (WAN).
- **Strong** applies a high compression level for fast data transfer at the expense of image quality. Select this option, for example, if you are working in a slow or very busy network.

Note

If images are displayed with reduced image quality because of streaming compression settings, a red bullet appears in the lower right corner of the viewer. Wait until the red bullet has disappeared to ensure that the images that you are looking at do not show any compression artifacts.

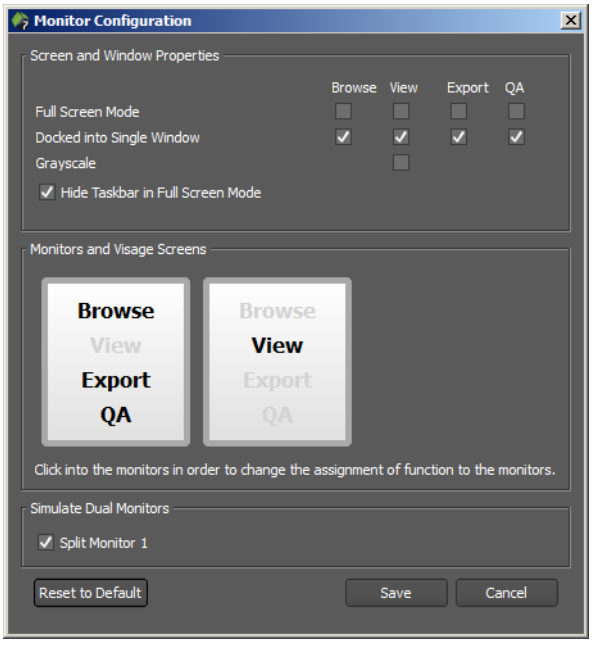
Monitor Configuration dialog box

If you are working with more than one monitor, you use this dialog box to define which Visage 7 window is shown on which monitor. For example, use a large high-resolution monitor exclusively for viewing images and use another monitor to find studies, create reports, or perform quality assurance.

1. Select **File > Preferences > Monitor Configuration**.

Tip

Point to a monitor box to show the resolution of this monitor as a tooltip.



2. Select display settings for each window.

   Select **Full Screen Mode** to show the windows on this monitor in fullscreen mode right after program start, that is without a window border. During a session you can return to window size with the **Restore Window** button in the upper right corner of the program window.

Select **Docked into Single Window** if you want to show all Visage 7 windows in the same program window. Clear this option to be able to show Visage 7 windows side by side on the monitor.

Note

The selections **Full Screen Mode** and **Docked into Single Window** become effective only if you select or clear these options for all windows of one monitor.

3. If the monitor that you use for reading images is a grayscale monitor, also select **Grayscale** for the **View** window.

   This selection enhances the readability of thumbnails and highlights the bright border that indicates the active viewer for grayscale monitors.

4. Select which windows you want to show on which monitor.

   Browse represents the **Study Browser**, **View** represents the **View** windows, **Export** represents the **Export** window, and **QA** the **Quality Assurance** window.

5. Decide whether you want to show the Windows taskbar when Visage 7 Client is shown in fullscreen mode.

   Showing the Windows taskbar facilitates switching over to other program windows such as the RIS (radiology information system).

6. Select **Split Monitor 1** if you are using only a single monitor with this Visage 7 Client but are used to dual monitors at your regular workplace.

   Splitting a single monitor allows you to use the same protocols that you are used to in dual-monitor mode.

7. Click **Save** to save the monitor configuration for your own user account.

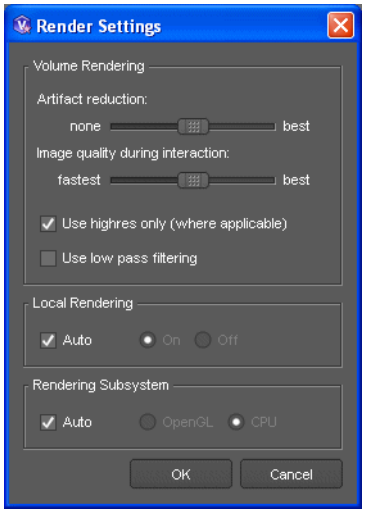
   -Or-

   Click **Reset to Default** to reset the monitor configuration to the system default.

Render Settings dialog box

In this dialog box, you can change technical parameters for the way 2D and 3D images are generated by Visage 7. Change these parameters only if your system administrators or Visage Imaging customer service instructs you to do so.

1. Select **View > Render Settings**.



2. Select **Auto** for **Local Rendering** and **Rendering Subsystem** to have the system identify and select the option best suited for your system configuration.

Caution

OpenGL is an advanced graphics standard that is not always properly supported by client-computer graphics hardware.

In the **View > Render Settings** dialog box, you should set **Rendering Subsystem** to **OpenGL** only if you are certain that this mode is supported properly by the graphics card of your client computer.

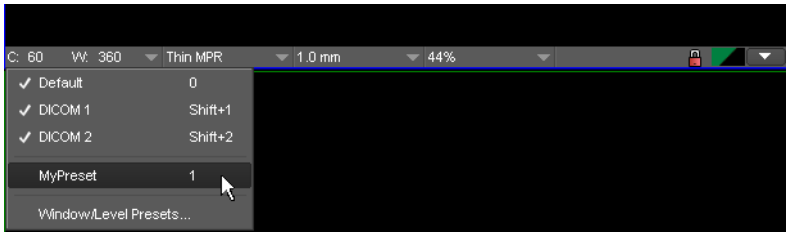
3. Also adapt **Volume Rendering** parameters, if necessary.
4. Click **OK** to save your settings.

Any modifications that you made to **Local Rendering** and **Rendering Subsystem** settings are stored permanently for your client. Modifications to **Volume Rendering** settings are reset to their defaults when you restart Visage 7 Client.

Configure Window/Level Presets dialog box

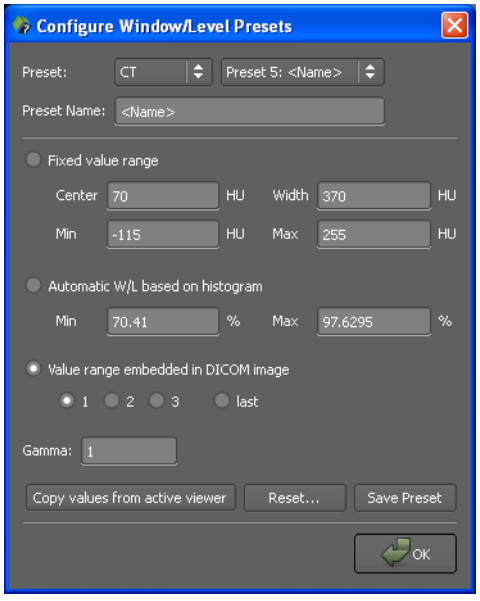
Window level presets are combinations of image brightness and contrast settings. You can save these presets for specific image types.

While you are reading images, you can select predefined window presets from a drop-down list in the viewer controls, from a list shown when you click the **Show Window Level Presets** button on the tool palette, or with a keyboard shortcut.



1. Select **File > Preferences > Window/Level Presets,** or select **Window/Level Presets** from the viewer controls.

   The image type of the currently loaded data is already selected.



2. Select the modality for which you want to define a preset and a preset number.

   Preset numbers correspond to the keyboard shortcuts that you can use to select presets quickly while you are reading images.

   Undefined presets are listed as *<Name>*.

3. Enter a **Preset Name**.

4. Enter or select window level settings.

   Fixed value range: Enter the window width as a range value or in terms of a minimum and maximum value. The **Center** and **Width** and **Min** and **Max** boxes are synchronized.

   -Or-

Automatic W/L based on histogram: This setting adapts the data window to the value range available in an image dataset.

-Or-

Value range embedded in DICOM image: Select one of the window level presets that are stored with the image. **Last** represents the most recently stored DICOM window preset.

-Or-

Click **Copy values from active viewer** to copy window level settings from the currently active viewer into the **Configure Window/Level Presets** dialog box.

5. Change the **Gamma** correction factor, if necessary.

   Gamma correction can be used to compensate for distortions in image brightness that are caused by the monitor.

6. Select **Save Preset** to save your settings.

   -Or-

   Select **OK** to close the dialog box and choose whether to save or ignore unsaved changes.

Configure Keyboard Shortcuts dialog box

Some of the functions and options that are represented by toolbar buttons can also be selected with keyboard shortcuts. These keyboard shortcuts are active even if a toolbar or button is currently not displayed in any of the toolbars on the screen.

Factory-default keyboard shortcuts

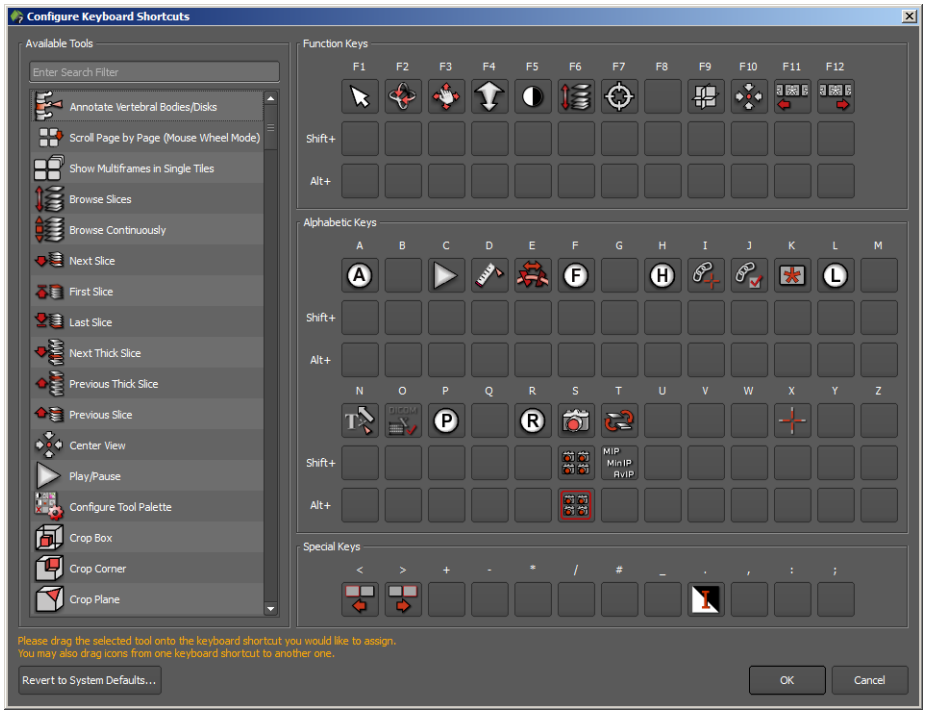
A number of keyboard shortcuts have been predefined for your system.

Select **Help > Keyboard Shortcuts** on the main menu to show the list of factory-default shortcuts.

Configuring your own keyboard shortcuts

If you feel that the factory-default shortcuts are not intuitive, you can redefine them and also assign other functions to keyboard shortcuts.

1. Select **File > Preferences > Keyboard Shortcuts**.



2. In the search filter box above the **Available Tools** list, type the name or part of the name of the tool that you are looking for.

   -Or-

   Scroll down the list of **Available Tools.**

3. Select a tool and drag it into the box of a keyboard shortcut on the right.

   You can assign tools to function keys, alphanumeric keys, or special keys and also to combinations of these keys with the **Shift** or **Alt** key.

   If you drag a function to the box of a key or key combinations that already contains a tool, this replaces the original key assignment.

Returning to factory defaults

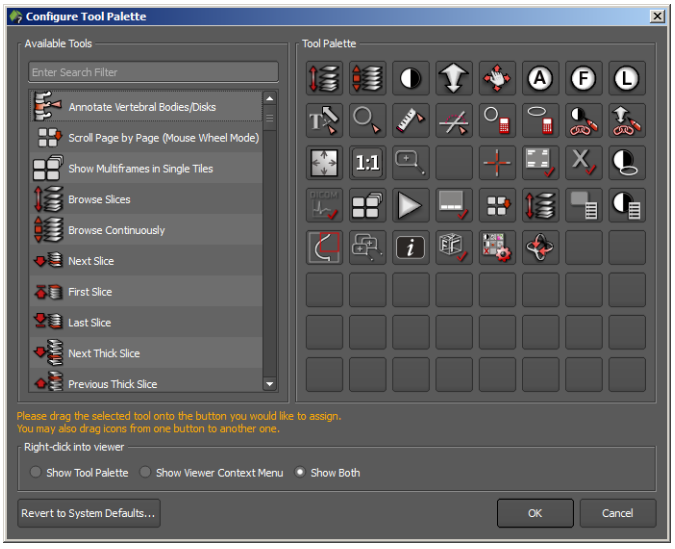
Click the **Revert to System Defaults** button to reject any recent or previous key assignments or reassignments.

The factory-default keyboard shortcuts, which you can also find under **Help > Keyboard Shortcuts**, are now active again.

Configure Tool Palette dialog box

When you right-click in a viewer, either the viewer context menu, or a tool palette, or both are shown. The tool palette offers a quick way of calling frequently used functions.

1. Select **File > Preferences > Tool Palette**.



2. In the search filter box above the **Available Tools** list, type the name or part of the name of the tool that you are looking for.

   -Or-

   Scroll down the list of **Available Tools.**

3. Select a tool and drag it onto the **Tool Palette** to the right.

   Moving a tool to a box that is already occupied by another tool replaces that tool.

4. Select whether to show the tool palette, the viewer context menu, or both when you right-click a viewer.
5. Click the **Revert to System Defaults** button to reject any recent or previous assignments or reassignments.
6. Click **OK** to confirm and close the dialog box.

Tip

You can even configure a shortcut to the **Configure Tool Palette** dialog box itself.

Properties and protocols

Properties and protocols are Visage 7 concepts for controlling and adapting the user interface and the default behavior of functions at various levels.

Properties dialog box

Properties define the default settings for many program functions. You can open the **Properties** dialog box either from the **File** menu or from various context menus or buttons. Depending on how you open the dialog box, it presents either the complete set of properties or only a context-dependent subset. You can change properties for your own user account, for all users, or for the currently active protocol, depending on your user rights.

1. Select **File > Preferences > Properties** from any of the Visage 7 windows to open a dialog box with all program properties.

   -Or-

   Select **View > Viewer Properties** in the **View** window if you want to redefine only a subset of user interface settings for the **View** window.

   -Or-

   Click the **Properties** or **Defaults** button in a dialog box or on a tool card to modify only the properties of the corresponding function.

   -Or-

   Right-click a configurable tool or tool card and select **Properties** to modify the properties of the corresponding function.

2. Decide on the level on which you want to save your changes.

   System: This saves your changes on a system-wide basis.

   User profile: This saves your changes in your user profile. The new settings will be effective in all studies that you view from now on.

   Protocol: This saves your changes in the protocol definition. The new settings will be effective in all studies that use this protocol.

   If you select **Protocol**, do not forget to save the protocol to make your changes permanent. See *Save Protocol dialog box*, page 189.

3. Open the tree view of the function or feature that you want to modify.

   The column **defined in** tells you the level of the currently valid values: factory default, system, user profile, or protocol.

4. Select the property that you want to modify and adapt its value in the second column.

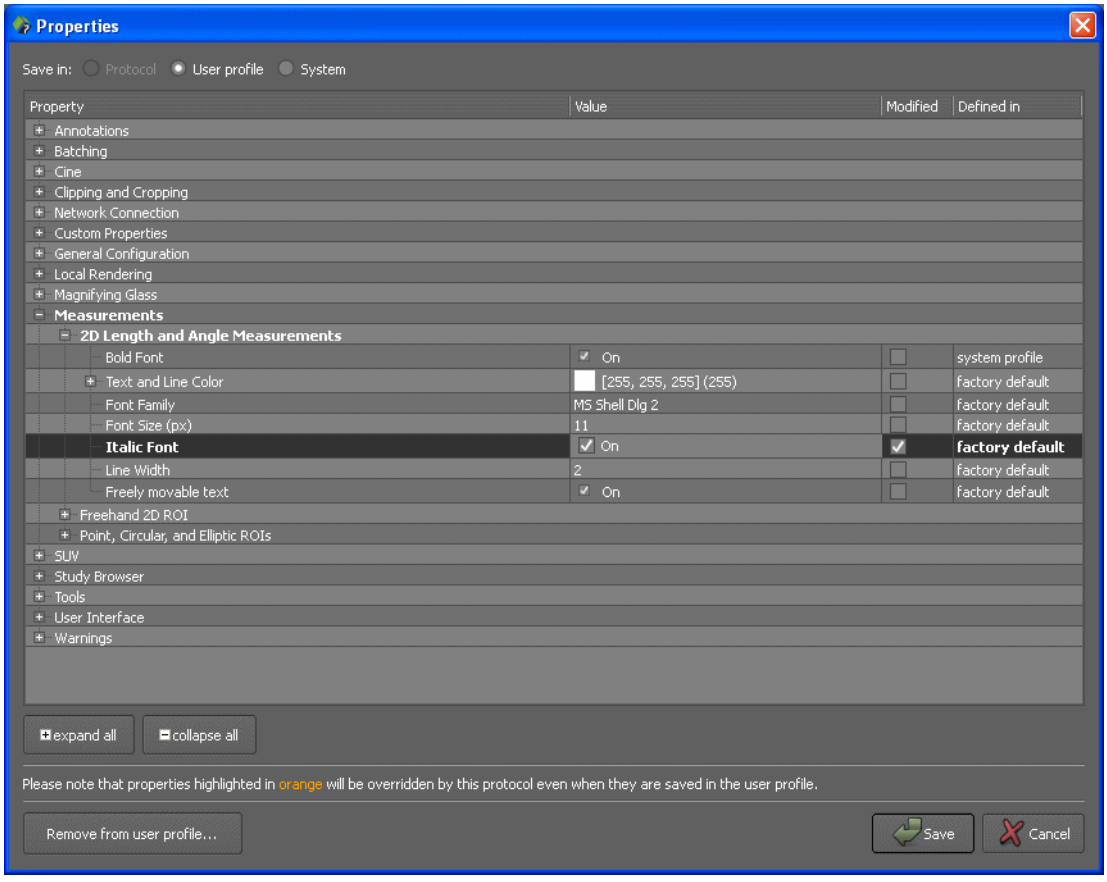
   Modified values have a check mark in the **Modified** column. When you clear this box, you undo changes for this feature.

Tip

When contradicting property settings exist at the various levels at which property settings can be defined, the following rule applies.

Protocol settings overrule user profile settings, user profile settings overrule system settings, and system settings overrule factory defaults.

Settings that will be overruled by settings of a higher priority are highlighted with orange text.



5. Click **Save** to save your changes and close the dialog box.

   -Or-

   Click the **Remove from ...** button to reset properties settings to the settings of the next higher level.

Automatic loading of prior studies

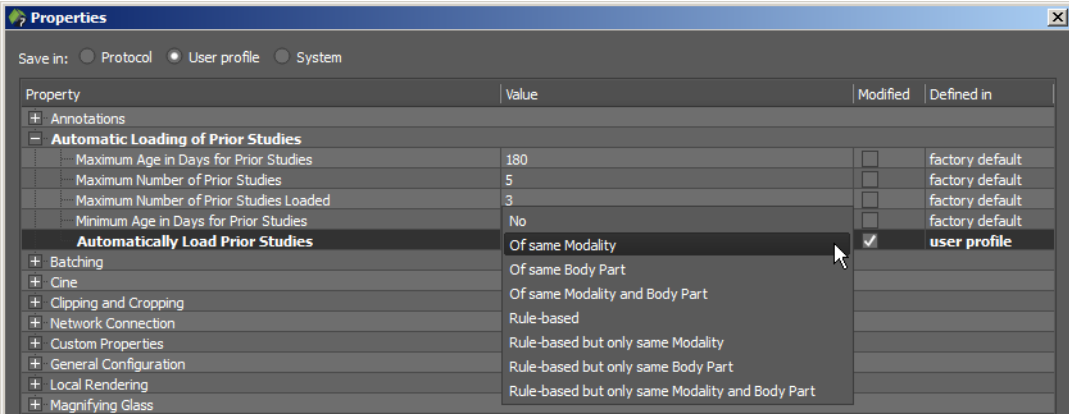
Automatic loading of prior studies can be configured either for the entire system, for specific user levels, or for individual user profiles.

When configuring automatic loading of prior studies you should consider the actual requirements of your users closely, because loading prior studies unnecessarily will slow down system performance.

Configuring automatic loading of prior studies

1. Select **File > Preferences > Properties**.
2. Open the list of options for **Automatic Loading of Prior Studies**.
3. Review and adjust settings.

If you select any of the rule-based options here, move on to the **Edit Auto-prior Rules** dialog box to review or define rules.



Editing rules for automatic loading of prior studies

1. Select **File > Preferences > Edit Auto-prior Rules**.
2. In the **Edit Auto-prior Rules** dialog box, select **System** or **User** below the rules list to show either only system rules or only the rules of your user profile.
3. Select a rule.

   -Or-

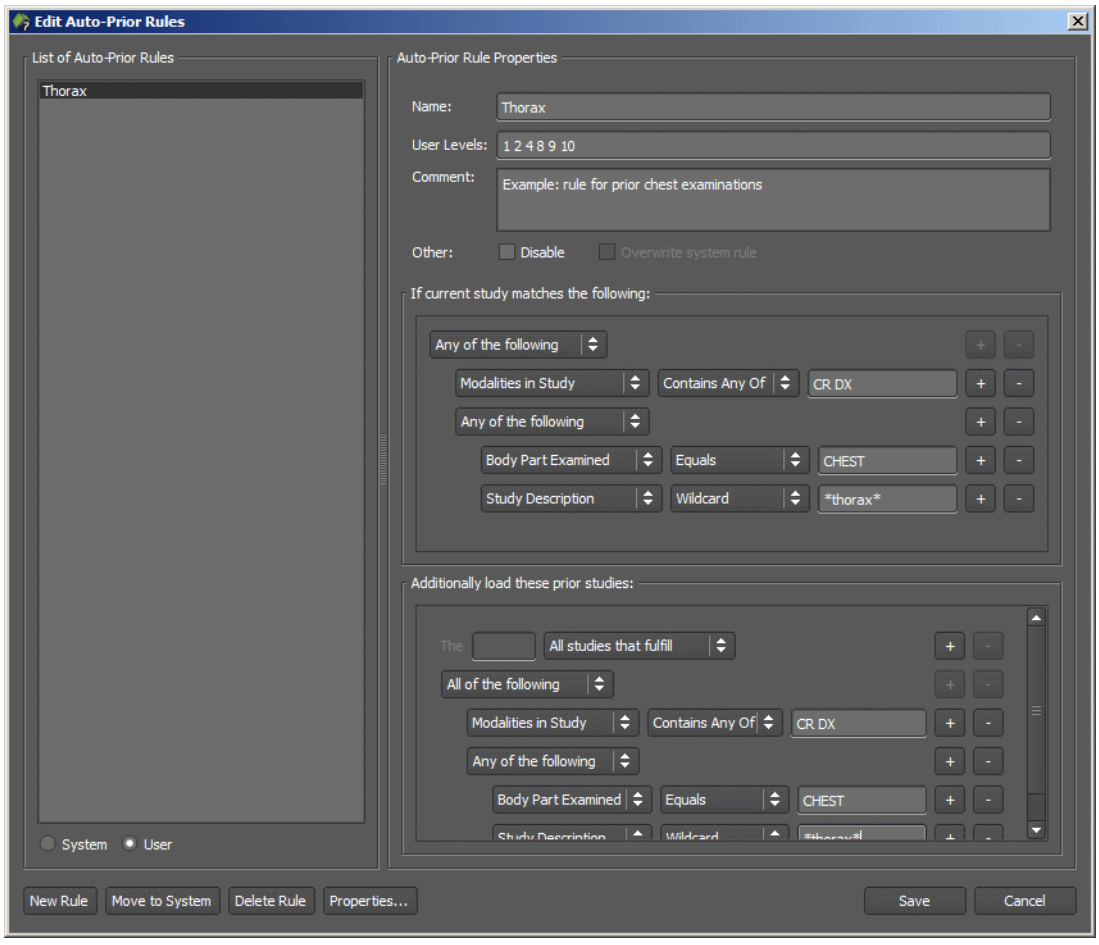
   Click **New Rule**.
4. For a system rule, you can specify for which user level or user levels the rule will apply.

   Type a user level number (e.g. `3`).

   -Or-

   Type several user level numbers separated by a space (e.g. `3 4 5`).
5. Under **If study matches the following**, define current studies for which the rule will apply.

6. Under **Additionally load these prior studies**, specify the prior studies that will be loaded together with the current study.



7. Always double-check your automatic loading configuration. Use the **Properties** button as a shortcut to the **Automatic Loading of Prior Studies** configuration.

   Parameters in the **Properties** dialog box and auto-prior rule settings are AND-combined. For example, you might define a rule intended to load prior studies of both the modalities CT and MR for current CT studies. However, you also select the option **Rule-based but only same Modality** for the property **Automatically Load Prior Studies** in the **Properties** dialog box. This will result in MR studies being ignored and only prior CT studies will be considered.

8. Click **Save**.

Tip

If you want to adapt a system rule for your user profile, you can copy it to your user profile. Likewise, and with appropriate user rights, you can move rules from your user profile up to system level. Use the buttons **Copy to User** and **Move to System** to copy and move rules.

Modifying and creating protocols

Protocols control the screen layout and the scope of functions that are available when a user loads different types of images or a combination of image types. Typically the system preselects the protocol best-suited for a selection of data when a user loads data into the **View** window. If users do not agree with this choice, they can select a different protocol. Users with appropriate user rights can prioritize protocols for specific image types or even edit or create protocols of their own.

Protocols are a very powerful and complex concept in Visage 7. Therefore, we recommend that you attend a dedicated training course before you attempt to perform complex protocol editing tasks.

Simple protocol editing

The easiest way to modify a protocol is to make changes in the **View** window and then to save these modifications.

Examples of simple protocol editing tasks

The following list presents some typical examples of simple protocol editing tasks:

- Hiding toolbars or showing additional toolbars
- Showing or hiding the thumbnail section or tool cards
- Changing viewer linking and viewer alignment
- Changing viewer types or viewer properties such as color maps, window level presets, image orientation, slice thickness, and rendering mode selection.
- Rearranging the **Layouts** toolbar.

Procedure in simple protocol editing

1. Load images into the **View** window.
2. Check which protocol is currently selected, or select a different protocol from the **Protocol** menu.
3. Make your changes.

   For example, show a toolbar that was previously hidden.
4. On the **Protocol** menu, select **Protocol Editing > Save Protocol**.
5. Change the protocol name and add a comment, if required.
6. Click **Save Protocol**.

When you proceed as described here and change no other parameters in the **Save Protocol** dialog box, the protocol is saved as a user-level protocol. The priority of the new protocol is the same as the priority of the original protocol. User-level protocols have a higher priority than system-level protocols. Therefore, the new user-level protocol will be selected the next time you load images of this image type.

Prioritizing protocols

As a further step, you might want to call up the **Protocols** dialog box. In this dialog box you can change the priority of the modified protocol and disable obsolete protocols for your user account.

For more information, see *Protocols dialog box*, page 183.

Protocols dialog box

In the **Protocols** dialog box, you prioritize, activate or deactivate protocols in your own user profile.

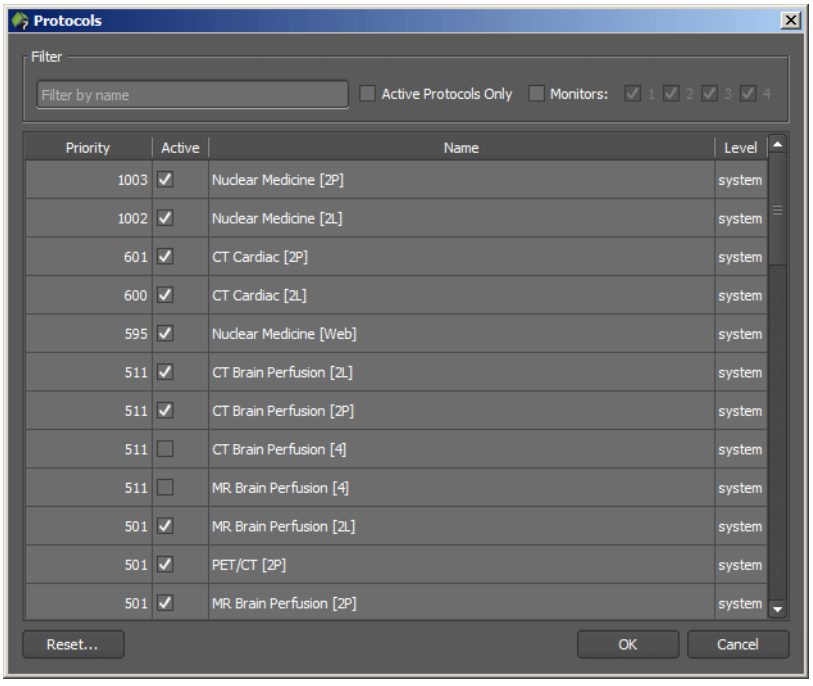
Changing protocol priorities does not change the protocol definition itself but only stores customized protocol priorities in your user profile.

When you load images, Visage 7 automatically identifies the protocol best-suited for these images. Each protocol contains a number of matching criteria, which include a monitor configuration, DICOM tags, and other metadata. The software uses these matching criteria to identify protocols that are suitable for the selected image data. From among these candidates the software chooses the protocol with the highest priority in your user profile.

1. Select **File > Preferences > Protocols** from any of the Visage 7 windows.

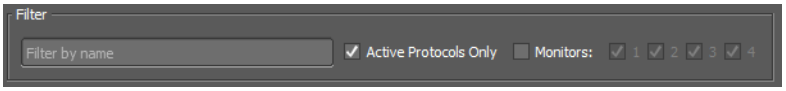
   -Or-

   Select **Protocol > Protocol Editing > Protocols** in the **View** window.



   Because the list of protocols that you find here is most likely very long, filter the list before you begin.

2. Select if you want to show **Active Protocols Only**.

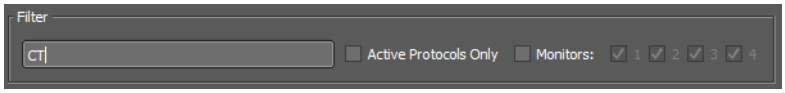


   -Or-

   Filter by protocol name. Type a search string in the **Filter** box and press **Return**.

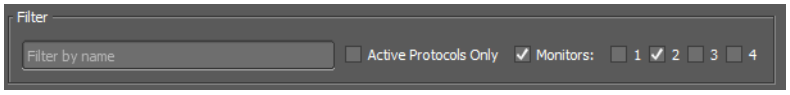
   For example, show only those protocols that apply to CT datasets or to a combination of CT and other modalities.

Note that you cannot use wildcards in the **Filter** box.



-Or-

Show only those protocols that apply to specific monitor configurations.



-Or-

Combine any of these filter criteria.

3. Select **Active** for all protocols that will be considered when you load data. From these protocols the system selects the one best suited for the selected data.

   Protocols for which **Active** is not selected are not considered. Also be aware that only active protocols are listed in the **Protocol** menu and available for manual protocol selection.

4. Double-click the priority rating of a protocol to overwrite the value.

   Protocols with a high priority ranking are more likely to be selected by the system when you load data into the **View** window. Protocols with a high priority ranking also show up at the top of the list when you drop down the **Protocol** menu.

5. Delete protocols only if you are sure you no longer need them.

   When you delete a protocol you remove it from the system. The protocol will no longer be available, either for your own user account or for all other users.

   To be able to delete protocols you need appropriate user rights.

6. Click **OK** to confirm your configuration settings and close the dialog box.

   -Or-

   Click **Reset** to reject any recent and previous changes in this dialog box and return to the factory-default settings.

Advanced protocol editing

Advanced protocol editing requires that you thoroughly understand the principles and concepts of the Visage 7 protocol mechanism.

Tip

We recommend that you attend a training course before you attempt to perform these tasks. Alternatively, leave these tasks to trained administrators or Visage Imaging service personnel.

Protocol definition workflow

Visage 7 expects you to base the definition of a new protocol on an existing protocol. Moreover, the system expects you to edit some aspects directly in the **View** window and adapt others with the protocol editing commands on the **Protocol** menu.

The workflow for protocol modification therefore comprises the following steps:

1. Loading appropriate image data into the **View** window

   Choose a study that is typical for the cases for which you want to create a new protocol.

2. Selecting a base protocol on the **Protocol** menu

   Choose a protocol that resembles the one you want to create.

   The protocol editing options of the Visage 7 Client do not permit you to modify or define **all** aspects of a protocol. Therefore, it is important that you start protocol editing with a protocol that interprets the data in the correct way. In particular, ensure that all images or image stacks that you want to present are available as thumbnails. If you cannot find a suitable protocol, contact customer service.

3. Creating and editing layouts

   A layout defines the arrangement of viewers on the screen. See *Edit Layout dialog box*, page 186.

4. Editing image assignment

   Image assignment defines criteria for selecting images or image stacks and for showing them in the viewers of a layout. Typically, you combine interactive image selection in the **View** window and definition of criteria in the **Image Assignment** dialog box in this step. See *Image Assignment dialog box*, page 188.

   If you define no image assignment rules, images are distributed across viewers in the order in which they were acquired.

5. Adapting image display and tool selection

   Use the tools of the **View** window to modify image display settings such as slice thickness, rendering modes, window level settings, or viewer linking. Also show tools and tool cards as required.

6. Saving the protocol

   Use the **Save Protocol** dialog box to save the modified protocol and to change its name, priority, access and matching criteria. See *Save Protocol dialog box*, page 189.

Defining conditions

Conditions are rules that help Visage 7 to identify specific types of images. See *Edit Conditions dialog box*, page 191.

Note

Only very advanced users with the most advanced user rights are permitted to edit conditions and therefore have access to the **Edit Conditions** dialog box.

Service-level protocol editing

The various options and dialog boxes for advanced protocol editing allow adaptation of existing protocols or definition of new protocols based on existing protocols.

Visage 7 Client users are not permitted to build protocols from scratch or to modify certain protocol properties which, if modified incorrectly, might render the system unusable. This level is reserved for service personnel who have been trained for these tasks specifically.

Tip

Do not hesitate to contact customer service if you require protocol changes that you cannot perform yourself, for example, because you do not have the necessary user rights.

Edit Layout dialog box

In the **Edit Layout** dialog box, you can configure layouts for the protocol that is currently active.

1. Before you open the **Edit Layout** dialog box, inspect the layouts of your current protocol.

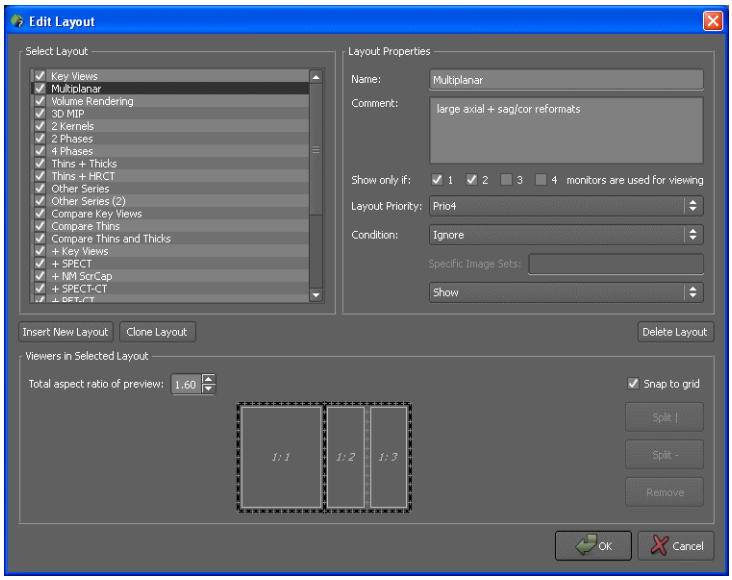
   

   By default, Visage 7 hides layouts that are not suitable for the currently loaded data. If you want to review these layouts nevertheless, select **Protocol > Protocol Editing > Show All Layouts**.

   -Or-

   Right-click in the **Layouts** toolbar and select **Show Layout** and a layout that is currently hidden.

2. Select **Protocol > Protocol Editing > Edit Layout**.



3. Select or clear the check box in front of a layout to activate or deactivate it.

   A layout that you deactivate is no longer shown on the toolbar irrespective of whether you select **Protocol > Protocol Editing > Show All Layouts**.

4. Drag a layout up or down in the **Select Layout** list to change its position on the **Layouts** toolbar.

5. Select an existing layout that you want to modify, or create a new layout.

   We recommend that you create new layouts by cloning existing ones.

6. Assign layouts to monitor configurations.

7. Use the **Layout Priority** and **Condition** boxes to define which layout is selected automatically when a user loads this protocol.

   Refer to customer service for detailed instructions about how to define priority settings and conditions.

8. Modify viewer arrangement and viewer sizes

   Use the buttons in the lower half of the dialog box to add or remove viewers from this layout.

   -Or-

   Resize viewers by dragging their borders in or out, or move viewers by dragging them to a different position.

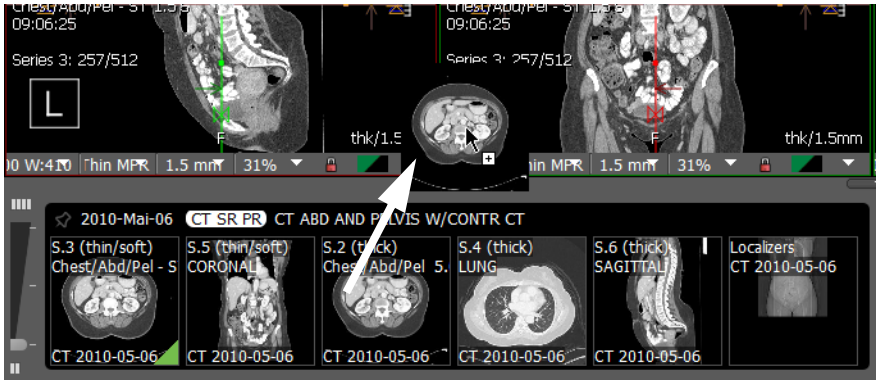
Image Assignment dialog box

Image assignment means assigning specific images to specific viewers by defining matching rules. For example, in MR studies you might want to assign axial T1 images to the upper left viewer.

Image assignment typically combines interactive steps, which you perform in the **View** window, and fine-tuning of rules in the **Image Assignment** dialog box.

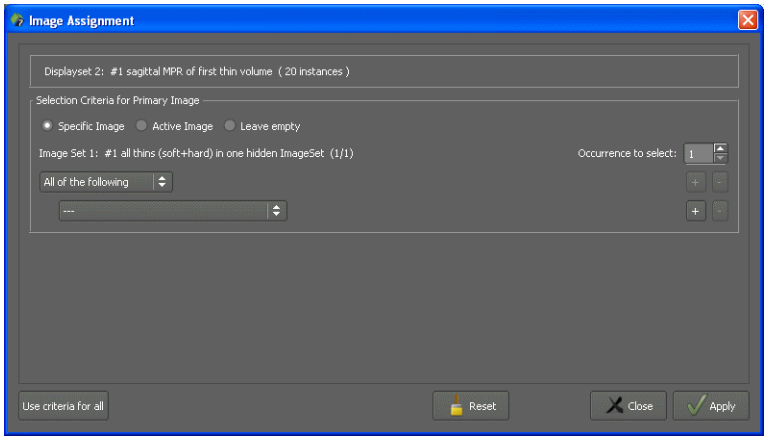
1. Switch to the layout whose image assignment you want to modify.

2. Drag images, image stacks, or series from the thumbnail section into the various viewers.



You can only drag image sets that are represented by a thumbnail. You cannot assign subsets of images or a combination of thumbnails to a viewer. Therefore, if the base protocol does not group the data in appropriate image sets, select a different base protocol, or contact customer service.

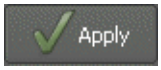
3. Select **Protocol > Protocol Editing > Image Assignment.**



4. In the **Image Assignment** dialog box, refine the criteria the system uses to select images for the active viewer.

   Refer to customer service for detailed instructions about how to define and combine conditions in image assignment rules.

5. Click **Apply**.



6. In the **View** window, select another viewer.

   You can leave the **Image Assignment** dialog box open while you select a different viewer in the background.

7. Define image assignment criteria for this viewer as well.

Save Protocol dialog box

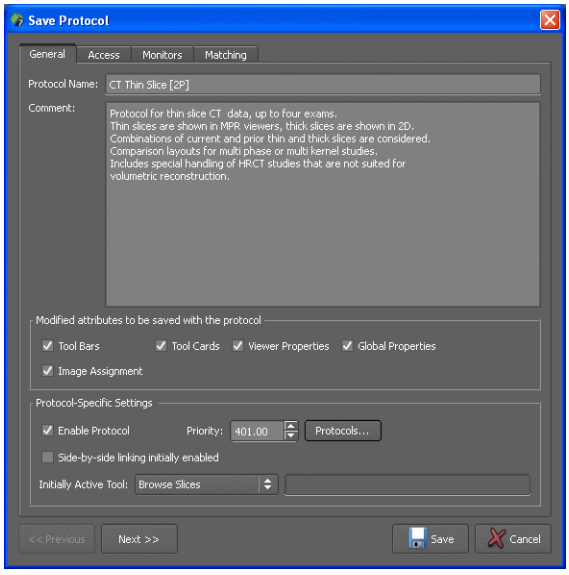
1. Select **Protocol > Protocol Editing > Save Protocol.**

   The **Save Protocol** dialog box has four tab cards.

2. On the **General** tab card, change the name, comment, and protocol priority.

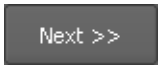
   For example, if you want to make sure that your new protocol is always chosen instead of an existing one, you should increase its priority by at least 1.

   Click the **Protocols** button to review the priority settings of all other protocols that are available for your user account.



3. Also select which of the attributes that you have changed since you selected this protocol you want to save.

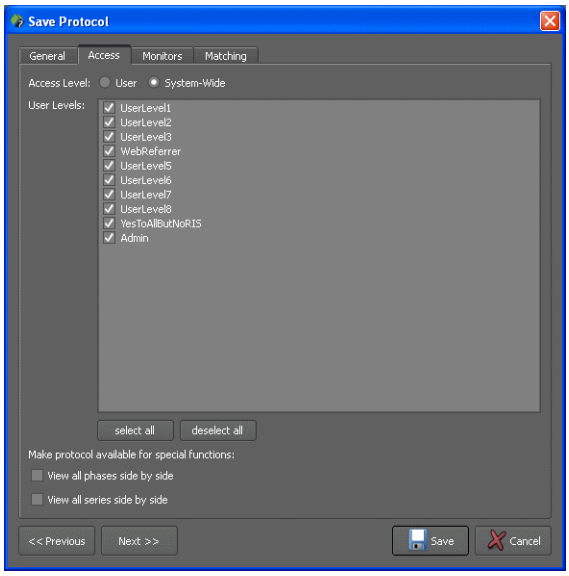
4. Click **Next** to move on to the **Access** tab card.



   -Or-

   If you do not want to change other aspects of the protocol, click **Save** to create a new user-level protocol.

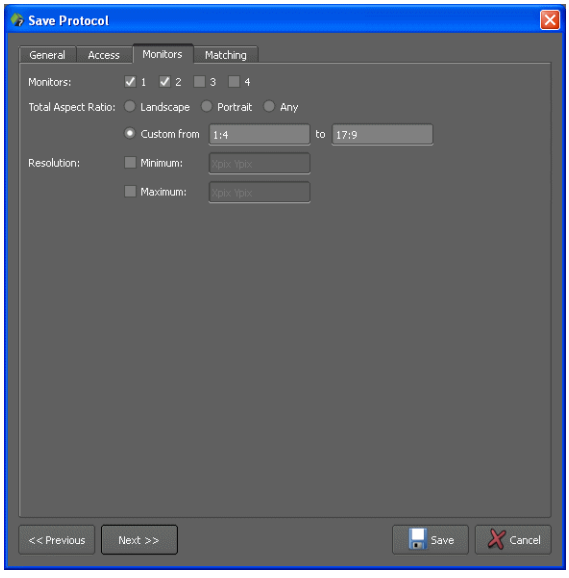
5. On the **Access** tab card, select whether you want to make this protocol available for all users or for specific user groups only.



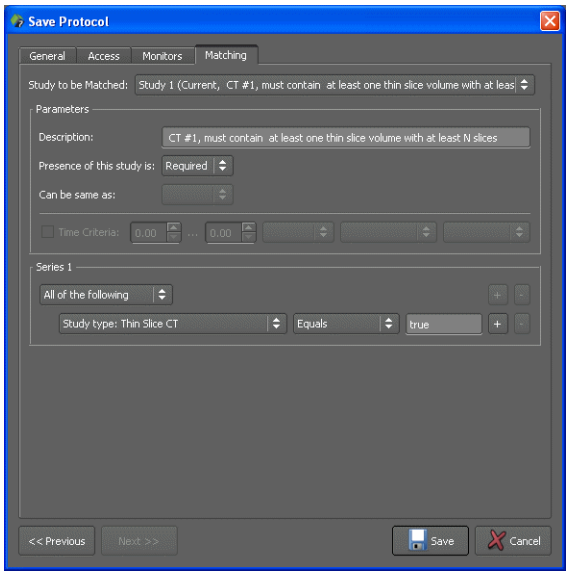
6. Click **Next** to move on to the **Monitors** tab card.
7. On the **Monitors** tab card, define the monitor configuration for which this protocol will be considered suitable by the system.

   The configuration considers only those monitors that display the **View** window.

   When users load images and their monitor configuration does not correspond to the configuration defined here, this protocol is not selected automatically by the system. Users can nevertheless select this protocol on the **Protocol** menu.



8. Click **Next** to move on to the **Matching** tab card.
9. On the **Matching** tab card, you define for which image type or image types the new protocol will be considered suitable by the system.



10. Refer to customer service for instructions about how to define conditions and build matching rules.

11. Click **Save** to save the protocol under the name you specified earlier and with the required access level.

Edit Conditions dialog box

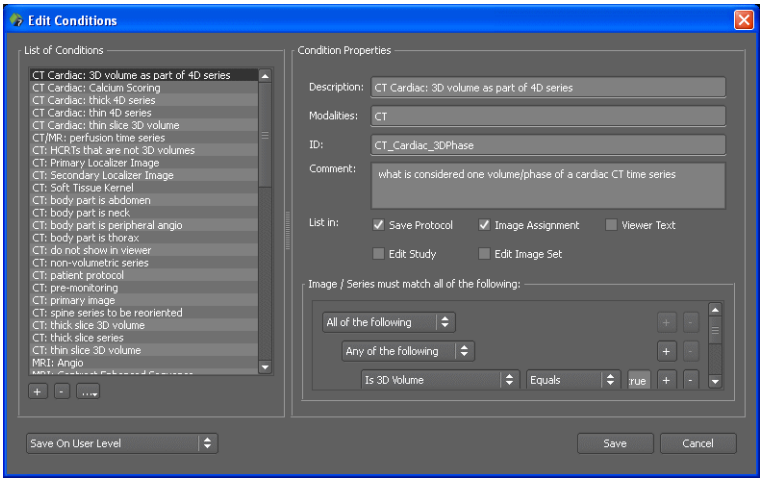
Conditions are rules that help Visage 7 to identify specific types of images. Conditions refer to the DICOM tags of images and series. Conditions combine these tags and their values to form complex selection criteria.

Conditions are used in various protocol definition steps:

- Definition of layout priorities: see *Edit Layout dialog box*, page 186.
- Image assignment to viewers: see *Image Assignment dialog box*, page 188.
- Matching of protocols to studies: see *Save Protocol dialog box*, page 189.

Moreover, conditions are used by the system to group images in image sets. Image sets are presented as thumbnails in the thumbnail section of the screen. The rules for this process are not visible on the Visage 7 Client user interface.

Only very advanced users with the most advanced user rights are permitted to edit conditions and therefore have access to the **Edit Conditions** dialog box.



Refer to customer service for instructions about how to define conditions.

VISAGE IMAGING®
Visioneering Science for Life