VISAGE IMAGING®
Visioneering Science for Life

Online Help

Visage® 7

MD $C\epsilon$ 0197

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The product lifetime of Visage 7 is regulated to two years after the product is discontinued, i.e., two years after the release date of the successor version of the product. Support is guaranteed only within the product's lifetime.

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.

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

Caution

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

Any serious incident that has occurred in relation to the medical device must be reported to the manufacturer and the responsible competent authority.

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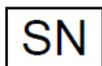
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Explanation of symbols

These symbols convey information that is essential for the proper use of the product.
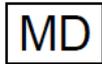
| MD | Medical device |

| SN | Serial number |

Production date

Manufacturer

Consult operating instructions

Caution, consult accompanying documents

CE 0197   CE-mark with reference number of VI's Notified Body (TÜV Rheinland LGA Products GmbH)

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Product description

Visage 7 is an imaging solution based entirely on efficient streaming technology. It scales easily from a single radiology practice to large distributed healthcare enterprises. Visage 7 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.

The Visage 7 server receives image data in DICOM format via network. This provides universal connections to archives, modalities, and workstations. The supported modalities are listed in the DICOM Conformance Statement.

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

- CT/MR angiography, e.g. 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 7 must only be used by trained healthcare professionals. It may support physicians and/or their medical staff in assessing medical cases. Any diagnostic or therapeutic decision resides with the doctors and/or their medical staff in their respective area of responsibility.

The web and thin-client technologies allow the software to be run on a variety of hardware platforms. For diagnostic purposes, the user must make sure that the reading environment complies with any applicable diagnostic requirements and the state-of-the-art.

Only DICOM for presentation images must be used on an FDA-approved monitor for primary image diagnosis in mammography.

Only uncompressed or lossless compressed images must be used for primary image diagnosis in mammography.

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 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 macOS clients**

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

- **Easy scalability**

  The fully scalable distributed server-side 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 shown 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.

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, Visage 7 uses streaming instead.

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 client computers running Visage 7 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 macOS. 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.

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 U.S. 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.

Loading studies from the 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 into a **View** window.

Note
Depending on your system configuration, the **Study Browser** might not be visible. Instead, you can use an integrated worklist, for example, the Visage RIS or the worklist tab of the Visage 7 client.

Finding studies

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.

Recent studies

The tab **Recent Studies** presents a list of the studies that you have loaded from the **Study Browser** recently.

If the **Recent Studies** tab is currently not shown, select it from the list of available servers and nodes.
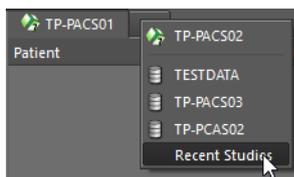
Defining filter and search criteria

Before you start defining search criteria for a database query, you select the database that you want to search. Queries apply only to the database whose tab is currently shown in the foreground. The leftmost tab is your Visage 7 server.

Patient

Enter the name, date of birth or age, or ID of the patient whom you are looking for.

If you do not remember the exact name, date, or number, use wildcard characters. For example, type `Mil` in the patient name box to find *Miller, Milford, Miltner*, or type `*mil` to find all of the above and also *Hamilton*. Or type `AB??34` in the patient ID box to find *AB1234, AB0034*, and *AB11345678*.

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 searches 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 semi-colon (;) or the pipe character (|). For example, `Anderson|Alexander` or `Miller;Milford`.

To exclude names or fragments of names, use the exclamation mark character (!). For example, `!A` in the patient name box searches for all patients whose names do not start with an A.

To search by date of birth or age, either specify the exact date, the year the patient was born, or the patient's age. Or search for patients of a specific age group. Point to **Date of Birth** to show a tooltip with examples of how to specify patient age or age group.

Date

1. Click the date box.

2. Select if you want to search by **Study Date** or **Insertion Date**.

   The **Study Date** is the date and time when the study started.

   The **Insertion Date** is the date and time when the study was transferred to the server from a modality or an archive.

3. Next to **From ... To**, specify 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.

-Or-

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

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

Modality

Select the checkboxes of all modalities whose studies you want to search for:

CT (computed tomography), **MR** (magnetic resonance imaging), **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`.

Use an exclamation mark to exclude a modality from your search. For example, specify `!CT` in the **Others** box to search for studies of all modalities except for modality CT.

Fields

1. Open the lists of additional criteria using the double-arrow buttons and select a criterion.

2. Specify your search string in the input box below the selected criterion.

Remember that you can use wildcard characters.

If you want to search for more than one reading physician, for example, separate names with a semicolon (;) or pipe character (|), for example, `Miller|Smith` or `Miller;Smith`. For **Accession Number**, **Study Instance UID**, and **Series Instance UID**, separation of numbers with a space is also possible.

If the search strings themselves contain semicolons, pipe characters, or backslashes, as in `Ward 4; Rm.6` or `Ward 1\Rm.2`, prefix these characters with a backslash. In this example:
`Ward 4\; Rm.6;Ward 1\\Rm.2` or `Ward 4\; Rm.6|Ward 1\\Rm.2`

To define exclusion criteria, use the exclamation mark character (!). For example, type `!Neuro` in the subspecialty field to search for studies that are not assigned to the subspecialty Neuro.

If you want to copy search criteria from a list, be sure that the list separates items as shown above or with the newline character (\n).

-Or-

Click the list button next to an input box and select one or several items.

3. If three search boxes are not sufficient for your filter definition, right-click the **Fields** section and select **Additional Search Fields**.

4. If you are using labels to organize your studies, use this field to search for a study with a specific label.

See *Finding studies with labels or comments*, page 222.

Study States

1. Click **Study States**.

2. In the **Study States** dialog, clear study states that you want to exclude from your search.

When you modify the selection of study states, the *Study States* button label is shown italic and the **Reset** button next to it is available.

3. Click **Reset** next to **Study States** if you want to reset only study states but none of the other search criteria.

Starting, resetting, or repeating a query

Use the following buttons to start a database search, to reset search criteria, or to repeat a recent query.

Starting a query

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

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

Resetting search criteria

Click **Reset** next to the **Query** button to remove all search criteria from the query section.

Repeating a recent query

1. Click **Reset** and hold the mouse button down to show a list of recent queries.
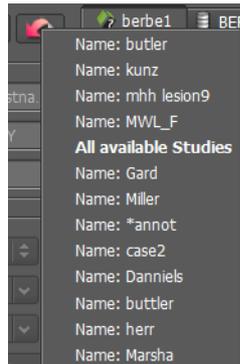
2. Click the query that you want to repeat.

   The filter and search criteria of this query now appear in the query section.

3. Click **Query** to start the database search.

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 only available to your own user account. You cannot make presets public.

Quick search with a preset

Click a preset button to retrieve its search criteria.
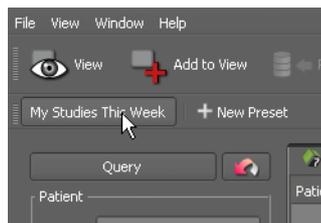
Depending on how you defined the preset, you might have to click **Query** to start the search.

Adding criteria

If the query preset finds too many studies, you can add criteria.

1. Select or type more search criteria in the query section.

2. Click **Query**.

> Query

Defining a preset

1. In the query section of the **Study Browser**, select and type your search criteria.

2. Click **New Preset**.

> + New Preset

3. In the **Preset** dialog, enter a name for your new preset.

4. Select **Default** or **Auto Query** or a combination of both.

Default automatically loads the search criteria defined in your preset when you start the Visage 7 client. You may still have to click **Query** to actually search the database.

Auto Query applies the search criteria defined in the preset and starts searching immediately. You do not have to click **Query** again.

Default plus **Auto Query** means the system will run this search every time you call up the Visage 7 software.

5. Save the preset.

A new preset button appears above the query section.

6. Drag the new preset to where you want to show it on the presets bar.

Modifying or deleting a preset

1. Click a preset button to select it.

2. Change filter and search criteria in the query section.

3. Right-click the selected preset button and select **Update Preset with Current Settings**.

-Or-

Right-click a preset button and select **Properties** to modify settings for the properties **Auto Query** or **Default**.

-Or-

Right-click a preset button and select **Delete Preset** to remove a query preset that you no longer need.

Selecting a different database

The study list may comprise two or more tabs:

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

• Any tabs further to the right represent more Visage 7 servers, connected DICOM network nodes, or external drives.

1. Click the **+** tab to show a list of available servers and nodes.
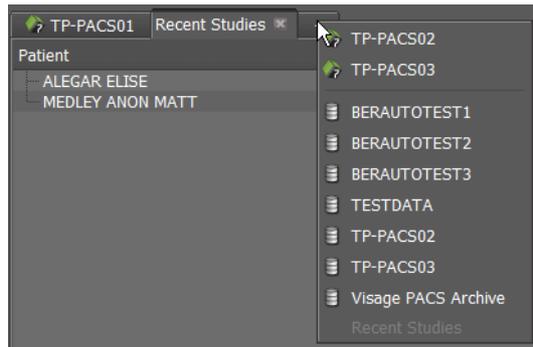
Servers with the Visage 7 logo are partner systems. You can load data from partner systems in the same way as you load them from the primary server. List items without the Visage 7 logo are connected DICOM network nodes. You need to retrieve data from these nodes before you can load the data.

See *Importing and exporting studies*, page 206.

2. Select a server or network node to add this tab.
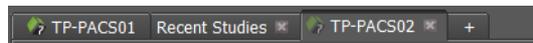
Remember that queries apply only to the database whose tab is currently shown in the foreground.

Loading data from the study list

After you have clicked the **Query** button or a query preset, the study list shows all the studies that were found on the server or on the selected network node.

Information in the study list

The study list is arranged in a hierarchical tree view.

1. Use the **+/-** buttons in front of the entries to expand or collapse this list.

2. Click a column header to sort the list for a better overview.

Clicking a second time reverses the search order.

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

The column **3D** tells you if 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.

The column **QA Status** indicates whether the study (performed procedure) could be matched to a RIS order (scheduled procedure). See *Information in the Performed and Scheduled Procedures lists*, page 236.

The **QA Status** column provides meaningful information only if your system is connected to a RIS (radiology information system).

Loading with double-click

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

2. Double-click a second study, series, or volume dataset.

   A new tab opens in the title bar. The active tab is highlighted with a green bullet.

3. Use these tabs to switch between cases.

   Tip

   Double-clicking a study, series, or volume dataset is a shortcut to selecting the study, series, or volume dataset and then clicking **View In New Tab**.
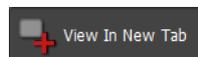
Replacing data on a view tab

1. Select a study, series, or volume dataset.

2. Click **View**.

   This replaces the data on the active tab.

Loading more than one study, series, or dataset onto one tab

1. Right-click a study, series, or volume dataset and select **Find All Studies For This Patient**.

2. Press the **Shift** key, or the **Ctrl/Cmd** key and click more studies, series, or volume datasets of this patient.

3. Click **View** to load all these studies, series, or volume datasets onto a single tab.

   -Or-

   Select one or several studies, series, or volume datasets and click **Add to View** to add this data to the active tab.

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. This Visage 7 client contains only this case and the **Export** window. A colored bar below the title bar reminds you that this is not the case that you worked on originally.

2. Return to your original case with **Alt + Tab** (Windows) or **Cmd + Tab** (Mac).

   The second case remains 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 you load 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 that you want to load.

2. Right-click and select **View All Series Side-By-Side**.

   -Or-

   For a time series, select **View All Phases Side-By-Side**.

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

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

-Or-

Point to the report in the **Interpretation** column.

Showing order details   If Visage 7 is integrated in a radiology information system (RIS), you can view order details right from the **Study Browser**.

Right-click a study for which an order exists and select **Order Details**.

A separate window opens which presents information about the corresponding RIS order.

Loading studies from the worklist

If Visage 7 is integrated in a radiology information system (RIS), you can use the **Worklist** window of the Visage 7 client for quick access to the studies that you want to read and report on.

The **Worklist** window presents orders from the RIS. Depending on the configuration of your system, these orders are grouped in so-called worklists. Worklists can be configured by Visage Imaging customer service. Worklists might reflect the departmental structure of your hospital (Emergency Room, Mammography, Neurology, etc.).

In the **Worklist** window, you can filter RIS orders so that only the cases that are relevant for your day's work are shown. You might choose to show all studies from a preconfigured worklist or filter a preconfigured worklist. So the **Worklist** window will always show only and exactly those cases that you want to read and report on next.

Loading data from the worklist

A worklist is a dynamic list of reading or imaging tasks that is updated when you or other users complete a task or when new tasks arrive on the server. Worklists are updated every few seconds.

Loading a study for reporting

Before you load a study from the worklist, decide whether you want to read and report on it now, or whether you want to preview its images only.

1. To load studies for reporting, select **Lock Studies For Reporting**.
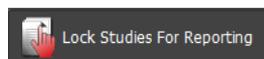
2. Double-click a study in the worklist.

In the **Worklist**, the study is now marked with a lock symbol. Other users are not permitted to open this study for reporting while you are reading it.

By locking a study for reporting, you make sure none of your colleagues accidentally reads the study that you are currently working on.

Loading a study for preview or reference

Clear **Lock Studies For Reporting** and double-click a study in the worklist.

-Or-

Right-click the study and select **View Only**.

The study is loaded. However, the study is not locked in the worklist. Another user can read it while you are looking at the images.

Loading studies onto separate tabs

If you want to load more than one case from the worklist at a time, load these studies onto separate tabs.

1. Turn **Lock Studies For Reporting** on or off, depending on whether you want to load these studies for reading or for preview or reference purposes only.
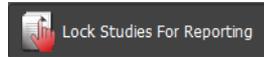
2. Double-click the first study in the worklist.

3. Return to the **Worklist** window.

4. Select a second study in the worklist.

5. Click **View in New Tab**.
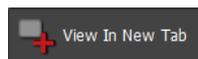
A new tab opens in the title bar. The active tab is highlighted with a green bullet.

6. Use these tabs to switch between cases.

Showing a study in the Study Browser

If you want to check which series a study contains before loading this study from the worklist, switch to the **Study Browser**.

Right-click the study in the worklist and select **Show in Study Browser**.

Showing order details

Click the info symbol in the **Priority** column to show order details in a separate window.

Organizing the workflow

For a radiologist, a worklist presents the cases that require reading. Typically, you proceed through this list from top to bottom. If the worklist does not present cases in a way suitable for this method, there are various options for optimizing your workflow.

Rearranging the worklist

The worklist presents information about studies in columns. With the exception of the leftmost columns **Priority** and **Status**, you can rearrange all columns according to your preferences.

1. Drag a column header to the right or to the left.

The new arrangement of columns is stored in your user profile automatically. This means that the worklist will present itself as you have arranged it, even if you close and then reopen the Visage 7 client.

2. Right-click a column header and select **Reset all Columns** to return to the default arrangement.

Sorting the worklist

By default, a worklist is sorted by priority and time elapsed since the studies were ready to read. However, you can change this sort order.

1. Click a column header to select the first criterion for sorting the worklist.

The column header shows a small arrow pointing up or down and the number 1.

2. Click a second time to reverse the sort order.

3. Hold the **Ctrl/Cmd** key down and click a second, third, or fourth column.

These column headers now also show an arrow and a number.

Assigning cases to users

If you share the task of reading the studies in a worklist with one or several colleagues, you can assign studies to specific users.

Click **Assign to me** to assign a study to yourself.

-Or-

Right-click a study and select **Assign to** to assign this case to a different user.

If other users attempt to open the study for reporting (**Lock Studies For Reporting** activated), a message opens informing them that this study is locked.

Skipping cases

Before you start reading the studies in your worklist, you can define your own priorities and decide which studies to process first and which ones you will reserve for later.

Click this button for studies that you intend to read at a later time.

These studies are marked with a skip symbol now.

The symbol is a marker or reminder to yourself only. The marker is not visible to other users.

As you proceed through your reading list, skipping the cases that you have marked and processing unmarked studies only, skipped cases will accumulate at the top of the list. When you close the Visage 7 client after your day's work and return the next day, the skip order symbol will have disappeared from these studies, which reminds you that these cases are due to be read next.

Marking an order as "Do Not Read"

Irrespective of the order status, a study can sometimes not be read immediately. One reason for this may be that a prior study needs to be imported first.

Right-click an order and select **Do Not Read** and a reason.

The priority indicator is now displayed striped.
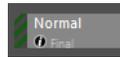
Linking related orders

In some situations, multiple RIS orders are scanned in a single DICOM study. For example, in a trauma workflow, separate orders may be created for the foot, knee, and leg. However, these parts of the body are scanned in a single study.

1. In the **Worklist**, right-click an order and select **Link Related Orders**.

   -Or-

   In a **View** window, click the **Link Related Orders** tool.

2. In the **Link Related Orders** dialog, select the orders that you want to link to this study.

If configured, the link status is shown in a separate column in the worklist.

Changing the order priority

Right-click an order and select **Priority Urgent**, **High**, or **Normal**.

Urgent orders are listed in the topmost position whereas orders with high or normal priority move further down the list.

Changing the order status

The various systems in your hospital communicate order status information in the background. This may take a few minutes. In urgent cases, you can speed up the order status update. For example, mark a study as ready to read as soon as the examination has ended and all images have arrived.

In the **Worklist**, right-click an order and select **Order Status > Exam Ended**.

-Or-

In a **View** window, click the **Mark Exam Ended (ready to read)** tool.

Tip

In the **Worklist**, you can also change other order status flags. For example, select order status **Finalize** even before a message to that effect has arrived from the system that you use for dictating reports.

Changing the subspecialty

The attribute subspecialty often defines on whose worklist an order will appear.

Right-click an order that was assigned incorrectly and select the correct **Subspecialty**.

Auto-advance   **Auto-Advance** helps to speed up your reading workflow.

1. Right-click in the worklist display section and select **Auto-Advance**.

2. Mark the cases that you do not want to read right now with a skip symbol.

   See *Skipping cases*, page 28.

3. Load the first study from your worklist for reporting.

4. Read the images and create your report.

5. Close the session.

The Visage 7 client will immediately open the next study in your worklist.

Finding orders

Click this button above the worklist to show the query section.

Filtering by order status

1. Use these buttons to select an order status.

You can select more than one status button.

2. Click the **Images in PACS** button in combination with order status **Exam Ended** to show only those studies for which the modality has already sent images to the Visage 7 server.

Defining filter and search criteria

When you are looking for a specific case, you use the query section of the **Worklist** to specify filter and search criteria.

Patient   Enter the name, date of birth or age, or ID of the patient whom you are looking for.

If you do not remember the exact name, date, or number, use wildcard characters. For example, type `Mil` in the patient name box to find *Miller, Milford, Miltner*, or type `*mil` to find all of the above and also *Hamilton*. Or `AB??34` in the patient ID box to find *AB1234, AB0034*, and *AB11345678*.

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 searches 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 semi-colon (;) or the pipe character (|). For example, `Anderson|Alexander` or `Miller;Milford`.

To exclude names or fragments of names, use the exclamation mark character (!). For example, `!A` in the patient name box searches for all patients whose names do not start with an A.

To search by date of birth or age, either specify the exact date, the year the patient was born, or the patient's age. Or search for patients of a specific age group. Point to **Date of Birth** to show a tooltip with examples of how to specify patient age or age group.

Date

1. Click the date box.

2. Select if you want to search by **Scheduled Date**, **Insertion Date**, **Study Date**, or **Completed Date**.

   The **Scheduled Date** is the date and time when the study was scheduled to be performed according to the RIS order.

   The **Insertion Date** is the date and time when the study was transferred to the server from a modality or an archive.

   The **Study Date** is the date and time when the study started.

   The **Completed Date** is the date and time when the study was marked as completed in the RIS.

3. Next to **From ... To,** specify 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.

   -Or-

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

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

Modality

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

CT (computed tomography), **MR** (magnetic resonance imaging), **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`.

Use an exclamation mark to exclude a modality from your search. For example, specify `!CT` in the **Others** box to search for studies of all modalities except for modality CT.

Fields

1. Open the lists of additional criteria using the double-arrow buttons and select a criterion.

2. Specify your search string in the input box below the selected criterion.

   Remember that you can use wildcard characters.

   If you want to search for more than one referring physician, for example, separate names with a semicolon (;) or pipe character (|): for example, `Miller|Smith` or `Miller;Smith`. For **Accession Number**, **Study Instance UID**, and **Series Instance UID**, separation of numbers with a space is also possible.

   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`

   To define exclusion criteria, use the exclamation mark character (!). For example, type `!Neuro` in the subspecialty field to search for orders that are not assigned to the subspecialty Neuro.

   If you want to copy search criteria from a list, be sure that the list separates items as shown above or with the newline character (\n).

-Or-

Click the list button next to an input box and select one or several items.

Institution Name

3. If three search boxes are not sufficient for your filter definition, right-click the **Fields** section and select **Additional Search Fields**.

Fields
Additional Search Fields
Accession Number

4. If you are using labels to organize your studies, use this field to search for a study with a specific label.

Study Labels

See *Finding studies with labels or comments*, page 222.

Study States

1. Click **Study States**.

Study States...

2. In the **Study States** dialog, clear study states that you want to exclude from your search.

When you modify the selection of study states, the *Study States* button label is shown italic and the **Reset** button next to it is available.

Study States...*

3. Click **Reset** next to **Study States** if you want to reset only study states but none of the other search criteria.

Starting, resetting, or repeating a query

Use the following buttons to start searching for orders, to reset search criteria, or to repeat a recent query.

Starting a query

Click **Query** to start a search.

Query

Resetting search criteria

Click **Reset** next to the **Query** button to remove all search criteria from the query section.

Repeating a recent query

1. Click **Reset** and hold the mouse button down to show a list of recent queries.
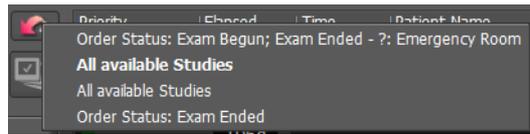
2. Click the query that you want to repeat.

   The filter and search criteria of this query appear in the query section now.

3. Click **Query** to start the search.

Query presets

Frequently used combinations of search criteria can be saved in presets. Query presets are listed above the query section and worklist.

Visage 7 makes a distinction between system presets, presets that are available to specific user groups, and user-level presets. Any presets that you define are only available to your user account. You cannot make presets public.

Quick search with a preset

Click a preset button to retrieve its search criteria and start the query.

The number in the upper-right corner of the preset button indicates how many RIS orders the preset will find at this point in time. This number is updated together with the worklist every few seconds.

The selected preset is highlighted.
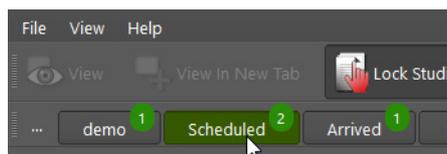
If you cannot find the preset that you are looking for, click the double-arrow button at the right edge of the presets bar to show all the available presets.

Adding criteria

If the query preset finds too many orders, you can add criteria.

1. Select or type more search criteria in the query section.

2. Click **Query**.

Combining presets

You can combine the search and filter criteria of several presets.

1. Click the first preset button.

2. Hold the **Ctrl/Cmd** key down and click a second preset.

Default preset Right-click a preset and select **Default**.

The system will select this preset every time you start the Visage 7 client.

Moving presets By default, query presets are listed in alphabetical order on the presets bar. If this bar contains a large number of presets, you will probably prefer to have the presets that you use most frequently in a prominent position.

Drag presets to a more suitable position if you like.

Showing or hiding system presets System presets are hidden, unless you subscribe to them.

1. Click the **New Preset** button.

    If system presets have been configured in your Visage 7 installation, a menu is shown.

2. Choose **Select System Presets**.

3. In the **Show or Hide Presets** dialog, select any system presets that you want to subscribe to.

4. Click **OK**.

    The presets bar now shows the selected system presets plus all your user-defined presets.

5. To hide a system preset, either go to the **Show or Hide Presets** dialog again, or right-click a preset button and select **Hide Preset**.

Modifying a preset You can modify user-defined presets as well as group-level presets and system presets as long as they have not been defined read-only. Modifications to system or group-level presets are available to your own user account only. Other users will not see your modifications.

1. Click a preset to select it.

2. Click this button above the worklist to show the query section.

3. Modify filter and search criteria.

4. Right-click the preset button and select **Update Preset with Current Settings**.

5. To discard your modifications to a system preset, right-click the preset button again and select **Reset to System**.

Defining a preset 1. Click this button above the worklist to show the query section.

2. Specify filter and search criteria.

3. Click the **Preset** button and select **Save User Preset**.

4. In the **Preset** dialog, enter a name for your new preset.

5. Save the preset.

A new preset button is displayed above the worklist.

Deleting a user-defined preset

Right-click a preset button and select **Delete Preset** to remove a query preset that you no longer need.

Viewing images

As soon as you have loaded images, they are shown in one or several **View** windows, which appear as tabs in the title bar. You use these tabs to switch between cases.

Tabs show the name of the patient whose data they contain. The active tab is highlighted with a green bullet, a yellow plus sign indicates that new images have arrived on the Visage 7 server since you loaded images onto a tab.

| Study Browser | Worklist | ● ROMERO | ● MCDONALD | Export | Quality Assurance | ▬ ▢ ✕ |
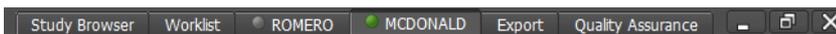
Basic navigation and image display

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 **Default Navigation** to select this tool.

2. Use the left mouse button to perform the function that is assigned to the default navigation tool.

Zoom

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

1. Click **Zoom** 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.

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

Pan

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

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

1. Click **Pan** to select this tool.

2. Drag the cursor across a viewer to move the image within the viewer.

-Or-

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

Inverse

Click this tool to invert the image in the active viewer.

Inversion means that light areas are displayed dark and dark areas are displayed light. Inversion is not possible in the 3D viewer.

Edge Enhancement

With this tool, you can optimize image quality and increase contrast between structures in slice images. The edge enhancement filter is particularly useful for improving the sharpness or definition of XA images.

1. Click **Edge Enhancement** to select this tool.

2. Drag the cursor up or down to adjust image sharpness.

-Or-

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

Adjusting the window level

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 **Window Level** to select this tool.

-Or-

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

2. Click a viewer and hold the mouse button (or mouse buttons) down.

3. Drag the cursor to the left or to the right to change the window width (contrast).

-Or-

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

If configured, dragging left or right only affects the upper window width value for PT, SPECT, ST, or NM images.

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 the way, you can hide it. See *Toggle Histogram*, page 58.

Tip
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. This tool is particularly useful for image data that is not calibrated. For example, use **Auto Window Level in ROI** in MR images in which the voxel intensity varies considerably.

1. Click **Auto Window Level in ROI** to select this tool.

2. 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.

Show Window Level Presets

With this tool, you can show a list of all window level presets that exist for an image type.

1. Click **Show Window Level Presets** to show a menu.

2. Select a window level preset from the list.

✓ Default	0
CT bone	1
CT organs	2
CT lung	3
CT brain	4
CT angio	5
Window/Level Presets...	

-Or-
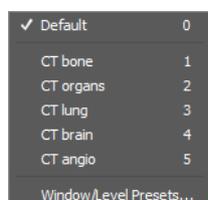
Select **Window/Level Presets** to define a new window level preset. See *Configuring window/level presets*, page 250.

Enlarge/Reduce Window Width

Click one of these tools to enlarge or reduce the window width step by step.

The adaptation factor and fix point can be configured in the property settings for these tools.

Adjusting the display size

In addition to interactive zooming, Visage 7 offers several other tools for optimizing image display size quickly.

Fit Width/Height, Fit Width, Fit Height

Click **Fit Width/Height** to fit images optimally within their viewers.

-Or-

Click **Fit Width** to make optimum use of the viewer width.

-Or-

Click **Fit Height** to make optimum use of the viewer height.

If an MPR viewer is active when you click one of these tools, 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%

Click this tool to show images in their original size.

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

For 2D viewers, original size 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 tool, 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.

Magnifying Glass

With this tool, you can see details without having to zoom the entire image.

1. Click **Magnifying Glass** 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.

3. Drag the cursor across the image to move the rectangle.

   This movement gives you the impression of holding a magnifying glass in your hand.

4. While holding down the mouse button, rotate the mouse wheel 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 into another viewer and use the magnifying glass there.

6. Click **Magnifying Glass** again to turn the tool off.

Tip

Choose multiple **Magnifying Glasses** rather than a single **Magnifying Glass** to inspect and compare magnified sections in more than one viewer. See also *Magnifying Glasses*, page 132.

Rotating and flipping images

With the tools described 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 (**View > Show in Viewer > Orientation Cube**, or **View > Show in Viewer > Orientation Labels**).

Rotate Clockwise, Rotate Counterclockwise

Click one of these tools to rotate the image in the active viewer by 90° clockwise or counterclockwise.

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

Flip Horizontally, Flip Vertically

Click one of these tools to flip the image in the active viewer along its vertical or horizontal axis.

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

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

Rotate in Plane

With this tool, you can rotate an image with the mouse. You use this tool, for example, to straighten up images that were acquired tilted.

1. Click **Rotate in Plane** to select this tool.

2. Click onto an image and hold the mouse button down.

3. Drag the cursor across the image to rotate the image.

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

Scrolling in image stacks

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

Browse Slices

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

1. Click **Browse Slices** to select this tool.

2. Drag the cursor up or down 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.

Browsing with the mouse wheel or arrow keys

Using the mouse wheel or arrow keys, you can browse slices without having to select a tool first.

Point to a viewer and start rotating the mouse wheel.

-Or-

Press the **Up** or **Down** arrow key on your keyboard.

Whether or not slices will be skipped depends on whether the tool **Mouse Wheel Acceleration** is also selected.

Mouse Wheel Acceleration

This tool affects the behavior of the arrow keys and the mouse wheel when you browse slices. With **Mouse Wheel Acceleration**, scrolling quickly with the mouse wheel or arrow keys results in slices being skipped.

Mouse Wheel Acceleration is selected by default.

Clear this selection explicitly if you want to see every single image in an image stack when you browse slices.

Deselecting this tool ensures that you will not skip images when browsing slices with the mouse wheel or arrow keys. Scrolling might become slower when the tool is deselected.

Instead of deactivating **Mouse Wheel Acceleration,** you might use the tool **Browse Continuously** to be sure you see all slices.

Browse Slices Sticky

This tool is an alternative to **Browse Slices**. With **Browse Slices Sticky**, you can browse slices simply by moving the mouse without clicking.

1. Click **Browse Slices Sticky** to select this tool.

The cursor changes shape.

2. Move the mouse up or down to start scrolling.

3. Click to end slice browsing.

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 **Browse Continuously** to select this tool.

2. Drag the cursor 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 property settings.

Browse in All Priors

With this tool, you can change the behavior of the **Browse Slices** tool.

✓ A current study and more than one prior study have been loaded.

✓ A layout is selected that shows the current and prior study side by side.

1. Click **Browse in All Priors** to select this tool.

2. Click **Browse Slices**.

3. Point to a viewer that shows the prior study.

4. Rotate the mouse wheel.

You now scroll images in all the viewers that show prior studies. Scrolling is synchronized so that you can compare the images of the current study with those of the various prior studies.

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 depending on whether the **Scroll Page by Page** tool is selected or not.

1. Click **Scroll Page by Page** to select this tool.

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

-Or-

1. Cancel the selection of the **Scroll Page by Page** tool.

2. Use **Browse Slices** or the mouse wheel or arrow keys to advance by just one image at a time in each viewer.

This gives the impression of images flowing through your viewers, for example, from the lower right to the upper left.

First Slice, Previous Slice, Next Slice, Last Slice

With these tools, you can scroll slices in viewers that show image stacks.

Previous Thick Slice, Next Thick Slice

If you have switched to thick-slice display in a volume dataset, use these tools to browse slices. The increment for scrolling is the selected slice thickness.

Show Multiframes in Single Tiles

Some protocols, for example, those for ultrasound images, present images as so-called tiles rather than in image stacks. Tiled presentation arranges images next to each other,

For multiframe objects, two alternative display modes are available in tiled display:

- Collapsed

  (**Show Multiframes in Single Tiles** is turned on)

  A multiframe object is shown in a single viewer as an image stack.
  When a multiframe object is shown in a single tile, you can play it back like a clip.

- Expanded

  (**Show Multiframes in Single Tiles** is turned off)

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

1. Click **Show Multiframes in Single Tiles** to show multiframe images collapsed or expanded.

2. Press the **Up** or **Down** arrow key or the **Home** or **End** key on your keyboard to scroll through the image stack of a collapsed multiframe.

   -Or-

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

   -Or-

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

Cine display

With the **Play/Pause** tool and the **Cine** tool card, you can play back images in a stack or time series, or you can rotate around a volume in a 3D viewer. This gives you the impression of a movie being played back.

Play/Pause

Starting playback   Click **Play/Pause** to start playing back.

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

Halting or stopping playback	While the movie is being played back, the button changes shape. Click **Pause** to interrupt or stop playback.

Play Images, Play Stack, Play in Time Mode

Click one of these tools to select a batching mode and start playback in one go.

These tools are shortcuts for selecting a batching mode on the **Cine** tool card and then starting playback from that tool card.

Cine tool card

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 (MPEG or H264). In a 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) onto the primary server or send them to another DICOM server. Or you can save images to your computer as an MPEG movie (.mpg), or as JPEG (.jpg), PNG (.png), or DICOM (.dcm) images.

On the menu, select **Tools > Cine** to open this tool card.

-Or-

Click **Show/Hide Cine Tool Card**.

The appearance of the **Cine** tool card is slightly different depending on the data loaded and the viewer selected.

Cine options for MPR viewers	1. Select a **Batching** mode. **Stack** scrolls through the slice images in a volume. **Images** scrolls through the slice images in consecutive volumes (stacked image sets). **Time** plays back a time series over the acquired time. 2. Under **Range**, select the first and last image in your movie. 3. If you select **Stack**, select the **Increment** for scrolling. The increment can either be the **Same as Slice Thickness** or any other value in millimeters (**Custom**).

4. Select a **Frame Rate**.

Select **Frame Time**, **Frame Time Vector**, or **Recommended Rate (DICOM)** to play back the movie at 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.

5. Use the **Speed** slider to slow down or speed up playback interactively.

6. If you select **Images**, select **All Viewers** to apply cine mode to all viewers.

Clearing **All Viewers** plays the film in the selected viewer only.

7. If you select **Images** plus **All Viewers**, decide whether to **Skip images if necessary**.

Clear **Skip frames if necessary** to be sure that all images are shown regardless of the playback speed. Clearing **Skip frames if necessary** might result in a slower playback speed than you have selected with the slider.

Cine options for 3D viewers

1. Select a **Batching** mode.

Rotation rotates the entire volume.

Crop moves a crop plane through the volume. This option is shown only if the **Crop Plane** tool is currently turned on.

Time plays back the volume over time. This option is available only if the loaded dataset is a time series.

2. If you select **Rotation**, select the rotation **Angle** (360° is full rotation) and **Increment**.

3. If you select **Rotation**, also select a rotation axis and decide whether this axis refers to the patient coordinate system (object) or to screen coordinates.

4. Select a **Frame Rate**.

Select **Frame Time**, **Frame Time Vector**, or **Recommended Rate (DICOM)** 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.

5. Use the **Speed** slider to slow down or speed up playback interactively.

6. Select the **Best 3D Quality** box for playback in best 3D quality. This may result in a slower playback speed.

Cine options for CPR or lumen viewer

1. Select a **Batching** mode.

   Stack scrolls through the slice images.

   Rotation rotates around the segmented structure or vessel.

2. If you select **Stack**, also specify the first and last image in your movie (**Range**) and an **Increment** for scrolling.

   The increment can either be the **Same as Slice Thickness** or any other value in millimeters (**Custom**).

3. If you select **Rotation**, also select the rotation **Angle** (360° is full rotation) and **Increment**.

4. Select a **Frame Rate.**

   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 is defined in your user profile.

5. Use the **Speed** slider to slow down or speed up playback interactively.

Cine options for 2D viewers

1. Select a **Batching** mode.

   Stack scrolls through the images of a dataset.

   Images scrolls through the images of consecutive (stacked) datasets.

2. Under **Range**, select the first and last image in your movie.

3. Select a **Frame Rate**.

   Select **Frame Time**, **Frame Time Vector**, or **Recommended Rate (DICOM)** 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.

4. Use the **Speed** slider to slow down or speed up playback interactively.

5. If you select **Images**, select **All Viewers** to apply cine mode to all viewers.

   Clearing **All Viewers** plays the film in the selected viewer only.

6. If you select **Images** plus **All Viewers**, decide whether to **Skip images if necessary**.

   Clear **Skip frames if necessary** to be sure that all images are shown regardless of the playback speed. Clearing **Skip frames if necessary** might result in a slower playback speed than you have selected with the slider.

Cine options for videos
1. Select a **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 pre-ferred frame rate, which is defined in your user profile.

2. Use the **Speed** slider to slow down or speed up playback interactively.

3. If your video includes audio recording, select a sound output device.
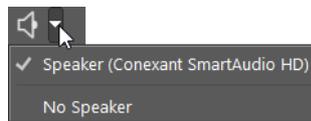
Playback tools

Use the following tools on the **Cine** tool card to start or halt cine display.

- **Play**

  This tool starts to play back your film once.

- **Pause**

  This tool pauses the playback.

- **Loop**

  This tool plays the film in an endless loop.

- **Swing**

  This tool plays the film in a bouncing loop.

  When playback reaches the last image, the movie is played backward to the first image, then forward again, and so on.

- Slider

  Use the slider to fast-forward or rewind the video.

Recording cine   1. Click **Record** to open the **Cine Options** dialog.

2. Select an **Image Format** and **Output Mode**.

3. Click **OK** to start recording.

The **Cine Options** dialog is not available for videos.

Browsing datasets

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

Previous Study, Next Study

✓ You have loaded more than one study.

Click **Previous Study** or **Next Study** to step through the loaded studies.

Previous Volume, Next Volume

✓ You have loaded more than one volume dataset.

Click **Previous Volume** or **Next Volume** to step through the loaded datasets.

Previous Image Set, Next Image Set

✓ You have loaded more than one image set.

Click **Previous Image Set** or **Next Image Set** to step through the loaded image sets.

Previous N Series, Next N Series

✓ You have loaded a large number of image sets into multiple viewers.

Click **Previous N Series** or **Next N Series** to step through the loaded image sets.

Previous Phase, Next Phase

✓ You have loaded a time series.

Click **Previous Phase** or **Next Phase** to step through the phases.

Previous Study from List, Next Study from List

1. Filter and sort the list in the **Study Browser** so that it shows the studies that you want to read next.

2. Load the first of these studies.

3. Click **Previous Study from List** or **Next Study from List** to load the study immediately above or below the study currently selected in the **Study Browser**.
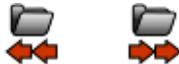
Menu bar, tools, and tool cards

Showing or hiding the menu bar

Select **View > Auto Hide > Auto Hide Menu Bar** to hide the menu bar.

The menu bar reappears when you move the mouse to the upper edge of the screen.

Showing or hiding tool-bars

Select **View > Auto Hide > Auto Hide Tool Bars** to hide toolbars.

Toolbars reappear when you move the mouse to the upper edge of the screen.

-Or-

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

Arranging toolbars   **1.** Click the toolbar handle to the left or above a toolbar.

2. Drag the toolbar to where you prefer it to be shown.

When you drag a toolbar to the left or right edge of the screen, a new toolbar section appears there. When you drag a toolbar to any other position 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.

Saving or resetting the toolbar arrangement   When you show or hide specific toolbars or move toolbars around on the screen, this toolbar arrangement is valid for the current session only.

To preserve the new toolbar arrangement, select **View > Show Toolbars > Save Toolbar Settings**.

-Or-

Select **View > Show Toolbars > Reset Toolbar Settings** to return to the original toolbar arrangement.

Resizing toolbars   Point to the toolbar section, hold the **Ctrl/Cmd** key down, and rotate the mouse wheel to show tools larger or smaller.

Tool palette and viewer context menu   A selection of your preferred tool buttons is also available within a viewer.

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

In your user profile, you can define whether tool palette, viewer context menu, or both are shown. See *Configuring the tool palette*, page 248.

2. Click **Show Context Menu** 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 tool buttons can also be selected with keyboard shortcuts. These keyboard shortcuts are active even if a toolbar or tool palette button is currently not displayed on the screen.

A number of keyboard shortcuts have been predefined for your system. Other keyboard shortcuts can be modified in your user account. See also *Configuring keyboard shortcuts*, page 246.

Select **Help > Keyboard Shortcuts** to show a list of all shortcuts.

Showing tool cards   **1.** Click the arrow button on the right edge of the screen to show tool cards.

2. Select a tool card from the dropdown list.
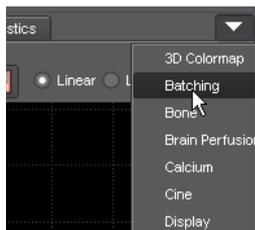
3. Double-click a tool card tab to show the tool card as a floating window.

-Or-

Select a tool card from the **Tools** menu.
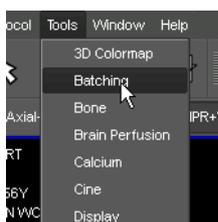
When you select a tool card from the **Tools** menu, it is shown as a floating window immediately.

Hiding tool cards

If the tool card area is temporarily in the way, you can hide it.

Click the arrow button between the tool card section and the viewers.

-Or-

Clear **View > Show Tool Cards** in the main menu to hide the tool card section.

Resizing the stack of tool cards

Some tool cards require more space than others. Therefore, you can 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.

-Or-

Point to the line that separates the tool card section and the viewers.

The cursor changes shape.

2. Drag the line that separates two tool cards up or down to resize the tool card above and below.
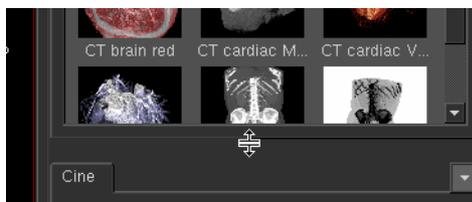
-Or-

Drag the line that separates the tool bar section and the viewers to the left or right to resize the entire tool card section.

Resizing floating windows

Floating windows are usually displayed in a size that ensures that they are not in the way while you are reading images. You can enlarge these windows, if necessary.

Click any of the four corners of a floating window and drag it out to show the tool card larger.
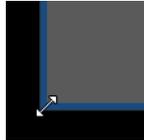
Warning symbols and viewer text

Aside from image information, viewers contain information about the loaded data as viewer 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 before the system has generated full image quality. The low-resolution warning also appears if a low streaming compression level is selected.

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.

Lossy image compression

This symbol indicates that the image is compressed with lossy image compression.

Miscellaneous warnings

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

Click the yellow triangle to find out more about these warnings.

Note

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

Showing or hiding viewer text

If the viewer text is in the way during image review, you can hide it.

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

-Or-

Use one of the following tools to show or hide image information.

Tip

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

Tools for showing/hiding text and graphics

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 show or hide 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.

The toggle tools can be configured to be shown in toolbars or on the tool palette, which you can show 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.

- **Toggle All**

    This tool shows or hides any texts or graphics that are currently selected for display in the **View > Show in Viewer** menu.

- **Toggle Patient/Study Data**

    This tool shows or hides patient or study information in all viewers.

- **Toggle Viewer Text Categories**

    This tool shows patient and study information in different levels of detail.

- **Toggle Orientation Labels**

This tool shows or hides 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**

This tool shows or hides 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. This tool hides or redisplays the window level histogram.

- **Toggle Scale**

In calibrated image types, for example, image types such as CT images, a scale can be shown on the right edge of the viewers. The scale looks like a small ruler and indicates centimeters, millimeters, or tenths of a millimeter when you zoom in. This tool hides or redisplays 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.

This tool shows or hides the color-map value-range indicator.

- **Toggle Annotations**

This tool shows or hides annotation text, annotation arrows, and measurement graphics and results.

- **Toggle Annotation Statistics**

This tool hides or shows the results of measurements only. When **Toggle Annotation Statistics** is off, measurement graphics are still visible, only the results of these measurements are hidden. This tool is particularly useful in the context of ROI statistics, which might hide underlying image information.

Tip

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**

This tool shows or hides 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**

These tools show or hide a box or cube that indicates volume borders in MPR viewers or 3D viewers.

- **Toggle 2D Crosshair, Toggle 3D Crosshair**

These tools show or hide scoutline crosshairs in MPR viewers or the 3D crosshair in 3D viewers.

- **Toggle Partial Crosshair**

This tool either shows the complete crosshair or hides the crosshair center.

When the full 2D crosshair is shown, the crosshair center turns into a move handle, irrespective of the tool that is currently selected.

Switching to partial crosshair display turns 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**

This tool shows or hides 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, this tool shows slice boundaries in MPR viewers of the same dataset.

- **Toggle Centerline**

  This tool shows or hides the curve definition or vessel centerline during vessel analysis or curved planar reformatting.

  Note that in curved view, centerline display must be activated in the context menu. Only then can you use this **Toggle Centerline** button to hide or redisplay the centerline.

- **Toggle DICOM Overlays, Toggle DICOM Annotations, Toggle DICOM Shutters**, **Toggle DICOM ECG curve**

  These tools show or hide DICOM overlays, DICOM annotations, DICOM shutters, or the ECG curve. These tools are available only if images contain this type of information.

- **Toggle Localizer Image**

  This tool hides or redisplays the embedded scout or localizer image in full-screen 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.

Resizing viewer text, orientation cube, scoutlines, or crosshair

Point to the viewer text, hold the **Ctrl/Cmd** key down, and rotate the mouse wheel to show the viewer text larger or smaller in all viewers.

-Or-

Point to the orientation cube, hold the **Ctrl/Cmd** key down, and rotate the mouse wheel to show the orientation cube larger or smaller and to show scoutlines or crosshair lines thicker or thinner.

Multiple viewers

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

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 tools to optimize how images are displayed.

Active viewer

In a screen layout with more than one viewer, only one viewer can be selected at a time. This viewer is the active viewer. Most image processing and changes to the display are applied to the active viewer only.

The active viewer is highlighted by a slightly brighter border color.

Click a viewer to make it the active viewer.

-Or-

Point to a viewer and start scrolling, zooming, panning, or any other activity. This viewer now automatically becomes the active viewer.

-Or-

Use the **Previous Viewer** or **Next Viewer** tools to select a different viewer as the active viewer.

-Or-

Click **Previous Viewer with Clip** or **Next Viewer with Clip** to move on to the next viewer that contains data that is suitable for cine display.

Protocol selection

The system preselects a different protocol depending on the modalities and ana-
tomical regions of the loaded data and also depending on the monitor configuration.
If you prefer a different screen layout, you can choose a different protocol or show a
different arrangement of viewers.

Drop down the protocol menu and select a protocol.
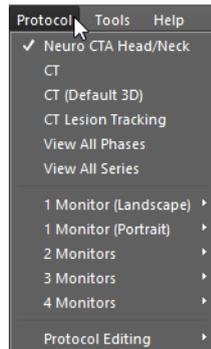
At the top of the **Protocol** menu, you will find alternative system suggestions for the
current dataset. Further down in the list, you will find all protocols that exist in your
system. These protocols are grouped by monitor configuration and by modality.

Layouts toolbar

With the buttons of this toolbar, you can switch between various viewer layouts.
These layouts have been defined in the active protocol. Different protocols offer dif-
ferent sets of layouts.

Selecting a layout   Click one of the buttons on the **Layouts** toolbar.

> **Tip**
>
> Double-click on a viewer in any of the available layouts or use this tool to show
> this viewer in full-screen mode.
>
>
>
> Double-click again to return to the original layout.

Adding a layout to the   If the layout that you are looking for is not available on the **Layouts** toolbar, add it to
toolbar   this toolbar.

1. Right-click the toolbar and select **Show Layout**.

2. Select the layout.

A new layout button has appeared on the **Layouts** toolbar.

Creating a new layout   You can create a new layout to arrange images in a way suitable for reading a particular case.

1. Right-click the **Layouts** toolbar and select **New Layout**.

2. Move the cursor across the matrix of available viewers.

    Selected viewers appear black.

3. Click to complete your viewer selection.

4. From the thumbnail section, drag images into the viewers.

Rearranging the   Drag a layout along the toolbar to show it in a more prominent place.
Layouts toolbar
                              -Or-

                              Add or remove layout buttons on the toolbar with **Show Layout** or **Hide Layout** from the context menu.

Default layouts   When you load a study, the system selects the protocol and layout best suited for the case at hand. By default, the system uses a number of criteria to define this layout. If you frequently prefer a different layout, you can define your own set of default layouts from which the protocol will choose..

                              Right-click your preferred layout on the toolbar and select **Add to Default Layouts**.

                              If you want to turn off criteria-based layout selection and show all studies with the same layout, select **Make Layout the only Default**.

Saving or resetting   To save any changes to the toolbar arrangement or your selection of default layouts,
changes   you need to explicitly save them.

                              Right-click the **Layouts** toolbar and select **Save Layout Preferences**.

                              -Or-

                              Right-click the **Layouts** toolbar and select **Reset Layout Preferences** to return to the toolbar presentation that is defined in the protocol.

Viewer controls

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

The viewer control 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 114.

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

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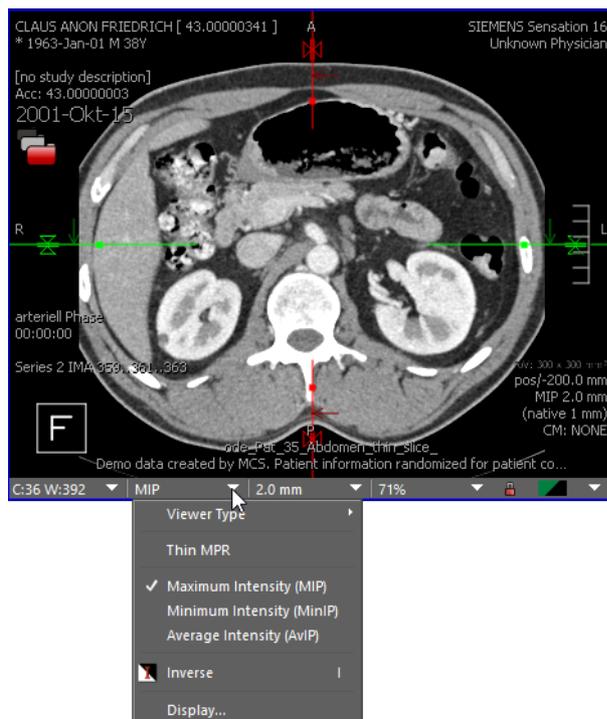
-Or-

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

3. Click the arrow button at the right edge of the viewer controls to show the viewer context menu.

Use this method to show the viewer context menu if right-clicking a viewer shows only the tool palette but no context menu.

Thumbnail section

The thumbnail section can be displayed 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.
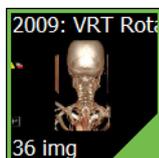
A **green border** around a thumbnail indicates that this image set is currently shown in the active viewer.

Click a thumbnail with a green border to highlight 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.

Click a thumbnail with a green triangle to highlight the viewer in which these images are shown briefly.

A **gray triangle** in the lower-right corner of a thumbnail indicates that this image set was displayed in a viewer at some time during the current session but is currently not shown.

If only the outline of a green or gray triangle is shown, only some but not all images of this image set are currently shown or were shown during the current session.

Thumbnails representing volume datasets are shown with a full triangle if at least one slice of the volume is or was shown in a viewer.

A **cube** symbol indicates that a thumbnail represents a volume.

In this example, the volume contains 10 images.

A **folder** symbol indicates that a thumbnail represents subsets of images.

In this example, the subset contains 6 images.

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

A **yellow plus sign** indicates that new images have arrived on the Visage 7 server since you loaded the study.

A **yellow star** in a thumbnail tells you that this series contains at least one key view.

Study dates are color-coded:

- Typically, the study date of the **current study**, that is, the study that you loaded from the **Study Browser** or from a worklist, has a white border.

- **Prior studies** have a red border.

- The study dates of **more recent studies** have a green border.

Showing the thumbnail section

Click the small arrow at the bottom of the screen.

Showing DICOM series

As soon as you load a study, image sets are arranged in the thumbnail section as defined by the active protocol.

Right-click the thumbnail section of a study and select **Show DICOM Series**.

Every DICOM series is now represented by exactly one thumbnail.

Sorting thumbnails by time

As soon as you load a study, image sets are arranged in the thumbnail section by relevance rather than in chronological order.

Right-click the thumbnail section and select **Sort by time**.
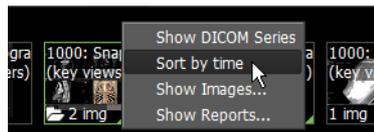
Thumbnails are now sorted by acquisition time.

Showing images or subsets of data

1. Right-click a thumbnail with a folder symbol and select **Show Images**.

   -Or-

   Click the folder symbol.

   The thumbnail folds out and shows the image sets it contains.

2. Click the **Close** button in the upper-right corner to close the foldout again.

Viewing reports

If a preliminary or final report exists for a study, you can preview it in the thumbnail section.

Right-click a study for which a preliminary or final report exists and select **Show Reports**.
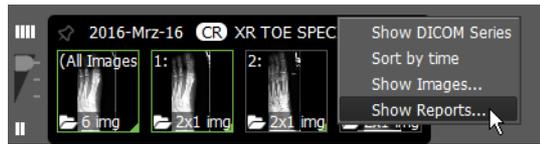
Scrolling in the thumb-nail section

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

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

-Or-

Click the white triangle.
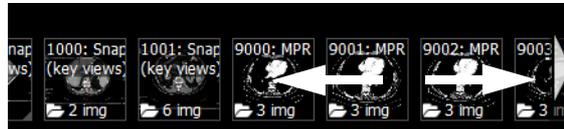
Collapsing or expand-ing studies

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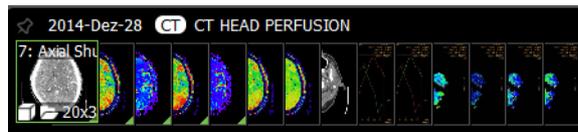
2. Click the study date a second time to collapse the study even further.

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

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 that you selected with a pin symbol.

Slider position center shows all the above studies plus studies preselected by the system as relevant prior studies based on auto-prior loading settings.

Slider position top shows all studies that exist for this patient on the Visage 7 server.
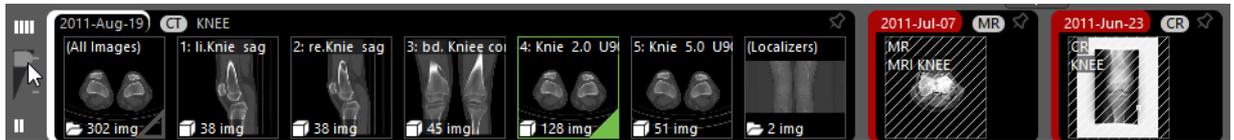
Showing all studies of a patient

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 to your case, select them.

Click the pin symbol to select a study.
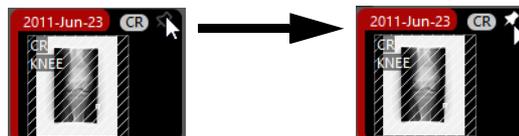
Pop-up viewer

In the pop-up viewer, you can show a scout image, for example. This viewer can remain open while you read images in the various viewers.

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

2. Double-click another thumbnail to replace the image in the pop-up viewer.

-Or-

Hold the **Shift** key down while you double-click another thumbnail to open an additional pop-up viewer.

3. To close a pop-up viewer again, double-click the thumbnail a second time or double-click in the pop-up viewer itself.

Loading image sets   Drag a thumbnail from the thumbnail section into a viewer to load this image set.
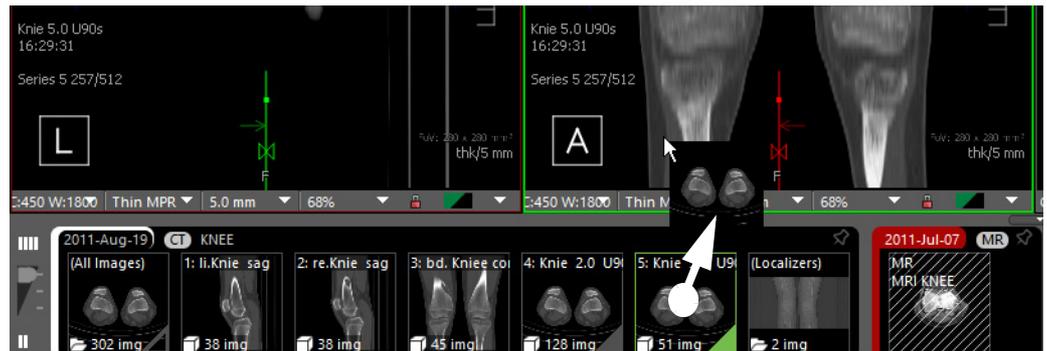
> **Tip**
>
> With large monitors or multiple monitors, dragging thumbnails into viewers might mean that you have to drag thumbnails a long way.
>
> Select **Show Mini Drop Zone (Thumbnail Browser)** for your user account in such a case (**File > Preferences > Properties > User Interface**).
>
> When you now start dragging a thumbnail, a small image appears in the thumbnail section. This image represents the monitor layout. Dragging a thumbnail into a viewer in the **Mini Drop Zone** has the same effect as dragging it all the way across the monitor to the target viewer.

Unloading image sets

1. Click any of the four corners of a viewer where the viewer text is shown and move the cursor a short distance.

2. Drag the thumbnail back to the thumbnail section to clear this 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.

-Or-

Select **Show Mini Drop Zone (Viewer)** for your user account and drag the thumbnail onto the small red **x** in the **Mini Drop Zone** to clear a viewer or to remove the overlay dataset.

Rearranging datasets in viewers

1. Click any of the four corners of a viewer where the viewer text is shown and move the cursor a short distance.

2. Drag the thumbnail that represents the data in this viewer to another viewer.

Loading an entire study   Drag a study date from the thumbnail section into a viewer to load the entire study.
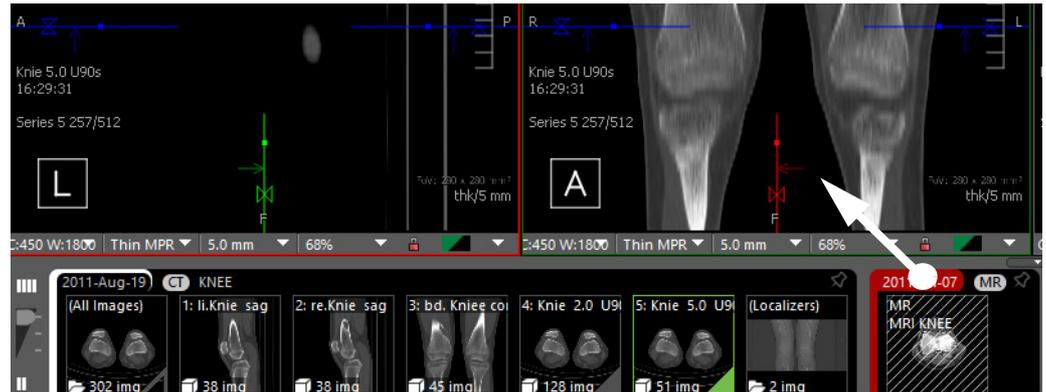
> **Tip**
>
> Drag with the left mouse button to replace the study in this viewer.
>
> -Or-
>
> Drag with the right mouse button to add this study to this viewer as an overlay dataset.

Study Navigator

From the **Study Navigator,** you can select and load more studies of the current patient.

Showing the Study Navigator

Click this tool to open the **Study Navigator** dialog.

-Or-

Use the keyboard shortcut that is assigned to the **Study Navigator** tool to open or close the **Study Navigator** dialog.

The tool is shown in 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. Prior studies that are potentially relevant to a case are displayed normally. Any other studies are slightly grayed out.
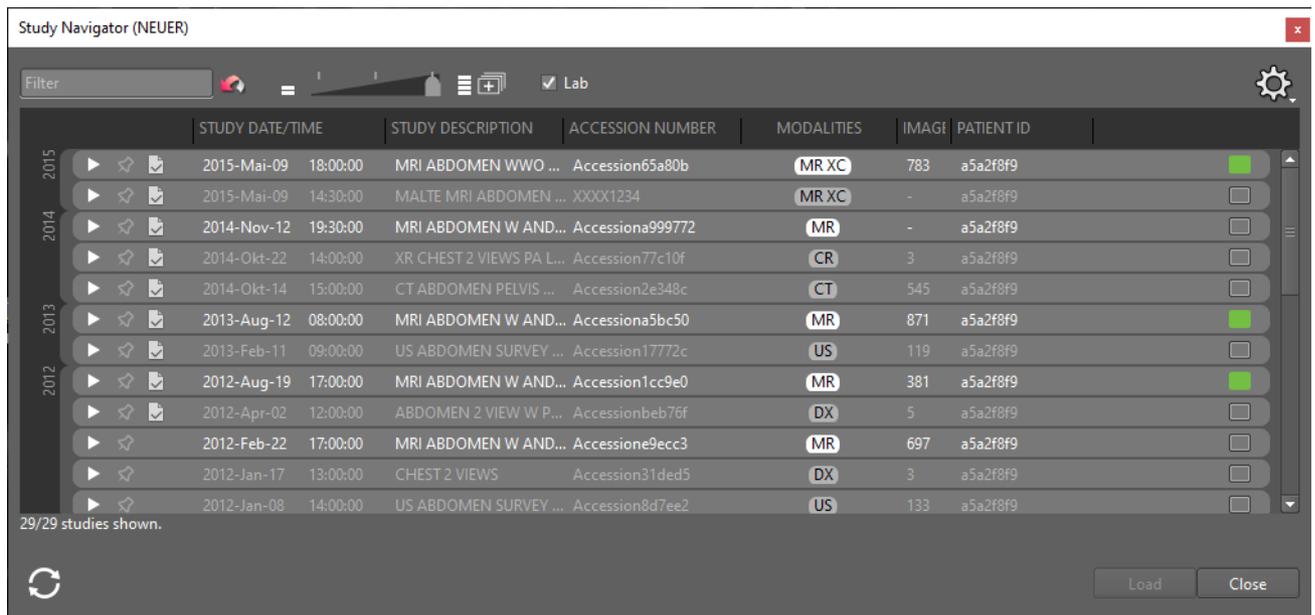
Selecting more relevant prior studies

You might consider more prior studies relevant to the case than those suggested by the system.

Click the pin symbol of such a prior study.
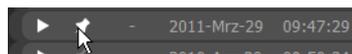
Controlling display of prior studies

If a large number of studies exist for a patient on the Visage 7 server, use the slider for a better overview.
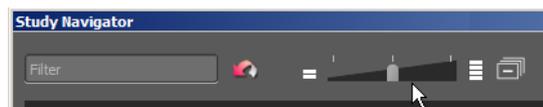
Slider position left shows only loaded studies and studies that you selected with a pin symbol.

Slider position center shows all the above studies plus studies preselected by the system as relevant prior studies based on auto-prior loading settings.

Slider position right shows all studies that exist for this patient on the Visage 7 server.

Filtering the study list

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

The study list is updated and now shows loaded studies, studies that you marked with the pin symbol, and studies whose study description, study date/time, or modality contains this string.

Expanding and collapsing studies

1. Click a study to show thumbnails of the images, series, and volume datasets that this study contains.

   -Or-

   Click **Expand** to show thumbnails for all studies.

2. Click the study again to hide thumbnails.

   -Or-

   Click **Collapse** to hide thumbnails of all studies.

Relative study date

Use the menu in the upper-right corner of the dialog to select a study date display mode.
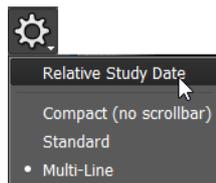
Choosing a display mode

Use the menu in the upper-right corner of the dialog to switch between different ways of displaying image thumbnails in expanded studies.
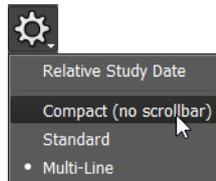
Loading studies from Study Navigator

1. Select the box to the right of a study.
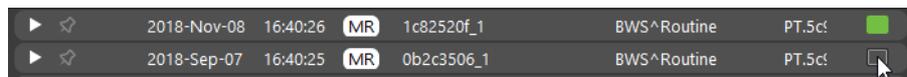
   The box turns green.

2. Click **Load**.

Loading individual image sets

1. Click a study to show thumbnails of its image content grouped into image sets.

2. Drag a thumbnail from the **Study Navigator** into a viewer.
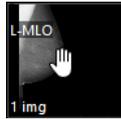
Tip

With large monitors or multiple monitors, dragging thumbnails into viewers might mean that you have to drag thumbnails a long way.

Select **Show Mini Drop Zone (Navigator)** for your user account in such a case (**File > Preferences > Properties > User Interface**).

When you now start dragging a thumbnail, a small image appears in the thumbnail section. This image represents the monitor layout. Dragging a thumbnail into a viewer in the **Mini Drop Zone** has the same effect as dragging it all the way across the monitor to the target viewer.

Multiple Protocols

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

1. Select the checkbox **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 the preliminary or final report in a separate window.

-Or-

Simply point to the report icon to show a preview of the report.
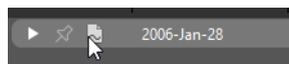
Additional images

If additional images are acquired at the modality while the study is already open in the Visage 7 client, these images appear in the **Study Navigator** automatically.

A plus sign on the **Study Navigator** icon alerts you to the fact that new images have arrived for your currently loaded study.

New images are marked with a plus sign in the **Study Navigator** and thumbnail section.
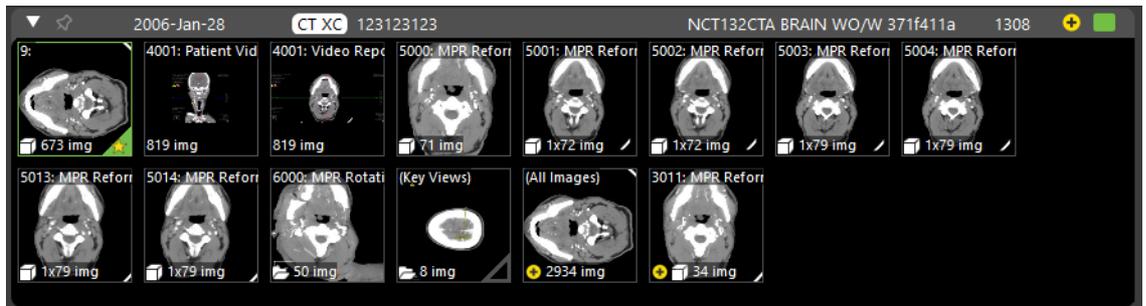
Load new images by dragging thumbnails into viewers.

-Or-

Click **Update Session**.

Update Session keeps all annotations and measurements and applies a protocol appropriate for the images that are loaded now.

Tip

If new images do not appear in the **Study Navigator** and thumbnail section automatically, the autorefresh mechanism has not been configured for your system

Click the **Refresh** button to update the the **Study Navigator** and thumbnail section manually in this case.

Linking viewers

In Visage 7, many image navigation and 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. Synchronized zooming means that not only is the image in the active viewer enlarged but all images in all linked viewers, too.

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

Activities that can be linked

The following activities can be linked across viewers:

- **Cursor Position/Navigation Synchronization** synchronizes **scrolling** in viewers.

- **3D Rotation Synchronization** synchronizes **3D rotation** in viewers.

- **Zoom Synchronization** synchronizes **zooming** in viewers.

- **Pan/Rotate Synchronization** synchronizes the following activities: **panning, rotation clockwise** and **counterclockwise, flipping horizontally** and **vertically.**

- **Tiled Navigation** creates a group of viewers for tiled image display. See also *Scroll Page by Page (Mouse Wheel Mode),* **page 46**.

- **Window/Level Synchronization** synchronizes **windowing** in viewers.

- **Time Synchronization** synchronizes playback of time series and browsing in time series.

- **Dataset Synchronization** synchronizes **loading of data** in these viewers, for example, from the thumbnail section.

Toggle Linking

Click this tool to switch viewer linking on or off.

Toggle Linking affects all viewers that are assigned to any of the linking groups. Assignment to a linking group is either specified by the protocol or it can be defined manually with the tools described below.

Automatically Link Viewers, Automatically Link Viewers (Frames of Reference)

Use these tools 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 use the same spatial orientation. While one of these tools is active, linking will be repeated when the viewer content changes, for example, by drag and drop.

For example, select automatic viewer linking 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.

Automatic viewer linking reads DICOM information to identify corresponding images.

1. Click **Automatically Link Viewers** to turn on linked scrolling in a single study.

-Or-

Click **Automatically Link Viewers (Frames of Reference)** to turn on linked scrolling across all loaded studies (current and prior studies).

Scrolling in one viewer will also scroll images in all linked viewers from now on.

Tip
Hold the **Shift** key down while you click **Automatically Link Viewers** or **Automatically Link Viewers (Frames of Reference)** to switch from one tool to the other.

2. Click **Automatically Link Viewers** or **Automatically Link Viewers (Frames of Refrerence)** a second time to turn linked scrolling off again.

Automatic Viewer Registration, Automatic Viewer Registration (Translation Only)

Click one of these tools to link scrolling in viewers that show corresponding images.

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.

The tools **Automatic Viewer Registration** and **Automatic Viewer Registration (Translation Only)** use a similar algorithm. However, whereas **Automatic Viewer Registration** considers 3D translation and rotation, **Automatic Viewer Registration (Translation Only)** only considers 3D translation but no rotation.

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

Adjusting viewer linking in two studies

If synchronized scrolling in two studies (or in data with different frames of reference) does not show corresponding images in the linked viewers, you can correct this interactively. Proceed in the same way if panning or rotation is synchronized across viewers and you need to correct viewer linking for these activities.

1. Scroll until one of the linked viewers shows an image with a clearly recognizable landmark.

2. Select one of the other linked viewers that does not show a corresponding image or that does not show the image correctly panned or rotated.

3. Press and hold the **Shift** key down.

   Scrolling, panning, or rotation will now only affect the selected viewer.

4. Scroll to an image that corresponds to the image in the first viewer (image show-ing the same landmark).

-Or-

Pan or rotate the image.

5. Release the **Shift** key.

Scrolling or panning and rotation will now be synchronized across all linked viewers again.

> **Tip**
>
> Within a single study, viewer linking for synchronized scrolling needs to be cor-rected only in very few and special cases. In such rare cases, detach a series from the other series in the study as described above. However, press and hold down the **Shift** plus **Ctrl/Cmd** keys while you scroll to the image that corre-sponds to the image in the first viewer.

Reset Viewer Linking

Click this tool to reset linking to the situation originally defined by the active protocol.

Link Scrolling

Link Scrolling is an alternative linking method, which can be useful for some data-sets for which the intended linking cannot be achieved with the **Automatically Link Viewers** tool. **Link Scrolling** requires a slightly more manual approach and allows the user to select the viewers to be linked.

Clicking **Link Scrolling** has a different effect on different viewer types.

You can use the **Link Scrolling** tool as a shortcut to **Edit Viewer Linking**. See also *Edit Viewer Linking*, page 80.

Only two viewers or two MPR groups shown

Click **Link Scrolling** to select this tool.

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

More than two viewers: 2D viewers

1. Click **Link Scrolling** to select this tool.

2. Select all viewers that show series with a similar orientation that you want to include in synchronized scrolling.

Selected viewers are highlighted with a gray 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 are 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 automatically linked by the protocol.

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

1. Click **Link Scrolling** to select this 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 gray border.

3. Click an MPR viewer in a second MPR group.

All six MPR viewers are now highlighted.

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. Click **Link Scrolling** to select this 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 gray border.

4. Click an MPR viewer in a second MPR group.

All six MPR viewers are now highlighted.

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

Visage 7 calculates a 3D registration for the two datasets using the 3D position of the reference point rather than the 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. Click **Link Scrolling** to select this tool.

2. Select all viewers in which you want to synchronize scrolling.

   Selected viewers are highlighted with a gray border.

3. Click **Accept and Exit** in the lower-right corner of the last selected viewer.

Unlinking viewers

1. Click **Link Scrolling** a second time.

2. Click a viewer.

   All viewers that you linked with the **Link Scrolling** tool earlier are now highlighted with a gray border.

3. Click linked viewers to remove the gray border and therefore 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.

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 two upper-left viewers and group 2 might combine the two lower-right 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.

Editing viewer linking   **1.** Click **Edit Viewer Linking** 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 in 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.

6. Continue and define more groups.

-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.

Group Editing tools

You can use these tools instead of **Edit Viewer Linking** as a quick way of linking viewers for one activity only. See also *Edit Viewer Linking*, page 80.

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

Overview of group editing tools

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

- **Modify Translation Navigation Group**

Assigns viewers to a translation navigation group for **synchronized scrolling**.

Datasets in a translation navigation group share the same reference point.

- **Modify Rotation Navigation Group**

Assigns 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**

Assigns 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**

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

- **Modify Tile Group**

Assigns viewers to a group for tiled image display. See also *Scroll Page by Page (Mouse Wheel Mode)*, page 46.

- **Modify Window Level Group**

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

- **Modify Time Phase Group**

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

- **Modify Dataset Group**

Assigns viewers to a dataset group to ensure that several viewers show the same dataset.

For example, if you load data into one viewer from the thumbnail section, all viewers in a dataset group are updated.

Quick linking of viewers

1. Click 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 linking.

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 temporarily.

1. Click the lock in the viewer controls.

   >

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

-Or-

1. Right-click the lock and cancel the selection of individual activities to detach the viewer from this group.
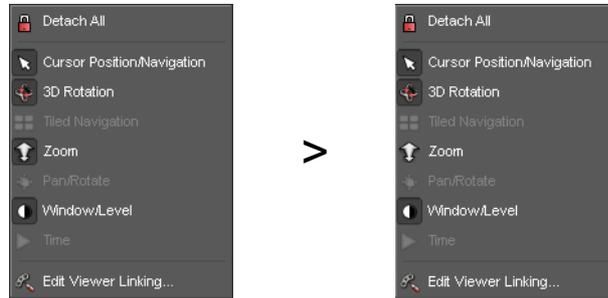
2. Right-click the lock again and reattach the viewer to its group later.

Changes to display settings, which you made while the viewer was detached from its group, are now reset to the group's settings.

Link Current Position

With this tool, you can align two 3D datasets, which are shown in side-by-side MPR viewers, based on a common reference point.

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.

    If necessary, deselect the tools **Toggle Linking** or **Link Current Position** first.

2. Click **Position Crosshair** and then click to position the crosshair on the same reference point in both datasets.

    -Or-

    Press and hold the **Alt** key down 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. Click **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.

Save Registration

Click this tool to save the registration (spatial alignment) of series for linked scrolling in current and prior studies permanently.

Clicking this tool saves the registration of series in current and prior studies in a DICOM object. In the **Study Browser**, this DICOM object appears as a new series with modality REG in the current study.

Link Display Properties

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

Annotations and measurements

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

Note

In the 3D viewer, measurements are only possible in orthographic projection but not in perspective projection. See also *Perspective projection*, page 116.

Every time you add an annotation to an image or perform a measurement, the Visage 7 client creates a screenshot and a key view and sends the screenshot to the **Export** window. From there, you can insert these screenshots into 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*, page 58 and *Toggle Annotation Statistics*, page 59.

Arrow/Text Annotation, Arrow Annotation

With these tools, you can add annotation text or draw arrows to point to observations.

Creating a text annotation

1. Click **Arrow/Text Annotation** to select this tool.

2. Click a point in an image.

3. In the **Edit Annotation** dialog, type your annotation text.

Creating an arrow plus text annotation

1. Click **Arrow/Text Annotation** to select this tool.

2. Click on a point and hold the mouse button down.

3. Drag the cursor across the image to create an arrow.

4. Release the mouse button.

5. In the **Edit Annotation** dialog, type your annotation text.

Creating an arrow with-out text annotation

1. Click **Arrow Annotation** to select this tool.

2. Click on a point and hold the mouse button down.

3. Drag the cursor across the image to create an arrow.

4. Release the mouse button.

Moving an annotation

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

2. Drag the entire annotation to move it.

   -Or-

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

Editing an annotation

1. Click an endpoint of the arrow.

2. Drag this point across the image.

   For example, move the arrow head until it points to a different observation.

Showing the annotation in all slices

1. Right-click the annotation.

2. Select **Show on all Slices**.

3. Start scrolling slices.

The annotation is shown in all slices.

Copying an annotation

1. Right-click an annotation and select **Copy Object**.

   -Or-

   Select the annotation and press **Ctrl/Cmd + C**.

2. Scroll to the slice into which you want to paste the annotation.

   -Or-

   Click the viewer into which you want to paste the annotation.

3. Right-click and select **Paste Object**.

   -Or-

   Press **Ctrl/Cmd + V**.

Circle Annotation (Text), Circle Annotation

With these tools, you can draw a circle around an area of interest or draw a circle and add annotation text that comments your observation.

Do not confuse the **Circle Annotation** tools with the **Circular ROI** tool. Annotation tools merely highlight an area of interest but do not evaluate image information. See also *Circular ROI, Elliptic ROI, Rectangular ROI*, page 101.

Creating a circle plus text annotation

1. Click **Circle Annotation (Text)** to select this tool.

2. Click a point in an image and hold the mouse button down to create a circle around this point.

3. Drag the cursor in or out to make the circle smaller or larger.

4. Release the mouse button.

5. In the **Edit Annotation** dialog, type your annotation text.

Creating a circle without text annotation

1. Click **Circle Annotation** to select this tool.

2. Click a point in an image and hold the mouse button down to create a circle around this point.

3. Drag the cursor in or out to make the circle smaller or larger.

4. Release the mouse button.

Moving or editing a circle annotation

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

   Four dots appear around the circle.

2. Drag the dots around the circle in or out to resize the circle.

   -Or-

   Drag the entire circle graphic to move the circle plus text.

   -Or-

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

Showing the annotation in all slices

1. Right-click the annotation.

2. Select **Show on all Slices**.

3. Start scrolling slices.

The annotation is shown in all slices.

Copying an annotation	**1.** Right-click an annotation and select **Copy Object**.

-Or-

Select the annotation and press **Ctrl/Cmd + C**.

2. Scroll to the slice into which you want to paste the annotation.

-Or-

Click the viewer into which you want to paste the annotation.

3. Right-click and select **Paste Object**.

-Or-

Press **Ctrl/Cmd + V**.

Sphere Annotation

With this tool, you can highlight a spherical volume of interest in MPR viewers.

Creating a sphere annotation

1. Click **Sphere Annotation** to select this tool.

2. Click a point in an image and hold the mouse button down to create a circle around this point.

3. Drag the cursor in or out to make the circle smaller or larger.

4. Release the mouse button.

The program highlights a spherical volume of interest, which has the radius and center of this circle.

5. Scroll through the image stack to see 2D representations of the selected spherical volume in various slices.

The sphere is only visible in MPR viewers but not in 3D viewers.

Default size of sphere annotations

1. Right-click your first sphere annotation.

2. Select **Set Size as Default**.

3. Click **Sphere Annotation** again.

4. Simply click (but do not drag) to create a second sphere annotation.

The sphere has exactly the same size as the first one.

Bracket Annotation

Bracket annotations mark areas for re-evaluation in a follow-up study. For example, use a bracket annotation to mark an observation that you do not consider a lesion in the current study but which might turn into a lesion in future. Bracket annotations have no text label or annotation text.

Creating a bracket annotation

1. Click **Bracket Annotation** to select this tool.

2. Click a point in an image and hold the mouse button down to create a bracket annotation around this point.

3. Drag the cursor in or out to make the brackets smaller or larger.

4. Release the mouse button.

Resizing a bracket annotation

1. Click a bracket annotation to select it.

   Dots appear on and around the annotation graphic.

2. Point to one of these dots.

   The cursor changes shape.

3. Drag the dot in or out to resize the annotation graphic.

Moving a bracket annotation

1. Click a bracket annotation to select it.

   Dots appear on and around the annotation graphic.

2. Point to the annotation graphic but not to one of these dots.

   The cursor changes shape.

3. Drag to move the entire bracket annotation.

Line Annotation

With this tool, you can draw a straight line in an image.

Do not confuse this tool with the distance measurement tool. The **Line Annotation** tool merely draws a line but does not measure its length. See also *Distance*, page 92.

1. Click **Line Annotation** to select this tool.

2. Click where you want to start the line and hold the mouse button down.

3. Drag the cursor across the image.

4. Release the mouse button at the endpoint of your line.

Tip
If configured, the system automatically corrects nearly horizontal or vertical lines so that they are exactly horizontal or vertical. If auto-snap mode has not been configured in your system, hold the **Ctrl/Cmd** key down while you draw the line to achieve the same effect.

Annotate Spine

With this tool, you can label vertebrae and intervertebral disks in images of the spine.

Labeling vertebrae or intervertebral disks

1. Click **Annotate Spine** to select this tool.

    -Or-

    Click one of the following tools.

    A new toolbar appears in the lower-right corner of the active viewer and the **Spine Labeling** tool card opens.

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

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

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.

-Or-

Click and drag the cursor 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 now selected.

6. Click the next vertebra or intervertebral disk in the image and continue until you have labeled all vertebrae or intervertebral disks.

7. Click **Show in all images**.

Spine labels appear in all other viewers that show this volume when you scroll to the corresponding slice.

8. Click **OK** to close the **Spine Labeling** toolbar and tool card.

Renaming spine labels

Right-click a spine label and select the correct label (**Rename to ...**).

Other spine labels in the image are also updated.

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 in the viewer in which you have labeled vertebrae or discs.

Spine labels are shown in all slices.

Distance

With this tool, you can 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 because zoom-out is applied. 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, inaccuracy may be even greater.

Measuring a distance   1. Click **Distance** to select this tool.

2. Click where you want to start your distance measurement and hold the mouse button down.

3. Drag the cursor across the image.

4. Release the mouse button at the endpoint of your distance line.

Depending on the modality, calibration information may be displayed in addition to the measured distance. See also *Image calibration*, page 110.

> **Tip**
>
> If configured, the system automatically corrects nearly horizontal or vertical distance lines so that they are exactly horizontal or vertical. If auto-snap mode has not been configured in your system, hold the **Ctrl/Cmd** key down while you draw the distance line to achieve the same effect.

Showing the measurement in all slices   1. Right-click the distance line.

2. Select **Show on all Slices**.

3. Start scrolling slices.

The distance line and measured distance are shown in all slices.

Moving a distance line that is in the way   1. Select the distance line.

Be sure not to click too close to an endpoint.

2. Hold the mouse button down and drag the line away from the measurement until it no longer hides important image information underneath.

Showing a line profile   A line profile is a grayscale or HU value profile of a selected distance line.

1. Draw or select a distance line.

2. On the menu, select **Tools > Line Profile** to open the **Line Profile** tool card.

-Or-

Click **Show/Hide Line Profile Tool Card**.

The x-axis shows the length of the line, 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.

If you have moved a distance line that was in the way, the line profile cannot be shown.

3. Select linear or logarithmic scale.

4. Click this button to create a screenshot of your line profile.

The screenshot is sent to the **Export** window. From the **Export** window, you can save it to your hard drive, or drag it into your report.

5. Click this button to save the data of your line profile onto your hard drive as a comma-separated list (*.csv file).

Curvilinear Distance

With this tool, you can measure the length of a structure that is not a straight line.

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 because zoom-out is applied. 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, inaccuracy may be even greater.

Measuring a curvilinear distance

1. Click **Curvilinear Distance** to select this tool.

2. Click where you want to start your distance measurement and hold the mouse button down.

3. Drag the cursor along the structure.

4. Release the mouse button at the endpoint of your distance line.

5. Click **OK** in the lower-right corner of the active viewer to complete the measurement.

Depending on the modality, calibration information may be displayed in addition to the measured distance. See also *Image calibration*, page 110.

Correcting the shape of a curvilinear distance line

1. Click a curvilinear distance line to select it and to reopen editing mode.

2. Click any point on the contour and drag in or out to correct the contour.

   -Or-

   Move away from the line.

   The cursor changes shape.

   Click anywhere near the curvilinear distance line and drag the cursor across the image to show a circle with which you can correct the line.

   The further from the line that you click, the larger the circle will be.

3. Push portions of the line in or out with this tool.

4. Click **OK** to end editing mode.

Extending or shortening a curvilinear distance line

1. Click a curvilinear distance line to select it and to reopen editing mode.

2. Click one of the end points of the curvilinear distance line.

3. Hold the mouse button down and drag the cursor out to extend the line.

   -Or-

   Hold the mouse button down and retrace the line to make it shorter.

4. Click **OK** to end editing mode.

Showing the measurement in all slices

1. Right-click the curvilinear distance line.

2. Select **Show on all Slices**.

3. Start scrolling slices.

The distance line and the measured distance are shown in all slices.

Horizontal Distance, Vertical Distance

With these tools, you can measure the horizontal or 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 because zoom-out is applied. 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, inaccuracy may be even greater.

Measuring a horizontal or vertical distance

1. Click **Horizontal Distance** or **Vertical Distance** to select the tool.

2. Click a point in the image.

3. Click a second point in the image.

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

Depending on the modality, calibration information may be displayed in addition to the measured distance. See also *Image calibration*, page 110.

Showing the measurement in all slices

1. Right-click the measurement.

2. Select **Show on all Slices**.

3. Start scrolling slices.

The lines and the measurement are shown in all slices.

Perpendicular Distance

With this tool, you can perform two distance measurements that are exactly perpendicular.

> **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 because zoom-out is applied. 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, inaccuracy may be even greater.

Measuring a perpendicular distance

1. Click **Perpendicular Distance** to select this tool.

2. Click where you want to start your distance measurement and hold the mouse button down.

3. Drag the cursor 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.

Depending on the modality, calibration information may be displayed in addition to the measured distance. See also *Image calibration*, page 110.

Tip

If configured, the system automatically corrects nearly horizontal or vertical distance lines so that they are exactly horizontal or vertical. However, if auto-snap mode has not been configured in your system, hold the **Ctrl/Cmd** key down while you draw your lines to achieve the same effect.

Showing the measurement in all slices

1. Right-click the measurement.

2. Select **Show on all Slices**.

3. Start scrolling slices.

The distance lines and measured distances are shown in all slices.

Distance Ratio

With this tool, you can measure two distance lines and 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 because zoom-out is applied. 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, inaccuracy may be even greater.

Calculating the distance ratio

1. Click **Distance Ratio** to select this tool.

2. Measure the first distance line.

Click the starting point, hold the mouse button down and drag, and release the mouse button at the endpoint.

3. Measure a second distance line.

Depending on the modality, calibration information may be displayed in addition to the measured distance. See also *Image calibration*, page 110.

Showing the measurement in all slices

1. Right-click the measurement.

2. Select **Show on all Slices**.

3. Start scrolling slices.

The distance lines and the results of the measurement are shown in all slices.

Angle

Caution

The accuracy of all angle measurements 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 because zoom-out is applied. 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, inaccuracy may be even greater.

Measuring an angle

1. Click **Angle** to select this tool.

2. Click the start point of the first leg of your angle.

3. Click the vertex.

4. Click the endpoint of the second leg.

**Showing the measure-
ment in all slices**

1. Right-click the angle.

2. Select **Show on all Slices**.

3. Start scrolling slices.

The angle graphics and measured angle are shown in all slices.

Angle (Two Lines)

<table>
<tr><td style="background-color:yellow">Caution</td></tr>
</table>

The accuracy of all angle measurements 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 because zoom-out is applied. 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, inaccuracy may be even greater.

Measuring an angle

1. Click **Angle (Two Lines)** to select this tool.

2. Click a point in the image and hold the mouse button down.

3. Drag the cursor to draw the first line.

4. Release the mouse button to finish the first line.

5. Click and drag the cursor to draw the second line.

6. Release the mouse button to finish the second line.

The system calculates both the acute angle and the obtuse angle.

<table>
<tr><td>Tip</td></tr>
</table>

If configured, the system automatically corrects nearly horizontal or vertical lines so that they are exactly horizontal or vertical. However, if auto-snap mode has not been configured in your system, hold the **Ctrl/Cmd** key down while you draw your lines to achieve the same effect.

Show Complement

Right-click the angle measurement and select **Show Complement**.

This calculates the difference between the obtuse angle and the 90° angle.

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

The angle graphics and measured angle are shown in all slices.

Cobb Angle

With this tool, you can measure Cobb angles in images of the spine.

<div style="background:yellow">

Caution

</div>

The accuracy of all angle measurements depends on the length of the shorter of the two angle legs. The longer the angle legs, 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 because zoom-out is applied. 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, inaccuracy may be even greater.

Measuring Cobb angles

1. Click **Cobb Angle** 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 angles.

6. Click **OK** to complete Cobb angle measurements.

Depending on the modality, calibration information may be displayed in addition to the measurement results. See also *Image calibration*, page 110.

Showing the measure-ment in all slices

1. Right-click one of the lines.

2. Select **Show on all Slices**.

3. Start scrolling slices.

Lines and Cobb angles are shown in all slices.

Circular ROI, Elliptic ROI, Rectangular ROI

A 2D ROI (region of interest) evaluates image information in the currently displayed image or slice.

<div style="background:yellow">

Caution
</div>

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

For example: Shorter radius or edge (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 because zoom-out is applied. 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, inaccuracy may be even greater.

Drawing a ROI

1. Click **Circular ROI**, **Elliptic ROI**, or **Rectangular ROI** to select one of these tools.

2. Click the center of your region of interest, hold the mouse button down, and drag the cursor out.

3. Release the mouse button when the ellipse, circle, or rectangle is large enough.

Depending on the modality, calibration information may be displayed in addition to the measurement results. See also *Image calibration*, page 110.

Showing or hiding ROI name and statistics

When you draw a ROI, ROI statistics appear.

Right-click the ROI or ROI statistics and clear **Show ROI Name** or **Show ROI Statistics** to hide the information for this particular ROI.

-Or-

Right-click the ROI or ROI statistics and select **Statistics in Corner of Viewer** to move the ROI name and ROI statistics to the right edge of the viewer.

<div style="background:#e6e6e6">

Tip
</div>

Default show/hide settings for ROI name and ROI statistics can be configured in your user profile.

Copying a ROI

1. Right-click a ROI and select **Copy Object**.

   -Or-

   Select the ROI and press **Ctrl/Cmd + C**.

2. Scroll to the slice into which you want to paste the ROI.

   -Or-

   Click the viewer into which you want to paste the ROI.

3. Right-click and select **Paste Object**.

   -Or-

   Press **Ctrl/Cmd + V**.

Default size of circular ROI

For circular ROIs, you can predefine the size of your next ROI.

1. Right-click your first circular ROI.

2. Select **Set Size as Default**.

3. Click **Circular ROI** again.

4. Simply click (but do not drag) to create a second circular ROI.

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

Rotating an elliptical ROI

When you draw or select an elliptical ROI a double arrow appears next to the ellipse.

1. Point to the double arrow.

   The cursor changes shape and indicates rotation.

2. Drag the double-arrow up or down or right or left to rotate the ellipse.

Spherical ROI, Spherical Probe

With this tool, you can evaluate 3D ROIs that are exactly spherical.

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).

Caution

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

For example: Shorter radius or edge (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 because zoom-out is applied. 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, inaccuracy may be even greater.

Drawing a spherical ROI

1. Click **Spherical ROI** to select this tool.

2. Draw a circle in a slice image.

    The program calculates the statistics of a spherical volume of interest (3D ROI), which has the radius and center of this circle.

3. Scroll through the image stack to see 2D representations of the selected spherical volume in various slices.

Depending on the modality, calibration information may be displayed in addition to the measurement results. See also *Image calibration*, page 110.

Showing ROI statistics and name

When you draw a ROI, statistics appear.

Right-click the ROI or ROI statistics and clear **Show ROI Name** or **Show ROI Statistics** to hide the information for this particular ROI.

-Or-

Right-click the ROI or ROI statistics and select **Statistics in Corner of Viewer** to move the ROI name and ROI statistics to the right edge of the viewer.

Note

When you draw a spherical ROI in PET data, Visage 7 also calculates the SUV peak and shows this value in the ROI statistics. In the images, the location of the SUV peak is shown as a small circle.
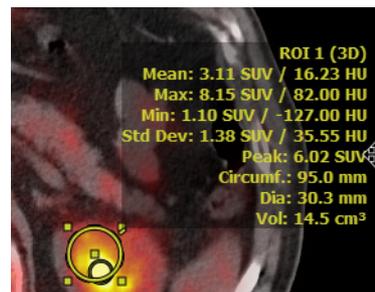
Tip

Default show/hide settings for ROI name and ROI statistics can be configured in your user profile.

Copying a ROI

1. Right-click a ROI and select **Copy Object**.

   -Or-

   Select the ROI and press **Ctrl/Cmd + C**.

2. Scroll to the slice into which you want to paste the ROI.

   -Or-

   Click the viewer into which you want to paste the ROI.

3. Right-click and select **Paste Object**.

   -Or-

   Press **Ctrl/Cmd + V**.

Spherical Probe

1. Click **Spherical Probe** to select this tool.

2. Click a lesion in an MPR viewer or in the 3D viewer.

All viewers now focus on this lesion. Statistics of a spherical volume of interest around the spot that you clicked are shown.

The program does not create a screenshot.

Changing the size of the sphere

The default size of the spherical probe is predefined in the tool properties. However, you can change the size of this sphere interactively.

1. Point to the circle that represents the sphere in one of the MPR viewers.

2. Hold the **Ctrl/Cmd** key down and rotate the mouse wheel to increase or decrease the size of the sphere.

   -Or-

   Right-click inside the sphere and drag in or out to increase or decrease the size of the sphere.

The new sphere size is used for subsequent measurements for the duration of this session.

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 ROI

1. Click **Point-Sized ROI** to select this tool.

2. Click a pixel in an image.

The grayscale or density value of this pixel is shown.

Showing ROI statistics and name

When you draw a ROI, statistics appear.

Right-click the ROI or ROI statistics and clear **Show ROI Name** or **Show ROI Statistics** to hide the information for this particular ROI.

-Or-

Right-click the ROI or ROI statistics and select **Statistics in Corner of Viewer** to move the ROI name and ROI statistics to the right edge of the viewer.

> **Tip**
>
> Default show/hide settings for ROI name and ROI statistics can be configured in your user profile.

Pixel Value

1. Click **Pixel Value** 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 screenshot.

Freehand 2D ROI, Freehand 3D ROI

Use the tool **Freehand 2D ROI** to draw a freehand shape and evaluate image information in this region of interest (ROI).

Use the tool **Freehand 3D ROI** to define a freehand 3D ROI by drawing contours in various slices of a volume dataset. You do not have to draw ROIs in every slice of the volume.

Caution

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

For example: Shorter radius or edge (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 because zoom-out is applied. 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, inaccuracy may be even greater.

When you click one of these tools, a new toolbar opens in the lower-right corner of the active viewer. Here you will find tools for drawing and refining freehand shapes.

New Elliptical Contour

1. Select **New Elliptical Contour** to circle the area of interest with an ellipse or a circle.

2. Click a start point, hold the mouse button down, and drag the cursor out.

Depending on the modality, calibration information may be displayed in addition to the measurement results. See also *Image calibration*, page 110.

New Freehand Contour

1. Select **New Freehand Contour** to draw a freehand shape.

2. Click a start point and hold the mouse button down.

3. Draw a contour line.

New Balloon Contour   1. Select **New Balloon Contour** to define a structure or area of interest of a specific brightness.

2. Click into the structure and drag the cursor out.

Append mode   1. Draw a contour or select a contour that you drew earlier.

2. Press and hold the **Shift** key down.

   The cursor turns into an arrow with a plus sign.

3. 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.

4. Add a third contour to this ROI, if necessary.

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

Refine Contour   After you have drawn a contour, the **Refine Contour** tool is active.

The cursor has changed shape.

Click anywhere in the image and drag the cursor to show a circle with which you can correct the ROI graphic.

The further from the contour line that you click, the larger the circle will be.

Click inside the ROI graphic to enlarge it by pushing the contour out.

-Or-

Click outside the ROI graphic to push the contour line in.

> **Tip**
>
> With freehand 3D ROIs, contours that you drew in a slice appear as solid lines. Interpolated contours in the slices in between appear as dashed lines. With the **Refine Contour** tool, you can correct both solid and dashed contours.

Undo   Click **Undo** to retrace your steps.

Copying a ROI

1. Right-click a ROI and select **Copy Object**.

   -Or-

   Select the ROI and press **Ctrl/Cmd + C**.

2. Scroll to the slice into which you want to paste the ROI.

   -Or-

   Click the viewer into which you want to paste the ROI.

3. Right-click and select **Paste Object**.

   -Or-

   Press **Ctrl/Cmd + V**.

Closing the Freehand 2D/3D ROI tool

Click **OK** when you have finished drawing and refining contours to close the tool.

The system now calculates ROI statistics.

Analyzing time series

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

1. Draw a circular, elliptical, rectangular, point-sized, or freehand ROI.

2. 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.

3. Draw a second ROI.

4. 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.

Replicate Annotation

With this tool, you can copy an annotation or measurement into several consecutive slices of a volume dataset.

The tool is only available in viewers that show images in standard orientations (axial, sagittal, coronal). The tool is not available in viewers that show oblique slices.

You can only replicate 2D objects but no 3D structures such as 3D ROIs or sphere annotations.

1. In the first slice in which you make an observation, add an annotation or make a measurement.

   For example, draw a circular ROI around a lesion in the slice in which the lesion is most prominent.

2. Scroll through the image stack in one direction until you reach the last slice in which the lesion is visible.

3. Click **Replicate Annotation**.

   The system copies the annotation or measurement into this slice and also into all the slices in between.

4. Scroll through the image stack in the other direction until you again reach the last slice in which the lesion is visible.

5. Click **Replicate Annotation** again.

Annotations tool card

The **Annotations** tool card gives you an overview of annotations, measurements, and key views in the currently loaded data.

1. On the menu, select **Tools > Annotations** to open this tool card.

   -Or-

   Click **Show/Hide Annotation Tool Card**.

   On the **Annotations** tool card, annotations, measurements, and key views are listed by study date. Symbols in front of each line indicate the annotation type.

2. Click the **Annotation** or **Series** column to show an annotation, measurement. or key view in a pop-up viewer.

3. Click a column header to sort the list according to the selected criterion.

   Clicking a column header again switches from ascending to descending sort order or vice versa.

4. Click a symbol in front of an annotation, measurement, or key view to open the **Edit Annotation** dialog.
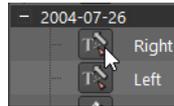
Image calibration

Depending on the modality, image data contain information about exact units, estimated units based on various data, or no unit information at all.

Units

When you measure a distance line, for example, the result is shown with one of the following units:

- mm

  Millimeters, exact units, for example, in images acquired with the modalities CT or MR.

- mm'

  Millimeters, reliable estimate based on image information sent from the modality.

- mm*

  Millimeters, less reliable estimate based on information in the image file.

- mm°

  Millimeters, value indication after manual calibration.

- pix

  Pixels, no unit information available.

Showing calibration information

For mm', mm*, and mm°, you can display the image information on which these units are based.

1. Right-click the distance line, for example.

2. Select **Calibration Info**.

A dialog with calibration details is shown.

Calibrate Image

If measurements yield only estimates or pixel values, you can calibrate the 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 because zoom-out is applied. 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, inaccuracy may be even greater.

1. Click **Calibrate Image** to select this tool.

2. Measure an object with known dimensions.

3. In the **Calibrate** dialog, enter the known length.

4. Click **OK**.

The program recalculates any previous measurements. In the upper-right corner of the image, the words **manual calibration** indicate that manual calibration has been performed on this image.

Delete All Measurements/Annotations

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

Clicking this tool removes **all** measurements and annotations in **all** images of **all** loaded studies. Moreover, key views and screenshots, which the program created automatically for each measurement or annotation, are also deleted.

3D navigation and volume data

The following 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.

> **Tip**
>
> Use the tools **Toggle MPR View** or **Next MPR View** to switch a viewer from 2D (original slice image) to MPR (reconstructed volume dataset) quickly.
>
> **Toggle MPR View** switches a viewer from 2D mode to MPR mode and back. **Next MPR View** switches a viewer from 2D to MPR and then cycles standard orientations.

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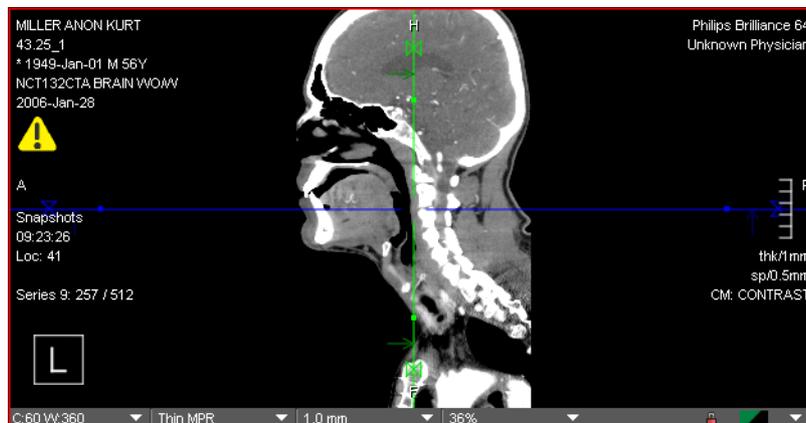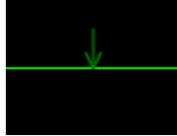
Small arrows that point to a scoutline indicate the viewing direction in the other two MPR viewers.

When you move the cursor over the center of the scoutline crosshair, the cursor changes shape. Use the 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. See also *Toggle Partial Crosshair*, page 59.
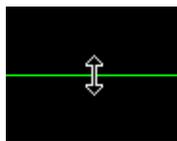
When you move the cursor over a scoutline, the cursor changes shape. Drag this line to move through the volume along one of the other two standard axes. Dragging a scoutline updates one of the other two MPR viewers.

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

When you click one of the small triangles on the scoutlines along the edges of the image, the scoutlines appear dotted.

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

Tip

The system behavior when moving or rotating the crosshairs is configured in your user profile. Therefore, dragging the small green dot can either mean crosshair movement or rotation.

Compositing modes for thick slices

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

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

1. In the viewer controls below a viewer, increase the slice thickness.

2. Change the compositing mode.
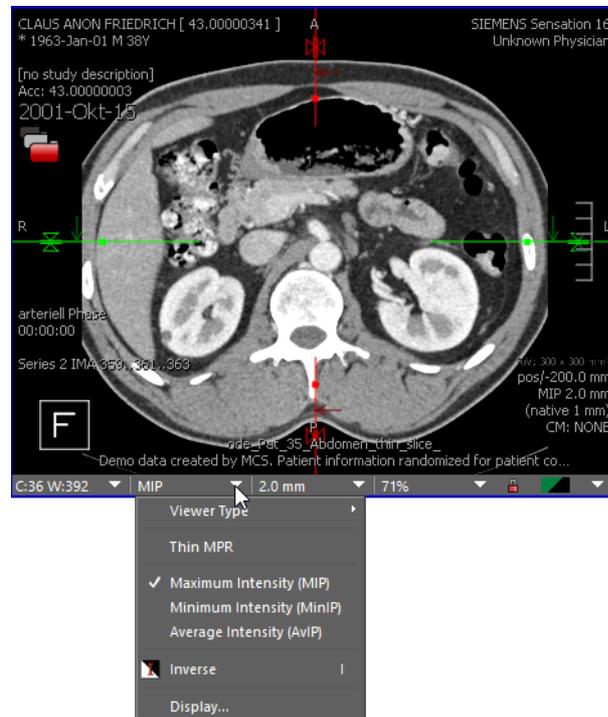
- Thin MPR

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

- Maximum intensity projection (MIP)

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

- Minimum intensity projection (MinIP)

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

- Average intensity projection (AvIP)

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

-Or-

Use the **Toggle Crop Slab / Thick MPR** tool to switch from display of thin slices to display of thick slices and vice versa.

-Or-

Use the **Next Thick Projection Mode** tool to switch compositing modes (MIP, MiniIP, AVIP).

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.

Volume rendering technique

Select a volume rendering technique from the viewer controls of the 3D viewer.

- 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.

- 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 depending on the angle between the incoming and reflected light. This means that on smooth surfaces users see highlights and shading becomes even more expressive than with diffuse shading. Specular shading is especially good for large surfaces with fine detail.

- VRT (advanced)

  This mode uses a direct volume renderer that comes with multiple modern features. Adaptive sampling allows to increase the quality while keeping the performance high. In addition, cubic filtering can be applied to reduce noise in the data as well as grid artifacts caused by the limited data resolution. The advanced illumination model used here supports ambient occlusion to approximate an important part of the global illumination. With ambient occlusion, regions in cavities or regions surrounded by opaque geometry appear darker because a smaller amount of light can reach these regions. This highly increases the perception of depth and looks more natural.

- Perspective projection

  This projection mode gives a more natural impression. Perspective projection corresponds to 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 telephoto lens. The viewing rays are 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. When perspective projection is activated, measurements cannot be performed.

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

- Smart sampling

  This option reduces artifacts in the volume display.

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

Templates

The tool card **Templates** offers a quick way of adjusting 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 117.

- Rendering and display settings for the volume display in the 3D viewer

A number of predefined templates come with the system. Advanced users can adjust these to their own requirements or define their own set of 3D templates. When you save a template, you can either make it available to all users or to your own user account only.

On the menu, select **Tools > Templates** to open this tool card.

-Or-

Click **Show/Hide Templates Tool Card**.

Applying a template   Click a template thumbnail on the tool card to select it.
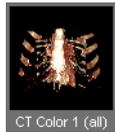
The tool card lists only those templates that were defined for the modality or modalities of the data that is currently loaded.

Creating a template

1. Select a template or start with the display settings suggested by the protocol.

2. Modify volume display settings in the 3D viewer.

3. Click **Reset** if you want to return to the original volume display and start again.

4. Click **Save** to save the 3D rendering and display settings currently applied to the volume in the active 3D viewer.

A dialog opens.

5. Enter a template name and decide whether the new template will be available to all users or to your user account only.

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.

A number of predefined color maps come with your system. Advanced users can adjust these or define their own set of 3D color maps. When you save a color map, you can either make it available to all users or to your own user account only.

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.

• You can select different colors for each graph or you can change the transparency settings for a tissue type.

• You can change the tissue type description.

• You can add or delete tissue type graphs.

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 only adjust the data windows of the tissue types. You cannot adjust the color and transparency settings. Nor can you save changes to these color maps.

On the menu, select **Tools > 3D Color Map** to open this tool card.

-Or-

Click **Show/Hide Colormap Tool Card**.

Moving or resizing the histogram

1. Click into the black area above or below the grayscale histogram and hold the mouse button down.

   The cursor changes shape to a double-headed arrow.

2. Drag the cursor to the right or left to move the histogram and show areas to the right or left that were previously hidden.

   -Or-

   Drag the cursor up or down to condense or expand the histogram.
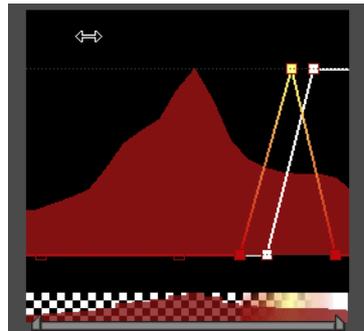
Editing a graph

1. Click a graph to select it.

2. Drag the boxes along the bottom line of the histogram to the right or left 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.
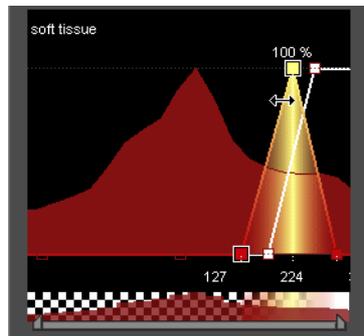
Renaming a graph

1. Select a tissue graph.

   The name of the selected tissue type appears above the graph section.

2. Click the tissue description text above the histogram and edit this text.

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-

   Click one of the listed tissue types to show or hide these graphs.

3D navigation tools

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 112.

> **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

With this tool, you can rotate the volume in the 3D viewer or in the MPR viewers.

3D Rotate is the standard navigation tool in the 3D viewer and in curved view.

3D rotation in the 3D viewer

1. Click **3D Rotate** to select this tool.

   -Or-

   Click **Default Navigation** or hold the **Ctrl/Cmd** key down.

2. Click anywhere in the 3D viewer and hold the mouse button down.

3. Drag the cursor across the image to rotate the volume in the direction of the mouse movement.

   -Or-

   Rotate the mouse wheel to rotate around the vertical axis only.

   -Or-

   Press and hold the **Shift** key down while you rotate the mouse wheel to rotate around the horizontal axis only.

4. Use any of the standard orientation buttons to reset rotation.

   See *Anterior, Posterior, Left, Right, Head, Foot View*, page 121.

3D rotation in MPR viewers

1. Click **3D Rotate** to select this tool.

2. Drag the cursor across the image to rotate the image plane.

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

> **Tip**
>
> Click **Reset Slice Orientations** to return to the original image orientation.

| Rotate in plane | 1. Click **3D Rotate** to select this tool. |
| | 2. Hold the **V** key down while you drag the cursor across the image 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 43.

Reset Slice Orientations

Click 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 immediately after loading.

Anterior, Posterior, Left, Right, Head, Foot View

Click one of these tools to display the image in one of the standard anatomical views in the currently active viewer:

A or **P** for anterior or posterior view, that is, view from the front or from the back.

L or **R** for view from the left or from the right.

H or **F** for view from head to feet or from feet to head.

Note

Clicking a standard orientation tool in a 2D viewer switches this viewer from 2D mode to MPR mode.

Position Crosshair

With this tool, you can focus on a particular point in the volume in **linked** viewers. **Position Crosshair** affects linked viewers only.

1. In a 3D viewer, show the 3D crosshair before you start positioning the crosshair.

2. Click **Position Crosshair** to select this tool.

3. 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.

Triangulation

With this tool, you can focus on a particular point in the volume in **all** viewers that show images or volume datasets that contain this point. **Triangulation** affects image display in **all** viewers and not only in linked viewers.

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

1. Click **Triangulation** to select this tool.

2. Click a point in any of the viewers.

Center View

Click **Center View** to move images in linked viewers in such a way that the scoutline crosshair is in the viewer center.

See also *Crosshair navigation in MPR viewers*, page 112.

Define View Plane (3 Points)

With this tool, you can define an arbitrary view plane in a volume dataset.

Defining a view plane

1. Click **Define View Plane (3 Points)** to select this tool.

2. Scroll to a slice that shows the first point that you want to use to define the plane.

3. Click this point (P1).

4. In the same viewer, scroll to a slice that shows the second point.

5. Click the second point (P2).

6. Scroll to a slice that shows the third point.

7. Click the third point (P3).

Clicking the third point completes view plane definition and rotates the volume.

Correcting point selection

After clicking the first or second point, you can correct your selection. You cannot correct P3 or the position of any of the three points after you have clicked the third point.

1. Scroll back to the slice that shows P1 or P2.

2. Point to the label or crosshair of P1 or P2.

3. Drag P1 or P2 to a more appropriate point.

Showing the definition points in all slices

1. Right-click a definition point.

2. Select **Show on all Slices**.

3. Start scrolling slices.

P1, P2, and P3 are shown in all slices.

Cropping

With cropping tools, you can 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

With this tool, you can cut away the outer parts of the volume.

Creating a crop box

1. Click **Crop Box** 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 but close to a border to move it.

-Or-

Drag a border line in or out to resize the box.
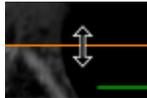
-Or-

Click a corner of the box and drag it up or down to rotate the crop box.
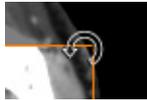
3. Click **Crop Box** a second time to show the entire volume again.

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

Click this tool to lock the crop region.

You can now move or rotate the volume within the crop box.

Rotation or movement of the crop region   Click this tool in the 3D viewer.

The tool switches the function of the mouse wheel from movement of the crop box to rotation of the crop box and vice versa.

Creating a box annotation   With **Create Box Annotation**, you can save the position and size of the 3D crop box in an annotation.

1. Click **Create Box Annotation** on the toolbar in the lower-right corner of the active viewer.

2. Click **Save Annotations as Presentation State** or **Save Result** to save the annotation in a presentation state. See *Presentation states*, page 190.

Crop Slab

With this tool, you can 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.

Cropping a slab

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

2. Drag slab boundaries out or in to change the slab thickness.

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

Locking the crop region

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

Click this tool to lock the crop region.

You can now move or rotate the volume within the slab.

Rotation or movement of the crop region

Click this tool in the 3D viewer.

The tool switches the function of the mouse wheel from movement of the slab to rotation of the slab and vice versa.

Crop Plane

With this tool, you can cut away a corner of the volume along an oblique cutting plane.

Cropping along a plane

1. Click **Crop Plane** to select this tool.

2. Drag the line that defines what will be cut away to move this plane in or out.

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

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

Click this tool to lock the crop region.

You can now move or rotate the volume within the remaining volume box.

Rotation or movement   Click this tool in the 3D viewer.
of the crop region

The tool switches the function of the mouse wheel from movement of the crop plane to rotation of the crop plane and vice versa.

Crop Corner

With this tool, you can cut away a box from the corner of the volume.

Cropping a corner   1. Click **Crop Corner** 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 border that defines the corner to be cut away to resize the box.

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

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

Click this tool to lock the crop region.

You can now move or rotate the volume within the remaining volume box.

Rotation or movement   Click this tool in the 3D viewer.
of the crop region

The tool switches the function of the mouse wheel from movement of the cropped corner to rotation of the entire volume and vice versa.

Subtracting image information

With this tool, you can subtract image information, for example, the baseline phase in a time series or a non-contrast image from a contrast-enhanced image or series.

Subtracting the baseline phase in a time series

1. Load the time series from which you want to subtract the baseline phase.

2. Click **Subtract Baseline Phase**.

　　　━

The tool identifies the baseline phase automatically and subtracts its image information from the other images in the time series.

As a result you see only those structures in which changes occurred over time.

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

Subtracting image information in other series or volume data

1. Load two volume datasets into an MPR viewer in fusion mode.

For example, load a contrast-enhanced series as a primary dataset and a corresponding native series as an overlay dataset.

2. Click **Subtract Baseline Phase**.

　　　━

The system subtracts the overlay dataset from the primary dataset.

3. Click **Subtract Baseline Phase** a second time to reset subtraction and show both primary and overlay datasets again.

Fused image display

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 or two CT series.

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.

Loading primary or overlay datasets

Multimodality studies can contain more than one series per modality. Multiple series are indicated by the **Viewer Objects (Primary)** and **Viewer Objects (Overlay)** tools in the MPR viewers and the 3D viewer.

When you load a suitable multimodality study, for example, an MR+PET study, Visage 7 overlays corresponding series automatically.

Viewer Objects (Primary), Viewer Objects (Overlay)

1. Click **Viewer Objects (Primary)** or **Viewer Objects (Overlay)** to show the study and image set that is the primary or overlay dataset in the current viewer.

2. Select a different image set as primary or overlay dataset, if necessary.

Loading primary or overlay datasets from the thumbnail section

Drag an image set from the thumbnail section with the **left** mouse button to load this image set as a primary dataset.

-Or-

Drag an image set from the thumbnail section with the **right** mouse button to load this image set as an overlay dataset.

Display tool card

On this tool card, you can adapt display settings for the active viewer.

The **Display** tool card offers slightly different controls depending on the selected viewer and whether fusion mode is active or not.

On the menu, select **Tools > Display** to open this tool card.

-Or-

Click **Show/Hide Display Tool Card**.

Display tool card in fusion mode

When you have loaded suitable data, you can use this tool card to turn fusion mode on and off and to adjust display settings.

1. Use the **Primary Dataset, Overlay Dataset** checkboxes to turn fusion mode on and off.

2. Select which dataset to display from the dropdown lists below the **Primary Dataset** and **Overlay Dataset** checkboxes.

3. Use the slider below a histogram to adjust the window settings for this dataset.

   -Or-

   Select a suitable color map from the dropdown list using the arrow button to the right of the histogram.

4. Use the 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 the slider 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 or grayscale inverse for a 100% PET image.

Display tool card in nonfusion mode

If you have loaded data that is not suitable for fusion display, you use this tool card to adjust window level and image resolution.

1. If you have loaded more than one dataset, use the dropdown list on the **Display** tool card to select which dataset to display.

2. Use the slider below the histogram to adjust window settings.

   -Or-

   Select a suitable color map from the dropdown list using the arrow button to the right of the histogram.

3. Select **Always Highest Resolution** to show full resolution images even during image processing.

   This selection might slow down system performance, therefore clear this checkbox to show a downsampled image during program interaction.

4. Use the **Edge enhancement** slider to adjust the sharpness of images.

Automatic Registration

Click this tool 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.

Note

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, Automatic Viewer Registration (Translation Only)*, page 77.

Manual Registration

1. 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.

2. Click **Manual Registration** to select this tool.

   The primary dataset is now shown pink and the overlay dataset is shown green in the active viewer. An outlined cross is also displayed in the viewer.

3. Drag the center of the cross so that corresponding structures in the green layer and in the pink layer are exactly overlaid.

   -Or-

   Use the arrow keys to move the green layer.

   -Or-

   Drag the ends of the cross to rotate the green overlay layer.

Tip

Hold the **Shift** key down in conjunction with the **Pan** tool to move only the green layer but not the pink layer. Or hold the **Shift** key down while you scroll images to scroll only on the green but not the pink layer.

4. Click **Accept Registration** when you have finished aligning your datasets manually.

-Or-

Click **Reset Registration** to undo manual alignment or automatic registration.

The two datasets are now registered in the same way as they were immediately after loading.

SUV tool card

You use the **SUV** tool card to check the calculation method and parameters for standard uptake values in PET or SPECT datasets.

On the menu, select **Tools > SUV** to open this tool card.

-Or-

Click **Show/Hide SUV Tool Card**.

Correcting calculation parameters

The upper half of the tool card shows calculation parameters stored in the DICOM data.

Correct values or add missing information, if necessary.

Information about the patient's weight, height, and sex is relevant for the calculation of SUV for lean body mass and SUV for body surface area.

-Or-

Click **Reset to DICOM values** to discard your corrections.

ROI statistics are updated immediately.

The parameters that you define on the **SUV** tool card will be applied to all ROI calculations in this study, even after you have closed the **SUV** tool card again.

Selecting a calculation method

In the lower half of the tool card, you can switch between different methods for calculating standard uptake values, or calculate activity in becquerel or counts.

Click **Make Default** to store your selection of a calculation method in your user profile.

Viewing mammography studies

Protocols for mammography studies feature a specific arrangement of images that is particularly well suited for comparing 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.

Magnifying Glasses

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

1. Click **Magnifying Glasses** 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 this rectangle across the image to move the magnifying glass.

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.

   For layouts that show images in more than one orientation, you can continue applying magnifying glasses to these other viewers as well.

6. Click the tool a second time to remove the magnified sections from all viewers.

> **Tip**
>
> The **Magnifying Glasses** tool is not limited to mammography studies but is also available for 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 42.

Quadrant Navigation

With this tool, you can enlarge the displayed images and read them quadrant by quadrant.

1. Click **Quadrant Navigation** 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 entire images again.

7. Continue pressing the **Right** arrow key to return to quadrant display.

Quadrant Navigation can be adapted to your screen size. **Quadrant Navigation** plus the **Right** arrow key will take you through four quadrants on medium-sized displays, as in the example above. Small displays may require six 'quadrants' to show all parts of the image in sufficient detail, while large monitors may only require two 'quadrants'. This affects the number of times you have to press the **Right** arrow key to see the full images again.

Tip

When entire images are shown, you can choose whether to show complete overview images or whether to cut away background information and show the overview image enlarged.

Quadrant Overview Enlarged shows the overview image enlarged and cuts away background pixels, burnt-in text, and markers.

Quadrant Overview shows either the full image or cuts away only background pixels, depending on the property settings for this tool. Choose this tool if you suspect that **Quadrant Overview Enlarged** might not display all diagnostically relevant information.

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

Click one of these tools to scroll through corresponding images in prior studies.

-Or-

Use **Browse in All Priors** for a similar effect. See also *Browse in All Priors*, page 45.

Viewing a DBT study

In digital breast tomography (DBT), multiple images may exist for each view:

- Projection images

  These are X-ray images of the breast acquired at different projection angles for a main viewing direction.

- Tomosynthesis images

  This is a volumetric reconstruction (3D series) of the projection images. Its layers focus on the anatomy at a certain tissue depth.

- Mammography images or reconstructed 2D images

  Mammography images are standard two-dimensional (2D) images resulting from digital mammography. Reconstructed 2D images are reconstructed from the DBT data so as to avoid additional X-ray exposure.

Symbols in the lower-right corner of a viewer indicate which of these images exist for a standard view.

Click one of these symbols to show the corresponding image type.

-Or-

Use the following tools to switch between 2D image, projection view, and 3D series display in the current viewer.

Tip

When tomosynthesis images are shown, the DBT position indicator in the lower left or right corner of a viewer shows you the position of the displayed image.

Select **View > Show in Viewer > Orientation Cube** to show or hide the DBT position indicator.

Toggle Dicom Mammo CAD

Click this tool to show or hide DICOM mammography CAD markers.

Segmentation

Visage 7 provides various tools and techniques for segmentation. Segmentation is the process of identifying objects and defining their contours. In all applications, segmentation is the first step before objects can be removed or before structures can be analyzed in greater detail. Visage 7 provides tools for manual segmentation of objects and structures in 2D images and for automatic, semiautomatic, or manual segmentation in 3D volume datasets and also permits a combined approach.

Automatic removal of structures

These tools segment and remove specific structures automatically. These tools are available for CT volume datasets only. The effect of automatic removal of structures is only visible in 3D viewers and MPR viewers in thick-slice display.

> **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 restore the removed structures.

Remove Patient Table

1. Click this tool to remove the patient table from a CT dataset with a single click.

2. Click the tool a second time to redisplay the patient table.

Remove Chest Wall

1. Click this tool to remove the chest wall or rib cage from a CT thorax dataset with a single click.

2. Click the tool a second time to redisplay the chest wall.

Bone removal

For CT angiography datasets, Visage 7 provides a tool for semiautomatic 3D segmentation of the bones of the legs, or of the pelvis and spine.

<table>
<tr><td style="background-color:yellow">**Caution**</td></tr>
<tr><td>

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, or legs. It is the responsibility of the user to check the plausibility and accuracy of the presented data.
</td></tr>
</table>

Bone segmentation   The **Bone** tool card guides you through the segmentation process step by step.

1. On the menu, select **Tools > Bone** to open this tool card**.**

-Or-

Click **Show/Hide Bone Removal Tool Card**.

2. Select **Run Segmentation Algorithm** and also which bones you want to remove.

3. Click **Find Aorta**.

The system attempts to find the aorta and asks you to verify the aorta position before you continue.

The system attempts to find the aorta and asks you to verify the aorta position before you continue. If a correction is necessary or if the system cannot identify the aorta and prompts you to identify it manually, move the scoutline crosshair so that its center points to the aorta.

4. Click **Compute**.

5. Use these buttons to switch between display of vessels only, bones only, or display of both bones and vessels.

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 will not have to perform bone removal again. Instead, load the results from the last segmentation run.

Select **Load Pre-Computed Segmentation** and click **Load**.

Load

-Or-

Click **Remove Leg Bones** 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

With this tool, you can segment structures in 3D datasets manually. The effect of freehand cropping is only visible in 3D viewers and MPR viewers in thick-slice display.

1. Click **Freehand Crop** to select this tool.

   When you click this tool, a new toolbar is displayed in the lower-right corner of the active viewer.

2. Select the viewer that shows the structure that you want to crop.

   If necessary, rotate the volume to show the structure more clearly.

3. Drag the cursor around the structure.

   When you release the mouse button, the system closes the shape.

4. Use the tools on this toolbar to remove the volume inside or outside the freehand shape.

Click **Remove Inside** to remove all that lies inside the shape that you have just drawn.

-Or-

Click **Remove Outside** 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.

5. Use these tools to correct cropping.

Click **Remove Last Contour** to delete the last shape that you drew in this viewer.

-Or-

Click **Reset Remove** to reset freehand cropping.

The complete volume is shown again.

6. Click **Accept and Exit** to accept cropping and to close the **Freehand Crop** tool.

Edit tool card

The **Edit** tool card offers tools for segmenting structures in 3D datasets and in 2D images.

On the menu, select **Tools > Edit** to open this tool card.

-Or-

Click **Show/Hide Edit Tool Card**.

Segmentation principles

We distinguish between three basic principles for identifying a structure:

- Explicit selection of voxels means that you color relevant voxels or areas of interest in an image or slice with a brush.

- Contour-based segmentation expects you to draw a contour around the structure that you want to segment. For 3D segmentation, the system expects you to do this in two or more slices. The system then connects contours throughout the volume and identifies all voxels that lie within the 3D contour as belonging to the selection.

- Threshold-based segmentation combines graphical identification of what to segment and definition of a range of grayscale or HU values.

Key terms for managing segmentation

To be able to manage segmentation results efficiently, you need to be familiar with the following key terms:

- Selection

  When you identify a structure by explicit voxel selection or 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 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.

Creating a selection

Use the tools on the **Edit** tool card to select portions of an image or a volume.

Connected Voxels in Value Range (3D)

1. Click this threshold-based segmentation 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 now visible.

2. 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.

3. 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 now creates a selection. The selection is shown red.

4. If the selection does not yet cover the relevant structure sufficiently, click the part that is still missing.

   -Or-

   If the selection covers more than the relevant structure, hold the **Shift** key down while you click to reduce the selection.

Encircle Voxels in Value Range (2D/3D)

1. Click one of these threshold-based segmentation tools.

   The system highlights structures of the range defined by the **Data Range** slider in the same way as for the tool above.

2. 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.

3. Now draw a freehand shape around the structure of interest.

   Encircle either a yellow structure in an MPR viewer or a visible structure in a 3D viewer.

   The system now creates a selection. The selection is shown red.

   If you click **Encircle Voxels in Value Range (2D)**, 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 will see that only a small ribbon is shown red.

   If you click **Encircle Voxels in Value Range (3D)**, the selection extends throughout the volume.

4. If the selection does not yet cover the relevant structure sufficiently, click and encircle the part that is still missing.

-Or-

If the selection covers more than the relevant structure, hold the **Shift** key down while you draw to remove part of the selection.

Define Contour in 3D

1. Click this tool to start contour-based segmentation.

Contour-based segmentation is independent of the data range that is defined by the **Data Range** slider.

When you click this tool, a new toolbar is displayed in the lower-right corner of the active viewer.

2. 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 2D ROI, Freehand 3D ROI*, page 106.

3. Use the **Refine Contour** tool to correct and refine contour lines.

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

Click inside the ROI graphic to enlarge it by pushing the contour out.

-Or-

Click outside the ROI graphic to push the contour line in.

4. 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.

5. Proceed in the same way in several slices until you reach the last slice in the image stack that shows the structure.

6. 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.

Brush (2D)

1. Click this tool to select voxels or to correct a voxel selection created with another segmentation tool or algorithm.

2. Click the arrow next to the tool to select the size of the brush.

3. Select **Range Only** from this dropdown menu and a **Data Range** to restrict voxel selection to a specific tissue type.

4. Click in an MPR viewer and hold the mouse key down while you move the cursor over the area that you want to select.

-Or-

Hold the **Shift** key down while you click and drag the cursor across the image to remove voxels from a selection.

Note that in 3D datasets, you use the **Selection Brush** tool to select voxels or correct voxel selection in one slice at a time.

Refining a selection

Use the tools **Enlarge Object** or **Enlarge Object x2** to expand the selection by a few voxels or **Shrink Object** or **Shrink Object x2** to reduce your selection.

-Or-

Use the **Brush (2D)** tool to select more voxels for this object or to remove voxels from this object.

-Or-

Use **Invert Object** to invert a selection.

-Or-

Use **Clear Object** to undo a selection and to start again from scratch.

Creating an object from a selection

By default, the objects list of the **Edit** tool card 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.

1. Right-click the list and select **Create Object**.

2. Type the object name.

   -Or-

   Type `category\object` if you want to organize objects in a hierarchical way.

3. Select the new object in the list.

4. Click the plus (**+**) button (**Add Selection to Object**).
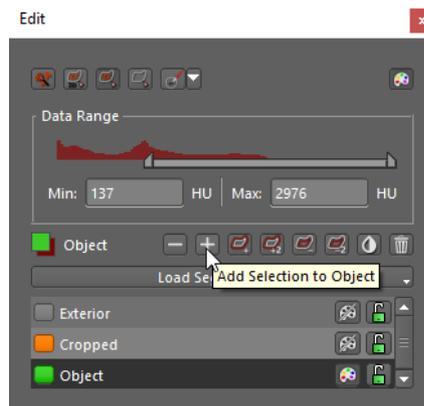
Editing an object

1. Select the object in the list.

2. Use the tools **Enlarge Object**, **Shrink Object**, **Invert Object**, or the **Brush (2D)** tool to select more voxels for this object or to remove voxels from this object.

   See also *Refining a selection*, page 143.

   -Or-

   Click **Connected Voxels in Value Range (3D)**, **Encircle Voxels in Value Range (2D/3D)** or **Define Contour in 3D** to create a new selection. Add the new selection to your object with the plus (**+**) button or remove it from your object with the minus (**-**) button.

> **Tip**
>
> Use **Lock/Unlock** to allow modification of an object or to protect an object from accidental modification.
>
>

> **Tip**
>
> To switch between objects while you correct them with the **Brush (2D)** tool, either select a different object on the **Edit** tool card, or hold the **Alt** key down while you click a different object in a viewer.

Showing segmentation results

1. Double-click an object to show it in the center of the active viewer.

Linked viewers are updated as well.

2. Click the show/hide color tool next to the object name to show or hide this particular segmentation in MPR viewers or 2D viewers.
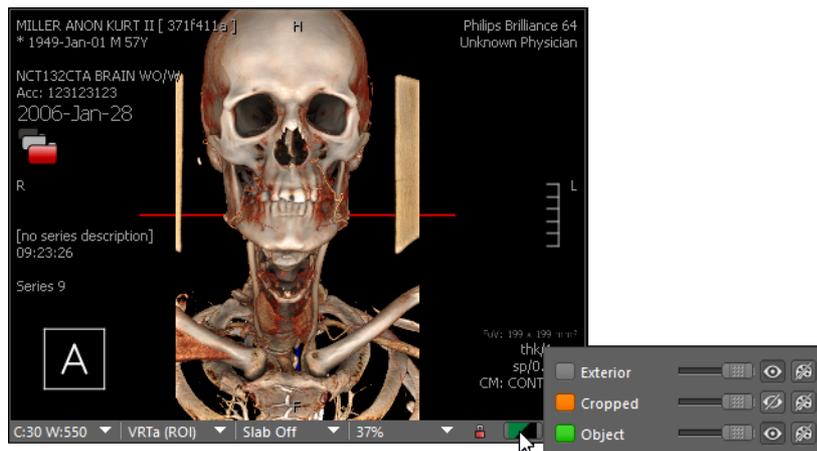

-Or-

Click **Toggle Segmentations** to show or hide all objects in MPR viewers or 2D viewers.

3. Use **Object Display** from the viewer controls to show or hide objects in a 3D viewer.

For example, you can show only a specific object but not any other objects. Hiding the object **Exterior** would crop objects in 3D.

Saving segmentation results

Create a presentation state to save your segmentation results.

See also *Presentation states*, page 190.

Loading alternative segmentations

When you load a study, segmentation results from the last (most recent) presentation state are loaded automatically. If more segmentation results exist for a study, you can load these instead.

1. Click the **Load Segmentation** button to show a list of all segmentations that exist for this study on the Visage 7 server.

2. Point to a segmentation in this list to show a preview image.
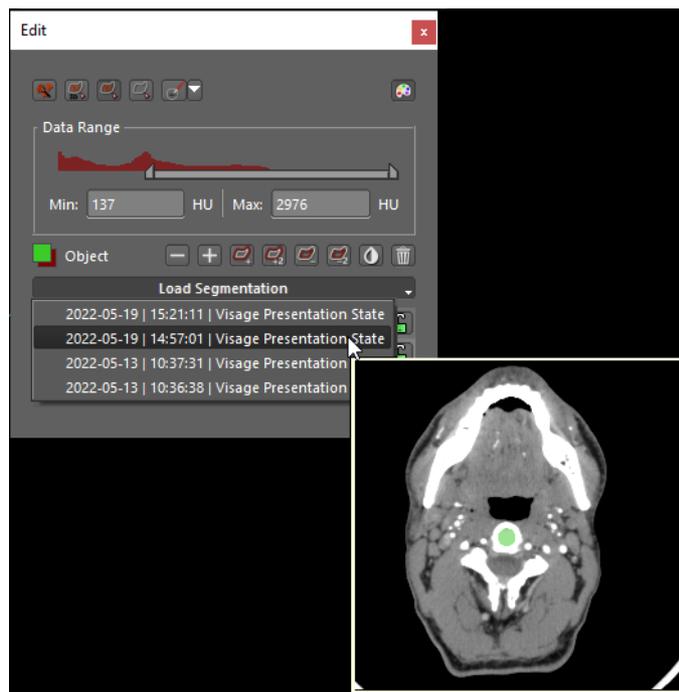
3. Click a segmentation in this list to load it.

Loading **replaces** the currently shown segmentation. Unsaved changes will be lost (no unsaved data message will be shown).

Creating freehand structures

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 for further analysis.

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 structure.

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, Freehand 3D ROI*, page 106 and *Freehand 2D ROI, Freehand 3D ROI*, page 106.

On the menu, select **Tools > Structures** to open this tool card.

-Or-

Click **Show/Hide Structures Tool Card**.

Freehand 2D structure, Freehand 3D structure

Click the **New 2D** or **New 3D** button on the **Structures** tool card.

A new toolbar opens in the lower-right corner of the active viewer. Here you will find tools for drawing and refining freehand shapes in 2D.

New Elliptical Contour

1. Select **New Elliptical Contour** to circle the area of interest with an ellipse or a circle.

2. Click a start point, hold the mouse button down, and drag the cursor out.

New Freehand Contour

1. Select **New Freehand Contour** to draw a freehand shape.

2. Click a start point and hold the mouse button down.

3. Draw a contour line.

New Balloon Contour

1. Select **New Balloon Contour** to define a structure or area of interest of a specific brightness.

2. Click into the structure and drag the cursor out.

Append mode

1. Draw a contour or select a contour that you drew earlier.

2. Press and hold the **Shift** key down.

   The cursor turns into an arrow with a plus sign.

3. 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.

4. Add a third contour to this ROI, if necessary.

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

Refine Contour

After you have drawn a contour, the **Refine Contour** tool is active.

The cursor has changed shape.

Click anywhere in the image and drag the cursor to show a circle with which you can correct the ROI graphic.

The further from the contour line you click, the larger the circle will be.

Click inside the ROI graphic to enlarge it by pushing the contour out.

-Or-

Click outside the ROI graphic to push the contour line in.

Tip
With freehand 3D ROIs, contours that you drew in a slice appear as solid lines. Interpolated contours in the slices in between appear as dashed lines. With the **Refine Contour** tool, you can correct both solid and dashed contours.

Undo

Click **Undo** to retrace your steps.

Copying a structure	**1.** Right-click a structure and select **Copy Object**.
	-Or-
	Select the structure and press **Ctrl/Cmd + C**.
	2. Scroll to the slice into which you want to paste the structure.
	-Or-
	Click the viewer into which you want to paste the structure.
	3. Right-click and select **Paste Object**.
	-Or-
	Press **Ctrl/Cmd + V**.

Completing a freehand 2D/3D structure

Click **OK** when you have finished drawing and refining the structure to close the tool.

The system now calculates ROI statistics.

Editing structures

Use the list of structures on the **Structures** tool card to select ROIs or contours for editing.

Refining contours

1. 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.

2. Refine the ROI or add more contours to a 3D structure.

Renaming structures

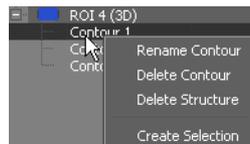Right-click a ROI or a contour to rename it.

Deleting contours or structures

Right-click a ROI and select **Delete Structure** to delete the entire structure.

-Or-

Right-click a contour in a 3D ROI and select **Delete Contour** to delete this contour only.

Showing or hiding structures

Select or clear the **MPR** and **3D** columns to show or hide ROI graphics in MPR viewers or the 3D viewer.

Converting a ROI into an object

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 *Creating an object from a selection*, page 144.

Statistical analysis of ROIs and structures

The **Statistics** tool card performs statistical analysis of all ROIs and structures that you have defined in your dataset.

On the menu, select **Tools > Statistics** to open this tool card.

-Or-

Click **Show/Hide Statistics Tool Card**.

Statistics for the report

1. Click **Compute** to update the results table on the **Statistics** tool card.

2. Click **Screenshot Statistics** in the upper-left corner of the **Statistics** tool card.

   This creates a screenshot of the entire results table and sends it to the **Export** window. You can drag the screenshot into your report from there.

   -Or-

   Select one or several rows in the results table and click **Screenshot Selected Statistics** if only selected measurements are relevant for the report.

Exporting results

If you want to evaluate ROI statistics further, export the entire results table or only individual lines as comma-separated lists (*.csv). Comma-separated lists can be imported into spreadsheet programs, such as Excel.

Click **Export CSV** to export the entire table.

Export CSV

-Or-

Select one or several rows in the results table and click **Export CSV Selected**.

Export CSV Selected

Vessel analysis

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.

Procedure overview

1. On the menu, select **Tools > Vessel** to open this tool card.

   -Or-

   Click **Show/Hide Vessel Tool Card**.

2. Select and name the vessel that you are about to trace.

   -Or-

   Right-click the vessels list and insert a new vessel.

3. Define and edit a curve and start vessel tracing.

4. Switch to **Curved View**, **Lumen View**, or **Cross-section View** for further vessel evaluation.

Curve definition and vessel tracing

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.

- Semiautomatic 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.

  To use semiautomatic vessel tracing mode, you click points between which you want the system to trace the vessel. This creates **green dots** in the images.

- Manual vessel tracing

  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 with straight lines.

  To use manual vessel tracing, you press and hold the **Shift** key down while you click to define manual control points. This creates **blue dots** in the images.

You can combine semiautomatic and manual vessel tracing to connect critical points.

Defining a new curve

1. Click **Define/Edit Curve** to start curve definition mode.

   You can use the **Define/Edit Curve** tool on the toolbar or on the **Vessel** tool card to start curve definition.

   When you click this tool, a new toolbar appears in the lower-right corner of the active viewer.

2. Now click control points along the vessel, either in the 3D viewer, or in MPR viewers, or in a combination of both.

3. Click **Show All Vertices** to project the curve that you have defined so far onto the currently shown slice.

   This tool is particularly useful if you are using MPR viewers and not the 3D viewer to define a curve along a vessel.

   If you switch off **Show All Vertices**, only those points that lie in the currently displayed slice are visible.

4. Click **Undo** to undo the last curve editing step.

-Or-

Click **Clear Points** to delete all points and start curve definition again from scratch.

5. When you have finished clicking points along the length of the relevant vessel section, have the system trace the vessel.

Click **Large Vessel Tracing** if you are analyzing a large vessel.

-Or-

Click **Small Vessel Tracing** if you are analyzing a small vessel and, in particular, a coronary vessel.

-Or-

Click **Trace Aorta** if you are analyzing the aorta.

-Or-

Click **Accept and Exit** to end curve definition without actually tracing a vessel and to create a curved view only.

Tip

Open the **Statistics** tool card for statistical analysis of the traced vessel segment. See *Statistical analysis of ROIs and structures*, page 150.

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/Cmd** key down.

For example, press and hold the **Ctrl/Cmd** key down and drag the cursor across 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.

1. If this happens, undo the last step.

2. Press and hold both the **Shift** and **Ctrl**/**Cmd** keys down 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.

2. Click **Define/Edit Curve** to start curve-editing mode.

Now you 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 cursor to change the 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 down 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 to define an additional control point between two existing points.

Curved View

Click this tool to open curved view, which is an additional viewer.

CPR

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 *Curve definition and vessel tracing*, page 153.

Navigating in curved view

If you have traced more than one vessel, use the context menu of the CPR viewer or the **Vessel** tool card to select which vessel you want to display.

1. Click **Toggle Centerline** for better orientation.

2. Rotate around the centerline in curved view.

   Rotation is the standard navigation tool in the CPR viewer.

3. Press and hold the **Alt** key down 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 any other curved structure.

1. For example, define a curve along the spine.

2. End curve definition with **Accept and Exit**.

3. Open curved view.

CPR

Lumen View and Cross-Section View

Lumen view and cross-section view are two views provided specifically for the analysis of vessels. Both views are not available in any other context.

If you have not yet defined a curve, these viewers are empty.

See *Curve definition and vessel tracing*, page 153.

Navigating along the vessel in lumen view

1. Open **Lumen View**.

   LUM

2. If you have traced more than one vessel, select which vessel you want to display.

   Use the context menu of the lumen viewer or the **Vessel** tool card to select the vessel.

3. Rotate around the vessel.

   Rotation is the standard navigation tool in the lumen viewer.

4. Drag one of the vessel sliders to a point of interest.

   The active vessel slider is displayed with an orange triangle at the bottom.

5. Click **Switch Active Vessel Slider** to switch between vessel sliders.

Navigation in cross-section view

Clicking and dragging a vessel slider in lumen view activates cross-section view in the upper-left viewer.

Scroll in cross-section view.

You are now 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

Stenosis calculation can either use line measurements or area measurements.

1. First, select a reference point along the vessel.

   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 the vessel cross-section.

-Or-

Use one of these area measurement tools.

In lumen view, measurement results are shown next to the vessel sliders.

3. Now select the point along the vessel where you suspect a stenosis.

4. In cross-section view, measure the vessel cross-section at this point.

Use the same tool as in the measurement at the reference point.

5. Right-click a measurement text and classify the measurement. For example, select **Stenosis n%**.
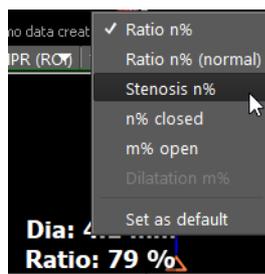
If **Stenosis n%** is not available, you might have right-clicked the vessel slider and not the text. Or you have clicked the text of the reference point, which is the higher value.

Measuring vessel seg-ment 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

Visage 7 provides tools specifically for reading cardiac studies.

LV Analysis

The **LV Analysis** tool card provides tools for LV segmentation and LV analysis in CT studies.

On the menu, select **Tools > LV Analysis** to open this tool card.

-Or-

Click **Show/Hide LV Analysis Tool Card**.

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.

Performing LV analysis

The **LV Analysis** tool card guides you through LV analysis step by step.

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.
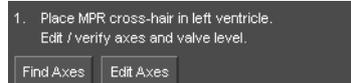
The system identifies the long and short axes of the left ventricle and turns on **Edit Axes** mode. The short and long axes are now shown as orange lines in the MPR viewers.

3. Correct the axes by moving or rotating the orange lines in the MPR viewers.

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 the 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 **Find LV (All Phases)** again when you have finished your adjustments.

-Or-

Proceed phase by phase and use **Clear LV (Current Phase)** and **Find LV (Current Phase)**.

When segmentation has been completed successfully, proceed with LV analysis step 3.

Step 3: time-volume analysis

Click **Results** to start time-volume analysis of the left ventricle.

Viewing LV analysis results

After you have clicked **Results** on the **LV Analysis** tool card, the **LV Results** tool card opens.

-Or-

On the menu, select **Tools > LV Results** to open this tool card.

-Or-

Click **Show/Hide LV Results Tool Card**.

LV Results consists of three segments:

- Bull's-eye view

    The segments in this bull's-eye view correspond to the classification of the American Heart Association (AHA).

    Move the cursor over a segment to show the segment designation as a tooltip. Or right-click anywhere in the bull's-eye view to switch between analysis results view and segment ID view.

- Curve display section

    Adjust the system's selection of the end-diastolic (ED) and end-systolic (ES) phases with the sliders, if necessary.

- Summary section

    Enter the heart rate of your patient here. The cardiac output value is updated automatically.

If only one or two of these segments are shown on your screen, drag out one of the corners of this floating window to make it wider.

Selecting a view

Use the dropdown selection box in the lower-left corner of the tool card to select a different view of your LV analysis results.

Global Volume
Regional Volume
Wall Motion

- **Global volume** shows a graph of the total LV volume over one heart cycle.

- **Regional Volume** shows 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 and clear the selection of regions that you want to hide. Or select **Show no Graphs** first and then select the regions that you want to show one by one. When you create a report, only those curves that are currently shown will be included.

- **Wall Motion** shows the accumulated wall motion in a bull's eye view.

Creating a report

Click **Report** in the lower-right corner of the **LV Results** tool card.

Report

Report sends screenshots of all graphs and analysis results to the **Export** window.

Calcium scoring

Visage 7 provides a tool card for identifying the extent of calcified plaque in coronary arteries in CT studies.

Select **Tools > Calcium** to open this tool card.

-Or-

Click **Show/Hide Calcium Scoring Tool Card**.

Identifying plaque

1. Click **Calcium Scoring**.

   All areas with an intensity of more than 130 HU are highlighted yellow.

2. Select or clear **Multi Slice Mode**.

   In multislice mode, voxels are assigned to plaque both in the slice into which you click and in adjacent slices. If multislice mode is not selected, only voxels in the currently displayed slice are assigned to plaque.

3. Now start scrolling through the image stack slowly.

4. If you observe plaque in an image, select the vessel in which the plaque is observed.

   To select a vessel, click one of these 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).

5. Next, click where you observe plaque in the image.

   -Or-

   Click and drag the cursor across the image to draw a line around the plaque.

   This assigns the plaque to the selected vessel.

6. Right-click one of the A1 to A3 artery buttons and select **Properties**.

7. Enter a label and select a color for this artery.

Reporting results

At the bottom of the **Calcium** tool card, you will find tools and input boxes that help you to prepare your report.

Under **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.

1. Correct information regarding the patient's sex and age, if necessary.

2. Select **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.

3. Click **Report** to send your findings to the **Export** window.

   Report

   -Or-

   Click **Export CSV**, to save your results as a comma-separated list on your computer.

   Export CSV

   *.csv files can be read by spreadsheet programs, such as Microsoft Excel.

Ejection fraction (echocardiography)

This tool calculates the left ventricular ejection fraction from echocardiography studies that contain end-diastolic and end-systolic images of the left ventricle in 2- and 4-chamber views.

Calculating the ejection fraction

✓ You have loaded an echocardiography study.

✓ Ideally, the study contains at least two clips: one clip of the 2-chamber view of the left ventricle and one clip of the 4-chamber view of the left ventricle.

1. Scroll slowly through the frames of the first clip (for example, the 4-chamber view).

   Use the slider of the **Cine** tool card or the mouse wheel for slow scrolling.

2. When you have reached a frame that shows the end-diastolic phase, click **Ejection Fraction (Echocardiography)**.

   When you click this tool, a new toolbar opens in the lower-right corner of the active viewer.

3. Click a start point, hold the mouse button down and draw a contour around the left ventricle. Leave the contour open over the mitral valve.

   The system closes the contour with a straight line automatically. The system also connects the center point of this line with the most distant point of the contour. The lumen is then approximated by a stack of 20 elliptical discs.

4. Click **New A4Cd Measurement** to define this contour as the 4-chamber view of the end-diastolic phase.

   The system now calculates the end-diastolic volume (EDV). A screenshot is sent to the **Export** window.

5. Scroll to the end-systolic phase in the 4-chamber view.

6. Draw a contour around the left ventricle.

7. Click **New A4Cs Measurement** to define this contour as the 4-chamber view of the end-systolic phase.

   The system now calculates the end-systolic volume (ESV) and the ejection fraction (EF) based on the 4-chamber view. A screenshot is sent to the **Export** window.

8. Select the second clip (in this example, the 2-chamber view).

9. Scroll slowly through the frames until you have reached the end-diastolic phase.

10. Draw a contour around the left ventricle and then click **New A2Cd Measurement.**

11. Scroll to the end-systolic phase of the 2-chamber view.

12. Draw a contour around the left ventricle and then click **New A2Cs Measurement**.

When you click **New A2Cd Measurement** and **New A2Cs Measurement**, the system updates measurement results taking data from biplanar (BP) measurements into account.

13. Right-click the contour and select **Show Single Plane Statistics** to show both single-plane and biplanar calculation results.

14. Click **Ok** to close the **Ejection Fraction** tool.

Showing contours in all slices

1. Right-click a contour.

2. Select **Show on all Slices**.

3. Start scrolling frames.

The contour is visible in all slices of the clip. However, the contour appears dimmed and light gray in all frames except in the frame in which you drew the contour.

Correcting a contour

You can correct a contour after you have completed it, either before or after you define the measurement.

However, you can correct a contour only in the frame in which you drew it, that is, when the contour is shown yellow. You cannot correct contour lines when they are shown light gray (**Show on all Slices**).

Click any point on the contour and drag in or out to correct the contour.

-Or-

1. Move away from the contour.

The cursor changes shape.

2. Click anywhere near the contour and drag the cursor across the image to show a circle with which you can correct the contour.

The further from the contour you click, the larger the circle will be.

3. Push portions of the contour in or out with this tool.

Evaluation of Doppler ultrasound curves

Visage 7 provides tools for evaluating Doppler ultrasound curves.

Doppler Curve

This tool calculates blood flow velocity, flow volumes, and pressure gradients from spectral Doppler images.

✓ You have loaded an echocardiography study.

✓ The active viewer shows a Doppler image.

1. Double-click the active viewer to show it in full-screen mode.

2. Click **Doppler Curve** to select this tool.

3. Draw a hull curve in the Doppler time-velocity diagram.

   The curve automatically starts and ends at zero velocity.

4. To correct the curve, click any point and drag in or out to correct the curve.

   -Or-

   Move the cursor away from the curve.

   The cursor changes shape.

   Click anywhere near the curve and drag the cursor across the image to show a circle with which you can correct the curve.

   The further from the curve you click, the larger the circle will be.

5. Push portions of the curve in or out with this tool.

6. Click **OK** to accept the calculation.

Measure Doppler Velocity

This tool calculates blood flow velocities, pressure gradients, and the velocity deceleration from spectral Doppler images.
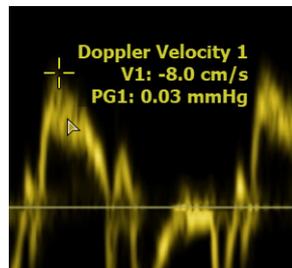
✓ You have loaded an echocardiography study.

✓ The active viewer shows a Doppler image.

1. Double-click the active viewer to show it in full-screen mode.

2. Click **Measure Doppler Velocity** to select this tool.
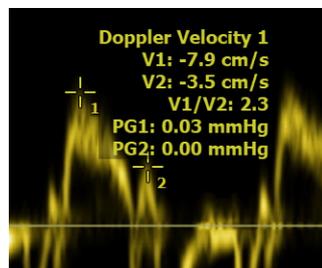

Single-click measurement

Click a peak in the Doppler plot.

The system calculates the blood velocity and the pressure gradient.

Comparing two peaks

1. Press and hold the **Shift** key down.

2. Click the first peak.

3. Click the second peak.

The system calculates the blood velocity and the pressure gradient for both peaks and also the velocity ratio.

Calculating the deceleration slope

1. Click the peak and hold the mouse button down.

2. Drag along the deceleration slope.

3. Release the mouse button at the bottom of the slope.
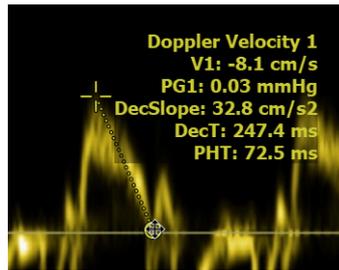
The system calculates the blood velocity, the pressure gradient, the deceleration slope, the deceleration time, and the pressure half-time.

Combined measurement

1. Click the peak and hold the mouse button down.

2. Drag along the deceleration slope.

3. Press and hold the **Shift** key down.

4. Release the mouse button at the bottom of the slope.

5. Click a second peak.
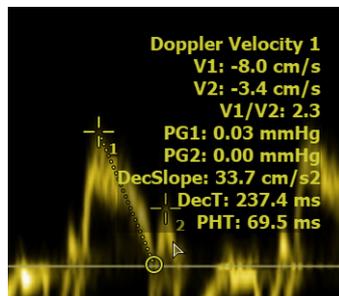
Synchronized display of pre- and post-stress cardiac echo

If an echocardiography study contains ECG information, Visage 7 synchronizes browsing and cine display in viewers showing pre- and post-stress images.

A typical application for synchronized display is a comparison of 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 browsing or playback of the post-stress sequence or speeds up browsing or playback of the pre-stress sequence. As a result, images of corresponding heart phases are shown side by side at any time during browsing or playback.

Synchronization of browsing or cine display is enabled automatically if the active viewer is a member of a time-phase group. See also *Linking viewers*, page 75. This is typically predefined in the protocol the system selects for echocardiography studies that contain ECG information.

Brain perfusion

Visage 7 provides tools for performing brain perfusion analysis.

Perfusion analysis

The **Brain Perfusion** toolbar comprises all the tools that you need to perform brain perfusion analysis. The tools are arranged left to right in the order in which you will need them.

> **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 and that the dataset is suitable for the calculations. It is the responsibility of the user to check the plausibility and accuracy of the result.

Excluding images

1. Browse the time series and decide whether all images can be included in the analysis.

   If individual images show motion artifacts, for example, you can exclude them from the analysis.

2. Show an image that you want to exclude from perfusion analysis.

3. Click **Exclude current Phase from Perfusion Calculation** on the toolbar.

4. Exclude more images, if necessary.

Creating a tMIP image

Click **Display tMIP** 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 more clearly.

Identifying the artery and the vein

1. Click **Define Artery** and then click 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 uptake curve for the artery is displayed red.

2. Next, click **Define Vein** and then click 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.

Calculating Perfusion

Click **Calculate Perfusion**.

This tool calculates the following functional maps: mean transit time (MTT), time to peak (TTP), cerebral blood flow (CBF), cerebral blood volume (CBV).

Mirror mode

In mirror mode, ROI measurements that you perform in one half of the brain are repeated in the other half of the brain. This helps you to compare relevant areas in both brain halves.

1. Select the tMIP image (large viewer).

2. Click **Mirror Mode**.

3. 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.

ROI measurement

1. Select one of the functional maps and click **Define ROI**.

    A new toolbar opens in the lower-right corner of the active viewer.

2. Use this toolbar to draw an elliptical ROI or a freehand ROI around an area of interest and to refine the contour.

    The tools on this toolbar are the same as those provided for evaluating freehand 2D ROIs in any other type of image. Therefore, for details on how to use these tools see *Freehand 2D ROI, Freehand 3D ROI*, page 106.

3. If the mirror line is in the way while you are analyzing functional images, click **Toggle Mirror Line** to hide it and redisplay it later.

Note that hiding the mirror line does not turn mirror mode off.

Saving perfusion results

1. Click **Save/Send Perfusion Result** to save the new series on the server or on a DICOM node.

Clicking the button opens the **Send perfusion results** dialog. Here you select send options.

2. Under **Destination**, select the server to which you want to save the new series.

3. Under **Save Options**, select how you want to save the maps that were calculated during perfusion analysis and which maps you want to save.

Each map will be saved as a separate series. The images will have the same slice thickness as shown on the screen.

Select **Original Maps** if you want to save perfusion maps as grayscale images.

This creates new series of DICOM images. These images can be windowed, resized, or evaluated in future postprocessing sessions, just like any other DICOM series.

-Or-

Select **Colorized Maps** if you want to save perfusion maps as color images (RGB).

RGB images are screenshots. This means that you cannot change any of their display parameters or perform measurements in these images in future postprocessing sessions.

Select **Mosaic** if you want to create and send an overview image showing the tMIP image plus the calculated maps side by side.

Select **Artery and Vein Positions** if you want to save the coordinates of the artery and vein position that you identified before you had the system calculate perfusion in a DICOM presentation state. In the **Study Browser**, the presentation state appears as a new series with modality PR. The next time you load this study, you can resume perfusion calculation or recalculate.

Select **Screenshots** to save or send all screenshots that were created during perfusion analysis.

If you want to save or send only selected screenshots, use the **Export** window to do so. See *Saving screenshots*, page 183.

4. Under **Perfusion results**, specify a series number and series description.

The various perfusion result series that will be created when you click **Send** will count up from the series number you specify here. The series description text that you enter here will be used as a prefix for the perfusion result series.

5. Select **Make Default** to save your settings as program suggestions for subsequent send jobs.

6. Send the perfusion result series to the selected server.

Send

Perfusion settings

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.

1. On the menu, select **Tools > Brain Perfusion** to open this tool card.

-Or-

Click **Show/Hide Brain Perfusion Tool Card**.

2. Select a preset.

Brain perfusion presets are parameter sets optimized for specific data acquisition protocols.

If no presets have been configured for your system, a default parameter set is automatically selected for CT or MR images respectively.

3. Modify individual calculation parameters, if necessary.

Brain Tissue: 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.

Default values are 0 HU (**Min**) and 120 HU (**Max**) for CT images and 20% and 100% of the grayscale value range in an MR dataset (indicated as US for "unspecified").

Remove CSF: To speed up the calculation and for ease of interpretation of the computed maps, voxels that contain cerebrospinal fluid (CSF) will not be processed.

Remove Vessels: For ease of interpretation of the computed maps, voxels that contain larger vessels will not be processed.

Smoothing: To improve the signal-to-noise ratio (SNR), a Gaussian image filter can be applied to all images before the computation. This parameter switches the smoothing filter on or off and also allows adjustment of the kernel width of the filter. Larger values improve the SNR at the expense of a diminished spatial resolution.

Pre-contrast Images: 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.

Last image: This parameter defines the last phase of the perfusion images series that is considered in the perfusion calculation.

Regularization Param.: This parameter is used to suppress noise in the source data. Lower values provide more accurate computation results but are more sensitive to noise.

Auto-Registration: If this option is selected, an automatic motion registration is performed on the perfusion time series when the user clicks one of the tools **Display tMIP**, **Define Artery**, or **Define Vein** for the first time. If the number of slices in the 3D volume is greater than or equal to the number of slices configured in the user interface, 3D rigid body motion registration is performed, otherwise only in-plane shifts and rotations are registered.

4. 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.

5. Click **Calculate Perfusion** at the bottom of the tool card or on the toolbar to recalculate functional maps after parameter adjustments.

Lesion tracking

Visage 7 provides tools for lesion tracking.

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 because zoom-out is applied. 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, inaccuracy may be even greater.

Lesion tracking

Click the **Lesion Tool** 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.

Automatic lesion segmentation

1. Click **Segment Lesion**.

2. Click the lesion in the current study and also in the prior study if the lesion is visible in both studies.

When you have identified a lesion in both studies, the system creates a lesion pair, labels it, and calculates activity.

Manual lesion segmentation

If automatic lesion segmentation is not possible because of poor image quality or because of artifacts in the images, resort to manual evaluation tools.

1. Select either the **Measure Lesion** or **Measure Lesion (2 Diameters)** tool depending on which standard you follow.

2. Drag the cursor across the lesion to measure its diameter.

   Also measure the second diameter if you work with the **Measure Lesion (2 Diameters)** tool.

3. Measure lesion dimensions in the prior study as well.

Mark Lesion

If a lesion does not exist in both datasets, click this tool to mark the spot where a lesion exists in the other dataset.

Deleting a lesion marker

Select a lesion by clicking on the lesion text and then use this tool to remove the marker from the dataset.

Lesion classification

Use this tool or keyboard shortcuts to classify a lesion or lesion pair.

RECIST

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.

Completing lesion tracking

Click **Accept and Exit** when you have identified and classified all lesions in your current and prior study.

This closes the lesion tool and creates a report in the **Export** window.

Reviewing lesions

On the menu, select **Tools > Lesion** to open the **Lesion** tool card.

-Or-

Click **Show/Hide Lesion Tool Card**.

The **Lesions** tool card displays an overview of the lesions that you identified in the loaded studies.

If lesions were identified during an earlier session, the system checks whether all the relevant prior studies have been loaded before moving on to the **Lesions** tool card.

Adding a lesion

1. On the **Lesion** tool card, click **Add Lesion**.

   Add Lesion

2. Use **Segment Lesion** or one of the **Measure Lesion** tools on the **Lesion** toolbar to identify a new lesion.

Editing the list of lesions

The **Name** column lists all lesions and a summary of lesion diameters in target lesions.

Click **Add Lesion** and measure a lesion in an image to identify a new lesion.

-Or-

Double-click a lesion name in this column to edit the lesion name.

-Or-

Right-click a lesion in this column or any of the other columns and select **Delete** to remove a lesion from the list.

-Or-

Click the **Name**, **Type**, or **Location in current** column to sort the lesion table.

-Or-

Click a lesion row, hold the mouse button down, and drag this line up or down to change the order in which lesions are presented in the table.

Editing the lesion classification

Double-click the **Type** column of a lesion and select a different lesion type from the list. See also *Lesion classification*, page 175.

-Or-

Double-click the **Type** column of a lesion type summary and select your mode of working. The DICOM structured report will consider the selected mode.

-Or-

1. In the **Non-Target Lesions** summary row, double-click the cell of the current study and assess the overall response of non-target lesions:

   CR (complete response), **PD** (progressive disease), **Non-CR/Non-PD** (neither of the above).

2. Repeat this step for prior studies if appropriate.

Current and prior studies

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.

Splitting or merging 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**.

-Or-

You have identified two areas of activity, one in the current study and one in the prior study and you have 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.

Last edited

This table row shows the name of the last user who edited lesions in a study and the date of the last edit.

Point to the table cell of each study to show the complete editing history in a tooltip.

Previous Lesion, Next Lesion,   Use these tools to browse through your lesion segmentations and to review your findings.

Browsing lesions in current and prior study   Select the **Follow** button to browse lesions in the current and prior studies simultaneously, even if viewers are not linked.

Follow

-Or-

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 for current and prior studies, selecting or clearing **Follow** has no effect on browsing.

Warning symbol   If the system detects inconsistencies in the segmentation and identification of lesions, a warning symbol appears on the Lesions tool card.

Point to this symbol to show a tooltip that explains the problem or inconsistency.

Saving results   Click **Export** and select a destination.
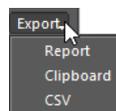
Report sends lesion statistics to the **Export** window as screenshots.

Clipboard copies lesion tables to the clipboard from where you can paste them into a document.

CSV saves your results as a comma-separated list onto your computer. *.csv files can be read by spreadsheet programs, such as Microsoft Excel.

-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).

Save

Sharing the Visage 7 client screen

With **Live Connect**, you can discuss studies with experts outside your Visage 7 network. For example, as a radiologist, you can discuss a case with a clinician even if the clinician has no Visage 7 user account or Visage 7 client software installed on the computer. To review the case with you, the clinician will only need a standard web browser plus a link and code, which you will provide.

1. Load the study that you want to discuss into a **View** window.

2. Click **Live Connect** or select **View > Live Connect** on the menu.

   The **Live Connect** dialog opens. This dialog contains an alphanumeric code and a link.
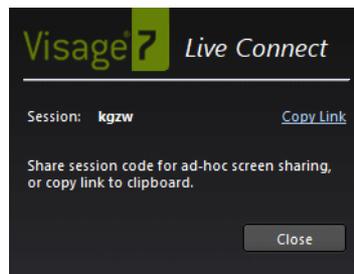
3. In the **Live Connect** dialog, click **Copy Link**.

4. Share the link with the clinician with whom you want to discuss the case.

   For example, send the link in an email.

   If you cannot email the link, clinicians should have a bookmark to the Visage 7 Live Connect landing page. From there, they can sign in to a session with their name and the alphanumeric code that you can communicate over the phone.

5. Tell the clinician to click the link or to copy it into a web browser.

   The link opens the Visage 7 Live Connect landing page, where the code has already been entered.

6. Tell the clinician to type their name and click **Connect**.

   As a Visage 7 user, you will now be prompted to permit the clinician to connect.

7. Click **Accept**.

The active viewer of your Visage 7 client is now shown in the clinician's web browser. Both you and the clinician have been assigned a color-coded cursor with your user name. You can use these cursors to point to structures of interest while you discuss the case over the phone.

The clinician can follow your activities in the active viewer in real time. When you switch to a different viewer, this is the viewer that the clinician will now see. Clinicians can maximize the image display in their web browser with the **Fit** button.

Screen sharing is active for as long as the **Live Connect** dialog is shown in your Visage 7 client.

8. Click **Stop Sharing** to end the **Live Connect** session.

Saving and documenting results

Visage 7 offers various tools and alternative approaches for saving evaluation results. These methods preserve your results and make them available for further evaluation or help you to include them in a report.

Screenshots

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

Visage 7 collects all screenshots that you create during a session in the **Export** window. From the **Export** window, you can save these screenshots, send or print them, or include them in your report.

Creating screenshots in a View window

Every time you add a text or graphical annotation or perform a measurement, the program takes a screenshot of the image in the currently selected viewer, complete with annotations, measurements, and viewer text, if shown. If you want to preserve an image without annotating it, you create a screenshot with one of the screenshot tools.

Screenshot

Click **Screenshot** to create a screenshot of the currently selected viewer.

One screenshot is sent to the **Export** window.

Screenshot All

Click **Screenshot All** to create screenshots of all viewers that are currently shown on the screen.

Several screenshots are sent to the **Export** window.

Combined Screenshot

Click **Combined Screenshot** to create a screenshot that shows all viewers that are currently displayed on the screen in one image.

One screenshot is sent to the **Export** window.

Screenshots in the Export window

Screenshots are bitmap images that you have created in your current session or that were created automatically to document observations or evaluation results. Because screenshots are bitmaps, you cannot edit them, even if you send them as a DICOM series or save them in DICOM format.

> **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.

Screenshot list

In the **Export** window, you will find the following types of screenshots:

- Screenshots that were created by the software when you stored a key view.

  These screenshots are labeled **Auto** in the lower-right corner. See *Annotations and measurements*, page 86 and *Key views*, page 189.

- Screenshots that you have created with one of the screenshot tools.

  These screenshots are numbered. Screenshots that you have created with **Screenshot All** have the same number. See *Creating screenshots in a View window*, page 181.

- Line profiles, which you have sent to the **Export** window with the screenshot tool on the **Line Profile** tool card. See *Showing a line profile*, page 93.

- ROI statistics, which you have sent to the **Export** window with the screenshot tool on the **Statistics** tool card. See *Statistical analysis of ROIs and structures*, page 150.

- Tables and graphs that result from an LV analysis or a calcium scoring analysis.

  You sent these analysis results to the **Export** window with the **Report** button on the corresponding tool card. See *LV Analysis*, page 159 and *Calcium scoring*, page 162.
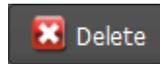
Displaying screenshots

1. Double-click a screenshot to show it in a floating window.

2. Use the **Previous Screenshot/Next Screenshot** buttons in this floating window to browse screenshots.

Deleting screenshots   1. Select a screenshot.

2. Click **Delete** to remove screenshots that you do not want to save.

Saving screenshots   Saving or sending screenshots means saving them on the Visage 7 server, on a partner system, or on a connected DICOM node.

1. Select the screenshots that you want to save.

    -Or-

    Press **Ctrl/Cmd + A** to select all screenshots in the **Export** window.

2. Click **Save/Send**.

3. In the **DICOM Send** dialog, select one or several DICOM servers.

    If the list of servers is very long, type the name or part of the name of the server in the **Filter** box above the list of destinations.

4. Enter a **Series Number** and **Series Description**.

    The program suggests 1000 as a series number. This adds the screenshot series to the end of the study.

5. For **Save Automatically**, select **Automatically (no confirmation)** and click **Make Default** to have the system save your screenshots automatically next time.

    The next time you close a study for which screenshots exist, Visage 7 creates a screenshot series and sends it to the server. If you have selected **Save Automatically (no confirmation)**, **Confirmation Dialog**, or **Confirmation Dialog (unchecked)**, the **Unsaved Data** dialog appears when you close a session, close the program, or try to load a new study.

6. Click **Send**.
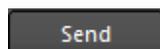
Exporting screenshots   Exporting screenshots means storing them on your local computer or in your network.

1. Select the screenshots that you want to export.

    -Or-

    Press **Ctrl/Cmd + A** to select all screenshots in the **Export** window.

2. Click **Export**.

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 screenshots

1. Select the screenshots that you want to print.

-Or-

Press **Ctrl/Cmd + A** to select all screenshots in the **Export** window.

2. Click **Print**.

3. In the **Print** dialog, select the printer and change printer settings, if necessary.

See *Printing images*, page 196.

Copying screenshots to the clipboard

If you want to show a screenshot in a presentation or in a text file, the easiest way is to copy it to the clipboard and paste it into your document from there.

You can only copy **one** screenshot at a time.

Right-click the screenshot and select **Copy**, or use the keyboard shortcut **Ctrl/Cmd + C**.

Batching

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 and rotational batching.

Stacked batching

Stacked batching is a process in which a new stack of coplanar reformats is created.

Click **Stacked Batching** to select this tool.

A new toolbar appears in the lower-right corner of the active viewer. Here you will find tools for creating a new image series.

Toggle Direction

Click **Toggle Direction** to reverse the direction in which you will walk through the volume.

Toggle Aspect Ratio

Click **Toggle Aspect Ratio** to plan 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

Click **Toggle RGB/Grayscale** to select the color scheme for the reformats: grayscale or RGB.

RGB

Grayscale creates a new series of DICOM images. These images can be windowed, resized, or evaluated in future postprocessing sessions, just like any other DICOM series.

RGB images are screenshots. This means that you cannot change any of their display parameters or perform measurements in these images in future postprocessing sessions.

Starting the batching process

Click **Save/Send** or **Export** to start the batching process.

See *Saving, sending, or exporting images*, page 188.

Rotational batching

Rotational batching is a process that creates new reformats from a volume dataset by rotating around a center axis. In 3D, this gives you the impression of walking around the volume. Rotational batching can be started from MPR viewers or from CPR viewers.

Click **Rotational Batching (Vertical)** or **Rotational Batching (Horizontal)** to select the tool.

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	Click **Toggle Direction** to reverse the direction in which you will walk around the volume.

Center Rotation Axis   Click **Center Rotation Axis** to move the rotation axis to the center of the preview image.

Toggle Aspect Ratio   Click **Toggle Aspect Ratio** to plan 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   Click **Toggle RGB/Grayscale** to select the color scheme for the reformats: grayscale or RGB.

RGB

Grayscale creates a new series of DICOM images. These images can be windowed, resized, or evaluated in future postprocessing sessions, just like any other DICOM series.

RGB images are screenshots. This means that you cannot change any of their display parameters or perform measurements in these images in future postprocessing sessions.

Starting the batching process   Click **Save/Send** or **Export** to start the batching process.

See *Saving, sending, or exporting images*, page 188.

Batching tool card

On this tool card, you can fine-tune parameters before starting the batching process.

1. Click **Show/Hide Batching Tool Card** to open the **Batching** tool card from the stacked batching toolbar or the rotational batching toolbar.

   -Or-

   On the menu, select **Tools > Batching**.

2. Click the lock symbol to 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 irrespective of whether they are locked or not.

3. In the **Number of images** box, define how many new reformats will be created.

4. In the **Angular increment** box, define the increments between slices.

   This parameter is available in rotational batching mode only.

5. In the **Image thickness** box, define the slice thickness of the new reformats.

6. In the **Overlap** box, indicate whether and how much images will overlap.

   A positive value creates overlapping slices, a negative value creates gaps between slices.

   This parameter is available in stacked batching mode only.

7. In the **Distance** box, define the distance between corresponding slice boundaries.

   This parameter is available in stacked batching mode only.

8. In stacked batching mode, click one of these buttons to define the direction in which you will walk through the volume.

   -Or-

   In rotational batching mode, click one of these buttons to define the direction in which you will walk around the volume.

9. Click **Save/Send** or **Export** to start the batching process.

See *Saving, sending, or exporting images*, page 188.

Saving, sending, or exporting images

You can save, send, or export images from the toolbars of the two batching modes or 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.

Save/Send

1. Click **Save/Send** to save the new series on the server or on a DICOM node.

The **DICOM Send** dialog opens. Here you select send options.

2. Under **Destination**, select one or several servers on which you want to save the new series.

3. Under **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.

4. Under **Reformatted Images**, enter a series number and series description. For example, enter a high number to append the series to the end of the study.

5. Click **Make Default** to save your settings as program suggestions for subsequent batching jobs.

6. Click **Send** to start the batching process and to send the new series to the selected server or servers.

Export

1. Click **Export** to export the new images to your local computer or to a folder in your network.

Depending on the color scheme that you selected earlier, clicking **Export** opens the **Export Grayscale** dialog or the **Export RGB** dialog.

2. Under **Export as**, select the file format of the new images.

The file formats *.jpg, *.mpg, and *.png are available only for RGB images and not for grayscale images.

When you select **DICOM Files** for RGB images, this creates screenshot images only. Windowing and measurements are only possible in new reformats of the type grayscale plus DICOM format.

3. Under **Destination**, select a drive and folder.

4. Under **Scout Images**, select whether you want to include the scout images in the series.

Selecting **Show Measurements and Annotations** and **Show Orientation Cube** under **Scout Images** applies to scout images and not to new reformats.

5. Enter a series number and series description for grayscale DICOM images.

-Or-

For RGB images of any file format, select whether patient information and orientation labels are to be shown permanently in the images.

6. Click **Export** to start the batching process and to save the images on your local computer or in a folder of your network.

Key views

When you read images, you make observations that you want to highlight and also save in order to return to them later.

Key views help you to return to an observation 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.

Key views are marked with a yellow star in the lower-right corner of an image or thumbnail. All the other images in a series that contains a key view are marked with a gray star.

Note
Key views exist for the duration of the current session. To preserve key views, save them as a presentation state. See *Presentation states*, page 190.

Store Key View

Click **Store Key View** to save what is currently shown in the active viewer to a key view.

When you save a key view this way, the program also creates a screenshot and sends it to the **Export** window.

Delete Key View

Click **Delete Key View** to delete a key view.

This tool is available only if a key view is shown in the active viewer.

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

Previous Key View,
Next Key View

Click **Previous Key View or Next Key View** to browse through the key views in the loaded images.

Presentation states

To store annotations, measurements, and other image evaluation and postprocessing results permanently, you create a presentation state.

A DICOM presentation state stores how an image is displayed. Depending on the system configuration, creation of presentation states can be triggered automatically or by clicking one of the following tools. When you unload data from a **View** window and your results have not yet been saved in a presentation state, you are prompted to save them.

In the **Study Browser**, a presentation state appears as a new series with modality PR. When you load a study, it is displayed together with its most recent presentation state. Presentation state series are archived together with the study.

Save Result

1. Click **Save Result**.

2. Select **Save as DICOM data** at the bottom of the **Unsaved Data** dialog.

3. Click **Save**.
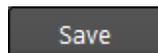
This saves any unsaved information such as annotations or measurements, or changes to the image representation in a presentation state.

Clicking this tool is a shortcut to saving the following aspects individually: **Save Current W/L as Presentation State**, **Save Flip/Rotate as Presentation State** and **Save Annotations as Presentation State**.

Save Current W/L as
Presentation State

Click **Save Current W/L as Presentation State** to save window level adjustments in a DICOM presentation state.

The next time you load this study, images will be displayed with the saved window levels.

Save Flip/Rotate as Presentation State

Click **Save Flip/Rotate as Presentation State** to save flips and rotations in a DICOM presentation state.

The next time you load this study, affected images will be displayed flipped or rotated.

Save Annotations as Presentation State

Click **Save Annotations as Presentation State** to save **all** annotations and measurements in the currently loaded dataset in a DICOM presentation state.

The next time you load this study, your annotations will be shown in the images.

Save Segmentations as Presentation State

Click **Save Segmentations as Presentation State** to save segmentation results in a DICOM presentation state.

The next time you load this study, segmentation results from a previous session will be available again.

See also *Edit tool card*, page 140.

Sessions

A session saves image evaluation and postprocessing results temporarily for a period of time. Session information is preserved for as long as the study is stored on the Visage 7 server. When a study is deleted from the database, session information might be lost depending on your system configuration. Session information is not archived together with the study.

Use cases

Typically, sessions are intended for the following use cases:

- You have to interrupt reading a case.

  When you resume reading later or on the next day, you want images to be presented in just the same way as you left them. If you have saved your session, you can continue with measurements and image evaluation exactly where you interrupted your work earlier.

  You might also use a session to store results to present them at a conference.

  See *Managing sessions*, page 192.

- You want to discuss a case with a colleague inside your Visage 7 network.

  See *Sharing cases*, page 194.

• Review of preliminary reading results

  Residents who are reading a case have their findings reviewed by an attending physician before they create the final report.

  See *Resident sessions*, page 194.

Session concept A session saves the following information and image processing results:

• All datasets that were loaded at the time the session was saved

• Protocol and display settings

• Key views and screenshots with or without annotations and measurements

• Segmentation results, such as 3D ROIs or vessel segmentation results

• Structures and contours

• Cardiac analysis results

Managing sessions

This section explains how to save a session and how to retrieve session information.

Saving a session You can save more than one session for a single study if you want to document stages or discuss different aspects.

1. Select **File > Save Session**.

   -Or-

   Select **File > Save Session As**.

2. In the **Save Session** dialog, enter a session name.
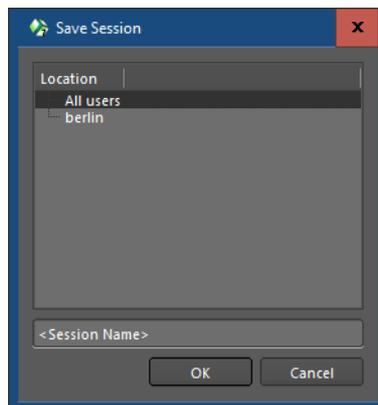
3. Also select who will be able to see and load this session: only your own user account or all users.

AutoLogoff session After an extended period of no user interaction, the system logs you off automatically. Unsaved data is stored in an **AutoLogoff** session.

The **AutoLogoff** session appears in the session list of the **Study Browser**.

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

Loading a session

If no study is selected in the study list, all your recent sessions are shown in the lower-right corner of the **Study Browser**.

If a study is selected in the study list, the session list displays only sessions of this particular study.

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.

Starting a new session from the Study Browser

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

1. In the study list, select the study.

2. Double-click **<New Session>** in the session list.

The system loads the original data as they were sent from the modality and ignores any intermediate evaluation results even if you have saved them in a session.

New Session in a View window

In a **View** window, click **New Session** to start a new session.

New Session removes annotations, measurements, or any changes to the display of images that you have made since you opened the study.

New Session also reapplies the protocol that was selected automatically when the images were initially loaded.

New Session does not load new or additional images. Use **Update Session** to add new images that have been acquired since you loaded the data. See also *Additional images*, page 73.

Sharing cases

When you save a session, you specify whether this session will be available to all users or only to your own user account. See also *Saving a session*, page 192.

Sessions that you made available to other users or all users are marked with the word **(shared)** in the session list of the **Study Browser**.

Sending a session link   You can send session links of shared sessions to colleagues.

1. Double-click a session in the session list.

2. Select **File > Copy Session Link**.

3. Open your email program and send the session link in an email.

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

Sending a study link   If you did not share a session or if you are not working with sessions, you can copy and send study links instead of session links. A study link will help the recipient of the email to find and open a study quickly. However, a study link will not communicate session-specific information.

1. Double-click the study in the study list.

2. Select **File > Copy Study Link**.

3. Open your email program and send the study link in an email.

> **Tip**
>
> If you want to discuss a case with a colleague outside your Visage 7 network, use **Live Connect**. See *Sharing the Visage 7 client screen*, page 179.

Resident sessions

Resident sessions are intended for a specific use case in which a resident reads a case and creates a preliminary report. Residents store these findings in a specific session type, namely a resident session.

Later, an attending physician will review these findings together with the resident. When they have reached a conclusion, they will save findings permanently as a DICOM presentation state and complete the report.

Resident sessions store annotations and measurements but not the complete set of session information that is stored when you select **Save Session**.

Saving a resident ses-
sion

1. As a resident, click **Save Result** when you have completed your preliminary reading session.

    -Or-

    Click **Close Session**.

    The **Unsaved Data** dialog opens.

2. Select **Save as resident session**.

3. Click **Save**.
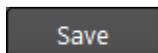
    In the **Study Browser**, the session is listed as **(shared) Resident Session**.

Opening a resident ses-
sion

1. As an attending physician who wants to review results, select the study in the study list.

2. Double-click the shared resident session in the session list.
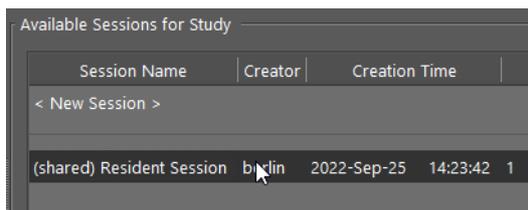
Saving findings perma-
nently

1. As an attending physician who has completed reviewing the findings of a resident session, click **Save Result.**

    -Or-

    Click **Close Session**.

    The **Unsaved Data** dialog opens, regardless of whether you have added or modified annotations, measurements, or other image evaluation results.

2. In this dialog, select **Save as DICOM data**.

3. Click **Save**.
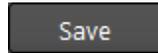
Save

This saves annotations, measurements, or other image processing results in a presentation state. A new series with modality PR is created for this study.

The resident session is now listed as **(shared) Obsolete Resident Session** in the **Study Browser** session list.

Printing images

You can print images on a DICOM printer or on a Windows printer, or save one or several images as a pdf file.

1. Right-click a viewer and select **Print**.

-Or-

Use the keyboard shortcut **Ctrl/Cmd + P**.

2. In the upper part of the **Print** dialog, select **DICOM printers** and one of the DICOM printers connected to your Visage 7 server.

-Or-

Select **Other Destinations** and select a Windows printer or **Save as PDF**.

3. Also select the number of copies.

4. Under **Images**, select which image or images you will print.

Active Image prints the image in the active viewer. Image orientation, zoom, and window settings in the printout are the same as in the active viewer. If viewer texts, annotations, or measurements are currently shown in the image, these are printed as well if you choose a Windows printer or **Save as PDF**. On a DICOM printer, annotations and measurements cannot be printed.

Active Image Set prints all images of the image set currently shown in the active viewer. All images are printed in their original orientation and together with any viewer texts, annotations, or measurements that are currently displayed on the screen if you choose a Windows printer or **Save as PDF**. On a DICOM printer, annotations and measurements cannot be printed.

Visible Images prints 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 select **Print**. This option is available only if all viewers show original images.

Visible Image Sets prints 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.

5. Under **Layout**, 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.

6. 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 for **Active Image** and **Visible Images** only.

   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 is displayed. **True Size** is available for DICOM printers only.

7. In the **Media Properties** section of the dialog, select medium type, size, orientation, and color mode. Which options are available in this section depends on the selected printer.

8. Click **Print** to start the printout.

   -Or-

   Click **Save** to create a pdf file.

Reporting

Depending on the overall organization of reporting in your hospital, you will proceed in a different manner. This section gives an overview of reporting options in the Visage 7 client.

Viewing reports

If a DICOM structured report, RIS report, or PACS or HL7 report exists for the study that you have loaded into a **View** window, you can use one of the following tools to display this report.

View Structured Reports

Click 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)

Click this tool to show reports that exist in the RIS for the currently loaded studies.

The reports are shown in a separate report window. In the report window, you can view and print reports.

The tool icon also indicates the report status (unsigned report, signed report, report for prior study only, no report at all).

View Reports (PACS)

Click this tool to view PACS reports or HL7 reports for the currently loaded studies.

-Or-

Use the keyboard shortcut that is assigned to the **View Reports (PACS)** tool to open or close the report window.

Depending on the configuration, this tool opens the **Export** window or a separate report window and displays the reports there.

The tool icon also indicates the report status.

Basic reporting

In this mode of working, you use the Visage 7 client **Export** window to summarize your findings on a study and save the result on your computer or in your network. However, the final report for the case is created on 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.
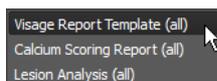
2. Use the **Insert Placeholders** command on the **Edit** menu to add more study data to the header or to the report text.

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.

5. Drag screenshots into the report where you want to show them.

Saving a report as Word or pdf file

Click **Export Word** or **Export PDF** to save your report as a Word file or as a pdf file on your local computer or in the network.

> **Note**
>
> **Export Word** is only available on Windows PCs and only if Microsoft Word is installed on your client PC.

Saving a DICOM or RIS report

1. Create screenshots of your report pages.

    📷

    Creation of a screenshot of your report requires that a printer is installed at your client PC.

2. Select all report pages in the **Screenshots** section.

3. Send these report pages as a screenshot series to the Visage 7 database or to a connected DICOM network node.

    ➡️ Save/Send

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**
>
> Use the **Start or Edit Report** tool from a **View** window to open the **Export** window and start reporting with only one mouse click.
>
>   📝

Creating a report

A standard report template is already selected in the **Export** window and basic patient data and study information have been entered in the report header.

1. If necessary, select a different report template.

    Visage Report Template (all)
    Calcium Scoring Report (all)
    Lesion Analysis (all)
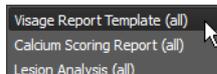
2. Click **Start Reporting** above the report template.
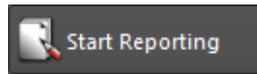
3. Fill out the report template.

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 screenshots into the report where you want to show them.

4. Save the report.
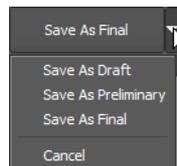
Editing a report

You can edit a draft or preliminary report that 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 the **Study Browser** and move on to the **Export** window, the most recent version of the report is shown here.

1. Click **Edit Report**.
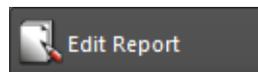
If you try to edit or create a report that another user has worked on since you loaded the study, a message will ask you to update the report first.

Click **Options > Refresh** near the right edge of the **Export** window.
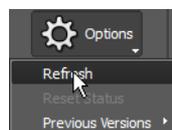
Click **Edit Report** again.

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.

Select **Options > Previous Versions** and an earlier version of this report.
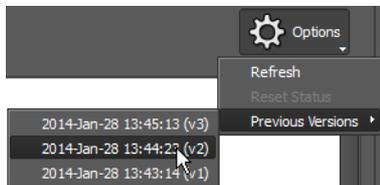
The Visage 7 client opens this earlier version of the report on a separate tab. You can read but not edit or sign off this report version.

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**.
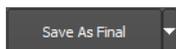
A report with report status final can no longer be edited.

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 is necessary if you need to add findings to a report that has already been signed off.

Select **Options > Reset Status**.

The report status is reset to preliminary. You can now open it (**Edit Report**) and add any new findings, comments, or images and then save the report 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. In the **Export** window, select a template or a report.

2. Select **Edit > Edit Template**.

3. Add all the required placeholders and standard texts.

4. Format placeholders and standard texts.

5. Click **Save** next to the template selection list.

6. In the **Save** dialog, enter a template name.

7. Decide whether you want to make this template available to all users or to your own user account only.

8. Click **OK**.

Video reports

The **View** window offers a tool card for creating short video reports in addition to standard radiology reports. Video reports are short recordings (approximately 30-60 seconds) in which a radiologist explains findings while showing the relevant images.

Video reports are intended to be presented to patients because they are easier to understand than standard radiology reports. Video reports can also serve as internal reports or memos.

Creating a video report

1. In a **View** window, display the images in which you want to explain your findings.

2. On the menu, select **Tools > Video Report** to open this tool card.

   -Or-

   Click **Show/Hide Video Reports Tool Card**.

3. Check that the correct microphone has been selected.
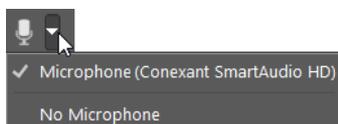
   -Or-

   Select a macro.
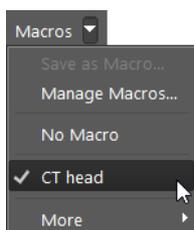
   See also *Recording and managing macros*, page 205.

> **Note**
>
> You can either use a macro or record explanatory text with the microphone, you cannot combine both methods in a single video report.
>
> A macro not only provides the audio track but typically also predefines the duration of the recording. You can interrupt the video report before the audio track has been played back entirely. However, if you use a macro, you cannot create a video report that is longer than the prerecorded audio track.

4. Select what you want to show in the video: the active viewer, all viewers on the active monitor, or all viewers on all monitors.

5. Click the **Record/Pause** button to start recording.

6. Point to your findings in the images and explain what can be seen.

7. Click the **Record/Pause** button to pause or finish recording.

Previewing a video report

1. Click **Play/Pause** again to check your report before you save it.

2. Use these buttons or the slider to fast forward or rewind the video.

Resuming a recording

As long as you have not yet saved a video report, you can modify it. You can add to the report, correct it from a certain point onward, or discard what you have recorded so far and start again.

Play the video back to the point from where you want to continue.

If the slider is at the end of what you have recorded so far, you will add to the report. If the slider is somewhere in the middle of the recording, you will correct your recording from this point onward.

Click **Record/Pause** again to resume recording.

-Or-

Click **Reset** and then **Record/Pause** to discard all that you have recorded so far and to start again from the beginning.

Saving a video report

1. Click **Send**.
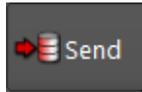
2. Select a location for saving your video report.

   Select **Save Locally** to create a video file (typically an mp4 file) on your local computer.

   Select **PACS** or **Patient Report** to save the video as a new series on the Visage 7 server. **PACS** marks the video for internal use. **Patient Report** marks the video as intended for the patient portal if your hospital provides such a service.

3. If you have loaded current and prior studies, also select the study to which the video report series will be assigned.

   The system suggests the current study.

   Sending the video report also closes the report.

Recording and managing macros

Macros are audio recordings with explanatory text, which you frequently use in your video reports. When you record a video report, you combine this prerecorded text with patient-specific images. The macros that you create are available to your own user account only.

1. Create a video report.

   Creating a video report, page 203.

2. Select **Macro > Save as Macro**.

3. Enter a macro name.

4. Define the modality for which this macro will be available.

   To define a combination of modalities, separate modality abbreviations with a space, for example, `CT PT`.

5. Specify the part of the body that this macro refers to.

   A macro is available for studies of the modality or combination of modalities plus the part of the body specified here. Leave the **Body Part** box empty if you want to make this macro available to all studies of a certain modality irrespective of the part of the body examined.

6. Click **OK**.

7. Select **Macro > Manage Macros** to edit or delete a macro.

Importing and exporting studies

Visage 7 can import and export study information in various formats.

Importing and exporting studies (DICOM format)

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

Importing a study from CD, DVD, or USB drive

1. Insert a patient CD, DVD, or connect a USB drive.

   If Visage 7 finds DICOM data (DICOMDIR file) in the root directory of this medium, the **DICOM data detected** dialog opens.

2. Click **Import.**

   In the study list of the **Study Browser**, a new tab appears.

3. On this new tab, select the study or studies that you want to import.

4. Click **Import**.

   The **Import DICOM Data** dialog opens. In this dialog, 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 ID is a prerequisite for Visage 7 to identify the imported study as a prior study of a patient who already exists in the Visage 7 database.

5. From the **Import Presets** list, select **Create new UIDs** and modify the **Patient ID**, for example.

   Other import presets might also be available in your Visage 7 client. These presets were configured to meet the requirements for patient data import in your particular institution.

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

7. If you have selected the import preset **De-identify**, also select **Remove private tags** and **Remove other demographic tags**, if relevant.

8. If your Visage 7 is connected to a RIS (radiology information system), select a RIS order in the lower part of the dialog.

   If you skip this step now, you can assign the imported study to a RIS order later. Use **Assign to Order** on the context menu of the study list.

9. Click **Import Data**.

   Import Data

   Tip

   If DICOM data is not stored directly in the root directory of the CD, DVD, or USB drive, Visage 7 cannot detect these data automatically. In this case, select **File > Import DICOM Directory** from the menu. Open the folder that contains the DICOMDIR file and click **Select Folder**.

Exporting studies

You can export studies either from the **Study Browser** or from a **View** or **Export** window. In the **Study Browser**, you explicitly select studies from the study list of your Visage 7 server (primary server). You cannot export data from partner systems or connected DICOM nodes. To export studies from a **View** window, you load the relevant studies first. All the loaded studies will be exported. You cannot exclude loaded studies from data export. Data export from the **Export** window considers the study or studies loaded in the active **View** window (green bullet).

1. In the **Study Browser**, select the study or studies that you want to export, right-click and select **Media Export**.

   -Or-

   In a **View** window or the **Export** window, select **File > Media Export**.

2. Select a **Destination**.

   Select **Export files to local client folder** to download data onto your local computer or onto a USB drive at your local computer. Also select the drive and folder to where you want to export the data.

   Select **Burn Patient CD/DVD** to create a CD or DVD on a CD/DVD writer at your local computer.

   Select **Export files on server** to export data to a predefined folder on the Visage 7 server. From there, the data can be picked up by a CD/DVD producer station, for example.

   Select **CD Producer Station** 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. This option is only available if a CD producer station is connected to the Visage 7 server.

   If CD producer stations have been configured as DICOM nodes, one or more additional CD producer stations in your hospital might be available here.

   Select **Send to** and a DICOM node that has been configured to receive studies from Visage 7.

3. Select export options.

    Select **Include Media Viewer** to allow the recipient of the CD, DVD, or USB drive to view the study data directly from this medium. No other software is required. Also select **Autorun Media Viewer** if you want Media Viewer to be started automatically when the CD or DVD is inserted into the CD/DVD drive or when a USB drive is connected to a computer.

    Select **Uncompressed only** to export data according to the IHE standard.

    Select **De-Identify** to export an anonymized copy of the selected data.

4. Click **Export**.
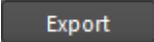
    Export

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.

Retrieving a study from a DICOM node

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

1. Select the tab of a connected DICOM node.

2. Define search criteria in the query section and click **Query**.

    Query

3. In the study list, select the study that you want to retrieve.

4. Click **Retrieve**.

5. Return to the leftmost tab. This is the tab 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 tabs 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.

Sending data from the primary server

1. In the study list of the Visage 7 server, right-click the study that you want to send.
2. 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.

Sending data from a partner system

1. On the partner system, right-click the study list and select **Switch over to [system]**.
2. Select the leftmost tab.
3. Right-click the study and select **DICOM Send** or **DICOM Quick Send**.

Configuring DICOM Quick Send

1. In the study list of the primary server, right-click a study and select **DICOM Send**.
2. In the **DICOM Send** dialog, select the **DICOM Quick Send** tab.
3. Select the server or servers to which you want to send data with the **DICOM Quick Send** function from now on.
4. Either click **Send** to send the selected study now.

   -Or-

   Click **Cancel** to close the dialog.

The next time you select **DICOM Quick Send** from the context menu, studies will be sent to this destination or these destinations.

Importing studies (non-DICOM format)

You use these functions when you receive study data in a non-DICOM format (for example, jpg, pdf, or as a paper printout).

You can import new studies either from the **Study Browser** or from a **View** window. To import studies from a **View** window, you use the **Import From Non-DICOM Files** and **Import from Document Scan** tools, which you can add to your tool palette.

Importing a study from a file

1. On the menu of the **Study Browser**, select **File > Import New Study > From Non-DICOM Files**.

-Or-

From a **View** window, click **Import From Non-DICOM Files**.

2. On the **Select Patient** page of the **Import New Study** dialog, select the patient or order to which you want to attach the study.

-Or-

Select **<New Patient>** from the patient list and specify at least patient ID, patient name (family name and given name), date of birth, and sex in the **Patient Details** section of the dialog.

3. Enter a **Study Description** and the **Study Date**.

By default, the system suggests the date when you import the study (today's date) as the **Study Date**. Overwrite this information if you know the date when the study was performed.

4. Click **Next**.

5. On the **Select Files** page, click **Browse** and select one or several files in your file system.

6. Modify series information, if necessary.

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

8. Click **Import**.

Scanning a study

1. On the menu of the **Study Browser**, select **File > Import New Study > From Document Scan**.

   -Or-

   From a **View** window, click **Import from Document Scan**.

2. On the **Select Patient** page of the **Import New Study** dialog, select the patient or order to which you want to attach the study.

   -Or-

   Select **<New Patient>** from the patient list and specify at least patient ID, patient name (family name and given name), date of birth, and sex in the **Patient Details** section of the dialog.

3. Enter a **Study Description** and the **Study Date**.

   By default, the system suggests the date when you import the study (today's date) as the **Study Date**. Overwrite this information if you know the date when the study was performed.

4. Click **Next**.

5. On the **Scan Documents** page, select your scanner and scan settings.

   Note that the highest resolution that you can select here might be lower than the maximum resolution of your scanner.

6. Click **Scan** to scan one or several pages.

7. Use these buttons to review the scanned pages.

8. Click **Rotate** to correct the orientation of a scanned page.
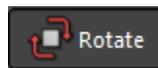
9. Click **Delete** if a page was scanned with bad image quality and you need to scan it again.
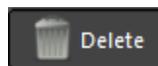
10. Modify series information, if necessary.

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

12. Click **Import**.

Attaching documents to studies

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

Attachments are appended to a study as a separate series. The suggested series number ensures that the attached series will be added to the end of the study.

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

Attaching files to studies

Only pdf files, image files, and MP4 videos can be imported from the file system and attached to a study.

1. In the study list of the **Study Browser**, right-click a study and select **Add Attachment**.

   -Or-

   In a **View** window, select **Add Attachment** from the **File** menu.

2. In the **Import Series** dialog, click **Browse** and select one or several files in your file system.

   -Or-

   Simply drag files from the **File Explorer** into this dialog.

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 only affect attachments and not the study as such.

5. Click **Import**.

Scanning attachments

1. In the study list of the **Study Browser** or in the **Worklist**, right-click a study and select **Add Document Scan**.

2. In the **Import Series** dialog, select your scanner and scan settings.

   Note that the highest resolution that you can select here might be lower than the maximum resolution of your scanner.

3. Click **Scan** to scan one or several pages.

4. Use these buttons to review the scanned pages.

5. Click **Rotate** to correct the orientation of a scanned page.
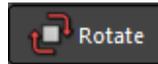
6. Click **Delete** if a page was scanned with bad image quality and you need to scan it again.
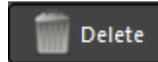
7. Modify series information, if necessary.

8. 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 only affect attachments and not the study as such.

9. Click **Import**.

Marking and presenting studies

Visage 7 provides functions for marking and commenting on studies for various purposes and for presenting images without disclosing protected health information (PHI).

Planning a conference

You use conference labels to mark cases for discussion in a conference or meeting on a specific day and at a specific time. Visage 7 features a calendar for planning conferences and for assigning studies to them.

Assigning a conference label

1. In the **Study Browser** or **Worklist**, right-click a study and select **Conference Labels**.

   -Or-

   In a **View** window, click **Schedule for Conference**.

   The **Conference Labels** tab in the **Labels** dialog shows a calendar with recurring conferences and scheduled one-time meetings. If the selected study has already been assigned to a conference in the week that is currently shown, this conference has a check mark.
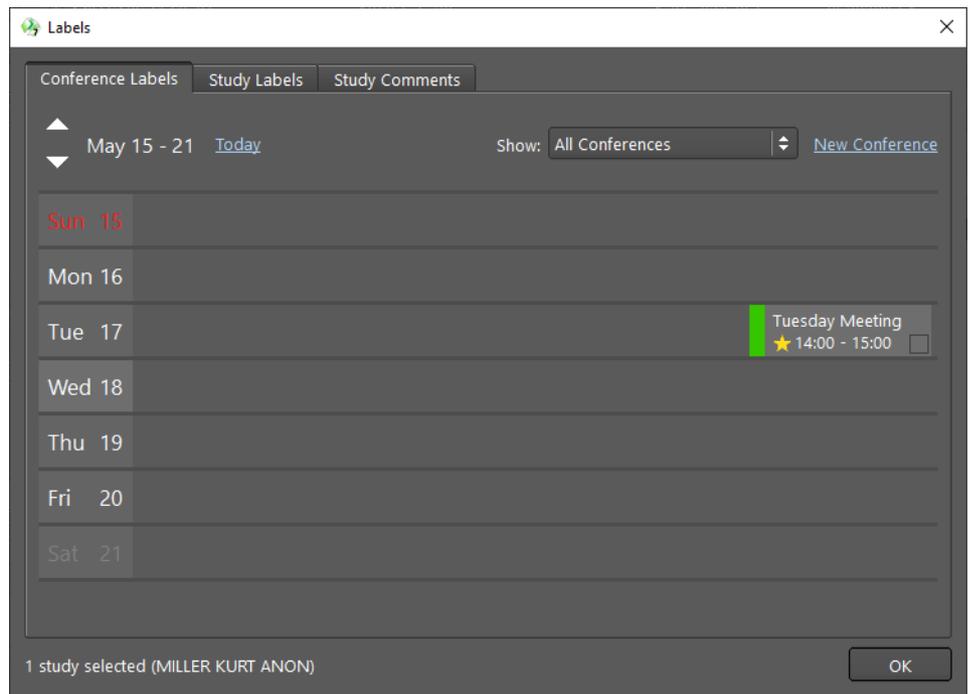
2. To assign the study to a conference, first select the week.

3. Select the conference at which you want to discuss this case.
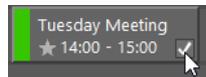
4. If necessary, also assign a study label and add a study comment.

See *Assigning a public or private label*, page 217 and *Creating a study comment*, page 220.

Scheduling a conference

You also use the **Conference Labels** tab of the **Labels** dialog to plan conferences or recurring meetings regardless of whether you will assign cases to them immediately.

1. In the **Study Browser** or **Worklist**, right-click any study and select **Conference Labels**.

-Or-

In a **View** window, click **Schedule for Conference**.

2. Click **New Conference**.

New Conference

3. In the **New Conference** dialog, specify a subject or the name of the conference.

4. Select the date, time, and duration.

5. Select a specific color to highlight this conference.

6. Define a recurrence pattern, if required.

7. Specify who will be allowed to take part in this conference under **Permissions**.

Public will allow all Visage 7 users to assign studies to this conference and to view the studies assigned to this conference.

Private allows you to restrict access to this conference and its studies to individual users or user groups.

8. Click **OK**.

You and the users whom you granted permission to take part in this conference can now start assigning studies to it.

The new conference is marked as one of your favorite conferences.

9. Click the yellow star if you want to remove this conference from your list of favorite conferences.

Assigning and managing 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 label.

  Teaching 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 labels. However, a public label with the name `class1` or `course2-teaching` would not be identified as a teaching label but as a public label for other purposes.

  See *Creating anonymized teaching files*, page 226.

- Public labels for other purposes

  You use a label of this type, for example, to mark studies that you want to discuss with a colleague.

- Private labels

  Private labels are only visible for your own user account or for user accounts with which you have shared them. You use labels of this type, for example, to collect cases for research purposes or simply to find a study again quickly.

Assigning a public or private label

1. In a **View** window, click a predefined study label button on the **Labels** toolbar to assign this label immediately.
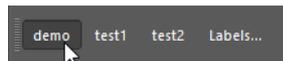
   -Or

   In the **Study Browser** or **Worklist**, right-click a study and select **Study Labels**.

   -Or-

   In a **View** window, click **Assign and Manage Labels** on the **Labels** toolbar or tool palette to open the **Labels** dialog.

   On the **Study Labels** tab of the **Labels** dialog, you will find a list of all public labels, your own private labels, as well as private labels that other users shared with you.
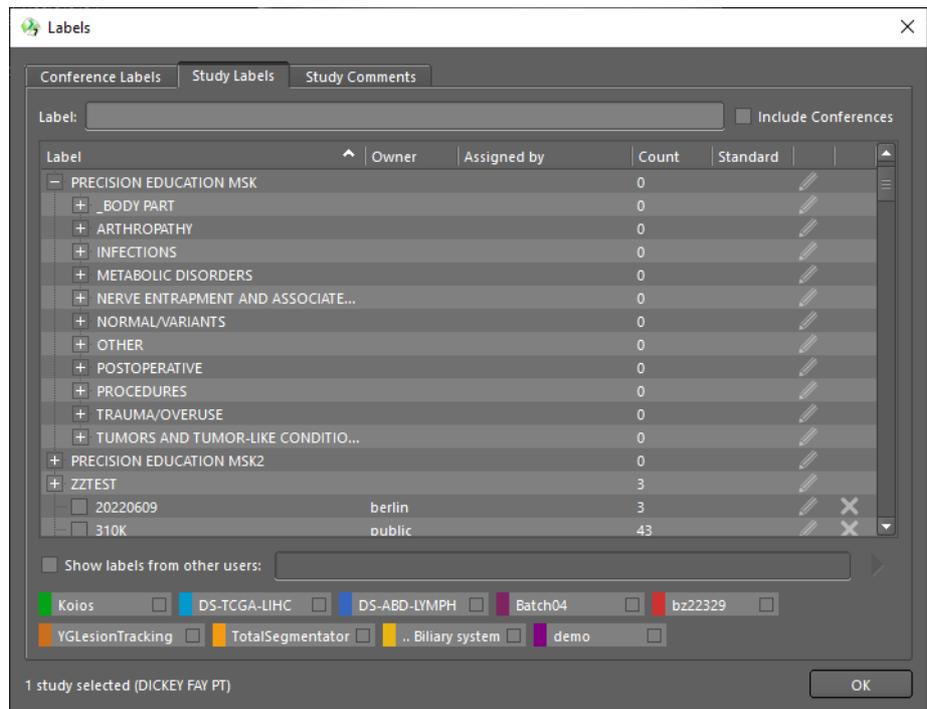
2. Select **Include Conferences** to show conference labels as well.

3. Select the checkboxes of one or several labels.

4. Click **OK**.

Creating a new study label

1. In the **Study Browser** or **Worklist**, right-click a study and select **Study Labels**.
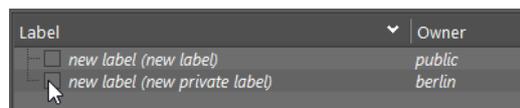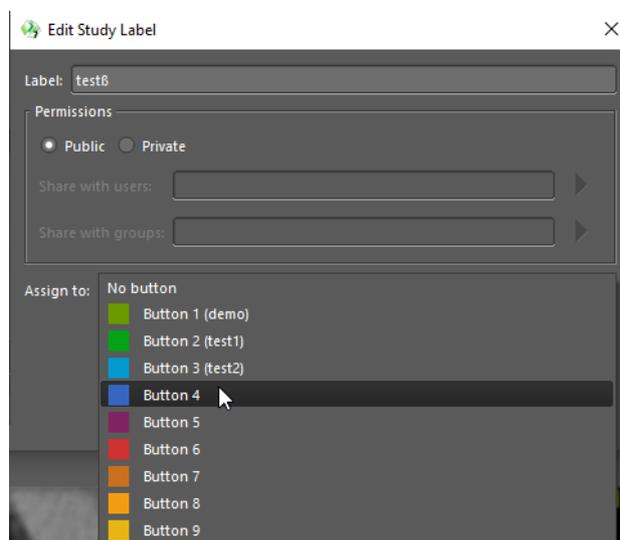
   -Or-

   In a **View** window, click **Assign and Manage Labels** on the **Labels** toolbar or tool palette.

2. On the **Study Labels** tab of the **Labels** dialog, type the new label name.

   Visage 7 now offers two versions of the new label, *new label* and *new private label*. Select the checkbox in front of the public or private version.

   Visage 7 creates the new label and assigns the selected study to it.

3. To share a private label, click **Edit Label** next to the label.

4. In the **Edit Study Label** dialog, click the arrow button next to the **Share with users** or **Share with groups** box.

5. Select users or user groups from these lists.

Creating a label button

For quick and easy assignment of labels, you can create label buttons on the **Labels** toolbar and on the **Study Labels** tab of the **Labels** dialog.

1. In the **Study Browser** or **Worklist**, right-click a study and select **Study Labels**.

-Or-

In a **View** window, click **Assign and Manage Labels** on the **Labels** toolbar or tool palette.

2. On the **Study Labels** tab of the **Labels** dialog, click **Edit Label** next to a label.

3. In the **Edit Study Label** dialog, assign the label to a button placeholder.

4. The next time you want to assign this label, click the button on the **Labels** toolbar or in the **Labels** dialog.

Deleting a study label

1. In the **Study Browser** or **Worklist**, right-click a study and select **Study Labels**.

-Or-

In a **View** window, click **Assign and Manage Labels** on the **Labels** toolbar or tool palette.

2. On the **Study Labels** tab of the **Labels** dialog, click the **Delete Label** button next to a label.

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

Commenting on studies

You can add one or several comments on a study either while you are reading the images or from the **Study Browser** or **Worklist**.

In the **Study Browser** or **Worklist**, comments on a study can be shown in the list.

Patient	Date of Birth	Study Comments	Patient ID	Accession Number	Study UID	Modali
⊞ ABUS_3D			ABUS_3D_2022...	ABUS_3D_1234	1.2.276.0.7230010.3.1.4.3823309873.2348.1529...	OT PR
⊞ MILLER ANON KURT	1949-Jan-01	Demo data created by MCS. Patien...	PMCS0006	43.135_1	9.9.840.113704.1.111.7176.1138457491.1	CT PR
⊞ ADAMS ELIZABETH	1942-Okt-24		4989481		1.3.12.2.1107.5.1.4.48658.30000009081322375...	CT PT
⊞ AUTOTEST-SCHAAF ELLEN ANON	1998-Jan-01		AT_43.00000239	AT_43.403_1	1.2.276.0.45.1.7.2.159493823762.16022314413...	CR
⊞ BUTLER ANON MARSHA		Demo data created by VI. Patient i...	43.00000221	43.00000214	9.9.840.113619.2.234.60341928380.14749.1208...	CT
⊞ SingleAndMultiframes	1943-Jan-01		298b0209	01451020	1.2.276.0.45.1.2.7.2.964244282638.2012101913...	US
⊞ 1zzm1			1zzm1		1.2.826.0.1.3417726.3.145744.20060519114833...	CT

Creating a study comment

1. In the **Study Browser** or **Worklist**, right-click a study and select **Study Comments**.
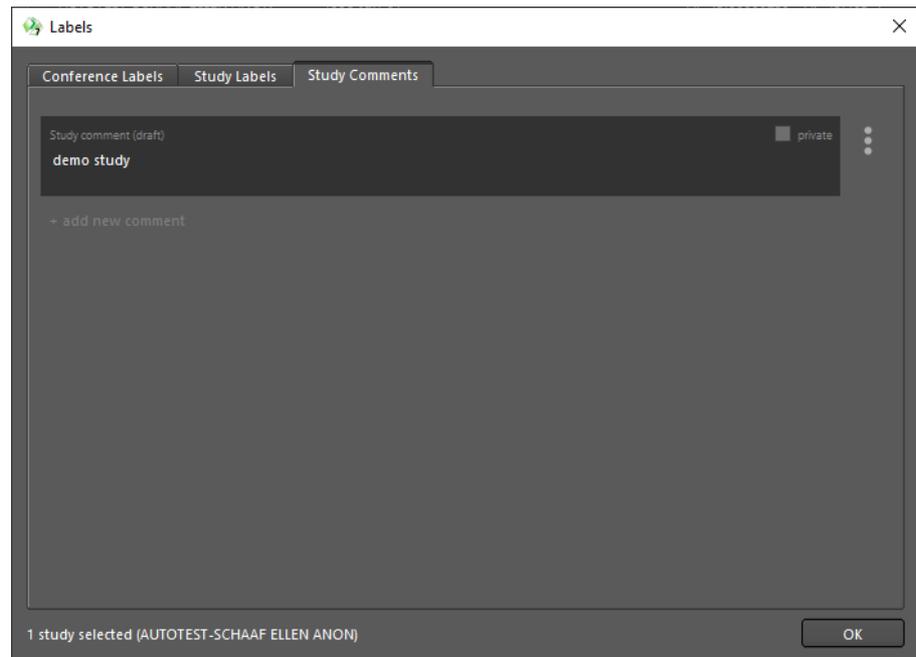
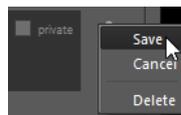-Or-

In a **View** window, click **Study Comments**.

The **Study Comments** tab of the **Labels** dialog opens.
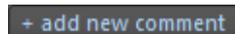
2. Type your comment.

3. Select **private** in the upper-right corner of the comment box if this comment should be visible for your user account only.

4. To add a second comment, click the three dots to the right of your first comment and select **Save**.

5. Click **add new comment**.

6. Type your second comment.

Deleting a study comment

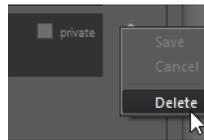1. In the **Study Browser** or **Worklist**, right-click a study and select **Study Comments**.

   -Or-

   In a **View** window, click **Study Comments**.

2. On the **Study Comments** tab of the **Labels** dialog, click the three dots to the right of the comment that you want to delete.

3. Select **Delete**.

Finding studies with labels or comments

In the **Study Browser**, in the **Worklist**, and in the **Quality Assurance** window, you can search for studies with specific labels or comments.

Quick search for studies with labels or comments

In the **Study Browser** and **Worklist**, the **Search Conferences and Labels** button offers a particularly quick and convenient way to find studies with a specific label or comment.

Finding studies that are assigned to a conference

1. Click **Search Conferences and Labels.**
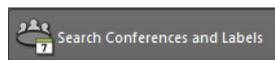
2. On the **Conference Labels** tab of the **Labels** dialog, scroll to the week of the conference or click **Today**.

3. If a very large number of conferences have been scheduled for a particular week, show only those conferences that you marked as being relevant to you.
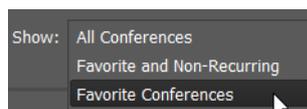
Your favorite conferences are marked with a yellow star.
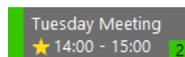
The number in the lower-right corner of a conference tells you how many studies are assigned to this conference.

4. Click a conference.

The study list now shows all studies that are assigned to this conference.

Finding studies that are marked with a study label

On the **Study Labels** tab of the **Labels** dialog, click a label button, or click a study label in the list.
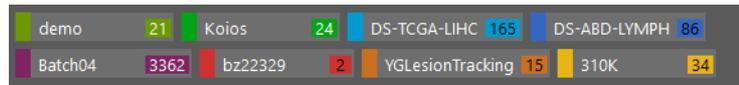
The number on a label button tells you how many studies are assigned to this label.

The study list now shows all studies that are assigned to this study label.

Finding studies by study comment

1. On the **Study Comments** tab of the **Labels** dialog, type the comment or part of the comment text that you are looking for.

   -Or-

   Use the pipe character (|) to search for more than one comment.

   For example, `comment|test` searches for studies that have a study comment that contains the words *comment* or *test*.

2. If you want to search for your own comments or for comments made by specific users only, select the **Created by** box.

   Then select either **me** or **user** and specify the user whose comment you are looking for. Use the pipe character (|) to search for more than one user.

   For example, `user1|user2` searches for studies that were commented on either by *user1* or by *user2*.

3. If you want to search for comments that were created at a specific time, select **Creation date** and specify a time range.
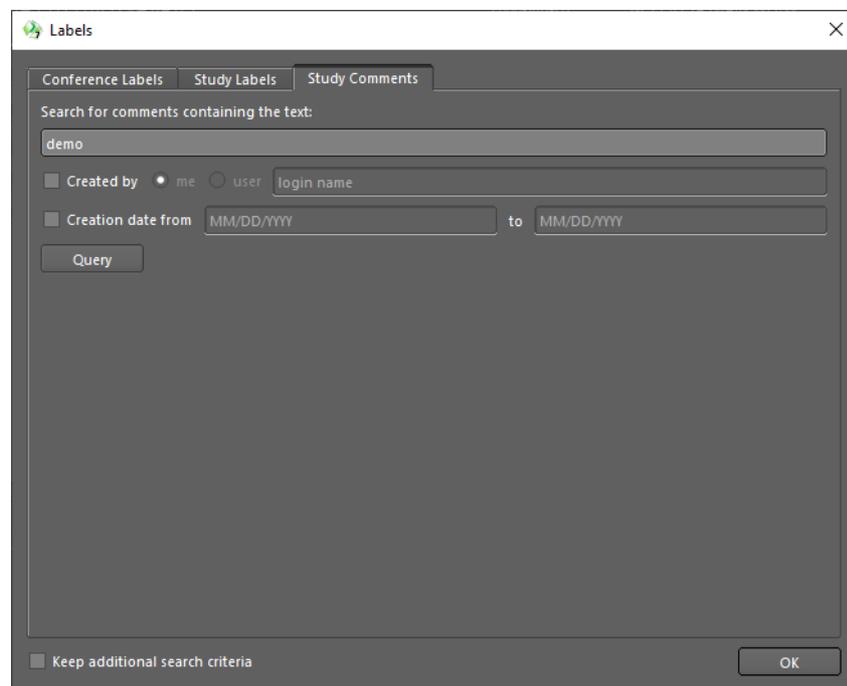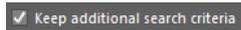

4. Click **Query**.

The study list now shows all studies that have a study comment that contains this text string.

Combined search in Labels dialog

You can combine search criteria from all three tabs of the **Labels** dialog.

For example, you can search for studies with a specific study label that also have a specific study comment.

1. On the **Study Labels** tab of the **Labels** dialog, select a label.

2. Select **Keep additional search criteria**.

   ☑ Keep additional search criteria

3. Move on to the **Study Comments** tab and type the comment or part of the comment text that you are looking for.

4. Click **Query**.

Combined search with query section and Labels dialog

You can also combine search criteria in the query section of the **Study Browser** or **Worklist** with a label or comment search.

For example, you can search for last week's CT studies with a specific study comment.
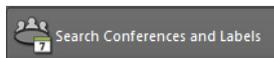
1. In the query section of the **Study Browser** or **Worklist**, define filter and search criteria.

   See *Finding studies*, page 17, *Finding orders*, page 30.

2. Click **Query**.

   Query

3. Click **Search Conferences and Labels**.
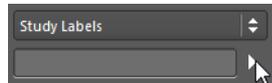
   Search Conferences and Labels

4. In the **Labels** dialog, select **Keep additional search criteria**.

5. On the **Study Comments** tab, type the comment or part of the comment text that you are looking for.

6. Click **Query**.

## Study labels in the query section

You can use **Study Labels** in the query section to search for studies with conference or study labels or with comments. This box is also available in the **Quality Assurance** window.

Searching for conference or study labels

1. Under **Fields**, select **Study Labels**.

2. Click the arrow next to the input box.

The **Study Labels** dialog lists study labels and conference labels. You can recognize a conference label by the date in square brackets.
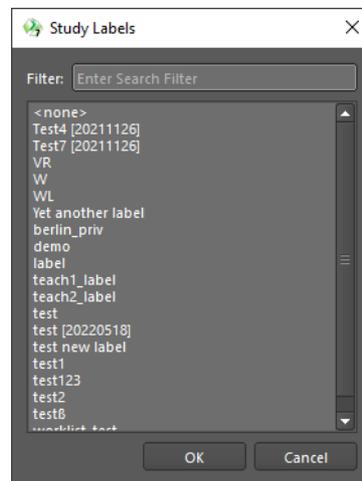
3. Select one or several labels.

Combined search for study labels

Type the label or labels that you are looking for in the **Study Labels** box.

`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.

If you are searching for labels that contain spaces, use quotation marks: `"Label A" "Label B"` - this string searches for all studies with either Label A or Label B.

Also remember that you can use wildcard characters in your search.

Searching for study comments

To use the **Study Labels** box to search by study comment, observe the following syntax:

`"type:comment demo"` - this string searches for all studies with a study comment that contains the word *demo*.

Anonymizing cases and anonymized display of data

Visage 7 provides mechanisms for anonymizing data and for anonymized display of data.

## Creating anonymized teaching files

De-identification or anonymization of a case means removing any information that would identify the patient from a copy of a case permanently.

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

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

In the **De-identification and Teaching Files** dialog, the **Create De-identified Copy** checkbox is selected. Do not clear this box.

Moreover, the system has replaced patient and study data with random codes.
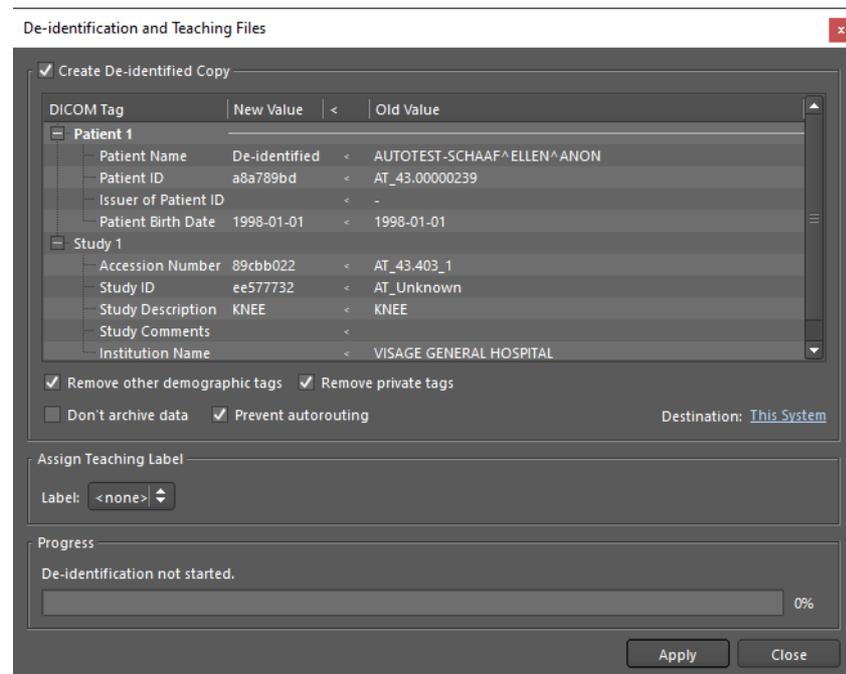
2. Double-click an item in the **New Value** column and change this random data if you want.

3. Select the following options for anonymization:

Remove other demographic tags and **Remove private tags**: Aside from the data shown in this dialog, 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.

Destination: Here you can choose to send the de-identified copy of the study to a connected DICOM node.

4. Select a teaching label for the anonymized copy.

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

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.

Anonymizing cases for other purposes

If you want to create an anonymized copy of a study 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 Browser**, right-click a study and select **De-identification and Teaching Files**.

2. Proceed as described in *Creating anonymized teaching files*, page 226. However, do not assign a teaching label.

Marking the anonymized case with a private label

1. In the **Study Browser**, search for the anonymized case.

2. Right-click the anonymized case and select **Study Label**.

3. Assign a public or private label.

See *Assigning a public or private label*, page 217.

Anonymized data export

Some modalities, such as ultrasound, have patient and study information burnt into the images. Visage 7 offers a tool for anonymizing and exporting such images and video clips to the local computer.

Export Image or Clip is available for 2D images, multiframe images, or MPR images in standard orientations. When you use this tool for modalities that show patient and study information as viewer texts, hide these viewer texts before you start data export.

See *Showing or hiding viewer text*, page 57.

Export Image or Clip is not available for oblique MPR reformats or in curved view, lumen view, or in 3D viewers.

1. In a viewer that shows a suitable image, select **Export Image or Clip**.

2. For individual images, select the **Image Target**.

   File saves the image to the file system on your local computer. Also specify the target folder on your computer and modify the suggested file name, if necessary. Video clips can be saved to file only.

   Clipboard sends the image to the clipboard from where you can paste it into a document.

   Export tab creates a screenshot in the Visage 7 **Export** window.

3. Select **Mask Patient Header** to anonymize the image.

   Mask Patient Header works only for image types where patient and study information is burnt into the image.

Privacy mode

In privacy mode, any information that would identify a case is temporarily hidden. You can use this mode for presentation purposes, for example.

You can switch to privacy mode either from the **Study Browser** or from a **View** window.

Select **File > Privacy Mode > Study Browser and View Screen.**

-Or-

Select **File > Privacy Mode > View Screen Only**.

Privacy mode will remain active until you end it again (**File > Privacy Mode > Off**).

Quality assurance

Visage 7 provides tools and a platform for performing quality assurance.

Quality assurance on images

Sometimes it might be necessary to correct images so that these corrections apply even if the images are viewed with viewer software other than Visage 7.

Such corrections include the following:

- 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.

On other occasions, it might be necessary to delete images with poor image quality.

Permanent Text Label

With this tool, you can overwrite patient or study data or orientation labels that are burnt into 2D images (ultrasound, mammography, or X-ray images).

1. Click **Permanent Text Label** to select this tool.

   The **Edit Permanent Labels** dialog opens. Text label creation and editing mode is active as long as this dialog remains open.

2. In the image, click the patient information or orientation label that you want to hide or overwrite.

3. Drag the cursor across the image.

   This creates a black box that covers image information.

4. Type the correct information in the **Label properties** box of the **Edit Permanent Labels** dialog.

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. Click **Save Modified Image** to save your changes.

8. Close the dialog.

Closing the dialog ends label creation and editing mode.

> **Tip**
>
> To change a text label that you just entered or to delete one of your labels, return to label editing mode.
>
> Click **Permanent Text Label** again and click a label that you entered earlier to select it. You can now change the label text, or move or resize the label. To delete a text label, right-click it and select **Remove**.

Save Modified Image

With this tool, you can save changes to image content permanently.

1. Click **Save Modified Image**.

2. Select which changes you want to save.

You can save changes to window level settings, flip or rotate operations, sort order changes, and permanent text labels.

Save Modified Image combines the tools **Save Current W/L as Presentation State**, **Save Flip/Rotate as Presentation State**, and **Save Sort Order** with saving permanent text label changes.

See also *Presentation states*, page 190.

Delete Image for Quality Reasons

With this tool, you can delete individual images with poor image quality. Deletion of images for quality reasons might be restricted to images from certain modalities.

1. Select the viewer that shows the image you want to delete.

2. Click **Delete Image for Quality Reasons**.

3. Click **OK** to confirm deletion.

Finding studies and orders

In the **Quality Assurance** window, quality assurance means checking the assignment of studies to orders from the RIS (radiology information system) and correcting patient, study, and series information.

The quality assurance workflow may differ from organization to organization. For example, in many cases editing patient information (for example, correcting the patient name) can only be performed in the RIS or the HIS (hospital information system). Such functions may be disabled in Visage 7. Please discuss site-specific details with your PACS Administrator.

Defining filter and search criteria

The query section of the **Quality Assurance** window comprises two tabs.

- **Study** tab

  Data that you find as a result of a search on the **Study** tab is listed in the **Performed Procedures** list.

- **Order** tab

  Data that you find as a result of a search on the **Order** tab is listed in the **Scheduled Procedures** list.

Patient

Enter the name, date of birth or age, or ID of the patient whom you are looking for.

If you do not remember the exact name, date, or number, use wildcard characters. 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 type `AB??34` in the patient ID box to find *AB1234, AB0034*, and *AB11345678*.

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 semi-colon (;) or the pipe character (|). For example, `Anderson|Alexander` or `Miller;Milford`.

To exclude names or fragments of names, use the exclamation mark character (!). For example, `!A` in the patient name box searches for all patients whose names do not start with an A.

To search by date of birth or age, either specify the exact date, the year the patient was born, or the patient's age. Or search for patients of a specific age group. Point to **Date of Birth** to show a tooltip with examples of how to specify patient age or age group.

Date

1. Click the date box.

2. Select if you want to search by **Study Date**, or **Insertion Date** (**Study** tab), or by **Modification Date** (**Order** tab).

   The **Study Date** is the date and time when the study started.

   The **Insertion Date** is the date and time when a study was transferred to the server from a modality or an archive.

   The **Modification Date** is the date and time when an order was created or modified on the RIS (radiology information system).

3. Under **From** ... **To** specify 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.

   -Or-

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

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

Modality

Select the checkboxes 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`.
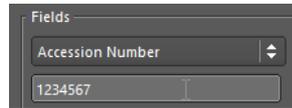
Use an exclamation mark to exclude a modality from your search. For example, specify `!CT` in the Others box to search for studies of all modalities except for modality CT.

Fields (Study tab)

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

2. Specify your search string in the input box below the selected criterion.

Remember that you can use wildcard characters.

If you want to search for more than one reading physician, for example, separate names with a semicolon (;) or pipe character (|). For example, `Miller|Smith` or `Miller;Smith`. For **Accession Number**, **Study Instance UID**, and **Series Instance UID**, separation of numbers with a space is also possible.

If the search strings themselves contain semicolons, pipe characters, or back-slashes, as in `Ward 4; Rm.6` or `Ward 1\Rm.2`, prefix these characters with a backslash. In this example: `Ward 4\; Rm.6;Ward 1\\Rm.2` or `Ward 4\; Rm.6|Ward 1\\Rm.2`

To define exclusion criteria, use the exclamation mark character (!). For example, type `!Neuro` in the subspecialty field to search for studies that are not assigned to the subspecialty Neuro.

If you want to copy search criteria from a list, be sure that the list separates items as shown above or with the newline character (`\n`).
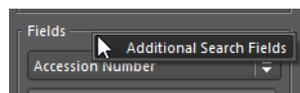
-Or-

Click the list button next to an input box.

Select one or several items.

3. If three search boxes are not sufficient for your filter definition, right-click the **Fields** section and select **Additional Search Fields**.
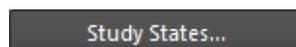
4. If you are using labels to organize your studies, use this field to search for a study with a specific label.

See *Finding studies with labels or comments*, page 222.

Study States (Study tab)
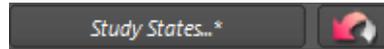
1. Click the **Study States** button.

2. In the **Study States** dialog, clear study states that you want to exclude from your search.

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.

3. 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)

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

2. Then specify your search string in the input box below the selected criterion.

Remember that you can use wildcard characters in your search.

3. If two search boxes are not sufficient for your filter definition, right-click the **Fields** section and select **Additional Search Fields**.
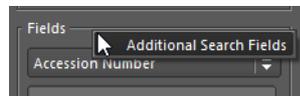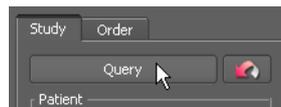

Status (Order tab)

Here you can filter the **Scheduled Procedures** list.

Choose whether to display either only those scheduled procedures that are assigned to performed procedures or only those that cannot be assigned.
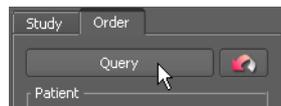
Starting and resetting a search

Click **Query** on the **Study** tab to update the **Performed Procedures** list.

-Or-

Click **Query** on the **Order** tab to update the **Scheduled Procedures** list.

-Or-

Click **Reset** to return to the default query preset.

See also *Defining a preset*, page 235.

If no default query preset has been defined, **Reset** removes all search criteria.
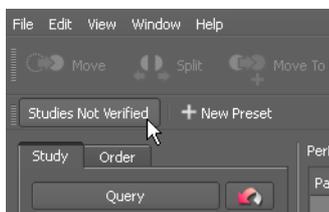
Query presets

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 to your own user account only. You cannot make presets public.

> **Tip**
>
> A preset stores filter and search criteria on both tabs (**Study** and **Order** tabs). It also stores the size and arrangement of the **Performed Procedures** and **Scheduled Procedures** lists.

Quick search with a preset

Click a preset button to retrieve its search criteria.

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

Adding criteria

If the query preset finds too many studies or orders, you can add criteria.

1. Select or type more search criteria in the query section.

2. Click **Query**.

Defining a preset

1. On the **Study** and **Order** tabs, select and type search criteria.

2. Click **New Preset**.

3. In the **Preset** dialog, enter a name for your new preset.

4. Select **Default** if you want to make this preset the default query preset.

   -Or-

   Select **Auto Query** if you want the system to re-enter 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**.

5. Save the preset.

A new preset button appears above the query section.

Modifying or deleting a preset

1. Click a preset button to select it.

2. Change filter and search criteria in the query section.

3. Right-click the selected preset button and select **Update Preset with Current Settings**.

   -Or-

   Right-click a preset button and select **Properties** to modify settings for the properties **Auto Query** or **Default**.

   -Or-

   Right-click a preset button and select **Delete Preset** to remove a query preset that you no longer need.

Information in the Performed 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.

Performed Procedures

Performed Procedures lists all studies that are currently stored on the Visage 7 server.

The column **QA Status** 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 has been terminated.

- NOT SCHEDULED (column remains empty)

  This QA status indicates that no matching of a performed procedure to a scheduled procedure is planned for this study.

The **QA Status** column provides meaningful information only if your Visage 7 is connected to a RIS (radiology information system).

Use the **Study States** button on the **Study** tab to search for studies of a specific QA status.

Scheduled Procedures

Scheduled Procedures lists all orders that have been sent from a connected RIS (radiology information system).

The column **Assigned** 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 to search for scheduled procedures that have already been assigned or that cannot be assigned.

If your Visage 7 is not connected to a RIS, the **Scheduled Procedures** list remains empty.

Organizing and rearranging procedure 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** list.

2. Cancel the selection for any columns that you want to hide or move.
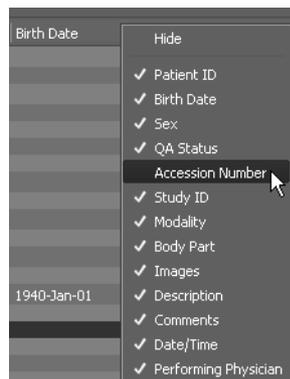
3. Point to a column to the right of which you want to reinsert a hidden column.

4. Right-click and select the column again.

Keep patient in Per-
formed Procedures list

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 subsequent performed procedures queries (that is, queries on the **Study** tab).
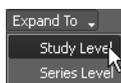
Expanding or collaps-
ing the Performed Pro-
cedures list

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 **Expand To** 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 a level

-Or-

Click **Collapse All** to show only the patient level.

Sorting the Scheduled
Procedures list

1. Click a column header to sort the list.

2. Clicking a second time reverses the sort order.

Selecting data for quality assurance in the Study Browser or View window

1. Open the **Study Browser** and search for the study or studies that require quality assurance.

2. In the study list, select one or several studies, series, or volume datasets.

3. Right-click and select **Quality Assurance**.

-Or-

1. In a **View** window, select an image.

2. Click **Select for Quality Assurance**.

In the **Quality Assurance window,** you will find the selected case in the **Performed Procedures** list.

Quality assurance with RIS

If your Visage 7 is connected to a radiology information system, quality assurance is performed automatically and in the background.

Automatic data consolidation

If a RIS connection exists, Visage 7 is typically 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

If your Visage 7 is connected to a RIS, you only need to perform manual quality assurance if automatic matching of studies and RIS orders fails. A common scenario for this is when scans are performed without a modality worklist and incomplete or incorrect information was entered at the modality.

1. In the **Performed Procedures** list, search for studies with **QA Status** *SCHEDULED*.

   Use the **Study States** button on the **Study** tab to define such a query. See also *Study States (Study tab)*, page 233.

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, select *NOT ASSIGNED*. See also *Status (Order tab)*, page 234.

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. On the toolbar, click **Assign Order to Study** and confirm.

Assigning series to orders

1. In the **Performed Procedures** list, search for and select the series that you want to reassign.

2. In the **Scheduled Procedures** list, search for and select the order to which you want to assign the series.

3. On the toolbar, click **Assign Order to Study** and confirm.

The system now splits the study from the **Performed Procedures** list, assigns the series to the new study and the new study to the selected order in one step.

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, search by study date and modality, for example.

2. Click **Query**.
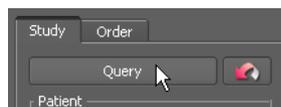
3. Select an emergency patient in the **Performed Procedures** list.

4. Click **Edit**.

5. Overwrite any preliminary information with the correct patient information.

6. Select **Apply to partner systems** to apply this change not only to the primary server but to all partner systems as well.
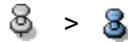
7. Click **OK**.

The **Performed Procedures** list is now updated automatically.

Merging patients

1. Search for the patient that you want to merge with another patient.

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, choose the emergency patient or misspelled patient.

5. Press and hold **Ctrl/Cmd** down while you also click the correct patient name.

6. Click **Merge Patients**.

7. In the **Merge Patients** dialog, 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, you can move the data to another patient, study, or series. You proceed in a similar way in all these operations.

Move to another patient, study, or series

1. Select the study, series, or images that you want to move.

2. Press and hold **Ctrl/Cmd** down while you also click the patient, study, or series that you want to move the data to.

3. Click **Move**.

4. Read the message and confirm.

5. Select **Apply to partner systems** to apply this change not only to the primary server but to all partner systems as well.

Move to a new patient, study, or series

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 **New Patient**, **New Study**, or **New Series** dialog.

4. Select **Apply to partner systems** to apply this change not only to the primary server but to all partner systems as well.

5. 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, click **Move to New Patient** 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.

4. Select **Apply to partner systems** to apply this change not only to the primary server but to all partner systems as well.

5. Click **OK** to confirm.

Deleting patients, studies, series, or images

Before you delete data, ensure that the data is no longer required by any user. After you have deleted a study from the server, you cannot restore it again, unless an independent copy exists to which you have access, such as a copy in a long-term archive. Note that in some configurations, delete operations may propagate to other systems, such as long-term archives.

1. Select one or several patients, studies, series, or images.

2. Click **Delete**.

A dialog opens prompting you to specify a reason.

3. Select a reason for data deletion and click **OK** if you are certain that you no longer need this data on the server.

Undeleting studies deleted for quality reasons

With appropriate configuration settings, data that you deleted for quality reasons do not disappear from the **Quality Assurance** window entirely. Even though the data is no longer available in the **Study Browser**, the data remains in the **Performed Procedures** list of the **Quality Assurance** window where it is marked with an asterisk (*). You can revoke deletion of such data.

1. Select a patient, study, series, or image with an asterisk (*).

2. Click **Undelete**.

The asterisk is removed from the patient, study, series, or image in the **Performed Procedures** list and the data is available again in the **Study Browser**.

Modifying patient ID mappings

If subsystems that send data to the Visage 7 server or that receive data from the Visage 7 server use different patient IDs than Visage 7, IDs can be mapped. In the **Quality Assurance** window, you can edit patient ID mappings.

1. Right-click a patient, study, series, or image and select **Mapped Patient IDs**.

2. In the **Mapped Patient IDs** dialog, add new patient ID mappings or delete a mapping that is no longer valid.

Customizing the Visage 7 client

Visage 7 users can customize the Visage 7 client in various ways.

Note

Some of the configuration options in this section are not available on all Visage 7 client screens.

UI appearance and display size

1. On the menu, 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.

2. Point the cursor to a screen or section of a screen, hold the **Ctrl/Cmd** key down, and rotate the mouse wheel to display viewer text larger or smaller.

Monitor configuration

If you are working with more than one monitor, you use this dialog 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.
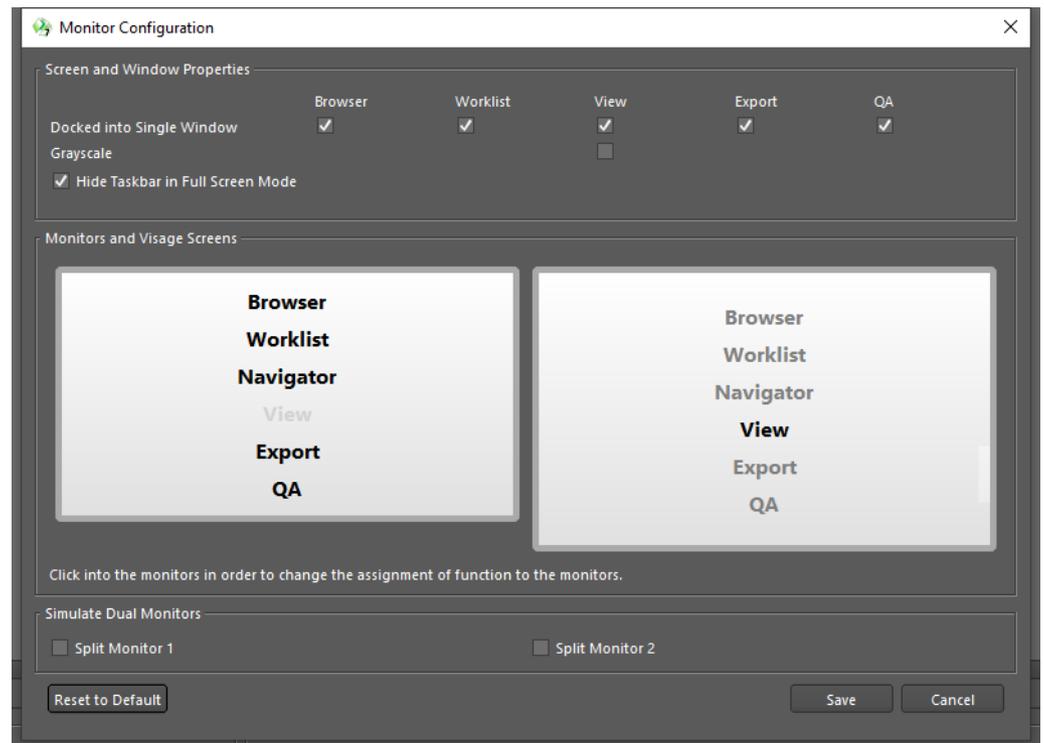
2. In the **Monitors and Visage Screens** section, click a window to select it or to clear its selection on one of the available monitors.

   Select **Docked into Single Window** if you want to show all Visage 7 windows in the same program window. Clear this option for display as a floating window. Floating window display is indicated by square brackets.

   Tip

   Floating window or tab display of the **Study Navigator** cannot be defined with a **Docked into Single Window** checkbox. The **Study Navigator** moves to a tab automatically as soon as you move **View** windows to a separate 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. Decide whether you want to show the Windows taskbar when the Visage 7 client is shown in full-screen mode.

   Showing the Windows taskbar facilitates switching over to other program windows such as the RIS (radiology information system).

5. Select **Split Monitor** if you want to simulate dual monitors.

   For example, split the monitor 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.

6. 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.

Tip

If studies are loaded in more than one **View** window (more than one tab with a patient name is shown in the title bar) when you change the monitor configuration, reload these studies so that the new monitor configuration becomes effective in all **View** windows.

Configuring keyboard shortcuts

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

You can redefine some of these shortcuts and also assign other functions to keyboard shortcuts.

1. Select **File > Preferences > Keyboard Shortcuts**.
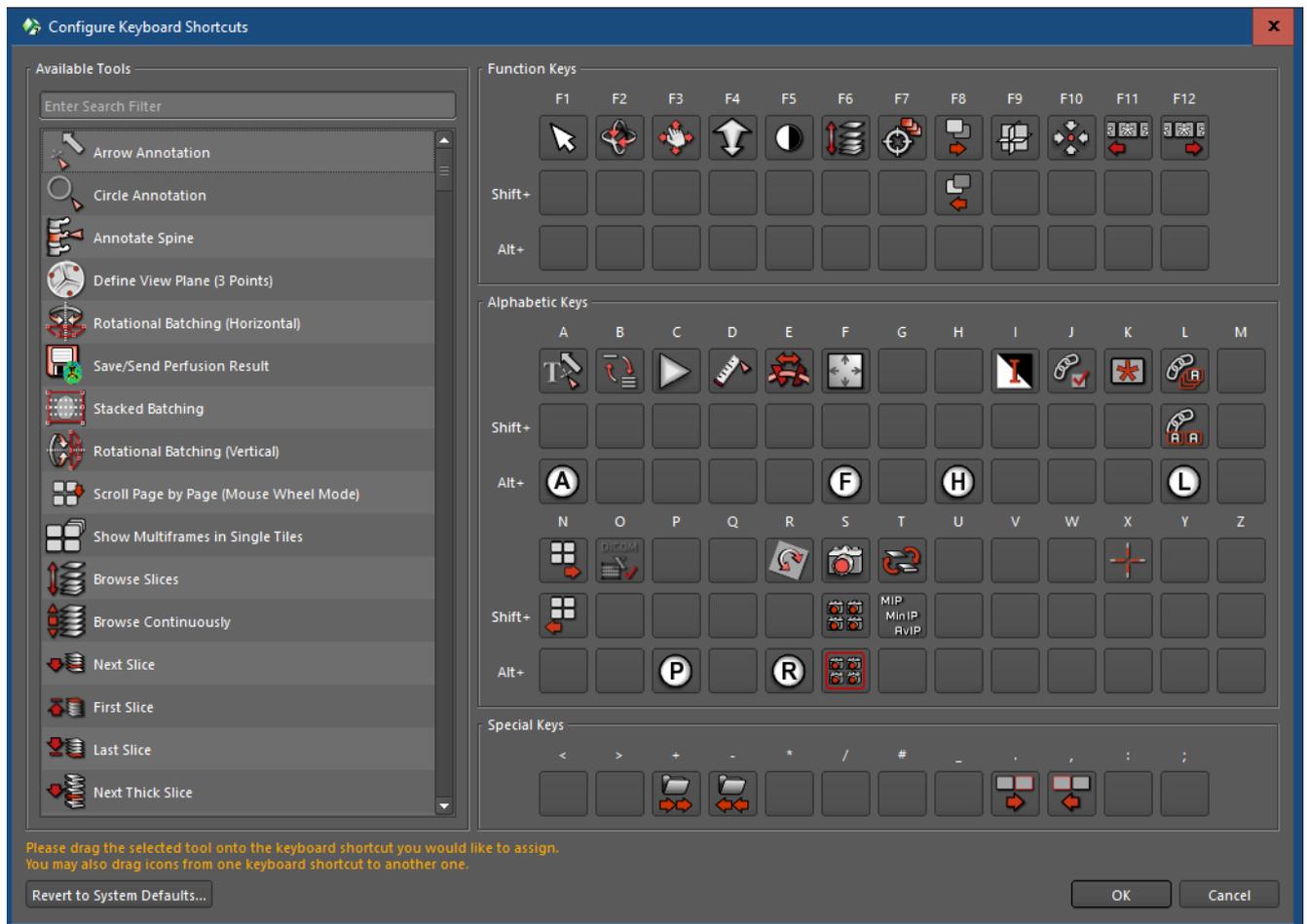
2. In the search filter box above the **Available Tools** list, type the name or part of the name of the tool that you are looking for.

-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, alphabetic 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.

4. Click **OK** to confirm your new keyboard shortcuts.

The keyboard shortcuts list, which you can display with **Help > Keyboard Shortcuts**, is updated automatically.

**Returning to factory defaults**

In the **Configure Keyboard Shortcuts** dialog, click the **Revert to System Defaults** button to reject any recent or previous key assignments or reassignments.

The factory-default keyboard shortcuts are now active again.

Configuring the tool palette

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**.
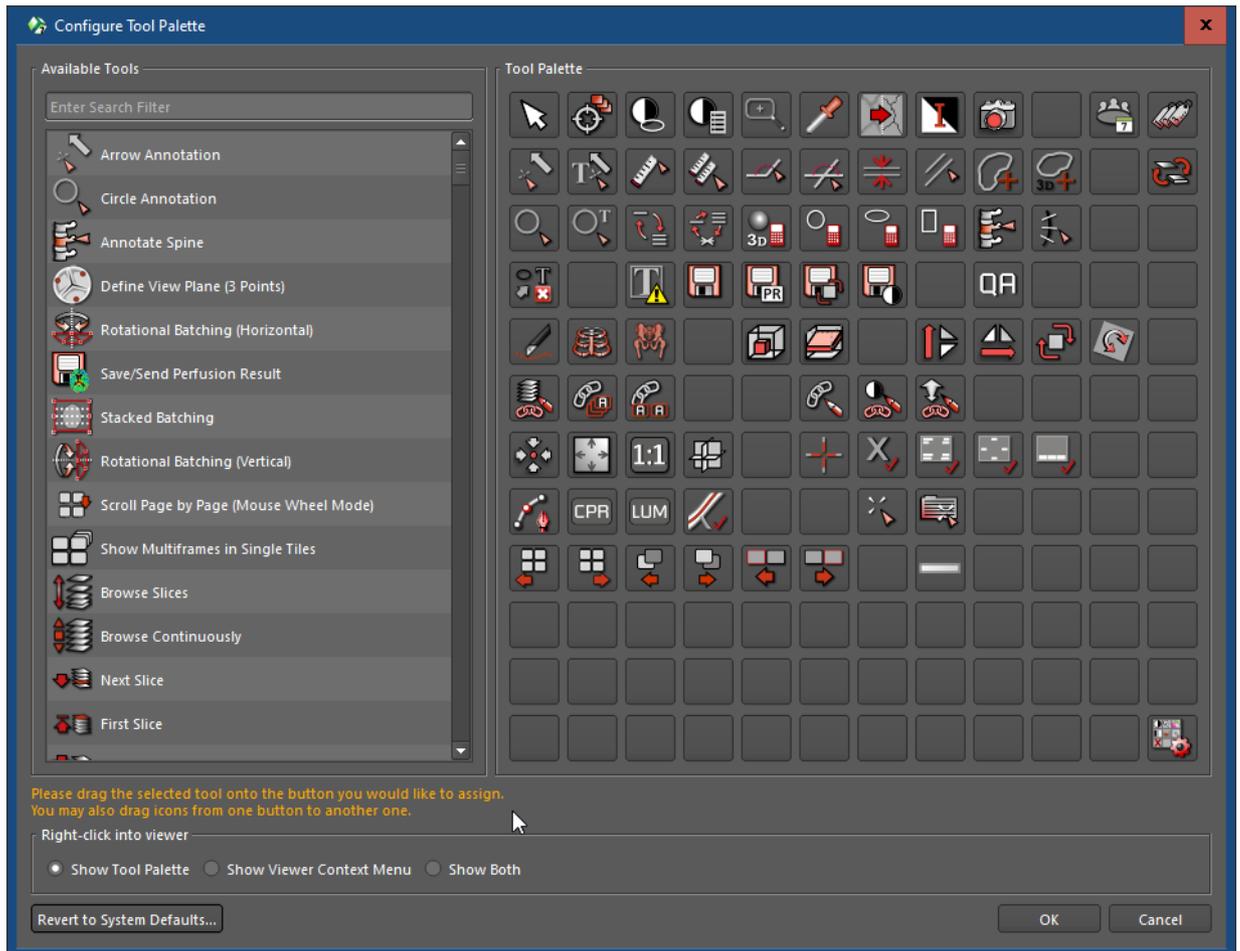
2. In the search filter box above the **Available Tools** list, type the name or part of the name of the tool that you are looking for.

-Or-

Scroll down the list of **Available Tools.**

3. Select a tool and drag it onto the **Tool Palette** on the right.

Moving a tool to a box that is already occupied replaces the tool.

4. Select whether to show the tool palette, the viewer context menu, or both when you right-click a viewer.

If you select **Show Tool Palette** here, use the arrow button at the right edge of the viewer controls to show the viewer context menu.

See *Viewer controls*, page 63.

5. Click **Revert to System Defaults** to reject any recent or previous assignments or reassignments.

6. Click **OK** to confirm and close the dialog.
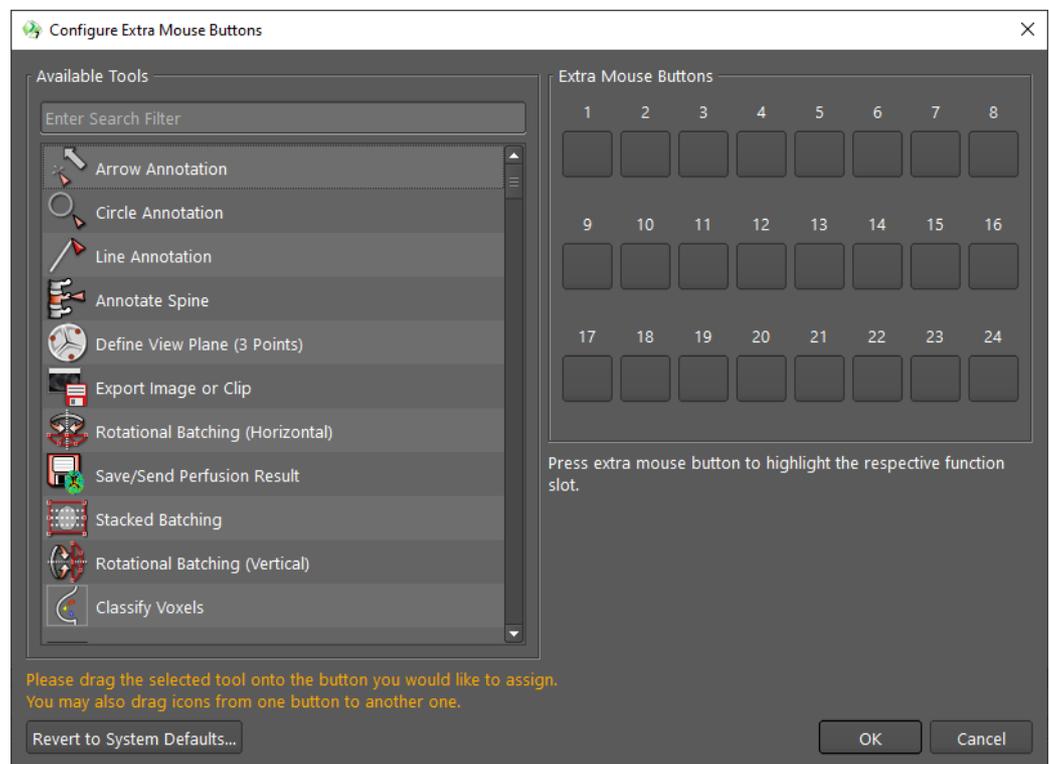
> **Tip**
>
> You can even configure a shortcut to the **Configure Tool Palette** dialog itself.

Configuring additional mouse buttons

If you are using a multibutton mouse, use the **Configure Extra Mouse Buttons** dialog to assign Visage 7 tools to these extra mouse buttons.

1. Select **File > Preferences > Mouse Buttons**.

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 an **Extra Mouse Button** slot to the right.

Moving a tool to a box that is already occupied replaces the tool.

4. Click the **Revert to System Defaults** button to reject any recent or previous assignments or reassignments.

5. Click **OK** to confirm and close the dialog.

Configuring window/level presets

Window level presets are combinations of image brightness and contrast settings. You can save such presets for specific image types.

While you are reading images, you can select predefined window presets from a dropdown list in the viewer controls, from a list that is displayed when you click the **Show Window Level Presets** button on the tool palette, or with a keyboard short-cut.
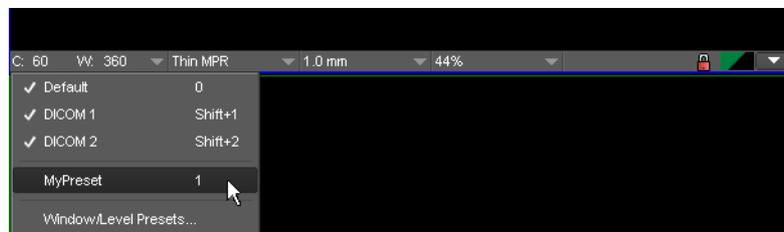
1. Select **File > Preferences > Window/Level Presets**, or select **Window/Level Presets** from the viewer controls.

The image type of the currently loaded data is already selected.
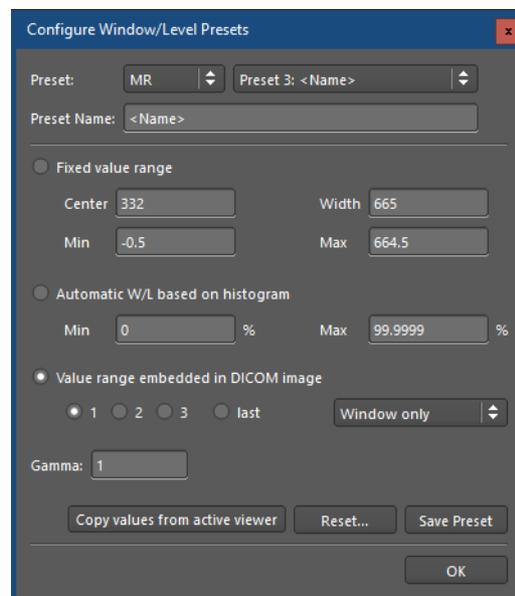
2. Select the modality for which you want to define a preset and a preset number.

   Preset numbers 1 to 9 correspond to the keyboard shortcuts that you can use to select presets quickly while you are reading images. Presets numbered 10 or higher do not have a keyboard shortcut. They can only be selected from the viewer controls.

   Undefined presets are listed as *<Name>*.

3. Enter a **Preset Name**.

4. Enter window level settings.

   In the **Fixed value range** box, enter the window width as a range value or as a minimum and maximum value. The **Center** and **Width** and **Min** and **Max** boxes are synchronized.

   -Or-

   Select **Automatic W/L based on histogram**.

   This setting adapts the data window to the value range available in an image dataset.

   -Or-

   Under **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.

   Also select whether to refer to window level data or to the VOI LUT, if such information is available in the DICOM data.

   -Or-

   Click **Copy values from active viewer** to copy window level settings from the active viewer into the **Configure Window/Level Presets** dialog.

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-

   Click **OK** to close the dialog and choose whether to save or ignore unsaved changes.

Render settings

In this dialog, 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.

Caution

OpenGL is an advanced graphics standard that is not always properly supported by client-computer graphics hardware.

In the **Render Settings** dialog, 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.

Reseting all warnings

If you have selected **Do not show again** for a warning that has appeared previously, **View > Reset All Warnings** revokes this selection. From now on, all warnings are shown again.