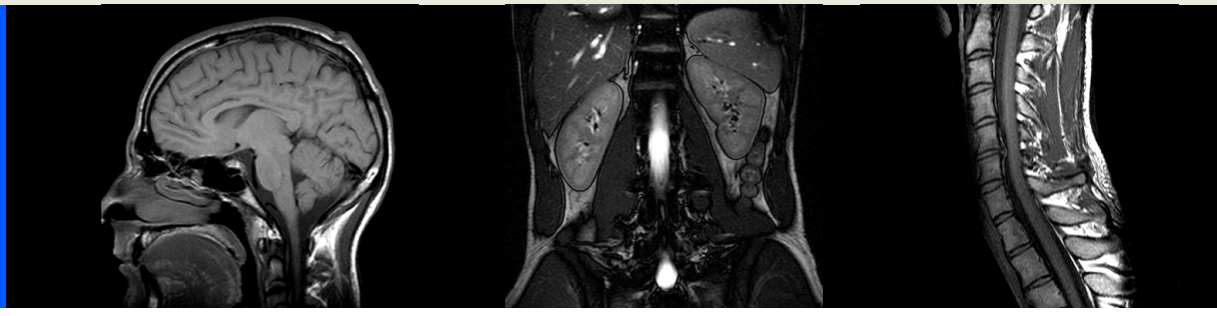
syngo MR Operator Manual



Magnetic Resonance

Operator Manual
Version *syngo* MR A40

SIEMENS

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MAGNETOM C!

MAGNETOM Symphony P

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Information on this Operater Manual

To operate the MR system accurately and safely, the operating-personnel have to have the necessary expertise as well as knowledge of the entire operator manual. It has to be read carefully prior to starting up the MR system.

Layout of Operator Manual

To improve readability, your complete operator manual has been broken down into several individual operator manuals with thematically distinct content:

- ❏ Hardware components (system, coils, etc.)
- ❏ Software (measurement, evaluation, etc.)

Information for the operator of the MR system is another part of the complete operator manual.

The volume of smaller operator manuals that you receivede-pends on your system configuration, and may vary.

! All parts of the complete operator manual may contain safety information requiring strict adherence.

The operator manual for hardware and software are intended for authorized users. They assume a basic knowledge of working with PCs and software.

This manual includes descriptions covering standard as well as optional software. Consult the respective Siemens sales organization to determine the type of software available for your system. The description of an option is not legally binding for providing this option.

The graphics, figures, and medical images used in this operator manual are examples only. The actual display and design of these may be slightly different on your system.

For the sake of linguistic simplicity, male and female patients are referred to as "the patient".

The term "Siemens Service" includes Service personnel authorized by Siemens.

Configuration

This manual consists of multiple parts (Part A, Part B, etc.). A comprehensive table of contents can be found at the beginning of each part.

! Please observe the content of the safety chapter during your daily activities.

The other parts contain descriptive and instructive chapters. The descriptive chapters explain the design, application, and function of the individual MR system components. The instructive chapters explain the operation of the individual components.

In addition, the software includes an Online Help derived from the Operator Manual.

Operator manuals *syngo* MR and *syngo*

The **Operator Manual - *syngo* MR** describes only MR-specific applications. General *syngo* applications, such as e.g. **Viewing** or **Filming**, also available for MR systems, are described in the ***syngo Operator Manual.***

Important icons

To improve readability, certain special content is identified accordingly. The following presents the icons used and their meaning:

✧ Requests for action
❏ List items

Additional information for the user

! Notes for optimal use of the MR system.



WARNING

Safety information

Indications for use

Your system is indicated for use as a magnetic resonance diagnostic device (MRDD) that produces transverse, sagittal, coronal and oblique cross sectional images, spectroscopic images and/or spectra, and that displays the internal structure and/or function of the head, body, or extremities.

Other physical parameters derived from the images and/or spectra may also be produced. Depending on the region of interest, contrast agents may be used. These images and/or spectra and the physical parameters derived from the images and/or spectra when interpreted by a trained physician yield information that may assist in diagnosis.

Your system may also be used for imaging during interventional procedures when performed with MR compatible devices such as in-room display and MR-safe biopsy needles.

Authorized operating personnel

The system must be operated according to the intended use and only by qualified persons with the necessary knowledge in accord with country-specific regulations, e.g., physicians, trained radiological technicians or technologists, subsequent to the necessary user training.

This user training has to include basics in MR technology as well as safe handling of MR systems. The user has to be familiar with potential hazard and safety guidelines the same way he is familiar with emergency and rescue scenarios. In addition, the userhas to have read and understood the contents of the operator manual.

Open source software included

The software delivery volume includes a separate Open Source DVD. This DVD contains the Open Source software packages as well as the associated licensing information installed in this product. For additional information, please read the following files on DVD:

❏ release-notes.pdf

PART A

Basics

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CHAPTER
A.1 Coordinate System

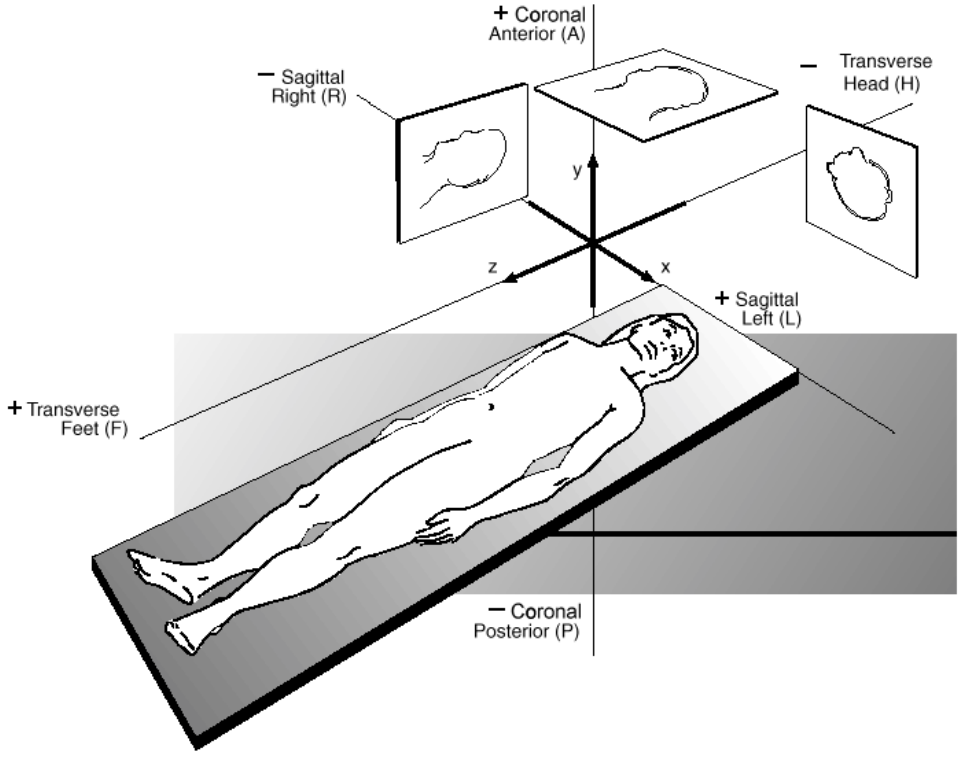
The software ***syngo* MR** and the previous version **Numaris** (including **Numaris 3.5**) use different patient coordinate systems.

It is important to remember this when diagnosing MR images acquired in **Numaris** under ***syngo* MR**.

If you have any questions about converting the different coordinate systems, please contact your applications specialist.

Coordinate system for Numaris 3 and Numaris 3.5 (+FAL)

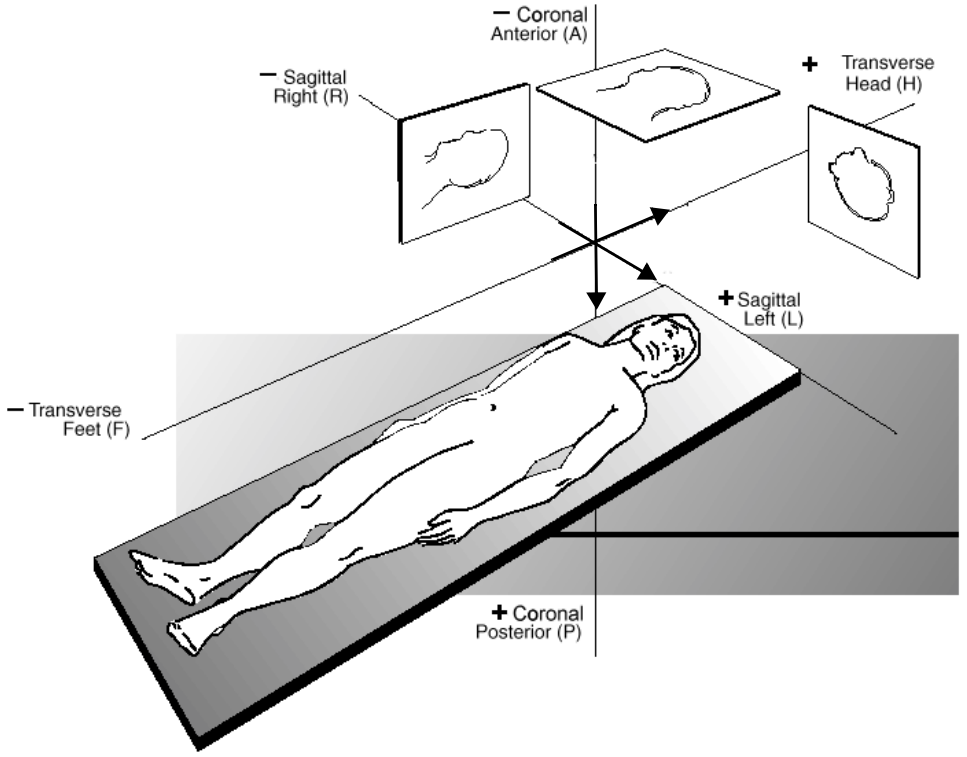
Slice positions as seen from the magnet isocenter into the direction of **F**eet, **A**nterior and **L**eft are positive.



MR images based on this patient-oriented coordinate system are only converted when exporting them into a DICOM format.

Coordinate system for syngo MR (DICOM standard, +LPH)

Slice positions as seen from the magnet isocenter in the direction of **L**eft, **P**osterior and **H**ead are positive.



The following overview shows how the direction of the slice position changes as it moves from minus to plus.

	Direction of slice position
Numaris 3 and Numaris 3.5	+FAL
syngo MR	+LPH

If the slice position ascends, the slices move toward the positive coordinates:

Numaris 3 and Numaris 3.5

- ❏ The transverse slice moves in the (F) direction of the feet.
- ❏ The coronal slice moves in the anterior (A) direction.
- ❏ The sagittal slice moves in the left (L) direction.

***syngo* MR**

- ❏ The transverse slice moves in the (H) direction of the head.
- ❏ The coronal slice moves in the posterior (P) direction.
- ❏ The sagittal slice moves in the left (L) direction.

! In **MRease**, position information in the PCS is shown in the form of abbreviations L=Left, R=Right, A=Anterior, P=Posterior, H=Head, F=Feet. They replace the algebraic signs "+" or "-" used in previous **Numaris** versions.

CHAPTER A.2

Differences between syngo and syngo MR

The ***syngo* MR** software on your system differs in some aspects from the *syngo* base version as described in the *syngo* Operator's Manual. This chapter provides information regarding these differences.

All applications and topic areas are presented where there are differences from the original *syngo* version. The following differences are described:

- *syngo* functions that are not available on your system with ***syngo* MR**
- ***syngo* MR** functions that operate differently than the original *syngo* version
- ***syngo* MR** functions called something different than in the original *syngo* version
- Functions that are not mentioned in the Operator's manual for the original *syngo* version

Common functions

Using the keyboard

Setting the keyboard focus

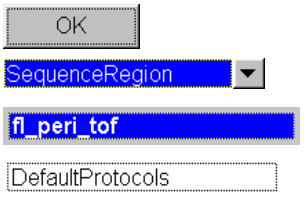
You can control and operate the input and operating elements of the user interface with the keyboard. In this case, you set a focus on the required operating element, which then reacts to subsequent input from the keyboard.

Within an object (e. g., a window, card, or special area), move the keyboard focus as follows:

✧ To move the keyboard focus to the next or previous element, press the **Tab** key or the **Shift + Tab** keys.

✧ Move the keyboard focus back and forth until you reach the element you want to operate.

Elements with the keyboard focus are highlighted.

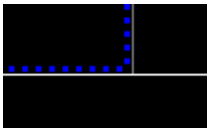


❏ Screen keys are highlighted by a dashed frame.

❏ List entries and entries in the program control change to a blue background and are highlighted by dashed frames.

❏ Entries on the program card are highlighted by a dashed frame.

Keyboard focus in the image area



The keyboard focus may be set only on the entire image area, not individual image segments. The image area is then indicated by a thin white frame. Within the image area you will see the input focus (dashed blue frame) indicating the image segment your entries will effect.

Scrolling within card stacks

If the keyboard focus is on a card stack, you can move individual cards to the foreground via keyboard commands.

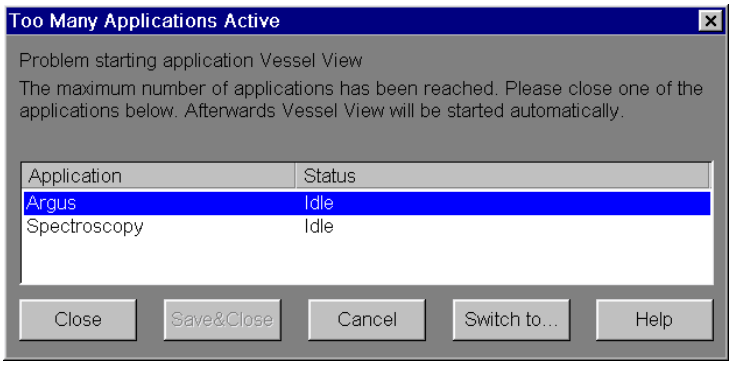
✧ Press the **Ctrl** + ← or **Ctrl** + → keys to move the keyboard focus to the left or right.

If the card in foreground is subdivided into cards, e.g., such as the **System** parameter card, you can also move these cards to the foreground with the keyboard.

✧ Press the **Shift** + **Ctrl** + ← keys or the **Shift** + **Ctrl** + → keys to move the keyboard focus to the left or right.

Too many active applications

You may only open six applications simultaneously on your MR system. If this number is exceeded, the **Too Many Applications Active** dialog window is displayed.



✧ To start the new application, close an application in the list that you are no longer using.

Configuring image text

The following text supplements the description of the **Image Text Editor** in the *syngo* Operator Manual. You access the **image text editor** via the **NUMARIS/4 – Configuration Platform** dialog window, which you select with **Options > Configuration**.

Highlighting image text

You can highlight selected image text. This can be helpful if text would otherwise appear too small in certain layouts (20 and 35 layout).

✧ Click the required image text in the image text overview.

The selected text is highlighted in gray and the **B** screen button is now active.



✧ Click **B**.

The marked text is displayed in bold.

➪ Image texts can be highlighted only if the **Selected Texts** option is selected. You can also cancel text highlighting in the same manner.

➪ Depending on your system configuration, some texts may not be able to be displayed.

! If the orientation marks are deselected, the patient name is not displayed.

Configuring the MR system

As an authorized user or system administrator, you will set ***syngo* MR** based on the concrete configuration of your MAGNETOM. For example, this includes specifying the MAGNETOM type, the optional system components, and the ambient conditions.

✧ Select **Options > Customer Service > Local Service**.

✧ Enter your password, and press the **OK** button in the **Authentication** dialog window.

Multi-Monitor operation

Multi-Monitor operation is not available on your MR system.

Patient registration

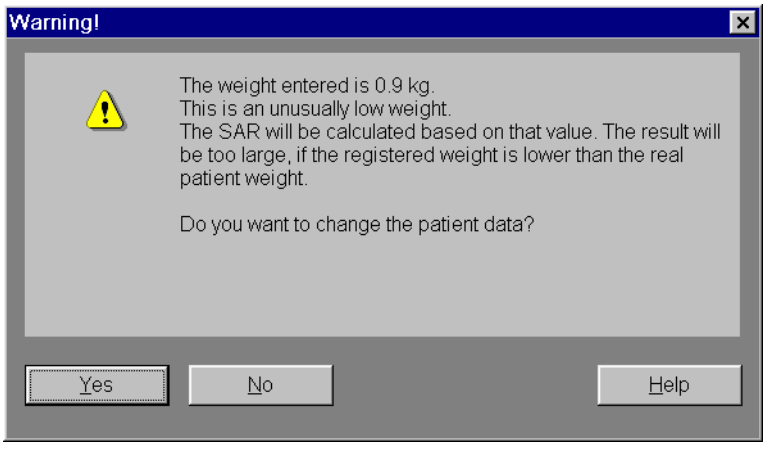
Emergency registration

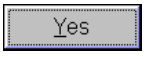
Emergency registrations are not intended for MR systems. The corresponding functions are not available.

Checking the weight during registration

During registration at an MR system, particular importance is placed on correctly entering the patient weight because the SAR threshold depends on weight. The following information supplements the description of patient registration in the *syngo* Operator Manual.

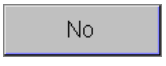
During registration, the system checks whether the relationship between age and weight is realistic. A warning window is displayed if there are discrepancies.





✧ If the entries have to be corrected, click **Yes**.

You return to the **Patient Registration** dialog window.



✧ To register and examine the patient with these settings, click **No**.

Patient position MR-System

MAGNETOM Symphony system use the typical patient positioning as described in the *syngo* Operator's Manual.

Direction

- ❏ **Head first**
  Patient lying with his head pointing toward the examination unit.
- ❏ **Feet first**
  Patient lying with his feet pointing toward the examination unit.

Position

- ❏ **Left side**
  Patient is lying on his left side.
- ❏ **Right side**
  Patient is lying on his right side.
- ❏ **In the supine position**
  Patient is lying on his back.
- ❏ **Prone position**
  The patient is lying on his stomach.

Patient Browser

Splitting mosaic images

Some post-processing functions, e.g. **3D**, cannot use mosaic images. So in special cases it may be necessary to split them into single images again.

Splitting a mosaic image

✧ In the **Patient Browser** select *one* mosaic image.

✧ Select **Applications > Mosaic > Split to one Series**.

The images of the selected mosaic image are saved in a new series under the same study.

Splitting several mosaic images

✧ Select several mosaic images or all mosaic images of a series in the **Patient Browser**.

✧ Select **Applications > Mosaic > Split to one Series**.

The images of *all* select mosaic images are saved in *one* new series.

Or

✧ Select **Applications > Mosaic > Split to one Series per Mosaic**.

A new series is created with the split images for each mosaic image selected.

Splitting images may take some time. The process runs in the background and is completed even if the current user logs off or another user logs on.

Canceling splitting

✧ Select **Applications > Mosaic > Abort Splitting process...**.

Canceling a splitting operation in progress after a user change is only possible if the new user has the necessary access rights.

syngo MR Workplace

The following important information on working with a *syngo* MR Workplace supplements the description of the Patient Browser in the *syngo* Operator Manual.

If you select the Patient Browser at a *syngo* MR Workplace, the Browser is not updated automatically.

✧ In this case, select **View > Refresh**.

Transferring images to the 3D task card

If you want to transfer selected images from the Patient Browser to the **3D** task card, note the following feature with ***syngo* MR**:

The corresponding menu items are available under **Applications > 3D** and *not* under **Patient**.

Procedure tracking with MPPS

On MR systems, the **Modality Performed Procedure Step** dialog window, which you can select in the **Patient Browser** for procedure tracking, does not contain the subtask card with information regarding **radiation dose**.

Media Browser

The **Media Browser** is not supported by your MR System.

Pixel lens in the Viewer

Basics

In an MR system, the **Viewing** task card has enhanced **pixel lens** functions.

The **pixel lens** displays the average value of gray scales of a small 5 × 5 pixel area. In ***syngo* MR** the patient coordinates are displayed together with this value.

The displayed coordinates refer to the **Whole Body patient coordinate system**. The zero point of the coordinate system is at the table position that was at the magnet isocenter during the first measurement of a series block (in practice, it is the position marked by the light localizer prior to the beginning of a new MR examination).
→ Chapter A 1, *Coordinate System*

Prerequisites for coordinate display

While the gray scale value can always be displayed in the **Viewer** image, the patient coordinates are displayed only if the reference image meets the following conditions:

- ❏ The image is a Siemens MR image
- ❏ The image is not a mosaic image
- ❏ The image has a defined DICOM image plane

Restrictions

- ❏ The images used *have to* belong to the same series block. → Page C.3–38, *Series block*
- ❏ The result images may contain distortion artifacts as a result of the non-linearity of the gradient field inside the magnet. Image distortion artifacts in the visible image are *not* corrected by the coordinates displayed.
- ❏ The patient coordinate is displayed only if the inaccuracy of the specified image coordinates lies within a 7 mm tolerance margin.
- ❏ In the case of Composing images, only the transverse part of the pixel lens coordinates is displayed in the image.
- ❏ The user is responsible for using the correct (mutually compatible) images for comparing the **pixel lens** coordinates.

Do not copy pixel lens markers from image to image.

If a pixel lens marking is copied, it does NOT displayed at the identical patient coordinates, but at the same distance to the upper left corner of each respective image.

Do NOT use the pixel lens when multiple images are selected.

If several pictures are selected, the pixel lens marking in the images is NOT displayed at the identical patient coordinate, but at the same distance to the upper left corner of each respective image.

Using the pixel lens

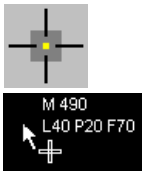
The **pixel lens** enables you to use gray scale and coordinate values as follows:

- ❏ Displaying the values of the pixel lens at the mouse pointer position
- ❏ Inserting the pixel lens marker at a fixed position
- ❏ Selecting, moving, or deleting the pixel lens marker
- ❏ Saving the pixel lens marker with the reference image

Activating / deactivating the pixel lens

When the **pixel lens** is activated, the values of the current mouse pointer position are displayed.

✧ Select **Tools > Pixel Lens**.
- Or -
Click this button of the **Tools** subtask card.



The mouse cursor changes shape. The grayscale value is shown in the first line. The second line shows patient coordinates.

➪ Deactivate the **pixel lens** in the same manner as you activated it.

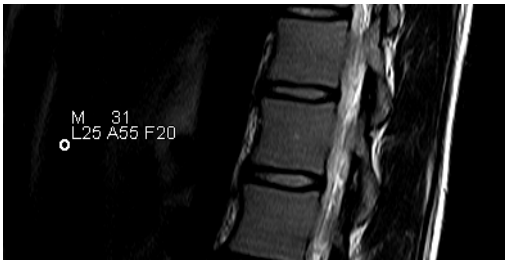
Inserting a marker at a fixed position

You can also enter the pixel values in an image.

✧ Activate the **pixel lens** function.

✧ Click the pixel of interest with the left mouse button.

The pixel is marked with a small circle. The grayscale value is shown in the first line. The second line shows patient coordinates.



! The circular marker of the **pixel lens** does not match the area measured to determine the grayscale value. It has a constant size and is independent of the zoom factor of the image.

The gray scale value is always determined by a 5 x 5 pixel area.

Selecting and moving the marker

You can move a fixed **pixel lens** marking that has been inserted.

✧ Deactivate the **pixel lens** function.
→ Page A.2–14, *Activating / deactivating the pixel lens*

✧ Move the mouse pointer to the marking.

The arrow cross is displayed in enlarged format.

✧ Press and hold the mouse button and move the marking with the mouse to the required position.

The grayscale value and patient coordinates are updated.

Application examples:

❑ **How to proceed with the application examples:**

The procedure is identical for the three examples presented:

✧ Ensure that only one image is selected.

! **Do NOT use the pixel lens when multiple images are selected.**

If several pictures are selected, the pixel lens marking in the images is NOT displayed at the identical patient coordinate, but at the same distance to the upper left corner of each respective image.

✧ With the **pixel lens** activated, mark the required vertebra in the first image via mouse click.

! **Do not copy pixel lens markers from image to image.**

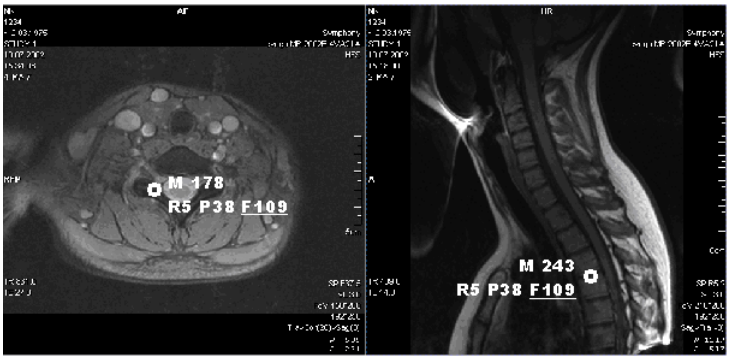
If a pixel lens marking is copied, it does NOT displayed at the identical patient coordinates, but at the same distance to the upper left corner of each respective image.

✧ Move the marker in the second image until the patient coordinates are the same as shown in the first image.

! Please note the inaccuracies that may be displayed when using this application.

❏ Example 1

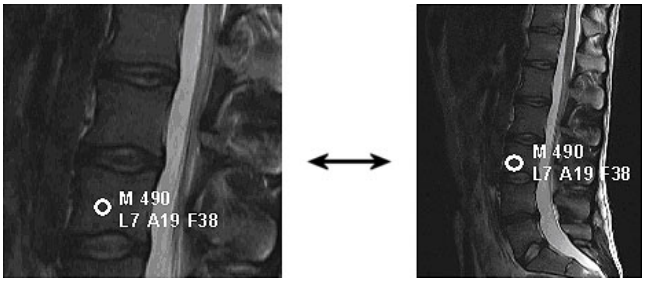
You are searching for the patient coordinates from the transverse image to the left in the second, sagittal image to the right.



❏ Example 2

You compare two sagittal images that belong to the same series block but have a different FOV.

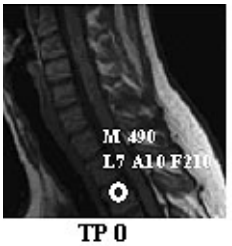
The first image shows only parts of the lumbar vertebrae, the second image shows the entire length of the lumbar vertebrae.



❑ **Example 3**

You compare two sagittal images of the same series block, but at different table positions.

The first image shows the upper section, the second image shows the lower section of the cervical spine.



TP 0



TP F15

Deleting a marking

You delete a marking when it is no longer required.



✧ Click the marker to select it.

The marker changes shape.

✧ Press **Del.**

The marker of the **pixel lens** is deleted.

Saving the marker with the image

When images are saved, the **pixel lens** markers in the images are saved as superimposed graphics.
→ *syngo* Operator Manual

The same applies to exporting and filming images.

Viewer

2D Evaluation

Adhere to the following information regarding 2D evaluation of MR images:

!

For optimum results, use quantitative analysis on distortion-corrected images only.

This is especially important for evaluations at the edge of the image and for large FOVs.

!

Note the following special feature for explicitly selected images of a different matrix:

If you draw a graphic in an image, this graphic is not displayed exactly at the same position in the other images and not in the same size.

Windowing with the keyboard

The following information supplements the description of windowing with the keyboard in the *syngo* Operator Manual:

!

If a dialog window is open and active in the **Viewing** task card, the keys of the symbol keypad may not function.

✧ In this case, click the image area to deactivate the dialog window or just close it.

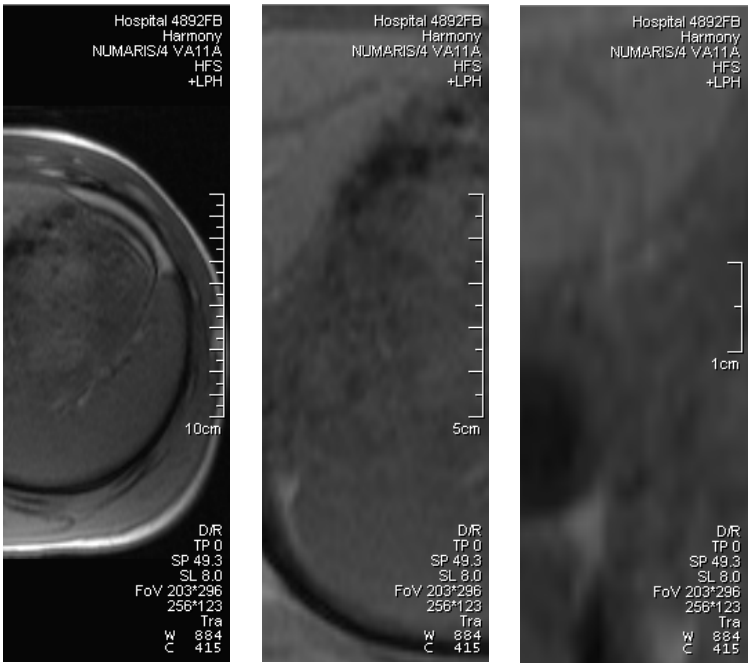
Displaying images with LUTs

The use of look-up tables (LUT) for the display of images is not supported by your MR system.

Scale in MR images

The scale is displayed at the right border of the segment and clarifies the proportions in the image.

The scale adapts to the current proportions in the image.



➪ The scale bar is not displayed if it would otherwise hide the image text.

Saving and data exchange

MOD storage medium

Your MR system supports the reading of MOD data storage media. Writing to MOD however is not possible.

Storage media CD and DVD

Your MR system does not provide **archiving functions**.

! The term **archiving** used in the *syngo* Operator Manual should be interpreted as **Save** for MR applications.

CDs and DVD-Rs can be kept only for a limited time, and are therefore only suited for limited data storage. For this reason, with ***syngo* MR** you can only use CDs as a storage medium, not for archiving.

Displaying images with a square matrix

The description of the display of images with a rectangular matrix presented in the *syngo* Operator Manual does *not* apply to ***syngo* MR**. The following section replaces that part of the *syngo* Operator Manual.

In some circumstances, images imported from an external storage medium or hard drive may be displayed with a reduced pixel matrix.

! When transferring edited, non-quadratic matrices/Viewer segments, diagnostically relevant image areas can be lost.

To prevent this, the original image should be included when edited images are exported or sent to another workstation.

We strongly recommend including the original images when performing the final diagnosis, and not to make it based solely on edited or modified images.

Occurrence of behavior

With the exception of the **3D** task card, this behavior occurs in all task cards when exporting or sending modified images.

It is caused by a mismatch between the size of the image matrix and the copy segment.

Example: A rectangular image matrix should be displayed in a square image segment or vice versa.

If an image has been zoomed, reduced, panned or rotated in a task card, the modified image is displayed correctly, i.e., it fills the entire image segment.

After being saved (using the **Save As** function), when this image is exported or sent, and then displayed again, the visible pixel matrix is reduced. At the edges, the image information of the newly displayed image is replaced by black borders.

If the image contains a ROI that is partially covered by black borders, the statistical information refers to the complete ROI and not just the area that remains visible.

Example 1

Zooming and panning rectangular images:

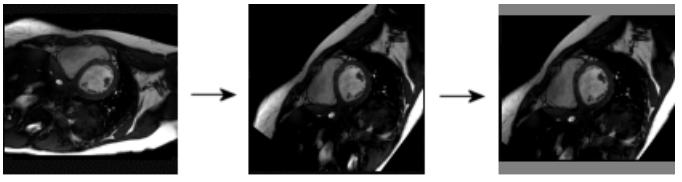


(1) (2) (3)

(1) Original image, Workplace 1
(2) Zoomed and panned image, Workplace 1
(3) Exported / sent image, Workplace 2

Example 2

Rotating rectangular images:

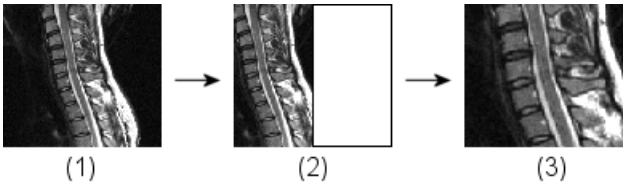


(1) (2) (3)

(1) Original image, Workplace 1
(2) Rotated image, Workplace 1
(3) Exported / sent image, Workplace 2

Example 3

Display of a square matrix in a rectangular Viewer segment:



(1) Original image, square matrix
(2) Image in a rectangular Viewer segment
(3) Image on Workplace 2

Running multiple movies

If you are working in study compare mode, you can use Auto Movie to simultaneously run all loaded studies and series as a movie. Note the following features with ***syngo* MR**:

The menu items for the corresponding functions are available under **Scroll > Sorting** and *not* under **Scroll > Link**.

Filming

Automatic filming

Automatic filming during the examination is not supported by your MR system.

Displaying the reference image

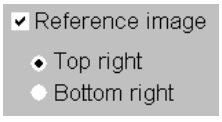
The following section replaces the section of the same name in the *syngo* Operator Manual:

You can display a small reference image (Mother) corresponding to the image (Child) in the film sheet segment. This simplifies the orientation and overview of the measured region.

You set the display of the reference image in the **Film Properties** dialog window, or when configuring a film sheet.

✧ Select **Filming > Properties...**.

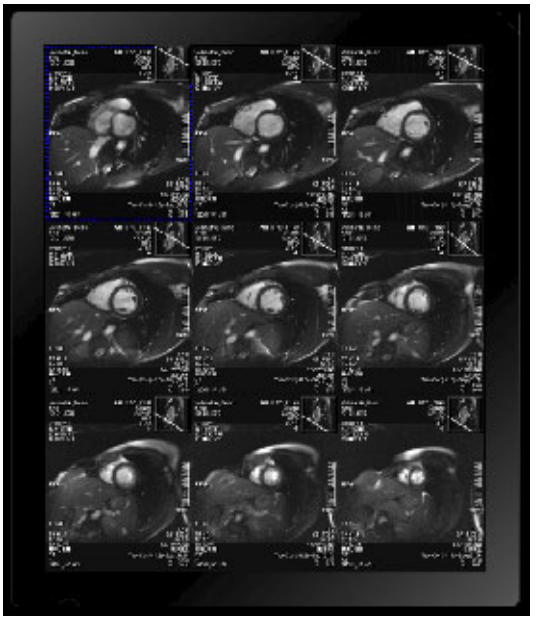
The **Film properties** dialog window opens.



✧ Activate the **Reference image** control box.

✧ Select an option for the position (**Top right** or **Bottom right**) of the reference image.

The system searches the database for a reference image used for slice positioning of the images to be filmed, and displays it in all segments of the current film sheet. The image text is moved to the left.



Displaying cut lines

To enable the position of the image (Child) to be displayed as a cut line in the reference image (Mother), the Mother and Child have to meet the same prerequisites as reference images.
→ Page C.3–4, *Requirements*

Similar rules apply for the display of cut lines as for graphical slice positioning:

❏ A perpendicular slice is represented by a solid line.

❏ An oblique slice is represented by a dashed line.

❏ No cut line is displayed if the angle between the Mother and Child is less than 30°.

Loading another image as the reference image

Instead of the displayed reference image, you can use any other image of the same examination as the mother as long as it was measured at the same table position.

✧ Activate the **Reference Image** option and select the position of the reference image.

✧ Open the **Patient Browser**.

✧ Drag a suitable image to the film sheet with the mouse.

➪ If additional images from the series to which the child belongs are loaded on the film sheet, the new reference image is also displayed there automatically.

Subsequently windowing the reference image

The small reference image may be displayed on the film sheet with unsuitable windowing values.

You cannot window the small reference image directly on the film sheet, but rather only in the **Viewing** task card:

✧ Load the reference image into the **Viewing** task card.

✧ Window the reference image and close the patient.

The new windowing values are permanently applied to the reference image.

✧ Drag the modified reference image from the **Patient Browser** to the film sheet with the mouse.

Reorganizing film sheets

The following section supplements the description on film sheet reorganization in the *syngo* Operator Manual.

You can change the order of images of a series on the **Filming** task card.

✧ Place the input focus on an image from this series that you want to select.

✧ Select **Edit > Select series**.
- Or -
Select **Select Series** in the context menu.

✧ Delete the selected series from the filming request.
→ *syngo* Operator Manual

✧ Change the sorting of images in the **Patient Browser**
→ *syngo* Operator Manual.

✧ Load the new series into the **Filming** task card.
→ *syngo* Operator Manual

The images are displayed in the new sort order.

3D evaluation

Preferred orientation

Menu item **Orientation Control** to activate automatic default alignment is available under **Orientation**, and *not* under **Options**.

Clip planes

Clip planes on the **3D** task card are not supported by your MR system.

Fly-Through

The **Fly-Through** task card is not supported by your MR System.

CHAPTER
A.3 Position Display

For series containing a large number of images, is often useful to display the position of the scanned images in an overview.

The cut lines are calculated for acquired images with the original reference images or other suitable images.

You may display single images, complete series, or several series in the position display.

You may configure the display and labeling of cut lines yourself.

Basics

The position display is used to show the cut lines of acquired images on other images. A new series is generated as a result.

You can display single images, all images of a series, or multiple series as cut lines on reference images.

Terms

When calculating the position display, it is important to understand the following terms:

- **Data image**
  Image whose position line is to be displayed
- **Data series**
  Series containing the data image
- **Reference image**
  Image on which the position line of a data image is to be displayed
- **Reference series**
  Series containing the reference image

Requirements

Both data images and reference images must fulfill the following conditions for successful calculation of position lines:

- ❏ The images are **MR images** only.
- ❏ The images are part of the current examination of the current patient.
- ❏ The images are part of the same series block.
  → Page C.3–38, *Series block*
- ❏ The images were acquired at the same table position.

The following images cannot be used for the position display:

- ❏ Distortion-corrected images
  → Page H.1–69, *FoV compensation filter (large FoV)*
- ❏ Mosaic images
  See Application Guide
- ❏ Secondary capture images
  (e.g. alpha images of the BOLD evaluation)
  → Page D.4–11, *Automatic calculation of the alpha images*
- ❏ Curved cuts of the 3D evaluation
  → *syngo* Operator Manual

Defining data and reference images

The images and series to be used as data images for the position display are already loaded on the **Viewing** task card.

You may define data images and reference images by selecting them explicitly or implicitly.

The order in which you select them determines whether they are used as a data or reference image.

✧ Select the images or series.

NOTICE

Calculation of the position display requires that the user has full access rights to the patient data to be evaluated.

Please observe the information given in the *Safety Standards* book.

Selected images are part of series S1

You have selected some or all images from an S1 series. These images are used as data images. The system identifies the reference series R1 used for slice positioning of S1 and uses R1 as a reference series for the position display.

- If the S1 series was planned using images from different R1 and R2 reference series, the sum R1 + R2 will be used as the reference series in the position display.

- The images of S1 will be mapped onto themselves if no reference series exists for S1 and if it is possible to calculate cut lines.

The selection includes several series (S1, S2, and S3)

You have selected series S1, S2, and S3.

All images from the series selected *last* (S3) (or all images from the series to which the image last selected belongs) will be used as reference images.

The images of series S1 and S2 will be used as data images.

Starting calculation

Single images or all images of one or more series may be displayed in the position display.

Displaying whole series

✧ Select **Evaluation > Position Display > Series**.

Or



✧ Click the **Position Display: Series** button on the **Patient** subtask card.

The cut lines with the reference images are calculated and displayed for *all* images of the data series.

Displaying some images

✧ Select **Evaluation > Position Display > Selection**.

Or



✧ Click the **Position Display: Selection** button on the **Patient** subtask card.

The cut lines with the reference images are calculated and displayed *only* for the selected images of the data series.

- Messages are shown on the status bar during calculation. You may continue working on the **Viewing** task card while the position display is being calculated.
- A message will notify you if you did not select suitable images and it is not possible to calculate cut lines.

The new position display series

Calculating the position display generates a new series.

This new series includes the reference images for which at least one cut line can be calculated and displayed.

The image at the top of the stack in the new series is the image with the greatest number of perpendicular (or nearly perpendicular) cuts.

All images of the new series are fitted to the segment size, even if they had been zoomed or panned prior to calculating the position display.

You may edit images in the position display series.
→ *syngo* Operator Manual

Name of the new series

The name of the new series consists of **PosDisp:**, the series number set in square brackets, plus the name of the first data series.

Example: **PosDisp: [2] t1_se_sag**

Number of the new series

The number of the new series is the highest series number assigned thus far +1.

If a series number has not yet been assigned, e.g, after system installation, the **PosDisp** series will be give the number 5000.

Display and labeling of cut lines

The slice positions of the data images are drawn in the **Pos-Disp** images and labeled as cut lines.

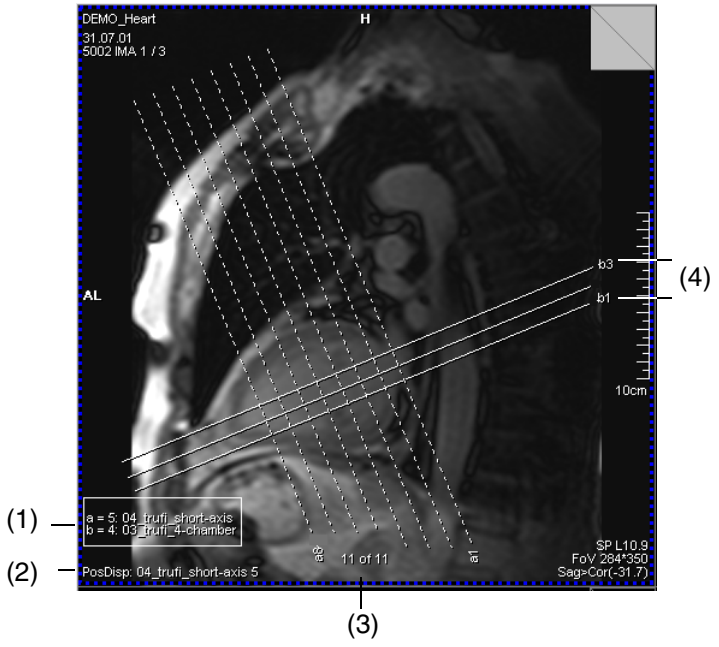
The length of the cut lines does not always represent the spatial extent. They may be cut off at the edges of the images to make space for image text and cut line labels.

Display rules

The following rules apply to the display of cut lines:

- ❏ Perpendicular cuts are displayed as solid cut lines.
- ❏ Oblique cuts (angle ≥ 30°) are drawn as a dashed line.
- ❏ Oblique cuts with smaller angles are not displayed on the reference image.
  (Example: Transverse images are not displayed on transverse reference images.)
- ❏ The cut lines are always displayed with shading lines.
  → Page C.4–38, *Shadow lines*

Labeling rules

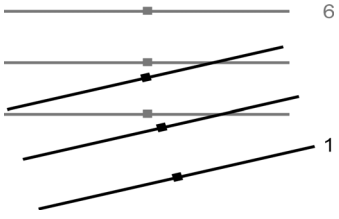


(1) Assignment of lower-case letters to series names
(2) Name of the new position display series
(3) Number of cut lines displayed and number of all data images
(4) Image numbers

The cut lines are labeled with the number of the image if the **PosDisp** series only shows images of *one* series.
→ Page C.6–67, *Numbering of reconstructed images*

If the **PosDisp** series shows images of *several* series, the cut lines are labeled with a lower-case letter to identify the series plus the number of the image. If cut lines coincide, the lowest image number plus **...** is shown.

The comment line of the **PosDisp** images (3) shows how many data images are displayed as cut lines in the PosDisp.



NOTE

If you have configured the position display so that not all cut lines are labeled, the allocation of overlapping cut lines to cut-line numbers that are no longer visible may be incorrect. In such cases, select the labeling option **All** to be on the safe side.

→ Page A.3–16, *Configuring the display of cut lines*

Examples for calculating the position display

Example 1 (series)

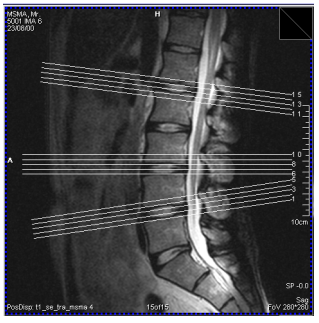
All 15 images of a transverse series are to be displayed on the original reference images. The original reference series consists of a transverse, a coronal, and a sagittal image.

✧ Load the transverse series into the **Viewing** task card.

✧ Place the input focus on an image from this series.



✧ Select **Evaluation > Position Display > Series** or click the **Position Display: Series** button on the **Patient** subtask card.



The position display is calculated. The new **PosDisp** series contains the sagittal and coronal reference images, each with 15 cut lines.

Example 2 (selection)

A coronal series and a transverse series are loaded into the **Viewing** task card. The cut lines of selected coronal images are to be displayed in the transverse images.

✧ Explicitly select the coronal images of interest.

✧ Select an image from the transverse series.



✧ Select **Evaluation > Position Display > Selection** or click the **Selection** button on the **Patient** subtask card.

The position display is calculated. The new **PosDisp** series contains all images of the transverse series for which cut lines of the selected coronal images exist.

Example 3 (several series)

A coronal, a transverse, and a sagittal series are loaded into the **Viewing** task card. The cut lines of all transverse and sagittal images are to be displayed in the coronal images.

✧ Explicitly select a transverse and a sagittal image.

✧ Select an image from the coronal series.



✧ Select **Evaluation > Position Display > Series** or click the **Position Display: Series** button on the **Patient** subtask card.

The position display is calculated. The new **PosDisp** series contains all images of the coronal series including the cut lines of the transverse and sagittal images.

Configuring the position display

You can configure the number of slices to be drawn in the reference images, the location of cut line labels, and how many cut lines are to be numbered.

Opening the Position Display dialog box

To change the settings for the position display while no **PosDisp** series is loaded on the **Viewing** task card, open the **Position Display** dialog box via the menu.

✧ Select **Evaluation > Position Display > Settings**.

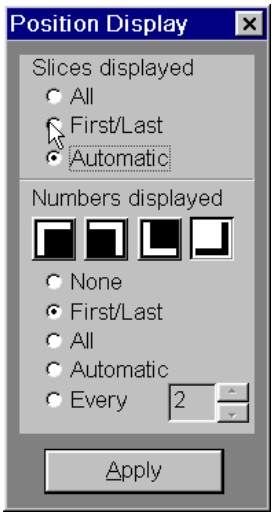
If you want to change how the current **PosDisp** series is displayed, you can also open the **Position Display** dialog box with the **Position display**: **Series** and **Position Display: Selection** buttons.

✧ Place the input focus on the **PosDisp** series.




✧ Click the **Position Display**: **Series** or **Position Display: Selection** button on the **Patient** subtask card.

The **Position Display** dialog box opens.



Configuring the display of cut lines



You can choose the number of cut lines to be displayed.

- **All**
  All cut lines are displayed.
- **First/Last**
  Only the first and last cut lines of a parallel line group are displayed.
- **Automatic**
  Cut lines that are too close to one another are automatically hidden. Overlapping cut line labels are avoided.

✧ Select an option under **Slices displayed**.

NOTICE

The system automatically switches from **First/last** to **Automatic** as soon as the first and last cut line of a group can *not* be calculated.

This does not affect any other line groups.

The above occurs if a data image does not intersect the reference image.

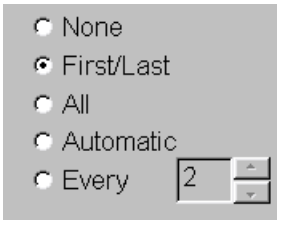
Defining the position of the cut line labels



You may set a preferred position for the cut line labels in the **PosDisp** image.

✧ Click the appropriate button to place the labels on the top left, top right, bottom left or bottom right.

Defining display of the cut line labels



If you are editing a **PosDisp** series containing several slices, it is not advisable to label every cut line.

✧ Click one of the following options:

❏ **None**
No cut lines are labeled.

❏ **First/Last**
Only the first and last cut lines from each parallel and equidistant line group are labeled.

❏ **All**
All cut lines are labeled.

❏ **Automatic**
All cut lines are labeled as long as the labels do not overlap. Individual labels are hidden if they do overlap.

❏ **Every**
Only every nth cut line is labeled. Sorting is based on image numbers and starts at 1.

✧ Enter an increment in the text input field for the **Every** option.

Applying the settings



You may save the configuration settings for the position display.

✧ Click the **Apply** button in the **Position Display** dialog box.

The dialog box will stay open.

The position display settings will still apply the next time you restart the system.

CHAPTER A.4

File Browser

Introduction

The **File Browser** provides you with the opportunity to access and manage a clearly defined portion of the NUMARIS/4 file system.

The **File Browser** enables:

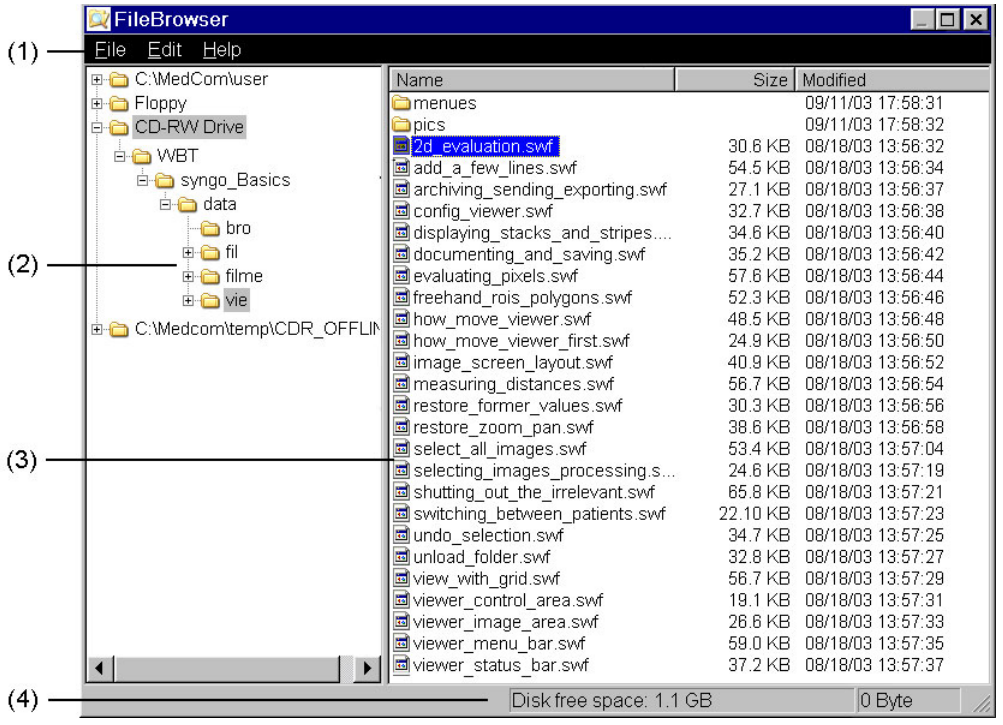
- ❏ Copying or moving files (DICOM image data), i.e., to the CD folder for export
- ❏ Access to generated reports and AVI files,
- ❏ Access to files downloaded via NUMARIS *life*.

⇨ If Security (HIPAA) is activated, you need export authorization for the **File Browser**. Detailed information regarding all security settings in *syngo* are included in the *syngo* Security Package brochure.

Selecting the File Browser

✧ Select **Options > File Browser** from the main menu.

The **File Browser** opens.



(1) Menu bar
(2) View of the directory
(3) Directory view with subdirectories and files
(4) Status bar with display of free disk space

➪ You cannot open more than one **File Browser** at a time.

Closing the File Browser

✧ Select **File > Close** in the **File Browser** menu.

Functions of the File Browser

Opening files and folders

✧ Double-click the desired file or folder.

Or

✧ Select a file or folder.

✧ Select **File > Open**.

Exporting Files and Folders

You are able to export files and folders to the following target destinations:

❏ Floppy disk (A:\)
❏ Memory stick (depending on the system setting)
❏ CD burn folder
❏ Additional enabled folders (depending on the system setting)

✧ Select a file or folder.

✧ Select the export destination under **File > Send to**.

The file or folder is copied to the export target.

Managing Files and Folders

The **File Browser** provides the standard functions of the usual file explorer.

Function	Comment
Cut	You move an object (file or folder) via cut and paste.
Copy	You copy an object (file or folder) via copy and paste.
Paste	Inserts a previously cut or copied object (file or folder) into the current directory.
Rename	Displays the name of the file or folder to be processed in an input field.
New folder	Creates a new folder and displays an input field where you can enter a new name.
Deleting	Deletes the selected file or folder once you confirm the safety query.

✧ Select files or folders.

✧ Select the desired function from the **File** or **Edit** menus.
- Or -
Select the desired function in the context menu of the **File Browser**.

✧ When creating or renaming a file or folder, enter a new name.

➪ Preinstalled folders and files cannot be deleted, moved, or renamed.

PART B

Managing and Adjusting the System

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CHAPTER B.1

System Manager

Your MR system consists of various components: The main component is the MR scanner located in the examination room. In addition, there is an image reconstruction system and the *syngo* Acquisition Workplace for operating ***syngo* MR**. You may also have an optional *syngo* MR Workplace.

These components comprise your MR system. The ***syngo* MR System Manager** is a module that allows you to monitor, as well as start and stop the individual components of the scan system.

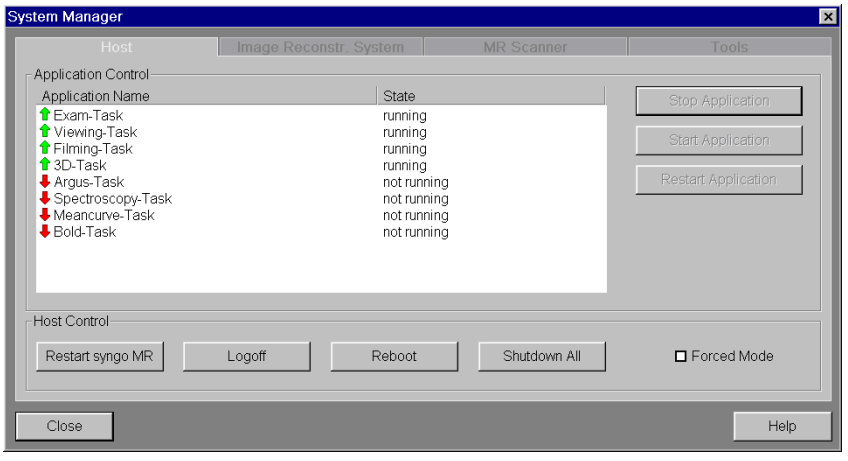
Using the image control system and syngo MR

You control and operate your MR system from the *syngo* Acquisition Workplace. using the ***syngo* MR** program which runs on the Windows XP operating system. The ***syngo* MR** program consists of different applications, such as image processing or 3D. You may sometimes find that one or more applications no longer respond, i.e. your commands are not accepted. If this happens, you may close these applications separately without having to shut down ***syngo* MR** or the operating system.

✧ Select **System > Control** from the main menu.

The **System Manager** dialog box opens.

✧ Click the **Host** card.

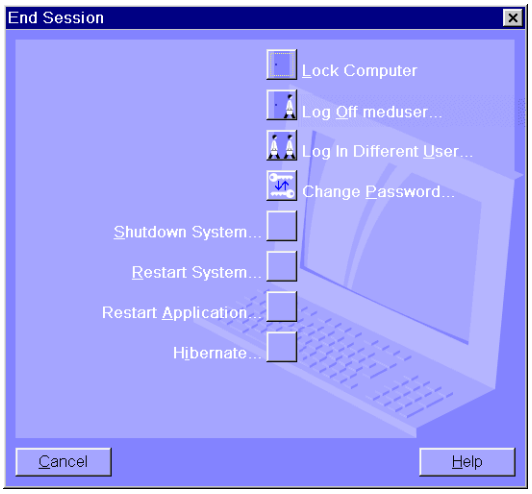


Shutting down the entire system

You can shut down the entire system at once, i.e. the *syngo* Acquisition Workplace, the MR scanner and the image reconstruction system, for example, at the end of the day or to disconnect the system from the power supply for service work or reinitialization of the hardware and software.

✧ Select **Options > End Session** from the main menu.

The **End Session** dialog box opens.



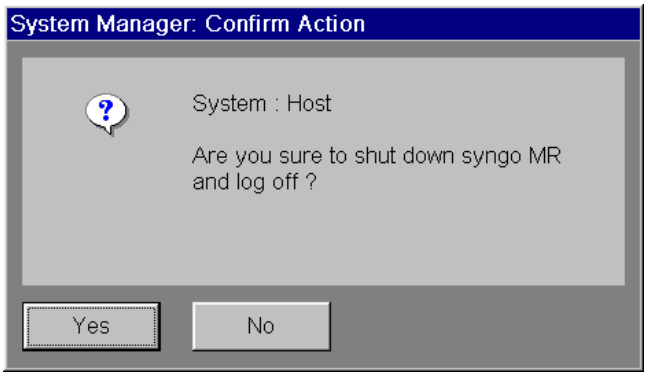
✧ Click the **Shutdown System** button.

Or



✧ Click the **Shutdown All** button in the **System Manager**/ **Host** card.

The **Confirm Action** dialog window opens.



✧ Click the **Yes** button.

➪ Or click **No** to cancel the operation. The system does not shut down.

➪ Once you have closed down all programs and the operating system, you have to switch off the components of the scan system from the alarm box. This is the only way to ensure that the image reconstruction system will start when you restart the system.
See System Manual

Shutting down and rebooting the image control system

An error in the operating system or in ***syngo* MR** can mean that you only need to shut down the *syngo* Acquisition Workplace. The other components of the system such as the MR scanner are not affected.

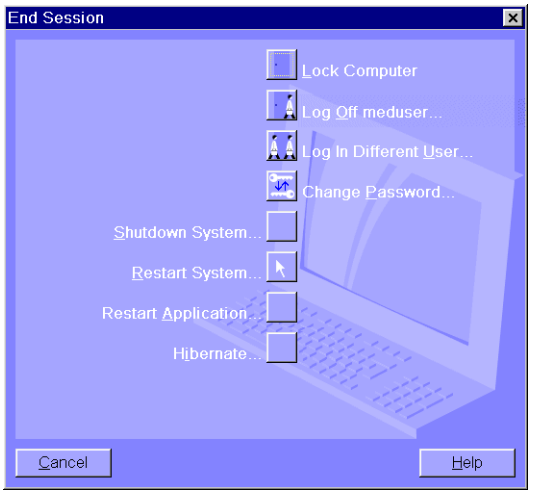
Reboot

✧ Click the **Reboot** button in the **System Manager**.

Or

✧ Select **Options > End Session** from the main menu.

The **End Session** dialog box opens.



✧ Click the **Reboot** button.

***syngo* MR** and the operating system are shut down and then automatically rebooted.

Closing syngo MR and rebooting

You may have to close ***syngo*** **MR** if it no longer responds. You may then restart it automatically.

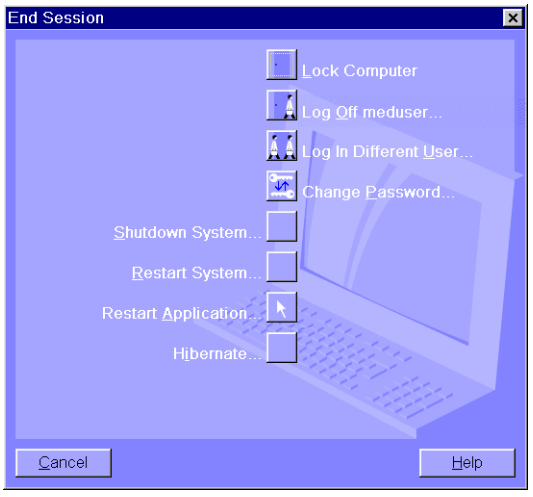
Restart syngo MR

✧ Just click the **Restart *syngo* MR** button in the **System Manager**.

Or

✧ Select **Options > End Session** from the main menu.

The **End Session** dialog box opens.

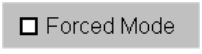


✧ Click the **Restart Application** button.

syngo **MR** is closed and then restarted immediately. The operating system is not affected.

Forced shutdown/reboot

If errors occur in the operating system or in the ***syngo* MR** application, you may respond either by properly shutting down the software or forcing the system to shut down. Following a forced shutdown, the system will be operational again in a short time.



✧ Select the **Forced Mode** option in the system manager.

✧ Click the **Reboot** button on the **System Manager/Host** card.

Or

✧ Click the **Shutdown All** button in the **System Manager/Host** card.

Or

✧ Click the **Restart *syngo* MR** button in the **System Manager/Host** card.

The system shuts down.

CAUTION

After a forced system shut down, all unsaved data and unfinished filming or storage jobs will be lost. All background activities are forced to terminate.

Handling applications

***syngo* MR** includes a series of applications that may be started and closed individually.

The applications that run under ***syngo* MR** on your *syngo* Acquisition Workplace are listed under **Application Name** in the **System Manager**.

The status of each application is also displayed:



❑ **Running**
The application is running.



❑ **Not running**
The application is not running.



❑ **Undefined**
The application status has not been received shortly after starting the System Manager.



❑ **Not responding**
It is not possible to communicate with the software components.



❑ **Unknown name**
Certain components of the application are not available.



❑ **Stop in progress**
The application is shutting down.

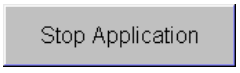


❑ **Startup in progress**
The application is starting up.

Stopping an application

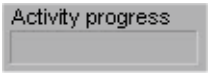
You may stop an individual application (e.g. the 3D module) to save memory space.

✧ Select the application from the list.



✧ Then click the **Stop Application** button.

⇨ Initially, the application shows the status **stop in progress**. Then it changes to status **not running**.



The **Activity Progress** window shows you how far the selected action has progressed. The progress bar allows you to monitor the progress of actions that take a long time.

Starting an application

You may explicitly start applications that you have stopped or that do not start automatically.

✧ Select the application from the list.



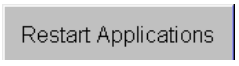
✧ Click the **Start Application** button.

⇨ Initially, the application shows the **start up in progress** status, and then **running** once the application is running.

Restarting an application

You can shut down and restart applications, e.g. if they are no longer responding.

✧ Select the application from the list.



✧ Click the **Restart Application** button.

Locking the computer

If you have to leave the MR system for a short time, you can protect the data on the computer from unauthorized access without having to log off.

➪ This function is available only if the *syngo* security system is activated on your system.

✧ Select **Options > End Session** from the main menu.

The **End Session** dialog box opens.



✧ Click the **Lock Computer** button.

A login window opens. It hides the user interface of the program.

When you want to resume work on the workstation, you only need to log on again.

➪ Detailed information about logging on and off in ***syngo* MR** and access rights in general can be found in the *Safety Standards* book.

Logging off

When you have finished working with the system, you must log off.

✧ Select **Options > End Session** from the main menu.

The **End Session** dialog box opens.



✧ Click the **[user name] Logoff** button.

NOTE

When a user logs off, unsaved data are irretrievably lost.

Check whether data still needs to be saved and save any data you want to keep before you log off.

A login window opens. Opened patient data are unloaded. It hides the user interface of the program.

Another user can now log onto the system.

➪ Detailed information about logging on and off in ***syngo* MR** and access rights in general can be found in the *Safety Standards* book.

Logging on a new user

A new user can log onto the system even if the current user has not logged off.

➪ This function is available only if the *syngo* security system is activated on your system.

✧ Select **Options > End Session** from the main menu.

The **End Session** dialog box opens.



✧ Click the **Log on new user** button.

A login window opens. It hides the user interface of the program.

✧ Enter a new user name in the dialog box.

➪ If you have the same user rights as the previous user, you can work with the loaded data again. If you have fewer rights, the data used by the previous user will be unloaded.

➪ Detailed information about logging on and off in ***syngo* MR** and access rights in general can be found in the *Safety Standards* book.

Changing your password

You can change your password in an input dialog box.

➪ This function is available only if the *syngo* security system is activated on your system.

✧ Select **Options > End Session** from the main menu.

The **End Session** dialog box opens.



✧ Click the **Change Password** button.

An input dialog box is displayed.

✧ Enter the old password in the first field for authentification.

✧ Enter the new password in the next field. Repeat the new password in the third input field for checking.

Upper and lower case letters are treated as different characters.

➪ Detailed information about logging on and off in ***syngo* MR** and access rights in general can be found in the *Safety Standards* book.

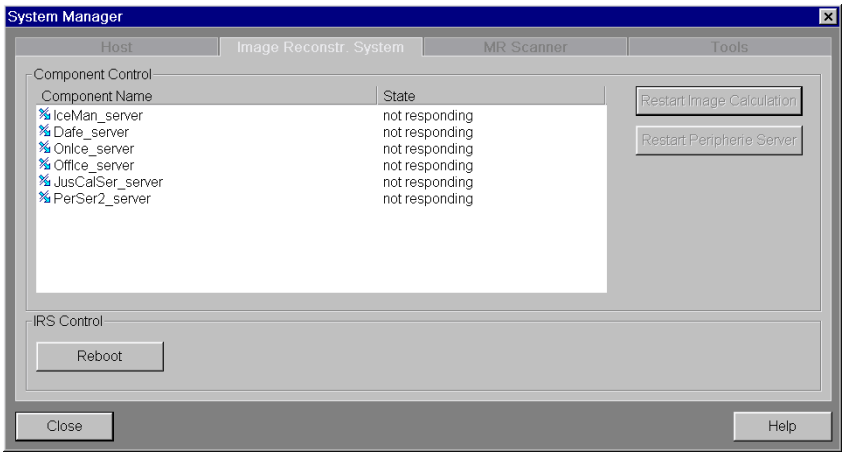
Monitoring the image reconstruction system

The raw data supplied by the scan system are reconstructed by the image reconstruction system. Like the image control system, you can also close down and restart this system, for example, if a fault occurs.

✧ Select **System > Control** from the main menu.

The **System Manager** dialog box opens.

✧ Go to the **Image Reconstr. System** card.



Displaying the status of the image reconstruction system

The status bar of the system contains an icon indicating the status of the image reconstruction system:



Status: *The image reconstruction system is ready.*

If the image reconstruction system is not ready, the icon has a red line through it.

➪ Double-clicking on the icon opens a dialog box with an explanation.

Rebooting the image reconstruction system

In the event of a fault, you can shut down and reboot the entire image reconstruction system.



✧ Click the **Reboot** button.

The image reconstruction system will be shut down and rebooted. It will not be operable again until the status of the monitored applications changes from **not running** to **running**.

Shutting down and rebooting components

The **Component Control** window of the **Image Reconstr. System** card shows which software components of the image reconstruction system are running and what status they have.

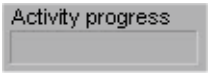
If a software error occurs during scanning or image reconstruction, you may restart the components of the image reconstruction system separately.

Restarting software components

If errors occur during image reconstruction, all software components running on the image reconstruction system, except the **Peripherie Server** (peripheral server), will be shut down and restarted.



✧ Click the **Restart Image Calculation** button.



The **Activity Progress** window shows how long it will take to shut down and restart the software components.

The system is ready for scanning again once the components of the image reconstruction system have restarted.

➪ The status of the **Peripherie Server** (peripheral server) component must be **running** while the software components restart.

Restarting the Peripherie Server (peripheral server) component

The **Peripherie Server** (peripheral server) component establishes the connection with the MR scanner and is restarted separately.



✧ Click the **Restart Peripherie Server** button.

The **Peripherie Server** (peripheral server) component is shut down and restarted.

The status of the image calculation components stays **running**.

➪ Shutting down and restarting the **Peripherie Server** (peripheral server) component of the image reconstruction system takes longer than restarting the image reconstruction components.

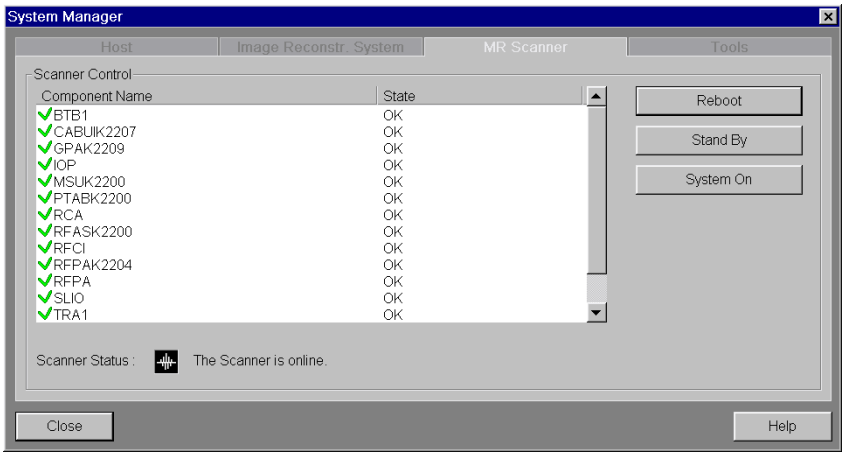
Controlling the MR measurement system

The computer system of the MR scanner also has an operating system. You can display the current status of individual components of the MR scanner and switch the power supply on and off.

✧ Select **System > Control** from the main menu.

The **System Manager** dialog box opens.

✧ Go to the **MR Scanner** card.



Operating status of the individual components

All the components of the MR scanner are listed under **Component Name**.

The current status of the components (**ok** or **not ok**) is shown in the **State** column.



OK



Not OK

➪ The list is updated automatically. The **MR scanner** is not always online while it is rebooting. Therefore, it is not possible to display the status of scanner components during booting. During this time, the **MR Scanner** window shows the message "The Scanner is not online".

Status of the MR scanner

The status of the MR scanner is shown both on the **MR Scanner** subtask card and on the status bar of the system.

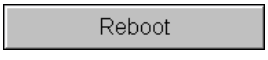


Status: *MR scanner is ready.*

If the MR scanner is not online or is booting, the icon has a red line through it.

Rebooting the operating system

If an error occurs in the operating system of the MR scanner during operation, you can eliminate the error by shutting down and rebooting the operating system.



✧ Click the **Reboot** button.

Switching the Power Supply to Standby

Switching the MR scanner to standby

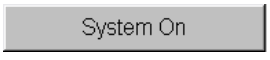
If you do not intend to perform scans for a longer period of time or only want to process or evaluate images at the *syngo* Acquisition Workplace, you can disconnect the MR scanner from the power supply in order to save energy.



✧ Click the **Stand By** button.

Switching the power supply on again

If your MR scanner is in **Stand By** mode, you can switch on the power supply again to resume scanning.



✧ Click the **System On** button.

➪ The power supply of the MR scanner can also be switched on or off in the alarm box.
See System Manual

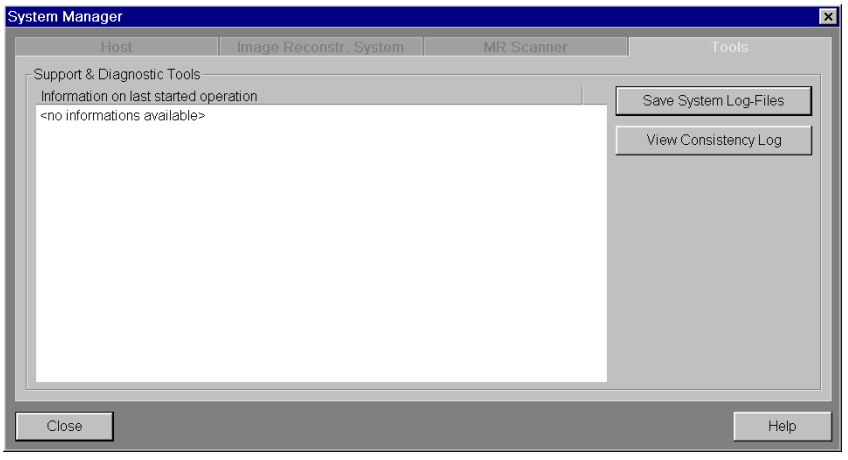
Tools

The **Tools** card is used to acquire diagnostic information or check important system files.

✧ Select **System > Control** from the main menu.

The **System Manager** dialog box opens.

✧ Go to the **Tools** card.



Gathering diagnostic information

If a software error occurs during scanning, it is recommended to create a "MrSaveLog" file immediately. This allows you to gather valuable diagnostic information.



✧ Click the **Save System Log-Files** button.

The "MrSaveLog" file is created. It contains all diagnostic information valid at the time the error occurred. It is stored in the C:\MedCom\MriDiagnostic folder as a ZIP file. Siemens Service will be able to use the ZIP file for subsequent analysis.

➪ The diagnostic information contained in it can be used to help locate the error.

Displaying changed files

The most important system files are checked every time the system boots.



✧ Click the **View Consistency Log** button.

The "MrConsistency-Checker" checks the system files for changes every time the system boots. The result is saved in a log file. You can view the content of this file in the **Support&Diagnostic Tools** window by clicking the **View Consistency Log** button.

➪ Never install additional software on the system. Installation could replace existing system files and impair the scanning capability of the system.

Displaying system information

***syngo* MR** also displays information about your scan system. This includes information regarding memory capacity and available disk space.

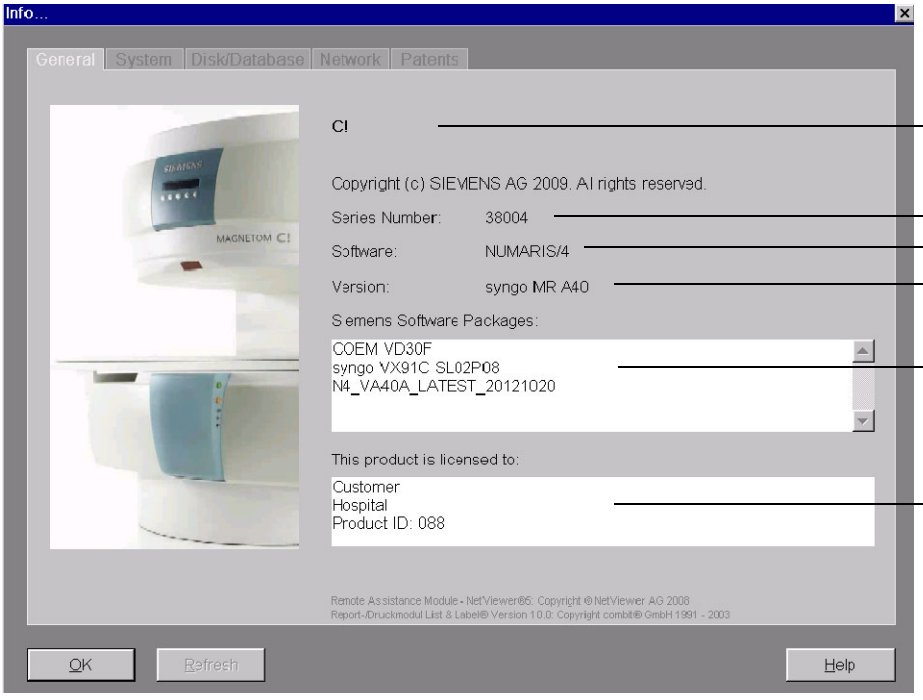
General system information

General system information is required, e.g. when you contact Siemens Service regarding problems. Problems can be solved more quickly if you specify the serial number of the system and the software version.

✧ Select **Help > Info ...** from the main menu.

✧ Go to the **General** card.

The **Info ...** dialog window opens.



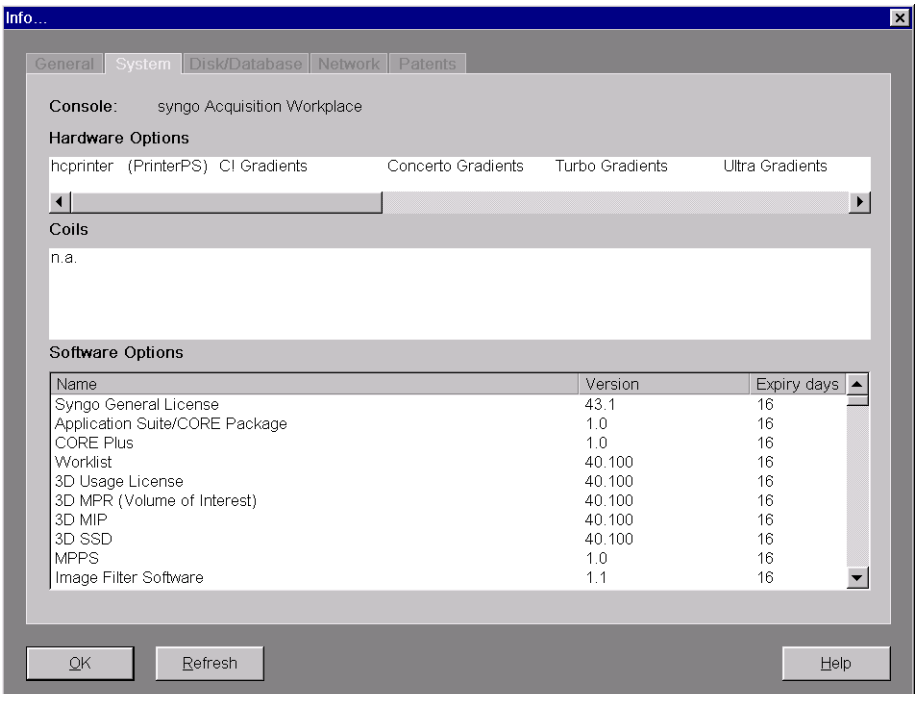
(1) Product name
(2) Series number
(3) Software used
(4) Software version
(5) Software name
(6) Information about license holder; name, hospital or practice, and product identification number (product ID)

Information about the system

The **System** card provides further information about your scan system. Here, you will find information about hardware and software options (e.g. cameras and printers) as well as the coils currently available.

✧ Select **Help > Info ...** from the main menu.

✧ Go to the **System** card.

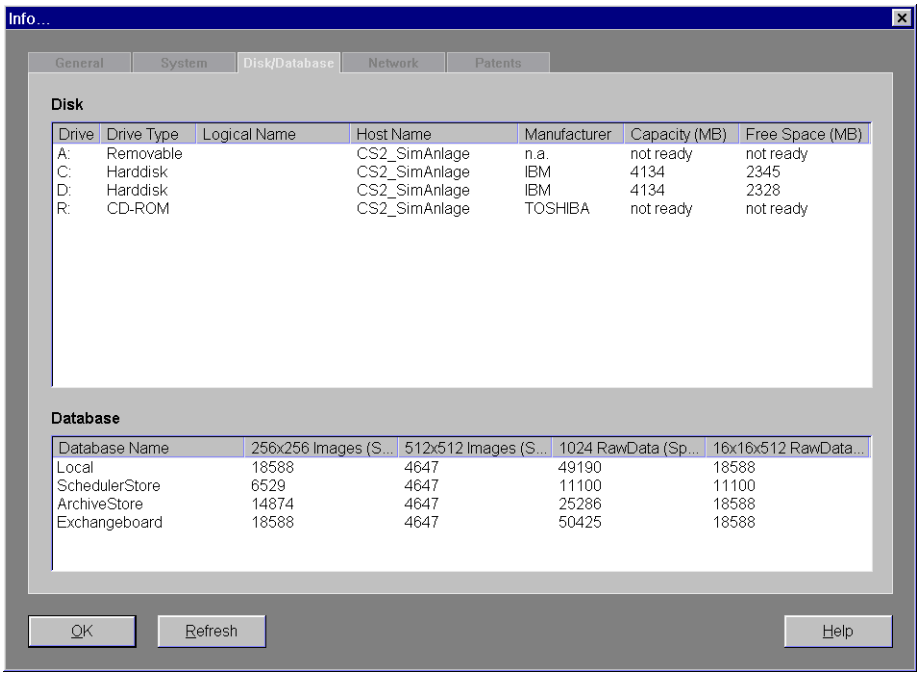


Drive and database information

The **Disk/Database** card displays the drives and hard disks currently connected, including information about the capacity and free space still available. It also displays how much space is available in terms of images.

✧ Select **Help > Info ...** from the main menu.

✧ Go to the **Disk/Database** card.



Displaying the drives

The **Disk** list displays all physical (e.g. CD-ROM) and logical (e.g. network drives) drives. The capacity and free space still available is listed next to them.

The following information about these drives is displayed:

- ❏ drive letter, e.g. diskette drive A
- ❏ type of drive, e.g. CD-ROM
- ❏ logical name of the hard disk
- ❏ name of computer to which memory medium is connected
- ❏ manufacturer of the memory medium
- ❏ capacity of the memory medium (in MB)
- ❏ free disk space in MB

Displaying the databases

All local databases are listed under **Database**. You are also told how many images can still be stored for each matrix.

The following information is displayed:

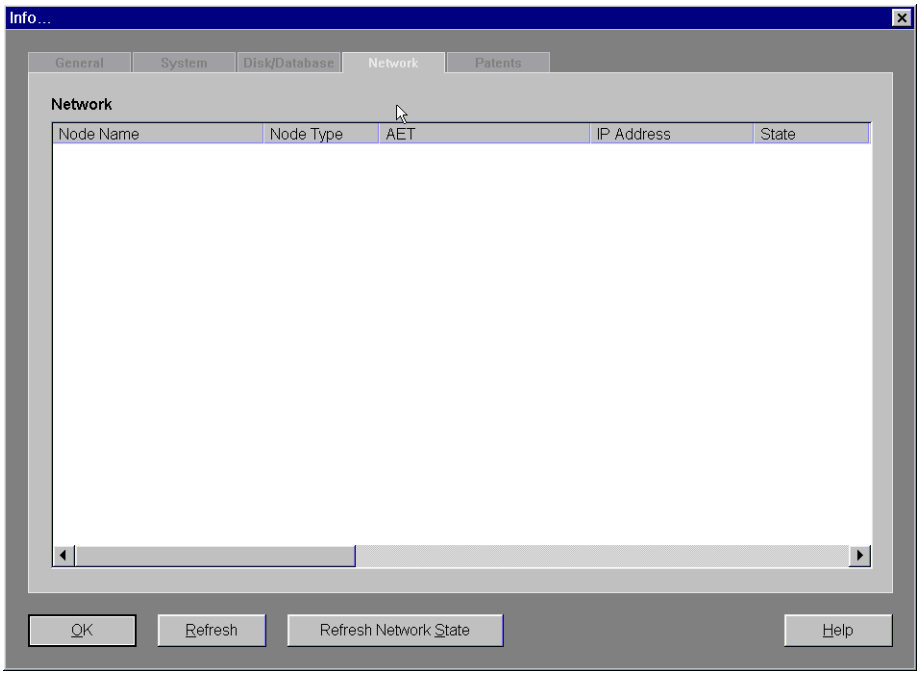
- ❏ Name of the database
- ❏ Number of images 256 × 256 matrix images that can still be stored
- ❏ Number of images 512 × 512 matrix images that can still be stored
- ❏ Number of raw data sets (1024) that can still be stored
- ❏ Number of raw data sets (16 × 16 × 512) that can still be stored

Network information

If your *syngo* Acquisition Workplace or *syngo* MR Workplace is connected to a network, you can view network-specific information on the **Network** card.

✧ Select **Help > Info ...** from the main menu.

✧ Go to the **Network** card.



Updating the network display

If the dialog window has been open for a while, you may refresh the network information display.



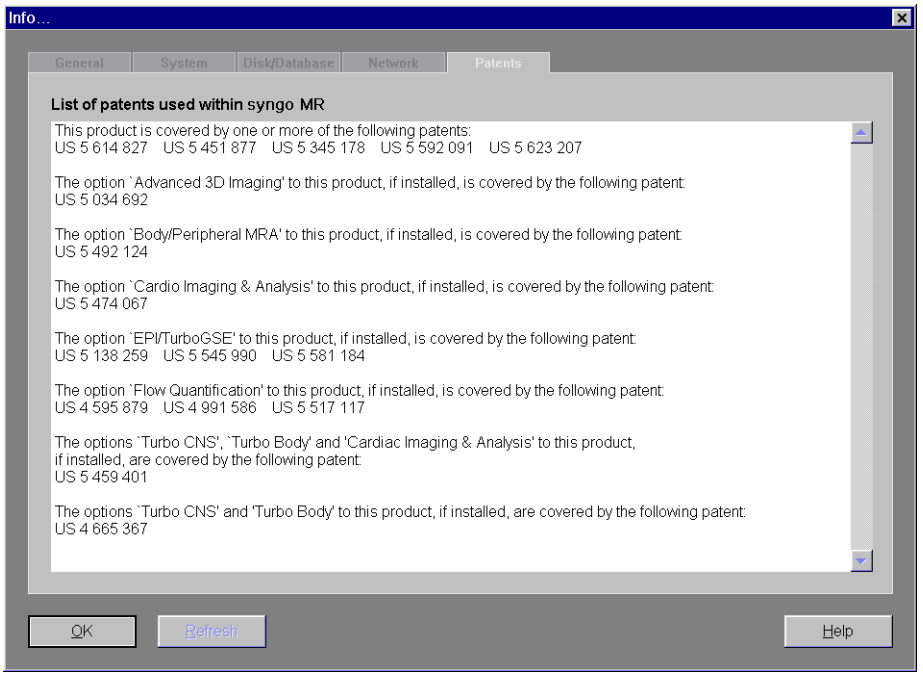
✧ Click the **Refresh Network State** button.

Displaying patents

The **Patents** card lists all the patents used by ***syngo* MR**.

✧ Select **Help > Info ...** from the main menu.

✧ Go to the **Patents** card.



Updating the display

If the **Info...** dialog window has been open for a while, you may refresh the data displayed.



✧ Just click the **Refresh** button.

➪ The button is only active if you have selected the **System**, **Disk/Database**, or **Network** card.

CHAPTER B.2

Adjusting the System

To consistently obtain high-quality images, it is important to adjust the scan protocol prior to each protocol. For this purpose, individual settings are available for automatic adjustments prior to each protocol.

However, manual adjustment of the scan system is sometimes required for special scanning methods such as spectroscopy.

With shimming you compensate for inhomogeneities of the magnetic field.

An adjustment volume is defined for each protocol. Most adjustments refer to this volume, which you may display during graphic slice positioning. You may change it there or on the **System** parameter card, as required.
→ Page B.2–8, *Adapting the adjustment volume*

Configuring automatic adjustment

Automatic adjustment of the system is performed prior to each scan. In most cases, it is not necessary to change the settings during routine operation. You can check these parameters, however, you should not modify them under normal circumstances.

Opening a protocol

It is only possible to view the parameters of a protocol if it is open.

✧ Select a protocol in the program control.

✧ Click the **Open** button or double-click the selected program.

The protocol opens and the specific parameters are displayed.

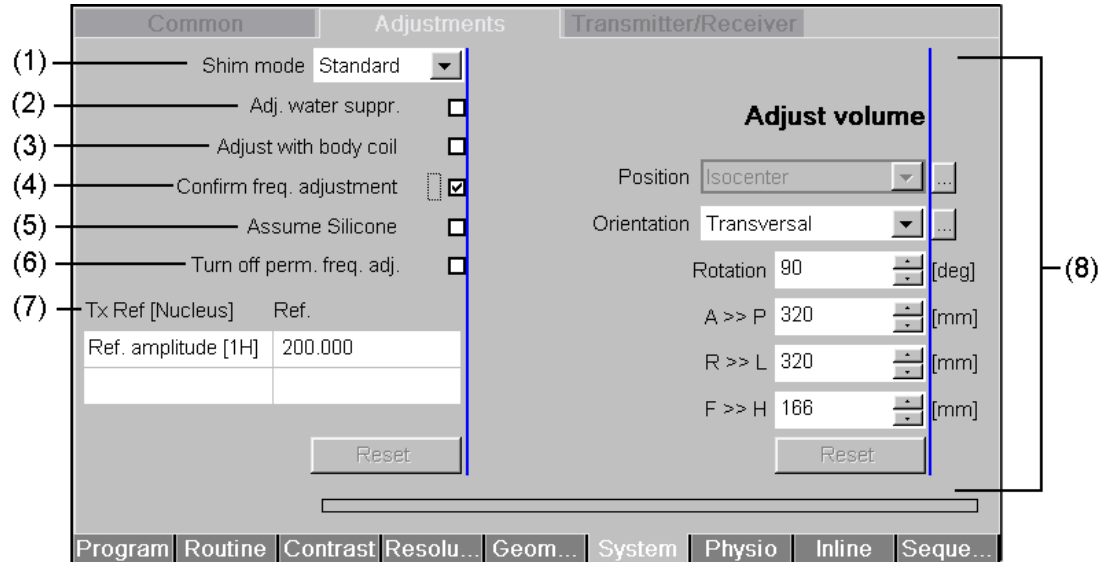
You may view and edit (if required) the automatic adjustment parameters on the **System** parameter card.

✧ Go to the **System** parameter card.

> **NOTE**
>
> All system adjustment settings made on the **System** parameter card *only* apply to the protocol currently open.

Settings on the Adjustments card

✧ Go to the **Adjustments** card.



(1) Selecting shim mode
(2) Performing water suppression adjustment
(3) Performing adjustment with the body coil
(4) Changing the resonance frequency
(5) Adjustment in silicone mode
(6) Suppression of standard frequency adjustment (only with "Concerto", "C!" and "Symphony Mobile" systems)
(7) Changing the reference amplitude
(8) Geometry of the adjustment volume

Setting the shim mode

For the 3D-shim, up to three settings are available per protocol depending on the various measurement requirements:

- **Tune-up**; neither adjustment scans nor evaluations are necessary. The system uses the values set during system tune-up by Siemens Service. This setting is sufficient for standard imaging protocols without special requirements.
- **Standard**; Adjustment scanning and evaluation are performed in standard mode. This mode is suitable for imaging protocols with special requirements, for example, for fat saturation or EPI.
- **Advanced**; Adjustment scans and evaluation are performed in advanced mode. This mode is used mainly for spectroscopy protocols. Advanced mode is time consuming and is only necessary for scans that place the greatest demands on the homogeneity of the magnetic field.

Each protocol is preset to the mode required for optimum image quality.



✧ Select a shim mode from the list.

It is also possible to use the manual interactive shimming method, independent of this protocol setting.
→ Page B.2–69, *Interactive shim*

Performing adjustments with the body coil

Normally, all adjustments are performed using the coil elements defined in each protocol and used during subsequent imaging. You may also perform the adjustment measurements using the body coil only. This method saves time, since it is not necessary to make readjustments after changing the selection of coil elements.

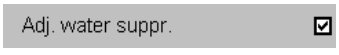


✧ Click the **Adjust with body coil option.**

➪ For spectroscopy protocols, it is not possible to perform adjustments using the body coil.

Performing water suppression adjustment

For spectroscopy measurements, special pulse trains are used that suppress the water signal.



✧ Select the **Adj. water suppr.** check box to optimize the pulse train.

Confirming or changing the resonance frequency

After an inline adjustment, you may pause the system and accept or change the resonant frequency.



✧ Click the **Confirm freq. adjustment** check box.
→ Page B.2–86, *Changing the resonant frequency after inline adjustment*

Adjustment in silicone mode

The **Assume Silicone** option optimizes measurements taken for patients with silicone implants.



✧ Click the **Assume Silicone** check box.

Suppression of standard frequency adjustment

On "Concerto", "C!" and "Symphony Mobile" systems, frequency adjustment is performed before each imaging scan, even if the scan parameters have not changed. You may switch off this automatic frequency adjustment.

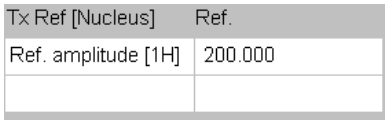


✧ Click the **Turn off perm. freq. adj.** check box.

➪ On "Symphony Mobile" systems, this option can be selected only for time-critical scans.

Changing the reference amplitude

The **TxRef/Ref** display field shows a list of reference amplitudes for the selected primary or secondary nucleus.



✧ Enter new values for the reference amplitude.

All manually modified values are marked with an exclamation point ("!") and will be ignored during the next optimization.

You can undo your manual settings at any time.



✧ Click the **Reset** button on the **Transmitter/Receiver** parameter card.

The automatically calculated values are now displayed again.

Adapting the adjustment volume

A localized volume, the adjustment volume, is defined for each protocol for tuning the transmitter and receiver. The adjustment volume defines the space in the magnet for which the parameters will be optimized. It is determined automatically but may also be adjusted manually.

Imaging protocols

The default setting of the adjustment volume depends on the slices and slabs. In most cases, an orthogonal cuboid completely encloses the slices or slabs to be measured.

Spectroscopy protocols

Here, the adjustment volume is equivalent to the VOI.

NOTE

Protocols requiring neither shim adjustment measurement (e.g. tune-up mode) nor water suppression adjustment use a fixed adjustment volume in the form of a large central cuboid.
This saves time since readjustment is not necessary after slice positioning.
Of course, you may also manually adapt the adjustment volume at any time.

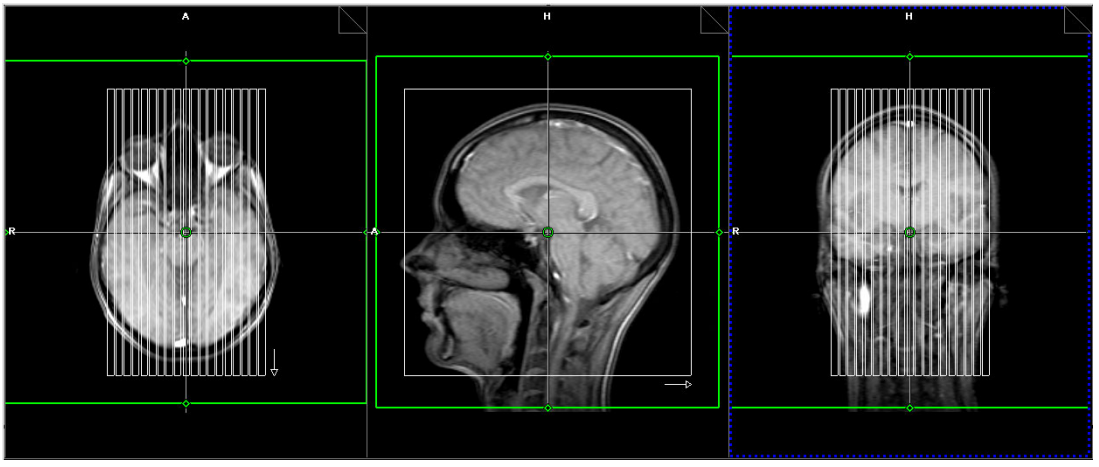
Editing the adjustment volume graphically

During graphic slice positioning, you may display the adjustment volume as an additional graphic object in the reference images.



✧ Click this button on the **Position Toolbar**.

The adjustment volume is shown as a green rectangle in each reference image and may now be edited graphically.

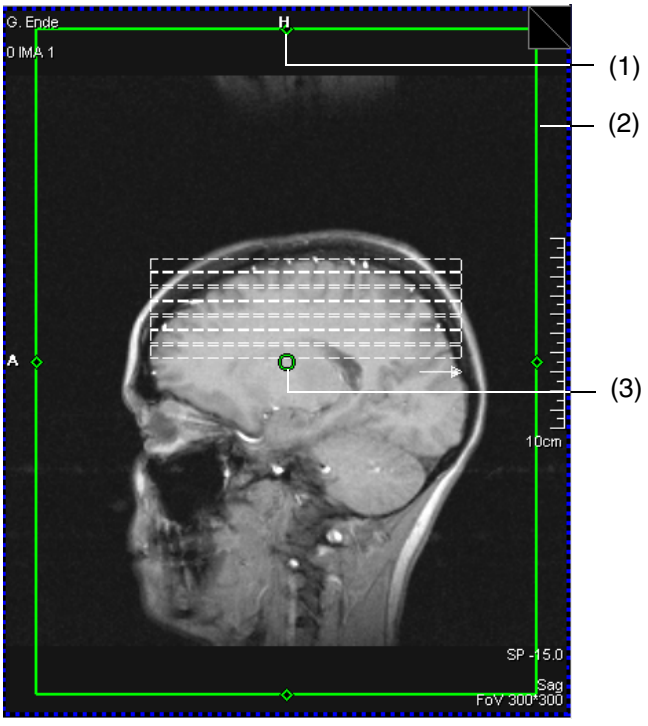


Selecting an adjustment volume

To enlarge/minimize you must first select the adjustment volume.

✧ Click the contour line of the adjustment volume.

The adjustment volume turns bright green. The center and resizing handles are displayed.



(1) Resizing handles/contour line
(2) Contour line
(3) Center for moving

Moving the adjustment volume



✧ Place the mouse pointer on the center of the adjustment volume.

The mouse pointer changes shape.

✧ Press the left mouse button and drag the adjustment volume to its new position.

Or

✧ Place the mouse pointer on a contour line or a handle, press the **Shift** key and left mouse button, and drag the adjustment volume to its new position.

Resizing the adjustment volume



✧ Click a contour line of the adjustment volume if the handles of the adjustment volume are not yet visible.

✧ Place the mouse pointer on one of the handles.

The mouse pointer changes shape.

✧ Press and hold the left mouse button while dragging the handle in the desired direction.

The size of the adjustment volume is increased/decreased *symmetrically*.

The center of the adjustment volume remains unchanged.

To change the size of the adjustment volume *asymmetrically*, i.e. increase/decrease its size in only one direction:

✧ Also press the **Alt** key while performing the steps described above.

The center of the adjustment volume is moved accordingly.

Rotating the adjustment volume

The volume element may be rotated about its center point. The rotational axis is now perpendicular to the reference image.

✧ Place the mouse pointer on the contour line of the adjustment volume, but not on a handle.



The mouse pointer changes shape.

✧ Hold down the left mouse button and drag the contour line of the volume element in the desired direction.

The adjustment volume may be rotated about the center in one spatial direction only.

Tilting the adjustment volume

The volume element can be tilted about an axis that runs parallel to the reference image and through the center point.

✧ Press the **Alt** key and drag the contour line in the required direction.

The tilting axis is perpendicular to the movement of the mouse.

Rotating the adjustment volume freely

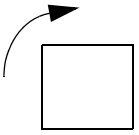


Free rotation of the adjustment volume is a combination of rotation and tilting and is supported in all three spatial directions.

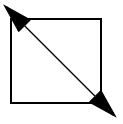
- ✧ Click a contour line of the adjustment volume if the adjustment volume handles are not yet visible.
- ✧ Press the **Ctrl** key and drag a handle or a contour line.
- ✧ Drag the adjustment volume tangentially towards the adjustment volume to rotate it.

Or

- ✧ Perform a radial movement (radiating away from or toward the center) to tilt the adjustment volume.



tangential movement

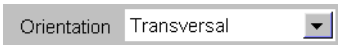


radial movement

The rotational axis runs through the center of the volume element and is perpendicular to the reference image.

Numerically setting the adjustment volume

To set the adjustment volume with millimeter precision, you may also enter the parameters numerically. The respective input fields can be found on the **Adjustment** subtask card of the **System** parameter card.



✧ To manually set the adjustment volume, first select an orientation.

Or



✧ Enter an orientation in the **Orientation** dialog box.



The **Position** field displays the current position of the adjustment volume.



✧ Enter a new position for the adjustment volume in the **Position** dialog box.
→ Page C.5–25, *Geometry parameter card*



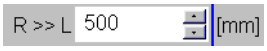
✧ Enter the angle for rotating the adjustment volume in the **Rotation** spin box.



✧ Enter the edge length of the adjustment volume in the **A >> P** (anterior/posterior) direction.



✧ Enter the edge length of the adjustment volume in the **F >> H** direction (feet/head).



✧ Finally, enter a translation of the edge length of the adjustment volume in the **R >> L** direction (right to left).

Applying the settings

✧ To apply the settings simply press the **Return** key after numeric input.

Or

✧ Click the image area with the mouse to update the graphic display.

Restoring the default settings

✧ Click **Reset** to reactivate automatic calculation of the adjustment volume.

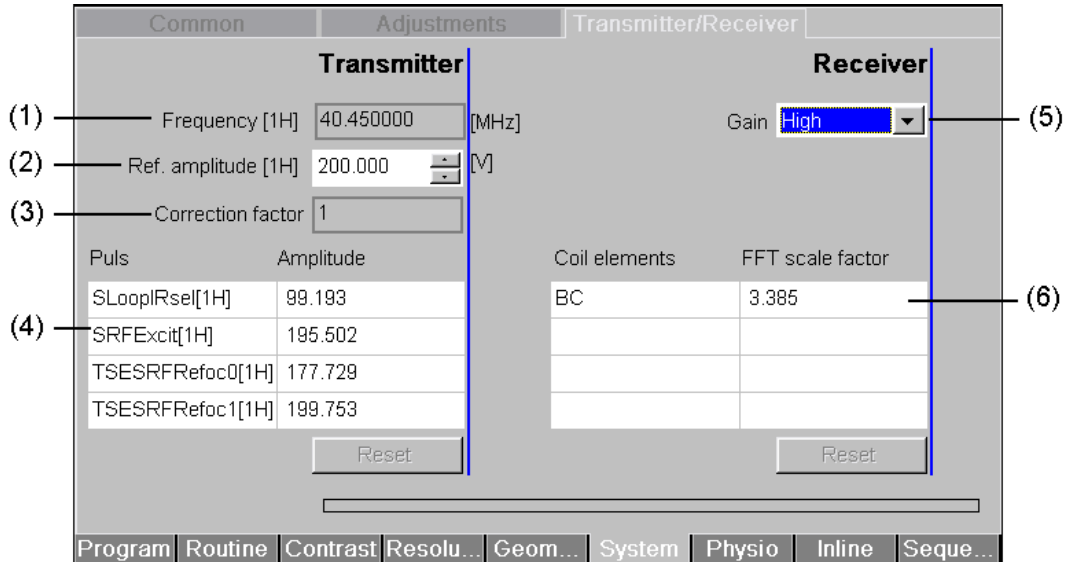
The exclamation points are now hidden.

Adjustment parameter display in the protocol

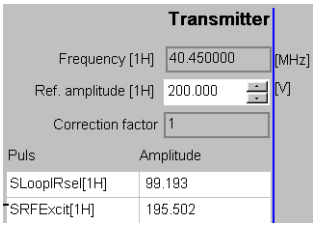
The **System Transmitter/Receiver** parameter card shows the results of the last automatic and successful adjustment.

✧ Click the tab of the **System** card to move it into foreground.

✧ Click the **Transmitter/Receiver** card into foreground.



(1) Display system frequency
(2) Display reference amplitude
(3) Display the correction factor for water suppression
(4) Amplitude of the RF pulses used in the protocol
(5) Receiver gain
(6) FFT scale factors of the individual images from each coil element

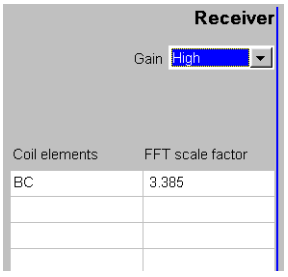


The left side of the parameter card displays the values of the last successful transmitter tuning:

- ❏ the MR system frequency under **Frequency**
- ❏ the pulse amplitude calibration under **Ref. amplitude**
- ❏ the factor for water suppression under **Correction factor**

All pulse amplitudes are calculated from the reference amplitude and, if necessary, the correction factor.

This parameter card also allows you to overwrite the automatically corrected pulse amplitudes by entering new values.



The right side of the **Transmitter/Receiver** parameter card shows the values for the receiver gain automatically calculated by the system:

- ❏ the gain level of the receiver
- ❏ the FFT scale factors for the individual images of each coil element

Here, too, you have the option of overwriting the automatically calculated values by entering new values.

Undoing changes

All manually changed values and settings are marked by an exclamation point ("!").

You can undo your manual settings at any time.



✧ Click the **Reset** button on the **Transmitter/Receiver** parameter card.

The automatically calculated values are now displayed again.

Automatic sequence of adjustment steps

Special adjustments are performed automatically for each protocol. To avoid having to perform a complete adjustment each time, the system checks the adjustment status and uses adjustment results from a previously scanned protocol, if possible.

The results can normally only be applied if the following parameters of the two protocols remain unchanged:

- ❏ the table position
- ❏ the coil elements used
- ❏ the shim mode (standard/advanced/tune-up)
- ❏ the adjustment volume

Dependencies between adjustments

When adjusting the system, the sequence of adjustment operations is important since some adjustments may invalidate the results of previously performed adjustments. After 3D-shim, for example, frequency adjustment is automatically performed again because changing the magnetic field causes the system frequency to change.
These dependencies are always taken into account by the automatic adjustments.

Validity of the adjustment parameters obtained

The adjustment parameters obtained after successful adjustment may be used for further protocols. They become invalid in the following cases:

- ❏ A new patient is registered
- ❏ The parameters are invalidated explicitly
  → Page B.2–92, *Rejecting all adjustment results*
- ❏ The coils on the patient table are changed

As already mentioned, dependency on the coil elements can be avoided by selecting **Adjust with body coil**. The dependency on the adjustment volume may be avoided via the shim mode tune-up without water suppression.
→ Page B.2–3, *Settings on the Adjustments card*

This reduces the number of adjustment steps and saves time.

Manual adjustment

Manual adjustments must only be performed by experienced users and are mainly intended for test purposes, error analysis, or for special applications such as spectroscopy.

The following adjustment options are available:

- ❏ Adjusting the transmitter coil
- ❏ Adjusting local coils
- ❏ Optimizing the resonance frequency
- ❏ Optimizing the multinuclear resonance frequency
- ❏ 3D shim and interactive shim
- ❏ Tuning the transmitter
- ❏ Tuning the multinuclear transmitter
- ❏ Optimizing water suppression

➪ Interactive shimming may only be performed manually.

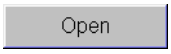
➪ The number of adjustment options available depends on your system.

➪ Multinuclear adjustments are only available with the appropriate license.

NOTE

Manual adjustment of the system should only be performed by experienced users and should not be performed during routine operation.

Opening a protocol



Open the protocol that requires manual adjustment.

✧ Click the **Open** button in the program control or double-click the entry.

The protocol-specific parameters are displayed on the parameter cards.

The individual steps of manual adjustment are described below.

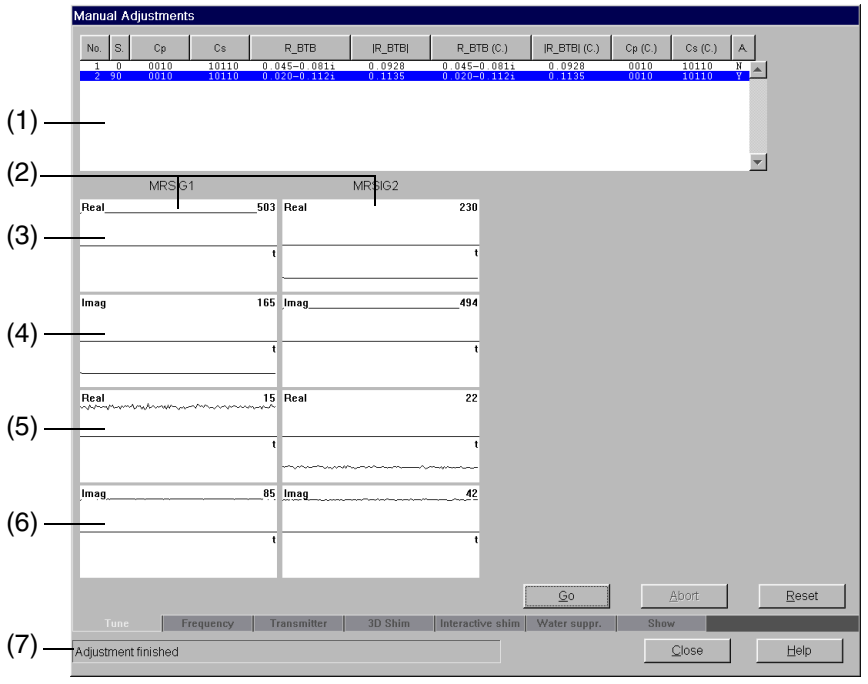
Adjusting the transmitter coil

If the body coil has been selected as the transmitter coil for the selected protocol, you may tune it with this adjustment. The input impedance of the body transmitter coil depends on the patient. It is adapted to the output impedance by switching additional capacitance values in the body tune box (BTB). The reflectance is calculated from the transmission and reflection signals. When the reflectance reaches a minimum value, the coil is tuned. For this purpose, several adjustments may be required.

Preparing the adjustment

✧ Select **Options > Adjustments** from the menu and go to the **Tune** card.

The **Manual Adjustments** dialog box is displayed with the **Tune** card.

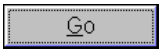


(1) Numeric results of the adjustment
(2) 0° scale system (left) and 90° scale system
(3) Real part of the measurement signal of the forward wave (transmission signal)
(4) Imaginary part of the measurement signal of the forward wave
(5) Real part of the measurement signal of the reverse wave (receiver signal)
(6) Imaginary component of the measurement signal of the reverse wave
(7) Status bar

Starting the adjustment

Once you have completed the preparations for scanning, you may start the adjustment.

⇨ It is not possible to enter parameters for coil adjustment. It runs automatically. You only launch it manually.



✧ Click the **Go** button in the **Manual Adjustment** dialog box.

⇨ You can monitor the progress of adjustment on the status bar.

The results are displayed numerically and graphically.

Numeric results

A line is displayed with the following parameters for each iteration:

- ❏ **No.**; running number of the measurement
- ❏ **S.**; measured scale system (0° or 90° system)
- ❏ **Cp**; switch position of the parallel capacitors (0/1) (1: switch closed or 0: switch open)
- ❏ **Cs**; switch position of the serial capacitors (0/1)
- ❏ **R_BTB**; measured complex reflectance on the body tune box (BTB)
- ❏ **|R_BTB|**; absolute value of the measured reflectance at the body tune box
- ❏ **R_BTB (C)**; calculated minimum reflectance
- ❏ **|R_BTB| (C)**; absolute value of the calculated reflectance.
- ❏ **Cp (C.)**; optimum switch position of the parallel capacitors derived from the calculation (0/1)
- ❏ **Cs (C.)**; optimum switch position of the serial capacitors derived from the calculation (0/1)
- ❏ **A.**; successful adjustment of the system (Y/N)

NOTE

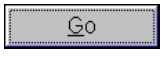
The 0° and 90° scale systems are adjusted in mutual dependence. An **N** may therefore appear in column **A.** after the 0° scale system has been scanned. Once the 90° scale system has been scanned, convergence of the adjustment is indicated by a message in the footer and a **Y** in column **A**.

Graphic display of the results

The forward and reverse wave signal (real and imaginary part) for the current iteration are displayed in the time domain in the graphic display. The raw data maximum is displayed numerically.

Repeating the adjustment

✧ Repeat the adjustment until reflectance has reached a minimum and "**Y**" appears in the numeric display.



✧ Click **Go** again to start scanning.

Aborting adjustment



✧ Click the **Abort** button to cancel an adjustment scan.

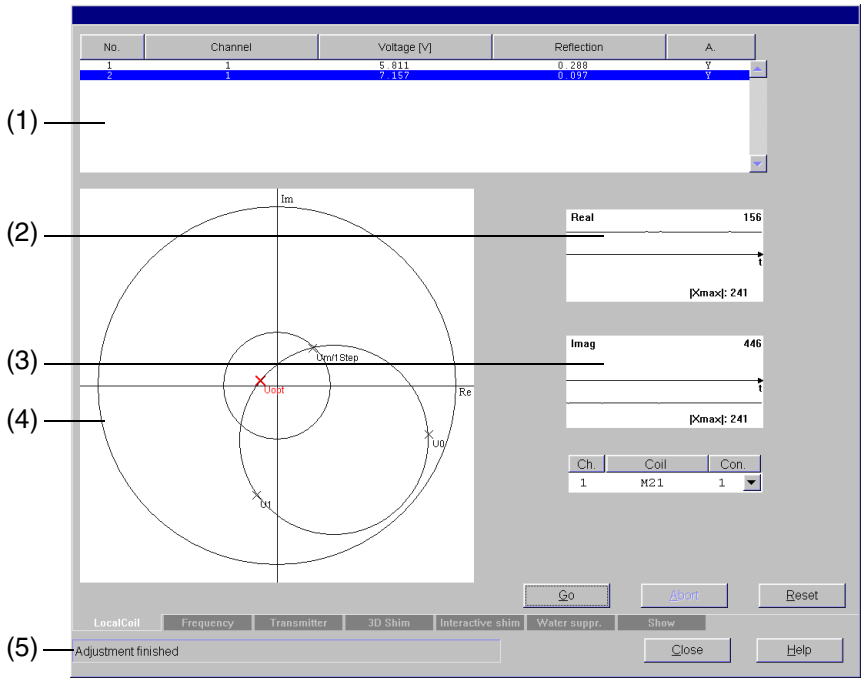
Adjusting local coils

This adjustment tunes the local receiver coils required for the selected protocol. The input impedances of the local receiver coils (which are dependent on the patient, etc.) are optimized by varying a continuously adjustable capacitance. The system calculates the reflectance from the reflection signal. When the reflectance reaches a minimum value, the coil is tuned. For this purpose, several adjustments may be required.

Preparing the adjustment

✧ Select **Options > Adjustments** and go to the **Local Coil** card.

The **Manual Adjustment** dialog box with the **Local Coil** card is displayed.

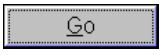


(1) Numeric results of the adjustment
(2) Real part of the reflection signal for the active measuring point
(3) Imaginary part of the reflection signal for the active measuring point
(4) Smith diagram with tuning measuring point
(5) Status bar

Starting the adjustment

Once you have completed the preparations for scanning, you may start the adjustment.

⇨ It is not possible to enter parameters for coil adjustment. It runs automatically. You only launch it manually.



✧ Click the **Go** button in the **Manual Adjustment** dialog box.

⇨ You can monitor the progress of adjustment on the status bar.

The results are displayed numerically and graphically.

Numeric results

A line is displayed with the following parameters for each iteration:

- ❏ **No.**; running number of the measurement
- ❏ **Channel**; tuning channel used for coil adjustment
- ❏ **Voltage [V]**; adjustment voltage used
- ❏ **Reflection**; Measured reflectance
- ❏ **A.**; successful adjustment of the system (Y/N)

Graphic display of the results

The scan points acquired during adjustment scanning are displayed in a Smith diagram (diagram in the complex number plane). The measuring points are shown as crosses. For the active measuring point (highlighted in color), the real and imaginary components of the reflection signal are also displayed as a diagram.

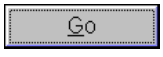
Selecting scan points

✧ Click a measurement point with the mouse to select it.

➪ For more detailed information about a particular measuring point, refer to the information box displayed when you move the mouse toward the measuring point.

Repeating the adjustment

✧ Repeat the adjustment until reflectance has reached a minimum and "**Y**" appears in the numeric display.



✧ Click **Go** again to start scanning.

Aborting adjustment

If you want to cancel an adjustment scan in progress:



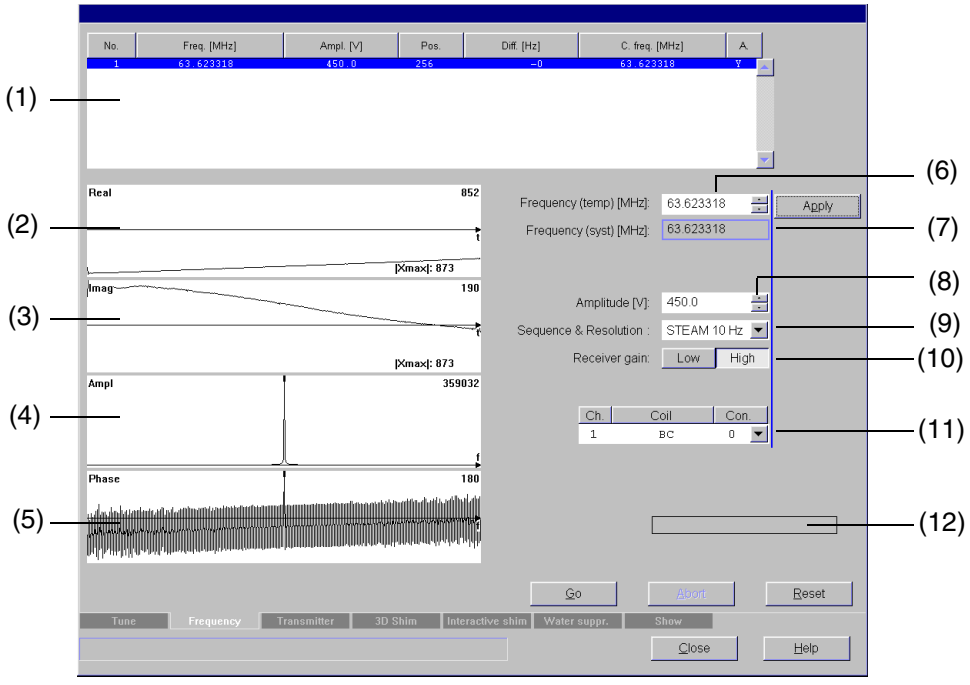
✧ Click the **Abort** button.

Optimizing the frequency

When optimizing the frequency, you may determine the exact proton resonant frequency. For this purpose, you may enter various parameters and accept the frequency calculated for the scan system following adjustment. The results are first transferred from the time domain into the frequency domain via Fourier transform. The resonance frequency of the water protons is calculated from the peak position of the water.

Preparing the adjustment

✧ Select **Options > Adjustments** and go to the **Frequency** card.

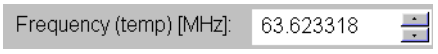


(1) Numeric results
(2) Real part of the measurement signal in the time domain
(3) Imaginary part of the measurement signal in the time domain
(4) Amplitude in the frequency domain
(5) Phase in the frequency domain
(6) Temporary transmit frequency
(7) Display of system transmit frequency
(8) Transmit amplitude
(9) Search range
(10) Receiver gain
(11) Selection of the coil measurement signal for graphic display
(12) Specific display when entering frequency or amplitude

Certain parameters have to be entered prior to performing the frequency adjustment.

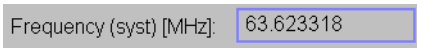
Entering the frequency

A different transmit frequency may be used for each iteration.



✧ You can enter a new transmitter frequency in the **Frequency (temp)** input field.

➪ You can also determine the frequency graphically and transfer it to the input field.
→ Page B.2–39, *Transferring the frequency*



The frequency currently used is displayed in the field underneath for comparison.

➪ The temporary frequency that you may enter yourself is only used for adjustment scans. The system frequency is used for examinations.

Amplitude



✧ You can enter the transmitter amplitude to be used for the scan.

Range display

You can use the range display to verify whether your inputs for the frequency and amplitude are correct. You have to correct them if they are out of range.



➪ When you enter the amplitude, the labeling of the range display is modified accordingly. It will then show the amplitude values.

Sequence and resolution

The following options are available:

- ❏ Broadband not volume-selective (FID 400 Hz)
- ❏ Narrowband not volume-selective (FID 10 Hz)
- ❏ Narrowband volume-selective (STEAM 10 Hz)

If the frequency lies outside the narrowband standard range (no resonance line in the spectrum), it is recommended to search a wide frequency band first to limit the frequency. To subsequently adjust the transmit frequency, you will have to work with a narrow frequency band.

➪ Following each non-volume-selective adjustment measurement, it is necessary to perform at least one volume-selective adjustment.



✧ Select a sequence and resolution from the list.

Selecting the gain

You may set the receive gain to match the intensity of the measured signal.



✧ Click the **Low** button if the receive signal is strong.

Or

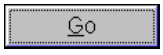


✧ Click the **High** button if the receive signal is weak.

➪ If necessary, the system will adjust this setting automatically.

Starting the measurement

After you have entered all parameters, you can start the adjustment.



✧ Click the **Go** button.

Canceling the measurement



✧ Click the **Abort** button to cancel an adjustment scan in progress.

Results display

The results are displayed both numerically and graphically.

Numeric results

The results are listed below the running numbers. The following parameters are displayed:

- ❏ **No.**; running number of the measurement
- ❏ **Freq. [MHz]**; transmit frequency in MHz
- ❏ **Ampl. [V]**; transmit amplitude of the adjustment measurement
- ❏ **Pos.**; position of the largest "peak" of the amplitude in the frequency domain (in units of the signal graph)
- ❏ **Diff [Hz]**; Difference between the transmit frequency and the calculated "better" frequency
- ❏ **C.freq. [MHz]**; calculated, "better" frequency
- ❏ **A.**; transmitter frequency successfully adjusted (Yes/No)

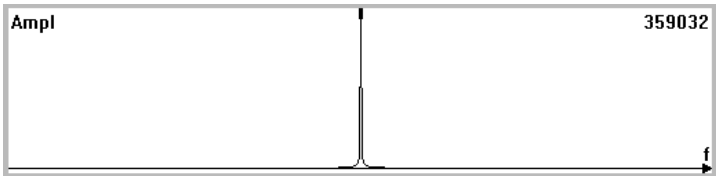
Graphic display of the results

The results are displayed graphically in both the time and the frequency domain. The maximum values of the raw data set are displayed numerically in the graphics.

If available, the "resonance peak" is highlighted.

Vertical marker

A vertical marker is shown when you position the mouse pointer inside the graphic display of the frequency domain. It indicates the delta frequency of the calculated resonance frequency. If no peak was detected during the adjustment, the absolute frequency is indicated instead.



➪ The position of the resonance frequency is indicated by a small line at the top of the graphic.

Transferring the frequency

You may select a frequency graphically by moving the vertical marker.

✧ Just left-click the line.

The frequency is entered in the **Frequency (temp)** field.

Inverting the frequency axis and zooming the graphic

A context menu is available when the mouse pointer is positioned inside the graphic display of the frequency domain.



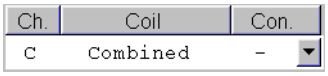
You can invert the default display of all frequency axes (from left to right) or zoom into the detected peak. If no peak is available, the program zooms into the center of the graphic.

➪ When you select a new patient, the default display of the frequency axes is restored. Any zoom applied is reset when you perform a new measurement.

Selecting a receive channel

The receive channel is used to select the signals of the local coils. In addition to the receive channel (**Ch.**), the coil name (**Coil**) and the connector (**Con.**) are displayed in the selection list.

➪ The **Combined** entry is used to select the combined signal of all coils selected.



✧ Select the receive channel whose signal you want displayed.

Accepting the frequency for the measurement system

After successful adjustment ("**Y**" in the numeric result field), the frequency is automatically loaded in the scan system. This may require several iterations.

Manual acceptance without successful adjustment

You may correct the frequency manually if the system cannot detect the correct frequency, e.g. due to the proximity of the resonance signals.

✧ Enter a value in the **Frequency** spin box.

Or

✧ Accept the frequency graphically using the vertical marker.



✧ Click the **Apply** button in the **Manual adjustments** dialog box.

This frequency is then used as the system frequency for subsequent scans.

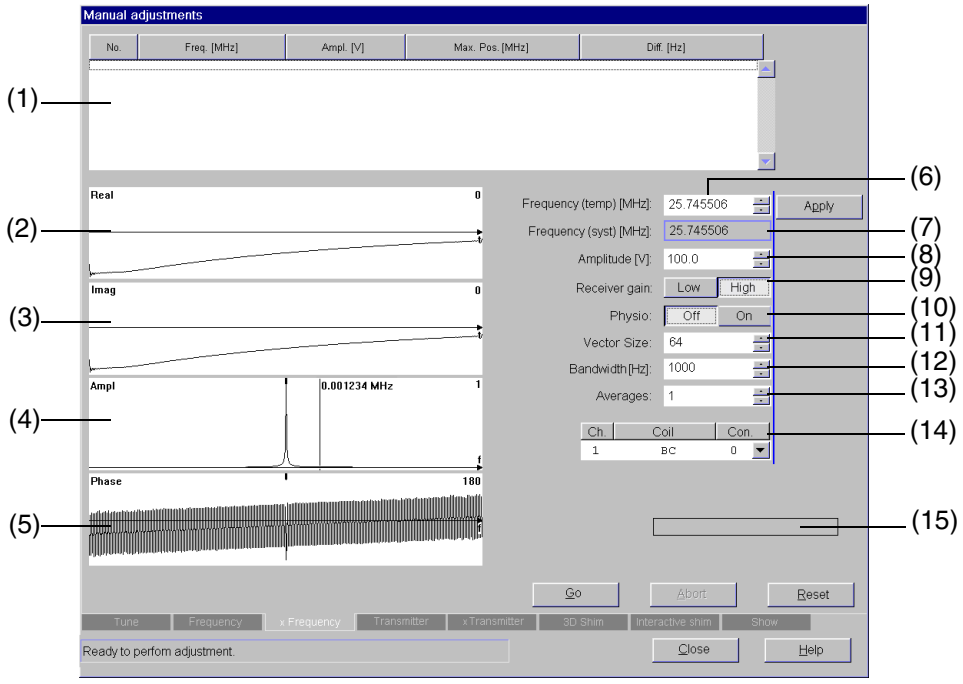
Optimizing the multinuclear frequency

A spectroscopy scan with multiple nuclei requires special frequency optimization.

With multinuclear frequency optimization, you can calculate the exact resonance frequency for the multinucleus determined by the protocol. For this purpose, you may enter various parameters and accept the frequency calculated for the scan system following adjustment.

Preparing the adjustment

✧ Select **Options > Adjustments** and go to the **X-Frequency** card.



(1) Numeric results
(2) Real part of the measurement signal in the time domain
(3) Imaginary part of the measurement signal in the time domain
(4) Amplitude in the frequency domain
(5) Phase in the frequency domain
(6) Temporary transmit frequency
(7) Display of system transmit frequency
(8) Transmit amplitude
(9) Receiver gain
(10) Physiological parameters
(11) Number of measurement points
(12) Bandwidth for measurement
(13) Number of averages
(14) Selection of the coil measurement signal for graphic display
(15) Specific display when entering frequency or amplitude

Before performing the multinuclear frequency adjustment, you first have to enter a few parameters.

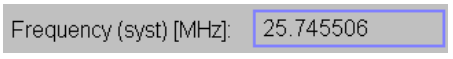
Entering the multinuclear frequency

A different transmit frequency may be used for each iteration.



✧ You can enter a new transmitter frequency in the **Frequency (temp)** input field.

➪ You can also determine the frequency graphically and transfer it to the input field.
→ Page B.2–39, *Transferring the frequency*



The frequency currently used is displayed in the field underneath for comparison.

➪ The temporary frequency that you may enter yourself is only used for adjustment scans. The system frequency is used for examinations.

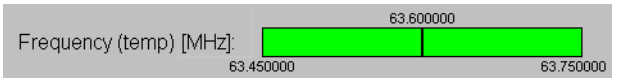
Entering the transmit amplitude



✧ You may enter the transmitter amplitude to be used for the multinuclear scan.

Range display

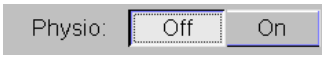
You can use the range display to verify whether your inputs for the frequency and amplitude are correct. You have to correct them if they are out of range.



➪ When you enter the amplitude, the labeling of the range display is modified accordingly. It will then show the amplitude values.

Physio selection

For the adjustment scan, you may apply physiological scan parameters from the relevant parameter card of the protocol.



✧ Change the selection by clicking the inactive button.

If **Off** is selected, no physiological scan parameters will be taken from the relevant parameter card of the protocol.

Entering measurement points

This sets the number of measurement points to be used during a scan.



✧ You may enter the number of measuring points.

Entering the measurement bandwidth

The scan bandwidth is determined by the range where the amplitude reaches its maximum.



✧ You can enter the overall bandwidth for a scan.

Entering the number of averages

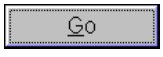
The individual measurements are averaged to determine the resonance frequency. This helps keep the noise as low as possible.



✧ You can enter the number of averages.

Starting the measurement

After you have entered all parameters, you can start the adjustment.



✧ Click the **Go** button.

Canceling the measurement



✧ Click the **Abort** button to cancel an adjustment scan in progress.

Results display

The results are displayed both numerically and graphically.

Numeric results

The results are listed below the running numbers. The following parameters are displayed:

- ❏ **No.**; running number of the measurement
- ❏ **Freq. [MHz]**; transmit frequency in MHz
- ❏ **Ampl. [V]**; transmit amplitude of the adjustment measurement
- ❏ **Max. Pos.**; position of the largest peak of the amplitude in the frequency domain (in MHz)
- ❏ **Diff [Hz]**; Difference between the transmit frequency and the calculated "better" frequency

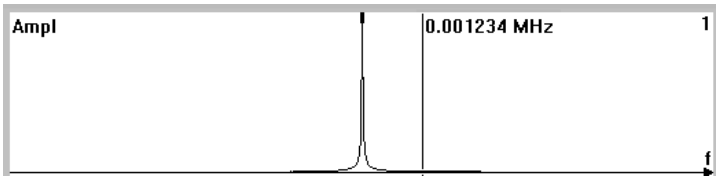
Graphic display of the results

The results are displayed graphically in both the time and the frequency domain. The maximum values of the raw data set are displayed numerically in the graphics.

If available, the "resonance peak" is highlighted.

Vertical marker

A vertical marker is shown when you position the mouse pointer inside the graphic display of the frequency domain. It indicates the delta frequency of the calculated resonance frequency. If no peak was detected during the adjustment, the absolute frequency is indicated instead.



➪ The position of the resonance frequency is indicated by a small line at the top of the graphic.

Transferring the frequency

You may select a frequency graphically by moving the vertical marker.

✧ Just left-click the line.

The frequency is entered in the **Frequency (temp)** field.

Inverting the frequency axis and zooming the graphic

A context menu is available when the mouse pointer is positioned inside the graphic display of the frequency domain.



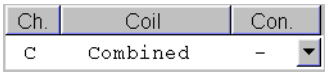
You can invert the default display of all frequency axes (from left to right) or zoom into the detected peak. If no peak is available, the program zooms into the center of the graphic.

➪ When you select a new patient, the default display of the frequency axes is restored. Any zoom applied is reset when you perform a new measurement.

Selecting a receive channel

The receive channel is used to select the signals of the local coils. In addition to the receive channel (**Ch.**), the coil name (**Coil**) and the connector (**Con.**) are displayed in the selection list.

➪ The **Combined** entry is used to select the combined signal of all coils selected.



✧ Select the receive channel whose signal you want displayed.

Accepting the frequency for the measurement system

After successful adjustment, the frequency is not automatically transferred to the scan system.



✧ Click the **Apply** button in the **Manual adjustments** dialog box.

The temporary frequency is then loaded in the scan system.

Manual acceptance without successful adjustment

You may correct the frequency manually if the system cannot detect the correct frequency, e.g. due to the proximity of the resonance signals.

✧ Enter a value in the **Frequency** spin box.

Or

✧ Accept the frequency graphically using the vertical marker.



✧ Click the **Apply** button in the **Manual adjustments** dialog box.

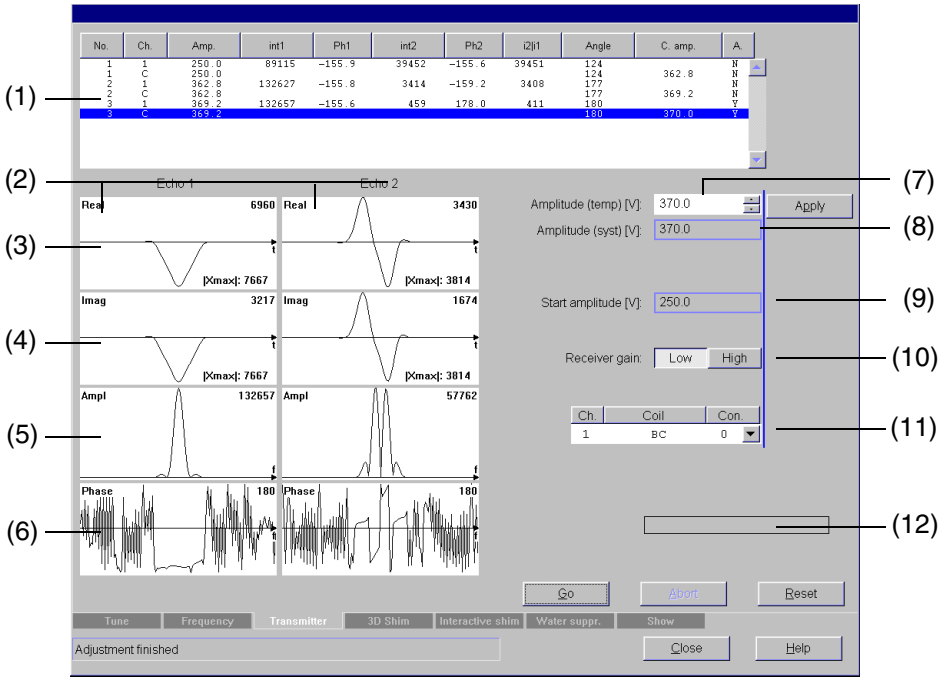
This frequency is then used as the system frequency for subsequent scans.

Transmitter adjustment

Transmitter adjustment is used for calibration of the transmitter. The reference amplitude is continuously varied until the spins are rotated 180° (flip angle) by the RF pulse. Two echoes are generated, one normal echo and one stimulated echo. The magnitude and the phase relation of both echoes is directly related to the flip angle.

Preparing the adjustment

✧ Select **Options > Adjustments** and go to the **Transmitter** card.



(1) Displaying numeric results
(2) Normal echo (Echo 1) and stimulated echo (Echo 2)
(3) Real part of the measurement signal in the time domain
(4) Imaginary part of the measurement signal in the time domain
(5) Amplitude of the measurement signal in the frequency domain
(6) Phase of the measurement signal in the frequency domain
(7) Enter the temporary reference amplitude
(8) System reference amplitude
(9) Start amplitude
(10) Receiver gain
(11) Selection of the coil measurement signal for graphic display
(12) Domain display

Transmitter calibration involves performing scans, each with a slightly different reference amplitude.

Entering the amplitude



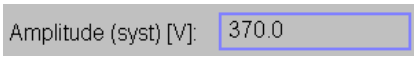
✧ For each scan, you can enter a new reference amplitude in the **Amplitude (temp)** spin box.

For comparison, the amplitude currently used by the system is displayed below.

➪ The temporary amplitude that you enter is only used for adjustment scans. The system amplitude is used for examinations.

Start amplitude

The **Start amplitude** text field shows the amplitude value (specific parameter of the transmitter coil) used for the first iteration.



Range display

The range displayed shows the range available for the reference amplitude. If your entry is outside the range, you have to correct it accordingly.

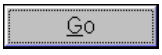


Selecting the gain

You can set the receiver gain depending on the signal intensity.
→ Page B.2–37, *Selecting the gain*

Starting the measurement

After you have entered all parameters, you can start the adjustment.



✧ Click the **Go** button.

Canceling the measurement



✧ Click the **Abort** button to cancel an adjustment scan in progress.

Results display

The results are displayed both numerically and graphically.

Numeric results

The results are listed below the running number of the iteration. The following parameters are displayed:

- ❏ **No.**; running number of the adjustment measurement
- ❏ **Ch.**; receive channel used to calculate the results
- ❏ **Amp.**; transmitter amplitude of the adjustment scan
- ❏ **int1**; integral data of the first echo
- ❏ **Ph1**; phase of the first echo
- ❏ **int2**; integral data of the second echo
- ❏ **Ph2**; phase of the second echo
- ❏ **i2/i1**; projection of the second echo on the first echo
- ❏ **Angle**; measured flip angle
- ❏ **C. amp.**; calculated "better amplitude"
- ❏ **A.**; transmitter successfully adjusted (Yes/No)

Graphic display of the results

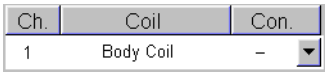
The following results are displayed graphically:

- ❏ Real and imaginary part of the echo in the time domain
- ❏ Amplitude and phase of the respective echo in the frequency domain

The graphics show the maximum value of each raw data set.

Selecting a receive channel

The receive channel is used to select the signals of the local coils.



✧ Select the receive channel whose signal you want displayed.

Accepting the frequency for the measurement system

After successful adjustment ("**Y**" in the numeric field), the amplitude is automatically transferred to the scan system.

Manual acceptance without successful adjustment

Within a certain range, you can also enter a reference amplitude and manually transfer it to the system without adjustment scanning.



✧ Click the **Apply** button.

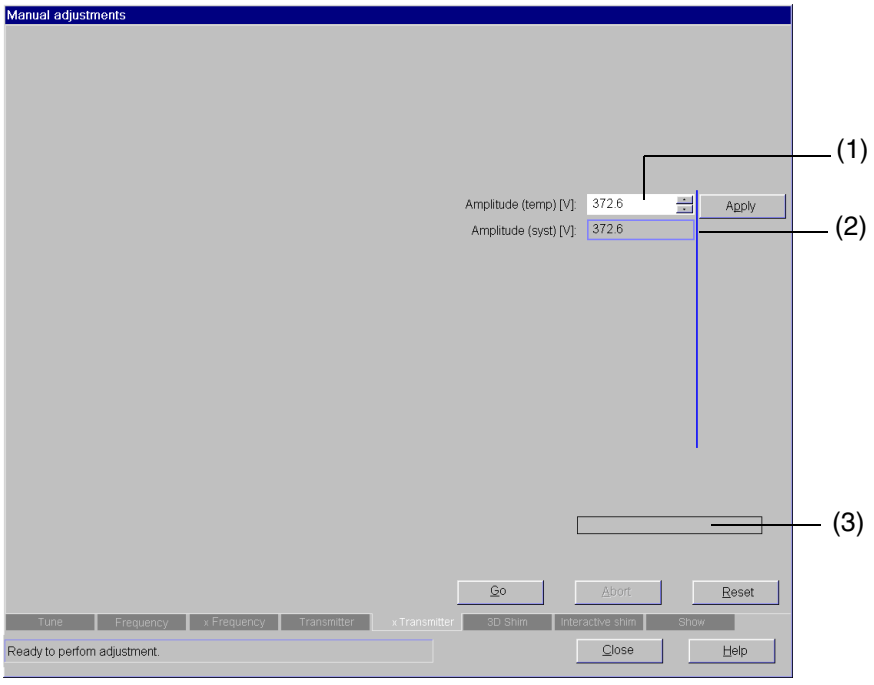
The amplitude is used as the reference amplitude for the following scans.

Multinuclear transmitter adjustment

You may not perform a transmitter adjustment for a multinuclear measurement because the signal strength is very low and the measurement field is not homogeneous. However, you may define a reference amplitude.

Preparing the adjustment

✧ Select **Options > Adjustments** and go to the **X-Transmitter** card.



(1) Entering the temporary reference amplitude
(2) System reference amplitude
(3) Range display

Entering the amplitude

You can manually enter a reference amplitude for a multinucleus determined in the protocol.



✧ You can enter a new reference amplitude within a certain range in the **Amplitude (temp)** spin box.

For comparison, the amplitude currently used by the system is displayed below.

➪ The system amplitude is used for examinations.

Manual acceptance

You can apply the selected reference amplitude to the scan system.

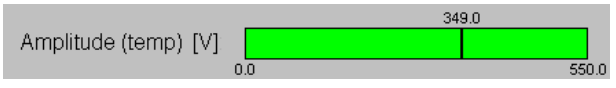


✧ Click the **Apply** button.

➪ The amplitude is used as the reference amplitude for the following scans.

Range display

The range displayed shows the range available for the reference amplitude. If your entry is outside the range, you have to correct it accordingly.



3D Shim

The 3D shim allows you to correct inhomogeneities of the magnetic field.

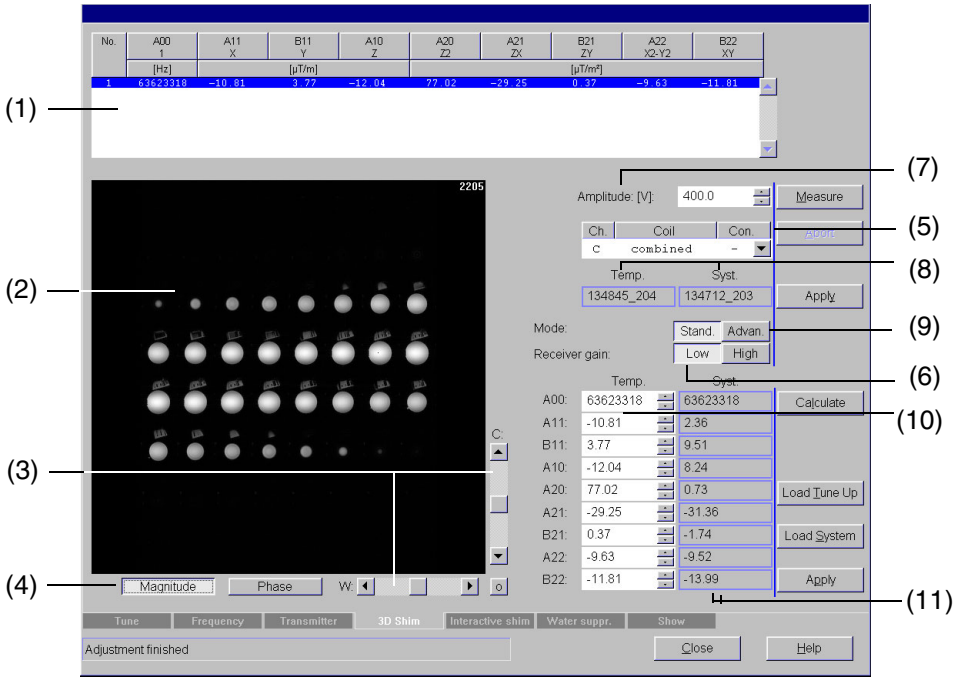
Scanning is performed in two steps:

(1) First, you generate a "field map" by acquiring a 3D data set. A "field map" is a three-dimensional description of the magnetic field.
(2) Subsequently, the shim parameters are calculated.

➪ After interactive shimming, you have to readjust the frequency. The frequency is automatically adjusted by the system if you do not do this yourself.

Preparing the adjustment

✧ Select **Options > Adjustments** and go to the **3D Shim** card.



(1) Displaying numeric results
(2) Image area for display of the field map (64 images)
(3) Slider for windowing the images
(4) Switchover between magnitude and phase display
(5) Transmit amplitude
(6) Selection of the coil measurement signal for graphic display
(7) Name of the field map (temporary and system)
(8) Mode selection for field map display (standard and advanced)
(9) Receive gain
(10) Temporary shim parameter set
(11) System shim parameter set

Before you can perform the 3D shim, you first have to enter the necessary parameters. The system suggests a default value.

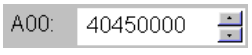
Entering the transmitter amplitude



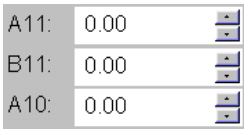
✧ You can enter the transmit amplitude for the adjustment.

Entering the shim parameters

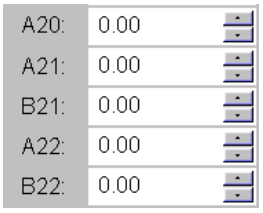
The nine parameters are part of a parameter set that describes the field correction.



✧ You can enter the transmitter frequency for the scan in spin box **A00**.



✧ You can enter the components of the linear gradients in spin boxes **A11**, **B11** and **A10**.



✧ Depending on the configuration of your system, you can enter the second order shimming currents in input fields **A20**, **A21**, **B21**, **A22** and **B22**.

These shim parameters are used for field map acquisition.

Loading from tune up

Alternatively, you can load the parameters from the last system tune up as temporary parameters.

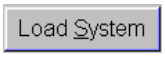


✧ Click the **Load Tune Up** button.

Or

Loading system parameters

Load the parameters currently used by the system as temporary parameters.



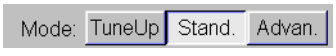
✧ Click the **Load System** button.

The system parameters are loaded.

Mode selection

The shim mode used to perform the adjustment is defined during protocol generation.
→ Page B.2–4, *Setting the shim mode*

The active button shows you which mode is active (tune-up, standard, or advanced).



✧ Switch modes by clicking the inactive button.

Selecting the gain

You can set the receiver gain to match the intensity of the measured signal (low/high).
→ Page B.2–37, *Selecting the gain*

Starting the measurement

After you have entered all parameters, you can start the adjustment. The scan takes approximately 20 seconds.



✧ Click the **Measure** button.

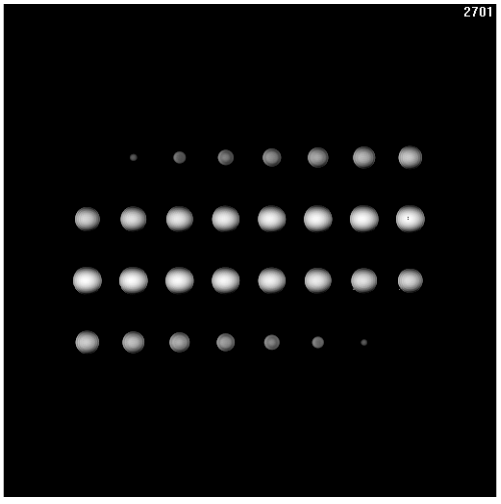
Or



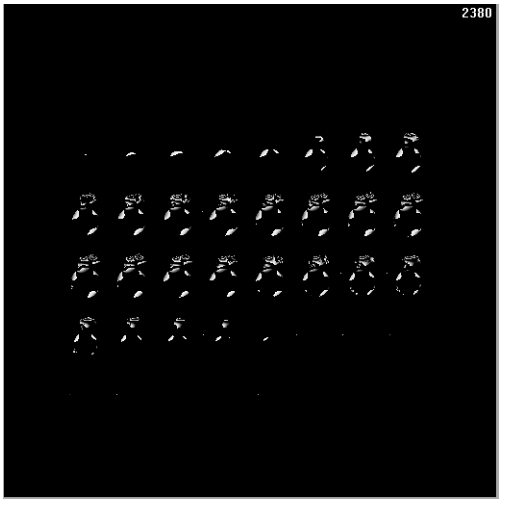
✧ Click the **Abort** button to cancel an adjustment scan in progress.

Displaying the field map

The field map is displayed in the image area of the dialog box. A maximum of 64 images with a maximum resolution of 64 × 64 pixels are displayed.



Field map, magnitude display



Field map, phase display

The tomographic images are displayed row by row.

Windowing images

If the window values of the images are not optimally set, you may readjust them manually using the two sliders in the bottom right-hand corner of the image area.

✧ Move the vertical slider to adjust the contrast.

✧ Move the horizontal slider to adjust the width.

Selecting magnitude or phase image

You may display the images as magnitude or phase images.



✧ Click the **Magnitude** button to display magnitude images.

Or

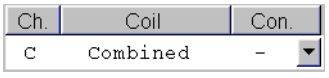


✧ Click the **Phase** button to display phase images.

Selecting the receive channel

The receive channel is used to select the signals of the local coils. In addition to the receive channel (**Ch.**), the coil name (**Coil**) and the connector (**Con.**) are displayed in the selection list.

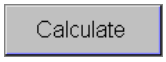
➪ The **Combined** entry is used to select the combined signal of all coils selected.



✧ Select the receive channel whose signal you want displayed.

Calculating the shim parameters

After scanning has been completed and the results are displayed, you may calculate the new shim parameters.



✧ Click the **Calculate** button to start the calculation.

The parameters are recalculated and may be used as a basis for the next field-map scan. They are displayed in the list of numeric results.

Numeric results

The results are listed below the running number of the iteration. The following parameters are displayed:

- ❏ **No.**; running number of the adjustment measurement
- ❏ **A00**; transmit frequency
- ❏ **A11, B11, A10**; linear gradients
- ❏ **A20, A21, B21, A22, B22**; second order shim currents

NOTE

The three-dimensional field map scan always shows the entire homogeneity volume of the magnet, irrespective of the adjustment volume.
The adjustment volume is taken into account and the field homogeneity is optimized only when the shim parameters are calculated. For this reason, changing the adjustment volume also results in different shim parameter settings for the same field map.

Accepting the field map for the scan system

The temporary field map (valid locally for the adjustment) may be applied to the scan system.



✧ Click the **Apply** button in the upper section of the dialog box.

Manual acceptance of the calculated parameters

After you have calculated the new parameters with **Calculate**, you may apply them directly to the scan system as temporary parameters.



✧ Click the **Apply** button in the lower part of the dialog box.

Manual acceptance without successful adjustment

You can also enter shim parameters and apply them to the scan system without performing a scan or calculation.



✧ Click the **Apply** button in the lower part of the dialog box.

The parameters will be applied to the scan system.

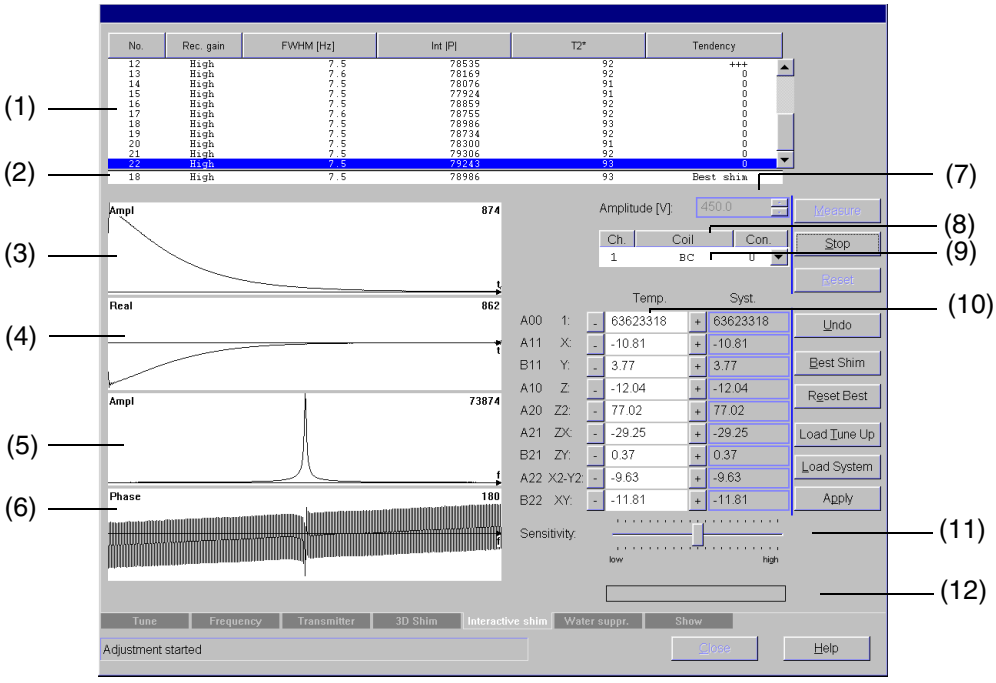
Interactive shim

Similar to 3D shim adjustment, interactive shimming compensates for inhomogeneities of the magnetic field. You can enter the shim parameters and monitor the measurement of the MR signal in real time. If you enter new parameters, the changes are reflected in the results of the following MR signal measurement. You may continue shimming the magnetic field until it meets your requirements.

➪ After interactive shimming, you have to readjust the frequency. The frequency is automatically adjusted by the system if you do not do this yourself.

Preparing the adjustment

✧ Select **Options > Adjustments** from the menu and go to the **Interactive shim** card.

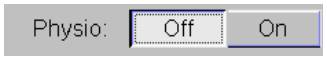


(1) Numeric results
(2) Display of best shim Result
(3) Amplitude of the measurement signal in the time domain
(4) Real part of the measurement signal in the time domain
(5) Amplitude of the measurement signal in the frequency domain
(6) Phase of the measurement signal in the frequency domain
(7) Transmit amplitude
(8) Physiological parameters
(9) Selection of the coil measurement signal for graphic display
(10) Temporary shim parameters and shim parameters currently used by the system
(11) Sensitivity when changing shim parameters
(12) Range display for entering the amplitude or the shim parameters

As soon as you go to the **Interactive Shim** card, the start parameters are displayed.

Physio selection

For the adjustment scan, you may apply physiological scan parameters from the relevant parameter card of the protocol.



✧ Change the selection by clicking the inactive button.

Entering the transmitter amplitude



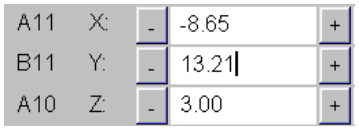
✧ You can enter the transmitter amplitude for the adjustment.

Entering the shim parameters

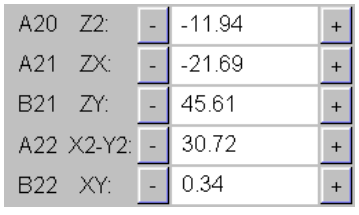
The nine parameters are part of a parameter set that describes the field correction.



✧ You can enter the transmitter frequency for the measurement in the **A00** input field.



✧ You can enter the components of the linear gradients in the **A11**, **B11**, and **A10** input fields.



✧ Depending on the configuration of your system, you can enter the second order shimming currents in input fields **A20**, **A21**, **B21**, **A22** and **B22**.

Using the plus and minus buttons

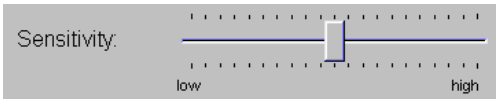
Instead of entering shim parameters numerically, you can increase or decrease their values using the plus or minus button.



The **Sensitivity** slider allows you to define the increments for value adjustments.

Fine tuning of shim parameters

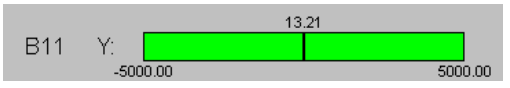
Shimming normally begins with significant changes to the parameter values and concludes with very small adjustments using the plus and minus buttons.



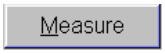
- ✧ Set the slider to **high** to change the shim parameters in larger increments.
- ✧ Set the slider to **low** to change the shim parameters in small increments.

Range display

The range display indicates at what interval you can change the transmit amplitude or shim parameters.



Starting the measurement



✧ Start the adjustment by clicking the **Measure** button.

The measurement is performed continuously using the current parameters. You can terminate continuous scanning with the **Stop** button.

Displaying results

When the measurement is complete, the results for each measurement are displayed numerically and graphically.

The following parameters are displayed numerically:

- ❏ **No.**; running number of the adjustment measurement
- ❏ **Rec. gain**; gain setting used
- ❏ **FWHM (Hz)**, (Full Width Half Maximum)
  Width of the pulse received (frequency domain) at half the maximum amplitude
- ❏ **Int |PI**; integral of the amplitude in the time domain
- ❏ **T2***; transverse relaxation time
- ❏ **Tendency**; indicates whether the parameter changes result in shim improvement (+++) or degradation (---).

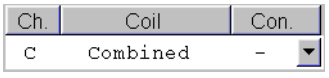
The following results are displayed graphically:

- ❏ The amplitude in the time domain
- ❏ The real part of the measurement signal in the time domain
- ❏ The amplitude of the measurement signal in the frequency domain (Fourier-transformed measurement signal)
- ❏ The phase of the measurement signal in the frequency domain

Selecting a receive channel

The receive channel is used to select the signals of the local coils. In addition to the receive channel (**Ch.**), the coil name (**Coil**) and the connector (**Con.**) are displayed in the selection list.

➪ The **Combined** entry is used to select the combined signal of all coils selected.



✧ Select the receive channel whose signal you want displayed.

Changing parameters

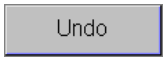
Once the measurement results are displayed, you can make changes while the measurement is in progress. The **Tendency** column provides valuable information.

✧ Change the parameters so that the full width at half maximum (**FWHM**) decreases and **T2*** increases.

➪ In the numeric display, the line with the highest **T2*** value is marked **Best Shim**.

Undoing changes

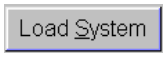
To undo the last change to the parameters:



✧ Click the **Undo** button.

Loading stored parameters

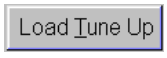
You can load the system parameters currently stored in the measurement system as temporary shim parameters and use them, for example, as start parameters.



✧ Click the **Load System** button.

Loading from tune up

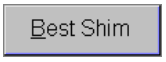
As an alternative, you can also load parameters from the last system tune-up as temporary parameters.



✧ Click the **Load Tune Up** button.

Loading the best shim parameters

The "best" shim parameters obtained in the current scan may be imported as temporary shim parameters. They are then used for the next adjustment measurement.



✧ Click the **Best Shim** button.

Deleting the best shim parameter

You may delete the best shim parameters obtained in the current scan, making them invalid. The corresponding display is deleted.



✧ Click the **Reset Best** button.

Applying parameters to the scan system

You can transfer the optimal shim parameters for the measurement to the measurement system.



✧ Click the **Apply** button.

They will be used in the next examination.

Stopping the measurement

To stop the measurement:



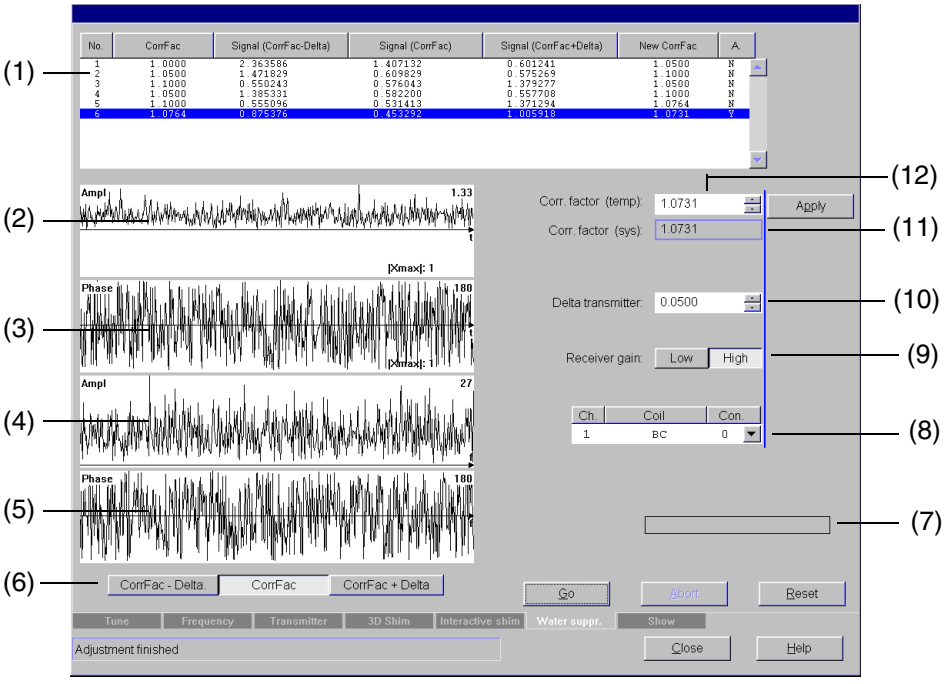
✧ Click the **Stop** button.

Manual water suppression

There are special RF pulses that are used for water suppression during scans. With this adjustment, you determine a correction factor for the transmitter amplitude for these RF pulses. Within the adjustment volume, the flip angles are set for optimal suppression of the water signal.

Preparing the adjustment

✧ Select **Options > Adjustments** and go to the **Water suppr.** card.



(1) Displaying numeric results
(2) Amplitude of the measurement signal in the time domain
(3) Phase of the measurement signal in the time domain
(4) Amplitude of the measurement signal in the frequency domain
(5) Phase of the measurement signal in the frequency domain
(6) Select signal graphs
(7) Range display for the correction factor and the transmitter increment
(8) Selection of the coil measurement signal for graphic display
(9) Receiver gain
(10) Transmitter increment
(11) Display of the system correction factor
(12) Input field for the temporary correction factor

Certain parameters have to be entered prior to the scan and checked after each scan.

Entering the correction factor

For the first iteration, the system suggests an amplitude correction factor of 1.0 which you may edit.



✧ You can enter a correction factor in the **Corr. Factor (temp)** spin box.

For comparison, the correction factor currently used by the system is displayed below.

Entering the transmitter increment (delta transmit amplitude)

To determine the correction factor, enter an increment so that three measurements can be performed with different correction factors (one measurement plus increment, one measurement without increment, and one measurement minus increment).



✧ You can enter an increment in the **Delta transmitter** spin box.

Selecting the gain

You can set the receiver gain depending on the signal intensity.
→ Page B.2–37, *Selecting the gain*

Starting the measurement

After you have entered all parameters, you can start the adjustment.



✧ Click the **Go** button.

The scan takes several seconds.

Canceling the measurement



✧ Click the **Abort** button to cancel an adjustment scan in progress.

Repeat the measurements using different parameters until the system has optimized the correction factor.

➪ A will "Y" appear in the numeric field following successful adjustment.

Results display

The measurement results are displayed both numerically and graphically.

Numeric results

The results are listed below the running number of the iteration. The following parameters are displayed:

- ❏ **No.**; running number of the adjustment measurement
- ❏ **CorrFac.**; correction factor of the adjustment scan
- ❏ **Signal (CorrFac - Delta)**; signal strength for measurement with correction factor minus transmitter increment
- ❏ **Signal (CorrFac)**; signal strength for scan with correction factor
- ❏ **Signal (CorrFac + Delta)**; signal strength for scan with correction factor plus transmitter increment
- ❏ **NewCorrFac**; calculated "better" correction factor

Graphic display of the results

The following results are displayed graphically:

- ❏ The real and imaginary part of the measuring signal in the time domain.
- ❏ The amplitude and phase of the measuring signal in the frequency domain.

Three different signal graphs are available for display.



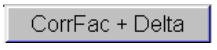
✧ Click the **CorrFac - Delta** button to display the signal graph of the "correction factor minus increment" scan.

Or



✧ Click the **CorrFac** button to display the signal graph of the measurement with the correction factor.

Or

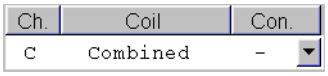


✧ Click the **CorrFac + Delta** button to display the signal graph of the "correction factor plus increment" scan.

Selecting the receive channel

The receive channel is used to select the signals of the local coils. In addition to the receive channel (**Ch.**), the coil name (**Coil**) and the connector (**Con.**) are displayed in the selection list.

➪ The **Combined** entry is used to select the combined signal of all coils selected.



✧ Select the receive channel whose signal you want displayed.

Accepting the correction factor

After successful adjustment, the correction factor is automatically loaded into the scan system.

Manual acceptance without successful adjustment

Within a certain range, you can enter a correction factor and manually accept it without adjustment measurement.



✧ Click the **Apply** button.

The correction factor is used for the following measurements.

Undoing changes

You have performed all adjustments and now want to undo the settings.

A **Reset** button is available for this purpose on every card (except 3D Shim).



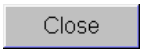
✧ Click **Reset**.

The parameters displayed when the dialog box was opened are re-loaded.

➪ System parameters that were changed during the adjustment cannot be restored to their initial settings before the adjustment.

Completing adjustment

Exit the adjustment platform with the **Close** button.



✧ Click the **Close** button.

The dialog box closes.

Starting protocol adjustments manually

All adjustments planned in the selected protocol may be manually started without starting the following protocol.

✧ Open the protocol first.

✧ Select **Options > Adjustments**.

✧ Go to the **Viewing** card.



✧ Then click the **Adjust All** button.

The adjustments are performed.

➪ If an error occurs during the measurement, the adjustment will be aborted and an error message is displayed.

Aborting adjustment

You can cancel a scan in progress at any time.



✧ Click the **Abort** button.

Changing the resonant frequency after inline adjustment

Inline adjustment is performed automatically before each scan.

You can pause the system after an inline adjustment to confirm or change the calculated resonance frequency.

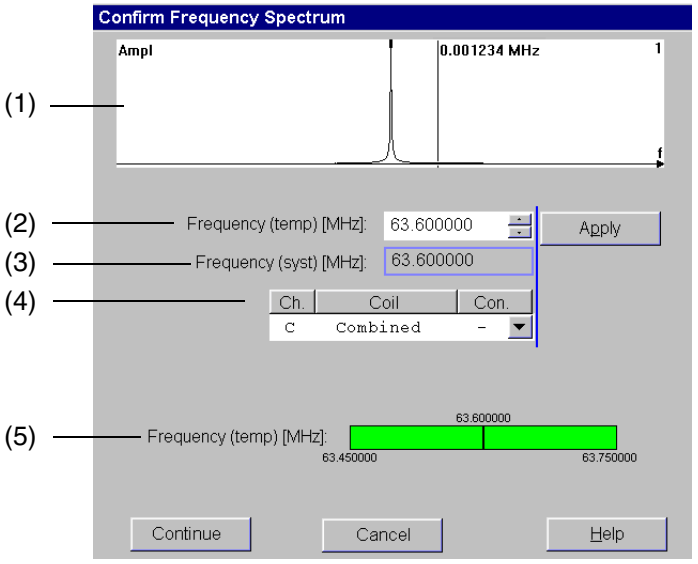
Settings on the Adjustments card

✧ Go to the **Adjustments** card.



✧ Click the **Confirm freq. adjustment** option.
→ Page B.2–3, *Settings on the Adjustments card*

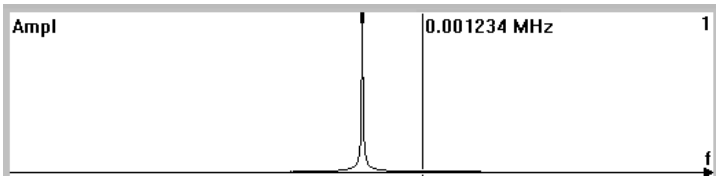
Once you have clicked the **Confirm freq. adjustment** option on the **Adjustments** card, the **Confirm Frequency Spectrum** dialog box is displayed after each inline adjustment. You may correct the resonant frequency or accept it without changes.



(1) Amplitude in the adjustment scan
(2) Temporary frequency
(3) Display of the system frequency
(4) Selection of the receive channel
(5) Range display for entering the frequency

Graphic display of the adjustment scan

The graphic display of the last frequency scan is displayed.



You can modify the frequency graphically by moving the vertical marker. Place the mouse pointer in the graphic display of the frequency domain. A vertical marker is displayed.

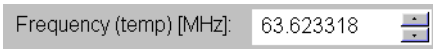
✧ Click on the line.

The newly selected frequency is transferred to the **Frequency (temp)** field.

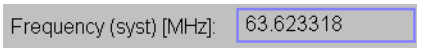
If no adjustment graphic is available, you will have to generate the data for graphic display by performing manual frequency adjustment.

Before manual frequency adjustment, you first have to enter a few parameters.

Entering the frequency



✧ You can enter a new transmitter frequency in the **Frequency (temp)** input field.



The frequency currently used is displayed in the field underneath for comparison.

➪ The temporary frequency that you may enter yourself is only used for adjustment scans. The system frequency is used for examinations.

Range display

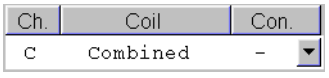
Use the range display to verify the accuracy of the selected frequency. If it is out of range, correct it accordingly.



Selecting a receive channel

The receive channel is used to select the signals of the local coils. In addition to the receive channel (**Ch.**), the coil name (**Coil**) and the connector (**Con.**) are displayed in the selection list.

➪ The **Combined** entry is used to select the combined signal of all coils selected.



✧ Select the receive channel whose signal you want displayed.

Starting the measurement

After you have corrected the resonance frequency, you may start scanning.



✧ Click the **Continue** button.

Canceling the measurement

You may stop the examination if you are not satisfied with the frequency spectrum.



✧ Click the **Abort** button.

Displaying adjustment results

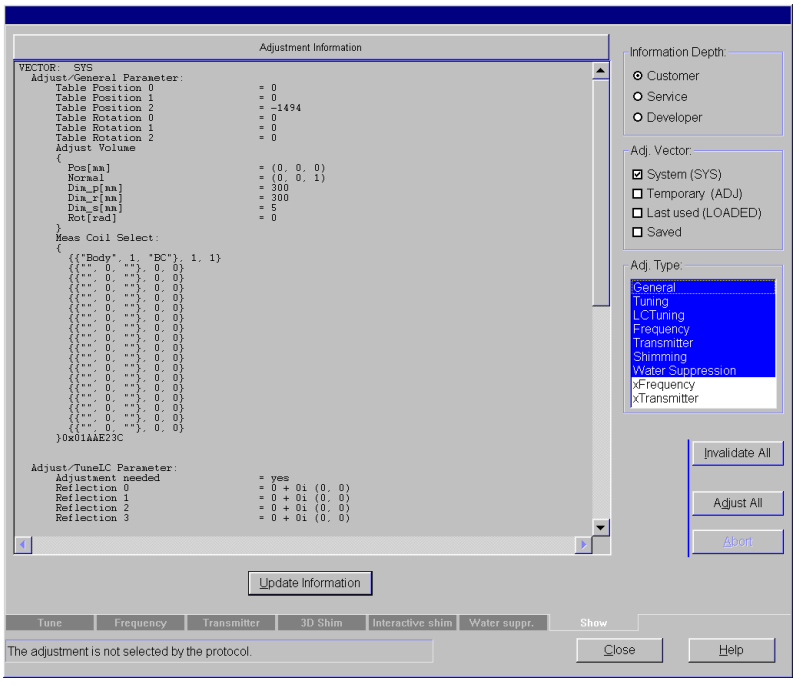
The **Show** card in the **Manual adjustments** dialog box displays the results of all the adjustments performed. It provides an overview of the current status of your scan system.

➪ Use the selection buttons to define the information to be displayed.

Displaying all adjustment parameters

✧ Select **Options > Adjustments**.

✧ Go to the **Show** card.



NOTE

This list is primarily intended for Siemens Service for diagnostic purposes.

Updating the display of parameters

You can update the scan results displayed on the card after each adjustment.



✧ Just click the **Update Information** button.

Rejecting all adjustment results

If you want to reject all the adjustments already performed:



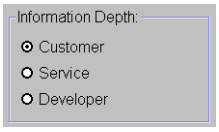
✧ Click the **Invalidate All** button.

The system is now in an unadjusted state.

Selecting parameters for display

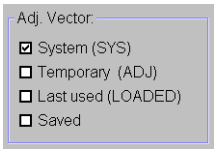
Detail of information for the parameters displayed

You can define the scope of the information to be displayed. All of the important parameters are displayed in "customer" mode.



Adjustment vector

Select the parameter sets you want to display.

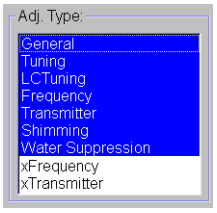


The following parameter sets may be selected:

- **System (SYS)**: Adjustment parameters applicable to the system.
- **Temporary (ADJ)**: Parameters acquired via the current adjustment process.
- **Last used (LOADED)**: Adjustment parameters used in the last scan.
- **Saved**: All saved adjustment parameters.

Adjustment type

Specify the adjustment types to be displayed.



The relevant adjustment parameters are displayed with the selected adjustment type.

PART C

Examination

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CHAPTER C.1

Introduction to the MR Examination

After registering a patient, you will make the necessary preparations in the examination room.

Preparations in the examination room

Position the patient in the orientation entered during patient registration. Observe the information regarding patient safety provided in the *System Manual*. Position the coil(s) and connect the coil cables to the connectors on the patient table. Mark the center of the region to be examined with the laser light localizer and move the patient into the magnet isocenter.
see System Manual

Working at the *syngo* Acquisition Workplace

Subsequently, you start the actual measurement at the *syngo* Acquisition Workplace in the control room. For this purpose, use the **Exam** task card. This card enables you to select, control, and monitor examination procedures.

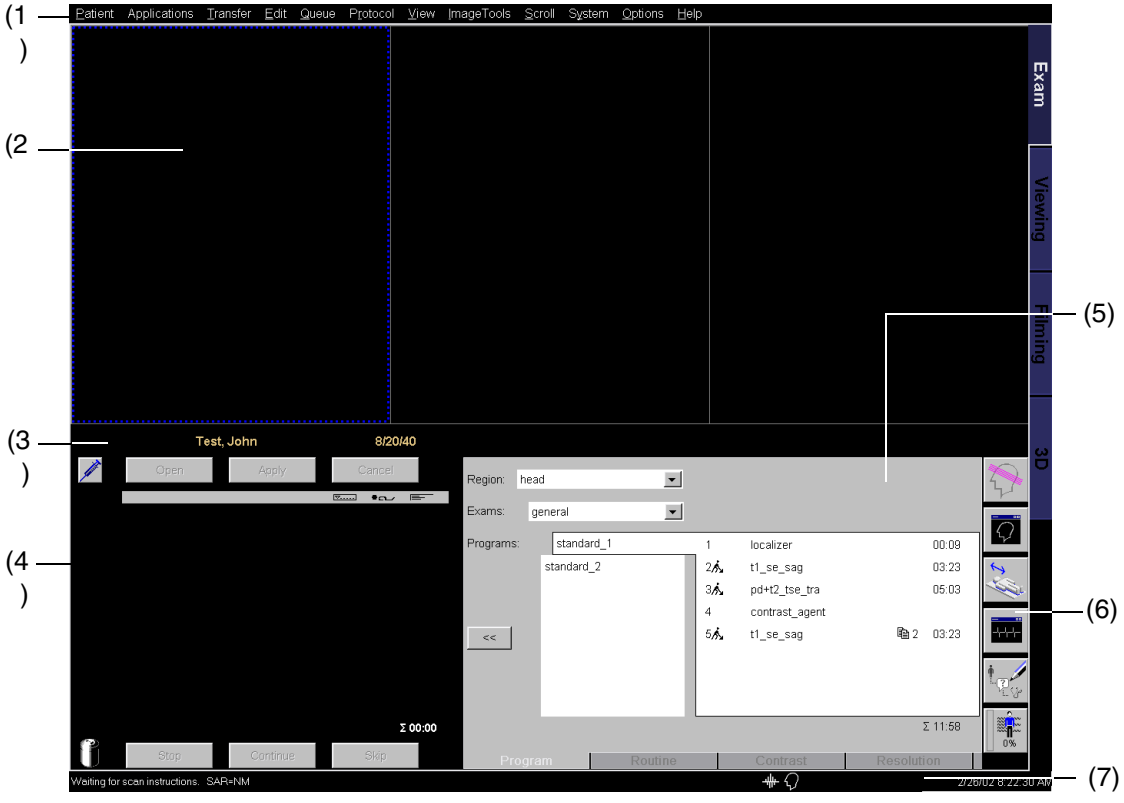
You are able to observe the patient through the window in the control room during the examination. Use the intercom system on the intercom console to listen or give instructions to the patient.

Subsequent chapters take you through an MR examination step by step. You will find detailed descriptions on how to perform special scans, organize and manage scan programs, and monitor thresholds relevant to the health of the patient.

The following pages provide an overview of the **Exam** task card, the scanning procedure, as well as important terms.

Layout of the Exam task card

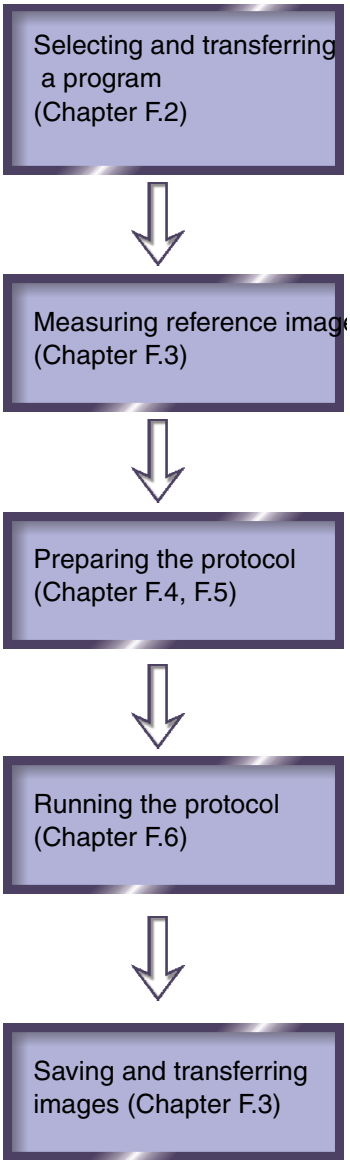
The **Exam** task card is displayed in foreground as soon as you register a patient for an examination.



This task card includes the following elements and areas:

(1) Menu bar
(2) Image area
Displays the reference images used to position graphic scan objects (slices, slabs).
(3) Info bar
Displays information regarding the current patient and the open protocol.
(4) Program control
After loading, the program control contains a list of the protocols to be processed (job list). It also includes buttons for controlling the program sequence.
(5) Parameter cards
The **Program** parameter card is used to select a scan program or protocol. You may use the other cards to adapt the parameters for the current examination.
(6) Toolbar
The buttons on the tool bar are used to open dialog boxes for editing and controlling the measurement.
(7) Status bar
The status bar displays system error and status messages.

Procedure for routine scanning



Select a scan program or protocol on the **Program** parameter card and transfer it to the program control.

Scanning reference images is the first program step, and usually starts automatically. The acquired reference images are displayed in the image area.

As the next step you prepare the next protocol in the program control. You graphically position the slices or slabs to be acquired on the reference images. Use the parameter cards to check or change the measurement parameters of the protocol.

Start the protocol.

During the scan you may prepare the next protocol, e.g., by positioning the slices and adjusting the measurement parameters. Alternatively, you may view the images acquired with the previous protocol.

You may save, export or transfer images to other task cards from the **Exam** task card.

You can interrupt a protocol, repeat scans, change the sequence of the program steps, and insert pauses (e.g. for administering contrast agent).

Use the **Online Display** or movie display to check the acquired images.

For physiologically triggered scans, you may use the **Physiological Display** dialog box to monitor the physiological signals and parameters.

During scanning, the system automatically monitors the SAR and dB/dt load on the patient (RF exposure and time-varying magnetic fields).

Use the **Exam Explorer** to organize examinations, scan programs, and protocols.

Important terms

It is very important to be familiar with the following terms associated with the examination procedure.

Sequence

A **Sequence** is the chronological sequence of RF pulses and gradient pulses for excitation of the volume to be scanned, for signal generation, and for position encoding. Each sequence requires a repeat time TR optimized for contrast.

Your MR system is equipped with a large number of sequences, allowing you to use different MR imaging techniques.
see Application Guide

Scan protocol

A **scan protocol** (**protocol**) is a sequence containing a full set of optimized parameters.

Scan pause

Scan pauses (**pauses**) are planned interruptions in an examination procedure, e.g. for contrast agent administration.

Program instructions

Scan protocols and scan pauses are known collectively as **program instructions**.

Scan program

A **Scan program** (**Program**) contains a list of program instructions suitable for clarifying diagnostic problems in a specific region of the body.

For greater clarity, the numerous scan programs are assigned to specific examinations and regions.

Examination

An **examination** contains all scan programs for an anatomical region that are required to obtain diagnostically useful information.

Examination region

Examinations for a specific region of the body are grouped together in an **Examination region** (**Region**).

CHAPTER C.2

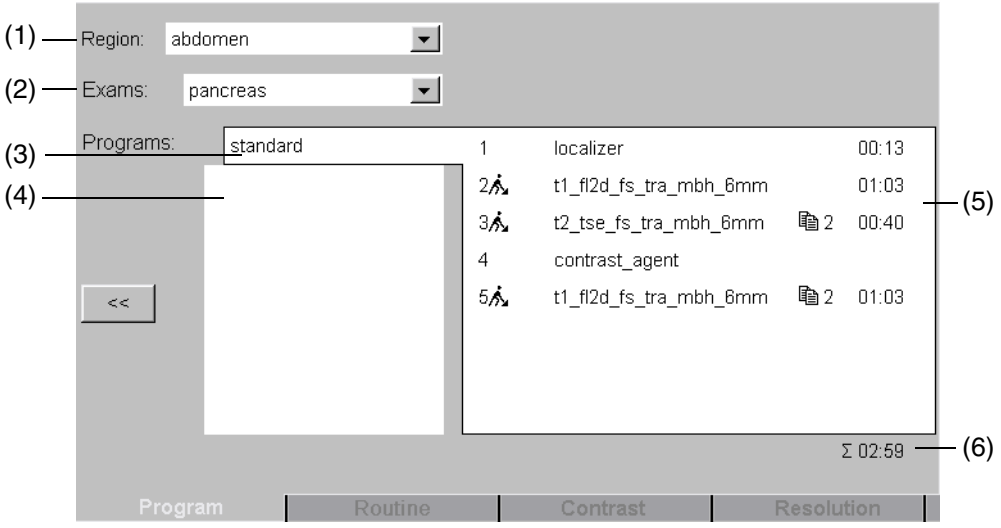
Loading the Measurement Program

After the preparations in the examination room, check the information you entered for the examination and region during patient registration.

Then select the scan program required for your examination and load it into the program control.
→ Page C.1–4, *Procedure for routine scanning*

Checking the region and examination

When you select the **Exam** task card, the **Programs** parameter card is in the foreground. The region and examination selected during patient registration are entered here.



(1) Region
(2) Available examinations for the selected region
(3) Selected scan program
(4) List of all available scan programs for the selected examination
(5) Program instructions for the selected scan program
(6) Sum of scan times of the individual protocols in the selected scan program

Changing the region



✧ Select a different examination region from the **Region** selection list, if required.

➪ The **Region properties** dialog box allows you to view the properties of the selected region (e.g. the short description or assignment to a body region). Select **Properties** from the context menu.

Changing the examination

An examination limits the region to be examined to a specific organ or part of the body.

As soon as you select an examination region, the **Exam** selection list contains the examinations available for this region.



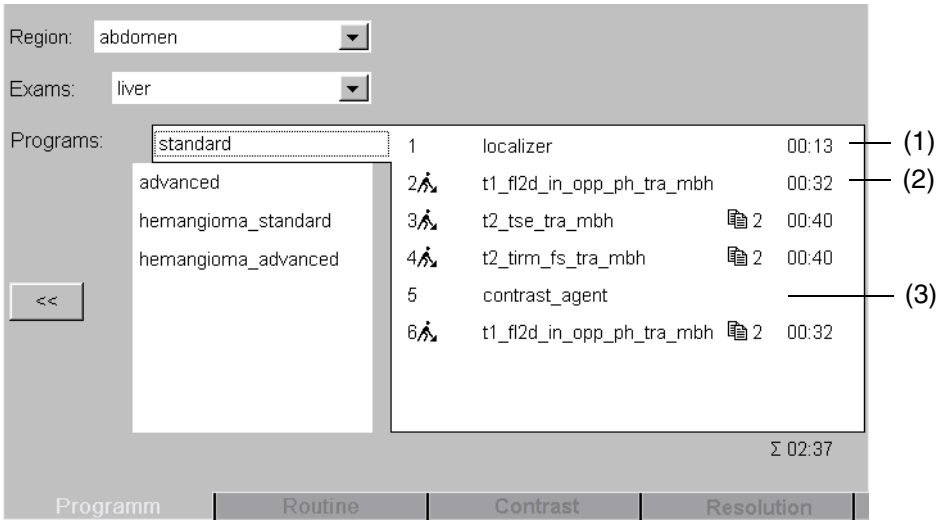
✧ Select a different examination, if necessary.

➪ The properties of the selected examination (e.g. the short description) may be viewed in the **Tree object properties** dialog box. Select **Properties** from the context menu.

Selecting a scan program

After you have selected an examination, **Programs** will display the scan programs that are available for this examination.

The first scan program is preselected in this list. The content of this scan program (i.e. the sequence of program instructions (scan protocols and scan pauses)) is displayed in the right-hand window of the parameter card.



(1) Overview measurement **Localizer**
(2) Scan protocol
(3) Scan pause (here: for contrast administration)

Selecting a scan program on the Program parameter card

If the preset scan program is not suitable for your diagnostic requirements, you may select one of the other scan programs offered on the **Programs** parameter card.

✧ Select the scan program you want to use for your examination by clicking on it in the list.

The right-hand window of the parameter card shows the program instructions of the newly selected scan program.

➪ The **Tree object properties** dialog box provides further information about the selected scan program (short description, time of last change, etc.). Select **Properties** from the context menu.

Selecting a scan program in the Exam Explorer

Switch to the **Exam Explorer** if you are unable to find a particular examination or scan program on the **Programs** parameter card. All examinations and scan programs are clearly listed there, and you can also access the Siemens tree, if necessary.
→ Page C.16–1, *Organizing Scan Programs*

✧ Select **Explorer** from the context menu.

The **Exam Explorer** dialog box is displayed. You may now search for the appropriate scan program in the **Exam Explorer** and then transfer it to the program control.
→ Page C.16–12, *Finding a scan program*
→ Page C.16–66, *Transferring a scan program to the program control*

You may close the **Exam Explorer** when you are finished using it.

✧ To do this, select **Object > Close** in the **Exam Explorer**.

NOTICE

Make sure that no program instruction is selected on the **Programs** parameter card. Otherwise the context menu will *not* contain the **Explorer** item.

Transferring a scan program to the program control

Before scanning you have to transfer a scan program from the **Programs** parameter card (or from the **Exam Explorer**, *see* → Page C.2–6) to the program control.

Transferring a routine scan program

In routine scans you will usually transfer a complete scan program.

✧ Select the required scan program.
→ Page C.2–4, *Selecting a scan program*



✧ Click the **<<** button on the **Programs** parameter card.

Or

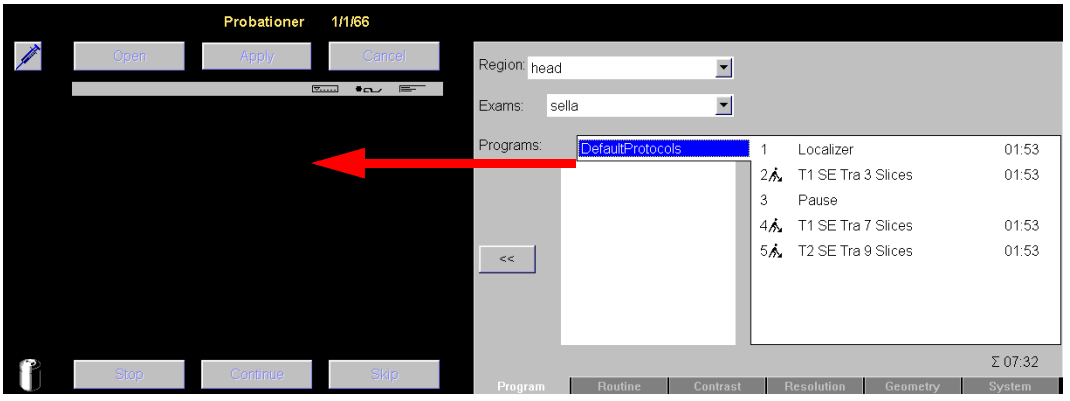
✧ Select **Queue > Append** from the main menu.

Or

✧ Select **Append** from the context menu.

Or

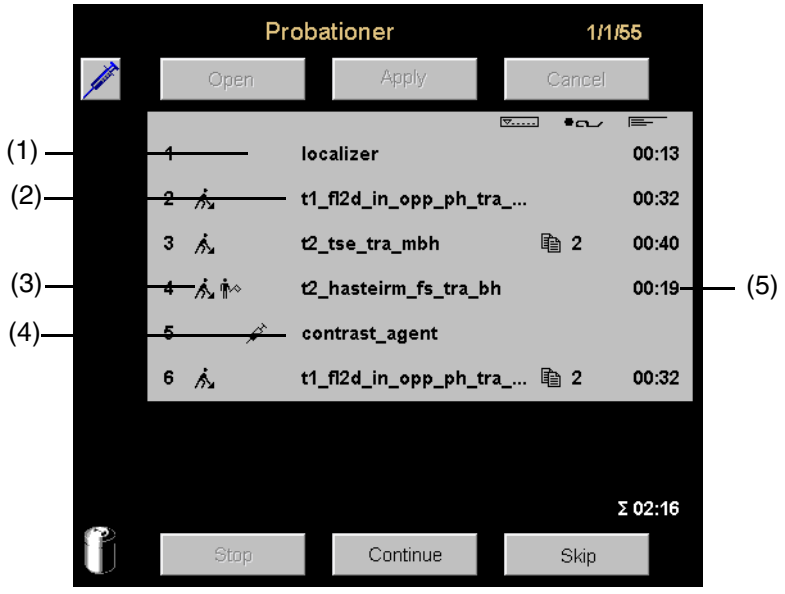
✧ Click the required program and *drag & drop* it in the program control.



The steps of the selected scan program will be transferred to the program control. This program will start automatically if it contains a **Localizer** with no additional start instructions.

The program control displays a sequence of program instructions with their expected scan time and the processing status of the protocols.

→ Page C.6–1, *Performing a Routine Examination*



(1) "Localizer" (overview measurement)
(2) Scan protocol
(3) Icons identifying the start options of a protocol
(4) Scan pause (in this case, for contrast agent administration)
(5) Scan time of a protocol

Transferring individual program instructions

You may also transfer individual protocols from one or more scan programs. This allows you to adapt the sequence of the current examination to your individual diagnostic problem.

✧ Select the scan program that you want to transfer.

➪ You may also several program instructions at once.
→ *syngo* Operator Manual



✧ Click the **<<** button on the **Programs** parameter card.

Or

✧ Select **Queue > Append** from the main menu.

Or

✧ Select **Append** from the context menu.

Or

✧ *Drag & drop* your selection into the program control.

The selected program instructions are transferred to the program control

Viewing protocol parameters

If you are not sure which scan protocol to transfer, you may view the measurement parameter settings first.

✧ Select a protocol from the **Programs** parameter card.

✧ Select **Edit > View Protocol** from the main menu.

Or

✧ Select **View protocol** from the context menu.

Or

✧ Double-click the protocol entry.

The **Protocol view** dialog box opens.

➪ In the Protocol view, you may view (but not change) the scan parameters of the protocol on the parameter cards.

Protocol or pause properties

The **Protocol step properties** dialog box provides information about the start options of a protocol, about copy references, and about automatic forwarding of images. The **Pause step properties** dialog box provides information about a scan pause (e.g. for administering a contrast agent).

✧ Select a protocol or pause from the **Programs** parameter card.

✧ Select **Properties** from the context menu.

Either the **Protocol step properties** or the **Pause step properties** dialog box will be displayed.

Adding further program instructions or scan programs

The program control includes a list of the transferred program instructions. You may add additional program instructions or scan programs to this list.

✧ Select additional program instructions or another scan program from the **Programs** parameter card (or in the **Exam Explorer**, *see* → Page C.2–6).



✧ Click the **<<** button on the **Programs** parameter card.

Or

✧ Select **Queue > Append** from the main menu.

Or

✧ Select **Append** from the context menu.

Or

✧ *Drag & drop* your selection into the program control.

The new scan program or the new program instruction are appended to the existing program instructions.

CHAPTER C.3

Measuring, Editing, and Managing Reference Images

Most measurement programs will prompt you to perform a localizer measurement first. The reference images generated with the localizer are used to position slices or define the field of view (FOV) for subsequent scans.
→ Page C.1–4, *Procedure for routine scanning*

Instead of the localizer images, you may also use other patient images acquired during the current exam as reference images.

You may view reference images in the image segments, improve image display, and select the images best suitable for slice positioning.

The image segments of the **Exam** task card may be used for other purposes besides graphic slice positioning. For example, they allow you to view, evaluate, and edit the acquired images. You can export images directly from the **Exam** task card to other task cards for postprocessing, export images, or save them in the **Patient Browser**.

NOTICE

To perform the examination, you need to have full access rights.

Please observe the information given in the *Safety Standards* book.

Measuring reference images

The localizer starts automatically as the first program instruction after you load a scan program into the program control.

While scanning is in progress, the localizer protocol has a white background in the program control.



The status bar successively displays the processes in progress:

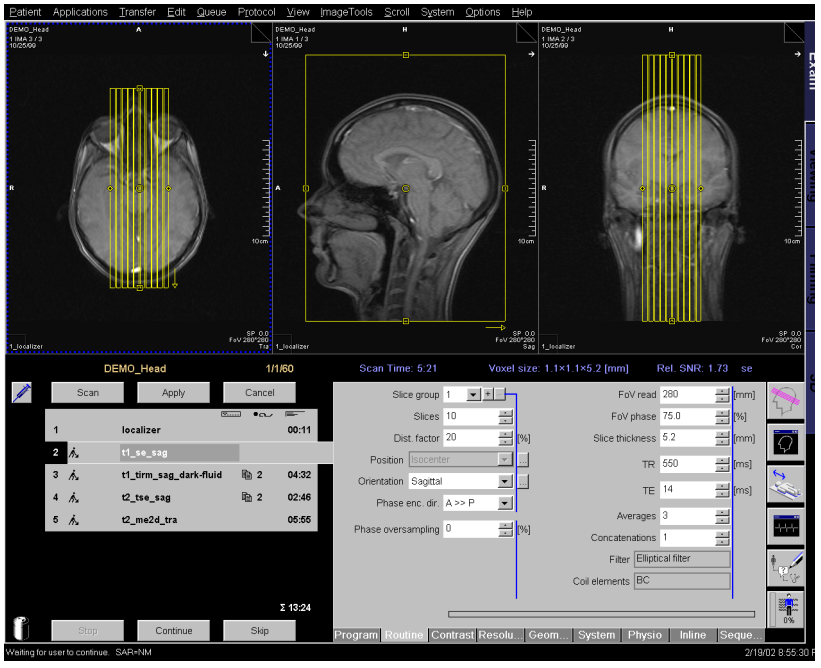
- **Adjusting (Tune)...**
  Adjustment of the system to the parameters and coils according to the program instruction.
- **Preparing...**
- **Scanning...**
  A scan is in progress. The remaining scan time of the protocol is displayed in countdown mode.

The series icon is displayed as soon as scanning and image calculation have been completed.



⇨ A half series icon means that the series has not been completed.

These reference images are displayed in the image area of the **Exam** task card once the localizer measurement and image calculation have been completed.



The reference images show the organ or part of the body to be examined, usually in the three main orientations (sagittal, transverse, and coronal).

The next program instruction (e.g. **t1_se_sag**) is normally incomplete and is opened for graphic slice positioning.



Using reconstructed images as reference images

If you have already performed scans and reconstructed series as part of your examination, you may use images from these series for graphic slice positioning as well.

Requirements

These images have to meet the following criteria:

- ❏ The images are part of the current examination of the current patient.
- ❏ The images are part of the same series block.
  → Page C.3–38, *Series block*
- ❏ The series were measured using the same table position.
- ❏ The images have NOT been filtered (distortion corrected) using the FoV compensation filter.
  → Page H.1–66, *Filter 🗀 Routine, Resolution-Common*

The following images cannot be loaded into the image segments:

- ❏ Mosaic images
  See Application Guide
- ❏ Secondary capture images
  (e.g. alpha images of the BOLD evaluation)
  → Page D.4–1, *Alpha image*
- ❏ Curved cuts of the 3D evaluation
  → *syngo* Operator Manual

Loading images into the image area

You can use either the program control or the **Patient Browser** to load images and series into the image area of the **Exam** task card.

Loading a series from the program control

✧ Select a completed protocol in the program control.

✧ Select **Queue > Load Series** from the main menu.

Or

✧ Select **Load series** from the context menu.

Or

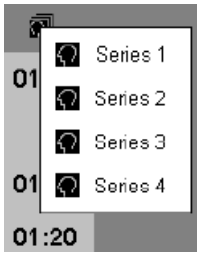


✧ Double-click the series icon.

Or

✧ Drag and drop the series into the image area.

The series is loaded into the image area of the **Exam** task card.



If the protocol generates several result series, a dialog window allows you to select the series to be transferred.

Loading from the Patient Browser

You can use the **Patient Browser** to load images for graphic slice positioning. Images already loaded into the image area will be ignored during this process.

✧ Open the **Patient Browser**.

✧ Select the images or series in the **Patient Browser**.
→ *syngo* Operator Manual

✧ Drag and drop the images or series into one of the image segments.

Or (if only *one* image or series has been selected)

✧ Double-click the selected image or series.

Images with different table positions

Each time you load series or images that were acquired at a different table position, the currently loaded images are cleared from the image area.
→ Page C.3–37, *Table position and reference images*

Display of loaded reference images

You can choose between different layouts to display the loaded images.

Three-segment layout

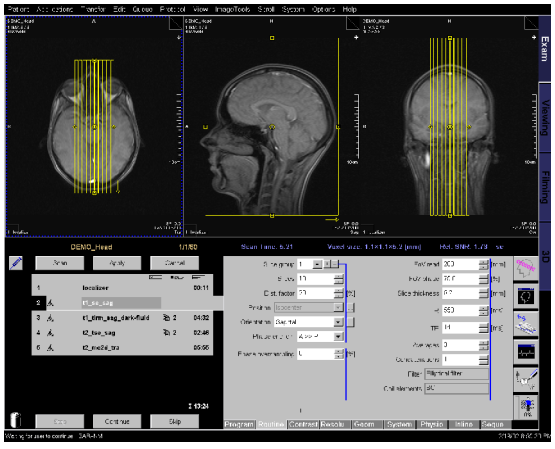
Select a three-segment layout if you want to display three reference images side by side.

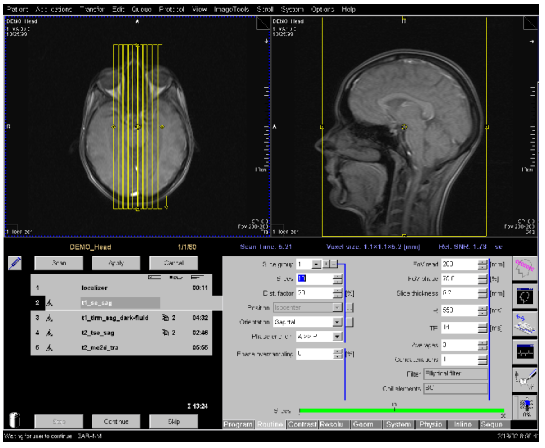
✧ Select **View > 3 Segments** from the main menu.

Two-segment layout

Select a two-segment layout if you want to display two reference images side by side. The reference images are displayed larger than in the three-segment layout.

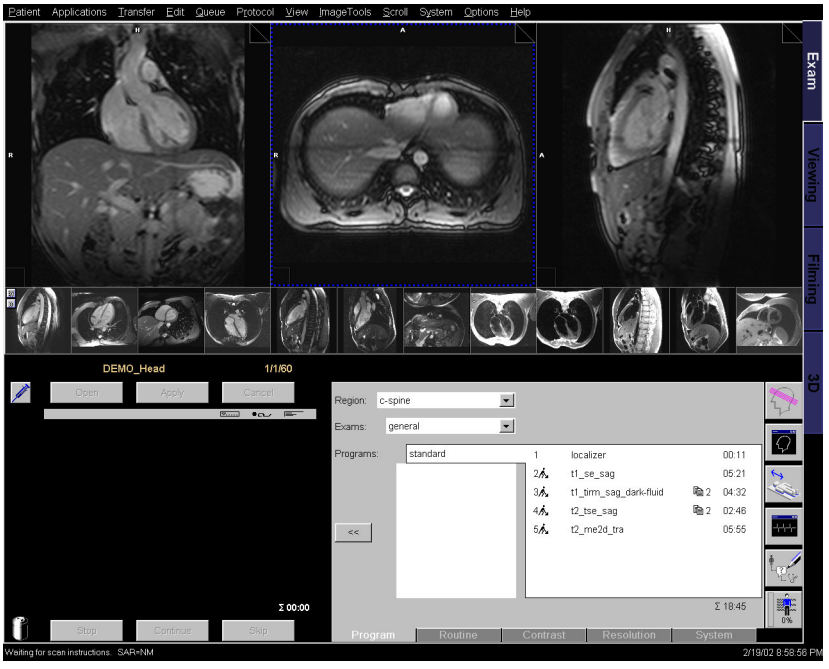
✧ Select **View > 2 Segments** from the main menu.





Maestro layout (optional)

Select the Maestro layout for improved management and evaluation of cardiac series. The acquired series are displayed in stamp segments below the three image segments.
’ Page C.17–2, *Maestro layout*



Distributing images across segments

The following rules apply:

- ❏ If the image area is empty, the loaded images will be distributed across the image area so that every segment displays at least one image.
- ❏ If only *one* series has been loaded into the empty image area, the images of this series will be distributed across the available segments (2 or 3).
- ❏ If *multiple* series have been loaded, one image representing a series will be displayed in each segment.
- ❏ If all the image segments are filled, the remaining series will be loaded in the background. You can move these series to the foreground by scrolling with **Series-**/**Series+**.
→ Page C.3–17, *Scrolling within image segments*

Representative image

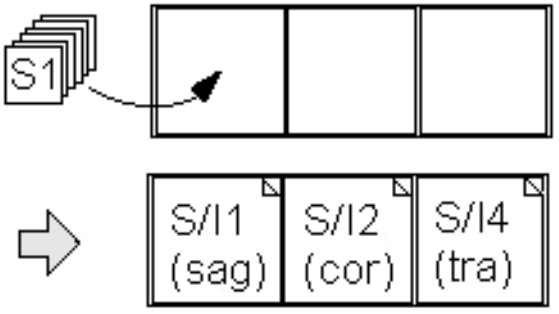
The image in the center of the anatomy is used as the representative image for a series with different slice positions.

If all images in a series use *the same* slice position, the first image of the current sequence is used as the representative image.
→ Page C.3–12, *Defining the scroll order*

Example 1

All three image segments are empty. A localizer with one sagittal, two coronal, and three transverse overview images has just been completed.

The images are distributed across the image segments as follows:

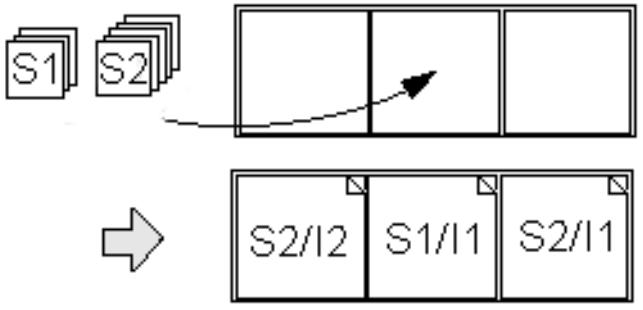


The series is duplicated twice and displayed in all three segments. The left segment shows the sagittal image, the center segment shows the first coronal image, and the right segment shows the first transverse image.

Example 2

All three image segments are empty. Two series of the current series block are dragged and dropped from the **Patient Browser** to the center segment.

The images are distributed across the image segments as follows:



The first series is loaded into the target segment (center segment), the second series is loaded into the right segment. The second series is duplicated and displayed in the left segment. The system automatically searches for another suitable image in the second series to be used as the representative image for the first segment.

Defining the scroll order

There is a difference between scrolling *within* a series and scrolling *between* series.

If multiple series are loaded into an image segment, you can scroll between series. The order of the series is defined by the series number. This number depends on the date and time of reconstruction. The order of the series *cannot* be modified.

However, you can define the order of the images within a series. You can select from various default sort options in the menu. You can also define your own sort schemes for the order of images.

The sort scheme also determines the order of the images during movie display.
→ Page C.17–13, *Movie display*

Sort criteria

The following sort criteria are available:

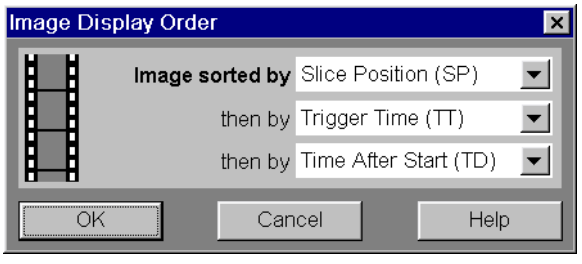
Abbreviation	Example
MO	Sorting according to the main orientation sag - cor - tra
SP	Sorting according to the main orientation tra - cor - sag Sorting according to membership in a slab group and the SliceShift value
TT	Sorting according to trigger time
TA	Sorting according to acquisition time
TE	Sorting according to echo time
TD	Sorting according to time after delay (perfusion or diffusion time)
BV	Sorting according to b-value
NR	Sorting according to image numbers
--	Sorting according to order of loading For this criterion, you cannot add another sub-criterion.

Defining your own sort scheme

You can define up to three levels for sorting images within a series. You define a sort criterion for each of the three levels.

✧ Select **Scroll > Display Order > User Defined**.

The **Display Order** dialog box opens.



✧ Select the sort criterion for the first sort level from the **Image sorted by** selection list.

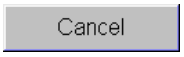
✧ Select the sort criterion for the second sort level from the **then by** selection list.

✧ Select the sort criterion for the third sort level from the **then by** selection list.

The sort criterion of the second level is used if the sort criterion values of the first level are identical.

The sort criterion of the third level is used if the sort criterion values of the first and second levels are identical.

➪ Select a different sort criterion for each sorting level. Exception: If you select the **Load Order** criterion for the first level, the **then by** fields will be grayed out. You cannot define additional sort criteria.



You can cancel the definition of the sort scheme and close the dialog box.

✧ Click **Cancel**.

The previous setting is still applied to the order of the images within the series.



You can apply the new sort scheme and close the dialog box.

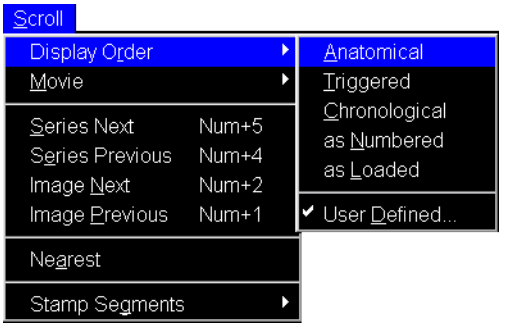
✧ Click **OK**.

Using a Siemens sort scheme

You may select from five different Siemens sort schemes for the order of images within a series.

Name	Sort scheme	Application
Anatomical	SP»TT»TA»NR	Standard sort scheme Localizer, anatomical examinations, multi-slice/multi-phase scans (grouped according to phases), multi-slice real-time scans
Triggered	MO»TT»TD»SP	Multi-slice/single-phase scans or multi-slice/multi-phase scans (if a slice package is viewed anatomically at defined trigger times) Perfusion and diffusion multi-slice scans
Chronological	MO»TA»SP»NR	Sorting by time of acquisition (TA), images with the same TA are sorted by SP, images with the same TA and SP are sorted by NR.
As numbered	NR»SP	Sorting by image number (NR) Images with the same NR are sorted according to SP.
As loaded		Sorting by load order

✧ Select a sort scheme from the menu under **Scroll > Display Order > .....**.



➪ The **Anatomical** sort scheme is selected by default. This is the optimal scheme for most applications.

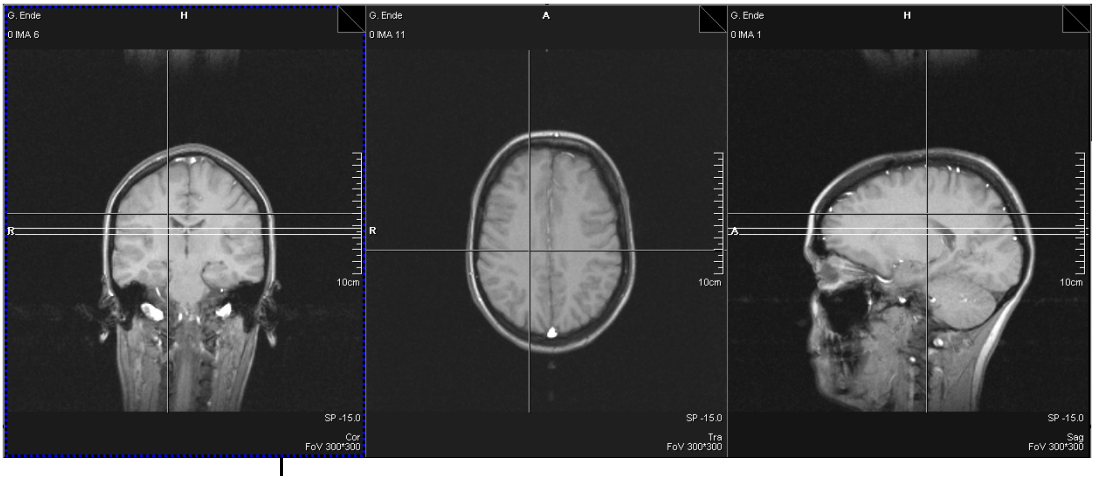
➪ The sort scheme selected is applied until you select another scheme.

Scrolling within image segments

After loading images into the image area, you can scroll the images within an image segment. This helps you select the images most suitable for slice positioning.

Setting the input focus

The **Input Focus** indicates the active segment of the image area. It is highlighted by a dashed blue border. Actions triggered via the keyboard (e.g., scrolling using the Image+/Image- keys) are always performed in the active segment.



Input focus

You can move the input focus into another image segment by pressing the **Left** or **Right** cursor keys or clicking the other segment.

Keyboard focus

The keyboard focus has to be on the image area if you want to use the keyboard for scrolling.
→ *syngo* Operator Manual

➪ Keep pressing the **Tab** key until a thin white border appears around the image area, or click inside the segment you want to scroll.

Scrolling between images

There are different ways of scrolling between images within a series.

✧ Select **Scroll > Image Next** or **Image Previous**.

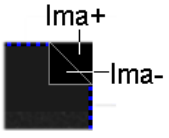
Or




✧ Press the **Image+** or **Image-** keys on the symbol keypad of the keyboard.

Or

✧ Scroll through the image stacks using the dog ears.



➪ When you reach the last image of the series, **Image+** scrolls to the first image of the series. **Image-** scrolls to the first image to the last image of the series.

Parallel scrolling

To compare images of two or three series, scroll in parallel through images in these series.

✧ Explicitly select the image segments you want to scroll in parallel.
→ Page C.3–21, *Explicit selection*

✧ Use the symbol keys or the menu commands to scroll between images.

⇨ It is also possible to scroll in parallel using the dog ears.

If the series do not contain the same number of images, parallel-scrolling stops at the end of the shorter series. Scrolling continues up to the end of the longer series. If you continue scrolling, parallel scrolling will start over with the first image of the series.

⇨ During parallel-scrolling, system performance depends on the number of images and series and may be affected by processes running in background.

Scrolling to the next/previous series

There are various ways of scrolling between series.

✧ Select **Scroll > Series Next** or **Series Previous** from the main menu when starting applications and functions.

Or




✧ Press the **Series+** or **Series-** keys on the symbol keypad of the keyboard.

➪ When you reach the last series of an examination, **Series+** scrolls to the first series of the examination (accordingly, **Series-** scrolls from the first series to the last series of the examination).

Editing reference images

You can edit reference images as follows:

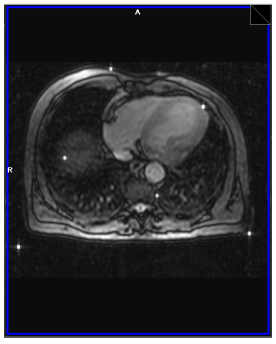
- ❏ Set brightness and contrast
- ❏ Zoom and reduce images and pan image content
- ❏ Fit to segment size
- ❏ Flip and rotate
- ❏ Display pixel coordinates, measure distances and angles
- ❏ Show/hide image text

Selecting images explicitly and implicitly

Before editing images using the various functions, you have to select the images explicitly or implicitly.
→ *syngo* Operator Manual

Explicit selection

Objects selected explicitly can be identified by their solid blue border.



✧ Press and hold the **Ctrl** key while left-clicking an image.

The image is selected explicitly.

You can select multiple images explicitly.

✧ Press and hold the **Ctrl** key while clicking multiple images.

You can also select a range explicitly.

✧ Press and hold the **Ctrl** key while clicking the first image within the range. Press and hold the **Shift** key *as well*. Click the last image within the range.

You can select multiple series explicitly.

✧ Start by selecting one image per series explicitly.

✧ Select **Edit > Select Series** from the main menu or **Select Series** from the context menu.

➪ You can cancel an explicit selection by left-clicking inside a segment. The segment is now selected implicitly.

Implicit selection



Objects selected implicitly can be identified by their dashed blue border (input focus).

The segment selected implicitly receives the function call from the menu.

If you open a context menu within a segment, the segment is automatically selected implicitly. This does *not* apply if the segment is part of a multiple selection.

Changing window values

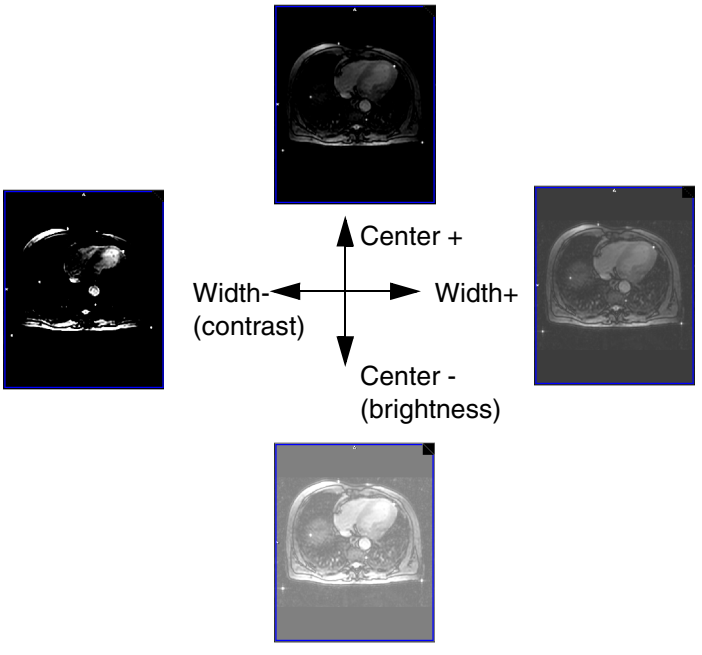
Windowing changes the grayscale values, the brightness, and the contrast of the reference images.

Windowing using the mouse



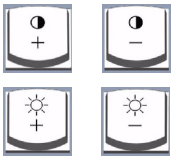
✧ Position the mouse pointer in the segment you want to window.

✧ Press and hold the *center* mouse button while dragging the mouse.



✧ Release the mouse button once the window values are set to your requirements.

Or



✧ Window by using these symbol keys on the symbol keypad of your keyboard.

➪ These symbol keys are mainly for fine adjustment. You may use the mouse for fast windowing.

Applying window values to the series

You can automatically apply the new window values of an image to all images in the respective series using the menu.



✧ Activate the **Window On Series** option under **Image Tools**.

This setting remains active even after the system is rebooted.

Auto windowing

This function allows you to set the contrast and brightness of the reference images automatically.

✧ Double-click an image segment with the *center* mouse button.

Or

✧ Select **ImageTools > Auto Windowing** from the main menu.

Or



✧ Press this key on the symbol keypad.

Enlarging, reducing, and panning reference images

You may want to reduce images for a better overview. You may want to enlarge images for a better view of details. After enlarging images, it is often helpful to pan them to move the relevant structure into the center of the screen.

Zooming with the mouse

You can enlarge, reduce or pan images using the mouse. This requires you to switch the functionality of the left mouse button from "Select" to "Zoom/Pan".

✧ Select **Image Tools > Zoom/Pan**.

Or

✧ Select **Zoom/Pan** from the context menu.

Or



✧ Click this button on the **Position Toolbar**.
→ Page C.4–4, *Position toolbar*

✧ Position the mouse pointer in the *outer* area of the image.



The mouse pointer changes shape.

✧ To enlarge the image, press and hold the *left* mouse button and drag the mouse pointer upward.

✧ To reduce the image, press and hold the *left* mouse button and drag the mouse pointer downward.

Panning with the mouse

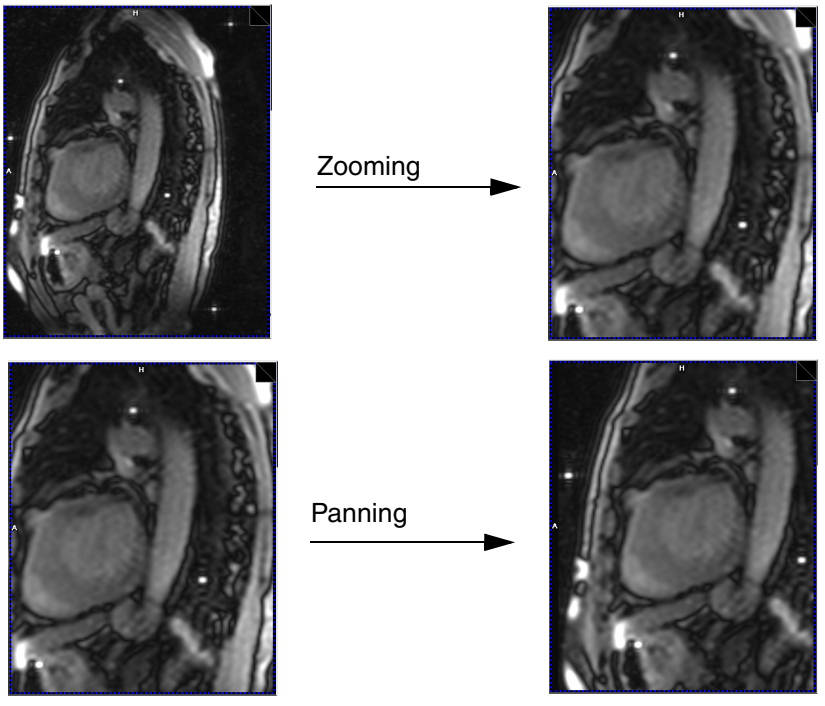
Next, you can use to the mouse to pan the enlarged or reduced image section in the image segment.

✧ Position the mouse pointer in the *inner* area of the image.



The mouse pointer changes shape.

✧ To pan the image contents, press and hold the *left* mouse button and drag the mouse upward, downward, to the right, or to the left.



Applying zooming/panning to the series

You can change the menu settings so that the changes to the visible image section are automatically applied to all images in the series.



✧ Activate the **Zoom/Pan On Series** option under **Image Tools**.

This setting remains active even after the system is rebooted.

Fit image to segment

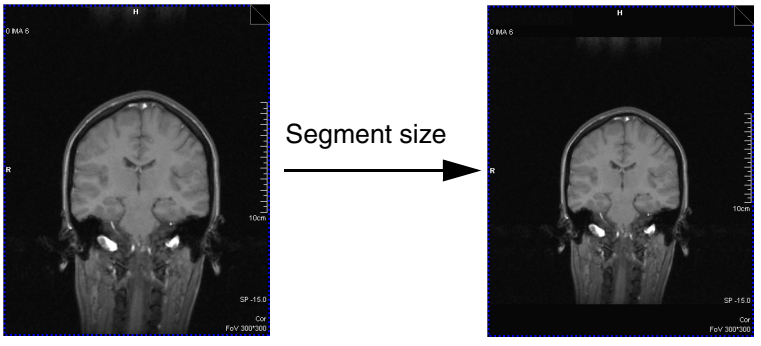
You can automatically enlarge/reduce an image for optimal fit of the image contents within the segment.

✧ Select an image.

✧ Select **Image Tools > Fit to Segment** to enlarge/reduce an image to fit the segment size.

Or

✧ Double-click the image with the *left* mouse button.

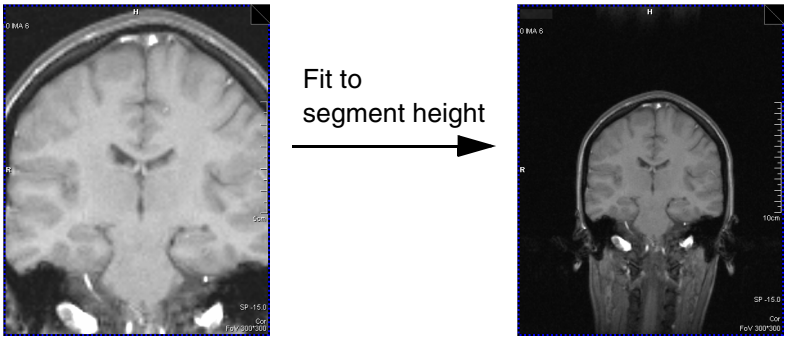


Fit to segment height

Use the **Fit to Segment Height** function to fit the height of the reference image precisely to the height of the segment.

✧ Select an image.

✧ Select **Image Tools > Fit to Segment Height**.



➪ In the two-segment layout, the **Fit to Segment** and **Fit to Segment Height** functions have the same effect.

Flipping and rotating images

You can flip images in the image segments horizontally and vertically and rotate them clockwise by 90°.

These functions are mainly used for improved viewing of breast biopsy images.

Flipping images horizontally and vertically

Horizontal flipping swaps the top and bottom of the image. The axis of rotation is horizontal.

Vertical flipping swaps the left and right side of the image. The axis of rotation is vertical.

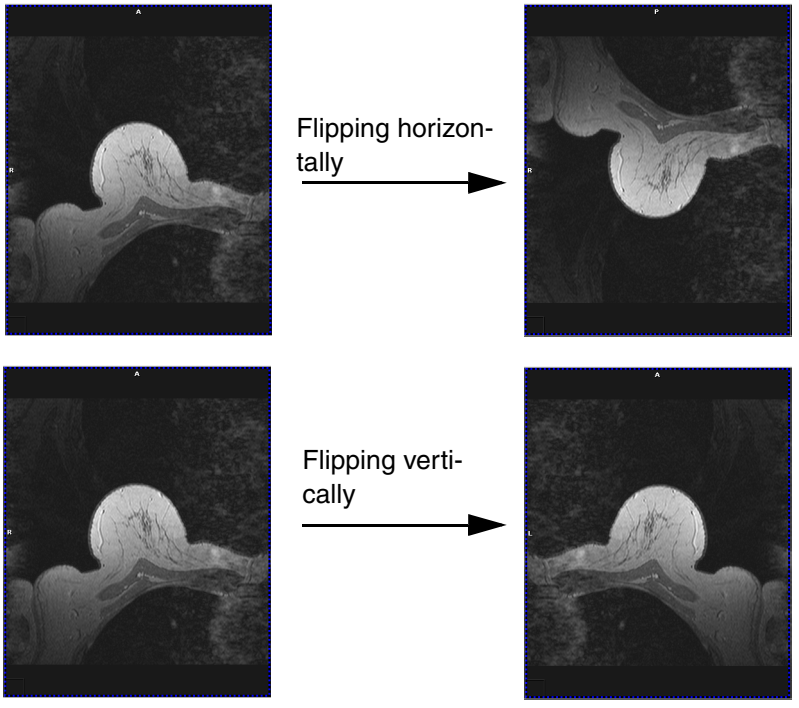
✧ Place the input focus on the image you want to flip.

➪ To flip multiple images, select the images explicitly.

✧ Select **Image Tools > Flip Horizontally**.

Or

✧ Select **Image Tools > Flip Vertically**.


Flipping horizontally
Flipping vertically

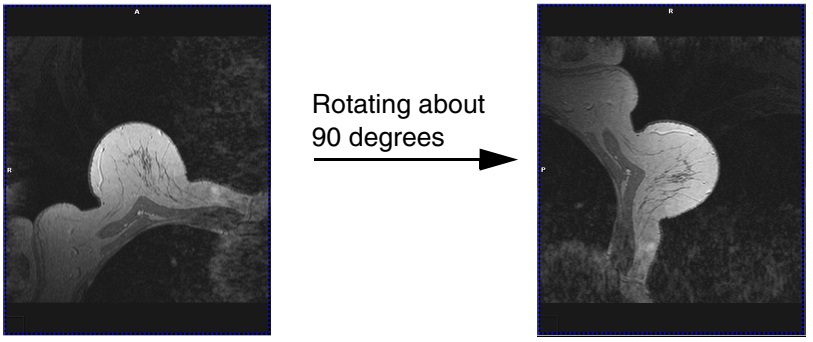
Rotating images about 90°

You are able to rotate images clockwise about 90°.

✧ Place the input focus on the image you want to rotate.

➪ To rotate multiple images, select the images explicitly.

✧ Select **Image Tools > Rotate 90**.



Showing/hiding image text

By default, image text is displayed in the image segments. When you edit images (e.g. windowing) the image text is often hidden temporarily.

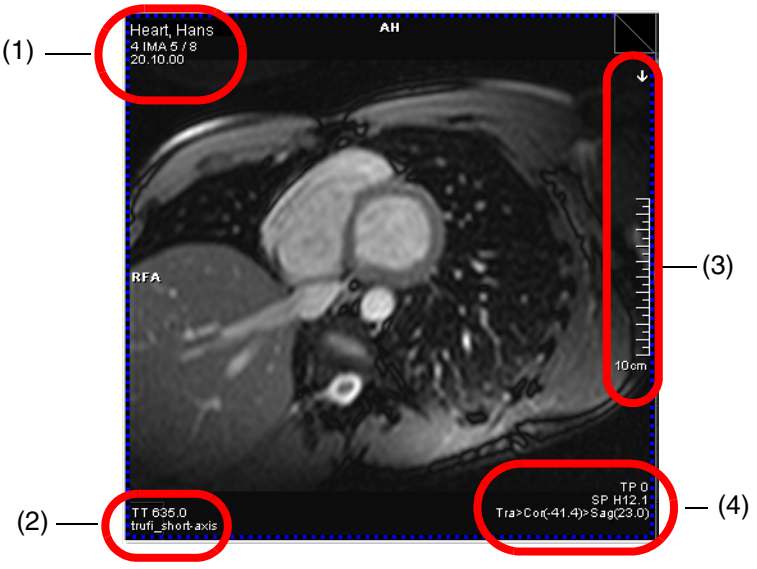
You can manually disable image text if necessary.

✧ Select **View > Image Text On** from the main menu.

Or



✧ Click this button on the **Position Toolbar**.
→ Page C.4–4, *Position toolbar*



(1) Patient data (name, series image number, date)
(2) Compression, trigger time, and protocol name
(3) Phase-encoding direction and scale
(4) Image data (FOV, slice orientation, table position, slice position)

Pixel coordinates, distances, and angles

You can display the position of the mouse pointer within the image as coordinates in the patient coordinate system.



✧ Select **Image Tools > Modify Graphics**.

The functionality of the mouse is switched from **Zoom/Pan** to **Modify Graphics**.

✧ Position the mouse pointer on the region of interest in the image.

✧ Press and hold the left mouse button.



The coordinates in the patient coordinate system are displayed without sign.

The coordinates of the table position are shown in the second line if the image was not acquired using the original table position of the series block, but after a relative table movement.

✧ Press and hold the left mouse button while moving the mouse pointer.

The new coordinates for the image position are displayed.

Measuring the distance between two points

In **Modify Graphics** mode, you can measure the relative distance between two image positions.



- ✧ Select **Image Tools > Modify Graphics**.
- ✧ Press and hold the left mouse button.
- ✧ Select the first position for the distance measurement while keeping the mouse button pressed.
- ✧ Press the Shift key and drag the mouse pointer.

This starts the distance measurement. You can release the Shift key as soon as the distance line is displayed.

- ✧ Drag the mouse pointer to the second position in the image.

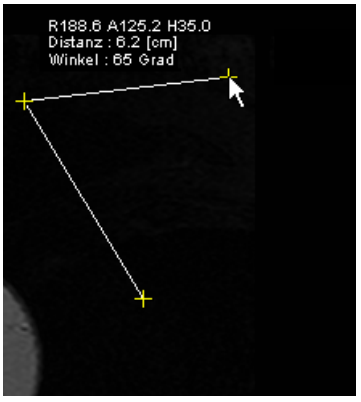


The distance to the first point is displayed below the coordinates.

The coordinates and the distance disappear when you release the mouse button.

➪ The **Viewing** task card also allows you to measure distances and save or film the distance line with the measured distance. → *syngo* Operator Manual

Measuring angles



After the distance measurement, you can select a third image position and determine the angle between the third, first, and second point.

✧ Select **Image Tools > Modify Graphics**.

✧ Measure the distance between two points.

✧ Continue pressing the left mouse button and temporarily add the **Ctrl** key while selecting a third image position.

The first and third points will be connected. The angle is displayed below the coordinates and the distance.

The coordinates, distance, and angle disappear when you release the mouse button.

➪ The **Viewing** task card also allows you to measure distances and save or film the distance line with the measured distance. → *syngo* Operator Manual

Removing images from the image area

You can clear the images from all segments if you no longer need the reference images loaded in the image area.

✧ Select **Edit > Clear All Segments**.

The images are removed. The image area is empty.

It is also possible to remove all images of one or more selected series from the image area.

✧ Select the series explicitly.
→ Page C.3–21, *Explicit selection*

✧ Select **Edit > Clear Document(s)**.

Repeating scans (Phoenix)

You can view and evaluate the measured images in the image segments.

You can repeat the complete scan of a protocol if, for example, the result images for a breath-hold scan are of poor quality.

✧ Select the poor quality image.

✧ Select **Append To Queue** from the context menu.

Or

✧ Drag and drop the image into the job list.

A copy of the protocol is generated and converted into an executable program instruction.

Table position and reference images

In most cases, reference images are scanned with the patient table in a certain position. This position is used for all protocols of the scan program.

In some cases, the area of examination may be so large that you have to move the patient table and run protocols at different table positions.

It is important to know the relation between the table positions of the reference images and the protocol parameters for positioning the scan region.
→ Page H.1–80, *Position of the scan region*

Series block

You can view and evaluate several series acquired at various table positions. In this case, they have to be grouped in a *series block*.

A series block groups all series with positioning data based on the same defined original table position. The series block remains valid in case of automatic table movement.

A new series block begins when you:

- ❏ **register a new patient**
  → *syngo* Operator Manual
- ❏ **reset the table position to zero**
  → Page C.6–36, *Defining a new center position*
- ❏ **move the table to the home position**
  see System Manual
- ❏ **change the patient position**
  see System Manual
- ❏ **set a new mark with the light localizer**
  see System Manual

You can end a series block explicitly.

✧ Select **Patient > Close Patient**.

Scanning at a table position

At the beginning of the examination, you mark the center of the examination region on the patient using the light localizer. Then you move the patient into the magnet. The position marked has to align with the magnet isocenter (center position).

Setting the origin

The light localizer is used to define a zero point (original table position) to which all subsequent scans will refer.

Localizer measurement

The image area is still empty. The localizer measurement is started from the original table position. The reference images are displayed in the image area after scanning and reconstruction are completed.

Transferring the table position of the localizer

Open the next protocol and plan the slices to be scanned on the reference images.

This protocol will be run at the same table position as the reference images.

Protocol with undefined table position

Protocols are scanned at the current table position if no reference images are displayed or you have cleared the reference images from the image area at the time of scan preparation.

This usually corresponds to the position of the light localizer marking (original table position). In this case, the protocol does not have a defined table position. The localizer is a typical protocol using an undefined table position.

Scans with patient table movement

You can set the offset of the patient table using the table position of the reference images or the **Scan region position** protocol parameter on the **System Common** parameter card.

Transferring the table position of a normal protocol

Instead of the localizer images, you load a different series already measured into the image area.

Open the next protocol and plan the slices to be scanned on these images. The next protocol is run at the same table position as the images loaded in the image area.

The patient table will automatically move to this table position if it is different from the original table position.

NOTE

The table position of the reference images overwrites the table position parameters of the open protocol.

Defining the table position using protocol parameters

The image area is empty, e.g., because you have cleared the reference images from the segments. A protocol is opened.

✧ Enter a patient table offset on the **System Common** parameter card.
→ Page H.1–80, *Position of the scan region*

The protocol now has a defined table position. As soon as you start running a protocol, the patient table will move to the new position.

NOTICE

If protocols have been scanned at various table positions within a series block, only one automatic adjustment will be performed for each table position.

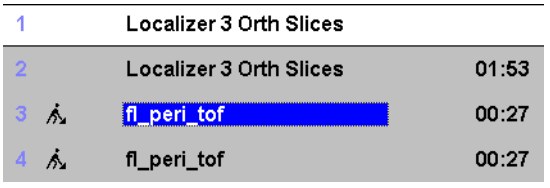
The adjustment results are stored and reused if additional scans are performed at the known table position.

Scan Program with More Than One Localizer

In some angiography examinations, the examination are is so large that multiple localizers have to be acquired at different positions. The subsequent protocols are run using the different table positions of the localizers.

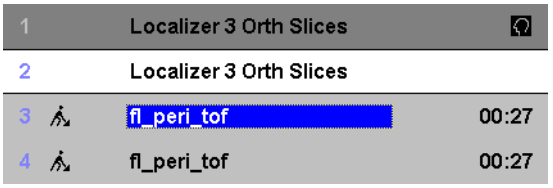
Example: Scan program with two localizers and two angio protocols

After transferring the scan program from the **Program** parameter card to the program control, the first localizer is scanned automatically at the original table position.



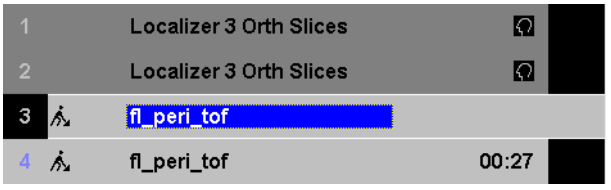
Once the first localizer is completed, the corresponding reference images are displayed in the image area. The patient table will *automatically* move to the preset table position of the second localizer.

The second localizer starts automatically at this position. After scanning, the series icon will indicate that reference images have been reconstructed for this localizer as well.



However, they will not be loaded into the image area.

The images of the *first* localizer are still displayed in the image area.



✧ Position the slices for the first angio protocol on these localizer images.

✧ Start scanning the first angio protocol.

The patient table will move back to the position of the first localizer (original table position). The first angio protocol will be scanned at this position.

✧ Load the reference images of the second localizer into the image area while the first angio protocol is running.

✧ Open the second angio protocol and plan this protocol on the images of the second localizer.

✧ Start the second angio protocol.



The patient table will move to the second table position. The second angio protocol will be scanned at the second table position.

Scanning will finish after all images have been reconstructed.

Saving, exporting, and transferring images

You may save, export or transfer images to other task cards from the **Exam** task card.

The image segments on the **Exam** task card may contain normal acquisition images or GSP images (reference images with drawn-in graphic objects).

NOTE

When a user logs off, unsaved data are irretrievably lost.

Check whether data still needs to be saved and save any data you want to keep before you log off.

Rules for saving, exporting, and filming

The following rules apply to GSP images:

- ❏ GSP graphics (slices, blocks, saturation regions, navigators) are stored with the GSP images.
- ❏ GSP graphics are saved in the non-selected version (without handles), with shadow lines and monochromatic.
- ❏ Distance lines, angles, etc. are *not* saved.
- ❏ GSP graphics on GSP images can no longer be edited on the **Viewing** task card.

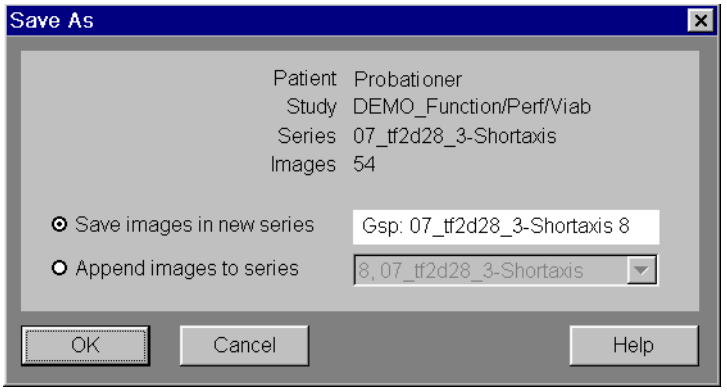
Saving images and GSP images

The **Exam** task card allows you to group a number of series and save them in *one* new series. These series must be part of the same series block and acquired at the same table position.

✧ Select the series or images explicitly.

✧ Select **Patient > Save As**.

The **Save As** dialog box is displayed.



A name for the new series is suggested. You can modify the suggested name.

✧ Select the **Save images in new series** option.

✧ Modify the new series name if necessary.

✧ Click **OK**.

Appending images to an existing series

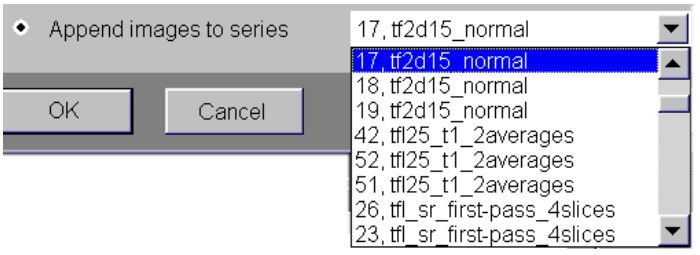
You can append individual GSP images to an existing series.

✧ Select the GSP images explicitly.

✧ Select **Patient > Save As**.

The **Save As** dialog box is displayed.

✧ Select the **Append images to series** option.



✧ In the list, select the series to which the GSP images should be appended.

✧ Click **OK**.

➪ The new images of the series have image numbers 5000 and up. This usually allows you to distinguish between old and new images within the series.

Appending an image to a reference series

You can append the GSP image with the input focus to the existing reference series in one step.

✧ Make sure the input focus is on the correct segment.

✧ Select **Patient > Copy Selection**.

The selected GSP image will be appended to the existing reference series.

Transferring images to other task cards

You can directly transfer images and series from the **Exam** task card to another opened task card for postprocessing.

This helps you save time, for example, when loading images into a postprocessing application.

✧ Make sure that the tab of the respective task card is visible.

✧ Explicitly select the images or series on the **Exam** task card.

✧ Drag and drop your selection onto the tab.

The selected images will be transferred to the task card. The **Exam** task card will remain in the foreground.

Filming, sending, and exporting images

Detailed information regarding filming can be found in the *syngo* Operator Manual.

Detailed information about data exchange via the network or Windows XP can be found in
→ *syngo* Operator Manual.

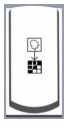
Copying images to the film sheet

Images that have been completely evaluated and edited can be copied directly from the **Exam** task card to the virtual film sheet.

✧ Select the images or series explicitly.

✧ Select **Patient > Copy to Film Sheet**.

Or



✧ Press this key on the symbol keypad of your keyboard.

➪ If you have not explicitly selected an image, the image from the segment with the input focus is copied to the film sheet.

Sending images

If your system is connected to a hospital computer network (HIS/RIS), you can send images to other network addresses directly from the **Exam** task card.

✧ Select the series explicitly.

✧ Select **Transfer > Send to**.

Or



✧ Press the **Send to Node 1** key on the symbol keypad.

Exporting images

You can save images on your hard disk as single files.

✧ Select the series explicitly.

✧ Select **Transfer > Export to file system**.

The **Export to File System** dialog box opens.

✧ Enter the path **C:\TEMP** and click **OK**.

Checking the data transfer

You can check and control the processing of export and network jobs.

✧ Select **Transfer > Organize Local Jobs** or **Transfer > Organize Network Jobs**.

Or

✧ Press the **Ctrl+L** or **Ctrl+N** key combination.

Or



✧ Click the corresponding icon on the status bar.

A dialog window for checking and controlling jobs is displayed.
→ *syngo* Operator Manual

CHAPTER C.4

Positioning Slices

After you have acquired and loaded reference images and optimized their display according to your diagnostic requirements, you can use them for defining the position, scope, and orientation of the region to be examined.
→ Page C.1–4, *Procedure for routine scanning*

Depending on the protocol, the system will scan slices or slabs for subsequent reconstruction.

You can plan saturation regions to avoid motion artifacts.

A number of special protocols - based on navigator sequences - contain additional navigator objects.

These graphic objects are displayed in the reference images as soon as you open a protocol.

The graphic objects of the protocol usually need to be adapted to the anatomy of your patient. The mouse and the graphic slice positioning tools allow you to perform tasks quickly and easily.

If these positioning tools are not accurate enough, you may set the parameters of the graphic objects on the **Geometry** parameter card.
→ Page C.5–79, *Adjusting the orientation and position of graphic objects*

Preparing for positioning

After completing the localizer, the next protocol automatically opens, allowing you to position the slices to be scanned.

Opening a protocol

If you want to adjust the slices of a subsequent protocol, open the protocol manually.

✧ Double-click a protocol in the program control.

Or

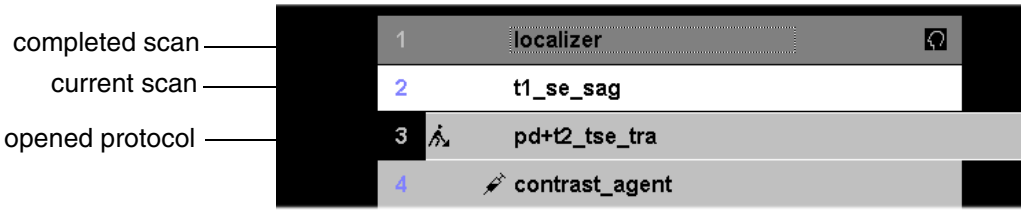
✧ Select a protocol in the program control.



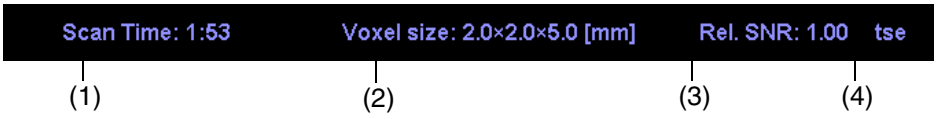
✧ Click the **Open** button or select **Open** from the context menu (right mouse button).

The program entry will be moved to the right in the job list. The protocol opens and its parameters are displayed on the parameter card.

➪ Each program instruction in the part of the job list that has not yet been processed can be opened for execution.
→ Page C.6–40, *Opening the next protocol for editing*



Various information about the open protocol is displayed below the image area.



(1) Scan time
(2) Voxel size (rounded up to the next $^{1}/_{10}$ mm)
(3) Relative signal-to-noise ratio
(4) Sequence type

➪ If you keep the mouse pointer near the voxel size display, a tool tip will be displayed stating the exact voxel size.

The graphic objects of the protocol (slices, slabs, navigators, and saturation regions) are displayed in the reference images in the image area.

Canceling slice positioning

You can cancel processing of the open protocol and restore the protocol to its original state.

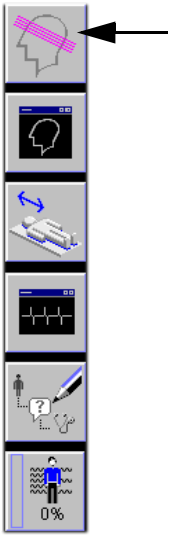


✧ Click the **Cancel** button in the program control.

All objects you have added or changed will be removed from the reference images. The reference images are still displayed in the image segments.

Position toolbar

Use the **Position Toolbar** to graphically position the objects to be scanned.



✧ Click on the **Position Toolbar** button on the tool bar of the **Exam** card.

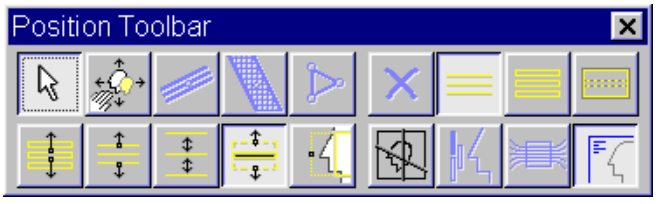
Or

✧ Go to the main menu and select **View > Position Toolbar**.

Or

➪ Select **Position Toolbar** from the context menu.

The **Position Toolbar** is displayed:



Graphical objects

Various graphic objects are displayed in the reference images, depending on the sequence preset in the protocol.

❏ Slice groups (for 2D measurements)
→ Page C.4–6

❏ 3D/Slabs (for 3D measurements)
→ Page C.4–8

❏ Saturation regions (possible for both 2D and 3D measurements)
→ Page C.4–10

❏ Navigator objects (for Navigator sequences)
→ Page C.4–15

❏ Spectroscopy volume elements
(e.g. for SVS protocols)

❏ Spectroscopy CSI slice
(e.g. for CSI protocols)

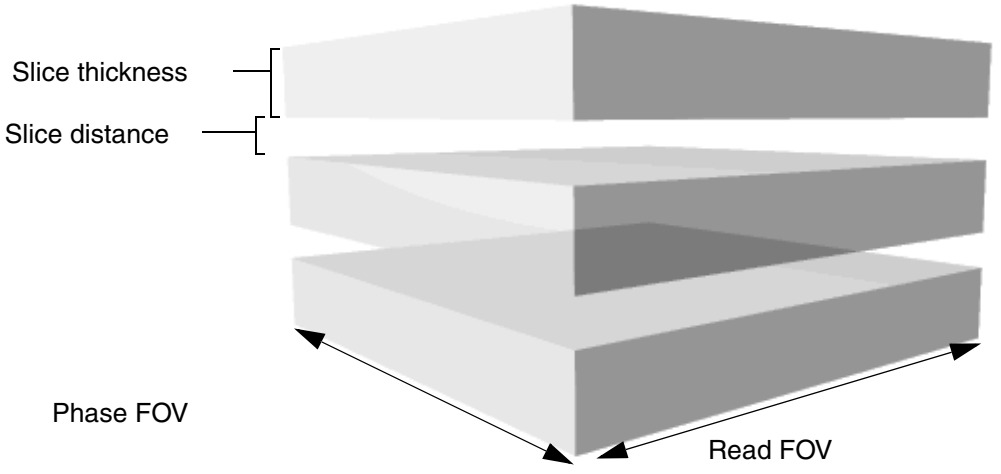
➪ Protocols and objects of spectroscopy are explained in a separate manual.
Refer to the MR Spectroscopy Operator Manual

Slices and slice groups

In 2D scanning, you use slice groups to define the extent, position, and orientation of the examination area to be scanned. Slice groups are composed of individual slices used for subsequent reconstruction of one or more tomographic images.

Slices always belong to a slice group. During graphic slice positioning you have to select an entire slice group. You are not able to select individual slices. The only exception is a slice group that consists of one slice only.

All slices of a group are located in parallel, have the same slice thickness, slice distance and field of view (FoV) as well as the same phase-oversampling factor (for reducing artifacts).



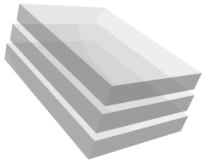
Field of view (FOV)

The field of view of a slice group is defined by its length and width. The length and width correspond to the read-out and phase-encoding directions in the magnetic field.
→ Page C.4–77, *Changing the field of view (FoV) via the mouse*

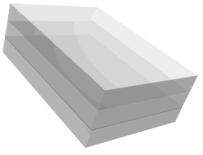
Slice thickness and slice distance

The distance between the slices of a slice group is expressed as a percentage of the slice thickness. In other words, as soon as you change the slice thickness of a group, the absolute slice distance changes as well.

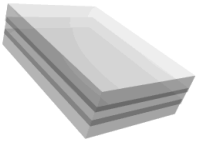
- ❏ 100%
  The slice distance is equal to the slice thickness.
- ❏ 0%
  The slices are contiguous.
- ❏ < 0%
  The slices overlap.
- ❏ -100%
  The slices overlap fully



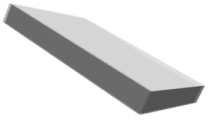
Factor > 0



Factor 0



Factor < 0



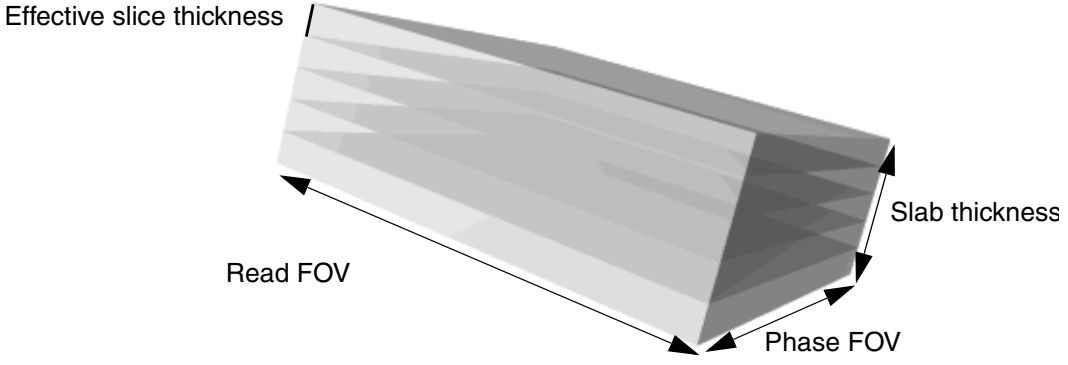
Factor -1

→ Page H.1–5, *Distance factor* 🗀 *Routine, Geometry-Common*
→ Page C.4–73, *Increasing the distance between slices/slabs*

Slabs and slab groups

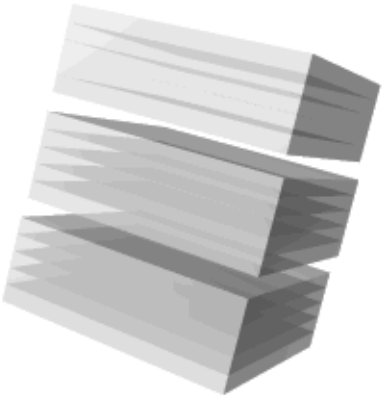
For 3D scans, phase-encoding is applied *to* the spins in the slice-selection direction. This allows you to measure entire volume ranges. In graphic slice positioning, these volume ranges are defined as 3D slabs.

Slabs are made up of contiguous slices (that is, slices without any overlap or distance between them). The thickness of a slab is the product of the effective slice thickness and the number of slices.



Slab groups

Similar to slices, 3D slabs are combined into slab groups.



A slab group consists of several parallel 3D slabs that have the same thickness and distance between them.

The slab distance is a percentage of the slab thickness:

- ❏ > 0%
  There is a distance between the slabs of a group.
- ❏ 0%
  The slabs of the group are contiguous (without any distance between them)
- ❏ < 0%
  The slabs of the group overlap.

Similar to a slice group, a slab group may only be positioned as a unit.

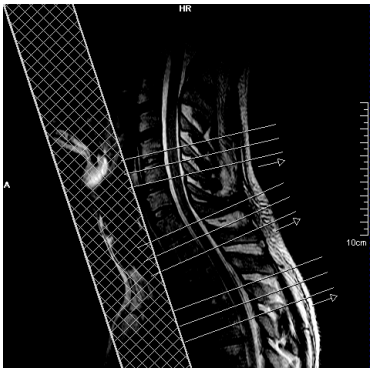
→ Page C.4–73, *Increasing the distance between slices/slabs*

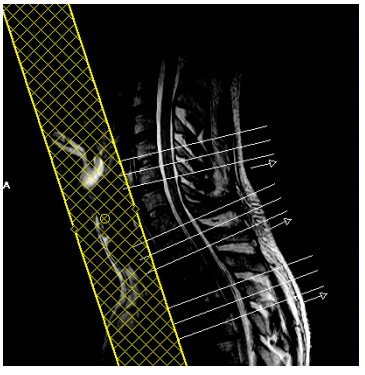
Saturation regions

A saturation region (sat) is an area in which the MR signal is suppressed by an RF saturation pulse.

Regular saturation regions

You are able to freely-define the position, orientation, and slice thickness for standard saturation regions. Several saturation regions can be planned in a single protocol. Their orientation, position, and thickness is freely-selectable. Regular saturation regions are not associated with a slice or slab group.

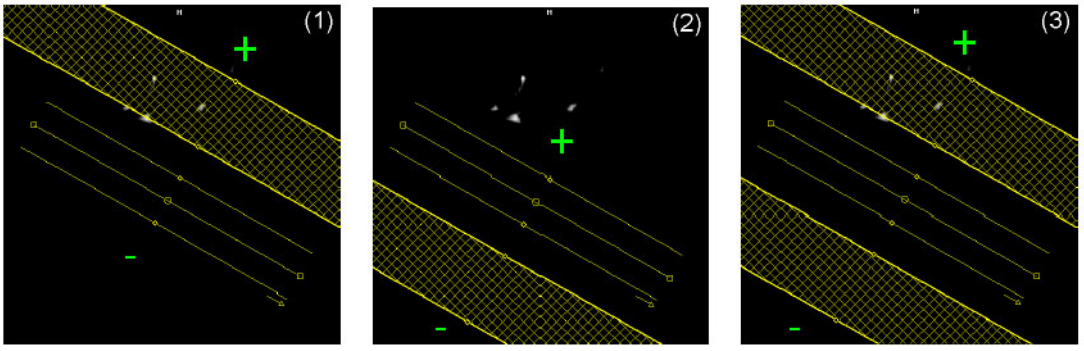




Parallel saturation regions

Parallel saturation regions may be positioned in pairs or individually (positive or negative sat). They are associated with and parallel to a slice or slab group. The distance from the saturation region to the outermost slices is specified via a protocol parameter.
→ Page H.1–19

If you translate, rotate, or change the particular slice or slab group, the two saturation regions are adjusted accordingly.



The names of the parallel saturation regions are derived from the preferred direction (orientation) of the slices/slab groups and may be selected accordingly in the **Geometry** parameter card.
→ Page C.5–31, *Geometry-Saturation parameter card*

Orientation of the slice group	Negative parallel sat	Positive parallel sat
Sagittal preferred	Parallel R (right)	Parallel L (left)
Coronal preferred	Parallel A (anterior)	Parallel P (posterior)
Transverse preferred	Parallel F (feet)	Parallel H (head)

Tracking saturation regions

You are able to plan tracking sat regions only for certain protocols. These protocols use sequences for sequential multi-slice scans and scan one slice group or slab group only.

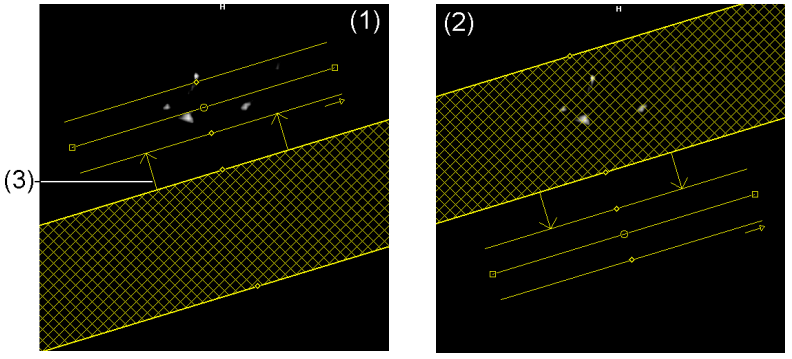
A tracking sat region is associated with and parallel to the slices of a slice or slab group. It may be positioned on either side of the slice or slab group.

The tracking sat region passes through the slice/slab group in either the ascending or descending direction. To avoid shifting the slice into a region that is already saturated, the sequential direction is always away from the sat band. For example, for transverse slices with the sat band above the slice, the excitation order (series) must be descending. Remember that DICOM defines 'ascending' as moving from foot to head. The name of the sat depends on the preferred direction of the slice/3D slab group. Suitable sats may be selected from the list on the **Geometry** parameter card.
→ Page C.5–31, *Geometry-Saturation parameter card*

Orientation of the slice group	Order of RF excitation	Sat name
Sagittal preferred	Ascending	Tracking R -> L
Sagittal preferred	Descending	Tracking L -> R
Coronal preferred	Ascending	Tracking A -> P
Coronal preferred	Descending	Tracking P -> A
Transverse preferred	Ascending	Tracking Sat F -> H
Transverse preferred	Descending	Tracking H -> F

During scanning, the saturation region tracks the most recently scanned slice. The distance between the sat and this particular slice is the same as at the beginning of the scan (distance to the first slice of the slice or slab group).

With transverse images, an ascending saturation region is located below and a descending saturation region is located above the slice group.



(1) Tracking Sat F -> H
(2) Tracking H -> F
(3) Normal vector

➪ The thickness and distance of a tracking saturation region may be set on the **Geometry** parameter card only.
→ Page C.5–31, *Geometry-Saturation parameter card*

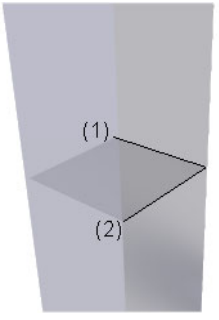
Navigator objects

Navigator objects are used in special navigator sequences, e.g., to record the movement of the diaphragm and uptake of contrast media, and to trigger the signal that starts the scan.

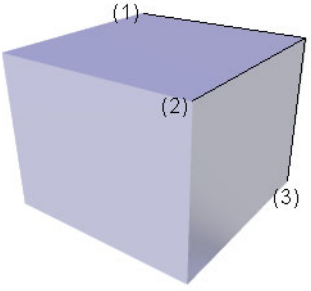
There are two types of navigator objects:

- ❏ **Navigator cuboid**
  finite cuboid volume
- ❏ **Navigator pen**
  unlimited long "pen"

Parameters of navigator objects



Navigator pen



Navigator cuboid

(1) Basic vector 1 (normal direction)
(2) Basic vector 2 (phase-encoding direction)
(3) Extent in the readout direction (navigator direction)

The base area of navigator objects is defined by the extent in the direction of base vector 1 and base vector 2.

Unlike navigator cuboids, navigator pens have an infinite extent in the navigator direction.

A two-dimensional excitation profile may be defined within the base area. This excitation profile is defined by the sequence. Depending on the application, it may have a rectangular, trapezoidal, or elliptical contour.

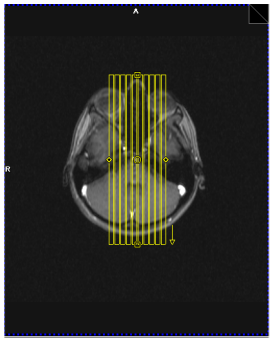
Navigator objects may be freely-positioned and oriented. It is not possible to add new navigator objects with *the mouse*. They may be added only on the **Geometry**/**Navigator** parameter card.

Display of graphic objects in the reference images

As soon as you have scanned or loaded reference images, the graphic display shows the intersection or projection of your planned slices or slabs together with the reference images.

The display used for these objects shows you their position and orientation with respect to the reference images.

Intersecting or projection areas



If a graphic object intersects the reference image at an angle ≥30°, the lines or areas of this intersection are displayed.

Example:
Sagittal slices in a transverse image



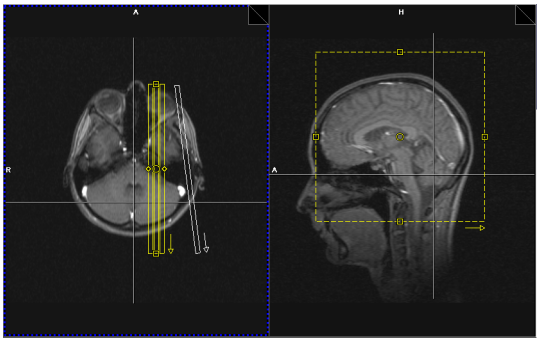
When graphic objects intersect the reference images at a shallow angle (≤30°), they are projected onto the reference image. In this case, a projection area is displayed instead of intersecting lines.

In a graphic object located parallel to the reference image, the projection area corresponds exactly to the dimensions of the field of view (FoV).

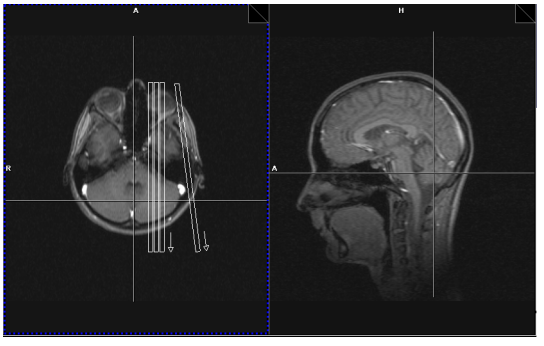
Example:
Sagittal slices in a sagittal image

➪ Upon request, Siemens Service will modify the default for the limit angle (30°). For CSI slices, the default for the limit angle is 45°.

If several graphic objects intersect the image at a shallow angle and one of these objects is selected, only the projection area of the selected object is displayed.

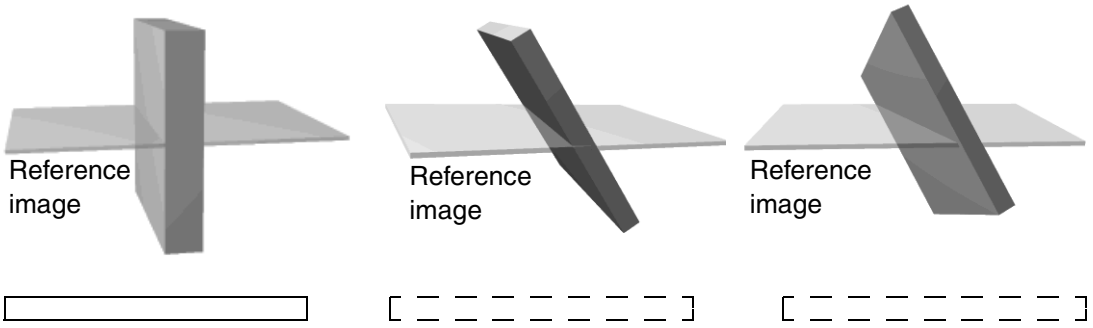


The projection area will not be displayed, if several graphic objects intersect the image at a shallow angle and none of the objects is selected.



Angle of intersection

The display of intersection and projection lines in reference images shows you whether a graphic object is located in perpendicular, single-oblique, or double-oblique orientation to the reference image.



Perpendicular intersection | Single-oblique intersection | Double-oblique intersection

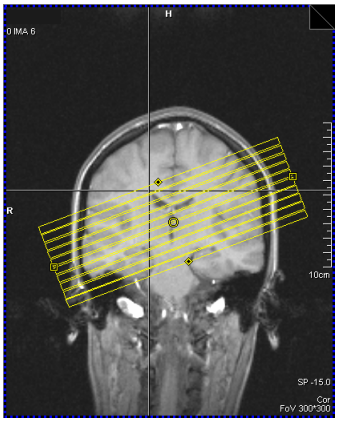
NOTE

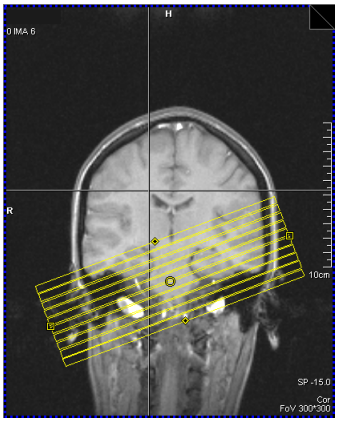
Intersections shown as a continuous or dashed line provide information only about the **position of the intersection with respect to the reference image**.

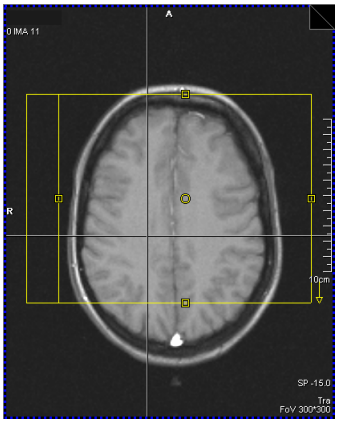
The display does **not provide information regarding the position** of the planned slice or slab **to standard anatomical views**, since oblique or double-oblique intersections may be used as reference images as well.

Single-oblique intersection

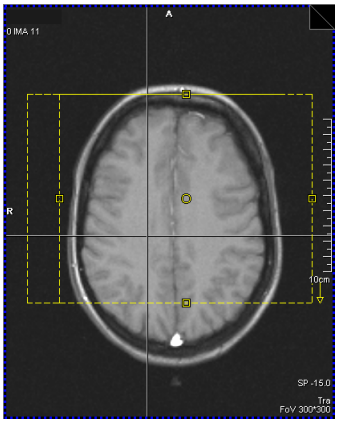
With single oblique intersections, one side of the field of view (FOV) is located in parallel with the intersecting line. The projection area shows a double border for this purpose. An arrow indicates the phase-encoding direction of the currently projected intersection area.







Single-oblique slice group intersecting the reference image

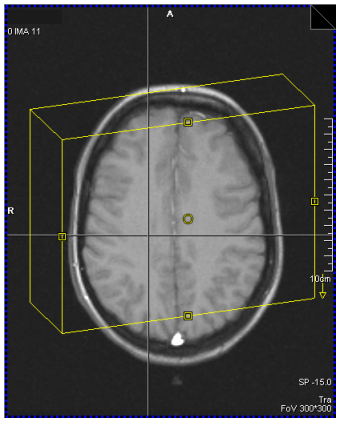


Single-oblique slice group that does not intersect the reference

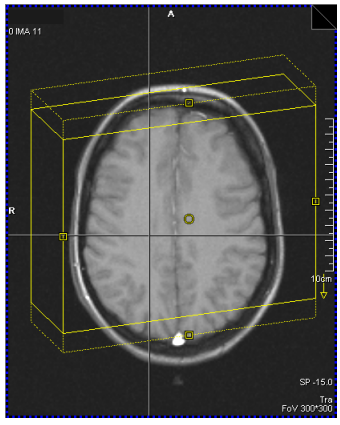
Double-oblique intersections

With double oblique intersections, neither of the two sides of the field of view (FOV) of the slice group is parallel with the common line of intersection with the reference image. Accordingly, two side areas are displayed on the projection area, providing a spatial impression. The arrows indicate the phase-encoding direction.

Slice group without phase oversampling



Slice group with phase oversampling



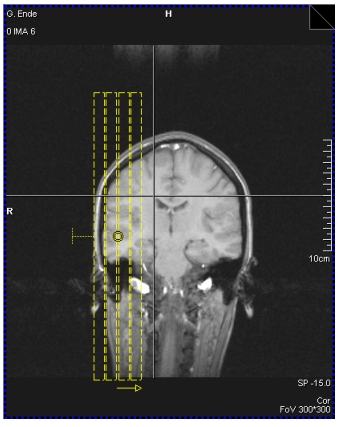
Partial views with oblique intersections

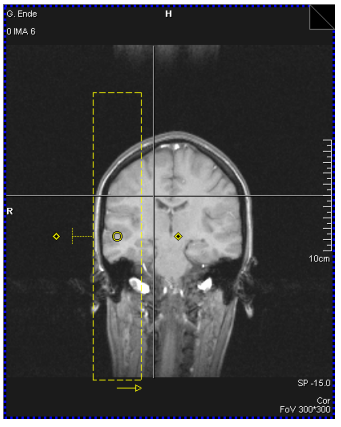
With oblique intersections, not all intersections of a slice or slab group will be intersecting the reference image. Some slices may be completely in front of or behind the reference image. As a result, they are not drawn as a line of intersection.

The bar in the reference image shows you the number of slices planned that do not intersect the reference image.

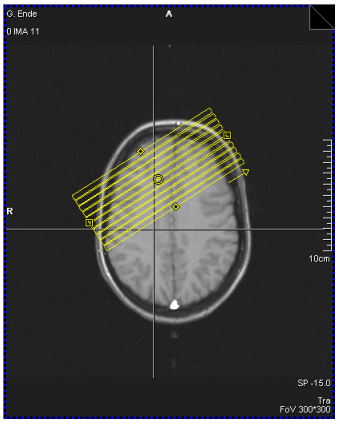


Oblique slice group in the coronal reference image

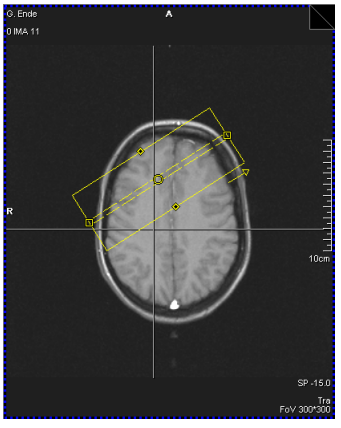




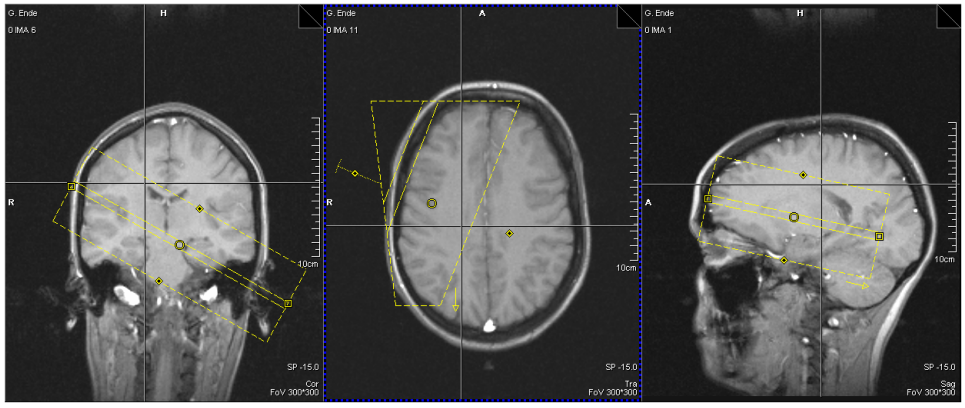
Oblique slice group in the transverse reference image



Box mode



Package mode



Partial view of an oblique slice group in the transverse reference image

If you have magnified a reference image and shifted the image content in the image segment, you may not be able to see the planned graphic object in the reference image.

✧ Reduce the reference image to its original size again.

Or

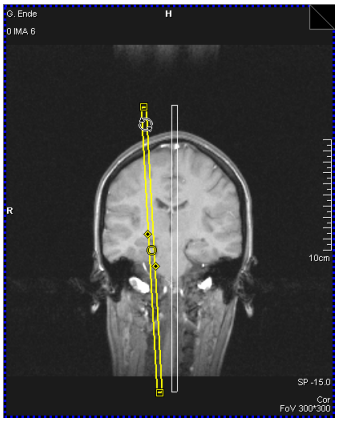
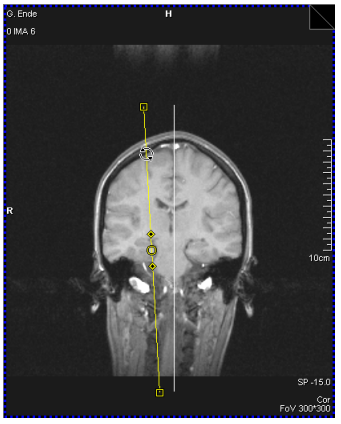
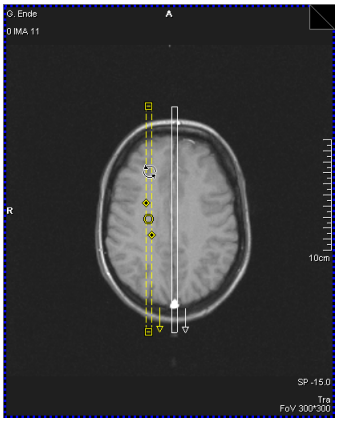
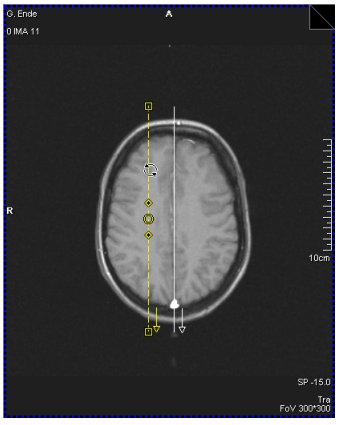
✧ Select the invisible slice/slab group on the **Routine/ Geometry** parameter card.

✧ Select **Fit to Image** or **Perpendicular** from the **Protocol** menu or the context menu to move the center of the slice group to the plane of the reference image.

➪ This function allows you to change the position of the slice/ slab group.

Display in line or box mode

The intersection of a slice through a reference image can be displayed either as a line (line mode) or as a rectangle (box mode).

	Box mode	Line mode
Oblique and perpendicular intersection in the coronal reference image		
Oblique and perpendicular intersection in the transverse reference image		

The box mode shows the actual intersection surface and therefore the anatomical region covered by the slice.

In line mode you are able to see the center line of an intersection area.




✧ Click the appropriate button on the tool bar.

Or

✧ Select **View > Display > Line mode ON /Off** from the menu.

Line mode is activated.

✧ Return to the menu **View > Graphics > Line mode ON/OFF** again.

The Box mode is activated.

Display in package mode

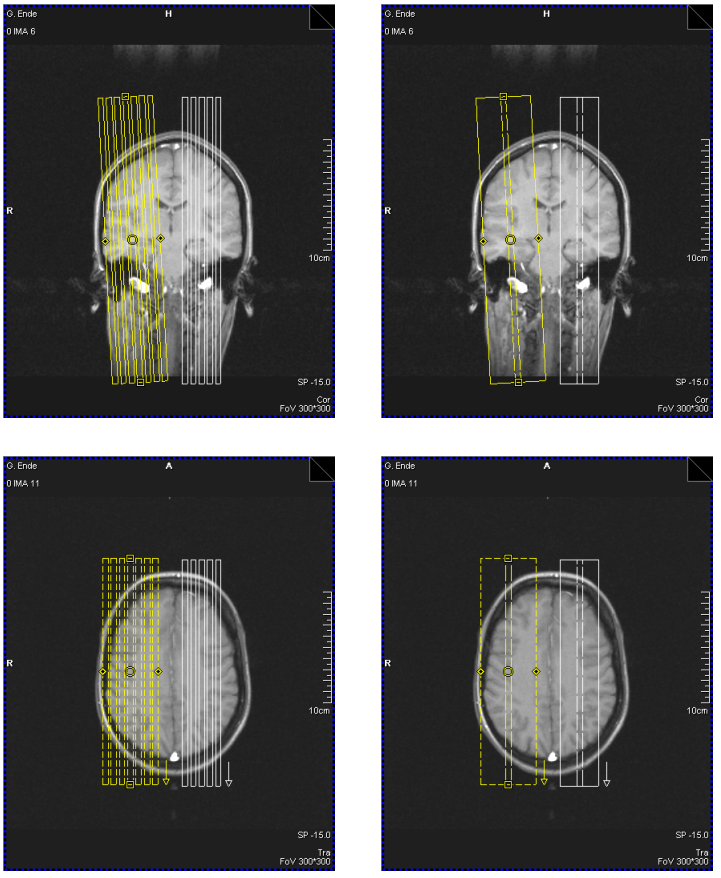
In package mode you are able to hide the individual lines of intersection of the slice/slab groups. Only the outline of the intersection area of the entire group and its thickness are visible.

Select package mode if your slice group contains a large number of individual slices to make your display clearer.



✧ Select **View > Display > Package mode ON/OFF** or click on-screen.

Package mode is activated. The dashed center lines show the thickness of the individual slices or individual 3D slab.



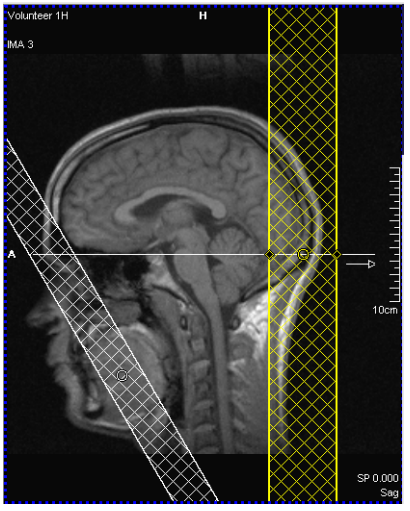
Box mode Package mode

➪ Slice or slab groups are automatically displayed in package mode if the elements of the group overlap or are very close together (depending on the zoom setting (factor) of the reference image).

Display of Saturation Regions

Saturation regions that intersect the reference image are displayed as cross-hatched bars.

Saturation regions that are perpendicular to the reference image have a continuous border. Oblique saturation regions have a dashed line border.



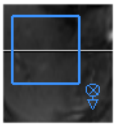
Oblique and perpendicular saturation region in the sagittal reference image

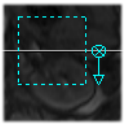
As you select a saturation region, the bar is highlighted. The center (pivot) and the handles are displayed.

A saturation region running parallel to the reference image completely covers the reference image with its cross-hatched shading if the region includes the image plane of the reference image.

➪ It is not possible to project saturation regions onto reference images.

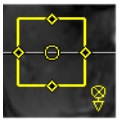
Display of Navigator Objects





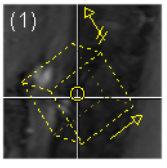
Non-selected navigator objects are displayed in turquoise in the reference images.

Non-selected navigator pens are displayed in blue.

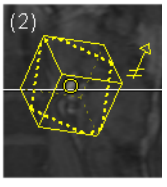


As soon as you select the navigator cuboid or navigator pen, it is displayed in yellow and the handles appear.

The navigator objects are always shown with projection lines. This gives you a spatial impression of the position and extent of the navigator object.



❏ If the navigator does *not* have a common intersection with the reference image, the projection lines will be shown as dashed lines.



❏ If the navigator *does* have a common intersection with the reference image, the projection lines will be shown as continuous lines. The intersection area, in this case, is shown with dashed lines.

The arrow next to the navigator object shows the direction of base vector 2 and the navigation direction.

The arrow may be displayed in four different ways to distinguish between four different situations.



(1) The arrow points in the direction of the base vector 2 (phase-encoding direction). The navigator orientation passes into *the* image plane.



(2) The arrow points in the direction of the base vector 2 (phase-encoding direction). The navigator orientation runs *out* of the image plane.



(3) The arrow with two lines points in the navigator direction. The direction of base vector 2 is *not* displayed, since the angle between the reference image and the direction of the base vector is between 45° and 90°.



(4) Two arrows are visible. The arrow points in the direction of the base vector 2 (phase-encoding direction). The arrow with two lines points in the navigator direction.

Graphic slice positioning (GSP)

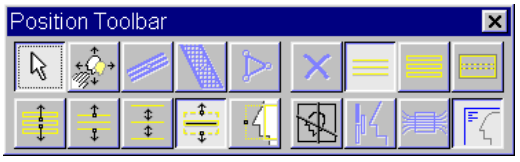
You can translate or rotate the graphic objects in the reference images (slices, slabs, saturation regions, navigators). You can also delete this object, add new objects, or change the parameters of the objects.

To this end, you are using the **Position Toolbar** or the mouse.

You may also use the parameter cards to manipulate graphic objects as described. In this case, you adjust the parameters numerically and work mainly in the **Geometry** parameter card.
→ Page C.5–26, *Geometry Common parameter card (2D)*

Displaying orientation aids

The buttons on the **Position Toolbar** and the menu commands display additional orientation aids in the reference images. This facilitates processing graphic objects.





Changing phase-oversampling
→ Page C.4–32, *Displaying the phase oversampling*



Reference lines on/off
→ Page C.4–34, *Reference image position lines*



Coil positions on/off
→ Page C.4–34, *Coil elements*



Adjust volume on/off
→ Page C.4–37, *Adjustment volume*



Image text on/off
→ Page C.3–31, *Showing/hiding image text*



Show/hide slice oversampling
→ Page C.4–33, *Display of slice oversampling*

Show/hide projection (menu)
→ Page C.4–36, *Projection display*

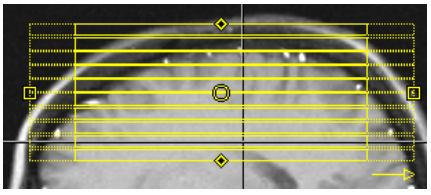
Displaying the phase oversampling



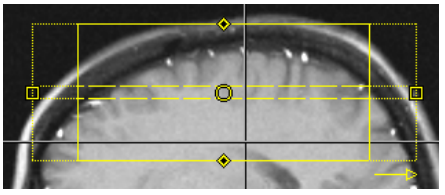
Phase oversampling is recommended to prevent aliasing artifacts. The field of view (FoV) is symmetrically expanded in the phase-encoding direction on both sides of the initial FoV.

This addition to the FoV is not visible in the final images The phase-oversampled area is displayed as dashed lines in the reference image.

Box mode



Package mode



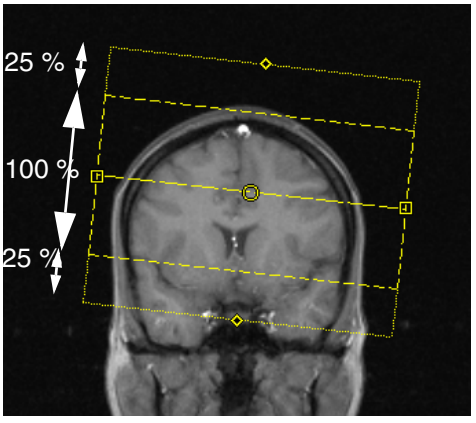
The percentage given refers to the field of view (FOV) in the phase-encoding direction. For example, 30% phase oversampling would increase the field of view (FOV) by 15% on both sides. The scan time is also prolonged by 30%.

You can change phase oversampling.
→ Page C.4–80, *Changing phase oversampling via the mouse*

Display of slice oversampling

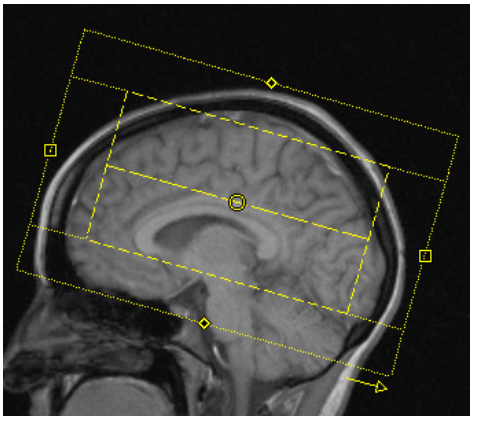
Slice oversampling is suitable for 3D scans only. Slice oversampling defines an area of a slice protruding on both sides (of a 3D slab). This additional area is excited during the scan.

Box mode: Slice oversampling



Phase-encoding direction

Box mode: Slice and phase oversam-



Phase-encoding direction

To improve the display of objects, deactivate the display of slice oversampling.



✧ Click this button.

Or

✧ Select **View > Graphics > Hide Slice Oversampling** via the main menu.

Reference image position lines

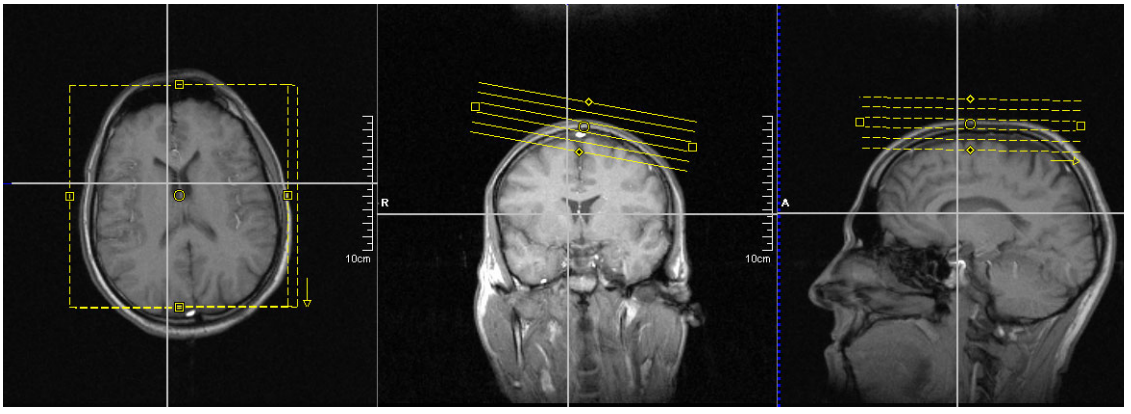
Reference image position lines make it easier for you to orient the images in space and position slices correctly.



✧ Click the button to activate display of the position lines.

Or

✧ Select **View > Reference Lines ON**.



Coil elements

The currently connected coils (and individual coil elements) may be displayed for support during the examination. This facilitates your selecting the correct coil elements for the region of the body to be examined.

Only coils with a fixed table position may be displayed. It is not possible to show coil elements with flexible positions (flex coils).

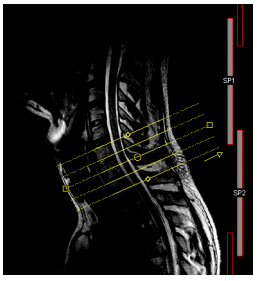
✧ Open the protocol with the coils you want to have displayed.



✧ Click this button.

Or

✧ Select **View > Coil Positions On**.



➪ Coil elements are *only* displayed on mostly sagittal and coronal reference images.

The coil elements are displayed symbolically as thin bars. The length of the bar corresponds to the length (sensitive region) of the coil element.

Coil elements selected for the examination are identified by *solid* white bars. Coil elements not selected for the examination are displayed as bars with a white border.

➪ You can select and deselect coil elements both via the mouse in the image segment and on the **System** parameter card.
→ Page C.5–40, *Selecting coils*

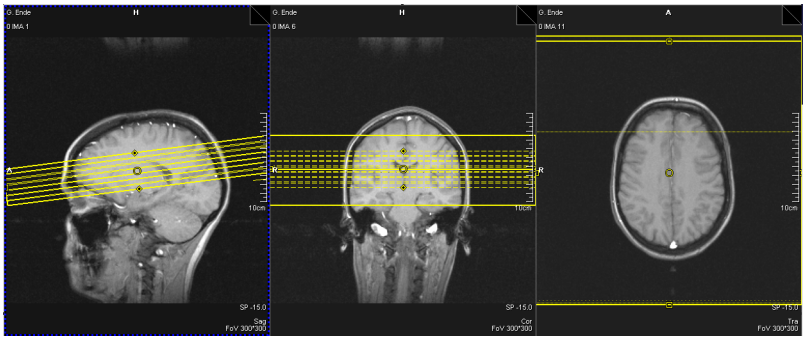
Projection display

Normally, the projection display of slices/slabs is active only when the angle between the graphic object and the reference image is less than 30°.

However, you may change this threshold.

✧ Select **View > Graphics > Projection On** from the main menu.

The menu item is now shown with a check mark.



The objects are displayed as a projection on the reference images.

Adjustment volume

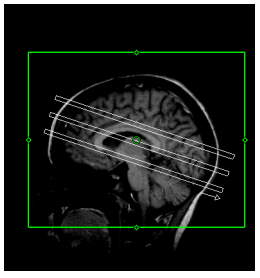
In some cases it may be useful to display the adjustment volume in the reference images.



✧ Click the button to activate display of the adjustment volume.

Or

✧ Select **Adjust Volume On**.



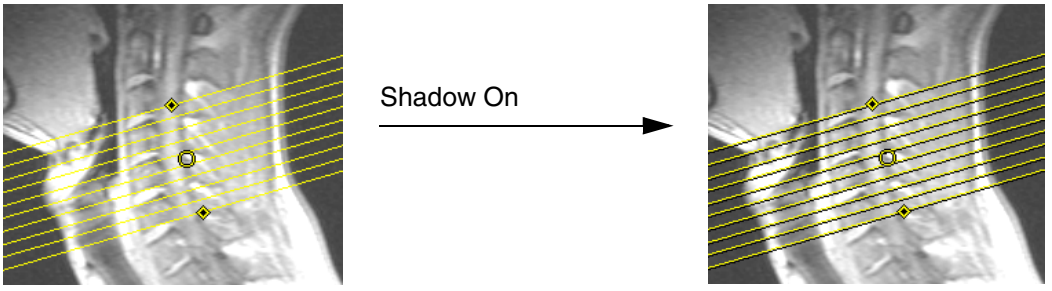
The adjustment volume is marked green in the reference images and allows for editing.
→ Page B.2–9, *Editing the adjustment volume graphically*

Shadow lines

To improve the display of graphic objects (GSP Graphic Slice Positioning objects) in light images, you can include shadow lines in the intersection and projection areas.

✧ Select **View > Graphics > Shadow On**.

The menu item is marked with a check mark.



➪ Whenever you save or copy reference images containing graphic objects to a film sheet, the shadow lines will be included and displayed. It does not matter whether the **Shadow On** option is activated or deactivated.

Selecting graphic objects

Before you can edit a graphic object in one of the reference images you must first select it.

You can select objects in one of two ways:

❏ Explicit selection

❏ Implicit selection (by direct manipulation)

Explicit selection

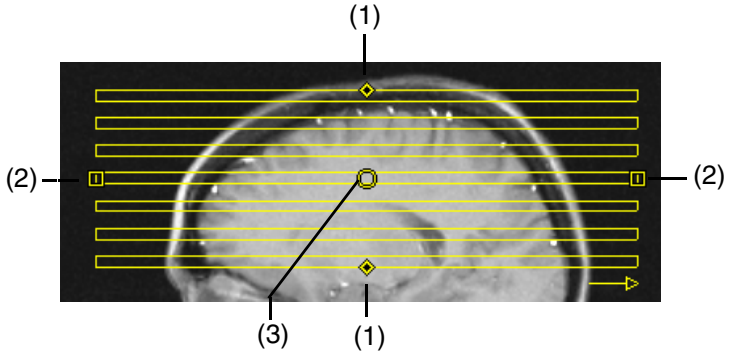


✧ Select an object by clicking an intersection or projection line.

Or

✧ Select an object from the **Slice Group, Slab Group,** or **Navigator** list on the **Geometry** or **Routine** parameter card.

The graphic object is now highlighted. The handles are displayed.



(1) Extend handle
(e.g. for changing the slice thickness;
not with projection areas)
(2) FoV handle or phase oversampling handle
(extend scan range)
(3) Pivot handle
(move)

You can now explicitly deselect objects again:

✧ Select **Edit > Deselect All** from the main menu.

Or

✧ Select another graphic object.

Implicit selection



✧ Move the mouse cursor over one of the graphic objects.

The mouse cursor changes shape allowing you to move or rotate the graphic object with the mouse.

➪ You may now directly move or rotate the graphic via the mouse without having to click it.

As soon as you edit a graphic object, it is implicitly selected. Its settings are displayed on the parameter cards.

Moving objects

Slice groups, slab groups, saturation regions, or navigator objects planned in a protocol usually need to be moved to fit the anatomy of the patient.

There are various ways of moving objects:

- ❏ Panning with the mouse
- ❏ Moving via menu commands
- ❏ Positioning to the millimeter on the Geometry parameter card

→ Page C.5–81, *Entering the slice position with millimeter precision*

Panning with the mouse



✧ Select a graphic object.

The pivot handle is displayed in the center of the object displayed.

✧ Place the mouse cursor on the pivot handle, hold the left mouse button down, and move the object to the required position.

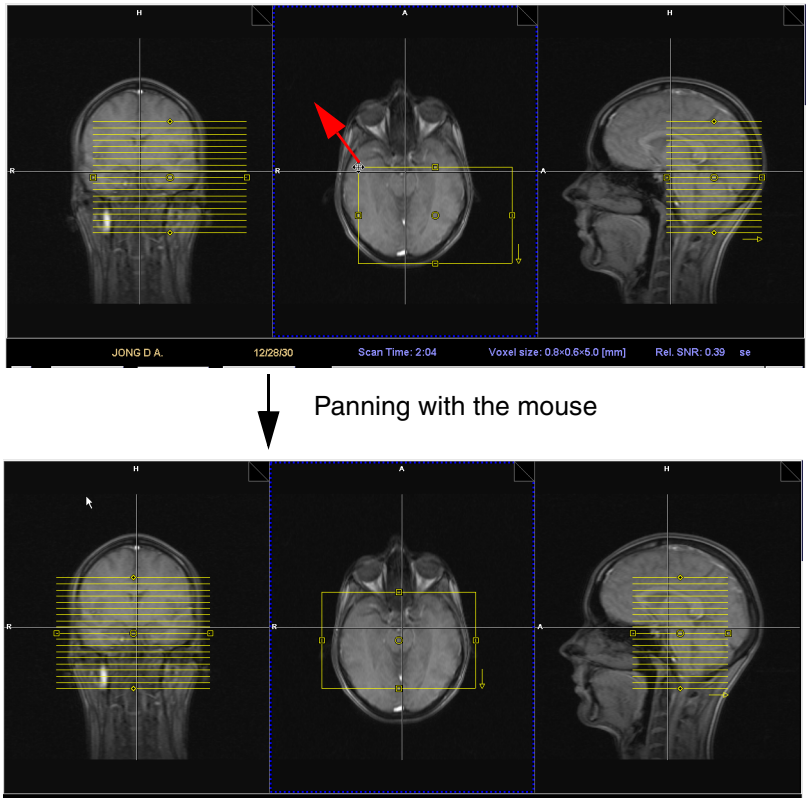
If the pivot handle of an object is no longer visible in the reference images:

✧ Press the **Shift** key on your keyboard and hold the key down.

✧ Place the mouse pointer on the intersection or position line of a graphic object.

✧ Move the object while holding the left mouse button down.

➪ To move graphic objects in the projection display, click on the contour line and move the object while keeping the mouse button pressed.



The display of the repositioned object is updated on all reference images.

➪ Parallel tracking saturation regions may *be* moved only together with slices or slabs assigned to them.

Moving a slice group by half a slice distance

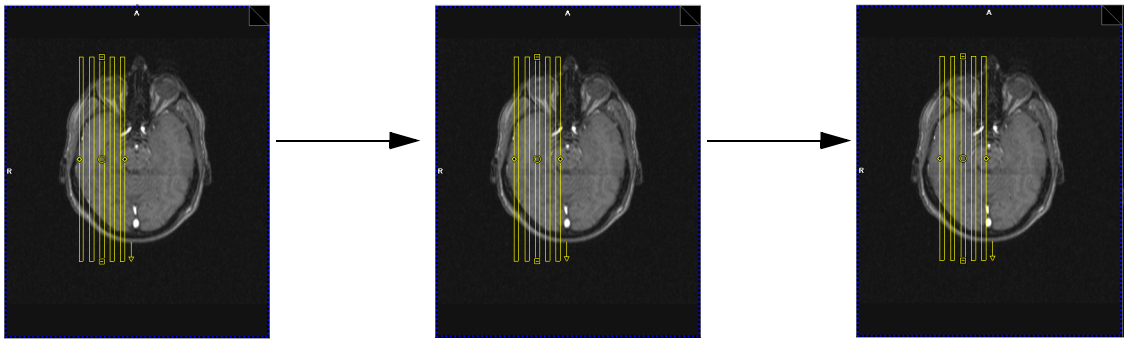
You can move slice groups by half the distance between slices in the positive or negative slice-selection direction.

This greatly simplifies the task of positioning a second scan to fill the gaps between the slices of the first scan. This is particularly helpful when the number of slices in one scan does not suffice to provide for a contiguous anatomic coverage of a specific volume (e.g., some breath-hold exams).

✧ Select **Protocol > Gap Filling +** or **Protocol > Gap Filling –**

Or

✧ Press the short cut **Ctrl + 6** (Gap filling +) or **Strg + 5** (Gap filling -).



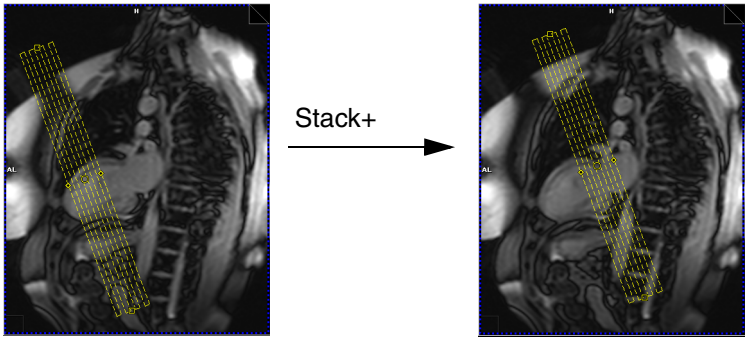
Moving the slice group as a whole

Unlike with the **Gap filling** function, you are able to move a slice group by the thickness of the entire group in one step. This function is especially suitable for multiple breathhold measurements.

✧ Select **Protocol > Stack +** or **Protocol > Stack –**.

Or

✧ Press the short cut **Ctrl + 4** (Stack +) or **Ctrl + 3** (Stack -).



➪ If the slice group contains only one slice, it will be moved across its slice thickness in or against the slice-selection direction.

Moving centers in the reference plane

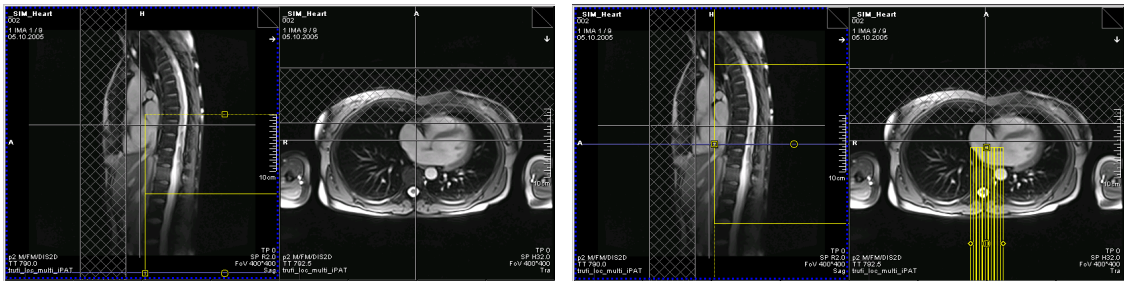
You are able to move the centers of slice/slab groups and navigator objects precisely into the reference plane (image plane of the reference image).

✧ Select the reference image to be used as the reference plane.

✧ Select **Protocol > Shift to Image**.
- Or -
Select **Shift to Image Plane** in the context menu of the reference image.

The centers of the graphic objects (except sat. regions) are moved in the reference plane and, if necessary, in the visible area of the image.

➪ You are *not* able to use this function for slice groups and slab groups located in parallel to the reference image.



Reference images before and after selecting the **Shift to image plane** with respect to the sagittal reference plane

Rotating objects

You can rotate graphic objects to fit them to an anatomical structure.

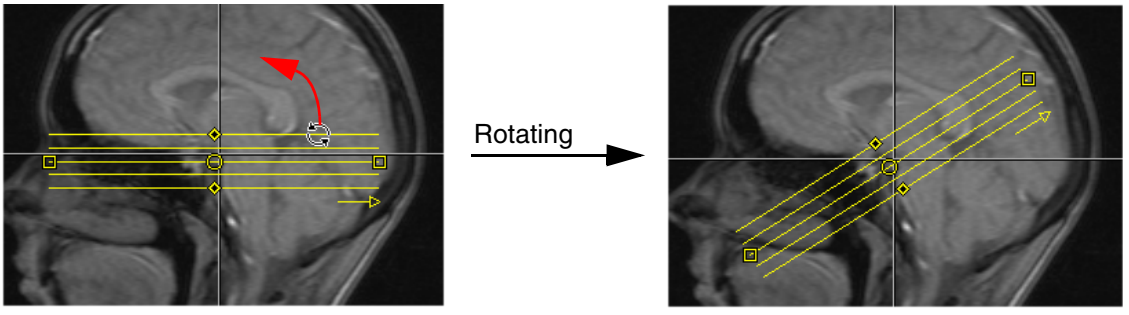
There are various ways of rotating objects:
- ❏ Rotating using the mouse
- ❏ Rotating using menu commands
- ❏ Setting the orientation at a precise angle on the Geometry parameter card
  → Page C.5–79, *Setting the slice orientation at a precise angle*

Rotating using the mouse

✧ Select the graphic object explicitly.

✧ Click on the selected object with the left mouse button and rotate it about its center.

The rotational axis is now perpendicular to the reference image.



Or

✧ Move the pointer over the object.



The pointer changes shape when placed over the delimitation lines.

✧ Hold the left mouse button down and rotate the object about its center.

Rotating a navigator cuboid

✧ Place the mouse cursor on one of the contour lines of the navigator cuboid. Do not use the handle.



The mouse pointer changes shape.

✧ Press the left mouse button and drag it in the desired direction of rotation.

Rotating a regular saturation region and navigator pen

Regular saturation regions and navigator pens are rotated similar to slice and slab groups.

The center (pivot) always appears at the position clicked with the mouse. This point is the center of rotation.

You can move the center of rotation by clicking another position in the Sat region.

➪ Parallel and tracking saturation regions may be rotated *only* with the slices or slabs assigned to them.

Combining rotate and shift functions

You may rotate and move objects in one step.

- ✧ Hold the **Shift** key down to move the objects.
- ✧ Release the **Shift** key to rotate it.
- ✧ Press the **Shift** key again to shift the object again.

Rotating Objects in the Plane

You can rotate slice and 3D block groups in the plane. These objects must be projection areas (flat section with reference image).

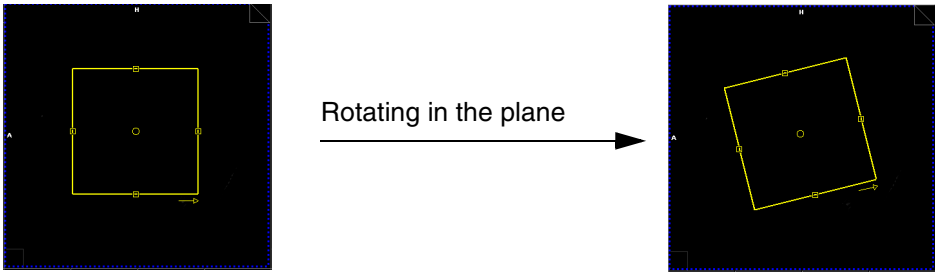


- ✧ Press the **Ctrl** key and move the cursor over the object.

The pointer changes shape when placed over the delimitation lines.

- ✧ Hold the left mouse button down, press the **Ctrl** key, and rotate the object about its center.

The rotational axis runs through the center of the graphic object and is perpendicular to the object.



Rotation of oblique intersections

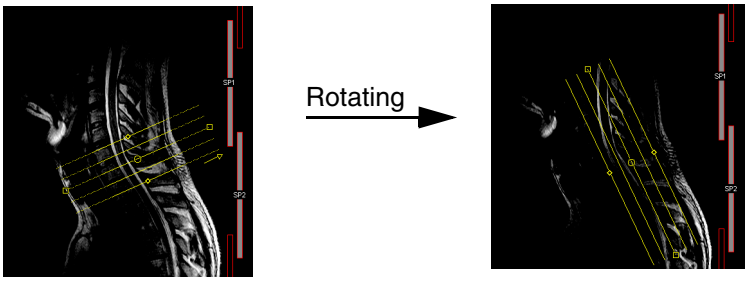
When you rotate slices whose center is not in the plane of rotation (oblique and double-oblique sections), the center of the slice moves as you rotate the slice.

Swapping the phase direction

The main orientation of the object may change as it is rotated.

If the object has a rectangular FoV, you may find that the intersection lines in the result display are noticeably longer or shorter than originally, because of the realigned phase-encoding direction of the FoV.

Example:
A mostly transverse slice group becomes a mostly coronal slice group.

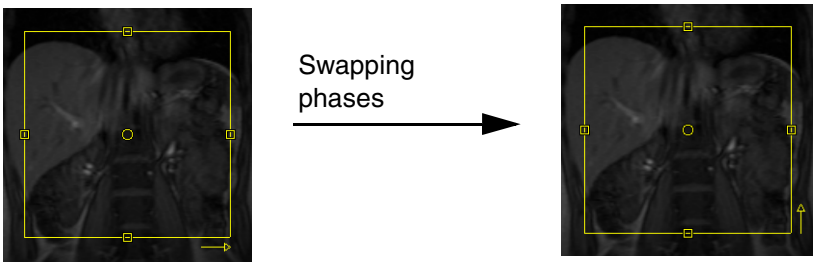


After the rotation, check the phase-encoding direction and swap it if necessary.

✧ Explicitly select a slice/slab group or a navigator object.

✧ Select **Protocol > Swap Phase** from the main menu or **Swap Phase** from the context menu.

The field of view of the selected object is rotated about 90°. The phase-encoding and readout directions are swapped.



➪ It is *not possible* to apply this function to saturation regions.

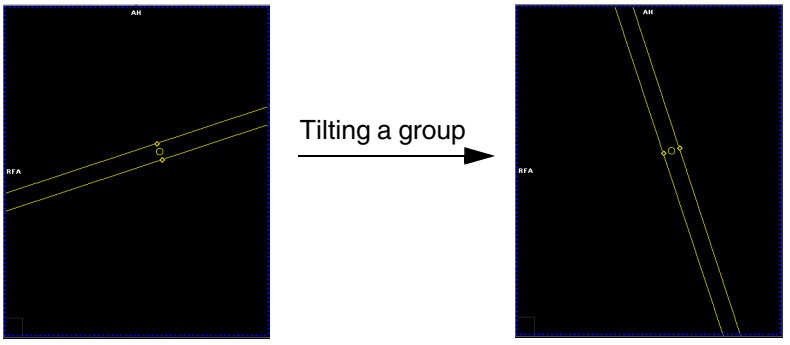
Tilt a slice group by 90°

When you tilt a slice group by 90°, the intersection line appears rotated counterclockwise by 90°.

✧ Select the saturation group.

✧ Select **Protocol > Turn Group**.

The center of the slice group remains unchanged.



Aligning graphic objects perpendicularly

You may change oblique intersections of the graphic object to align them perpendicularly to the reference image.

✧ Select a reference image.

✧ Select a graphic object that obliquely intersects the reference image.

✧ Select **Protocol > Perpendicular**.

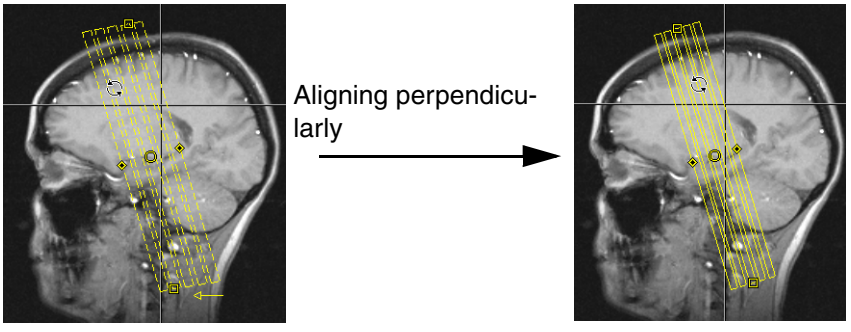
Or

✧ Select **Perpendicular** from the context menu.

Or

✧ Press the short cut **Ctrl + 1**.

The selected slice or slab group will be aligned perpendicularly to the reference image. Its center will then be moved into the reference image plane.



- If a navigator intersects the reference image at an angle ≥45°, the navigator direction will be aligned perpendicular to the image.
- If a navigator intersects the reference image at an angle ≤45°, the navigator direction will be aligned in the image plane.
- If no object is selected, **Perpendicular** will be applied to all oblique slice and slab groups. Oblique saturation regions or navigators are *not* aligned.

Making slices mutually orthogonal

You can align a slice group orthogonally to another planned slice group.

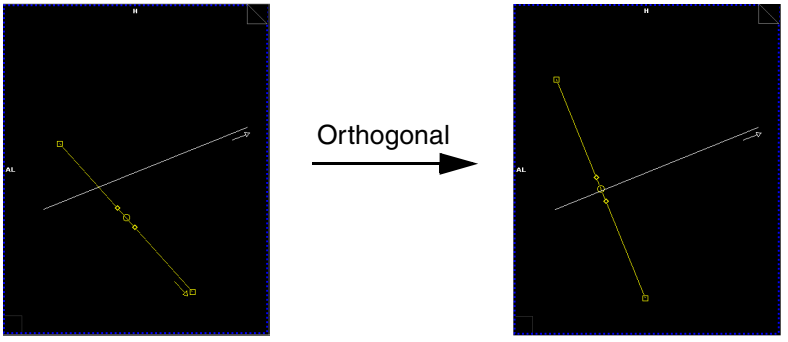
✧ Select the slice group you want to align.

✧ Select **Protocol > Orthogonal**.

Or

✧ Press the short cut **Ctrl + 2**.

The center of the aligned slice will be in the plane of the reference slice.



➪ The **Perpendicular** function is used to align objects to the reference image plane. The **Orthogonal** function is used to align the selected slice to the reference slice.

Grouping graphic objects

You can group graphic objects in order to rotate or move them together.

The following objects can be included in groups:
- ❏ Slice groups
- ❏ Slab groups
- ❏ Saturation

- ✧ To group the objects, select **Tools > Coupled Graphics On**.
- ✧ To eliminate a group, deselect **Tools > Coupled Graphics On**.

Adding slice and slab groups

If the slice or slab groups shown in the reference images are not suitable to your diagnostic question, other groups may be added.

The number of slice or slab groups that you can add depends on the protocol selected.
→ Page C.5–73, *Soft limits and extended limits*

The order in which new slices or slabs are drawn and edited does not affect the order of scanning or numbering reconstructed images.
→ Page C.6–67, *Numbering of reconstructed images*

There are various ways of adding new slice groups:

- ❏ Freely-selectable slice positioning via the mouse
- ❏ Positioning new slices in the center of the image segment
- ❏ Positioning a new slices using an orientation line
- ❏ Adding new slices in 3-point mode

Rules for adding

No slice group was selected before adding:

- ❏ The new slice group contains *one* slice.
- ❏ The center of this slice is in the reference image plane.

Another slice group was selected before adding:

- ❏ The new slice group inherits the properties of the selected group (number of slices, distance factor, swap, phase oversampling and slice oversampling).
- ❏ The new slice group has the same orientation as the reference slice group and is moved parallel to it in the slice selection direction (normal direction) about the thickness of the entire group (Stack+).

Freely positioning slice groups

Use the mouse to move new slice or slab groups to any position in the reference image.

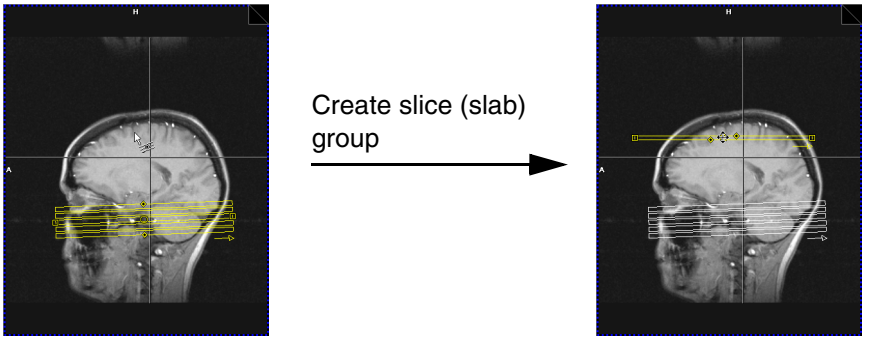


✧ Click the **Create Slice(Slab) Group** button.

The mouse pointer changes shape.

✧ Click the position in the reference image where you want to insert a new slice group.

The center of the slice or slab group will appear in the image plane of the reference image.



Hold the mouse button down and rotate/move the new slice or slab group with the mouse. direction. Click the image again to create the next slice/3D slab group.

Positioning graphic objects in the center of the image segment

You are able to insert new objects in the center of the selected image segment. The center of the newly created slice or slab group is positioned precisely in the image plane of the reference image.

✧ Select **Protocol > Add Slice(Slab) Group**.

If there already is a slice group with the same orientation of the new slice group in the center of the image segment, the new slice group will be shifted parallel so that it is equidistant and contiguous to the existing slice group.

Positioning slice groups using the orientation line

You may also position a new slice/slab group along an orientation line. To this end, draw the line into the reference image using the mouse. The slice/slab group is then positioned along the line and is located perpendicularly to the reference image. The center of the new slice/slab group is in the plane of the reference image and positioned exactly between the start and end point of the orientation line.

✧ Place the mouse cursor on the starting point of the line.

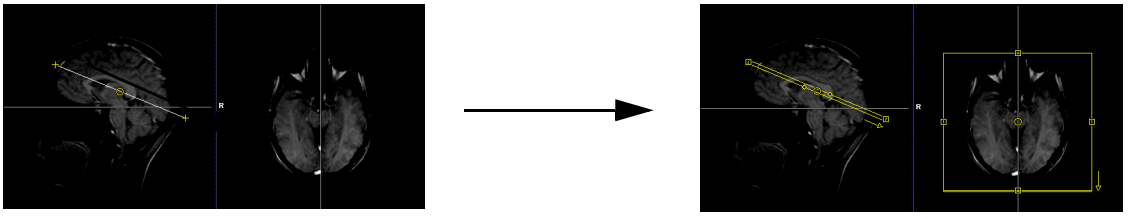
✧ Keep the left mouse button pressed and drag the mouse cursor to the point where you want to position the new slice/slab group.

The orientation line is drawn in.

You can change the direction and length of the line, as long as you hold the mouse button down.

✧ Release the mouse button.

The new slice/slab group is displayed.



Exiting "Create Slice(Slab) Group" mode

✧ Select another mode from the tool bar.

Or

✧ Select another mode from the main menu, for example, **Image Tools > Modify Graphics**.

Or

✧ Select another mode from the context menu, for example, **Zoom/Pan On**.

➪ If you reach the maximum number of slice(slab) groups, the **Create Slice(Slab) Group** mode will be automatically ended.

Adding a slice/slab group in 3 point mode

This mode allows you to use random reference images to determine 3 points that define a plane. You are now adding a new slice or slab group. The center slice or slab of this group passes exactly through this plane. You can also align an existing slice or slab group to this plane.

When selecting the 3 points, you may scroll through the reference images or load new ones.

➪ Ensure that no graphic objects are selected. Select **Edit > Deselect All**.

➪ If you want to change an existing slice or slab group, verify that it is not selected.



✧ Click the **Create Slice (Slab) Group (3 point)** button to activate this mode.

The mouse pointer changes shape.



✧ Click three positions successively in one or more reference images.

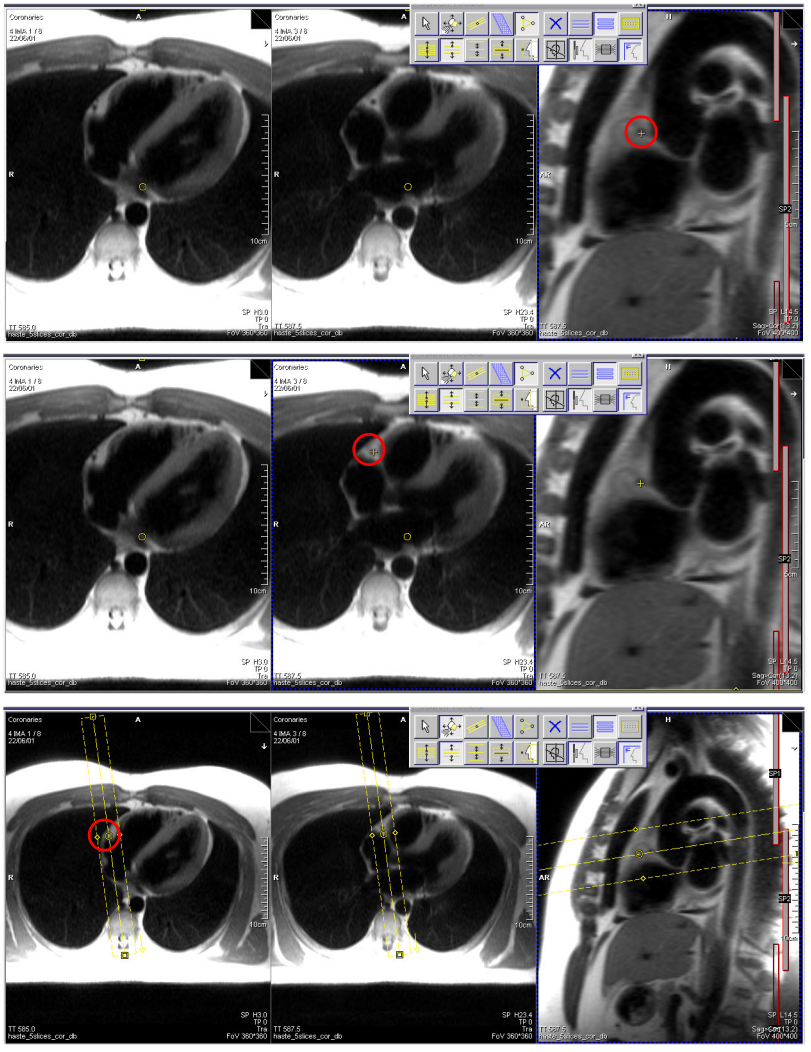
After each mouse click, a mark appears at the position you selected.

As long as the third mark is not positioned, you may move the corner marks by dragging them with the mouse. Click on them again for removal.

(1)

(2)

(3)



Example: Localization of the right coronary artery

(1) Define the first point
(2) Define the second point
(3) Define the thrid point,
the new slab is displayed

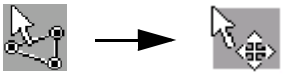
After you have defined the position of the third point, the new slice or slab group will appear in the reference images and/or the previously selected slice will be aligned with the three points.

➪ If you have created a new group, it will be selected automatically. You can align it by specifying 3 points again.

You can add additional groups in three-point mode as follows.

✧ Deselect the last group you created.

✧ Click three positions successively in one or more reference images.



✧ Finally, press the **Esc** key to deactivate **Create Slice (Slab) Group (3 points)** mode.

Or

✧ Select **Modify Graphics** mode on the tool bar.

Or

✧ Switch to another mode (using the tool bar, main menu, or context menu).

Adding saturation regions

You may add further regular saturation regions in a protocol just like slice or slab groups.

Parallel and tracking saturation regions may only be added on the **Geometry** parameter card. They *cannot* be added via graphic slice positioning.
→ Page C.5–31, *Geometry-Saturation parameter card*

Creating a regular saturation region in the center of the image segment

✧ Select a reference image.

✧ Select **Protocol > Add Sat** to position a regular saturation region in the center of the image.

The new saturation region appears perpendicular to the reference image with a vertical intersection area.

Freely positioning a regular saturation region

✧ Select a reference image.

✧ Select **Image Tools > Create Sat**.

Or



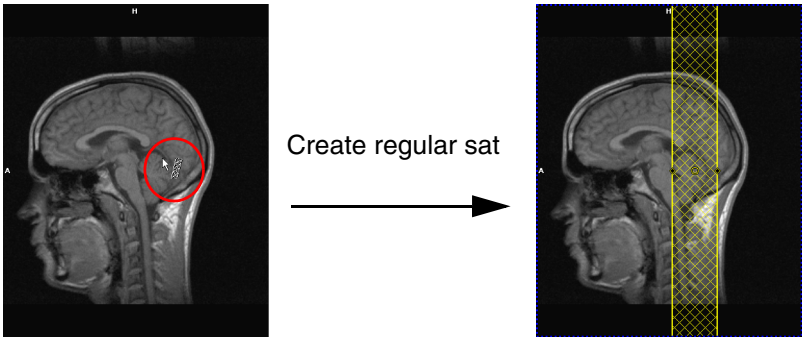
✧ Click the **Create Regular Sat** on the toolbar to activate this mode.



The mouse pointer changes shape.

✧ Click the position in the reference image where you want to insert the new saturation region.

The saturation region is located perpendicularly to the reference image. The intersection runs in vertical direction. The thickness of the region is calculated using standard protocol parameters.



You can change the course of the new saturation region by dragging the mouse while holding the mouse button down.

Regular sat using an orientation line

You may also place a regular saturation region along an orientation line. The saturation region is then located perpendicularly to the reference image.

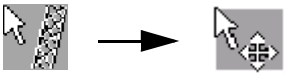
✧ Position the mouse pointer at the starting point of the orientation line.

✧ Hold the left mouse button down and drag the mouse cursor in the direction you want to place the saturation region.

✧ Release the mouse button.

The new saturation region is displayed.

Exiting the mode



You can exit **Create Sat** mode if you do not want to draw additional saturation regions.

✧ Press the **Esc** key.

The mouse is now in the **Modify Graphics** mode.

Or

✧ Switch to another mode (using the toolbar or context menu).

➪ When you have reached the maximum number of sat regions the **Create Sat** mode is automatically ended. The color of the icon changes from yellow to blue.

Changing graphic slice parameters

Use the mouse to change the following slice and slab groups parameter settings as well as edit standard saturation regions:



❑ **Slice thickness** or slab thickness



❑ **Number** of slices or slabs per group



❑ **Distance** between slices or slabs within a group



❑ **Slice oversampling**

As an alternative, you may change these parameters numerically on the **Geometry** card.
→ Page C.5–26, *Geometry Common parameter card (2D)*

➪ Ensure that the mouse is in the **Modify Graphics** mode. If necessary, press the **Esc** key to ensure that you are in that mode.

Increasing the thickness of the slices/slabs





◇

✧ Click the **Extent Thickness** button.

Or

✧ Select **Image Tools > Extent Mode > Extent Thickness**.

The mouse pointer changes shape.

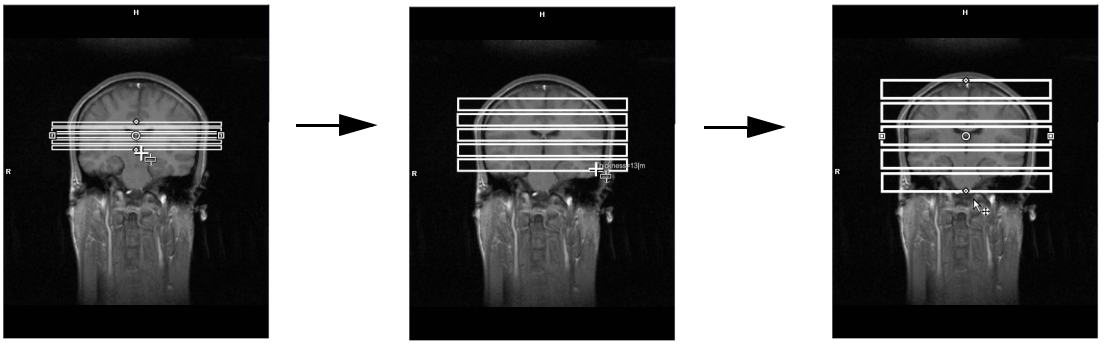
✧ Click the **Extent** handle, hold the mouse button down, and drag the handle in the required direction.

To increase the thickness of the slices/slabs, drag the extent handle away from the group.

To reduce the thickness of the slices/slabs, drag the extent handle toward the group.

The thickness will be displayed in millimeters on the reference image as long as you keep the mouse button pressed.

✧ Release the mouse button once the slices/slabs have the required thickness.



Changing the slice thickness also changes the distance between slices since the distance factor remains constant.

Increasing the number of slices/slabs



✧ Click the **Extent Slices (3D-group)** to switch to this mode.

Or

✧ Select **Image Tools > Extent Mode > Extent Slices (Slabs)**.



The mouse pointer changes shape near the pivot.

◇

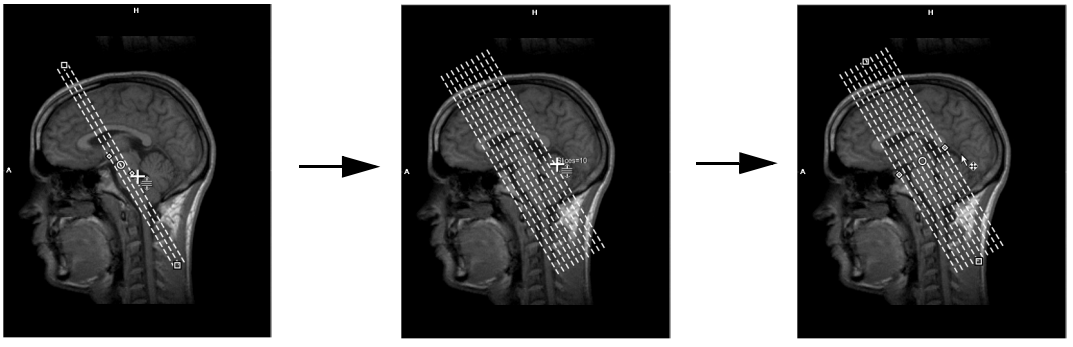
✧ Click the **Extent** handle, hold the mouse button down, and drag the handle in the required direction.

Drag the extent handle (mark) away from the group to increase the number of slices.

To decrease the number of slices drag the extent handle (mark) toward the group.

The number of slices will be displayed on the reference image as long as you hold the mouse button down.

✧ Release the mouse button as soon as you have generated the required number of slices or slabs.



The maximum possible number of slices is limited by other protocol parameters (for example, by TR). It is not possible to exceed this limit by dragging the extent handles. The highlighted display indicates when you have reached the limit (thick line).

Increasing the distance between slices/slabs





◇

✧ Click the **Extend Distance** button to switch to the appropriate mode.

Or

✧ Select **Image Tools > Extent Mode > Extent Distance**.

The mouse pointer changes shape.

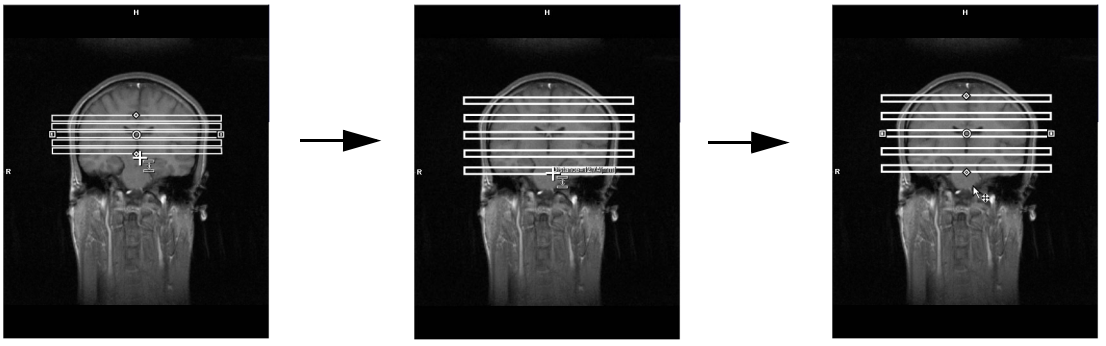
✧ Click the **Extent** handle, hold the mouse button down, and drag the handle in the required Keep the mouse button pressed.

Drag the extent handle away from the group to increase the distance between slices.

To reduce the distance between slices, drag the extent handle toward the group.

The distance between slices will be displayed on the reference image as long as you keep the mouse button pressed.

✧ Release the mouse button, when the slices/slabs show the required distance.



Changing slice oversampling

In 3D scans, you can change the slice oversampling.



✧ Click the **Extent Slice Oversampling** button.

Or

✧ Select **Image Tools > Extent Mode > Extent Slice Oversampling On**.



The mouse pointer changes shape.

◇

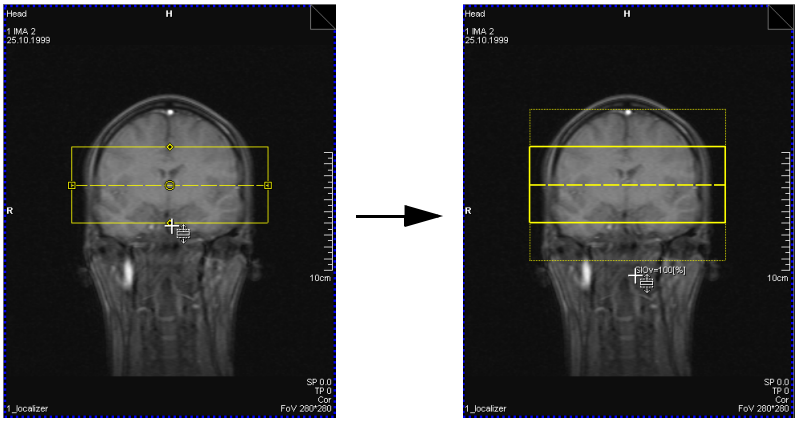
✧ Click the **Extent** handle, hold the mouse button down, and drag the handle in the required Keep the mouse button pressed.

To increase the slice oversampling, drag the extent handle away from the group.

To reduce the slice oversampling, drag the extent handle toward the group.

Slice oversampling is displayed on the reference image as long as you hold the mouse button down.

✧ Release the mouse button as soon as slice oversampling reaches the desired size.



➪ To change the thickness of the slices/slabs, press the **Alt** key to switch to the **Extend Thickness mode**. Release the **Alt** key to return to the **Extend Slice Oversampling** mode again.

Switching between the slice number/ slice distance/ and slice thickness mode

Changing the slice distance is just as easy as changing the slice thickness. Press the **Alt** key to switch to **Extent Number** mode, In this mode you can change the number of planned slices before returning to the **Extend Thickness** or **Extend Distance** mode (release the **Alt** key again).

Changing the field of view (FoV) via the mouse

✧ Select the slice or slab group whose field of view (FoV) you want to change.

✧ Drag the FoV handle in the phase-encoding direction.



If you drag the FoV handle in the readout direction, the icon (shown) will appear next to the mouse pointer.



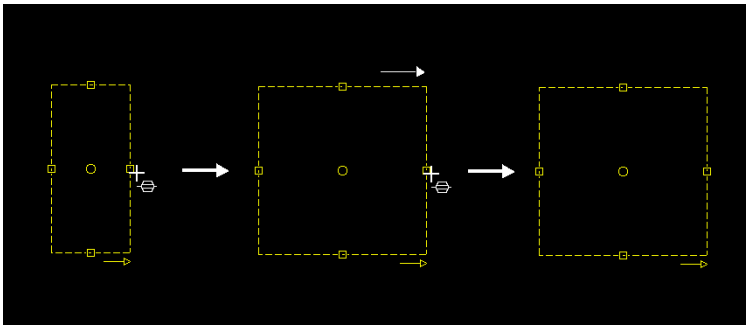
If you drag the FoV handle in the phase-encoding direction, the icon (shown) will appear next to the mouse pointer.

The dimensions of the current field of view (FoV) are displayed on the reference image as long as you hold the mouse button pressed.

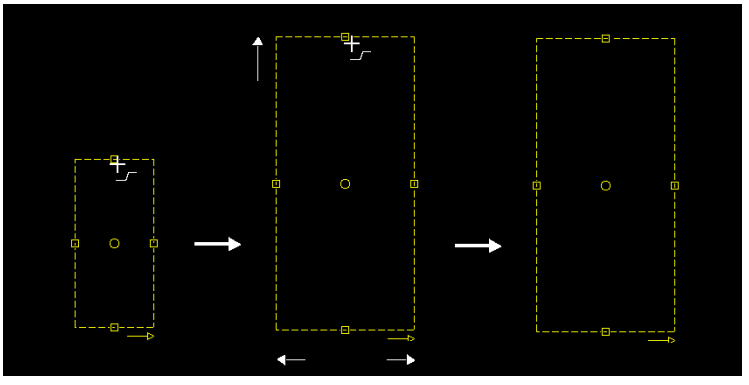
✧ Release the mouse button as soon as the field of view (FoV) has the required size.

Notes on enlarging the field of view (FOV)

❏ You may continue enlarging the field of view in the phase-encoding direction until you obtain a square field of view.

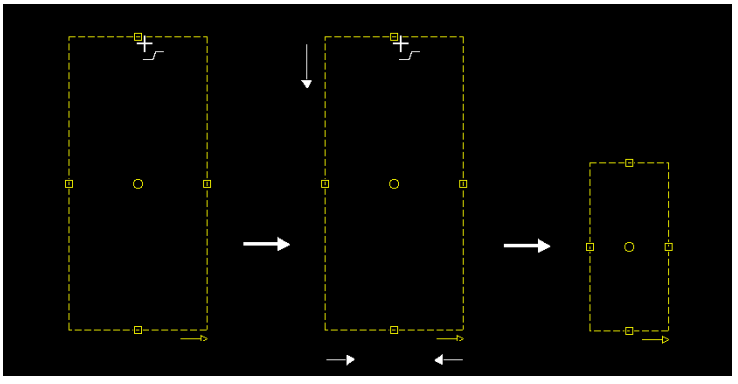


❏ You can only enlarge the field of view in the readout direction as a function of the FOV aspect ratio. The ratio between the length in the phase-encoding and readout direction remains constant. If you enlarge the field of view in the readout direction, the field of view will be enlarged as well in the phase-encoding direction.

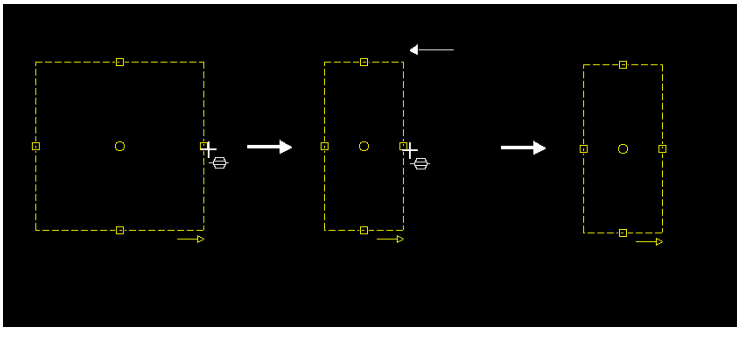


Notes on reducing the field of view (FoV)

❏ You may only reduce the field of view in the readout direction in conjunction with the phase-encoding direction. The FoV is also proportionally reduced in the phase-encoding direction to maintain a constant FoV aspect ratio.



❏ The FoV in the phase-encoding direction can be reduced independently of the readout direction.



Changing phase oversampling via the mouse



✧ Click this button to begin processing the phase oversampling.

Or

✧ Select **Image Tools > Extent Mode > Extent Phase Oversampling On**.

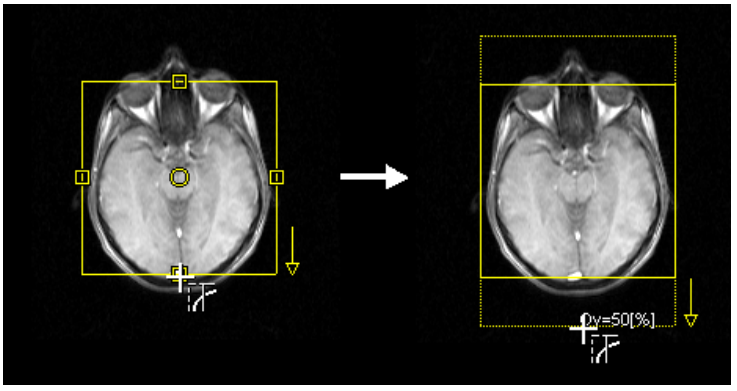
✧ Select the slice or slab group whose phase oversampling factor you want to change.



✧ Drag the FoV handle in the phase-encoding direction.

The current value of the phase oversampling factor will be displayed on the reference image as long as you keep the mouse button pressed.

✧ Release the mouse button as soon as the phase oversampling has been enlarged/reduced as required.



➪ Changes in phase oversampling have a symmetric effect on the slice or slab group. The size of the field of view (FoV) and its center remains constant.

Changing regular sat regions

You are able to move saturation regions, or change their orientation or thickness with the mouse. The procedure is the same as for processing slice/slab groups.

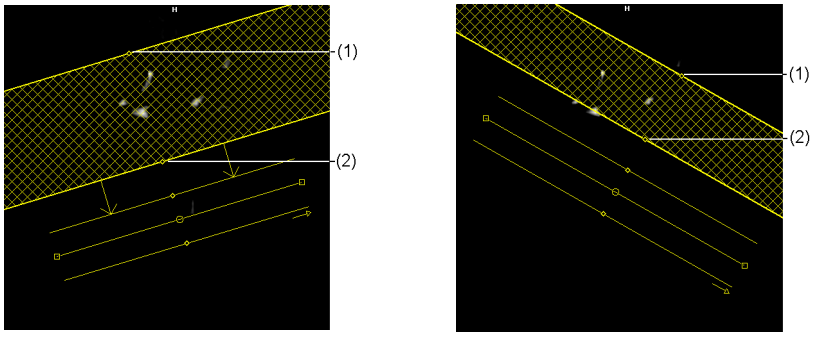
All other saturation region parameters can only be edited numerically on the **Geometry** parameter card.
→ Page C.5–31, *Geometry-Saturation parameter card*

Changing parallel and tracking saturation regions

You can change the position and orientation of a parallel/tracking saturation region via the slice/slab group associated with this slice group. The distance to the slice/slab group remains constant.
→ Page C.4–42, *Moving objects*

Depending on the extend handle clicked, you can change the thickness of the sat region or the distance to the slice/slab group.

⇨ With parallel saturation regions, modifying the slice thickness and the distance to the slice/slab group always affects both saturation regions symmetrically.



(1) Handle for changing the sat thickness
(2) Handle for changing the distance to the slice/slab group

To change the thickness of the parallel saturation region:

✧ Click the **Extent** handle facing away from the slice/slab group, press the left mouse button, and drag it.

To change the distance of the parallel saturation region:

✧ Click the **Extent** handle facing toward the slice/slab group, press the left mouse button, and drag it.

Switching between slice thickness and position editing

You are able to quickly and easily switch to position editing by pressing the **Shift** key while changing the slice thickness of saturation regions. You can then move the selected regular saturation region before returning to **Extend Thickness** mode (by releasing the **Shift** key again).

Deleting graphic objects

You can delete or replace graphic objects that you no longer need for scanning.

Deleting selected objects

✧ First select the slice object you want to delete.

✧ Select **Edit > Delete** from the main menu or **Delete** from the context menu.

Or



✧ Click the **Delete** button or press the **Del** key.

The selected object is deleted. The next object is selected in place of the deleted object.

The slice or slab group will not be deleted if the number of slices/slabs is below the minimum number defined for the protocol. Instead, the number of slices/slabs is reduced to a minimum.

Deleting all objects

✧ Select **Delete All** from the context menu.

All slice/slab groups and saturation regions of your protocol will be deleted except for the minimum number of slice/slab groups defined in the protocol. Parallel saturation regions are retained.

Transferring the position of reference images

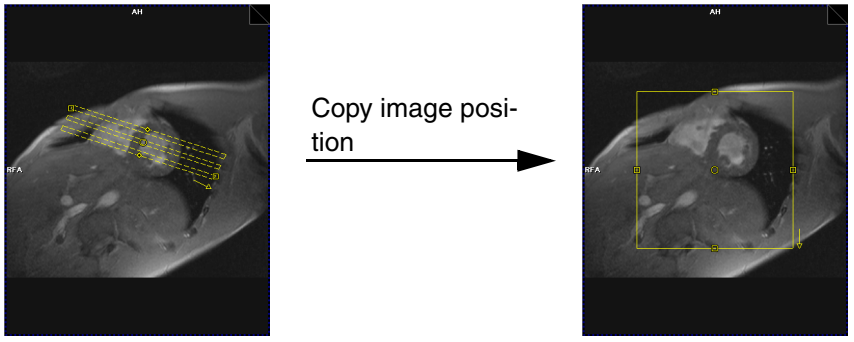
You can use the **Copy Image Position** function to temporarily store the position and orientation of a reference image and copy it to the selected slice of the open protocol.

✧ Select the reference image in one of the image segments.

✧ Select the slice.

✧ Select **Image Tools > Copy Image Position** from the main menu or **Copy Image Position** from the context menu.

The position and orientation are copied to the selected slice.



➪ If no slice (slab) group is selected, the position and orientation will be transferred to the first slice (slab) group of the protocol.

The position and orientation of the reference image is retained in temporary storage and may be copied to other selected slices as well.

✧ Select the slice.

✧ Select **Tools > Paste Image Position**.

Nearest

The **Nearest** function selects the best possible reference images for a region of interest.

As first step the center of the currently selected graphic object is automatically moved into the plane of the previously selected reference image. This shift runs perpendicular to the plane of the reference image. If the selected graphic object has already been positioned on the location of interest, this position is retained during the shift.

In addition, in the other two reference image segments, reference images are selected whose planes are closest to the position of the selected graphic object.

➪ The primary application of the **Nearest** function is spectroscopy.

Procedure:

✧ Select the required reference image in the loaded reference image series.

✧ Select the graphic object.

✧ Select **Image Tools > Copy Image Position** if you want the graphic object to have the same orientation as the reference image.
→ Page C.4–86, *Transferring the position of reference images*

✧ Select **Scroll > Nearest**.

Applying slice settings

Once you have correctly positioned the graphic objects, you may release the protocol for scanning.



✧ Click the **Apply** button in the program control.

The graphic objects in the reference images are now removed. However, the reference images are still displayed in the image segments.

When you have finished graphic slice positioning and completed the protocol, it is loaded into the scan system and run in the job list accordingly.
→ Page C.6–1, *Performing a Routine Examination*

The next, incomplete protocol of the program control will be opened automatically. You can now position the slices for this protocol and check the other parameter settings in the parameter card.
→ Page C.5–1, *Adjusting Measurement Parameters*

CHAPTER C.5

Adjusting Measurement Parameters

Siemens Service has set up a routine scan program on your system that requires minimal interactions on your part. Usually, you need to change just a few parameters prior to scanning.

The best time for you to adapt the scan parameters of your first protocol is directly after graphic slice positioning when your protocol is still open.
→ Page C.1–4, *Procedure for routine scanning*

The parameter cards of the **Exam** task card contain all measurement parameters of a protocol sorted by main topics.

During routine scan operations, it usually suffices to look at the parameters of the **Routine** parameter card to change the field of view (FoV) or other parameters that require frequent modification.

For more specialized diagnostic problems and special anatomical conditions, you can adjust additional measurement parameters in the **Contrast**, **Resolution**, and **Geometry** cards.

Depending on the sequence used for scanning, other application-specific parameter cards will be displayed.

An overview of the parameter cards and short descriptions of the parameters are provided on the following pages.

Next, the working procedure and input tools of the parameter card stack are explained. Finally, you learn how to save your parameter changes and copy them to other scan protocols.

NOTE

Detailed descriptions of the individual measurement parameters and notes on settings are provided in the reference section.
→ Part H

NOTE

The parameter cards for spectroscopy scans are described in the
MR Spectroscopy manual.

NOTE

This chapter also describes sequences and functions of optional applications packages.

Overview of parameter cards

The parameter card stack shows the measurement parameters of the protocol currently open.

The measurement parameters are organized on cards by topics. The parameter cards are arranged in a stack from left to right to provide easy access to the cards most frequently used and processed.

Different measurement parameters are displayed on the individual cards depending on the sequence associated with the current scan protocol.

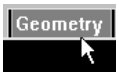
⇨ The following pages always list *all* the scan parameters that can be displayed and edited on a card for different examinations.
In some cases, parameters may be missing on the parameter cards shown, since the display depends on the sequence of the open protocol.

Some measurement parameters are available for verification and editing on several parameter cards. In other words, you will find a parameter on all cards for which it is relevant.

The detailed descriptions of scan parameters in the reference section also state the cards on which the individual parameters can be found.
→ Part H

Selecting a parameter card for editing

The **Routine** parameter card is always on top of the stack when you open a scan protocol.



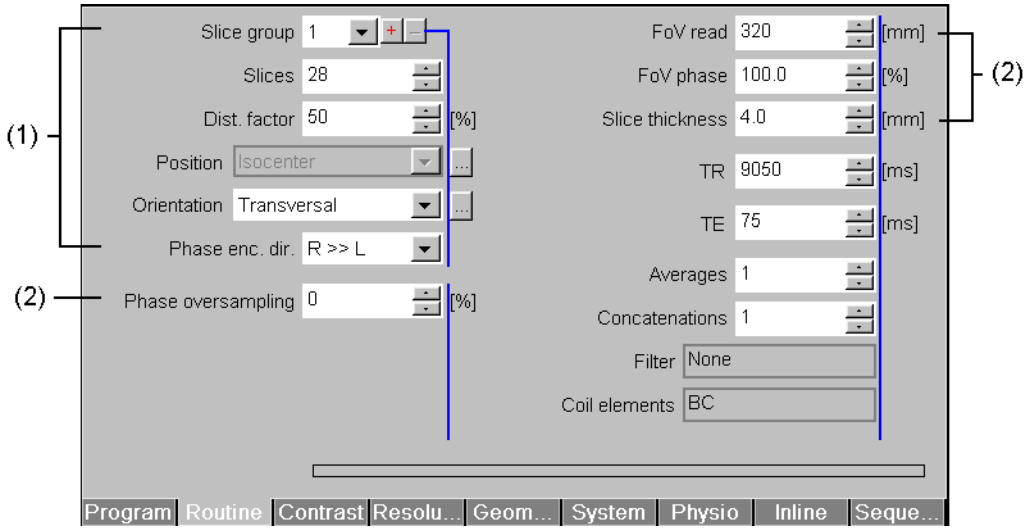
✧ Click the tab of another parameter card to place it on top.

Routine parameter card

The **Routine** parameter card includes all parameters of your scan protocols. You are able to check as well as modify them during scan preparations.

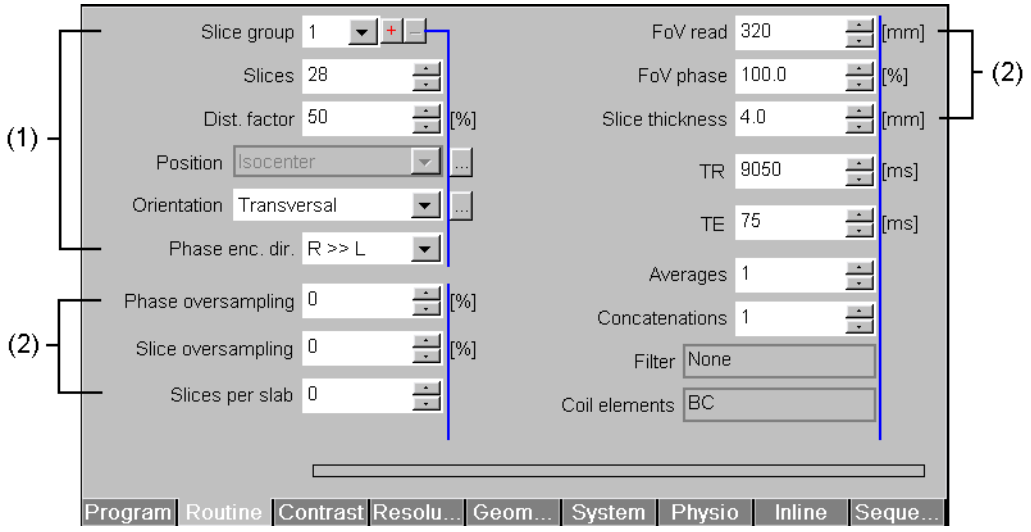
The parameters shown on the **Routine** parameter card depend on whether your protocol uses 2D or 3D scans.

Routine parameter card (2D)



(1) Parameters that may be different for each slice group
(2) Parameters that apply to all slice groups

Routine parameter card (3D)



(1) Parameters that may be different for each slab group
(2) Parameters that apply to all slices/slabs

Parameters for image resolution and contrast

- ❏ **FoV read**
  Field of view in readout direction, → Page H.1–51
- ❏ **FoV phase**
  Field of view in phase-encoding direction, → Page H.1–52
- ❏ **TR**
  Repetition time, interval between two consecutive excitations, → Page H.1–38
- ❏ **TE**
  Echo time, time between RF pulse and measured echo, → Page H.1–39
- ❏ **Averages**
  Number of scans, repetitions to improve the signal-to-noise ratio, → Page H.1–41
- ❏ **Filter**
  Display of the selected filter, → Page H.1–66

Parameters for monitoring the excitation sequence

- ❏ **Concatenations**
  Distribution of the slices to be measured across a given number of scans to avoid cross-talk, → Page H.1–34

Coils

- ❏ **Coil elements**
  Coils to be used for this protocol, → Page H.1–84

Slice parameters for 2D scans

❑ **Slice group**
Number of the slice group currently displayed,
→ Page C.5–78, *Adding or deleting graphic objects* and
→ Page H.1–3

❑ **Slices**
Number of slices in this group, → Page H.1–4

❑ **Distance factor**
Distance between the slices of the group as a percentage of the slice thickness, → Page H.1–5

❑ **Slice thickness**
Thickness of the slices (in mm), → Page H.1–6

❑ **Position**
Position of the slice group in the patient coordinate system,
→ Page C.5–79, *Adjusting the orientation and position of graphic objects* and → Page H.1–11

❑ **Orientation**
Orientation of the slice group in the patient coordinate system,
→ Page C.5–79, *Adjusting the orientation and position of graphic objects* and
→ Page H.1–8

❑ **Phase-enc. dir**
Phase-encoding direction, specified in the main orientations of the patient coordinate system, the angle of slice rotation can also be set in a lower-level dialog box,
→ Page H.1–13

❑ **Phase oversampling**
Extension of the field of view in the phase-encoding direction to avoid aliasing artifacts, → Page H.1–14

Slab parameters for 3D scans

❏ **Slab group**
Number of the slab group currently displayed,
→ Page C.5–78, *Adding or deleting graphic objects* and
→ Page H.1–3

❏ **Slabs**
Number of slabs in this slab group,
→ Page H.1–4

❏ **Distance factor**
Distance between slabs as a percentage of the slab thickness, → Page H.1–5

❏ **Slice thickness**
Thickness of the individual slices of the slabs,
→ Page H.1–6

❏ **Slices per slab**
Number of slices per slab,
→ Page H.1–7

❏ **Position**
Position of the slab group in the patient coordinate system,
→ Page C.5–79, *Adjusting the orientation and position of graphic objects* and
→ Page H.1–11

❏ **Orientation**
Orientation of the slab group in the patient coordinate system, → Page C.5–79, *Adjusting the orientation and position of graphic objects* and
→ Page H.1–8

❏ **Phase-enc. dir**
Phase-encoding direction, specified in the main orientations of the patient coordinate system; the angle of slice rotation can also be set in a lower-level dialog box,
→ Page H.1–13

❏ **Phase oversampling**
Extension of the field of view in the phase-encoding direction to avoid aliasing artifacts,
→ Page H.1–14

❏ **Slice oversampling**
Extension of the field of view in the slice selection direction to avoid aliasing artifacts,
→ Page H.1–16

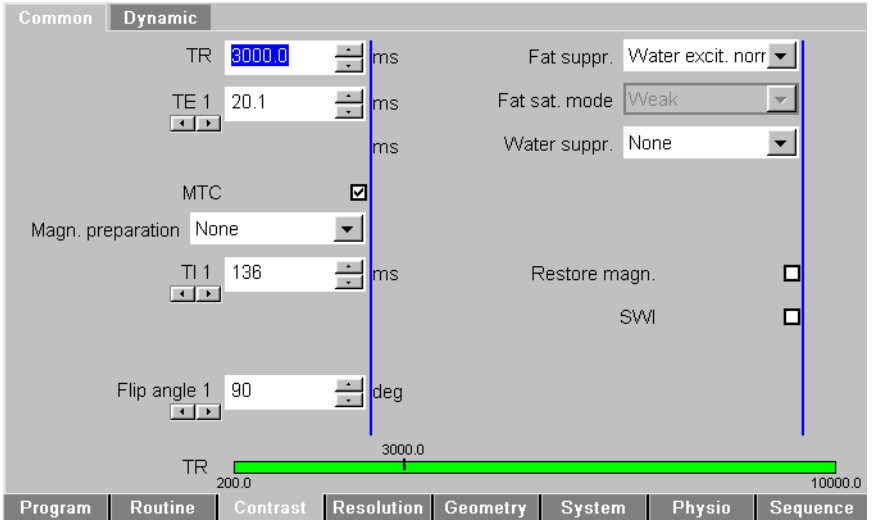
Contrast parameter card

The **Contrast** parameter card displays all the settings for changing the contrast in the images. Among other factors, image contrast is critical for correct diagnosis.

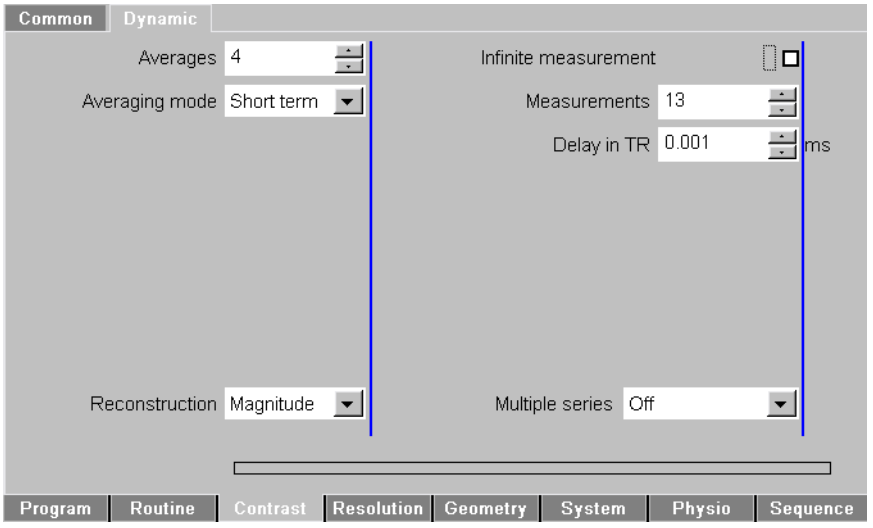
Depending on your diagnostic task, you can acquire images with different weightings by setting parameters on the **Contrast** card. Images with T1 and proton density weighting display anatomical structures especially well. T2 weighting, on the other hand, is more suitable to detect pathological changes.

Additional effects can be obtained by spin preparation. Using preceding RF pulses, contrast can be enhanced or signals can be suppressed completely.

Contrast-Common parameter card



Contrast-Dynamic parameter card



T1, T2, or proton density contrast

To determine the T1, T2, or proton density weighting for spin echo sequences, set the parameters TR (repetition time) and TE (echo time).

The values recommended for spin echo sequences are as follows:

- ❏ Short TR and short TE produces T1 contrast.
- ❏ Long TR and long TE produces T2 contrast.
- ❏ Long TR and short TE produces proton density contrast.

See Applications Manual

- ❏ **TR**
  Repetition time, interval between two consecutive excitations,
  → Page H.1–38
- ❏ **TE**
  Echo time, time between RF pulse and measured echo,
  → Page C.5–76, *Displaying and editing parameter groups* and → Page H.1–39
- ❏ **Flip angle**
  Flip angle of rotational axis of spins,
  → Page H.1–41

Settings for spin preparation

The actual scan should be preceded by an RF pulse (spin preparation) when you want to change the contrast or suppress certain signals (for example, for an inversion recovery sequence).

❏ **Magn. preparation**
Magnetization preparation for inversion recovery (IR) and saturation recovery (SR) sequences,
→ Page H.1–42

❏ **TI**
Inversion time,
→ Page H.1–40

Increasing signals

❏ **Averages**
Number of scans, repetitions to improve the signal-to-noise ratio,
→ Page H.1–41

❏ **Restore magn.**
Signal increase with T2 weighting by accelerated relaxation of the longitudinal magnetization,
→ Page H.1–47

Suppressing signals

The MR signal comprises the sum of signals from water and fat protons. This may result in chemical shift artifacts. Motion artifacts may be enhanced, and contrast may degrade.

Signal suppression may be used to decrease these effects.

- **Fat suppression**
  Suppression of the fat signal,
  → Page H.1–44
- **FatSat mode**
  Degree of fat suppression,
  → Page H.1–45
- **Water suppression**
  Suppression of the water signal,
  → Page H.1–46
- **Water excit. Offset** (only with MAGNETOM "Concerto" and "C!")
  Frequency offset to obtain an optimal water excitation; only appears if **Water excit.** is selected for fat suppression,
  → Page H.1–45
- **MTC**
  Presaturation through magnetization transfer,
  → Page H.1–47
- **SWI**
  Highlights susceptibility constants in brain tissue,
  → Page H.1–47
- **Dixon**
  Separate display of fat and water signal,
  → Page H.1–48

➪ For some types of sequences, the **Geometry Saturation** parameter card contains the **Saturation mode** parameter. If you select the **Quick** option for this parameter, the options for fat and water saturation change to **Q-fat sat.** and **Q-water sat.**

Magnitude, phase, and real images

The **Contrast** card lets you select the image types for reconstruction:

Magnitude images	Show the intensity of the MR signal
Phase images	Show the phase angle of the spins
Real images	Show the signed amplitude of the longitudinal magnetization after an inversion pulse

NOTICE

Reconstruction of image types is not possible in every protocol and every sequence.

❏ **Reconstruction**
Selection of the reconstruction mode and image type or types,
→ Page H.1–43

Parameters for dynamic scanning

- **TD**
  Delay time (e.g., for breath-holding commands)
  → Page C.5–76, *Displaying and editing parameter groups* and → Page H.1–40
- **Infinite measurement**
  The number of scans for realtime sequences is set to the maximum value,
  → Page H.1–76
- **Measurements**
  Number of measurements for dynamic scanning,
  → Page H.1–76
- **Pause after meas.**
  Delay between individual scans,
  → Page H.1–77
- **Delay in TR**
  Time between two or more consecutive scans in all ep2d sequences,
  → Page H.1–78
- **Multiple series**
  The images of each scan are stored as a separate series,
  → Page H.1–79

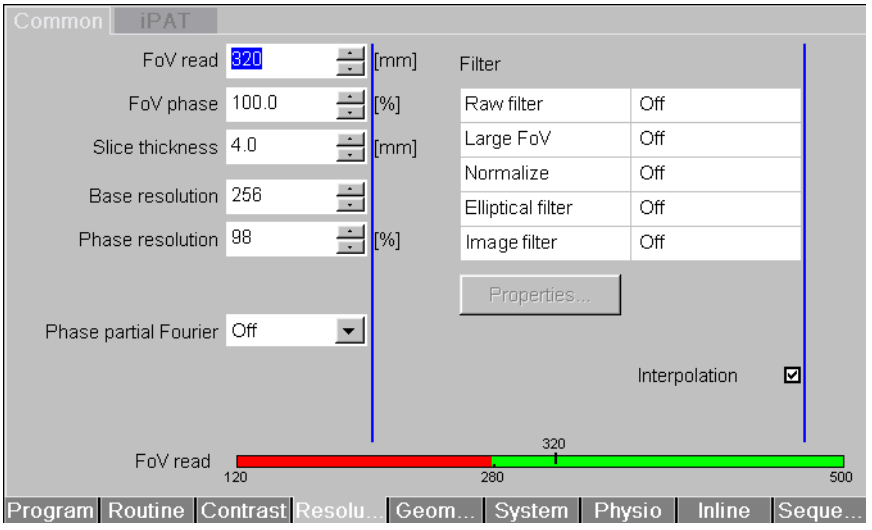
Resolution parameter card

The image resolution lets you determine the size and the level of detail shown by the images calculated from raw data. The higher the image resolution, the longer the acquisition time.

The **Resolution** parameter card consists of two subcards:

- **Common**
  All parameters affecting image resolution can be found on the **Resolution-Common** parameter card.
  The **Resolution-Common** parameter card differs for 2D and 3D measurements.
- **iPAT**
  The parameters for the PAT reconstruction method for shortening the scan time can be found on the **Resolution-iPAT** (PAT = parallel acquisition technique) parameter card.

Resolution-Common parameter card (2D)



Resolution Common parameter card (3D)

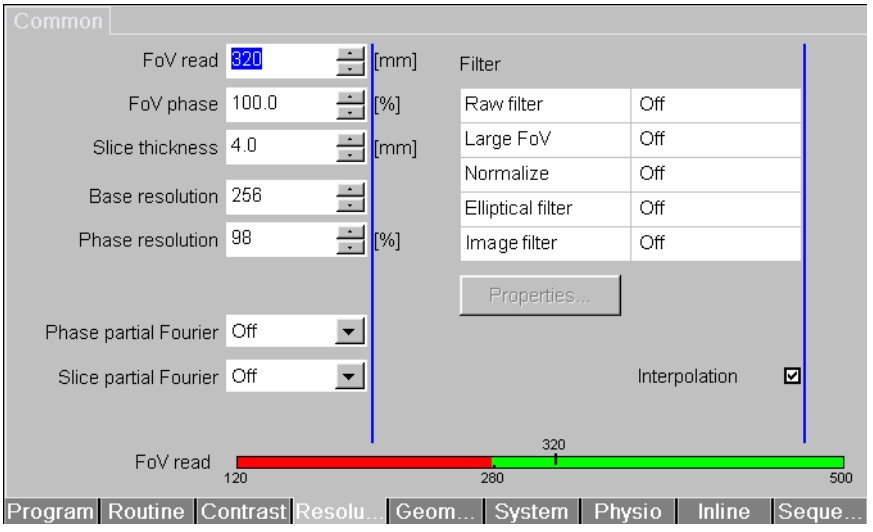


Image resolution for 2D scanning

❏ **FoV read**
Field of view in readout direction,
→ Page H.1–50

❏ **FoV phase**
Field of view in phase-encoding direction,
→ Page H.1–50

❏ **Slice thickness**
Thickness of the slices (in mm),
→ Page H.1–6

❏ **Base resolution**
Number of readout steps,
→ Page H.1–53

❏ **Phase resolution**
Ratio of readout to phase-encoding steps,
→ Page H.1–54

❏ **Phase partial Fourier**
Asymmetric scanning of raw data space in the phase-encoding direction to reduce the scan time,
→ Page H.1–59

Image resolution for 3D scanning

- ❑ **FoV read**
  Field of view in readout direction, → Page H.1–50
- ❑ **FoV phase**
  Field of view in phase-encoding direction, → Page H.1–50
- ❑ **Slice thickness**
  Individual slice thickness for all slabs (partitions), → Page H.1–6
- ❑ **Base resolution**
  Number of readout steps, → Page H.1–53
- ❑ **Phase resolution**
  Ratio of readout to phase-encoding steps, → Page H.1–54
- ❑ **Slice resolution**
  Ratio in slice selection direction, → Page H.1–57
- ❑ **Phase partial Fourier**
  Asymmetric scanning of raw data space in the phase-encoding direction to reduce the scan time, → Page H.1–59
- ❑ **Slice partial Fourier**
  Asymmetric scanning of raw data space in the slice selection direction to reduce the scan time, → Page H.1–62

Cartesian/Radial measurements

❏ **Trajectory**
Geometric shape of k-space sampling
→ Page H.1–60

❏ **BLADE coverage**
Number of radial blades for k-space sampling
→ Page H.1–61

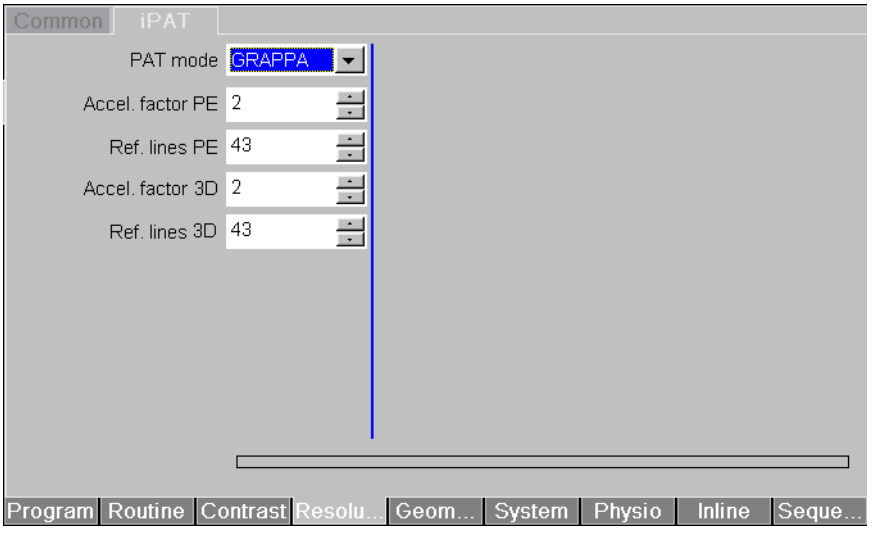
Filter

❏ **Filter**
Selection of a filter,
→ Page H.1–66

Interpolation

❏ **Interpolation**
Increasing the image matrix to twice the size,
→ Page H.1–56

Resolution - iPAT parameter card



- ❏ **iPat mode**
  Selection of the PAT reconstruction mode,
  → Page H.1–63
- ❏ **Accel. factor PE**
  Acceleration factor in the phase-endoding direction,
  → Page H.1–64
- ❏ **Ref. lines PE**
  Number of reference lines in the phase-encoding direction,
  → Page H.1–64
- ❏ **Accel. factor 3D**
  Acceleration factor in the slice selection direction,
  → Page H.1–65
- ❏ **Ref. lines 3D**
  Number of reference lines in the slice selection direction,
  → Page H.1–65

Geometry parameter card

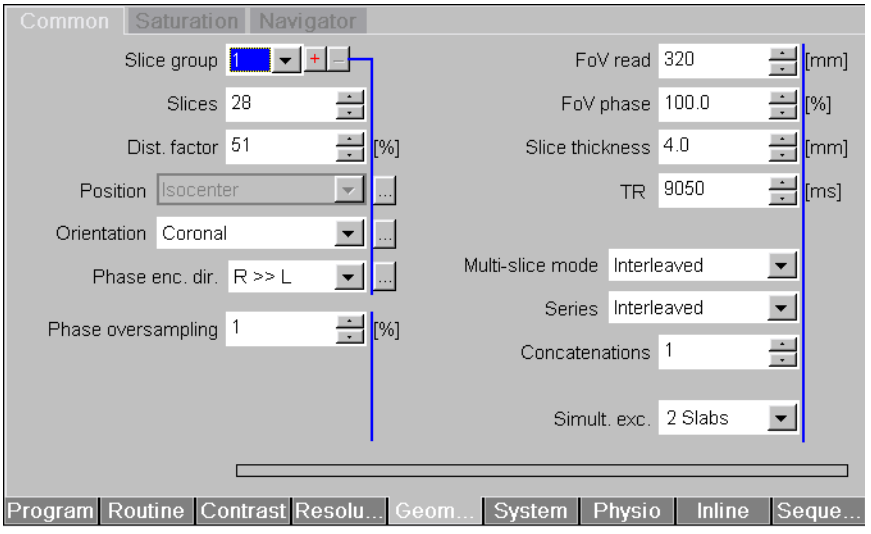
In routine examination mode, the position and orientation of slice and slab groups is planned graphically using the toolbar for graphic slice positioning and the mouse.

Use the **Geometry** parameter card if these tools are not sufficient for special diagnostic problems. This card also allows you to define the parameters for checking the excitation sequence, make settings for the saturation techniques, and position navigators.

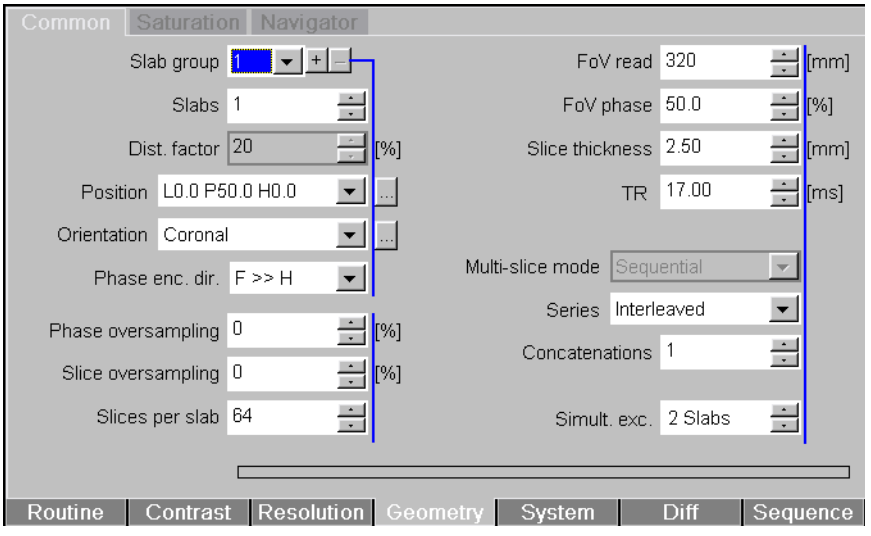
The Geometry card consists of three subcards:

- **Common**
  This card contains all the parameters for positioning and expanding the slices or slabs to be scanned. This parameter card differs for 2D and 3D measurements.
- **Saturation**
  This card displays the parameters relevant to the inclusion of regional or fat/water saturation.
- **Navigator**
  This card displays the parameters for navigator objects. It is only used for special navigator sequences.

Geometry Common parameter card (2D)



Geometry - Common parameter card (3D)



Slice parameters for 2D scanning

❏ **Slice group**
Number of the slice group currently displayed,
→ Page C.5–78, *Adding or deleting graphic objects* and
→ Page H.1–3

❏ **Slices**
Number of slices in this group,
→ Page H.1–4

❏ **Distance factor**
Distance between the slices of the group as a percentage of the slice thickness,
→ Page H.1–5

❏ **Position**
Position of the slice group in the patient coordinate system,
→ Page C.5–79, *Adjusting the orientation and position of graphic objects* and → Page H.1–11

❏ **Orientation**
Orientation of the slice group in the patient coordinate system, → Page C.5–79, *Adjusting the orientation and position of graphic objects* and
→ Page H.1–8

❏ **Phase-enc. dir**
Phase-encoding direction, specified in the main orientations of the patient coordinate system; the angle of slice rotation can also be set in a lower-level dialog box,
→ Page H.1–13

❏ **Phase oversampling**
Extension of the field of view in the phase-encoding direction to avoid aliasing artifacts,
→ Page H.1–14

Parameters for extending the measuring range

- ❑ **FoV read**
  Field of view in readout direction, → Page H.1–50
- ❑ **FoV phase**
  Field of view in phase-encoding direction, → Page H.1–50
- ❑ **Slice thickness**
  Thickness of the individual slices (2D) or thickness of the individual slices of the slabs (partitions, → Page H.1–6)
- ❑ **TR**
  Repetition time, interval between two consecutive excitations,
  → Page H.1–38

Parameters for monitoring the excitation sequence

- ❑ **Multi-slice mode**
  Sequential (slice by slice) or interleaved (row by row) scanning method, → Page H.1–31
- ❑ **Series**
  Slice excitation order, → Page H.1–33
- ❑ **Concatenations**
  Distribution of the slices to be measured across a given number of scans to avoid cross-talk, → Page H.1–34
- ❑ **Simult. excit.**
  Simultaneous excitation of 2 slices for a short TR even with a large number of slices, → Page H.1–35

Slab parameters for 3D scanning

❏ **Slab group**
Number of the slab group currently displayed, → Page C.5–78, *Adding or deleting graphic objects* and → Page H.1–3

❏ **Slabs**
Number of slabs in this slab group, → Page H.1–4

❏ **Distance factor**
Distance between slabs as a percentage of the slab thickness, → Page H.1–5

❏ **Position**
Position of the slab group in the patient coordinate system, → Page C.5–79, *Adjusting the orientation and position of graphic objects* and → Page H.1–11

❏ **Orientation**
Orientation of the slab group in the patient coordinate system, → Page C.5–79, *Adjusting the orientation and position of graphic objects* and → Page H.1–8

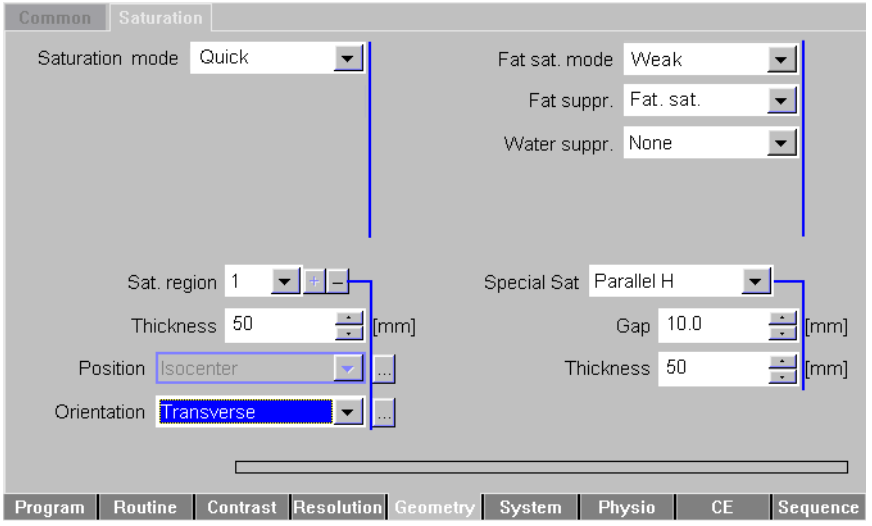
❏ **Phase-enc. dir**
Phase-encoding direction, specified in the main orientations of the patient coordinate system; the angle of slice rotation can also be set in a lower-level dialog box,
→ Page H.1–13

❏ **Phase oversampling**
Extension of the field of view in the phase-encoding direction to avoid aliasing artifacts,
→ Page H.1–14

❏ **Slice oversampling**
Extension of the field of view in the slice selection direction to avoid aliasing artifacts,
→ Page H.1–16

❏ **Slices per slab**
Number of slices per slab,
→ Page H.1–7

Geometry-Saturation parameter card



Saturation mode

❑ **Saturation mode**
Saturation pulses before each scan or only as often as necessary.

➪ The **Quick** saturation mode is available for some sequences. This mode ensures a shorter scan time and is used both for fat and water saturation as well as for regular and parallel saturation regions.

Suppression of the fat/water signal

- **Fat sat. mode**
  Degree of fat suppression, → Page H.1–45
- **Fat suppr.**
  Suppression of the fat signal, → Page H.1–44
- **Water suppr.**
  Suppression of the water signal, → Page H.1–46
- **Restore magn.**
  Signal increase with T2 weighting by accelerated relaxation of the longitudinal magnetization, → Page H.1–47

Saturation regions

Saturation regions are areas the signal of which is saturated by special RF pulses to avoid motion artifacts.

- **Saturation region**
  Number of the saturation slice displayed,
  → Page C.5–78, *Adding or deleting graphic objects*
- **Thickness**
  Thickness of this saturation region, → Page H.1–18
- **Position**
  Position of the saturation slice in the patient coordinate system, → Page C.5–79, *Adjusting the orientation and position of graphic objects* and → Page H.1–18
- **Orientation**
  Orientation of this saturation slice in the patient coordinate system, → Page C.5–79, *Adjusting the orientation and position of graphic objects* and → Page H.1–18

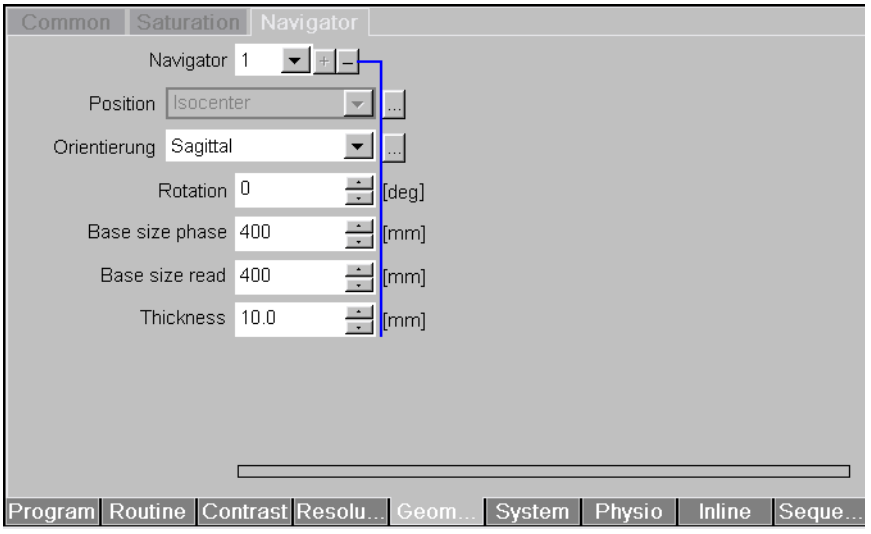
❑ **Special sat.**
Selection of a parallel or tracking saturation region, → Page H.1–19

➪ If you have selected the **Quick** saturation mode, a Quick option is available for all parallel saturation regions (for example, Q Parallel H). Tracking saturation regions cannot be planned in Quick mode.

❑ **Gap**
Distance between parallel or tracking saturation slice and slice group,
→ Page H.1–19

❑ **Thickness**
Thickness of the parallel or tracking saturation slice,
→ Page H.1–19

Geometry-Navigator parameter card



❏ **Navigator**
Type of navigator object currently displayed,
→ Page H.1–21

❏ **Position**
Position of the navigator object in the patient coordinate system,
→ Page H.1–22

❏ **Orientation**
Orientation of the navigator object in the patient coordinate system,
→ Page H.1–22

❏ **Rotation**
Angle about which the navigator object is rotated in the slice plane defined by the orientation,
→ Page H.1–23

❏ **FoV phase**
Extent of the navigator object in the phase-encoding direction, → Page H.1–23

❏ **FoV read**
Extent of the navigator object in the readout direction,
→ Page H.1–23

❏ **Thickness**
Thickness of the navigator slice,
→ Page H.1–23

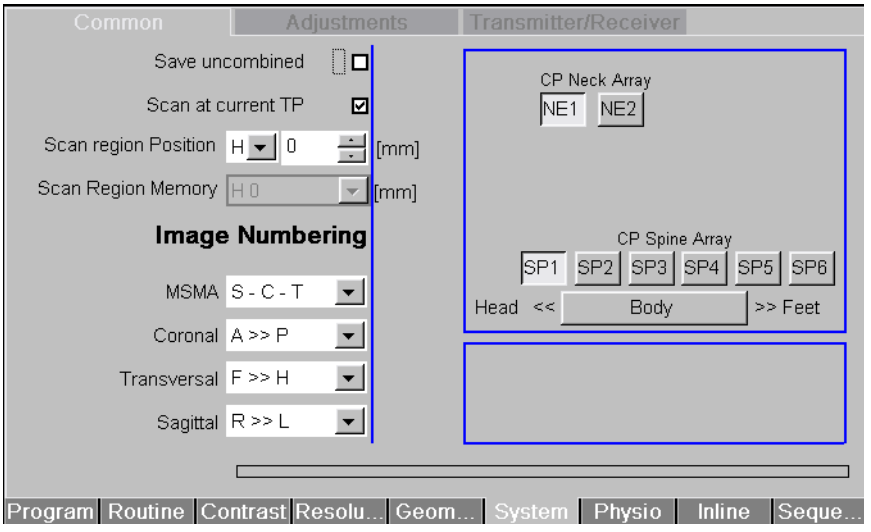
System parameter card

The **System** card is divided into three subcards:

- **Common**
  This subcard is used to define the position of the scan region. You may perform the scan using the current table position or define a different position.
  In the selection lists for image numbering you can define in which order the reconstructed images are to be numbered.
  In the right half of the card you can select the surface coils for your scan.

- **Adjustments** and **Transmitter/Receiver**
  These two parameter cards contain the settings for system adjustment. These cards are normally not used during routine operation. The adjustment settings should be changed only in exceptional cases and only by highly experienced users.
  → Chapter B 2, *Adjusting the System*

System-Common parameter card



Parameters for positioning the scan region

❑ **Scan at current TP**
The protocol is run at the current table position,
→ Page H.1–81

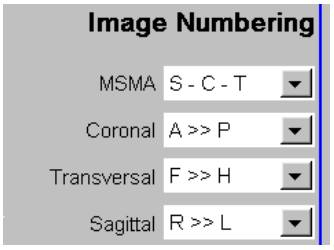
❑ **Scan region position**
Setting the position of the scan region, → Page H.1–81

❑ **Scan region memory**
Selection of a scan region position from the positions of the current series block, → Page H.1–82

NOTICE

The patient table is moved to adjust the position of the scan region. Depending on the patient positioning, the table will move toward the magnet or out of the magnet by the distance specified.

Parameter for image numbering



❏ **MSMA** (**M**ulti **S**lice **M**ulti **A**ngle) lets you define the order in which the scanned images are numbered with regard to their slice orientation (primary order).
→ Page H.1–36

❏ Use the **Sagittal**, **Coronal** and **Transversal** selection lists to define whether the scanned images are numbered according to ascending or descending slice positions (secondary order).
→ Page H.1–36

NOTE

The settings for image numbering are linked to the position of the scan region.
The settings for image numbering of the protocols already processed and completed are automatically applied when opening consecutive protocols sharing the same scan region position.

Selecting coils

You have a choice of surface coils for examining different regions of the body. As compared to the body coil, surface coils have a higher signal-to-noise ratio.

Please refer to the *System Manual* for a detailed description of the coils including their use.

NOTE

Coil selection is linked to the position of the scan region. Therefore, the coil selection of the protocols already processed and completed is automatically applied when opening consecutive protocols sharing the same position of the scan region.

➪ You can deactivate automatic coil selection. This is done by selecting **Queue > Automatic Coil select**.

NOTE

When you copy using copy reference, the target protocol inherits the coil configuration of the source protocol. The new coil configuration is stored at the corresponding position of the scan region.

The coils for the protocol are displayed on the **System Common** parameter card.

❏ **Array coils** and **body coil** (top right half of the card)
Selection of coils with fixed position and their coil elements, or the body coil,
→ Page H.1–84,
→ Page H.1–85

❏ **Flex coils** (bottom right half of the card)
Selection of coils with flexible position,
→ Page H.1–85

❏ **Uncombined images**
Saves array images uncombined. Two series are created: one containing the uncombined images of the individual coil elements *and* one containing the combined images (original images).
→ Page H.1–85

Physio parameter card

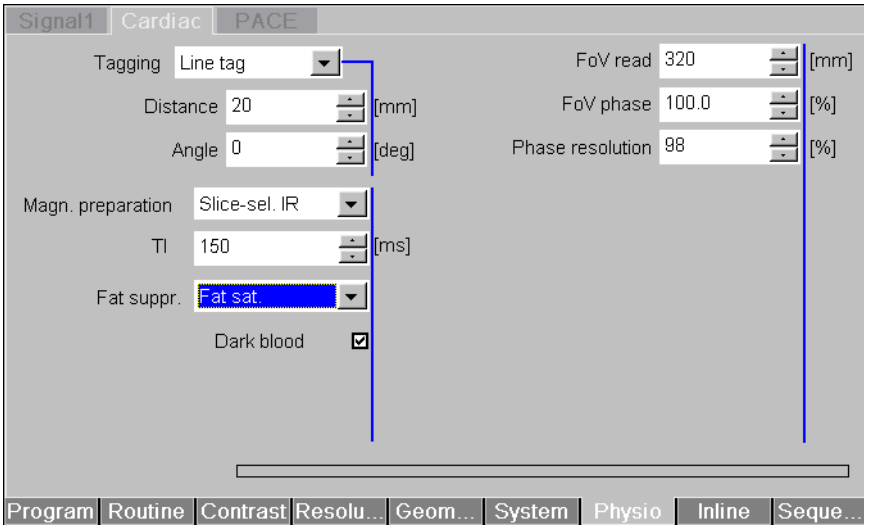
The **Physio** card is divided into three subcards:

- **Signal1**
  The **Physio Signal 1** parameter card lets you set the parameters for the 1st physiological signal.
  For a detailed description of the **Physio Signal 1** parameter card, please refer to chapter "Scans using physiological triggering", → Page C.15–1
- **Cardiac**
  The **Physio-Cardiac** parameter card allows you to set parameters for cardiological examinations.
- **PACE** (**P**rospective **A**cquisition **C**orr**E**ction)
  The **Physio-PACE** parameter card is used to set parameters for suppressing respiratory artifacts.

Physio-Cardiac parameter card

Cardiological sequences are used to examine and display cardiac functions. The resulting image data can be evaluated on the **Argus** task card.

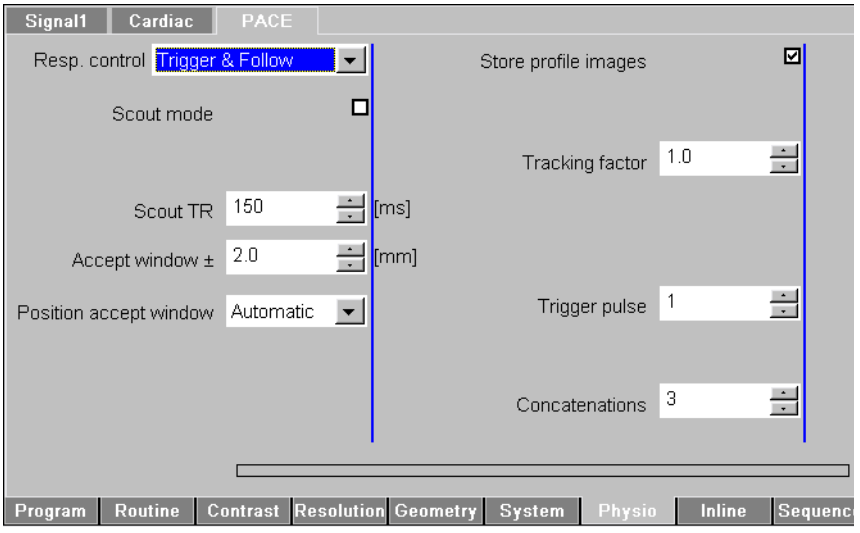
➪ The **Cardiac** parameter card is available only if the current scan protocol is based on a sequence supporting cardiological measurements.



- ❏ **Tagging**
  Displaying tagging (orientation) lines, → Page H.1–129
- ❏ **Distance**
  Distance between the tagging lines, → Page H.1–130
- ❏ **Angle**
  Angle of tagging lines, → Page H.1–130
- ❏ **Magn. preparation**
  Magnetization preparation for inversion recovery (IR) and saturation recovery (SR) sequences,
  → Page H.1–42
- ❏ **Fat suppression**
  Suppression of the fat signal,
  → Page H.1–44
- ❏ **Dark blood**
  Blood is displayed dark, → Page H.1–129
- ❏ **TI**
  Inversion time, → Page H.1–40
- ❏ **FoV read**
  Field of view in readout direction, → Page H.1–50
- ❏ **FoV phase**
  Field of view in phase-encoding direction, → Page H.1–50
- ❏ **Phase resolution**
  Ratio of readout to phase-encoding steps,
  → Page H.1–54

Physio-PACE parameter card

The **PACE** parameter card allows you to set parameters for suppression of respiratory artifacts.



- **Resp. control**
  Mode for compensating for the effects of breathing, → Page H.1–24
- **Scout mode**
  Preparation phase in which only the navigator signal is measured, → Page H.1–26
- **Scout duration**
  Duration of the preparatory phase, → Page H.1–26
- **Scout TR**
  TR of the navigator pulse, → Page H.1–26

- **Accept window±**
  Acceptable deviation from the tolerance center,
  → Page H.1–27
- **Position accept window**
  Position acceptance window, → Page H.1–28
- **Accept. position (green)**
  Centering position of the acceptance window,
  → Page H.1–28
- **Accept. position**
  Centering position of the acceptance window on triggering,
  → Page H.1–28
- **Search window ±**
  Size of the search window, → Page H.1–29
- **Search position (red)**
  Centering position of the search window, → Page H.1–29
- **Store profile images**
  Stores the navigator signal-time curve as an image,
  → Page H.1–29
- **Tracking factor**
  Correlation between the diaphragm movement and the anatomy to be scanned,
  → Page H.1–30
- **Chronologic position**
  Time when the navigator was used,
  → Page H.1–30

- **RF pulse type**
  Radio frequency pulse type, → Page H.1–97
- **Trigger pulse**
  Trigger counter, → Page H.1–143
- **Slices per resp. cycle**
  Slices per respiratory cycle, → Page H.1–146
- **Card. trig. per resp. cycle**
  Cardiac trigger per respiratory cycle, → Page H.1–146
- **Concatenations**
  Distribution of the slices to be measured across a given number of scans to avoid cross-talk, → Page H.1–34

Angio parameter card

The **Angio** parameter card is available only if the sequence used as a basis for the current scan protocol supports one of the following examinations:

- ❏ Time-of-flight angiography
- ❏ Contrast-enhanced angiography
- ❏ Phase contrast angiography (2D and 3D)
- ❏ Flow quantification

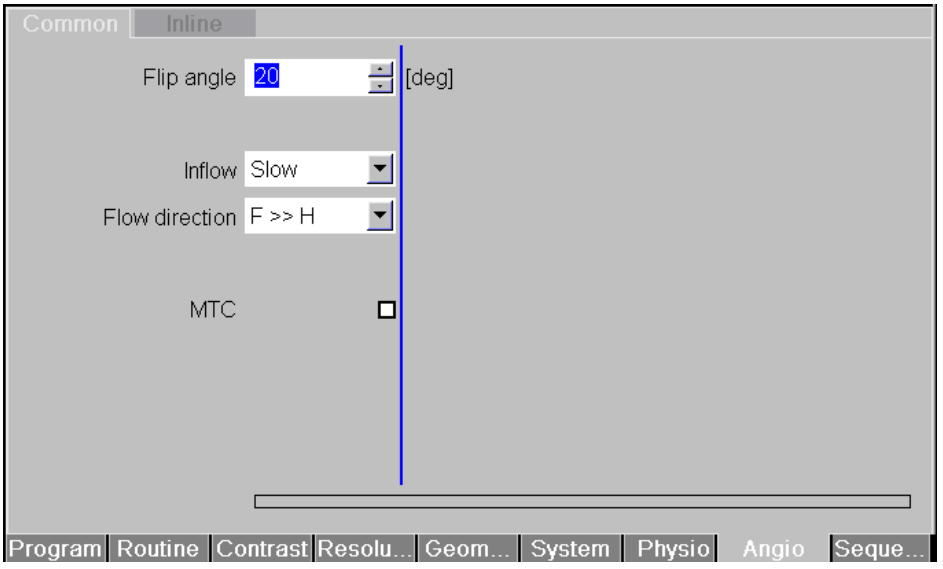
The **Angio** parameter card is divided into two subcards:

- ❏ **Angio-Common**
  Includes the parameters specific to one of the examinations mentioned above.
- ❏ **Angio-Inline**
  Includes the parameters for dynamic image evaluation for angiography examinations.
  → Page C.5–60

Angio - Common parameter card for Time-of-Flight angiography

In time-of-flight angiography sequences, unsaturated spins flow into the slice or volume to generate especially high signal intensity.

The **Angio Common** parameter card allows you to individually adjust specific parameters for magnitude angiography examinations.

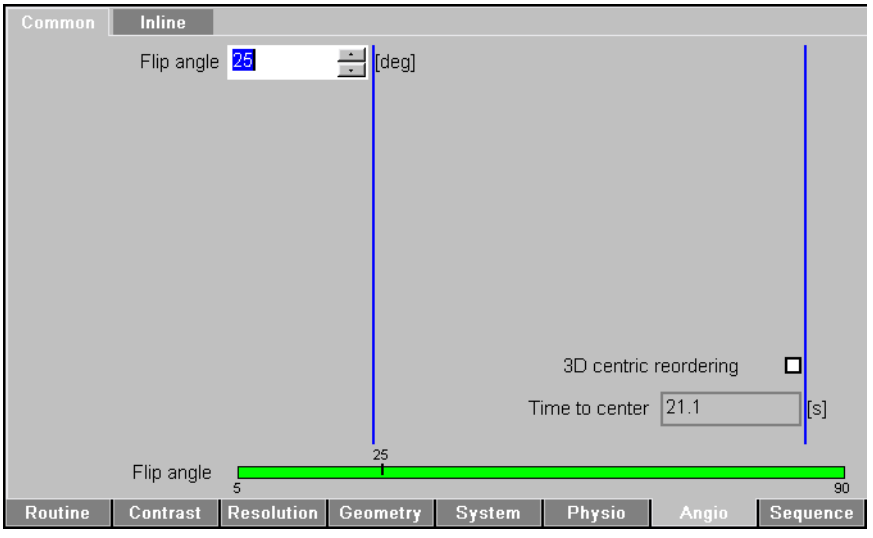


- **Flip angle**
  Flip angle of rotational axis of spins, → Page H.1–41
- **Inflow**
  Inflow velocity of blood, which defines the shape of the TONE excitation pulse, → Page H.1–108
- **Flow direction**
  Direction of blood flow, → Page H.1–108
- **MTC**
  Presaturation through magnetization transfer, → Page H.1–47

Angio - Common parameter card for contrast-enhanced angiography

Contrast-enhanced angiography takes advantage of the fact that contrast agent (gadolinium compounds) shortens T1 in the blood.

The **Angio Common** parameter card allows you to individually adjust specific parameters for contrast-enhanced angiography examinations.



- ❏ **Flip angle**
  Flip angle of rotational axis of spins, → Page H.1–41
- ❏ **3D centric reordering**
  Center of the raw data space is acquired as quickly as possible, → Page H.1–109
- ❏ **Time to center**
  Time it takes to reach the k-space center, → Page H.1–109

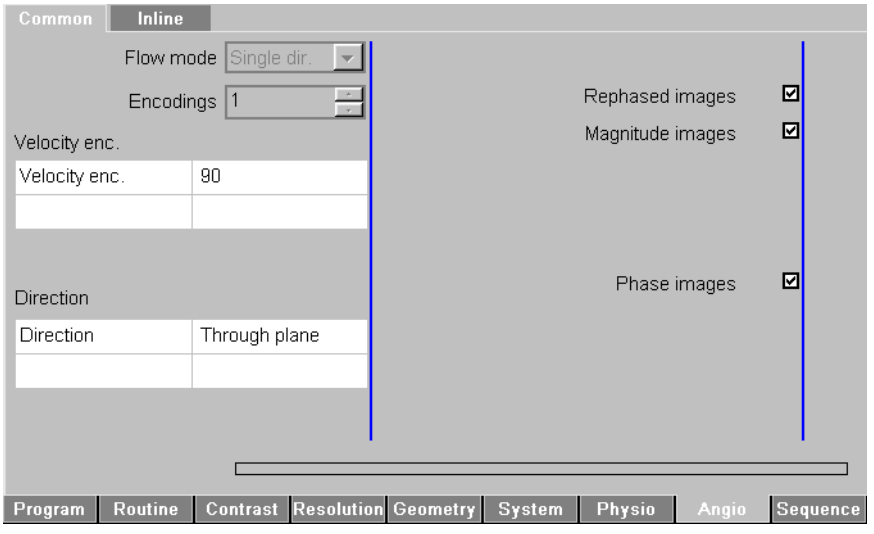
Angio - Common parameter card for phase contrast angiography and flow quantification

2D phase contrast angiography is used to display vessels within large scan volumes.

The intensity of each pixel is a measure of the velocity component at that location. Since only moving spins contribute to the signal, very thick slices can be displayed as well. The result is a projection image of all vessels in the excited slice volume.

To display special projections of vessel sections, **3D phase contrast angiography** allows you to process the entire data volume measured using the MIP technique.
→ *syngo* Operator Manual

The MR **flow quantification** technique allows for non-invasive examination and evaluation of blood flow.



❏ **Flow mode**
Flow-encoding mode, → Page H.1–110

❏ **Encodings**
Number of flow sensitivities to be set (flow velocity encoding),
→ Page H.1–111

❏ **Velocity enc.**
Definition of flow sensitivities in cm/s,
→ Page H.1–111

❏ **Direction**
Flow-sensitive axis, → Page H.1–111

❏ **Rephased images**
Magnitude image (flow-rephased), → Page H.1–112

❏ **Magnitude images**
Magnitude images (either for each flow direction or for each flow sensitivity), → Page H.1–112

❏ **Magnitude sum**
Magnitude sum image, → Page H.1–112

❏ **Phase images**
Phase images (either for each flow direction or for each flow sensitivity), → Page H.1–112

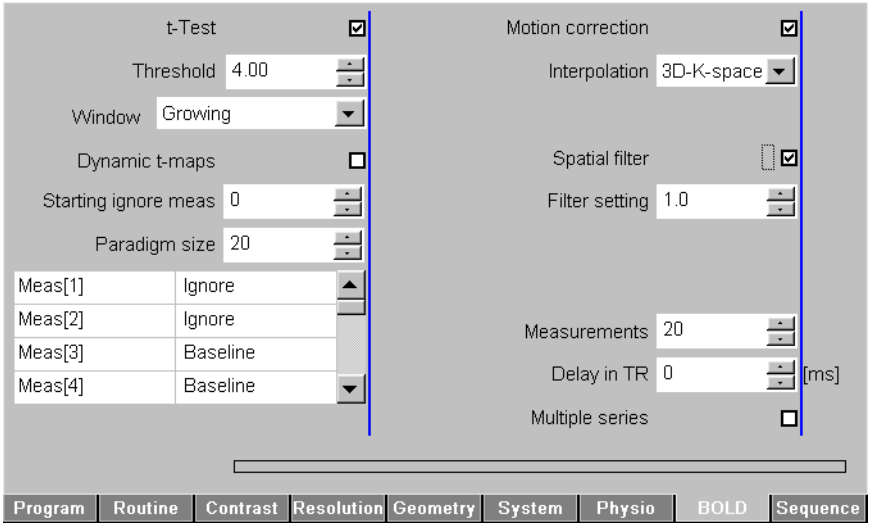
BOLD parameter card

The BOLD abbreviation stands for **B**lood **O**xygenation **L**evel **D**ependent Contrast.

BOLD imaging displays the change in the oxygenation state of blood. Generally, T_2*-weighted EPI sequences are used for this purpose.

While the patient is performing certain actions, e.g. finger movements, images of the brain are acquired during rest as well as active periods. Statistical analysis of these images (t-test) provides a parameter map that allows you to locate neurally active regions on the basis of intensity.

➪ The **BOLD** parameter card is available only if the current protocol is based on a sequence supporting BOLD imaging.



- **t-Test**
  Enables or disables t-test evaluation, → Page H.1–126
- **Threshold**
  Threshold value for calculating overlaid images, → Page H.1–127
- **Window**
  t-test calculation area, → Page H.1–127
- **Dynamic t-maps**
  Switching storage of the generated t-maps on or off, → Page H.1–126.
- **Starting ignore meas.**
  Number of initial scans excluded from the evaluation, → Page H.1–122
- **Paradigm size**
  Number of entries in the paradigm table, → Page H.1–127
- **Paradigm table**
  Table of single BOLD scans with information about stimulation, → Page H.1–128

❏ **Motion correction**
Switching motion correction on or off,
→ Page H.1–123

❏ **Interpolation**
Interpolation method for motion correction,
→ Page H.1–124

❏ **Spatial filter**
Switching Gauss filtering on or off, → Page H.1–125

❏ **Filter setting**
Window width of the Gauss filter, → Page H.1–125

❏ **Infinite measurement**
The number of scans for realtime sequences is set to the maximum value, → Page H.1–76

❏ **Measurements**
Number of scans, → Page H.1–76

❏ **Pause after meas.**
Delay between individual scans,
→ Page H.1–77

❏ **Delay in TR**
Time between two or more consecutive scans in all ep2d sequences, → Page H.1–78

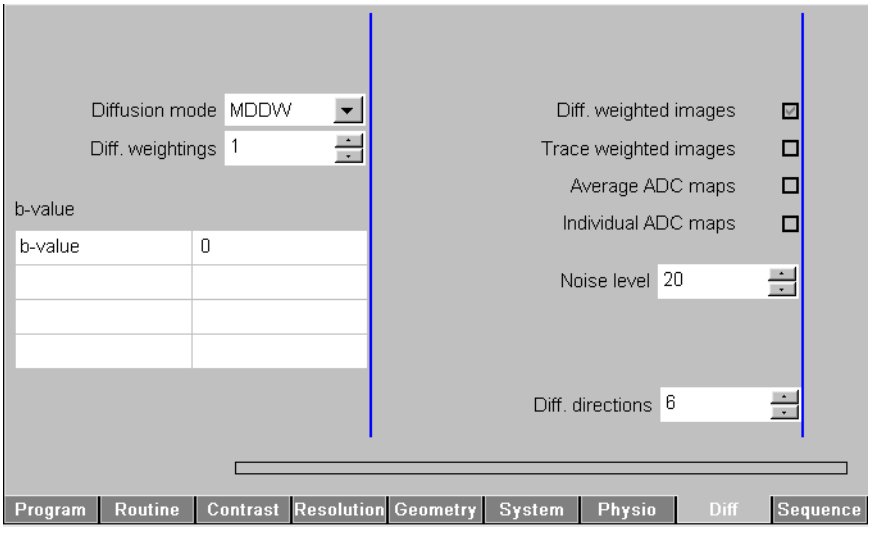
❏ **Multiple series**
The images of each scan are stored as a separate series,
→ Page H.1–79

Diff parameter card

The diffusion of water molecules along a field gradient reduces the MR signal. Signal loss is not as pronounced in areas where the water molecules are not able to diffuse as quickly. **Diffusion-weighted scans** are based on such diffusion-dependent differences in signal intensity.

The **Diff** parameter card allows you to set the parameters specific to diffusion-weighted scanning.

➪ The **Diff** parameter card is available only if the current scan protocol is based on a sequence supporting diffusion-weighted measurements.

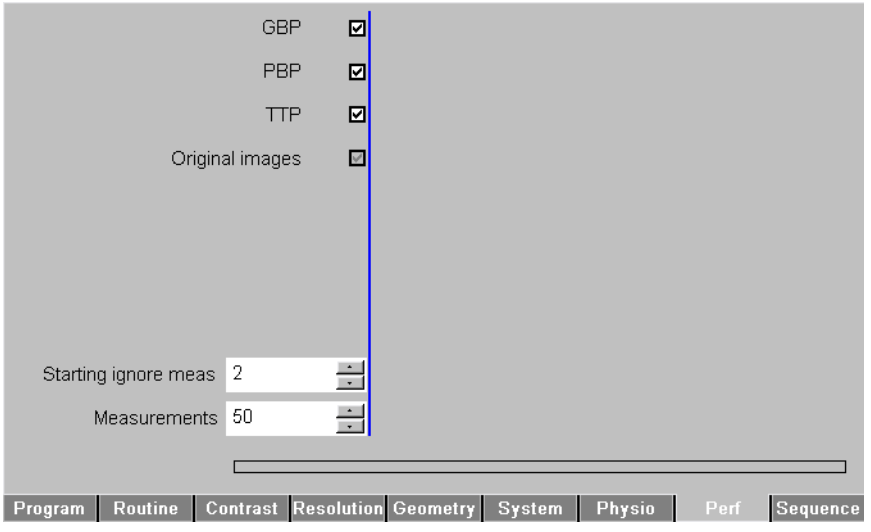


- **Diffusion mode**
  Diffusion-sensitive direction, → Page H.1–113
- **Diff. weightings**
  Number of diffusion weightings, → Page H.1–114
- **b-value**
  Value for diffusion weighting, → Page H.1–115
- **Diff. weighted images**
  Reconstructing original images with diffusion weighting, → Page H.1–115
- **Trace weighted images**
  Isotropically diffusion-weighted images, i.e. images are averaged in all spatial directions, → Page H.1–116
- **Average ADC maps**
  Grayscale values of images show diffusion coefficients averaged over different directions, → Page H.1–116
- **Individual ADC maps**
  Grayscale values of the images show diffusion coefficients along a gradient axis, → Page H.1–117
- **Noise level**
  Threshold value of the pixel intensity for calculating ADC maps, → Page H.1–117
- **Diff. moment** (only with **psif** sequence)
  Measure of the strength of diffusion weighting, → Page H.1–117
- **Diff. directions**
  Number of diffusion-encoding directions
  Selectable only in **MDDW** mode otherwise predefined by diffusion mode parameter.
  → Page H.1–118

Perf parameter card

One method of MR perfusion imaging is to determine the signal change in images as a function of time while injecting intravenous contrast agent. Generally, T_2*-weighted EPI sequences with a gadolinium contrast agent are used for this purpose.

➪ The **Perf** parameter card is available only if the current scan protocol is based on a sequence supporting perfusion measurements.



❏ **Global Bolus Plot (GBP)**
Calculating the global time-density curve, → Page H.1–120

❏ **Percentage of Baseline at Peak map (PBP)**
Calculating the signal change relative to the baseline, → Page H.1–120

❏ **Time-to-Peak map (TTP)**
Calculating the time-to-peak image, → Page H.1–119

❏ **Original images**
Saving the original images, → Page H.1–119

❏ **Starting ignore meas.**
Number of initial scans excluded from the evaluation, → Page H.1–122

❏ **Measurements**
Number of measurements for dynamic scanning, → Page H.1–76

Inline parameter card

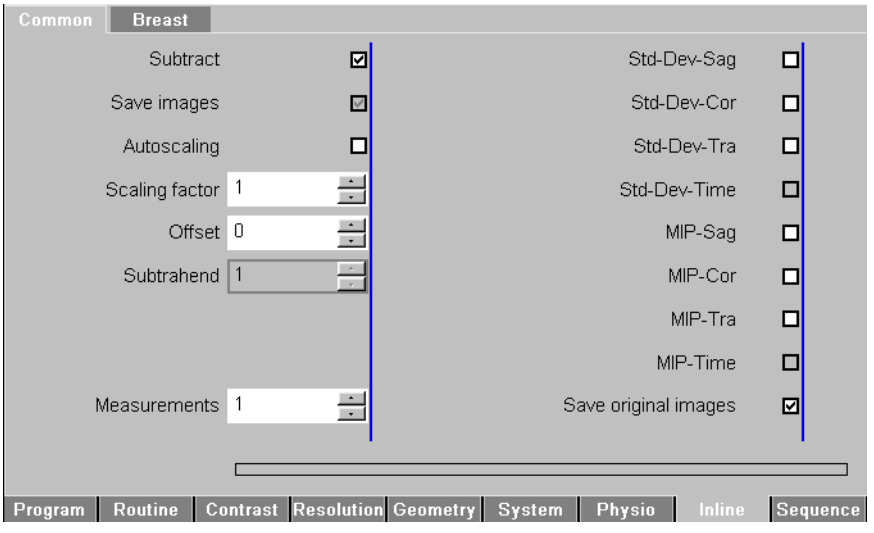
The **Inline** parameter card is divided into two subcards:

- ❏ **General Information**
- ❏ **Breast**

Inline-Common parameter card

The **Inline Common** parameter card allows you to set parameters for dynamic image evaluation.

➪ In case of scan protocols for angiography examinations, the **Inline** parameter card is displayed as **Angio Inline** subcard. In case of scan protocols for BOLD scans, diffusion-weighted scans, or perfusion scans, the **Inline** parameter card is not part of the parameter card stack.



❏ **Subtract**
Switching subtraction on or off, → Page H.1–131

❏ **Save images**
Saving the result images of the subtraction,
→ Page H.1–132

❏ **Autoscaling**
Automatic scaling of the result images of the subtraction,
→ Page H.1–132

❏ **Scaling factor**
Entering a scaling factor for the result images of the subtraction, → Page H.1–133

❏ **Offset**
Entering an offset value for the result images of the subtraction, → Page H.1–133

❏ **Subtrahend**
Defines the series to be subtracted,
→ Page H.1–134

❏ **Measurements**
Number of measurements for dynamic scanning,
→ Page H.1–76

❏ **Std-Dev-Sag**
Calculation of standard deviation result images in sagittal direction, → Page H.1–135

❏ **Std-Dev-Cor**
Calculation of standard deviation result images in coronal direction, → Page H.1–135

❏ **Std-Dev-Tra**
Calculation of standard deviation result images in transverse direction, → Page H.1–136

❏ **Std-Dev-Time**
Calculation of standard deviation result images in chronological sequence, → Page H.1–136

❏ **MIP-Sag**
Calculation of MIP images in sagittal direction,
→ Page H.1–137

❏ **MIP-Cor**
Calculation of MIP images in coronal direction,
→ Page H.1–137

❏ **MIP-Tra**
Calculation of MIP images in transverse direction,
→ Page H.1–138

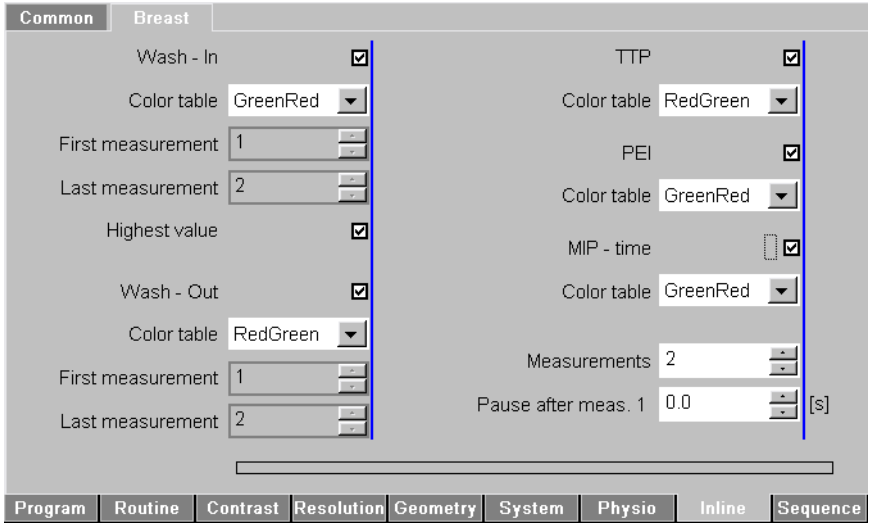
❏ **MIP-Time**
Calculation of MIP images in chronological sequence; (cannot be activated on **Inline-Common**, if MIP-Time is already activated on the **Breast** parameter card)
→ Page H.1–138

❏ **Save original images**
Saving the original images,→ Page H.1–139

Inline-Breast parameter card

The **Inline-Breast** parameter card allows you to set parameters for **Breast Evaluation**.

➪ For protocols for **BreastBreast Evaluation**, the **Inline** parameter card is shown as a sub-card **Inline-Common**. However, **MIP time** is available on this sub-card only if it has not been activated on the subcard **Inline - Breast**.



❑ **Wash-In**
Enabling/disabling calculation of the signal change in the starting range of the dynamic measurement series,
→ Page H.1–120

❑ **Color table**
Color palettes used to color-code the parameter cards
→ Page H.1–121

❑ **First measurement**
First measurement used for the wash-in or wash-out calculation,
→ Page H.1–121

❑ **Last measurement**
Last measurement used for the wash-in or wash-out calculation,
→ Page H.1–121

❑ **Highest value**
Defines whether the value of the last measurement or the highest value between the first and last measurement will be used for calculation of the wash-in parameter image,
→ Page H.1–121

❑ **Wash-Out**
Parameter for signal change in the end range of the dynamic measurement series,
→ Page H.1–122

❑ **TTP**
Display of the time-to-signal peak for each voxel,
→ Page H.1–119

❏ **PEI**
Positive enhancement integral, area under a signal intensity - time curve,
→ Page H.1–122

❏ **MIP-Time**
MIP images; highest pixel value along the time axis
→ Page H.1–138

❏ **Measurements**
Number of measurements for dynamic scanning,
→ Page H.1–76

❏ **Pause after meas.**
Delay between individual scans,
→ Page H.1–77

Sequence parameter card

Your system includes a number of different sequence types:

- ❏ Gradient echo sequences (GRE, FLASH, Turboflash, True FISP, MEDIC, PSIF, CISS, DESS)
- ❏ Spin echo sequences (se)
- ❏ Turbo spin echo sequences (tse)
- ❏ HASTE sequences
- ❏ Single-shot EPI sequences

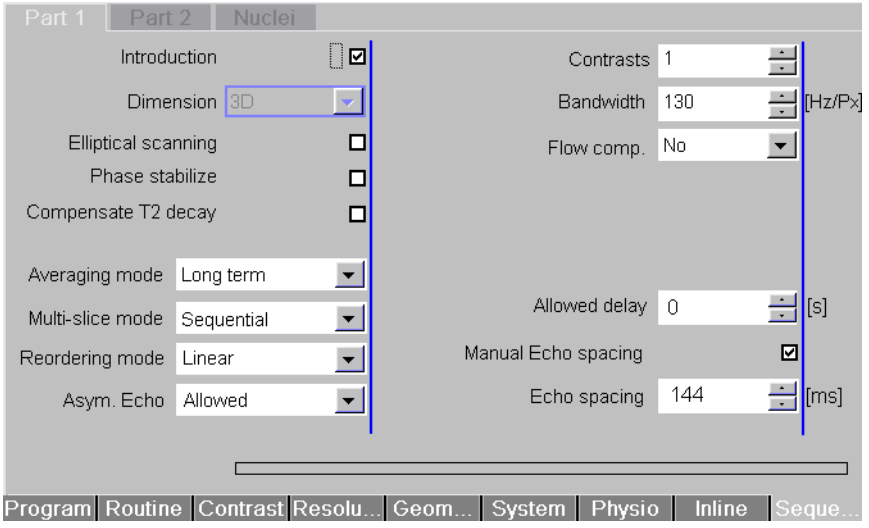
The **Sequence** parameter card groups all parameters specific to a given sequence type. Therefore, the display and input fields available vary depending on the sequence type selected. The parameter card is divided into the **Part 1** and **Part 2** subcards. In addition, the **Nuclei** subcard is displayed for protocols suitable for multinuclear measurements.



The sequence used as a basis for the current protocol is indicated in the right half of the info line above the parameter card stack.

➪ A tool tip including the name and type of sequence used will be displayed if you hold the mouse pointer over the sequence name.

Sequence-Part 1 parameter card



❏ **Introduction**
Initial knocking sound from gradient coil,
→ Page H.1–86

❏ **Dimension**
Setting for 2D or 3D scanning, → Page H.1–87

❏ **Elliptical scanning**
Elliptical k-space scanning, → Page H.1–87

❏ **Phase stabilization**
Prevents phase errors and improves image quality,
→ Page H.1–88

❏ **Compensation T2 decay**
Avoiding negative effects of the T2 decay,
→ Page H.1–88

❑ **Averaging mode**
Method for averaging several scans,
→ Page H.1–89

❑ **Multi-slice mode**
Scanning method for multi-slice scanning: sequential (slice by slice) or interleaved (line by line),
→ Page H.1–31

❑ **Reordering**
Acquisition sequence of raw data lines, → Page H.1–89

❑ **Asymmetric echo**
Defines whether echo asymmetry is permitted in the readout direction, → Page H.1–90

❑ **Contrasts**
Number of echoes, → Page H.1–90

❑ **Bandwidth**
Read-out bandwidth for contrasts, → Page H.1–91

❑ **Flow comp.**
Flow compensation of moving spins in the readout and/or slice selection direction, → Page C.5–76, *Displaying and editing parameter groups* and
→ Page H.1–92

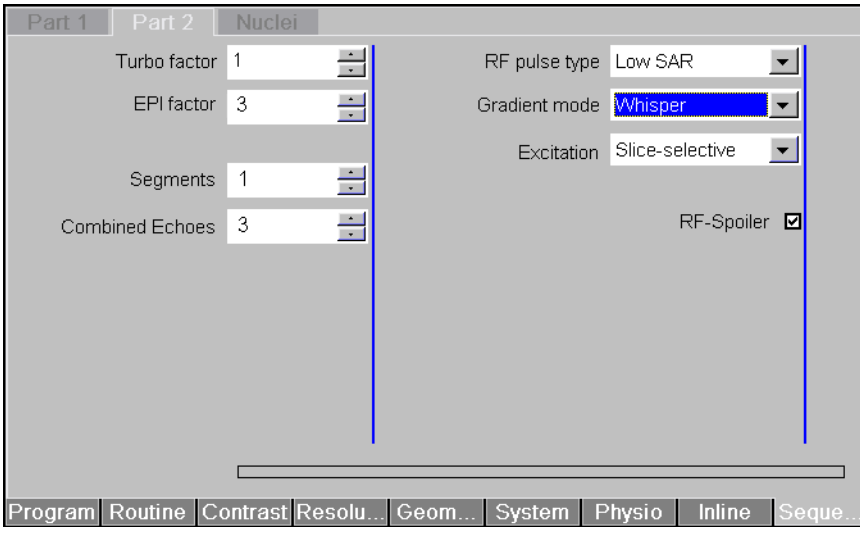
❑ **Allowed delay**
Maximum delay until the start of the next scan,
→ Page H.1–91

❑ **Manual echo spacing**
Allows you to define echo spacing, → Page H.1–93

❑ **Echo spacing**
Distance between echoes in the pulse train, → Page H.1–93

❑ **Readout mode**
Readout mode for gradient echo sequences (GRE),
→ Page H.1–94

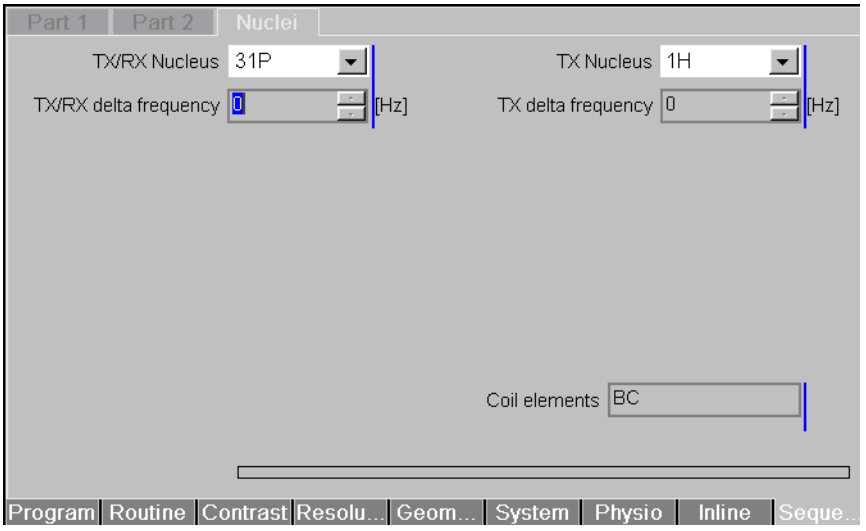
Sequence-Part 2 parameter card



- **Turbo factor**
  Number of echoes per RF excitation for turbo spin echo sequences, → Page H.1–95
- **EPI factor**
  Number of refocused gradient echoes per RF excitation, → Page H.1–95
- **Segments**
  Number of lines of a raw data matrix acquired during one TR, → Page H.1–96
- **Combined echoes**
  Combination of echoes with different T2 weighting for an image, → Page H.1–96

- ❏ **RF pulse type**
  Radio frequency pulse type, → Page H.1–97
- ❏ **Gradient mode**
  Gradient performance used, → Page H.1–98
- ❏ **Excitation**
  Mode for radio frequency pulse, → Page H.1–100
- ❏ **RF Spoiler**
  RF pulse for destroying phase coherence of gradient echo sequences, → Page H.1–100
- ❏ **Motion correction**
  Motion correction, → Page H.1–101
- ❏ **Flip angle mode**
  Excitation pulse of the flip angle over the echo train, → Page H.1–102
- ❏ **Echo train duration**
  Duration of echo train, → Page H.1–95
- ❏ **Fluid enhancement**
  Improvement of image contrast for self-weighted DESS images, → Page H.1–103
- ❏ **SNR optimization**
  Improvement of the signal-to-noise ratio for self-weighted DESS images, → Page H.1–103

Sequence-Nuclei parameter card



❏ **TX/RX Nucleus**
Selection of the primary nucleus, → Page H.1–104

❏ **TX/RX delta frequency**
Frequency shift relative to the adjustment frequency for the primary nucleus (can be edited only for spectroscopy protocols),
→ Page H.1–105

❏ **TX Nucleus**
Selection of the secondary nucleus, → Page H.1–105

❏ **TX delta frequency**
Frequency shift relative to the adjustment frequency for the secondary nucleus (can be edited only for spectroscopy protocols),
→ Page H.1–106

❏ **Coil elements**
Coils to be used for this protocol,
→ Page H.1–84

Working in the parameter card stack

The input and orientation tools on and above the parameter cards help you to quickly and easily adapt a scan protocol.

Protocol info line

After opening a scan protocol, the following information is displayed in the protocol info line (directly above the parameter card stack).



(1) Total scan time for the protocol
given the current parameter settings
(2) Voxel size
given the current parameter settings
(3) Relative signal-to-noise ratio (SNR),
SNR given the current parameter settings, based on the SNR when opening the protocol.
This allows you to monitor if and to what extent your parameter changes have improved or degraded the signal-to-noise ratio.
(4) Sequence type

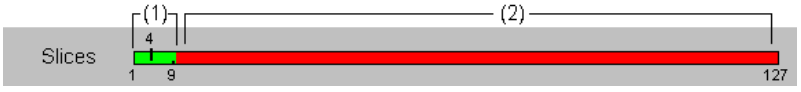
Changing parameter values and observing value ranges

Scan settings can be changed in the parameter card stack by clicking options, selecting options from a list, or changing values using spin boxes.

However, certain values and settings cannot be freely defined or combined. The value ranges of some parameters are limited by the technical capabilities of your scan system. Certain parameters depend on other measurement parameters. In this case, changing one parameter value will require that other measurement parameters be changed as well. The scan system informs you of these limitations.

Soft limits and extended limits

For parameter values that may be modified using spin boxes, the acceptable value range is displayed as a bar. When you click or modify a parameter value, the bar appears at the bottom of the parameter card.

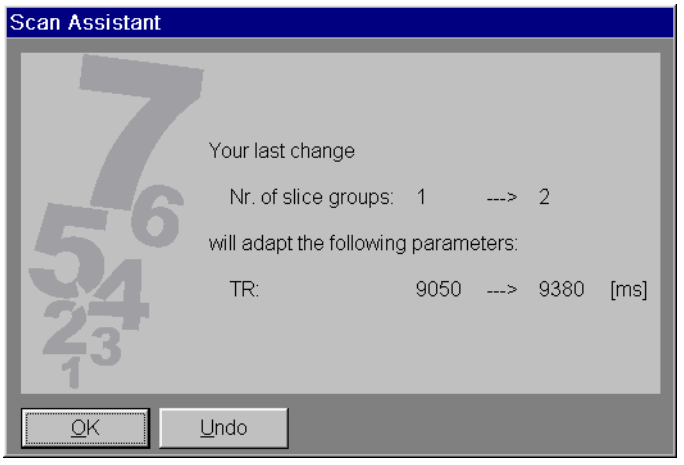


(1) Soft limits
(2) Extended limits

Within the **Soft Limits** (green bar), you can freely set parameter values without affecting other parameters.

Within the so-called **Extended Limits** (red bar), you are still able to change parameter values. However, changes within extended limits require that you adjust other measurement parameters as well.

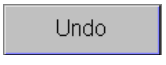
If you exceed the **Soft Limits**, the **Scan Assistant** dialog box will open.



It informs you about the necessary adjustments to other scan parameters and allows you to decide how to proceed:



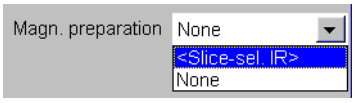
✧ Click the **OK** button or press the **Return** key to confirm your parameter change and the adjustments to other measurement parameters.



✧ Click the **Undo** button or press the **Esc** key to cancel your parameter change.

Restrictions when selecting options

Subsequent changes may be necessary also when checking or selecting options from lists.



In selection lists, these entries can be identified by pointed brackets.



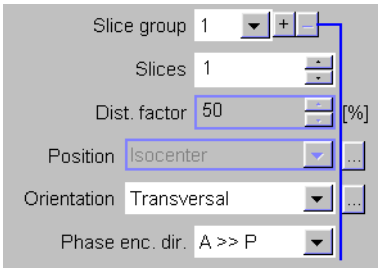
Check boxes requiring other parameter changes when selected are highlighted in red.



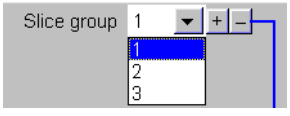
On the +/– buttons, the "+" and "–" signs are displayed in red.

Displaying and editing parameter groups

Certain parameters on the cards are grouped in sets. These parameter groups are indicated by blue brackets.



This example shows the parameter settings for a slice group.



✧ Expand the selection list of the **Slice group** field.

You can see how many slice groups are contained in the scan protocol.

✧ Select another slice group to display the corresponding slice parameters.

You can now change the parameters of the second group.

Other input or output fields allow you to access parameter sets.



In this example, the open scan protocol has several echo times.



✧ Click the arrow buttons in the lower left corner to scroll the echo times for the protocol.

The echo time currently displayed is indicated by square brackets.



✧ Click the arrow buttons of the spin box to change the value of the echo time currently displayed.

✧ Press the **Return** key or switch to another input field to confirm your parameter change.

Adding or deleting graphic objects

You usually use the graphic method to plan regions or volumes that will be excited when a protocol is run. You do this using the mouse and the graphic slice positioning tool bar. You are able to move, add, or delete slice or slab groups or saturation regions within the reference images.

Alternatively, you can use the parameter card stack to plan new objects or delete objects no longer needed.

New group or region



✧ Click the **Plus** button next to the selection list.

The new slice/slab group or saturation region is added to the selected reference image. It is slightly offset compared to the existing outermost object to avoid overlap.

✧ Move the new group or region to the desired position and adjust the orientation as required.

You can either use the mouse for graphical editing within the reference image or the **Position** and **Orientation** dialog boxes to work with maximum precision.

Deleting a group or region



- ✧ Select the slice/slab group or saturation region you want to delete from the selection lists.
- ✧ Click the **Minus** button to remove the group from the scan protocol.

Or

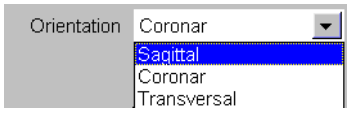
- ✧ Select **Delete** from the context menu for graphic slice positioning.

Adjusting the orientation and position of graphic objects

Similar to adding and deleting objects, you will normally position objects graphically in the reference images using the mouse.

Alternatively, you can use the parameter cards to position objects with more precision.

Setting the slice orientation at a precise angle

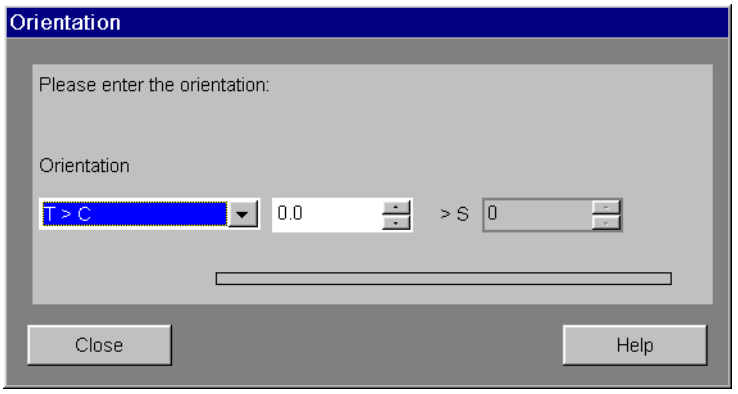


- ✧ Select the slice/slab group or saturation region for which you want to change the orientation.
- ✧ Next, select one of the three main orientations from the **Orientation** selection list.

Or

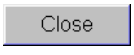


✧ Open the **Orientation** dialog box by clicking the button next to the selection list.



✧ Select the tilt direction (single slice) and enter a flip angle.
→ Page H.1–8

✧ Enter a flip angle for the direction of the third orientation plane if you want to generate a double-oblique slice.



✧ Close the dialog box to confirm your settings.

Entering the slice position with millimeter precision



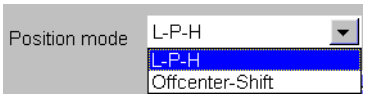
✧ Select the slice/slab group or saturation region for which you want to change the parameters.

✧ Next, select **Isocenter** from the **Position** list to position the slice/slab group or saturation region in the magnet isocenter.

Or



✧ Click the button next to the selection list to display the **Position** dialog box.

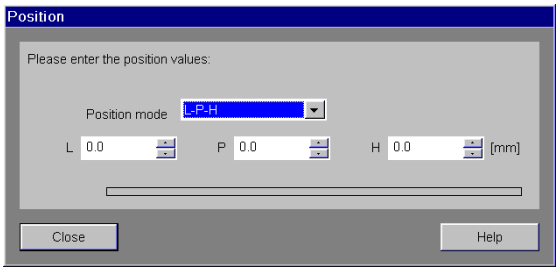


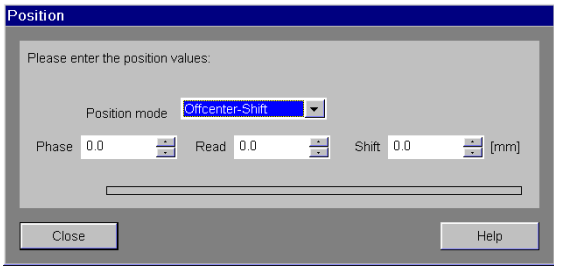
✧ Under **Position mode**, select the mode you want to use.

Depending on the position mode selected, the **Position** dialog box offers different options.

NOTE

During volume positioning (e.g., VOI, adjustment volume), you *always* work in **L-P-H** mode.
The **Position mode** selection list is *not* available.





In both modes, you proceed by defining the shift of the center of the object from the magnet isocenter.

❑ **L - P - H**
In this mode you enter the offset based on the patient coordinate system.
L - to the left (negative value for offset to the right)
P - to posterior (negative value for offset to anterior)
H - in the direction of the head (negative value for offset in the direction of the feet)

❑ **Offcenter-Shift**
In this mode you enter the shift in the gradient directions:
Phase - Offcenter in the phase-encoding direction
Read - Offcenter in the readout direction
Shift - Offcenter in the slice selection direction

CAUTION

When exchanging image data generated with the **Numaris** predecessor software, please note the following: ***syngo*** **MR** and **Numaris** use different patient coordinate systems. As a result, the slice position and orientation may have different signs.

➪ The selected position mode is maintained after the current positioning. When you open the **Position** dialog window the next time (even from another protocol), the position mode previously selected is still applied.

Keyboard operation

You can use both the mouse and the keyboard to select parameter cards from the stack or select and edit parameters.

The table below lists all actions in the parameter card stack that may be performed via the keyboard as well.

Action	Keyboard operation
Go to the next parameter card	Ctrl + right arrow
Go to the previous parameter card	Ctrl + left arrow
Go to the next parameter sub-card	Ctrl + Shift + right arrow
Go to the previous sub-card	Ctrl + Shift + left arrow
Go to the next parameter	Tab
Go to the previous parameter	Shift + Tab
Increase numerical value	Up arrow
Decrease numerical value	Down arrow
Accept numerical value	Enter or continue to next parameter (Tab)
Scroll to next parameter in the parameter set	Up arrow or right arrow
Scroll to previous parameter in the parameter set	Down arrow or left arrow
Scroll to first parameter in the parameter set	Home
Scroll to last parameter in the parameter set	End
Activate/deactivate check box	Enter or space bar
Expand/collapse selection list	Enter
Select entry from selection list	Up/down/right/left arrow button or Home - to the first entry or End - to the last entry

Action	Keyboard operation
Apply entry from selection list	Return or Esc or continue to next parameter (Tab)
Select button (e.g., for coil selection)	Enter or space bar
Toggle check box or disable button selection	Press Esc key while at same time pressing Return or Space bar

Accepting measurement parameter settings

After adapting the scan parameters of the open protocol to your requirements, save the new settings and close the protocol.



✧ Click the **Apply** button to accept your changes.

Or

✧ Select **Edit > Apply** from the main menu or **Apply** from the context menu of the program control (right mouse button).

When protocol reaches the top of the job list, it is loaded into the scan system. Depending on the start mode selected, the system starts scanning automatically or waits for your start command.

Copying measurement parameters

After adjusting measurement parameters, you can apply them to other protocols not currently open.

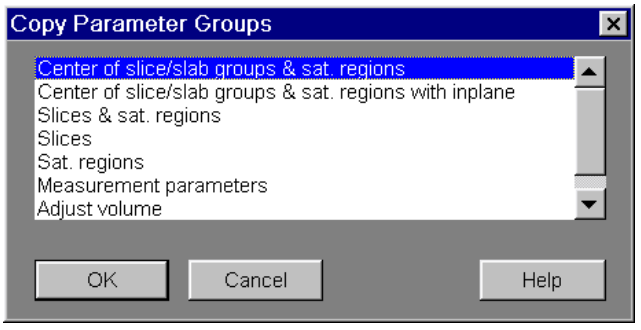
You can copy the settings and values of entire parameter groups from one protocol to another. This saves time during parameter entry and completion of the protocols.

✧ Open the pending protocol to which you want to apply the parameters of another protocol.
→ Page C.4–2, *Opening a protocol*

✧ Select the protocol containing the parameters you wish to copy (single click in the program control).

✧ Select **Queue > Copy Parameter** from the main menu or **Copy Parameter** from the context menu.

The **Copy Parameter Groups** dialog box is displayed.



✧ Select a parameter group and click **OK** to copy the corresponding settings.

The selected parameters are applied to the *open* scan protocol.

Parameter groups

The following table lists the parameters of the different parameter groups.

➪ Please note that some parameters are assigned to several parameter groups.

Parameter group	Parameters
Center of slice/slab groups & sat. regions	Coil elements Position, orientation of slices and slabs Position, orientation and thickness of saturation regions In-plane rotation angle of slice groups Position, orientation, rotation, and thickness of the navigators Extent of navigators in the phase-encoding and read-out direction
Center of slice/slab groups & sat. regions with plane rotation	Coil elements Position, orientation and rotation of slices and slabs Position, orientation and thickness of saturation regions In-plane rotation angle of slice groups Position, orientation, rotation, and thickness of the navigators Extent of navigators in the phase-encoding and read-out direction

Parameter group	Parameters
Measurement parameters	Coil elements Phase FOV Read FOV Slice thickness Base resolution Phase resolution Phase oversampling Slices per slab Slice resolution Slice oversampling Number of slice/slab groups Number of slices (or slabs) per slice group (or slab group) Position, orientation, distance factor, phase-encoding direction of the slice/slab groups Inplane rotation angle of slice groups Number of sat. regions Position, orientation, thickness of the saturation regions Special sat. regions (parallel or tracking sat. regions) including thickness and distance (gap) Saturation mode VOI (for spectroscopy scans) Interpolation resolution (for CSI protocols) Position, orientation, rotation, and thickness of the navigators Extent of navigators in the phase-encoding and read-out direction
Slices	Coil elements Slice thickness Slices per slab Number of slice/slab groups Number of slices (or slabs) per slice group (or slab group) Position, orientation, distance factor of the slice/slab groups Inplane rotation angle of slice groups Position, orientation, rotation, and thickness of the navigators Extent of navigators in the phase-encoding and read-out direction

Parameter group	Parameters
Saturation	Number of sat. regions Position, orientation, thickness of the saturation regions Special sat. regions (parallel or tracking sat. regions) including thickness and distance (gap) Saturation mode
Slices & sat. regions	Coil elements Slice thickness Slices per slab Number of slice/slab groups Number of slices (or slabs) per slice group (or slab group) Position, orientation, distance factor of the slice/slab groups Inplane rotation angle of slice groups Number of sat. regions Position, orientation, thickness of the saturation regions Special sat. regions (parallel or tracking sat. regions) including thickness and distance (gap) Saturation mode Position, orientation, rotation, and thickness of the navigators Extent of navigators in the phase-encoding and read-out direction
Adjustment volume	Shim mode Position, orientation, extent of the adjustment volume
Everything	All parameter settings including sequence

Inconsistencies

In case of inconsistencies between the parameter settings of the source and target protocol, the **Please Confirm** message window is displayed.

This message window appears in the following cases:

❏ At least one parameter of the group to be copied cannot be copied or not copied completely.

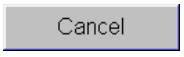
And/or

❏ At least one additional parameter has to be adapted to allow copying of the parameters of the selected group (e.g., number of concatenations).



✧ Click **OK** to accept the new settings and correct inconsistencies.

Or



✧ Click **Cancel** to discard the settings.

✧ Enter the measurement parameters manually.

Saving the Job List

You can save a scan program in the joblist under a new program name after adapting its protocols. This allows you to reuse protocols adapted during the examination for subsequent examinations.

✧ Select **Queue > Save As Program** from the main menu or **Save As Program** from the context menu of the program control (right mouse button).

The **Exam Explorer** is opened and displays the **Save Program As [Customer Tree]** dialog box. You can enter a name for the new scan program and assign it to an examination region and examination.
→ Page C.16–61, *Saving the scan program under a new name*

Saving a single scan protocol

Instead of the entire job list, you can also save individual protocols in the job list. This involves transferring the protocol to the Exam Explorer.

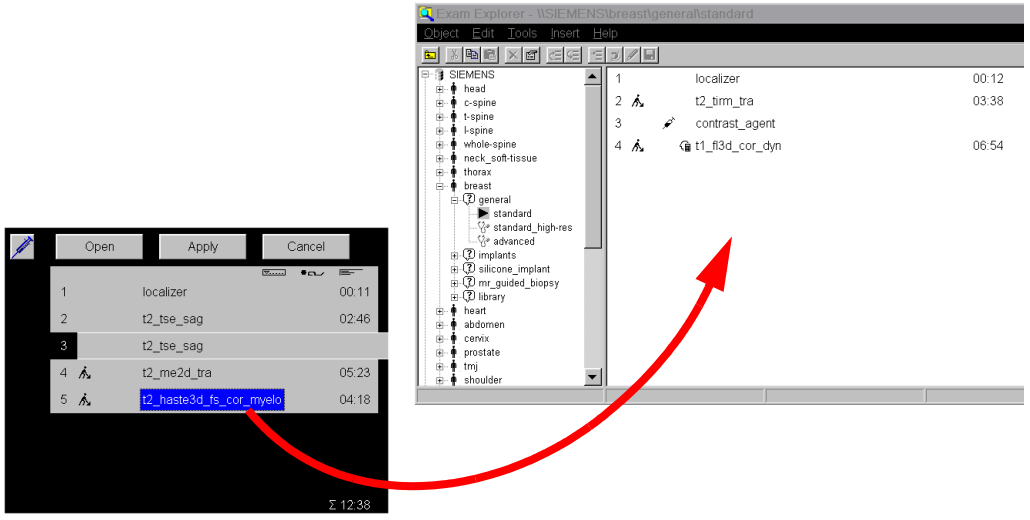
✧ Open the **Exam Explorer**.
→ Page C.16–3, *Calling up the Exam Explorer*

✧ In its navigation area, open the data level for the scan program where you want to save to the protocol.
→ Page C.16–12, *Finding a scan program*

➪ You can only save the protocol in a scan program of the customer level (USER).

✧ Click the required protocol in the job list of the **Exam** task card.

✧ Keeping the *left* mouse button pressed, drag-and-drop the selected scan protocol into the content area of the Exam Explorer.



✧ Select **Object > Save** from the main menu of the **Exam Explorer**.

Or



✧ Click this button on the toolbar.

The protocol transferred to the **Exam Explorer** is saved with the corresponding program.

CHAPTER C.6

Performing a Routine Examination

After completion of exam-related preparations, you acquired a localizer and graphically planned the slice or slab groups for the examination in the reference images. Any necessary changes to scan parameters have been made.
→ Page C.1–4, *Procedure for routine scanning*

⇨ In the case of the **"Symphony Mobile"** system, an automatic frequency adjustment is performed before each scan. For time-critical scans such as Care Bolus this automatic frequency adjustment can be deactivated.
→ Page B.2–7, *Suppression of standard frequency adjustment*

Routine scan procedure

Once you have finished adapting the parameters of the first protocol, apply the new settings.

The protocol is closed and the system automatically starts running this protocol. Once this protocol has been completed, the system automatically starts running the next protocol unless it is marked by an icon as not ready for scanning.

Utilizing scan times

Protocols usually take some time to run. This time can be used to prepare the following protocols or for postprocessing tasks.

After the initial scans have started, you can edit the portion of the job list not yet measured using the program control. You can complete the parameters of pending protocols and plan the examination sequence.
→ Page C.6–39, *Processing the job list while scans are being performed*

You can also use the time to view, evaluate, comment on, or film images of a series that has already run.
→ *syngo* Operator Manual

Stopping an examination

If the measurement procedure is interrupted (e.g., by patient movement) or you determine that all necessary images have been scanned, you can interrupt scanning at any time.

This does not affect the remaining program sequence.

Repeating scans

Protocols that have been interrupted can be repeated at any time. You can decide whether to repeat the most recent protocol only or a complete section of the job list.

Starting scans manually

Breath-hold scans to prevent motion artifacts are started manually. The protocol is automatically loaded into the scan system but does not start until you manually give the command.

For kinematic examinations, you can run protocols any number of times. In this case, start a protocol manually and run it as many times as required to complete all necessary scans.

Contrast medium examinations

For examinations using contrast agent, the scan program includes pauses that allow you to administer the contrast agent.
→ Page C.7–1, *Using a Contrast Agent*

Alternatively, you can perform contrast agent examinations using multiple scans.

→ Page C.6–24, *Starting a protocol manually - multiple scans*

Scans with patient instructions

Before and after measurements, you can automatically add patient instructions in different languages via protocols or manually play back voice-overs.
→ Chapter C 11, *Patient Instructions*

Automatic position correction

If you have a license for **AutoAlign**, the system performs slice positioning for head examinations, automatically and reproducibly, independent of the positioning of the patient's head.
→ Page C.18–1, *Automatic Position Correction*

Jobs

If you have the necessary license and your system is connected to a hospital information system (HIS), you can receive jobs for your MR system from the HIS via the network. When you register a patient, a reference to the job is created in the form of steps that appear as a range marker in the job list. All services rendered are automatically entered in the job. The information for the procedure step is now available for further processing within the hospital.
→ *syngo* Operator Manual

Conflict management

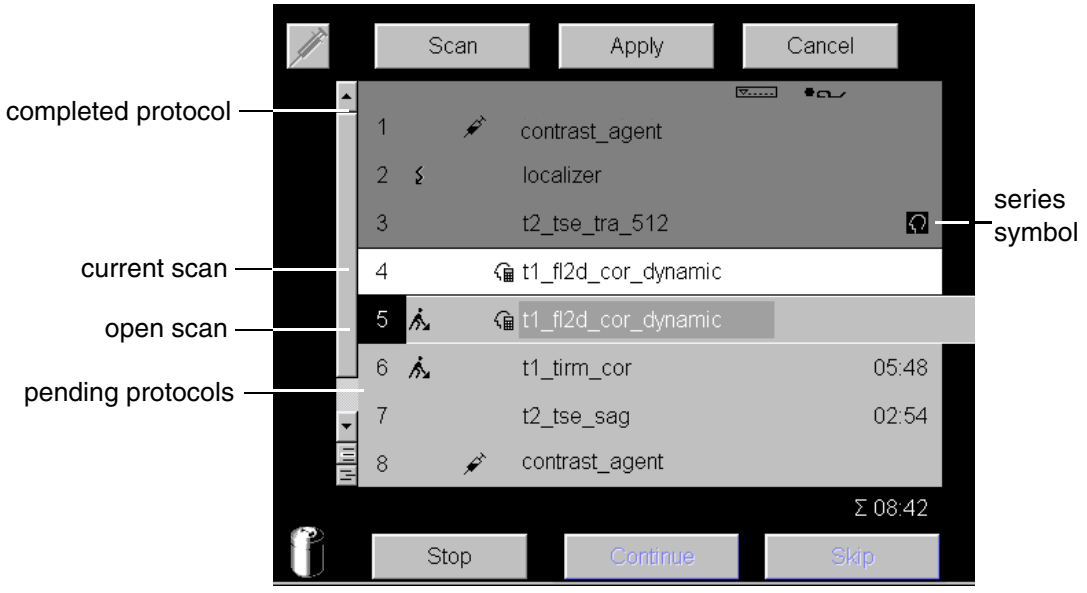
Before and during a scan, inconsistencies may occur between the scan program and the actual settings on the scan system (e.g., the coils actually connected do not match the coil configuration on the **System Common** parameter card). The system detects inconsistencies and helps you to eliminate them by displaying messages.

Displaying the queue in the program control

The program control allows you to trace and modify the course of an examination including all scans.

The program instructions are color-coded depending on the processing status:

- ❏ Executed protocols have a dark-gray background
- ❏ Protocols that are currently running are shown with a white background
- ❏ Opened protocols are marked with bars in light gray that are pushed to the right
- ❏ Protocols that are pending are shown against a light gray background



Tooltip

If you position and hold the mouse pointer over the name of a program instruction, a tool tip displays the following information:

❏ The full name of the program instruction.

❏ A short comment if entered in the properties dialog box.

Icons to identify the protocols

Icons before or after the protocol names identify additional properties of the program instructions.



A protocol marked with a construction worker icon cannot be automatically started at this processing state because the parameters are still incomplete.

The incomplete data usually relates to the positioning of the slices to be measured. All other data are typically predefined by the scan program.
→ Page C.4–1, *Positioning Slices*



A protocol identified by a flagman needs to be started manually. This is required for breath-hold scans, for example.
→ Page C.6–1, *Performing a Routine Examination*



A protocol identified by a flagman with several flags can be started and measured several times in a row. This is required for kinematic examinations, for example.
→ Page C.6–1, *Performing a Routine Examination*



This symbol identifies protocols that involve automatic image postprocessing following the scan, e.g. adding or subtracting series.



If you have planned a contrast agent pause for your scan program, the subsequent scans will be marked with a syringe icon indicating contrast agent scans.
→ Page C.6–1, *Performing a Routine Examination*



On a protocol with this icon, patient instructions are automatically played before and/or after scanning.



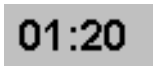
If you insert a protocol in the job list that is referenced with automatic patient instructions for which no voice output is available, the protocol is identified with this icon by the program control following a corresponding message.
→ Page C.6–55, *Program instruction with a patient instruction*



A protocol that is the target of a copy reference for which the copy reference exists is marked with this icon. The number next to the icon indicates the source of the copy reference.



Copy references crossed out in red are not valid. Invalid copy references occur when parameters change or when there are parameter conflicts between the source and target protocol. They cannot be included in a scan.



When you load a scan program into the job list for the first time, the estimated scan time is displayed in addition to all program instructions. Protocols displaying scan times are pending.

The scan time displayed next to a multiple-loading protocol indicates the duration of a single repetition.

The scan time is also shown in the Exam Explorer and the protocol overview.



Once program instructions are processed and the images have been calculated, the series icon is displayed to the right of the protocol name in the program control. This icon indicates that the protocol has been successfully completed.



If two or more series were created with one protocol, this is shown by an icon indicating several consecutive series.
→ Page C.3–5, *Loading a series from the program control*



Protocols that were canceled or skipped are identified by a lightning icon to the left of the protocol name in the program control.
→ Page C.6–1, *Performing a Routine Examination*

Information in the status bar

The status bar shows information while a scan is in progress.

- ❏ Information about the current status of the program control is shown in the left section (e.g. that the patient has not yet been positioned, program instructions have not yet been inserted, or the program control is waiting for input/actions).
- ❏ Results and error messages are shown in the middle section.

Scan is aborted due to a system error

If a system error occurs during a scan, the scan will be aborted automatically and marked as such.



Indicates that image calculation has been canceled.



Indicates that calculation has been canceled by the scanner.

Range markers

Within the job list, range markers provide information about different properties that are valid across multiple protocols.



This range marker indicates whether and which image comments have been entered for the scanned images.
→ Page C.9–13, *Editing an image comment*



This range marker indicates the body region examined.
→ Page C.9–3, *Editing a body region instruction range*



This range marker indicates that a job exists for the examination.
→ Page C.9–5, *Editing a work step in the instruction area*

The range marker for a step can have one of the following modes:



The step has been completed.



The examinations of a step have been canceled.

Scan procedure for a routine examination

After graphic slice positioning in the reference images and checking the routine scan parameters of your first protocol, you can apply the settings.
→ Page C.5–86, *Accepting measurement parameter settings*

For the most part, routine examinations run automatically.

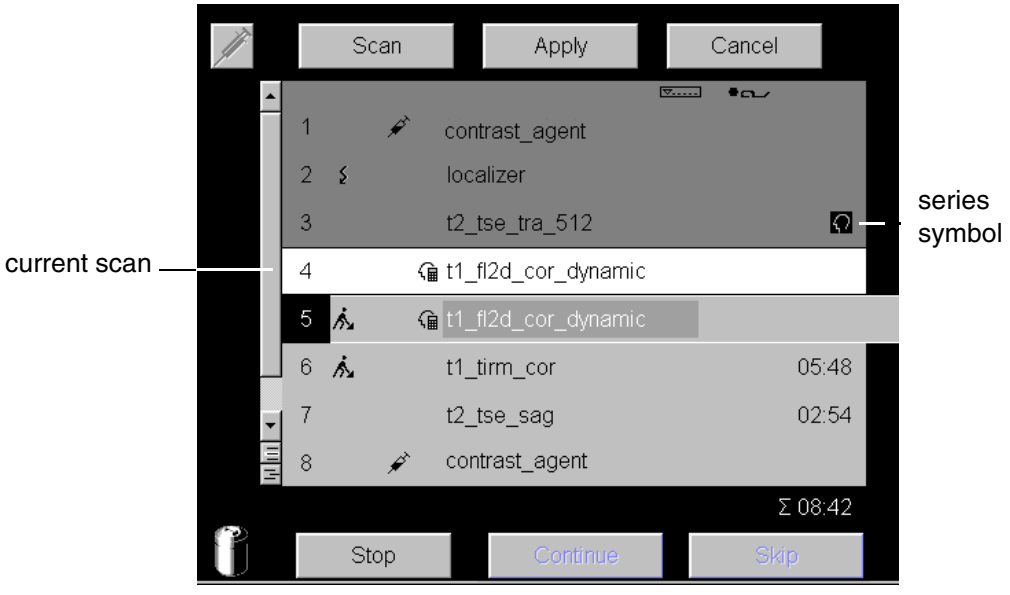
Running Complete Protocols

After completing the graphic slice positioning for the first protocol, you close the protocol. It is loaded into the scan system. Scanning will start automatically.

While the scan is in progress, the protocol is displayed with a white background in the job list. The remaining scan time is indicated in the status bar.

The images of the protocol are reconstructed immediately while scanning is in progress. After image reconstruction has been completed, the series icon is displayed.

If the next protocol has executable status (no construction worker icon), it will start immediately following the first protocol.



Completing and running a protocol with a construction worker icon

A protocol cannot be started automatically unless the slice positions have been adjusted in the reference images.



These protocols are marked by a construction worker icon in the job list.

Incomplete protocols ready to be run are opened automatically.

✧ Position the slices or slabs.

✧ Make necessary parameter changes on the cards of the parameter card stack.



✧ Click the **Apply** button.

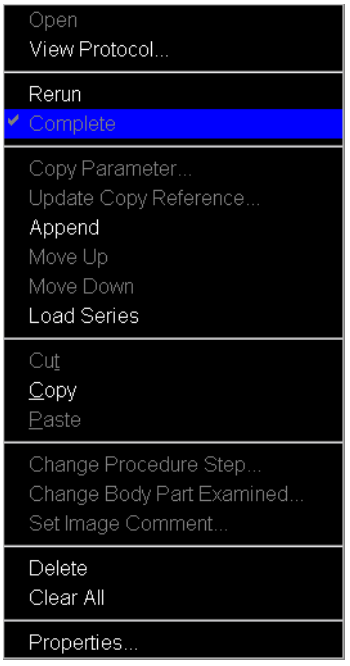
The protocol is closed and the scan is started.

Setting a protocol to executable without checking

You can mark a scan protocol identified by a construction worker icon as "executable" without checking it.

✧ Select the protocol from the job list.

✧ Right-click and select the **Complete** option from the context menu. A checkmark appears next to the menu item.



Or

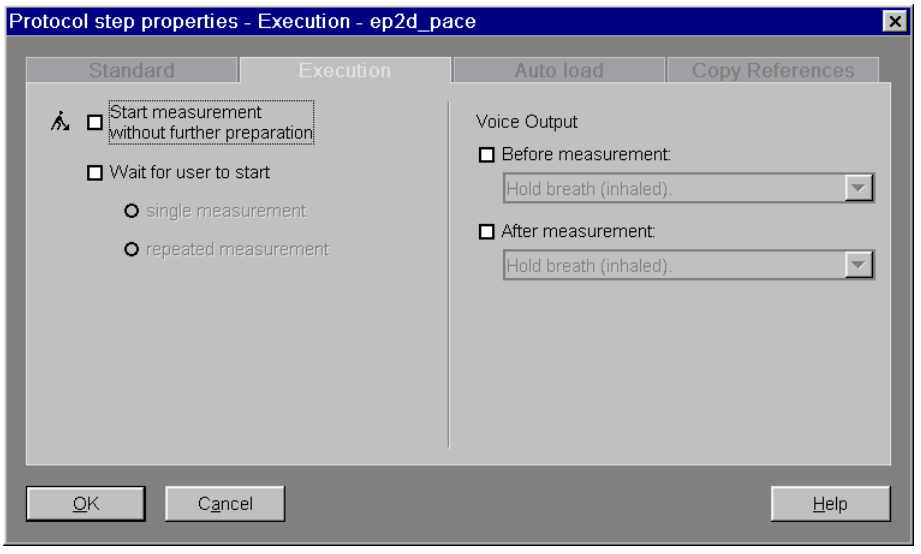
✧ Select **Edit > Properties** from the main menu or **Properties** from the context menu.

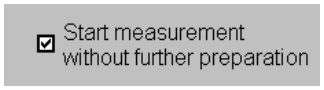
Or

✧ Press the **Alt + Return** keys on your keyboard.

The **Protocol step properties** dialog box opens.

✧ Go to the **Execution** subtask card.





✧ Select the **Start measurement without further preparation** check box.

✧ Click **OK**.

The protocol is set to executable and the construction worker icon is removed. The protocol may now be started.

You can also use this method to manually reset scan protocols with "executable" parameters to "not executable." Deselect the check box. The protocol will stop when it is ready to run.

NOTE

If you set a protocol to executable without checking to start the protocol immediately, the table immediately moves to the table position entered in the protocol if it does not match the table position currently set.

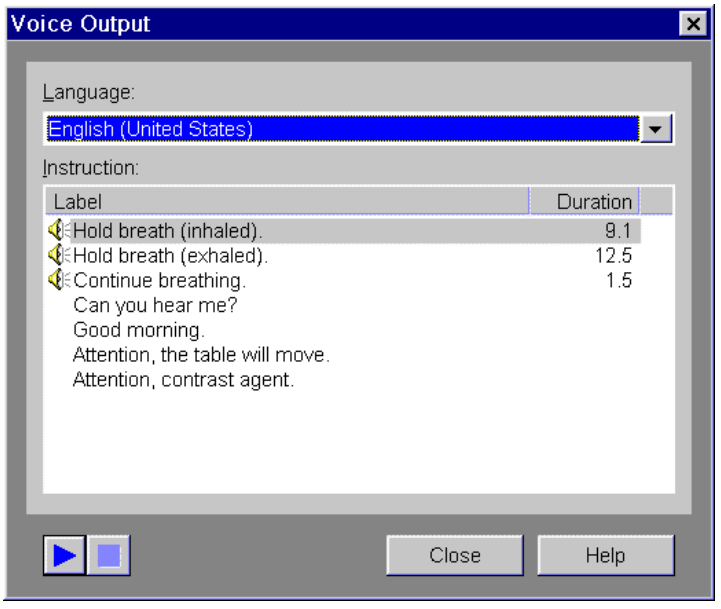
Playing back patient instructions manually

If you want to play back breathing or other patient instructions in the examination room, you can use the voice outputs. They are available in various languages.

Playing back an existing voice output

✧ Select **Queue > Voice Output > Play...** from the main menu or **Voice Output** from the context menu in the outer area of the program control.

The **Voice output** dialog box opens.



✧ Select the language from the selection list.

✧ Select the required patient instruction.



✧ Click the **Play back** button.

The selected voice output will be played back.

Recording patient instructions

If the list of voice outputs does not contain the patient instruction you require, you can record it yourself.
→ Page C.11–21, *Changing a voice output*

Voice outputs can be recorded or edited only if no patient is currently registered.

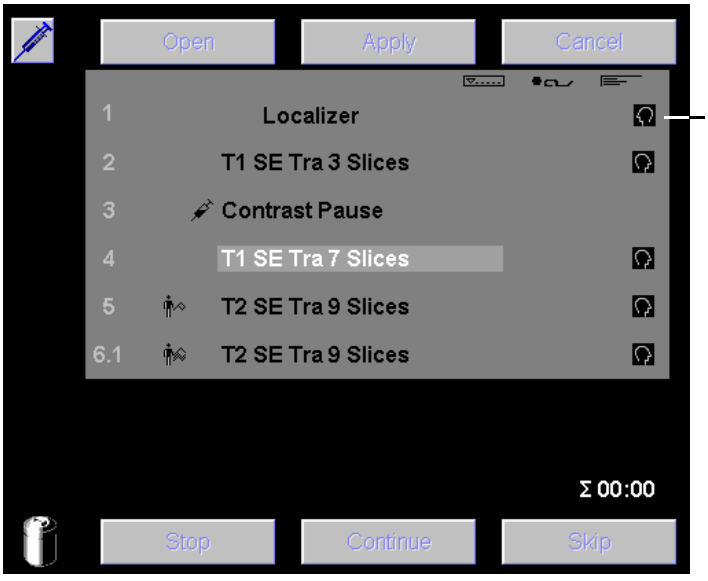
➪ If you have already registered the patient to be examined, close the examination again if necessary.
→ Page C.6–20, *Closing the patient*

Closing a routine examination

An examination is complete after all program instructions in the program control have been processed and all images have been reconstructed.

All protocols completed

All program instructions are now marked with the series icon.



Once you have determined that you do not need to perform additional scans or repeat protocols, you can end the examination.

Moving the table out of the magnet

The patient table is moved completely out of the magnet bore.

Use the **Table Positioning** dialog box or move the patient table using the buttons on the control unit near the magnet bore.
→ Chapter C 8, *Positioning the Patient Table* and *System Manual*

Closing the examination

The current examination is complete once you have moved the patient table into the HOME position, i.e., completely out of the magnet.

✧ You can now return the patient to the ward.

Subsequently, you can register a new patient.

Completing a job

Once all scans of the examination and all planned postprocessing steps have been completed, and the series have been transferred to the film sheet or printed, you can complete the procedure step.
→ Page C.6–20, *Closing the patient*

Closing the patient

If you release the last patient at the end of the working day, reset the program control to its original state.

✧ Select **Patient > Close Patient** from the main menu.

Or

✧ Right-click the name of the patient in the program control and select **Close Patient** from the context menu.

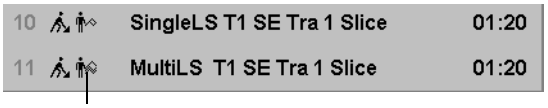
The job list is removed from the program control. All functions of the program control are disabled.

➪ If you need to correct the data of a registered patient during an examination, you have to remove the patient from the job list first by selecting **Close Patient**.

Starting a protocol manually

Some protocols should be started manually, e.g. protocols requiring breath-hold commands. It is helpful to have the scan system stop after the adjustments and wait for a manual start command.

Protocols that have to be started manually are marked by a flagman icon in the job list.



➪ The start mode of a protocol (manual or automatic) can be set using the **Execution** subtask card in the **Protocol step properties** dialog box.

NOTICE

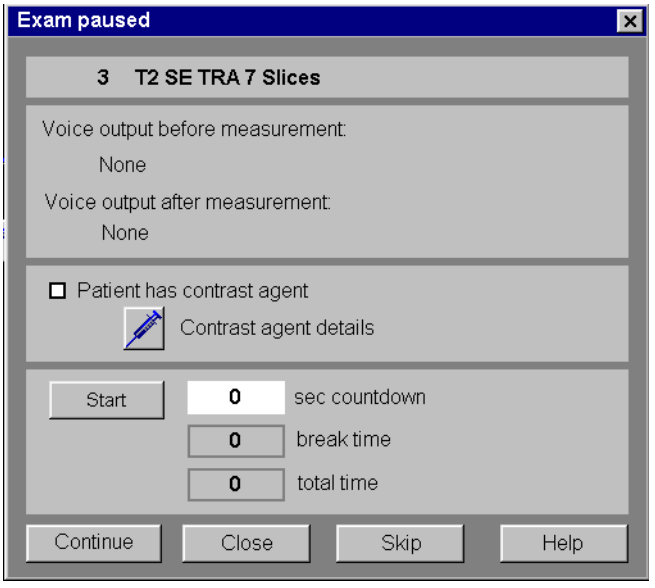
Multiple breath-hold scans are always started from the **Inline Display**.
→ Page C.10–27, *Starting multiple breath-hold scans*

Starting a protocol manually - single scan

Manual protocols can be started and run only once or several times in a row.

A protocol that you want to start manually and run once is automatically loaded into the scan system. After completion of adjustment, the program control waits for your start command

The **Exam paused** dialog box is displayed.



Give the breath-hold instructions. Click **Continue** to start the scan. The system does not have to load parameters or perform adjustments. This saves time and reduces patient stress.

➪ You can give breath-hold instructions automatically before or after the scan.
→ Page C.12–9, *Playing back voice output*

Starting the measurement



✧ Click the **Continue** button to start scanning immediately and close the **Exam paused** dialog box.

Or



✧ Click the **Close** button to close the **Exam paused** dialog box.

And



✧ Click the **Continue** button in the program control or select **Continue** from the context menu.

Canceling the measurement



✧ Click the **Skip** button to close the **Exam paused** dialog box. The loaded protocol is not run and the next program instruction is initiated.

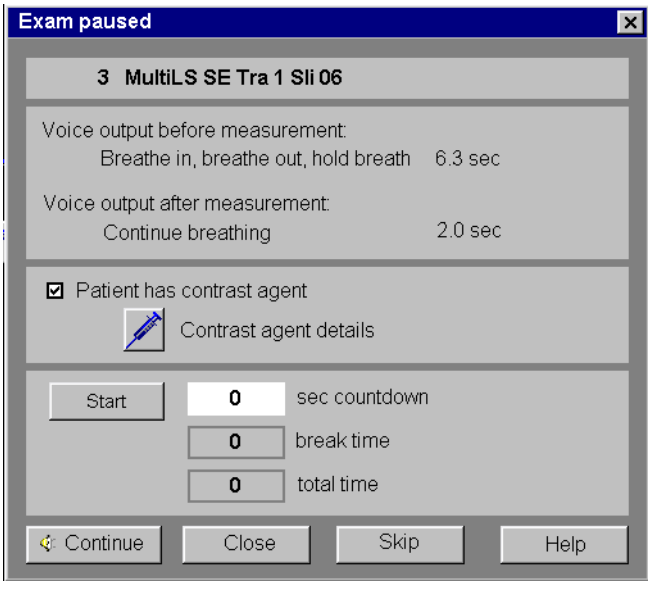


The protocol is marked "canceled."

Starting a protocol manually - multiple scans

Some protocols have to be started manually several times (e.g. a contrast agent, breath-hold examination of the liver). A series of the region of interest is acquired at regular intervals to document the progress of contrast agent uptake. The protocol is repeated using the breath-hold technique until all necessary data have been acquired.

The **Exam paused** dialog box opens as soon as the program control comes across this protocol while the program instructions are running.



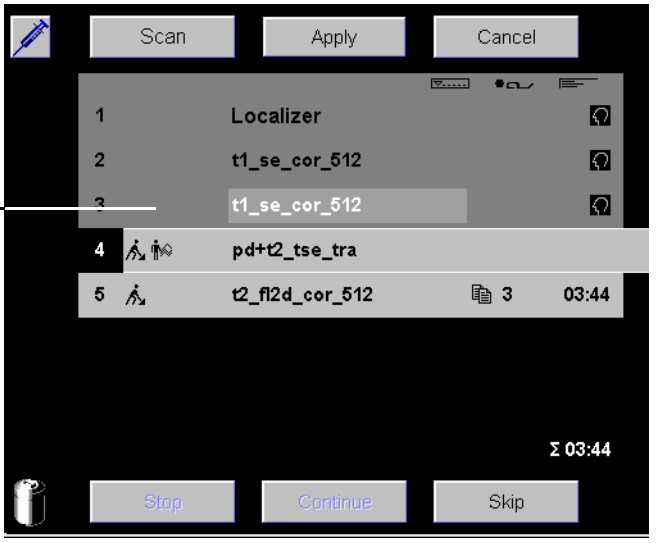
➪ Another application for multiple scanning includes kinematic examinations (e.g. when examining a joint).

Starting the protocol



✧ Click the **Continue** button to start the first scan.

The protocol starts.



Icon for multiple loading/starting

The **Exam paused** dialog box closes and reopens once the system is ready for the next scan.

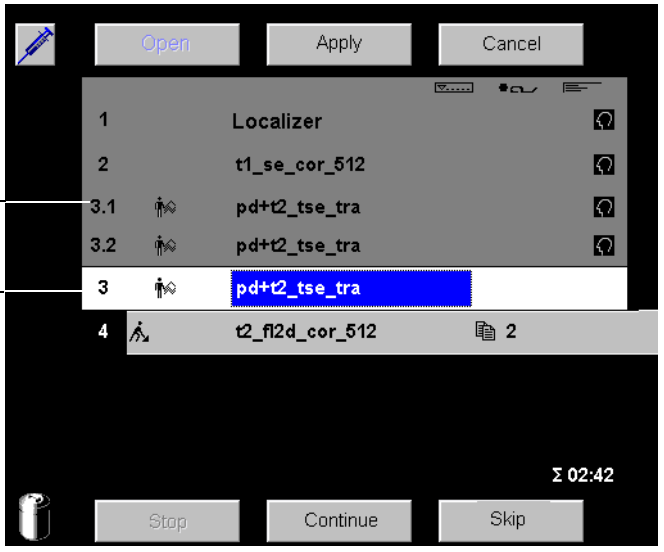
Starting the next measurement

Continue

The protocol parameters and slice position may not be modified during the pause.

✧ Next, click the **Continue** button again in the **Exam pause** dialog box to run the protocol a second time.

The same scan protocol as before is added to the job list and measured a second time.



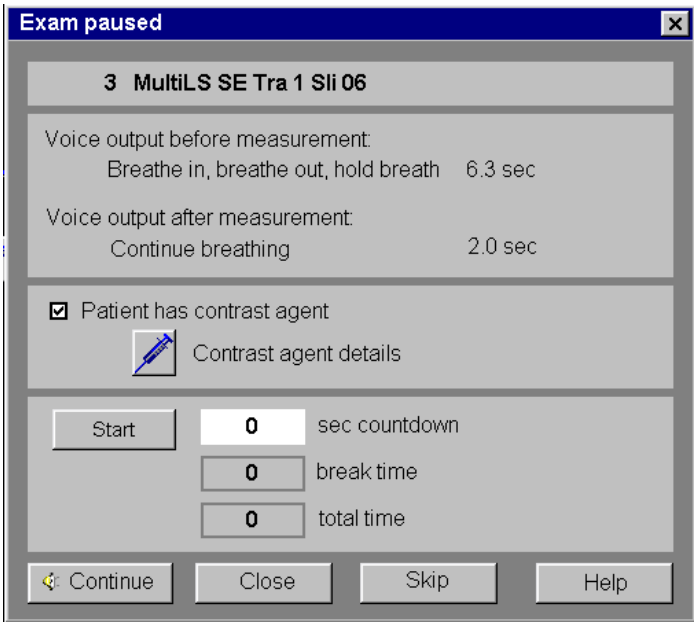
Completed protocol

Next running protocol

Protocols that have already run are numbered and appear in front of the multiple protocol. This shows you the sequence of scans.

Performing measurements with countdown

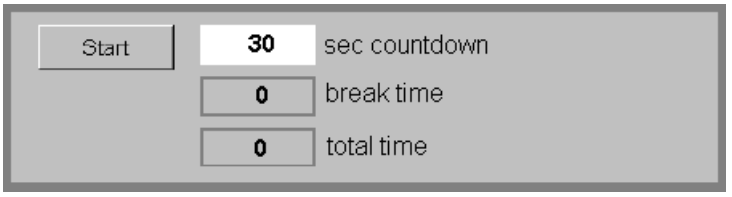
Contrast-enhanced examinations often require a precisely timed sequence of scans, especially following contrast agent administration.



Three fields are available to help you time the required sequence of successive scans:

- The **countdown** input field helps you plan the start of the next scan.
- The **break time** display field indicates the time since the end of the previous scan.
- The time elapsed since the start of the first scan of the current multiple scan is displayed in the **total time** display field.

✧ Enter the length of the pause in seconds in the **Countdown** field.



✧ Click the **Start** button.

The **Start** button will change to **Hold** and the length of the pause is counted down.

The total time elapsed since the pause dialog box was opened is counted as well and displayed in the **break time** display field.

➪ After the pause, the **countdown** field continues to count the time and displays it as a negative number.

Clicking the **Hold** button interrupts the timer in the **countdown** field or stops it after the pause. This allows you to reenter a pause time.

➪ Interrupting the countdown does not interrupt the **break time** and **total time**.

Interrupting scanning

Sometimes it is necessary to stop a scan, e.g. if the patient moves.



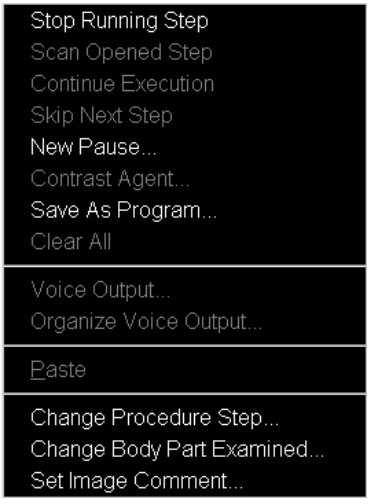
✧ Click the **Stop** button in the program control.

Or

✧ Select **Queue > Stop** from the main menu.

Or

✧ Right-click the outer area of the program control and select **Stop Running Step** from the context menu.



Or

✧ Press the **F3** key on your keyboard.

The scan will be stopped immediately. The protocol is stopped and marked with a cancellation icon (lightning).



➪ You can also interrupt a measurement in the examination room by using the STOP button on the control unit next to the magnet bore.
refer to the System Manual

Scan is aborted due to a system error

If a system error occurs during a scan, the scan will be aborted automatically and marked as such.




These icons appear in the status bar.
→ Page C.6–8, *Scan is aborted due to a system error*

Stopping one scan and starting the next

You may stop a scan in progress and immediately start the next scan. This is used, e.g. during contrast agent uptake to subsequently start a high-resolution protocol.

You can monitor the contrast agent uptake with the first localizer. As soon as it becomes visible in the image, you can start the next high-resolution sequence for imaging.

✧ Use the **Stop** button or the menu items to stop the scan in progress.



✧ Click the **Continue** button to start the next scan

Or

✧ Select **Queue > Continue** from the main menu.

Or

✧ Press the **Shift + F3** keys on your keyboard.

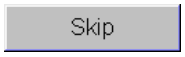
Or

✧ Select **Continue Execution** from the context menu in the (left-hand) outer margin of the program control.

➪ You can also continue the measurement by using the START button at the magnet bore in the examination room.
refer to the System Manual

Skipping a scan instruction

You may skip a program instruction in the job list that has not yet run and is open for editing.



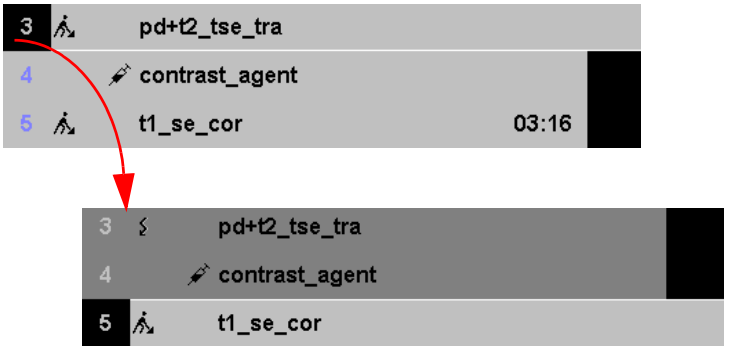
✧ Click the **Skip** button.

Or

✧ Select **Skip Next Step** from the context menu in the left margin of the program control.

The skipped program instruction is marked with a canceled icon (lightning) and has a dark gray background.

You can now resume the examination with the next program instruction.



Repeating scans

You may repeat individual as well as entire sections of previously processed program instructions.

In some cases (e.g., if you need to reposition the patient), it may be necessary to scan the entire job list again.

Repeating a canceled protocol

It is possible to repeat a canceled protocol.

✧ Select the canceled protocol from the job list.

✧ Select **Queue > Rerun** from the main menu.

Or

✧ Select **Rerun** from the context menu.

The protocol is automatically started and processed again.

Repeating previously processed protocols

✧ Select the protocol you would like to repeat.

✧ Select **Add** from the context menu (right mouse button).

Or

✧ Select **Queue > Append**.

The selected program instruction will be copied and appended to the end of the job list.

Repeating multiple program instructions

Similarly, you may rerun several program instructions up to the protocol you have just stopped.

✧ Select the program instruction from which you want to repeat all subsequent protocols.

✧ Select **Queue > Rerun** from the main menu or **Rerun** from the context menu.

The selected protocol will be automatically started and all subsequent, previously processed program instructions will be repeated.

➪ If you skipped the selected protocol the first time, it may still have the status incomplete. This protocol is automatically opened for completion.

Repeating the entire job list

If you interrupted an examination, for example, because of a serious error, you can reset the job list and start the examination again.
(Example: you notice that the patient was not positioned optimally on the patient table and you want to reposition the patient.)

✧ Select the first program instruction.

✧ Select **Queue > Rerun** from the main menu or **Rerun** from the context menu.

All protocols previously processed will be run again.

Defining a new center position

Resetting the table position to zero allows you to start a new series block. The current table position is now defined as the center position.

Setting the table position to zero

✧ Select **Patient > Reset Table Position** from the main menu.

Or

✧ Place the mouse pointer on the patient name in the program control and select **Reset Table Position** from the context menu (right mouse button).

All planning images in the graphic segments and all series symbols in the program control are removed from protocols that have already run.

All protocols ready for measurement are reset to incomplete if indicated as such in the property dialog box. They must be planned again.

The job list in the program control is now ready for scanning again.

Scanning an open protocol more than once

For examinations with scans that differ only slightly in their protocol parameters (e.g. for cardiac and angio applications), you may perform the scans with an open protocol.

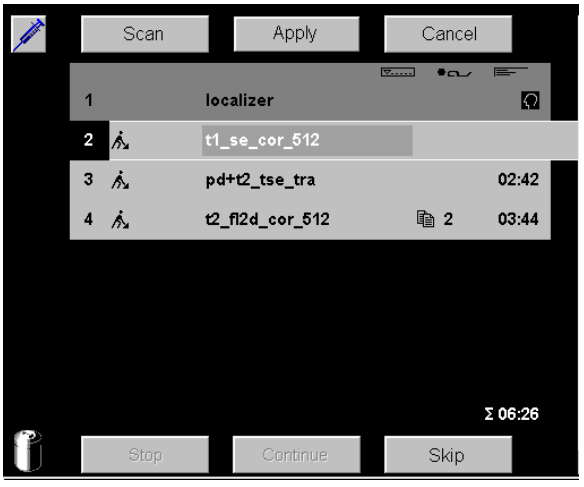
➪ When you repeatedly scan an open protocol, it is not necessary to close protocols following each parameter change with **Apply** and then reopen the job list again.

✧ Change your parameters as required.

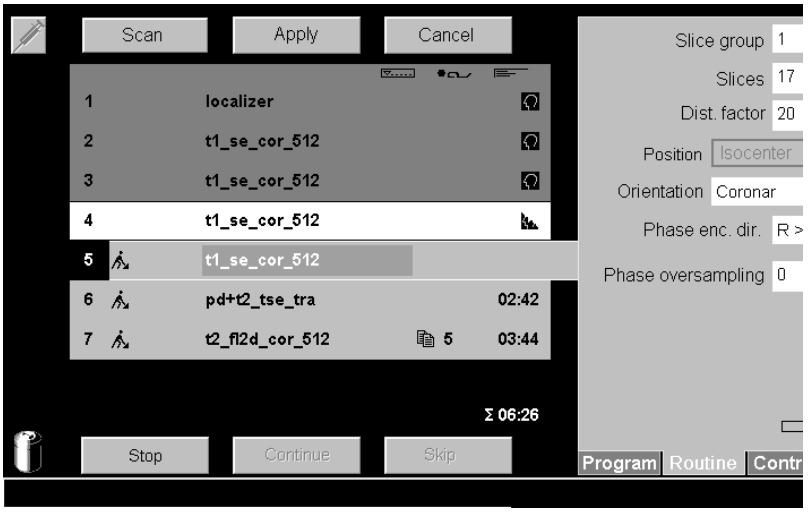
✧ Select **Queue > Scan Opened Protocol** from the main menu or **Scan Opened Step** from the context menu in the left (outer) margin of the program control

Or

✧ Click the **Scan** button in the Program Control.



A copy of the open protocol is generated and inserted in the job list below the open protocol.



The protocol is complete and ready to run immediately. The protocol will be executed as soon as it reaches its turn in the queue.

➪ You may repeat this process as often as necessary.

Processing the job list while scans are being performed

Scanning individual protocols usually takes some time. You can reduce the duration of the overall examination by effectively using the scan time for postprocessing and preparing the scan sequence. This eliminates unnecessary stress from the patient.

Completing protocols

While the first protocols are in progress, you may check and complete the parameter settings of subsequent protocols. Thus you can avoid unnecessary pauses between individual scans.

Opening a protocol

✧ Double-click a protocol in the section of the job list that is still pending.

Or

✧ Select the protocol and click the **Open** button.

The protocol opens. Its measurement parameters are displayed in the parameter card stack. You may add to these parameters or modify them, if necessary.



✧ Then click the **Apply** button.

The protocol closes. It is now complete and executable.

Opening the next protocol for editing

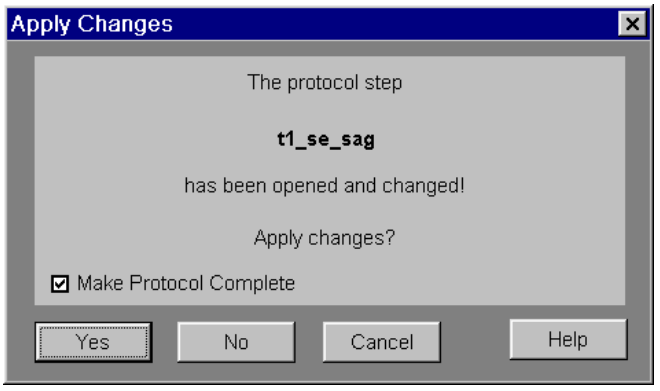
Even if a protocol is open, you can open and edit an additional program instruction from the part of the job list that is still pending. Any changes you have made must be saved first.

✧ Double-click another protocol in the section of the job list that still needs to be excecuted.

Or

✧ Select the protocol and click the **Open** button.

The already opened protocol is closed, and the **Apply Changes** dialog box appears (even if you have not made any changes).



✧ Select the **Make Protocol Complete** option to "complete" the program instruction.

➪ If this option is not activated, you must open the protocol again before scanning and set it to complete.

✧ Click **Yes** to accept the changed parameter settings of the protocol last opened.

The program instruction is now ready to run.

Or

✧ Click **No** to reject the parameter changes.

Or

✧ Click **Cancel** to continue editing the last protocol to be opened.

Viewing parameters of protocols previously run

You may also view the parameters of protocols that have been run already. This enables you to compare the parameters of previous protocols with the program instructions to be run.

✧ Double-click a previously scanned protocol.

Or

✧ Select a previously scanned protocol by clicking it.

✧ Select **Edit > View Protocol** from the main menu or **View Protocol** from the context menu (right mouse button).

The **Step Protocol number- Protocol name (read-only)** window opens. The parameters may be viewed but not changed.

➪ Move the window across the screen so that the parameter card stack is visible. This enables you to compare the measurement parameters of a previously scanned protocol with those of a protocol still to be performed.

Applying parameter settings

To apply the parameter settings of one protocol to another protocol, copy the parameter settings or set a copy reference.

Copying parameters from a protocol

✧ First open the (target) protocol into which you want to copy the parameters (double-click).

✧ Select the (source) protocol from which you wish to transfer the settings (single-click).

✧ Select **Queue > Copy Parameter** from the main menu or **Copy Parameter** from the context menu.

✧ In the **Copy Parameter Groups** dialog box, select the parameter group with the settings you want to copy.
→ Page C.5–87, *Copying measurement parameters*

➪ It does not matter if the source protocol is positioned behind the target protocol in the job list.

Copying parameters from an image in the GSP segment

You may also select a GSP segment for copying parameter settings, if the GSP segment contains an image, the protocol of which is still pending in the job list.

- ✧ First open the (target) protocol into which you want to copy the parameters (double-click).
- ✧ Place the mouse pointer on the GSP segment containing the image.
- ✧ Select **Copy Parameter** from the context menu in this segment.
- ✧ In the **Copy Parameter Groups** dialog box, select the parameter group with the settings you want to copy.
  → Page C.5–87, *Copying measurement parameters*

Parameter conflicts may occur on copying parameters settings. A message box will indicate the conflict.
→ Page C.6–49, *Inconsistencies in parameter settings*

Setting a copy reference

Copy references provide another way of transferring parameter settings from one protocol to another. This simplifies manual copying of parameter settings.

✧ Select a pending target protocol from the section of the job list.

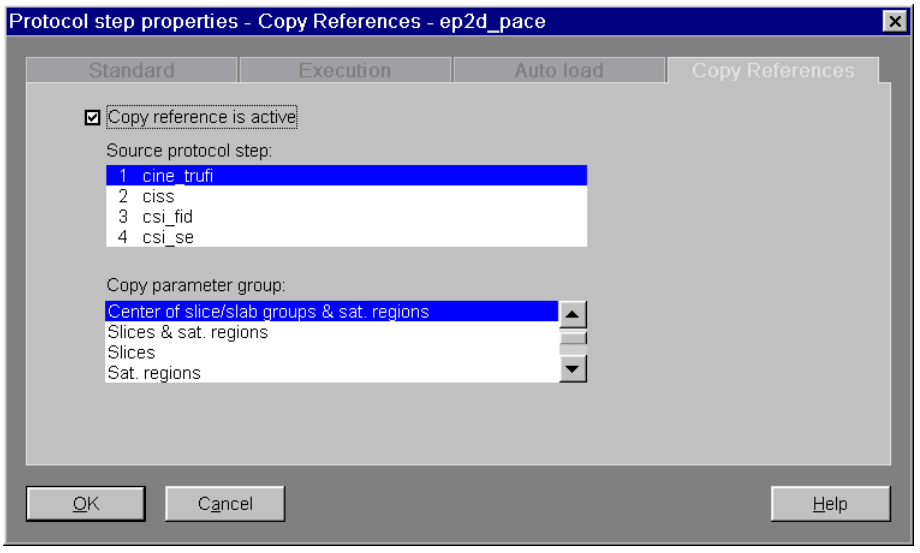
✧ Select **Edit > Properties** from the main menu or **Properties** from the context menu.

Or

✧ Press the **Alt + Return** keys on your keyboard.

The **Protocol step properties** dialog box opens.

✧ Go to the **Copy References** subtask card.



✧ Check the **Copy reference is active** check box.

Once the copy reference has been activated, the **Source protocol** and **Copy parameter group** lists are available.

✧ In the **Source protocol step** list, select the protocol with the parameter settings you want to copy.

This list contains all the protocols located **in front of** the selected protocol in the scan program that are not the target of a copy reference.

✧ In the **Copy parameter group** list, select the parameters to be copied from the source to the target protocol.

Only parameter groups may be copied with a copy reference, not single parameters.
→ Page C.5–87, *Copying measurement parameters*



✧ Click **OK** to close the **Protocol step properties** dialog box.

The target protocol is now marked by a reference icon in the job list.



Reference symbol



The number next to the reference symbol identifies the source protocol with the settings to be copied.

➪ You cannot see which parameter group has been applied. To view this information you need to reopen the properties window.

Parameter conflicts may occur when setting copy references. A message box will indicate the conflict.
→ Page C.6–49, *Inconsistencies in parameter settings*

Updating a copy reference

If a target protocol has a copy reference, the referenced parameter settings are copied and updated from the source protocol to the selected program instruction.

✧ Select the target protocol with a reference icon.

✧ Select **Queue > Update Copy Reference** from the main menu or **Update Copy Reference** from the context menu.

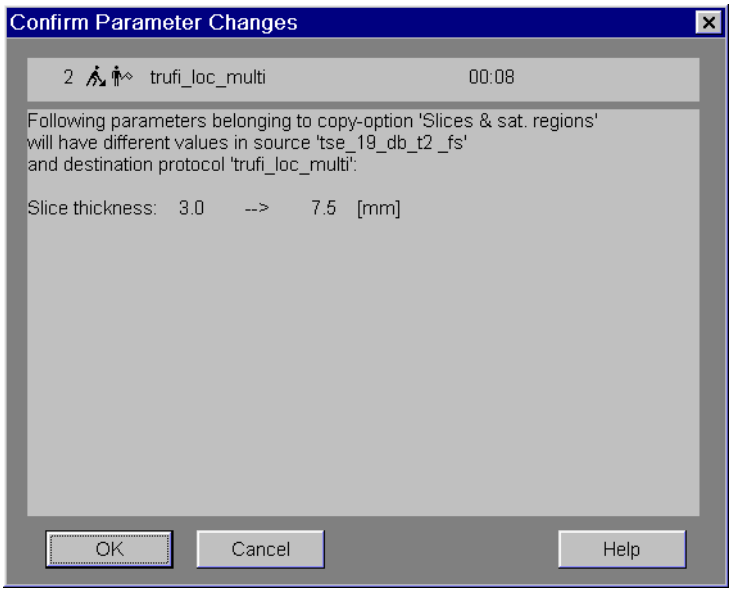


The copy reference will be updated and used in the scan process.

Parameter conflicts may occur when you update parameter settings from a source to a target protocol. A message box will indicate inconsistencies.
→ Page C.6–49, *Inconsistencies in parameter settings*

Inconsistencies in parameter settings

The **Confirm Parameter Changes** message box will be displayed in case of inconsistencies between the source and target protocol for the parameter settings, that is, parameter settings are not valid or executable.



The message box displayed includes proposals for resolving the conflict.

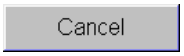
Parameter change by copying



✧ Click **OK**.

The new settings are applied. This resolves the inconsistency.

Or



✧ Click **Cancel**.

The new settings are not applied.

Parameter change by copy reference

✧ Click **OK**.



The suggestion is applied and a valid copy reference is set.

Or

✧ Click **Cancel**.

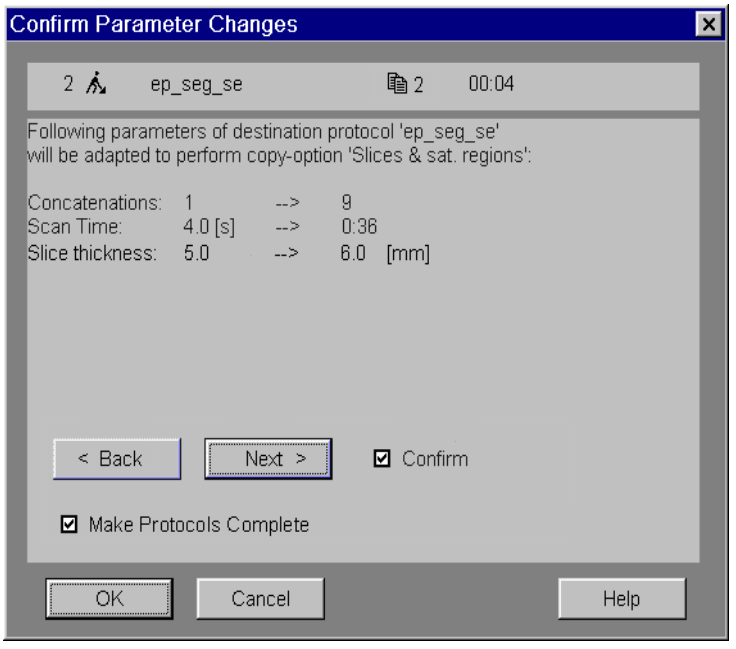


The new settings are not applied. The copy reference has been recorded by the system, however, it is not valid.

Copy reference for multiple target protocols

Updating copy references may cause multiple conflicts when several target protocols are updated.

The message box **Confirm Parameter Changes** appears.



Applying all parameter changes

✧ Select the **Confirm** check box and click **OK**.

The parameters are copied to *all* target protocols.

Not applying parameter changes

You have a choice to not involve certain target protocols in the suggested parameter change.

✧ Use the **<Back** and **Continue>** buttons to switch between target protocols.

➪ If the **Confirm** check box is not selected, the suggested change will not be applied even if you close the window with **OK**.

Making a source protocol complete

✧ Select the **Source protocol complete** check box and click **OK**.

The source protocol is set to complete.

Inserting new scan instructions

You may add further program instructions to the job list in addition to the selected scan program.

Inserting a new protocol

✧ Click the **Program** parameter card to move it into foreground.

✧ Select the required protocol.



✧ Click the **<<** button on the **Program** parameter card to append the selected protocol *to the end* of the job list.

Or

✧ Select **Queue > Append** from the main menu.

Or

✧ Select **Append** from the context menu.

Or

✧ Open the **Exam Explorer**.
→ Page C.16–3, *Calling up the Exam Explorer*

✧ Select a protocol in the **Exam Explorer**.

✧ Select **Tools > Append To Queue**.

Or

✧ Select **Append To Queue** from the context menu.

The selected protocol is appended to the end of the job list.

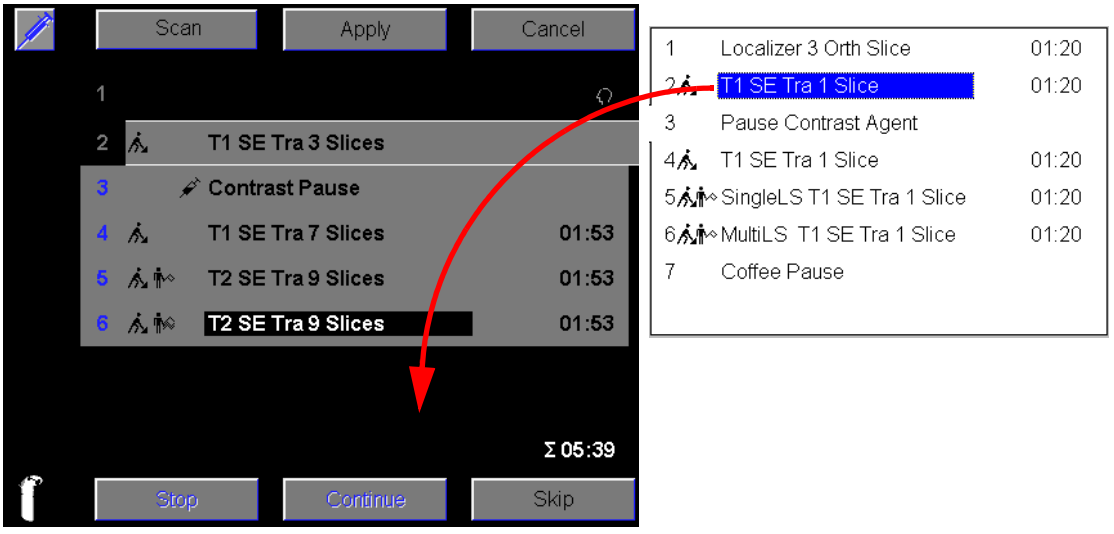
You may now position the protocol at the required location among the pending protocols.
→ Page C.6–60, *Changing scan sequence*

Or

✧ Press the mouse button and drag the required protocol from the **Program** parameter card or the **Exam Explorer** to the job list (*drag* & *drop*).

✧ Release the mouse button when the mouse pointer is at the correct position.

➪ If you drag the protocol into the empty part of the program control, the program instruction will be placed at the end of the job list.



Program instruction with a patient instruction

For example, you have selected a protocol with voice output or included patient instructions for automatic playback via the protocol properties.
→ Page C.12–9, *Playing back voice output*

When you insert the protocol into the job list the system checks whether the voice outputs are available in the set language.

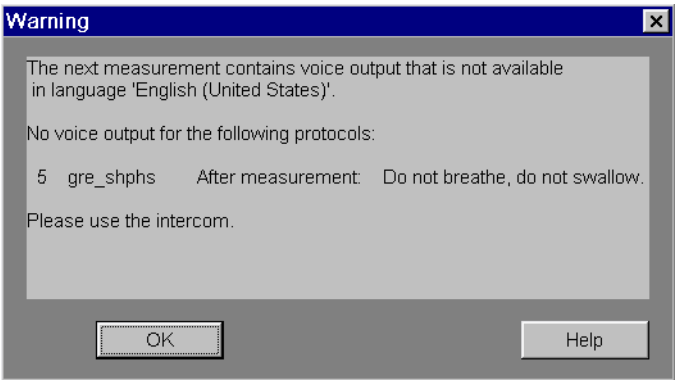


If the voice outputs are available, the protocol is marked with a loudspeaker icon in the job list.

Or



A message box opens if the voice outputs are not available. The protocol is then marked with a crossed out loudspeaker icon in the job list.



✧ Click **OK** and announce your instructions over the intercom system.

There are also other ways to respond to the message:

❏ You can set another language.
→ Page C.11–8, *Setting playback of voice outputs*

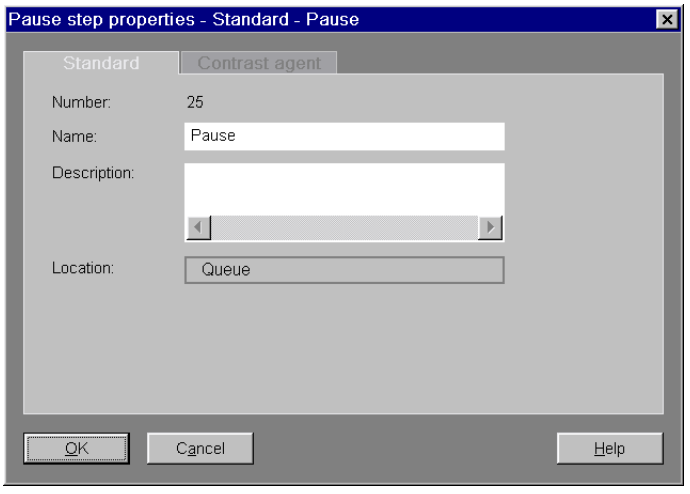
❏ You can record the voice output in the set language.
→ Page C.11–21, *Changing a voice output*

➪ If you close the message box without switching languages or recording a new patient instruction, a message box will appear when you start the affected protocol. You will be prompted to remove the missing voice outputs from the protocol and speak the instructions through the intercom.

Inserting a new pause

✧ Select **Queue > New Pause** from the main menu or **New Pause** from the context menu in the outer margin of the Program Control.

The **Pause Step Properties** dialog box is displayed.



✧ Enter a **Name** and, if necessary, a **Description** in the input fields.

✧ Click **OK**.

The new pause is appended to the end of the job list. You can now move the pause to the correct position.
→ Page C.6–60, *Changing scan sequence*

➪ If you want the pause to be a contrast agent pause, you can define contrast agent administration on the **Contrast Agent** subtask card.

→ Page C.7–15, *Inserting and planning contrast agent pauses*

Generating a protocol from acquired images (Phoenix)

You may reconstruct a new protocol from acquired series or single images and add it to the job list. For this purpose, you may select images from different sources (stamp segments, large segments, or **Patient Browser**).

NOTE

Protocols may be reconstructed from existing images aquired with MAGNETOM systems running with the *syngo* software version MR 2002B or higher. The different coil concept of the MAGNETOM systems permits exchange of image information between MAGNETOM Harmony, MAGNETOM Symphony, and MAGNETOM Sonata with different gradient configurations.

The Phoenix function only permits reconstruction of protocols from a MAGNETOM system of the same type for images from MAGNETOM Concerto, MAGNETOM C!.

✧ Select a series or image from the stamp segments of the Maestro layout, from the large image segments, or from the **Patient Browser**.

✧ Press the mouse button and drag your selection into the program control (*drag* & *drop*).

Or

✧ Select **Append To Queue** from the context menu in one of the large image segments.

A protocol is generated from the series or image and contains all measurement parameters used to acquire the image. The reconstructed protocol is appended to the end of the job list.

You may now position the protocol at the required location among the pending protocols.
→ Page C.6–60, *Changing scan sequence*

Reconstructed protocol through conversion

If images or series have not be scanned with the same software version or originate from different MAGNETOM types, the underlying protocols have to be converted to adapt the reconstructed protocols to your type of MAGNETOM system.

➪ In this case, selection is not possible in the stamp segments of the Maestro Layout or in the large image segments.

✧ Therefore select a series or image in the **Patient Browser**.

✧ *Drag&drop* the image/series into the job list with the *left* mouse button held down. Also press the **Shift** key after you start dragging.

➪ If conversion fails, an error message appears.

Changing scan sequence

If the sequence of the routine scan program is not suitable for the current examination, you can modify the sequence while it is running.

You can, however, only change the lower part of the job list that is still pending.

Moving a program instruction

✧ Select the protocol or scan pause that you want to move.

✧ Select **Queue > Move Up** or **Move Down** from the main menu or **Move Up** or **Move Down** from the context menu.

Or

✧ Use the **Alt +** ↑ and **Alt +** ↓ shortcuts.

You may also move a program instruction via *drag & drop*.
→ *syngo* Operator Manual

✧ Select the program instruction that you want to move.

✧ Press the left mouse button and drag it to its new position in the job list.

Cutting/copying and pasting a program instruction

✧ Select a program instruction.

✧ Select **Edit > Copy** from the main menu or **Copy** from the context menu to copy the entry.

Or

✧ Select **Edit > Cut** from the main menu or **Cut** from the context menu to cut the entry.

Or

✧ Use the shortcuts **Ctrl + C** (copy) or **Ctrl + X** (cut).

The selected entry is copied or cut to the clipboard.

✧ Select the program instruction, **in front of** the position where you want to insert the cut protocol.

✧ Select **Edit > Paste** from the main menu or **Paste** from the context menu.

Or

✧ Use the **Ctrl + V** shortcut.

➪ If no program instruction was selected before pasting it, the cut protocol or the cut pause will be appended to the end of the job list.

You can also copy a program instruction via *drag* & *drop*.
→ *syngo* Operator Manual

✧ Click the program instruction you want to copy.

✧ Keep both the **Ctrl** key and the left mouse button pressed and drag it to the desired position in the job list.

➪ Copying via *drag & drop* does not work with open program instructions.

Deleting program instructions

You may remove individual program instructions from the job list.

Deleting a program instruction

✧ Select the program instruction that you want to remove from the job list.

✧ Select **Edit > Delete** from the main menu or **Delete** from the context menu.

Or

✧ Use the **Del.** key on the keyboard.

Or



✧ Click the recycle bin.

You may also remove a program instruction easily via drag & drop.
→ *syngo* Operator Manual

✧ Select the program instruction that you want to remove from the job list.



✧ Hold down the left mouse button and drag it to the recycle bin at the bottom left next to the job list.

Deleting a complete program instruction list

✧ Select **Queue > Clear All** from the main menu or **Clear All** from the context menu.

All program instructions are deleted from the job list.

➪ This menu item is not available when a scan is in progress.

Changing protocol properties

You can adjust the properties of the pending protocols and pauses during an examination.

Examples of protocol properties:

- ❏ Automatic loading of a measured series into the image area or other task cards
- ❏ Setting automatic voice outputs
- ❏ Changing the protocol's start type
- ❏ Changing the name of the protocol

➪ Already opened protocols can also be changed. However, it is not possible to adjust the voice output for these protocols.

✧ Select the protocol from the job list.

✧ Select **Edit > Properties...** from the main menu.

Or

✧ Select **Properties...** from the context menu.

The **Protocol step properties** dialog box opens.

✧ Click the relevant subtask card into foreground.

✧ Change the properties of the protocol.

The properties of protocols and pauses are described in detail in a separate chapter.
→ Chapter C 12, *Protocol and Pause Properties*

Saving a job list as a new program

If you want to save a modified scan program for subsequent examinations, you can save it as a new program.

✧ Select **Queue > Save As Program** from the main menu or **Save As Program** from the context menu of the program control (right mouse button)

The **Exam Explorer** is opened and displays the **Save Program As [Customer Tree]** dialog box. Assign your modified scan program to an examination region as well as an examination and enter a name for the scan program.
→ Page C.16–61, *Saving the scan program under a new name*

Numbering of reconstructed images

Numbering is determined by the orientation and position of the images. It is *independent* of the slice positioning, excitation sequence, and number of concatenations in multi-slice measurements.

Numbering rules

The following rules apply:

(1) **Primary order**
Acquired images are divided into sagittal, coronal, and transverse groups according to their main orientation.

(2) **Secondary order**
Within these groups, the slices are numbered according to their position in ascending or descending order.

- You can define the primary order (for example, **cor - tra - sag** as one of six possible combinations) and the secondary order (**ascending** or **descending**) when you adapt the protocol parameters.

- The images are numbered by default in the primary order **sag - cor - tra** and in the secondary order **R >> L, A >> P, F >> H**.

NOTE

The settings for image numbering are linked to the position of the scan region.
The settings for image numbering of the protocols already processed and completed are automatically applied when opening consecutive protocols sharing the same position of the scan region.

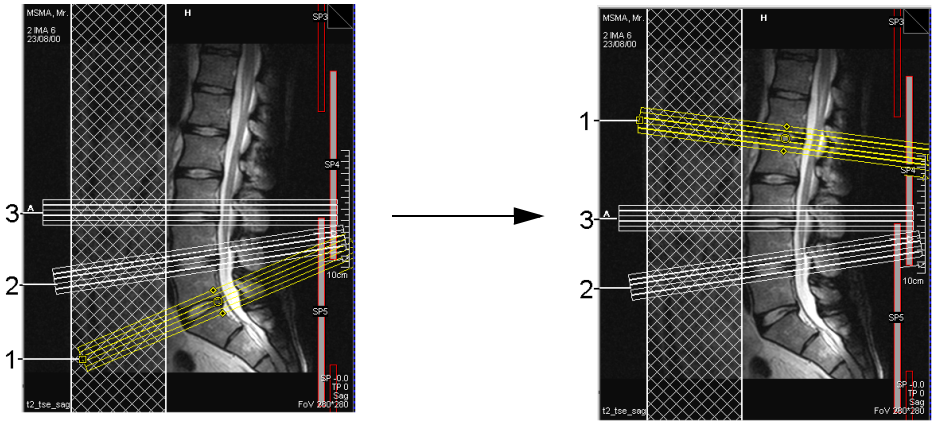
Example

You are planning a scan with 3 slice groups. You can move or rotate the slice groups without changing the numbers of the slice groups.



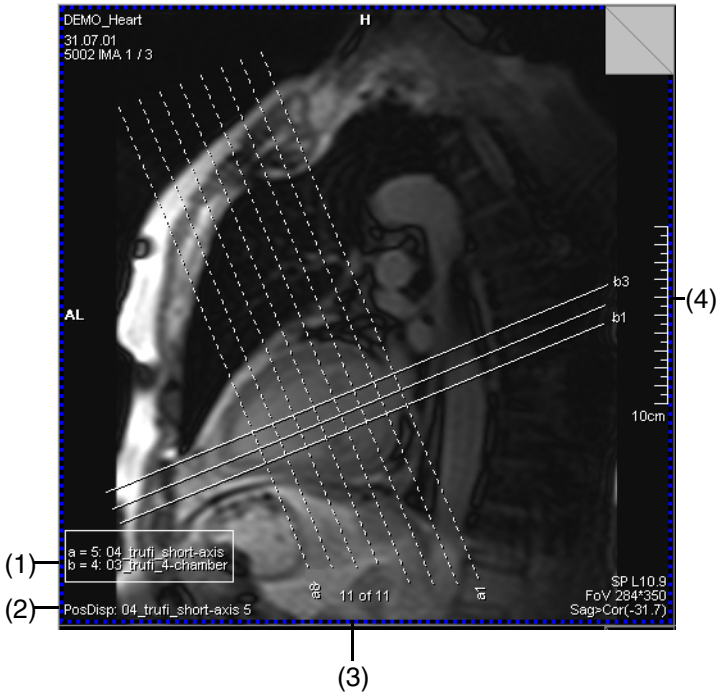
➪ The number of the selected slice group is displayed on the **Geometry** parameter card under **Slice group**.

In the display, slice group 1 is moved up:

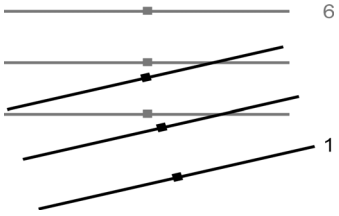


After the measurement, you may view the numbering of the reconstructed images in the **Position Display** of the **Viewer** task card, in the image area of the **Viewer** or in the **Patient Browser**.

In the **Position Display** you can see the position and numbers (right side) of the reconstructed images.



(1) Assignment of lower-case letters to series names
(2) Name of the new position display series
(3) Number of images on the reference image
(4) Image numbers



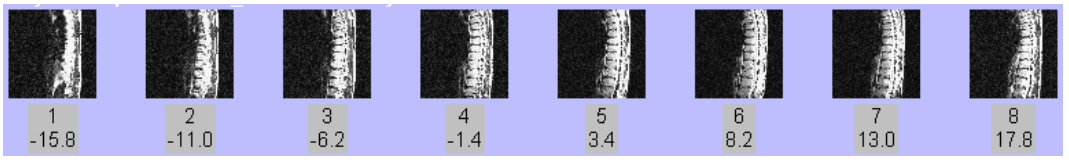
NOTE

If you have configured the position display so that not all cut lines are labeled, the allocation of overlapping cut lines to cut-line numbers that are no longer visible may be incorrect. To be on the safe side in such cases, select the settings for the cut line labeling in the position overview so that **all** cut lines and image numbers are displayed.

→ Page A.3–16, *Configuring the display of cut lines*

The display of images in the **Patient Browser** is defined by the sort criterion. If you select the criterion **Instance Number** on the series level, the images will be displayed in the order of their slice position.

You can uniquely assign the images in the **Patient Browser** to the images in the **Position Display** using the images numbers displayed in both cases.

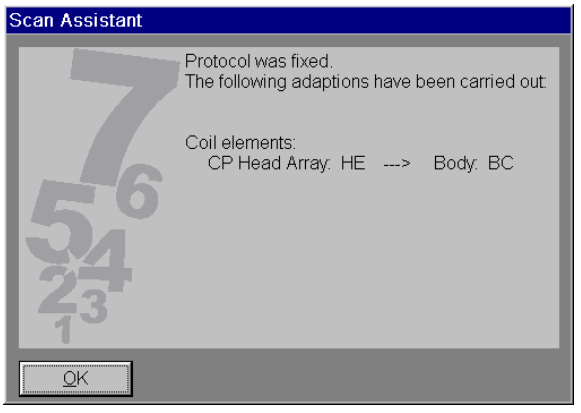


Resolving conflicts and inconsistencies

Before or during the examination, inconsistencies can occur between the data in the currently loaded scan program and the actual settings in the scan system.

Inconsistent Coil Configuration

The protocol requires coils different from the ones plugged into the patient table. A message box will appear if one or more coils is not connected.

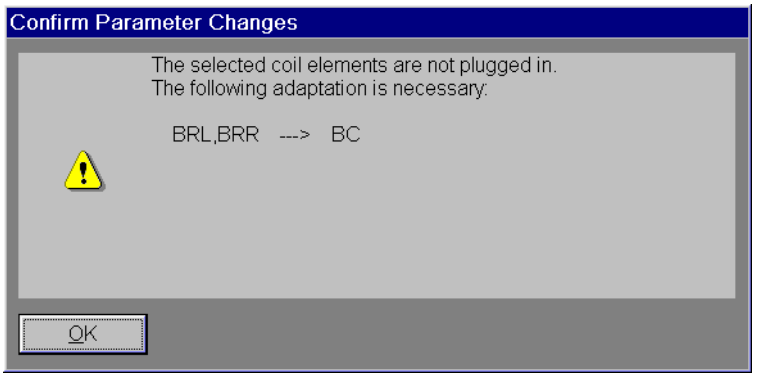


✧ Click **OK**.

✧ Open the scan protocol (double-click).

Since the required coils are not plugged in for this protocol, the system automatically adjusts the coil configuration.

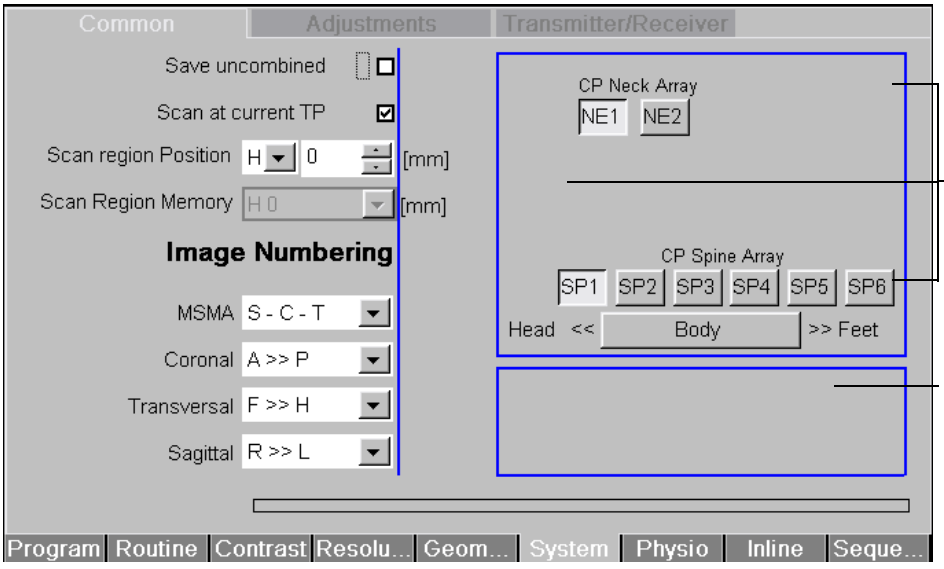
The message window **Confirm Parameter Changes** appears.



✧ Confirm your changes with **OK**.

✧ Connect the missing coils to the patient table.

✧ Go to the **System Common** card in the parameter card stack.



✧ Select the coils for scanning.

Apply

✧ Click this button in the program control to confirm your settings.

The protocol is closed and you may start the measurement.

Inconsistencies Resulting from a Changed Table Position

Sometimes it is necessary to move the patient table prior to a scan, e.g. to administer contrast agent to the patient.

Use the **Table Positioning** dialog box to control the table movement from the control room. Or, you can move the table by using the keys on the control panel next to the magnet bore.
→ Chapter C 8, *Positioning the Patient Table* and *System Manual*

At the start a scan the system automatically checks whether the information about the table position in the subsequent protocols matches the current table position.

If it does not, a appears indicating that the table will move. If you answer the dialog box with **Yes**, the table moves to the position entered in the protocol and scanning starts.

NOTE

However, do not move the table completely out of the magnet
(**do not move it into the HOME position!**).
Otherwise the examination will be considered completed.

You will not be able to perform any more scans, and you will have to start the entire examination again from the beginning (patient registration, overview scan, position slices... etc.).

CHAPTER C.7

Using a Contrast Agent

Contrast agents may be required for a variety of MR examinations. Paramagnetic contrast agents (usually Gd compounds) enhance the signal of many pathological structures.

If you want to run a protocol with contrast agent, use a measurement program that already contains pauses for administering contrast agent.
→ Page C.2–4, *Selecting a scan program*



All protocols *after* this pause are marked with a syringe icon in the job list.

If no contrast agent pauses are planned in a scan program, you can insert them into the job list while the examination is in progress. Or, you may utilize other unrelated pauses in the examination sequence to administer contrast agent to the patient and document it accordingly.

Procedure for a Contrast Agent Measurement

This is the usual procedure for examinations using contrast agent:

❏ Perform a native scan.

❏ Stop the examination before the first contrast agent protocol.

❏ Check whether the contrast agent protocol has a "complete" status (no construction worker icon).

Please observe the following when applying dynamic contrast agents:

❏ Document contrast agent administration in the **Exam Paused** dialog box
→ Page C.7–5, *Documenting the use of contrast agent in the examination pause*,
Administer contrast agent
→ Page C.7–7, *Documenting contrast agent administration without pause*,
New Pause or in the **Pause step properties dialog**
→ Page C.7–15, *Inserting and planning contrast agent pauses*.

❏ Move the patient table out of the magnet using the tabletop control.

You can also use the injector to administer the injection in the magnet.

NOTE

Do **not move** the table fully out of the magnet **into the HOME position**).
Otherwise the examination is considered completed.

You are not able to perform additional scans, and you will have to start the entire examination again from the beginning (patient registration, overview scan, position slices... etc.).

❏ Administer the contrast agent.

❏ After injecting the contrast agent move the table back into the magnet isocenter.



❏ Start the first contrast agent protocol, e.g. with **Continue** in Exam Paused.



All program instructions after the pause will be marked as contrast agent scans via a syringe icon to the left of the protocol name.



The syringe icon is displayed next to the patient's name above the program control.

❏ Following the contrast agent uptake, reset the contrast agent icon.
→ Page C.7–12, *Resetting the contrast agent icon*

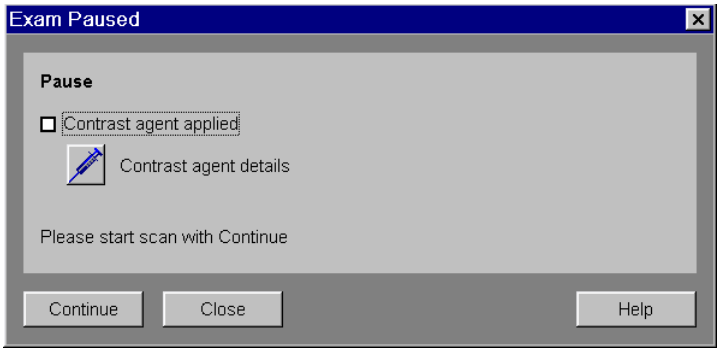
The subsequent protocols are no longer identified with the contrast agent icon.

Documenting the use of Contrast Agent

There are various ways of documenting the use of contrast agent. While you are able to identify an exam as a contrast agent exam, you are also able to enter data about the type and quantity of contrast agent.

Documenting the use of contrast agent in the examination pause

If your scan program includes a contrast agent pause, the examination will stop at the pause. The **Exam Paused** dialog box is displayed.



✧ Select the **Contrast agent administration** check box.

➪ If you want to document further details of the use of contrast agent (type and quantity) for subsequent invoicing, click the syringe icon to select a substance from the contrast agent catalog.
→ Page C.7–9, *Specifying contrast agent details*



✧ Click **Close** to close the dialog box.

✧ Administer the contrast agent to the patient and start the scan with **Continue** in the program control.

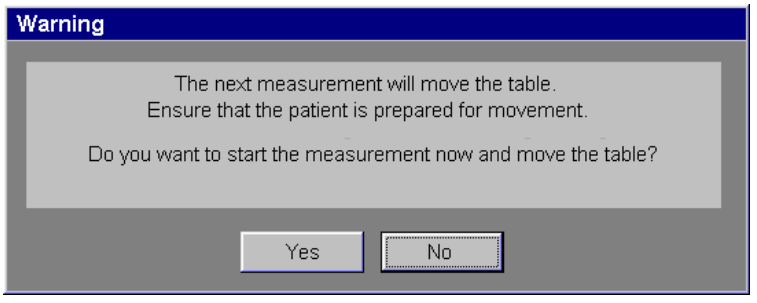
Or

✧ Administer the contrast agent to the patient.



✧ Click **Continue** in the **Exam Paused** dialog box to close the window and start scanning immediately.

The system checks whether the patient table is being moved automatically before the next protocol starts. If it is, a warning indicates table movement and the possible danger to the patient.



✧ Click **Yes**.

The table is moved. The table is moved to the position entered and scanning is started.

Documenting contrast agent administration without pause

You may also perform a contrast agent examination, even if the selected program does not include contrast agent pauses. Instead of a pause, you may use a break in the measurement, e.g. while you check and complete the parameters of the next protocol.

Administer the contrast agent to the patient, document it in the **Apply Contrast Agent** dialog box, and continue with the examination.

✧ Select **Job list > Contrast agent** from the main menu.

Or

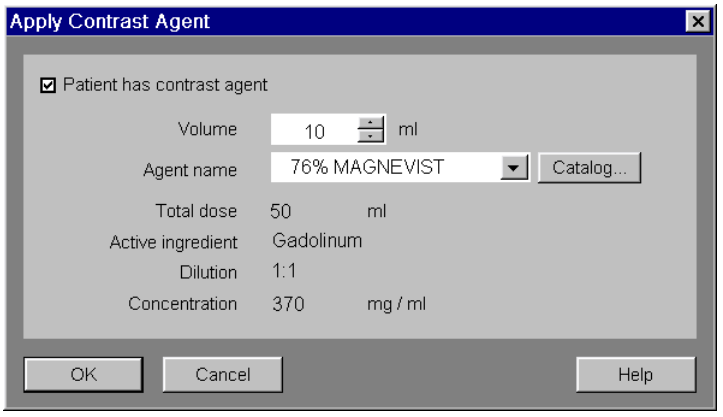


✧ Click the syringe icon located at the top left next to the job list (queue).

Or

✧ Select **Contrast Agent** from the context menu in the left-hand (outer) margin of the program control.

The **Apply Contrast Agent** dialog box is displayed.



✧ Select the **Patient has contrast agent** check box.

Contrast agent administration

The input fields for volume and contrast agent names are activated.

✧ Enter the name and quantity of the contrast agent administered.

Or

✧ Click the **Catalog** button.

The following dialog box allows you to select the required contrast agent from the contrast agent catalog.
→ Page C.7–9, *Specifying contrast agent details*

✧ Click **OK**.

Scanning continues.

➪ To document a scan as a contrast agent scan, it is not mandatory to specify the name and quantity of the contrast agent. Contrast agent administration is identified by the image text.

Specifying contrast agent details



✧ Click the syringe icon in the **Exam Paused** dialog box.

Or

✧ Click the syringe icon located in the upper left next to the job list.

The **Apply Contrast Agent** dialog box is displayed.



➪ The syringe icon is shown as depressed in both the **Exam Paused** dialog box and the program control next to the job list.

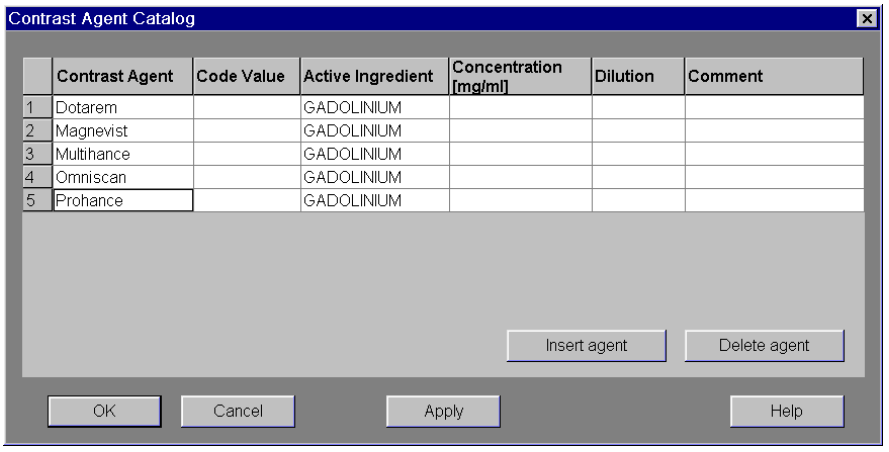


✧ Select the **Contrast agent administration** check box.



✧ Click the **Catalog** button in the **Apply Contrast Agent** dialog box.

The **Contrast Agent Catalog** dialog box is displayed.



Selecting a contrast agent

✧ Select the desired contrast agent from the contrast agent catalog.

OK

✧ Click **OK**.

The **Contrast agent catalog** closes. The program returns to the **Apply Contrast Agent** dialog box. The selected contrast agent is displayed in the **Agent name** selection window.

✧ Click **OK**.

The **Apply Contrast Agent** dialog box closes. Information about the contrast agent is transferred to the **Exam Paused** dialog box, if you called the contrast agent dialog box from the pause.

The syringe icon becomes active again and you may start the scan by clicking the **Continue** button.

Resetting the contrast agent icon

If you notice that the contrast agent no longer affects image contrast during the scan, you may remove the syringe icon for all subsequent measurements.

✧ Select **Job list > Contrast Agent** from the main menu or **Contrast Agent** from the context menu in the left (outer) margin of the program control.

Or

✧ Click the syringe icon located in the upper left next to the job list.

The **Apply Contrast Agent** dialog box is displayed.

✧ Deselect the **Patient has contrast agent** check box.

Or

The **Exam Paused** dialog box opens again if an additional contrast agent pause is planned as the next step in the job list.

✧ Deselect the **Contrast agent administration** check box.

Subsequent scans are now no longer marked as contrast agent scans.

Editing the contrast agent catalog

To make your work easier, you can enter all substances used as contrast agents in scans in the catalog. You can also add or remove contrast agents during an examination.

Inserting a contrast agent into the catalog

If the contrast agent you would like to use is not entered in the ccontrast agent catalog, you may insert it in the **Contrast Agent Catalog** dialog box
→ Page C.7–9, *Specifying contrast agent details*



✧ Click the **Insert Agent** button.

A new line is inserted into the catalog.

✧ Enter a name for the contrast agent, the code value, the active component, concentration, dilution and, possibly, a comment.

➪ You need the code if you want to document the contrast agent used via the HIS (hospital information system) The data are entered as consumables.
→ Page C.9–1, *Job*



✧ Click the **Apply** button.

The newly entered contrast agent is now included in the catalog.

The **Contrast Agent Catalog** dialog box remains open.

Deleting a contrast agent from the catalog

In case the catalog includes contrast agents you no longer want to use, they can be deleted as follows.



✧ Select the substance you want to remove.

✧ Click the **Delete agent** button.

The selected substance is deleted from the catalog.

The **Contrast Agent Catalog** dialog box remains open.

Inserting and planning contrast agent pauses

If your scan program does not include contrast agent pauses, you may insert them during an examination. If your program already contains a contrast agent pause, you can document contrast agent administration here while the first protocols are running.

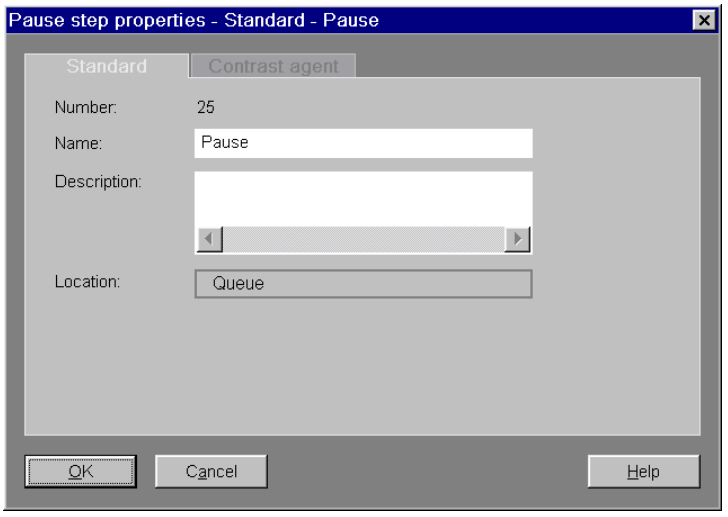
Inserting a new contrast agent pause

✧ Select **Job list > New Pause** from the main menu.

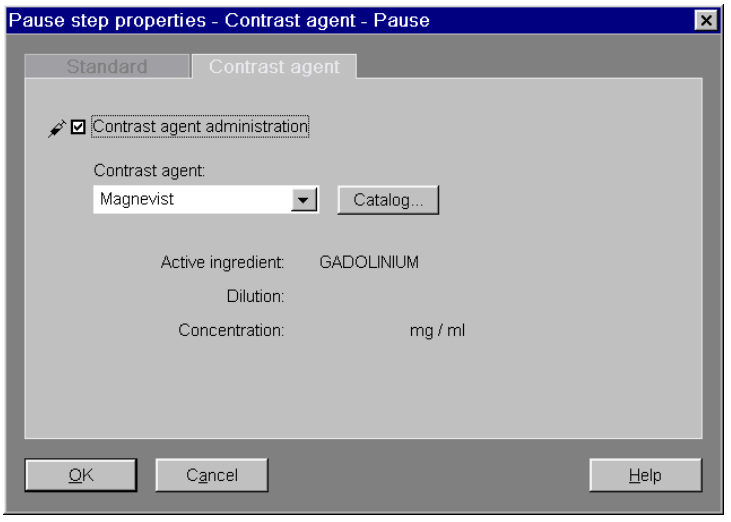
Or

✧ Select **New Pause** from the context menu in the (left-hand) outer margin of the program control.

The **Pause step properties-Standard Pause** dialog box is displayed.



✧ Click the **Contrast Agent** card into foreground.



Existing contrast agent pause

Contrast agent administration is also documented in the properties window for contrast agent pauses already positioned in the job list.

✧ Select the pause from the section of the job list that still needs to be run.

✧ Select **Edit > Properties** from the main menu.

Or

✧ Select **Properties** from the context menu of the Program Control.

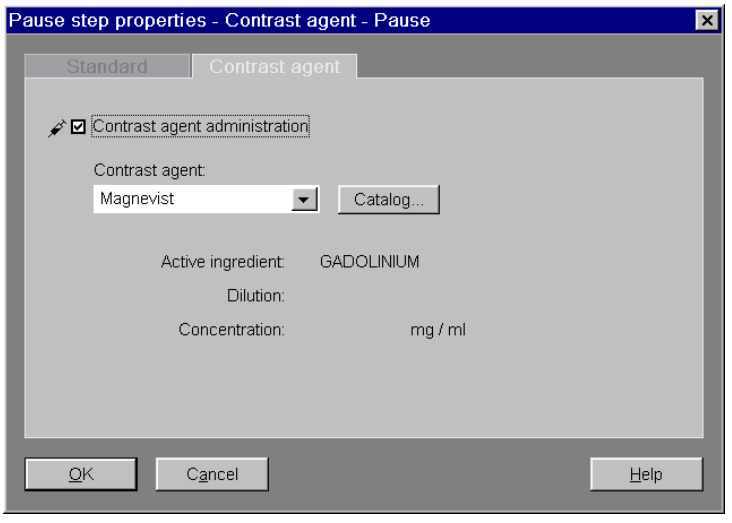
The **Pause step properties-Standard Pause** dialog box is displayed. Click the **Contrast Agent** card into foreground.

Planning contrast agent administration



✧ Select the **Contrast agent administration** check box.

The **Contrast agent** selection field and the **Catalog** button become active.



✧ Select the contrast agent you want to administer from the list.

Or

✧ Click the **Catalog...** button and select the contrast agent in the **Contrast agent catalog** dialog box.
→ Page C.7–9, *Specifying contrast agent details*

✧ Confirm your entry with **OK**.

If you have inserted a new pause, the contrast agent pause will be appended to end of the job list.

You can now move the contrast agent pause to the correct position in the job list.
→ Page C.6–60, *Changing scan sequence*

Scanning stops as soon as the pause reaches the top of the job list. The **Exam Paused** dialog box is displayed.



✧ Administer the contrast agent and start the contrast agent scan with **Continue**.

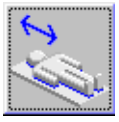
CHAPTER C.8

Positioning the Patient Table

You will have to move the patient table at various points during the examination to, for example, administer contrast agent.

You can control the patient table movement by using either the control panel next to the magnet bore or the software at the *syngo* Acquisition Workplace in the control room.

Selecting table positioning

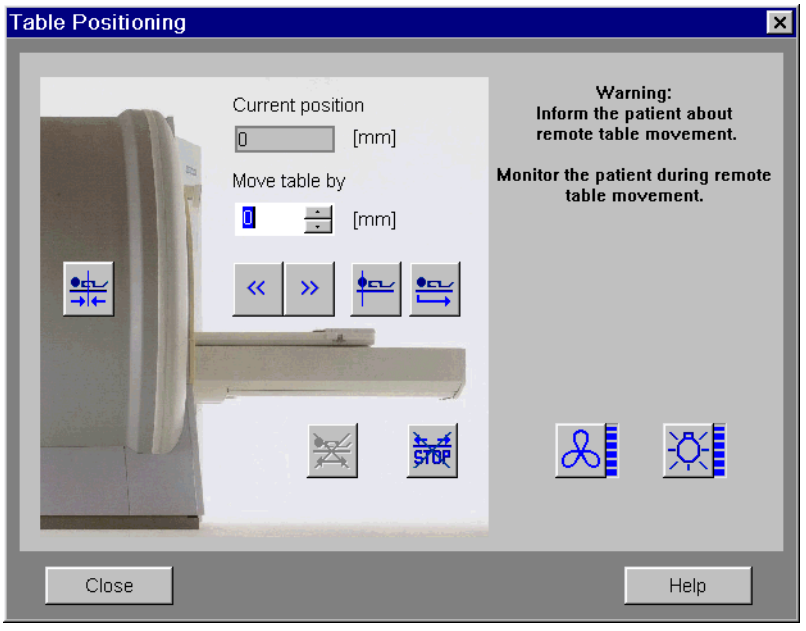


✧ Click the **Table Positioning** button on the tool bar of the **Exam** task card.

Or

✧ Select **View > Table Positioning...** from the main menu.

The **Table Positioning** dialog box opens.

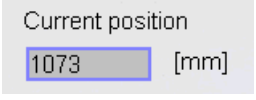


The current table position is displayed, and you can control various horizontal movements of the patient table.

NOTE

When performing table movements, ensure that the table is *not* simultaneously moved via the operating panel at the magnet bore.

Current table position

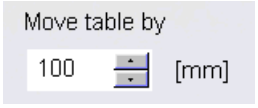


The current, relative table position is displayed here.

The relative table position is the distance between the magnet isocenter and the point marked using the light localizer when preparing for the examination.

Moving the table by a certain distance

You may position the patient table with millimeter precision in the **Table Positioning** dialog window.



✧ Enter the distance you want to move the patient table in the **Move table by** field.



✧ Then click this button to move the patient table into the magnet (i.e. toward the isocenter) by the specified distance.

Or



✧ Click this button to move the patient table out of the magnet by the distance specified.

NOTE

The **Current position** and **Move table by** displays (as well as the buttons for moving the patient table by a certain distance) are only available if you have the "Panoramic Table" license.

Moving the table into the isocenter



✧ Click the **Move to Center** button to move the patient table precisely into the isocenter.

The isocenter is usually the point that you marked with the light localizer during the preparation for the examination.

If you have not marked a point, the table position of the last scan is considered the center. If you have not yet performed a scan, the table will move to the scan level of the head coil when you click the **Move to Center** button (default setting).

Moving the table almost completely out of the magnet



✧ Click this button to move the patient table almost completely out of the magnet.

You will move the table to this position, e.g., for contrast administration. The information regarding the position of the scan center does not change.

Canceling a table movement



✧ Click this button if you want to cancel a table movement.

The patient table will stop at the point it has already reached.

Canceling table STOP

As soon as you press the **STOP** button on the intercom system or at the *syngo* Acquisition Workplace (e.g. in an emergency), the table will stop moving. The buttons for table positioning are also disabled.

Before you can resume table positioning, you have to first cancel the table STOP.



✧ Click the **Cancelling table stop** button.

Switching magnet opening lighting on/off

Some examinations require you to set or switch the tunnel lighting on/off.



✧ Click this button to switch on the magnet opening lighting, if it is off.

✧ Click the **Lighting of magnet opening** button several times in quick succession to set the intensity of the lighting (3 levels: low, medium, high).



The current setting for magnetic opening lighting is shown to the right of the button.

You may set the magnetic opening lighting to three different brightness levels. The more times you click the button, the brighter the lighting. Once maximum brightness has been reached, clicking the button again will dim the lighting.

➪ To switch the magnet opening lighting off, first set the lighting to the lowest brightness level.

Switching magnet opening ventilation on/off

You can adjust the ventilation of the magnet opening at the *syngo* Acquisition Workplace in the control room.



✧ Click the **Ventilation of magnet opening** button to switch on the ventilation in the magnet opening, if it is off.

✧ Click the **Ventilation of magnet opening** button several times in quick succession to adjust the ventilation (3 levels: low, medium, high).



The current setting for tunnel ventilation is shown to the right of the button.

➪ To switch the magnet opening ventilation off, first set the ventilation to the lowest level.

Closing the examination



✧ Click the **Move to Home** button to move the patient table completely out of the magnet.

NOTE

Never move the patient table into the HOME position if you want to resume the examination afterward.

Clicking the **Move to HOME button** always terminates the current examination.

The system assumes that you now want to register and examine the next patient.

All reference images are removed from the image area.

CHAPTER C.9

Working with Instruction Areas

Instruction ranges are used to define the common properties of different program instructions in the job list. The steps have to be grouped by range markers.

There are different types of instruction areas:

- **Job**
- **Body region**
- **Image comment**

Job

With the necessary license and connection to a hospital information system (HIS), you can access the HIS via the network to receive jobs for your MR system in the form of work steps. A job reference is created in the job list during patient registration. All acquired series and contrast agent administrations will be automatically entered in the job. You are also able to enter results series (e.g. from post-processing) or consumables on your own. The information for the procedure step is now available for further processing within the hospital.
→ *syngo* Operator Manual

Body region

The body region to be examined is defined by selecting the scan program during patient registration. The body region set in the program control can be useful when sorting images later (e.g. on another image archiving system).

Image comment

Instruction areas also include the display of image comments to be saved with scanned images in the image database. They are also marked in the program control using range markers.

Editing a body region instruction range

When you select your scan program, the first range marker for the body region is defined automatically.

Changing the body region range marker

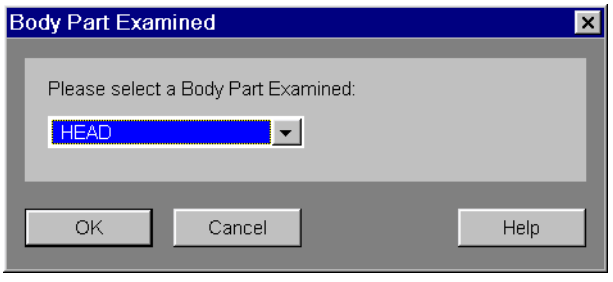
If you decide to examine another body region during the examination, you may change the region setting.

✧ Select **Queue > Change Body Part Examined** in the main menu.

Or

✧ Select **Change Body Part Examined** from the pop-up menu in the program control (right mouse button).

The **Body Part Examined** dialog box opens.



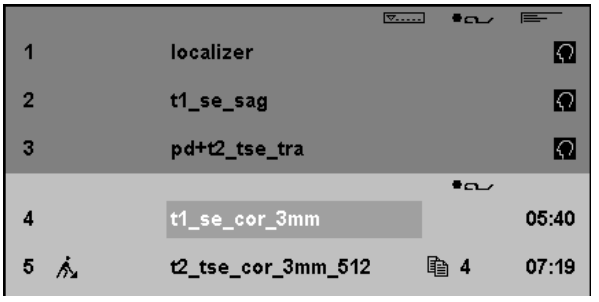


✧ Select a new body region from the selection list.

✧ Click the **OK** button.



A new range marker is inserted with the new body region.





If you position the mouse pointer over the instruction range, the new scan region of the program instructions will be displayed as a tool tip.

Deleting the body region range marker

✧ Select the range marker of the body region you want to delete.

✧ Select **Delete** from the context menu of the program control.

The body region is no longer entered in the images.

Editing a work step in the instruction area

As soon as a patient is registered, a range marker is automatically generated for the work step determined. The defined procedure step causes all scans and material consumed (e.g. for contrast agent administration) belonging to the examination to be available for further editing within a license-dependent hospital information system.



Hovering the mouse pointer over the range marking of the procedure step displays the starting time of the scan and information about the procedure step in a tool tip.

➪ If you have to repeat scans or insert new protocols, they will be assigned to the existing procedure step.

Adding the range marker for the procedure step

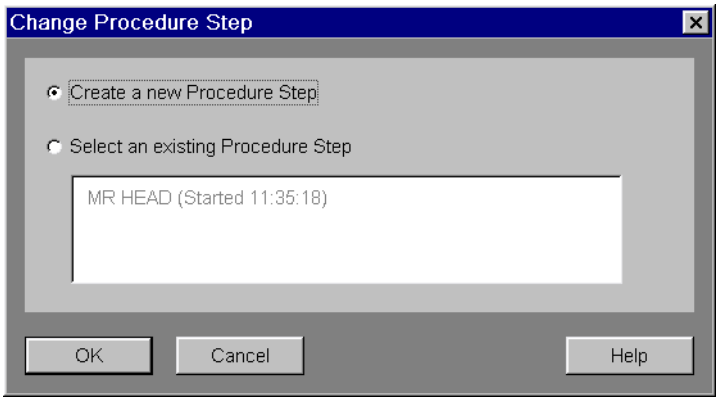
If you need an additional procedure step during the examination, insert it using the program control.

✧ Select **Queue > Change Work Step** from the main menu.

Or

✧ Select **Change Procedure Step** from the pop-up menu of the Program Control.

The **Change Procedure Step** dialog box is displayed.



The dialog box contains a list of predefined work steps. You can apply one of the work steps offered or create a new one.

✧ Select the **Create a new Procedure Step** option.

✧ Click the **OK** button.



A new range marker is inserted in the queue.

❏ If a program instruction was selected, the range marker above the program instruction will be inserted into the job list.

❏ If you have not selected a program instruction, the range marker will be appended to the end of the job list.

This option creates a new work step in the patient database.

This work step records subsequent examination steps for billing purposes.

➪ The range marker of the previous procedure step is retained and indicates the processing status.

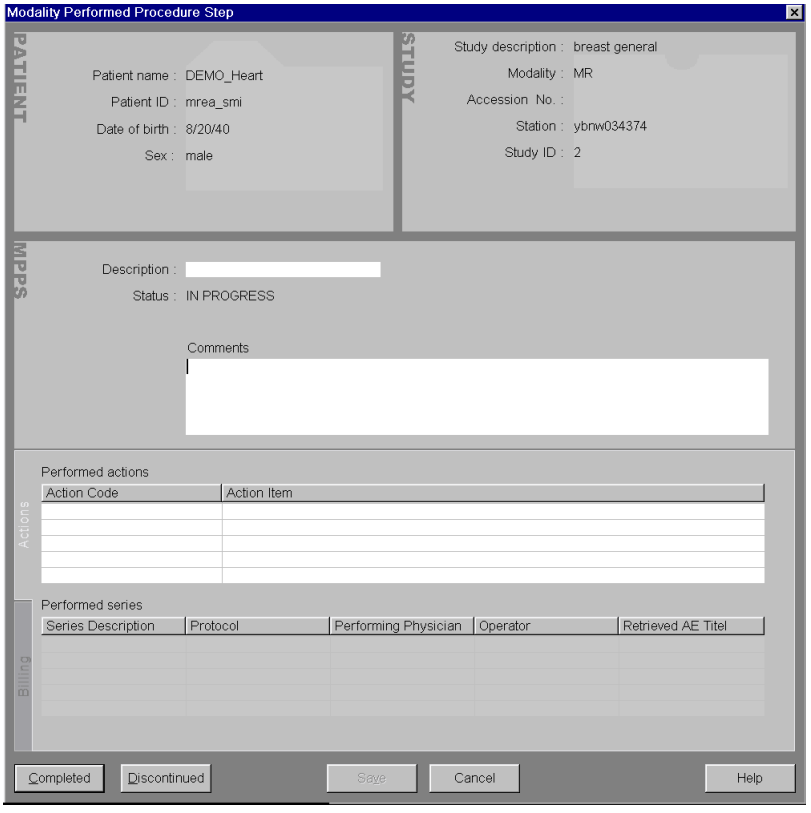
Editing a new work step

You may define the newly created work step from the program control.

✧ Select the newly inserted range marker.

✧ Select **Properties** from the context menu.

The **Modality Performed Procedure Steps** dialog box is displayed.

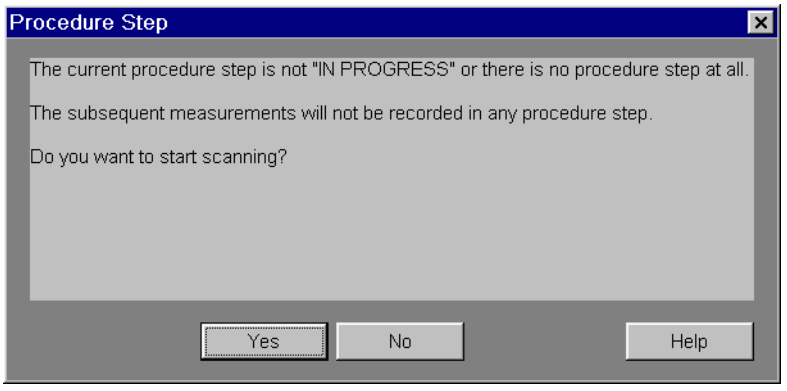


✧ Enter a designation in the **Description** field for billing purposes.

✧ Record all services to be included for billing.
→ *syngo* Operator Manual

Response to a missing work step

A message box will appear when you start a protocol, if no procedure step exists or if the procedure step has already been completed. It indicates that the following scans will not be recorded in a job for billing.



✧ Click **Yes** if you want to start scanning.

Or

✧ Click **No** if you want to create a procedure step.

Canceling a procedure step

If you are unable to perform an examination as initially planned, just cancel the procedure step.

✧ Select the range marker and **Cancel** from the pop-up menu of the Program Control.

Or

✧ Select the range marker and **Properties** from the pop-up menu.

The **Modality Performed Procedure Steps** dialog box then opens.

✧ Click the **Cancel** button.

The work step icon is marked with a red cross.



Subsequent scans are no longer entered in the procedure step.

Completing a procedure step

You can complete the procedure step when the last scan of the examination and all planned postprocessing operations have been completed, and the series has been printed or transferred to a film sheet.

✧ Select the range marker and **Complete** from the pop-up menu of the Program Control.

Or

✧ Select the range marker and **Properties** from the pop-up menu.

The **Modality Performed Procedure Step** dialog box then opens.

✧ Click the **Completed** button.



The procedure step icon is marked with a green checkmark.

Image calculations still in progress are no longer recorded for this procedure step.

➪ If you unregister the patient being examined or register a new patient, there will be *no* indication that the procedure step has not been completed. However, you may complete it later via the Patient Browser. This can be helpful if you want to enter series of subsequent postprocessing steps (e.g. spectroscopy) in this procedure step.
→ *syngo* Operator Manual

Deleting the procedure step range marker

You can delete a procedure step from the job list of the program control.

✧ Select the range marker you want to delete.

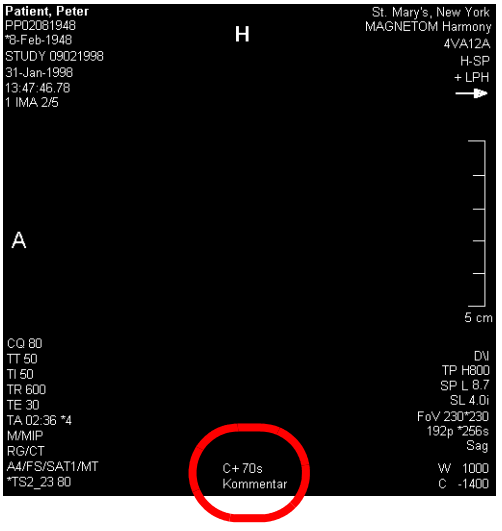
✧ Select **Delete** from the context menu of the program control.

➪ The work step is deleted but is retained in the patient database.

Editing an image comment

When registering of a patient, a range marker is automatically generated for image comments. Initially it is empty. You are able to enter an image comment for all protocols waiting to be processed, including the selected or open protocol. This comment appears as an annotation in the center of the lower image margin of the series.

➪ If you do not enter an image comment in the program control, comments entered during patient registration will be inserted. The image comment line remains empty if this activity does not generate a comment. Special image calculation programs (IDEA) can enter a comment as well.



Entering an image comment

If no image comment has been assigned, you may enter the required image text.

✧ Select **Queue > Set Image Comment** from the main menu.

Or

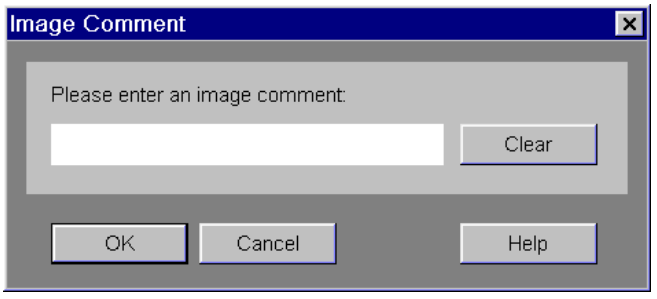
✧ Select **Set Image Comment** from the pop-up menu in the outer area of the program control.

Or



✧ Select the icon for image comment and select **Properties** from the context menu.

The **Image Comment** dialog box appears.



✧ Type a comment in the input field.

✧ Confirm your comment with **OK**.

The dialog box closes. All images to be acquired contain this image comment.



Now hover the mouse pointer over the image comment icon to display the image text you entered.

Inserting a new image comment

To assign a different image comment to subsequent program instructions, proceed as follows:

✧ Select the program instruction starting from which you want to change the image comment.

✧ Select **Queue > Set Image Comment** from the main menu.

Or

✧ Select **Set Image Comment** from the pop-up menu in the outer area of the program control.

The **Image Comment** dialog box appears.

✧ Type the new text.

✧ Click the **OK** button.

Another image comment icon is inserted in front of the program instruction in the job list.

Changing the image comment

You may change an existing comment for program instructions that are still waiting to be processed.



✧ Select the icon for image comment and select **Properties** from the context menu.

The **Image Comment** dialog box appears.

✧ Click the **Delete** button

The input field for the image comment is cleared.

✧ Enter a new text in the input field.

Or

✧ Select the image comment in the input field and overwrite it.

✧ Click the **OK** button.

The images acquired in subsequent protocols will include the new image comment.

➪ The current image comment will also be used if you repeat protocols previously scanned with a different comment.

Deleting an image comment

An image comment can be deleted again if necessary.

✧ Select the icon for the image comment with image text you want to delete.

✧ Select **Delete** from the context menu.

The image comment icon is removed from the job list of the program control.

Images acquired in subsequent protocols are assigned the *previous* image comment or stored *without* an image comment, if none is available.

CHAPTER C.10

Inline Display

You can use inline display for the following applications:

- ❏ You are able to view the reconstructed images during scanning. This allows you to decide when to intervene in a scan by checking the acquired images.
- ❏ You can locate the required slice position and orientation of a real-time protocol interactively using the space mouse.
- ❏ Inline display lets you trace contrast agent build-up in CARE bolus scans before starting the high-resolution protocol.
- ❏ You are able to trace the navigator signal (respiratory curve) and start a multiple breath-hold scan.
- ❏ You are able to monitor the MR spectrum and stop scanning as soon as an adequate signal-to-noise ratio is attained.
- ❏ You are able to filter the display of BOLD images to display just the images of a certain slice.

Starting Inline Display

You can start Inline Display manually or automatically. as well as change the appearance and size of the inline display.

➪ The display includes only images that are loaded automatically from the image calculation. It is not possible to load, manual images into the Inline Display and then to page back to previously displayed images.

➪ You may start the Inline Display only if you have full access rights to the data of the patient being scanned. Please observe the information given in the Safety Standards book.

Starting Inline Display manually



✧ Select **View > Inline Display** from the main menu.

Or

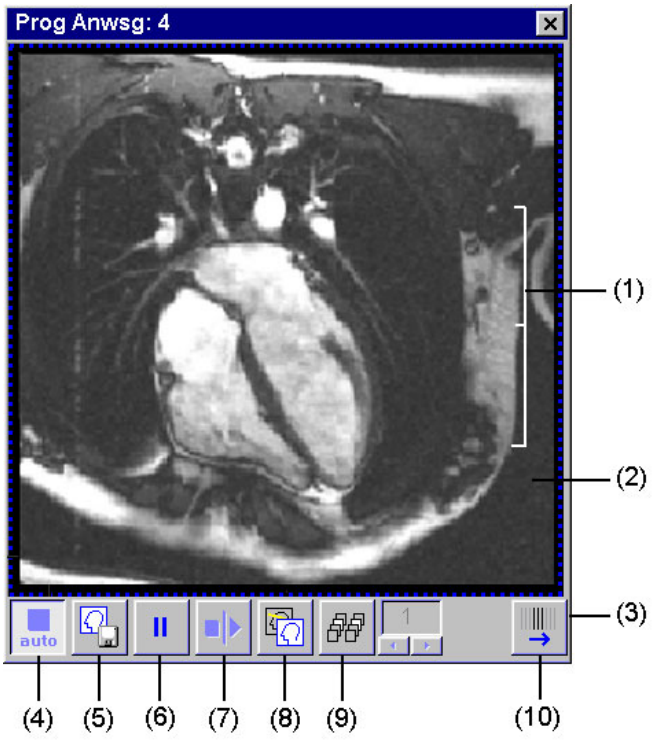
✧ Click this button in the toolbar of the **Exam** card.

The Inline Display is displayed. Two views are possible: with "frame" or without "frame".
→ Page C.10–6, *Changing the Inline Display*

If **Frame on** is activated, the image segment is displayed with the title bar and several function keys.

The title bar shows the number of the program step. You can move this window to a new position.

Inline Display with frame:



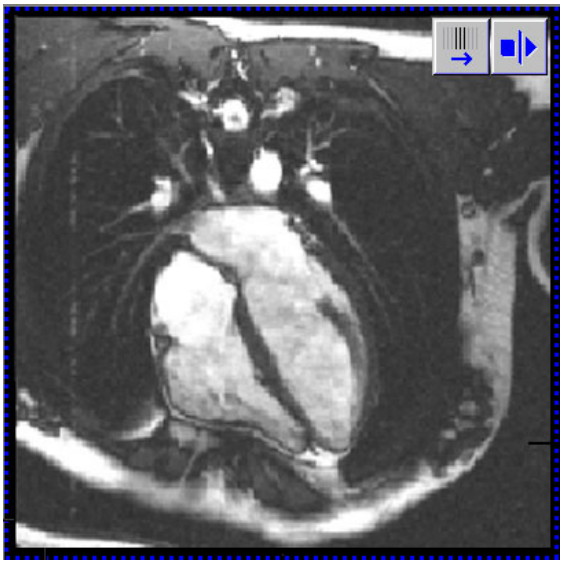
(1) Scale bar
(2) Image range
(3) Control area with buttons
(4) **Store Images On/Off** button
(5) **Save** button
(6) **Display Pause** button
(7) **Stop & Continue** button
(8) **Copy Image Position** button
(9) **Display Filter On/Off** button
(10) **Scan Breathhold** button

Starting Inline Display automatically

Inline Display is opened automatically when a protocol with the **Auto open Inline Display** property is about to run in the job list.
→ Page C.12–13, *Opening Inline Display automatically*

The Inline Display appears either with or without a "border", depending on whether **Frame on** is activated or not. Without a frame, the Inline Display appears in the position of the right GSP segment.
→ Page C.10–6, *Changing the Inline Display*

Inline Display without frame:



If **Zoom/Pan On** is deactivated, you can move the Inline Display as required.
→ Page C.10–14, *Zooming and panning an image*

NOTE

The **Auto open inline display** option is available *only* if you have installed a **Maestro Class System** or an **Advanced Workflow Package**.

The Inline Display is closed as soon as the **Inline movie** option is enabled in the protocol properties, and the program step has been completed.
→ Page C.17–15, *Starting the movie display*



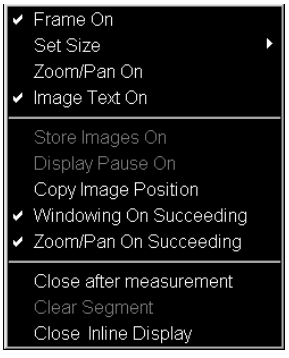
Changing the protocol parameters (e.g. increasing the number of coils by propagation) may deactivate the inline display This is indicated by the **+** sign in the protocol info line.

Display of the current protocol

The number of the protocol steps as well as the images displayed in the inline display, appear on the Inline Display title bar and as a tool tip in the bottom left corner of the Inline Display (drag & drop area).

Changing the Inline Display

The Inline Display may be displayed with or without a "frame", i.e. without title bar and control area.



✧ Deselect **Frame On** in the pop-up menu of the Inline Display.

The Inline Display is displayed without a title bar and switching area. It takes the position of the right-hand GSP segment.

If **Zoom/Pan On** is deactivated, you can move the Inline Display as required.
→ Page C.10–14, *Zooming and panning an image*

NOTE

The **Frame on** function is available *only* if you have installed a **Maestro Class System** or an **Advanced Workflow Package**.

To display the title bar and functional area again.

✧ Select **Frame On** from the context menu.

Setting the size of the Inline Display

You can set the size of the Inline Display freely or select one of three predefined sizes.

Setting the size freely

✧ Place the mouse pointer on the edge of the Inline Display.

✧ Drag the Inline Display to the required size holding the left mouse button down.

Image display is temporarily stopped.

Selecting a predefined size

If you have installed a **Maestro Class System** or an **Advanced Workflow Package**, select one of the following predefined sizes for the Inline Display:

❏ **Inline**
The Inline Display has the size of a GSP segment in the three-segment layout.

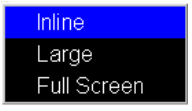
❏ **Large**
The Inline Display is as high as the monitor. This setting is useful for examinations with intervention.

❏ **Full screen**
The Inline Display fills the entire monitor.

✧ Make sure **Zoom/Pan On** mode is switched off in the pop-up menu.

✧ Switch between the predefined sizes **Inline** and **Large** by double-clicking on the Inline Display with the left mouse button.

Or



✧ Set the required size with **Set Size** in the context menu.

➪ Exit **Full screen** size again by pressing the **Esc** key.

Switching to another task card

Inline Display closes if you switch to another task card (e.g. **Viewing**).

➪ If you return to the **Exam** task card, the inline display will be open again with the same settings as applicable for manual starting. Only the last **Frame On** setting is retained.

Image display

Inline display shows the images in sequence, similar to a fast slide show.

How reconstructed images are displayed depends on the sequence used and the protocol settings:

❏ If image calculation provides images very quickly, it may not be possible to display all the images. In this case, you will only see the most up-to-date image.

❏ If the slices are scanned with interleaving, the inline display will initially remain empty. The images are reconstructed only when all data have been acquired.



✧ Click the **Display Pause On** button.

Or

✧ Select **Display Pause On** from the context menu.

The presentation pauses at the image currently displayed.

➪ It is not possible to pause the display if automatic image storage is deactivated.
→ Page C.12–10, *Setting automatic saving and loading*

Restarting image display

You are able to resume image display at any time. The image displayed next is the last one reconstructed. Images that have been reconstructed since the display has been paused are no longer available for inline display.



✧ Click the **Display Pause On** button.

Or

✧ Select **Display Pause On** from the context menu.

Image display continues.

Changing image display

The images are transferred from image calculation using standardized window values and aspect ratios.

You can modify this image display: You may window, zoom, and pan the images during Inline Display.

NOTE

If displayed very quickly on the inline display, your changes may not be visible due to windowing, zooming, or panning.

✧ In this case, pause the display.

NOTE

The changed settings for image display in the Inline Display are *not* stored.

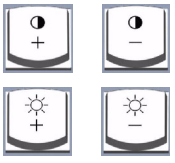
Windowing an image

Windowing with the center mouse button, allows you to modify the brightness and contrast of the displayed image.

✧ Position the mouse pointer on the image displayed in the inline display.

✧ Press and hold the center mouse button while dragging the mouse up/down or right/left.

Or



✧ Window by using these symbol keys on the symbol keypad of your keyboard.

Windowing images up to the end of the series

Using the mouse, you are able to automatically apply the new window values of an image to subsequent images in the respective series.

✧ Select **Windowing On Succeeding** from the context menu.

Windowing images automatically

You can also assign automatic window values to the image.

✧ Double-click the image currently displayed with the center mouse button.
→ *syngo* Operator Manual

Or



✧ Press this key on the symbol keypad.

Zooming and panning an image

The images shown in inline display are shown to fit the segment size. You can change this display.

✧ Select **Zoom/Pan On** from the pop-up menu.



✧ Position the mouse pointer in the *outer* area of the image.

✧ Hold the *left* mouse button down and drag the mouse pointer up to enlarge the image or down to reduce the image.



✧ Position the mouse pointer in the *inner* area of the image.

✧ To pan the image contents, press and hold the *left* mouse button and drag the mouse upward, downward, to the right, or to the left.

Zooming images up to the end of the series

You can change the menu settings so that the changes to the visible image section are automatically applied to all images in the series.



✧ Select **Zoom/Pan On Series** from the context menu.

Resetting changes

You can undo the zooming/panning in the Inline Display.

✧ Double-click the image with the *left* mouse button.

The images are again fitted to the segment size.

Hiding image text

You can hide image text for improved viewing of reconstructed images.

✧ Deselect **Image Text On** in the context menu.

Image text is hidden on the transferred images.

You can show image text in the transferred images again.

✧ Select **Image Text On** from the context menu.

When you restart image display, all subsequent images will be shown with (or without) image text.

Removing an image

For example, if you have interrupted a scan and the image displayed last remains in the image area.

✧ Right-click the Inline Display.

✧ Select **Clear Segment** from the context menu.

The image currently displayed is cleared from the image area.

Saving images

The calculated images in inline display are usually automatically stored in the **Patient Browser**.

In some cases you may deactivate automatic storage and manually store single images shown in the Inline Display.

Automatic image storage

For each protocol, the system defines whether automatic images storage may be switched off or not.

If automatic image storage is switched off, the images will be deleted after initial display in the Inline Display.

For protocols involving offline image calculation (e.g. spectroscopy), automatic image storage is not possible.

For real-time scans, on the other hand, it makes sense to switch off automatic image storage and just save single images manually.

Disabling automatic image storage

You will disable automatic storage if the images are not necessary for diagnostic purposes (e.g., in case of real-time scans).
→ Page C.12–10, *Setting automatic saving and loading*



✧ Click the **Store Images On/Off** button.

Or

✧ Deselect **Auto store images** in the context menu.



The images of your current scan are no longer stored. They are only displayed in the Inline Display.

CAUTION

When you disable automatic image storage, image data will be lost!

➪ Automatic image storage can be disabled for a current measurement only.



➪ The **Display Pause** button is not available while automatic image storage is disabled. In this case, you cannot pause image display.



➪ The **Store Images On/Off** button is disabled if image reconstruction is completed or the **Auto store images** option cannot be deselected.

Enabling automatic image storage



If you require all images for diagnosis, you can enable automatic image storage.

✧ Click the **Store Images On/Off** button in the Inline Display.

Or

✧ Select **Store Images On** from the context menu.

When the **Store Images On/Off** button appears depressed, images are automatically stored in the **Patient Browser** as they are acquired.

Manual image storage

You can still store individual images manually when automatic image storage is disabled.



✧ Click the **Save** button.

The image currently displayed in the image area of the Inline Display will be saved.

➪ If the Inline Display does not contain an image, the **Save** button is not available.

Copying the image position

You are able to copy the slice position and orientation of the current image in inline display to the protocol opened in the program control.

This position and orientation are then transferred to the selected graphic object of the opened protocol. If no graphic object is selected, the position and orientation will be transferred to the first slice group of the protocol.

The slice position and orientation are also stored in a buffer.

If no protocol is open, the slice position and orientation will remain in the buffer. You can transfer these settings to another protocol later with Image **Tools > Paste Image Position**.

Copying the image position via button



✧ Click the **Copy Image Position** button.

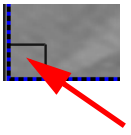
Or

✧ Select **Copy Image Position** from the context menu.

➪ You may select **Copy Image Position** as many times as required. The buffer contents will be overwritten.

Copying the image position via drag & drop

The prerequisite for this step is an open protocol.



✧ Place the mouse pointer on the bottom left corner of the inline display (drag & drop area).

✧ Drag and drop the image position of the current image into the GSP segment.

The current slice position and orientation will be copied to the open protocol.

Selective image display (BOLD)

With respect to **BOLD**, it is sometimes useful to only display a certain slice in the Inline Display (instead of having all images displayed).

The slice is selected by using its image number.
→ Page C.6–67, *Numbering of reconstructed images*



✧ Click the **Display Filter** button to enable image display selection.

When the button is selected, a field is shown that lets you select the slice to be displayed.



✧ Enter the number of the slice to have the images displayed.

Use the arrow buttons to change the slice number during scanning.

Interactive scanning in real-time mode (optional)

Your system contains various protocols that support real-time mode similar to fluoroscopy.

When performing scans in this mode, you are able to use the space mouse to continuously change slice position and orientation.

This allows you to interactively locate a slice of interest and transfer its position and orientation to another (high-resolution) scan protocol.

Interactive scans in real-time mode run as continuous loops. After locating the desired slice position and orientation, you may close the measurement in the program control.

Interactive scanning procedure

- ✧ Select a real-time protocol from the program card.
  → Page C.2–4, *Selecting a scan program*
- ✧ Transfer the protocol to the program control.
  → Page C.2–7, *Transferring a scan program to the program control*
- ✧ Set automatic opening of Inline Display in the protocol properties.
  → Page C.12–10, *Setting automatic saving and loading*
- ✧ Deselect the **Auto store images** option on the **Auto load** subtask card in the protocol properties.
- ✧ Prepare the protocol for the scan.
  → Page C.4–1, *Positioning Slices*
  → Page C.5–1, *Adjusting Measurement Parameters*



- ✧ Click **Apply** in the program control to start the protocol.
- ✧ View the first reconstructed images in the Inline Display.

The slice position and orientation specified here are the initial values that you are changing interactively during scanning.

✧ Vary the slice position and orientation during the measurement by moving the space mouse .
refer to the System Manual

The new slice position and orientation are already applied to the following reconstructed images. Once a suitable slice is displayed, you may apply the image position.



✧ Click the **Copy Image Position** button.
→ Page C.10–19, *Copying the image position*



✧ Click the **Stop** button in the program control.

Scanning stops.

As a next step, you prepare the high-resolution protocol. Copy the slice position and orientation of the real-time protocol from the buffer.

✧ Select **Tools > Paste Image Position**.
→ Page C.4–86, *Transferring the position of reference images*

Inline display for CARE Bolus scans

The inline display allows you to check acquired images while scanning is in progress. This is especially helpful in cases where you may want to stop the current scan and continue with the next scan, e.g. during contrast agent scans where you are monitoring the uptake of contrast agent. As soon as the contrast agent becomes visible in the image, you may immediately proceed to the next high-resolution sequence.

NOTE

The **Stop & Continue** function is available *only* if the **CARE Bolus** license has been installed.

✧ Place the keyboard focus (dashed border) on the **Stop / Continue** button.
→ Page C.3–18, *Keyboard focus*

✧ Press the **spacebar** or the **Enter** key.

Or



✧ Click the **Stop / Continue** button in the Inline Display.

The scan in progress stops and the following scan starts immediately.

NOTE

Using the keyboard provides you with the advantage of focussing on the inline display instead of the mouse pointer.

Starting multiple breath-hold scans

A multiple breath-hold protocol is started in the inline display and run in several steps.

After positioning the slices in GSP, you can define the number of breath-hold intervals by entering the **Concatenations**. The acquisition time required for each breath-hold interval is displayed as a tool tip in the information line below the image area.



After each breath-hold command, the image rows of the slices belonging to *one* concatenation are measured. → Page H.1–31, *Excitation sequence of slices*

You are starting by scanning each concatenation (=breath-hold interval) from the Inline Display. With navigator protocols, you can also observe the respiratory movement of the diaphragm in the Inline Display.

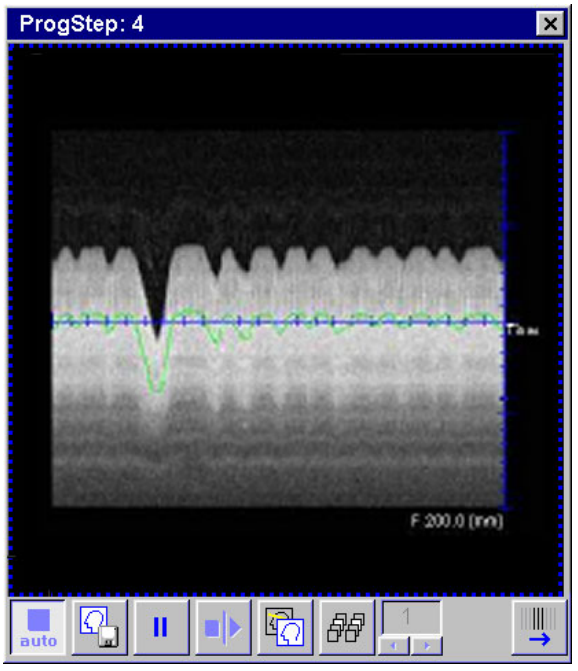
✧ Prepare a navigator protocol for scanning. Select a mode for **Respiratory Control** and include a preparation phase (**Scout Mode**).
→ Page H.1–21, *Navigator* 🗀 *Geometry-Navigator*

✧ Open the Inline Display.



✧ Click **Apply** in the program control to start the protocol.

The position of the diaphragm (navigator signal) is displayed as a function of time in the Inline Display.



✧ Follow the respiratory curve on the Inline Display.

✧ Apply the breath-hold command.



✧ Click the **Scan Breathhold** button.

The measurement is started.

TIP

If the keyboard focus (dashed border) is on the **Scan Breathhold** button, you may want to press the **spacebar** to start scanning.

Navigator signals are *not* recorded during scanning. After the slices of the first concatenation have been scanned, the navigator signal is scanned and displayed again.

The position of the diaphragm during the "first" scan is displayed as a yellow line.

✧ Apply the command to breathe again.

The patient should draw several normal breaths.

✧ Apply the breathhold command to scan the image lines of the next concatenation and click the **Scan Breathhold** button again.

To stop the multiple breath hold scans.

✧ Click the **Stop** button in the program control.

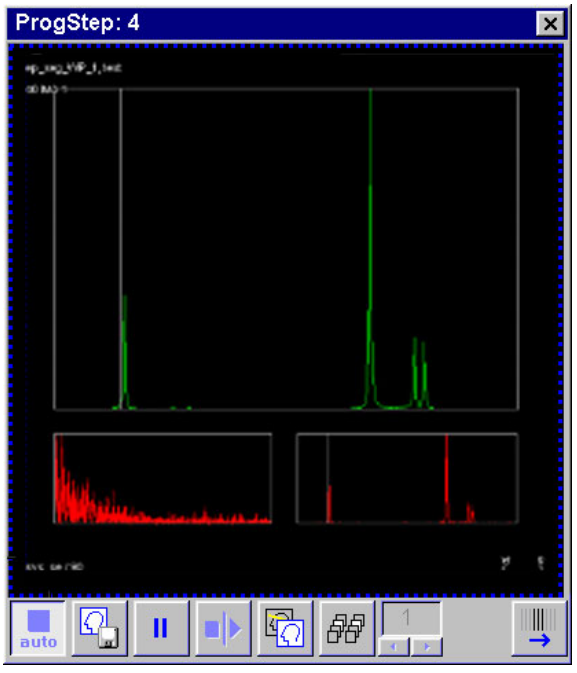
The results of all slices that have been scanned are stored. Partially scanned slices are lost.

NOTE

When you cancel a protocol with multiple **Scans**, all images from the current scan are lost.

Display of the spectroscopy time signal

You may use the inline display to track the MR spectrum while a scan is in progress. The current and accumulated spectroscopy data are displayed as a vector graphic in the Inline Display window.



➪ For spectroscopy sequences, the **Store Images On/Off** button is not available, because it is not possible to deselect the **Auto store images** option in the protocol properties.

Ending Inline Display

Inline Display can be terminated either manually or automatically.

Ending Inline Display manually

When you close inline display, you are no longer able to view reconstructed images or graphics of a scan (online or offline).



✧ Click the **Close Window** button in the top right corner of the inline display.

Or



✧ Click the **Inline Display** button again on the tool bar of the **Exam** task card.

Or

✧ Press **Alt + F4** on your keyboard.

Or

✧ Select **Close Inline Display** from the context menu.

The Inline Display is closed.

Ending Inline Display automatically

In the context menu you can set the Inline Display to close automatically as soon as image calculation is completed.



✧ Select **Close after measurement** from the pop-up menu.

The Inline Display closes as soon as the current image calculation is completed.

You can also deactivate this setting.

✧ Deselect **Close after measurement** in the pop-up menu.

➪ If reconstruction of a protocol has been completed with the **Inline movie** option, the inline display automatically closes and movie display starts.

➪ The inline display is automatically cleared when protocol reconstruction is complete and a new scan protocol has been enabled.

Tips on optimum performance with real-time scans

- ❏ Check whether one or two receiver coils are connected.
- ❏ Deactivate the image text display.
- ❏ Disable automatic image storage.
  The images of this scan will *not* be stored in the **Patient Browser**.
- ❏ Finish all other processes, e.g. archiving and sending.
- ❏ Optimize the protocol parameters, e.g., minimize TE and TR, reduce phase-encoding steps, and deactivate fat saturation.

CHAPTER C.11

Patient Instructions

Two essential factors in obtaining useful MR images are patient communication and cooperation.

Patient information and instructions are given during an examination by means of manual or automatic voice outputs, e.g. breathing control instructions.

Sample files for voice outputs are supplied in two languages with your system. You may record additional voice outputs in various languages. You can assign these voice recordings to a protocol as a property. This allows you to automate communication with the patient. You are also able to play back these voice outputs manually without reference to a scan.

➪ Voice outputs are not suitable for patient instructions with multiple measurements, e.g. multi-breathhold **abdomen**.

Voice output A single spoken instruction to the patient. Instructions are available in various languages.

Label A unique name for each voice output. The label is displayed in the selection list and is used to identify a voice output.

Do not confuse voice outputs with music played to the patient. The intercom has a separate input for connecting a CD player, radio, etc.

NOTICE

Never insert a commercial music CD into the CD drive of the *syngo* Acquisition Workplace. The copy protection on the CDs could cause the system to crash and damage the drive.

When using automatic voice outputs to give instructions to the patient, it is advisable not to play music at the same time.

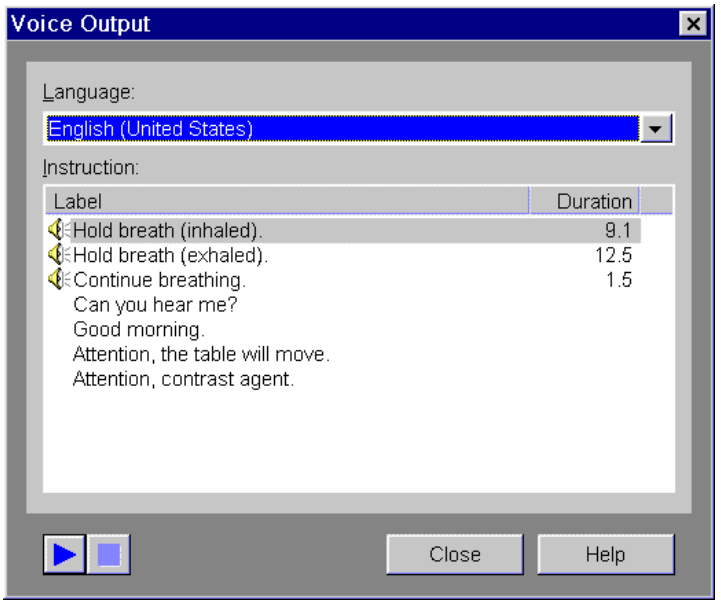
Playing back an existing voice output

For many examinations it is important to instruct the patient before and/or after the scan (e.g. to breathe in and hold his breath). Existing voice outputs may be played back manually or automatically. You may also set the volume for the voice output and play back the patient instructions either in the control room or in both the control room and the examination room.

→ Page C.11–11, *Changing the volume*
→ Page C.11–12, *CV/CBT switch*

✧ Select **Joblist > Voice Output > Play...** or select **Voice Output** from the context menu of the program control.

The **Voice output** dialog box opens.



Existing voice outputs are marked with a loudspeaker icon and indicate the playback duration. The language of the label does not correspond to the set language.

➪ The dialog will open only if no scan is active.

Playing back patient instructions manually

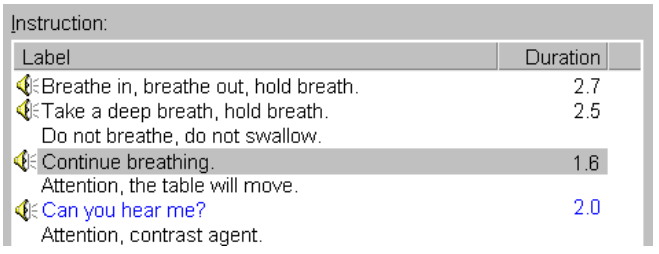
Voice outputs are available in several languages. They can be played back as often as necessary and at any time. This may be helpful, e.g. to familiarize patients with the sound.

➪ Patient instructions can be played back before and after but not during a scan.

The language in the **Voice Outputs** dialog box is the default setting. You may select a different language from the selection list.



✧ Select the required language from the **Language** selection list.



✧ Select the voice output, e.g. "Continue breathing", from the **Instruction** selection list.



✧ Click the **Play** button to play back the voice output.

The patient hears the instructions in the examination room via headphones or loudspeakers.

Pausing a voice output

You can stop if you do not want to play back an entire voice output or have selected the wrong voice output.



✧ Click the **STOP** button.

Playback of the voice output stops.

Automatic playback of a voice output

If you want to play back voice outputs automatically before and/or after a scan, the required voice outputs have to be referenced to the protocol.

The voice outputs are integrated

❏ via the protocol properties during program set-up in the **Exam Explorer**

Or

❏ in the program control during the examination
→ Page C.12–9, *Playing back voice output*

When a protocol with reference voice output is ready to run or if you have integrated patient instructions for automatic playback via the protocol properties, the voice output will be played back automatically. If the referenced voice output does not exist, a message box appears. In that case, acknowledge this message box and give your instructions via the intercom system.
→ Page C.6–55, *Program instruction with a patient instruction*

Setting playback of voice outputs

You can adjust the voice outputs to the individual requirements of a patient, i.e. by selecting the language and adjusting the volume.

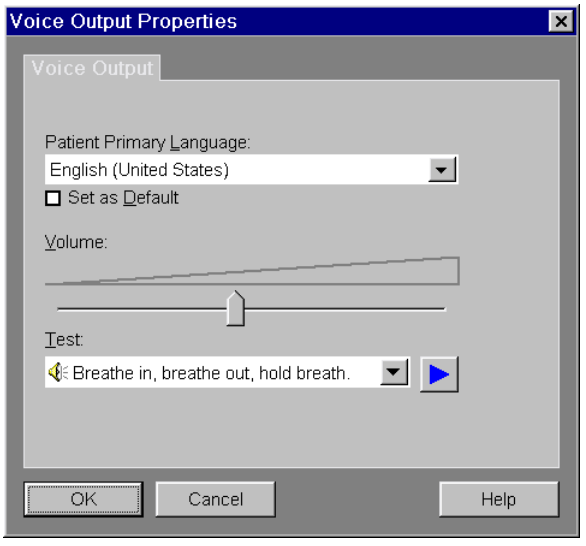
➪ If your system is not able to play back voice outputs, the **Test** selection list and the **Play** button will not be active.

✧ Select **Patient > Voice Output Properties**.

Or

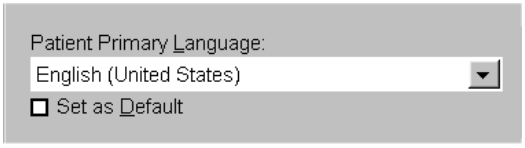
✧ Right-click the name of the patient in the program control and select **Voice Output Properties** from the context menu.

The **Voice Output Properties** dialog box opens.



Changing the language for the current patient

Voice outputs should be played back in a language the patient can understand.



✧ Select the language, e.g. English (United States), from the **Patient Primary Language** selection list.

If the **Set as Default** check box is *not* clicked, the language entered in the **Exam UI Configuration - Voice Output** dialog box will be used again for the next patient.

➪ You can only select from the languages that are available on your system. It is not possible to add new languages.

NOTICE

It is not possible to change the patient language once scanning has started.

➪ You may record voice outputs in other languages.

Changing the default language setting



You can use the same newly selected language again for the next patients.

✧ Click the **Set as Default** check box to save the selected language as the default language.

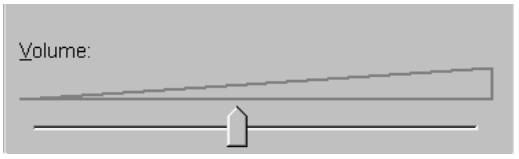
The changed default language setting will become the default in the **Exam UI Configuration - Voice Output** dialog box.

You can redefine the default language in the **Exam UI Configuration - Voice Output** dialog box.
→ Page C.11–29, *Configuring voice output*

➪ The default language for patient instructions does not have to be the same as the language of the user interface.

Changing the volume

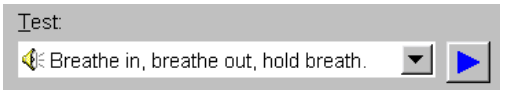
The volume of voice outputs is also preset in the **Exam UI Configuration - Voice Output** configuration window. You may change the volume set in the **Voice Output Properties** dialog box.



✧ Move the **Volume** slider to the right to increase the volume for voice output, or to the left to decrease it.

Testing voice output

After you have selected the language and set the volume, you are able to select and play back a voice output for test purposes.



✧ Select a voice output from the **Test** selection list.



✧ Click the **Play** button.

The selected voice output will be played back.

CV/CBT switch

Use the toggle switch on the intercom system to select whether the patient instructions will be played back in the control room only or in both the control as well as the examination room.

✧ Push the CV/CBT toggle switch on the intercom system toward **CBT**.

The patient instructions will be played back in the control room only.

➪ This may be useful to test, for example, voice outputs right after you have recorded them.

Or

✧ Push the CV/CBT toggle switch on the intercom system toward **CV**.

The patient instructions will be played back in the control as well as the examination room.

➪ The toggle switch must be set to **CV** during examinations.

Recording and editing voice outputs

Patient instructions may be recorded or edited only if no patient is currently registered.

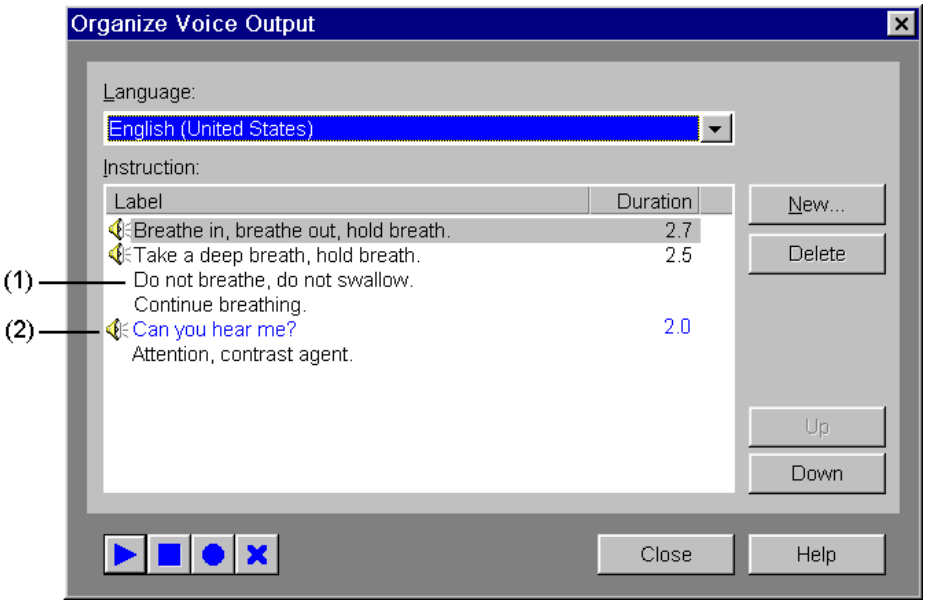
✧ Select **Patient > Close Patient** from the main menu of the **Exam** task card.

Or

✧ Select the name of the patient in the program control with a right-click and select **Close Patient** from the context menu.
→ Page C.6–20, *Closing the patient*

✧ Select **Joblist > Voice Outputs > Organize**.

The **Organize Voice Outputs** dialog box opens.



(1) Default voice output (black)
(2) User-defined voice output (blue)

Recording new voice output

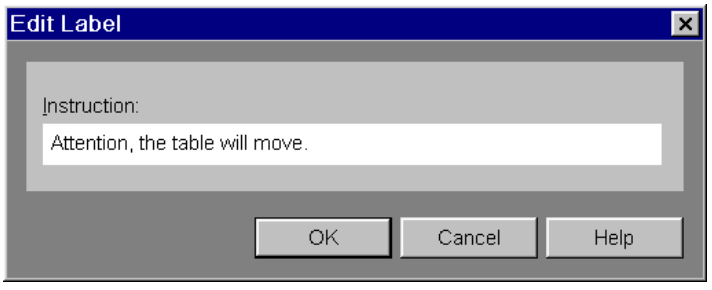
The files available on your system are shown with a loudspeaker icon in the **Instruction** selection list in the **Organize Voice Outputs** dialog box. You may record additional instructions, if required.

Creating a voice output

To create a new voice output, you first have to create a label for the instructions and then start recording.

- ✧ Select the language for the new instructions in the **Organize Voice Outputs** dialog box.
- ✧ Click the **New** button in the **Organize Voice Output** dialog box.

The **Edit Label** dialog box is displayed. The input field is empty.



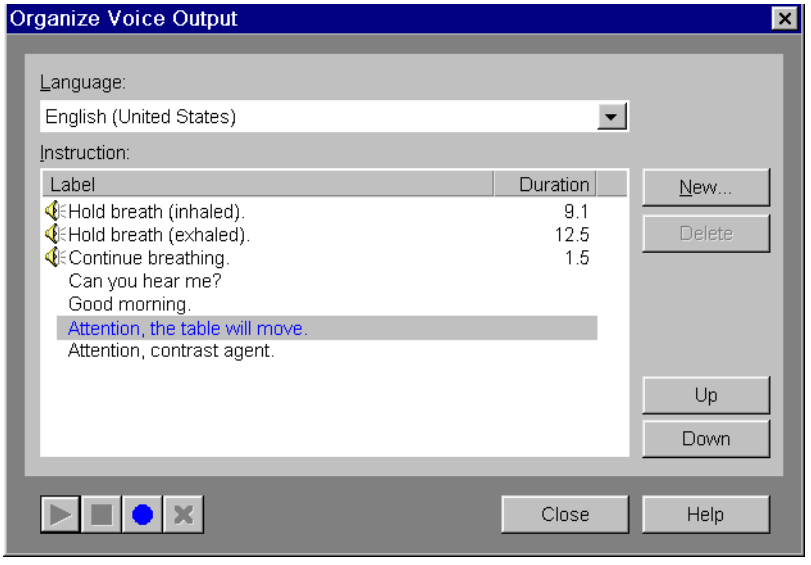
✧ Enter a name for the new voice output.

➪ The name for the new label cannot be more than 31 characters long and must start with a letter
(a to z or A to Z). The following characters cannot be used: ?, ", *, |, :, \, /, >, <.

✧ Confirm with the **OK** button.

The **Edit Label** dialog box closes and the newly created voice output is appended to the end of the **Label** selection list in the **Organize Voice Outputs** dialog box.

➪ The label for the new voice output is now available in all languages and the voice output can be recorded in any other language necessary.



➪ User-defined voice outputs are blue in the **Label** selection list.

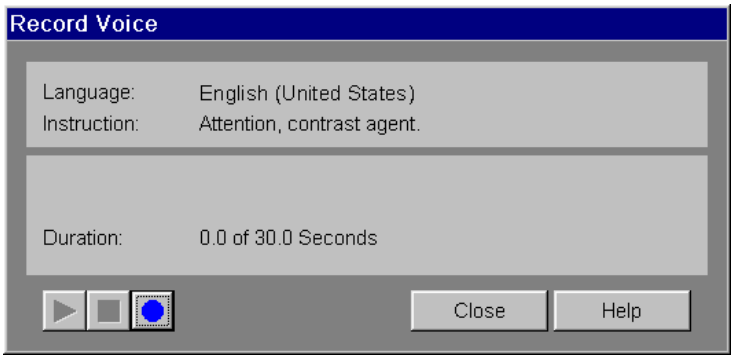
Recording a new voice output



To record a voice output you will need to use both the **Record Voice** dialog box and your system's intercom.

✧ Click the **Record** button in the **Organize Voice Output** dialog box.

The **Record Voice** dialog box opens.



The dialog box shows the language selected in **Organize Voice Output** and the label of the voice output that is being recorded.

➪ If your *syngo* Acquisition Workplace has a volume indicator, the dialog box will contain an additional bar for monitoring the volume.



✧ Press the **Talk** button on the intercom system and hold it pressed.



✧ Click the **Record** button in the **Record Voice** dialog box to activate recording mode.

✧ Speak the new instruction into the built-in microphone.

The duration is displayed during recording.

➪ A voice output can be up to 30 seconds long.

NOTICE

To ensure good recording quality, we recommend maintaining a distance of 30 cm from the microphone and speaking in a normal voice. You can also adjust the recording volume with the **Record Volume** slider during configuration. The volume slider in the exam room has no effect on the recording volume.



✧ Press the **STOP** button in the **Record Voice** dialog box to stop recording.

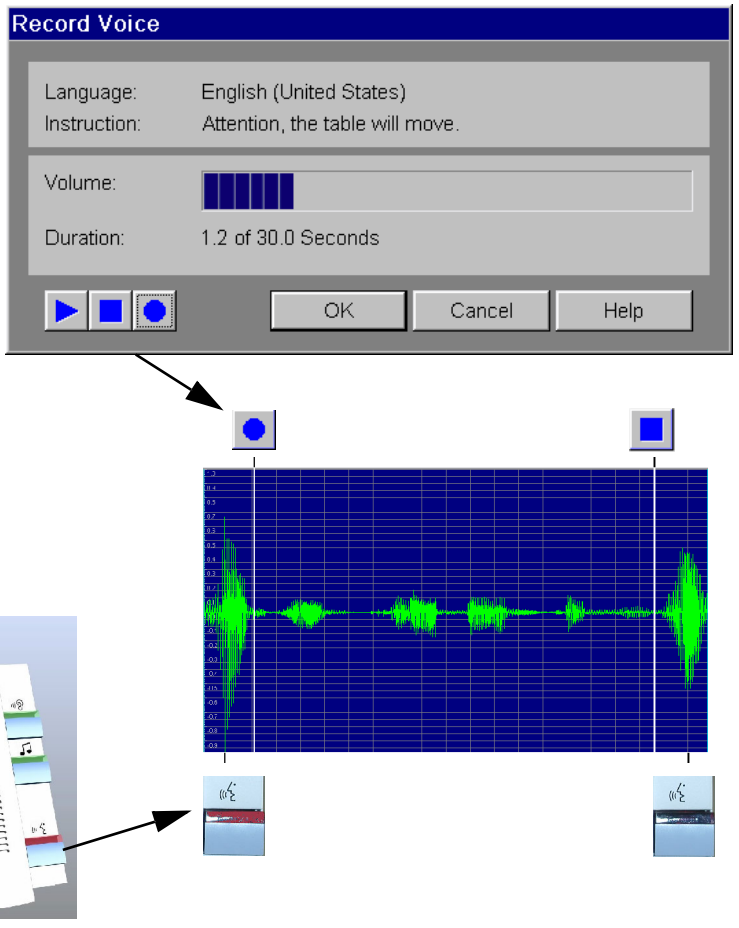


✧ Release the **Talk** button on the intercom.



✧ Click **Close** to close the dialog box.

The newly recorded voice output will now appear in the selection list of the **Organize Voice Outputs** dialog box with its playback time and the loudspeaker icon.



➪ Proceed in this sequence to avoid unwanted noise at the beginning and end of the recording.

Testing a new voice output

You can play back the new patient instructions after recording the voice output to test comprehensibility.

After the recording the **Play** button will be active.



✧ Click the **Play** button.

The voice output is played back.

Voice outputs are played back through the loudspeakers or headphones (set with the CBT/CV switch) both in the control and the examination rooms, just as they would be during an examination.



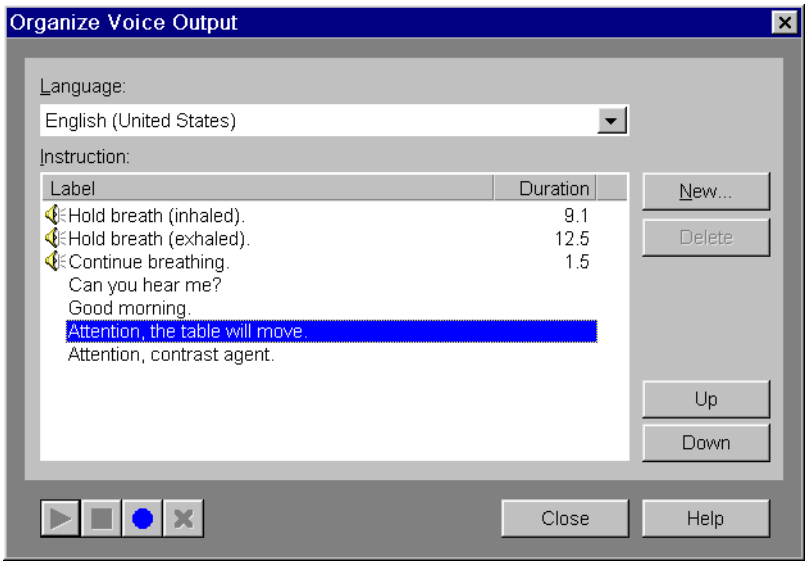
✧ Click the **STOP** button to stop playback of the voice output.

Changing a voice output

If an existing voice output does not meet your requirements, you can record a new one in its place.

Editing a voice output

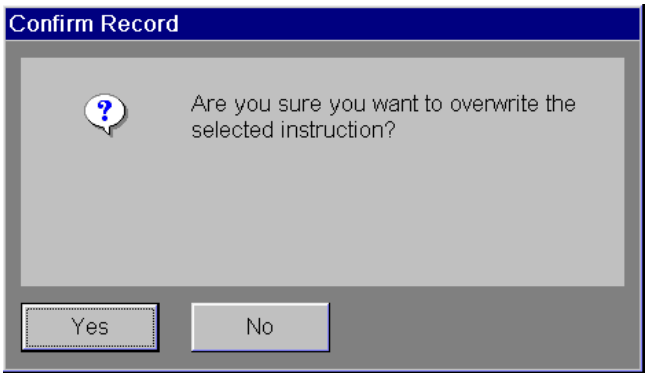
✧ Select the instructions to be modified from the **Labels** selection list in the **Organize Voice Outputs** dialog box.

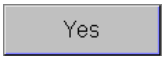




✧ Click the **Record** button.

If you select existing instructions to record over, the **Confirm Recording** message box appears.





✧ Click the **Yes** button.

The **Record Voice** dialog box opens.

You can now record the patient instructions.
→ Page C.11–17, *Recording a new voice output*

Reordering voice outputs

Manual playback of patient instructions is much easier if the instructions are already organized in the correct order. This enables you to access voice outputs quickly and helps prevent mistakes.

✧ Select the voice output from the **Instruction** selection list in the **Organize Voice Output** dialog box.



✧ Click the **Up** button to move a selected voice output up in the selection list.

Or



✧ Click the **Down** button to move a selected voice output down in the selection list.

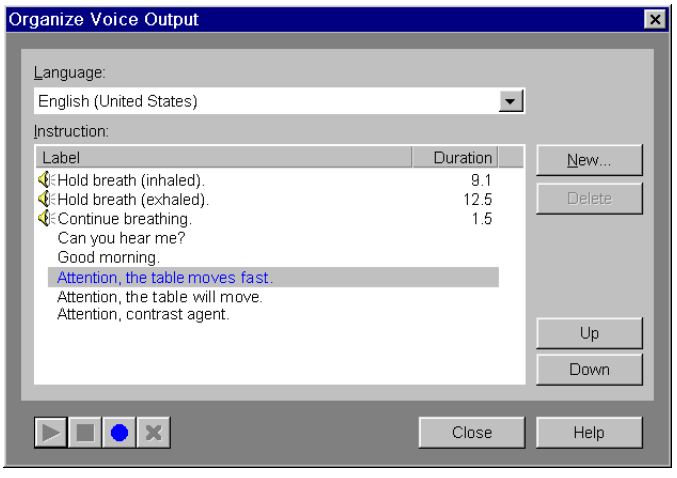
Deleting user-defined voice outputs

When you no longer require a voice output, you can delete it. However, remember that voice outputs may have been linked to program instructions for automatic playback. If the deleted voice output does not exist when a protocol is running, a message appears and you have to deliver the patient instructions via the intercom system.

➪ It is not possible to delete standard pre-installed voice outputs.

Deleting a voice output from the current language

✧ In the **Organize voice output** dialog box, select the voice output to be deleted from the **Instruction** selection list.

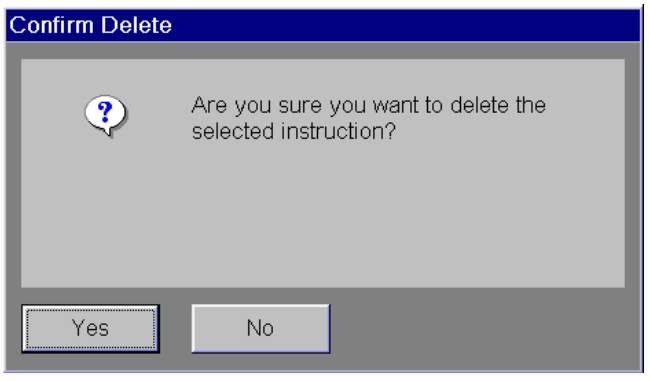


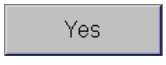


✧ Click the **Delete** button

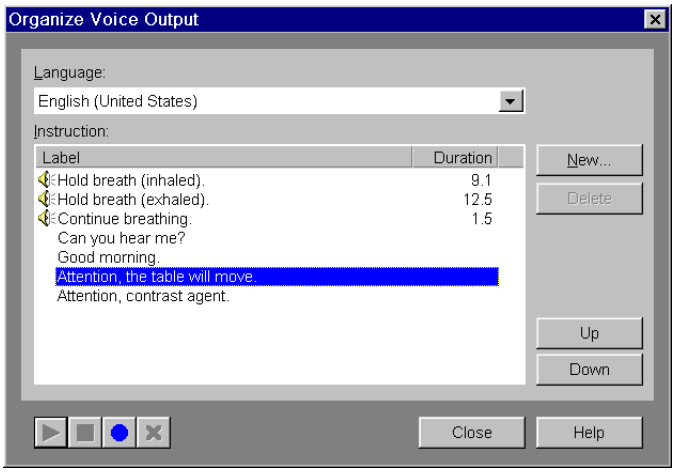
➪ The button is only active if a voice output exists for the selected instruction, i.e. it is marked with a loudspeaker icon.

The **Confirm Delete** message box will appear.



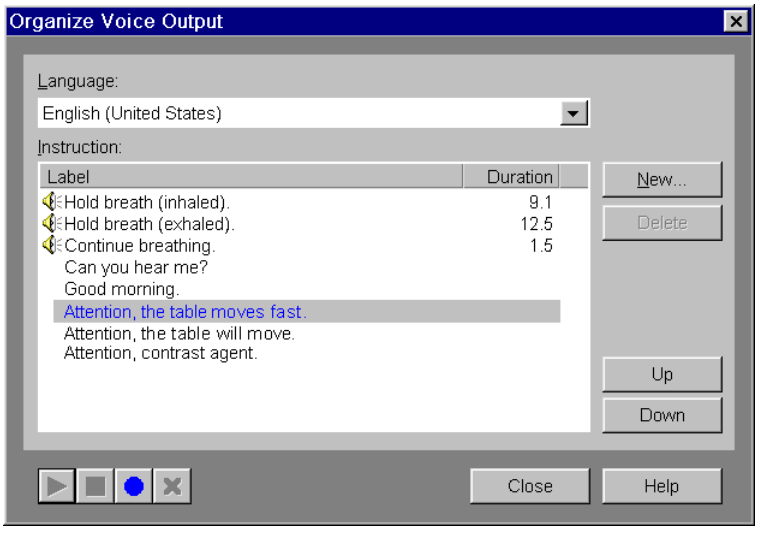


✧ Click the **Yes** button.



The loudspeaker icon in front of the label disappears and the voice output is no longer available in the selected language. Deleting voice outputs in the current language does not automatically delete them in other languages (if available).

Deleting a voice output from all languages



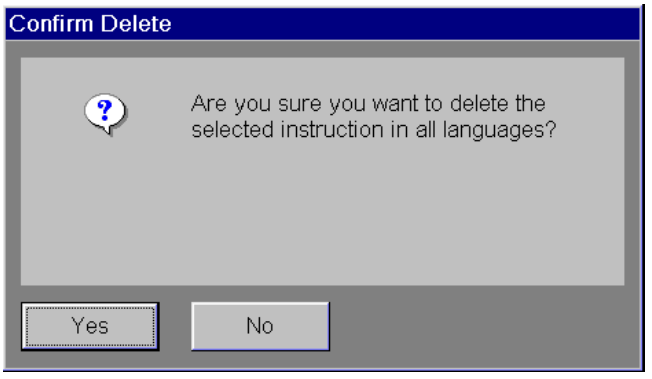
✧ In the **Organize voice output** dialog box, select the voice output to be deleted from the **Instruction** selection list.



✧ Click the **Delete** button.

➪ The button is not active, if a default instruction is selected.

The **Confirm Delete** message box will appear.



Yes

✧ Click the **Yes** button.

The voice output will be deleted from all languages and the label will be removed from the **selection list**.

NOTICE

The changes you make in the **Organize Voice Outputs** dialog box are implemented immediately. It is not possible to undo them.

Configuring voice output

You can configure the voice output in the **Voice Output Properties** dialog box or in the **Exam UI Configuration - Voice Output** dialog box.

The settings in the **Voice Output Properties** dialog box only apply to the current patient.
→ Page C.11–8, *Setting playback of voice outputs*

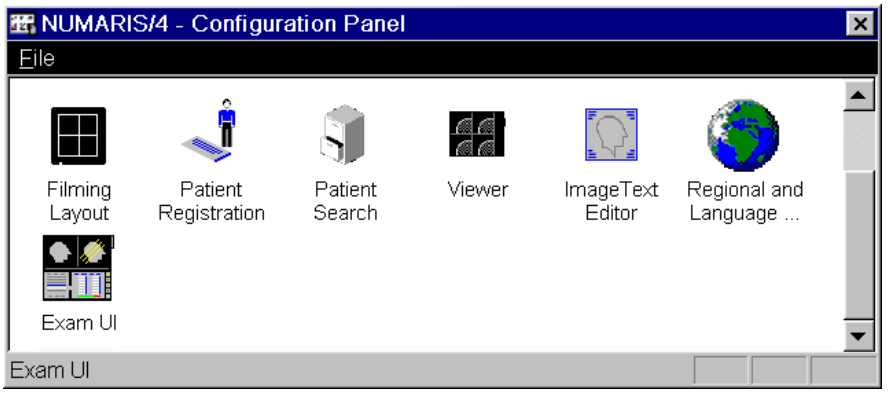
The settings in the **Exam UI Configuration - Voice Output** dialog box are global. These defaults will be used when all patients are registered.

You are able to perform the following settings:

- ❏ Preselection of patient language
- ❏ Volume

✧ Select **Options > Configuration**.

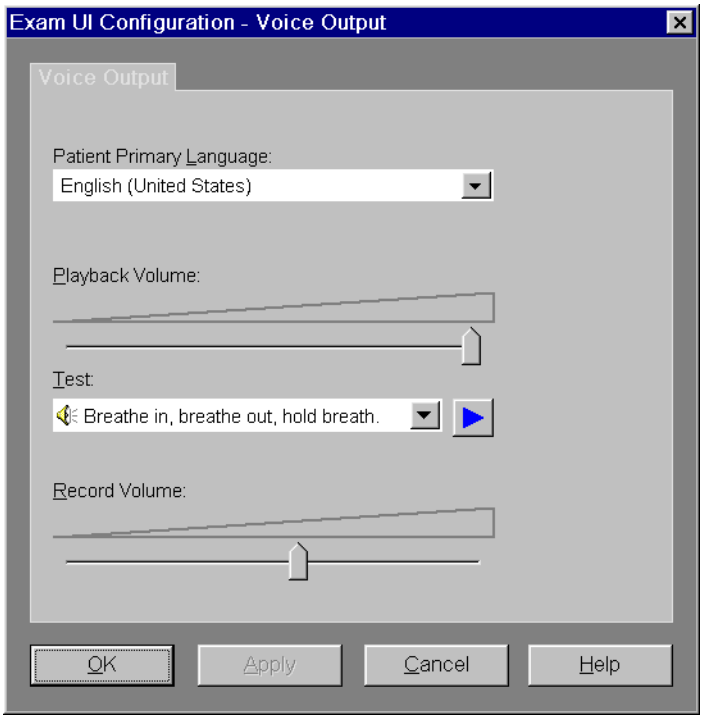
The **NUMARIS/4 Configuration Panel** dialog box opens.





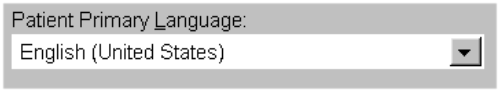
✧ Double-click the **Examination** icon.

The **Exam UI Configuration - Voice Output** box opens.



Selecting the patient language

Voice outputs should be played back in a language the patient can understand. The language used by most patients should be set as the default language of your system.

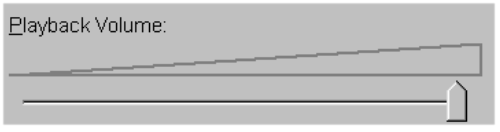


✧ Select the required language from the **Patient Primary Language** selection list.

You can only select from the languages that are available on your system. It is not possible to add new languages.

Setting the output volume

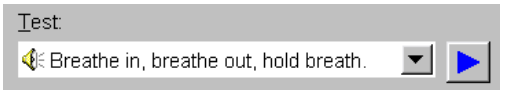
You can set the volume for playback of voice outputs.



✧ Move the **Output Volume** slider to the right to increase the volume for voice output playback, or to the left to decrease it.

Testing the selected voice output

After you have selected the language and set the volume, you are able to select and play back a voice output for test purposes.



✧ Select a voice output from the **Test** selection list.

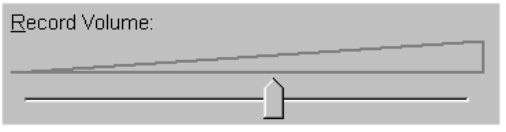


✧ Then click the **Play** button.

The selected voice output will be played back.

Setting the recording volume

You can set the volume for playback of the voice outputs you have recorded.



✧ Move the **Recording Volume** slider to the right to increase the volume for recording voice outputs, or to the left to decrease it.

Closing the dialog box

After you have entered your settings, you may save them.



✧ Click the **OK** button.

All settings will be saved.

Or



✧ Click **Cancel**.

The **Exam UI Configuration - Voice Output** box closes. All settings remain unchanged.

CHAPTER C.12

Protocol and Pause Properties

The protocols and pauses are characterized by numerous properties.

These properties include, e.g. their name, comment, copy references, start properties, and automatic loading of scanned images into other task cards.

You can change the properties of protocols and pauses to influence how an examination is performed and evaluated.

You can adjust the properties of the pending protocols and pauses during an examination.

Editing protocol properties

The properties of a protocol is changed in the **Protocol Step Properties** dialog box. You can open this dialog window from the **Exam Explorer** or from the job list.

Calling from the Exam Explorer

✧ Select a protocol in the **Exam Explorer**.

✧ Select **Edit > Properties** from the main menu of the **Exam Explorer**.

Or

✧ Select **Properties** from the context menu.

Or



✧ Click this button on the tool bar.

Or

✧ Press the shortcut **Alt + Enter** on your keyboard.

The **Protocol step properties** dialog box opens.

Calling from the job list

✧ Select the pending protocol from the job list.

✧ Select **Edit > Properties** from the main menu.

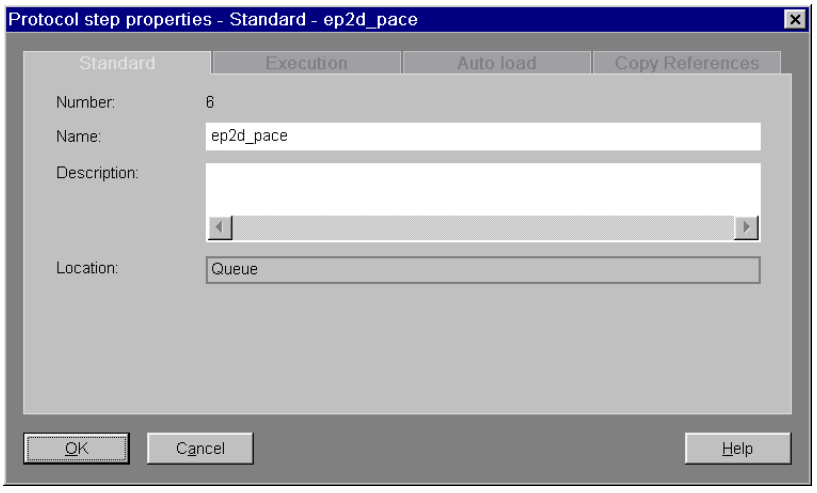
Or

✧ Select **Properties** from the context menu.

Or

✧ Press the shortcut **Alt + Enter** on your keyboard.

The **Protocol step properties** dialog box opens.



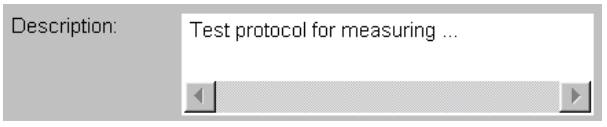
Entering a protocol name

When you first open the **Protocol step properties** dialog box, the **Standard** card is in the foreground. Enter a name and description for the protocol on this card.

Give the protocol a unique name. The name of the protocol is used as a series description for the images acquired with this protocol and is shown, for example, in the **Patient Browser**. A unique name should also clarify the function that the protocol has in the scan program.



✧ Enter a descriptive name for the protocol.



✧ Add a description to the name, if necessary.

➪ If you hover the mouse pointer over a protocol entry in the **Exam Explorer** or program control, a tool tip shows you the name of the protocol and the respective comment.

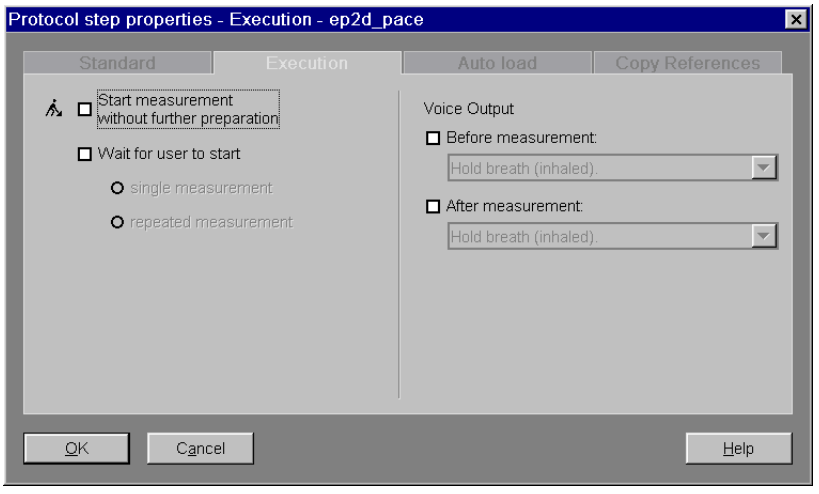
Defining start options

Before scanning, you normally have to position the graphic objects defined in the protocol to make them match the anatomy of the patient. Only localizers and protocols not requiring exact positioning can be started immediately (automatically).

You can set the following start options on the **Execution** card:

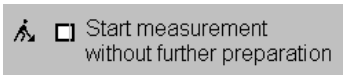
- ❏ Starting a protocol without further preparation
- ❏ Starting a protocol manually, once or several times
- ❏ Automatic voice playback before and after the measurement

✧ Go to the **Execution** subtask card.



Starting scanning with / without preparation

You will normally check the parameters and slice positioning of the protocol before each scan.



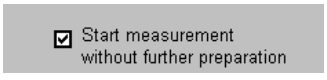
✧ Deselect the **Start measurement without further preparation** check box.



The protocol will be marked with a construction worker icon.

➪ A protocol marked with a construction worker icon has the "incomplete" status and cannot be started automatically by the system.

Localizers are normally started immediately without checking the parameters and slice positioning.



✧ Select the **Start measurement without further preparation** check box.

The construction worker icon is removed.

➪ A protocol without a construction worker icon has the status "complete" and is started automatically as soon as it reaches its turn in the queue.

Starting scanning manually

A protocol run is performed in three steps. 1) adjustments are performed, 2) data are acquired, and 3) the images are reconstructed either afterward or at the same time.

For some examinations (e.g. protocols with breath-hold commands), it is better to set manual starting. In this case, the system will pause following adjustment. You can then give the breathhold command and start the measurement manually.
→ Page C.6–21, *Starting a protocol manually*



✧ Check the **Wait for user to start** check box.

➪ If you have recorded an appropriate voice output on your system, you can perform this type of examination without manual start-up.
→ Page C.12–9, *Playing back voice output*

Running a protocol once/ more than once

After you change the means of starting the protocol to manual, you can also define whether to start the protocol once or several times in succession.





✧ Click the **Single Measurement** option.

Protocols set to run once only are marked in the scan program with a "flagman with one flag" icon.

Multiple loading and starting of protocols is used, for example, for examinations with contrast agent.





✧ Click the **Multiple Measurement** option.

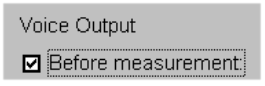
Protocols that can be loaded and run more than once are marked in the scan program with a "flagman with several flags" icon.

Prior to each new scan, a dialog window is displayed allowing you to start the protocol.

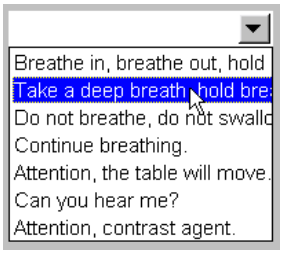
Playing back voice output

Communicating with patients is an essential part of an examination. You need to tell the patient when scanning starts and ends and give instructions such as breath-hold commands. Frequently required patient instructions are stored in your system as voice outputs.

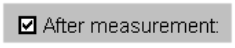
The **Execution** card is used to define whether a voice output will be played back *before* scanning. Actual scanning then starts automatically. You can also play back a voice output after the end of scanning.
→ Chapter C 11, *Patient Instructions*



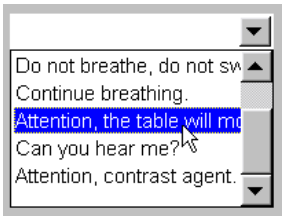
✧ Activate the **Before measurement** option.



✧ Select a suitable voice output from the selection list.



✧ Activate the **After measurement** option.



✧ Select a suitable voice output from the selection list.

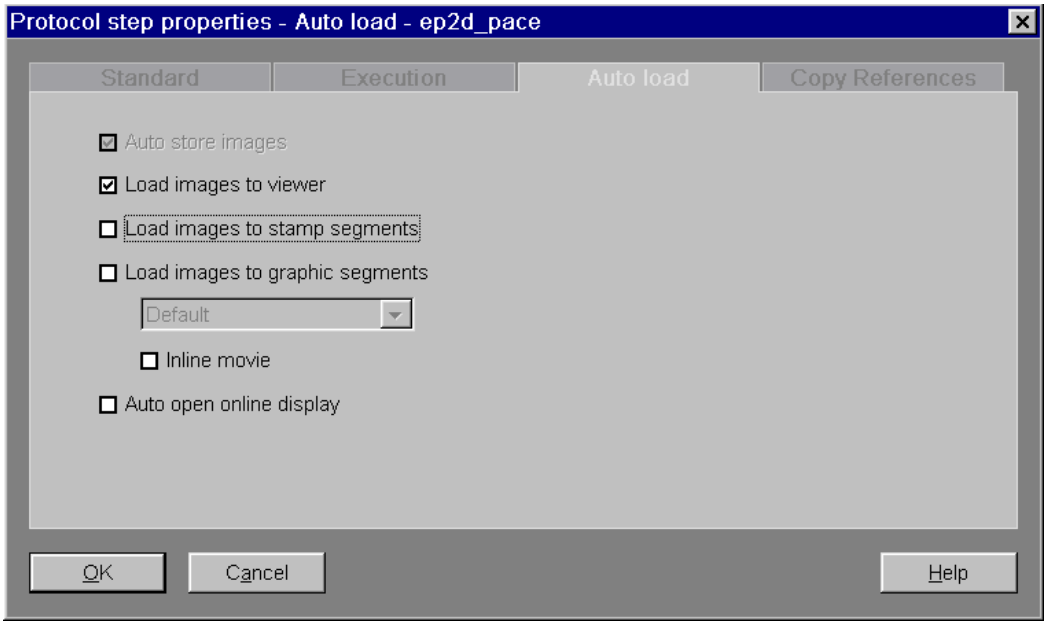


➪ Protocols with voice outputs are marked with a loudspeaker icon in the scan program.

Setting automatic saving and loading

Images and series acquired through scanning can be saved automatically and loaded into other applications. These properties are set on the **Auto load** card.

✧ Go to the **Auto Load** card.



NOTICE

The **Load images to stamp segments**, **Inline movie**, and **Auto open inline display** options will only appear on the **Auto load** subtask card if you have a **Maestro Class System** or you have installed the **Advanced Workflow** package.

Automatic image storage

For most protocols, the **Auto store images** property is defined and cannot be deactivated.

In some cases (e.g. real-time protocols), you may deactivate automatic storage and manually store single images from the inline display.
→ Chapter C 10, *Inline Display*

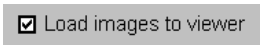


✧ Select the **Auto store images** check box.

Loading images into the Viewing card

You can automatically load acquired series into the **Viewing** task card after reconstruction for viewing, postprocessing, or evaluation.

➪ Automatic loading into the Viewing task card is not possible, if more than 400 images are reconstructed from one protocol run.

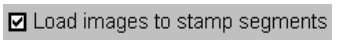


✧ Select the **Load images to viewer** check box.

The images are loaded into the Viewer in the order of the image numbering. You can affect image numbering in the protocol editor on the **System-Common** measurement parameter card.
→ Page C.5–39, *Parameter for image numbering*

Loading images into stamp segments

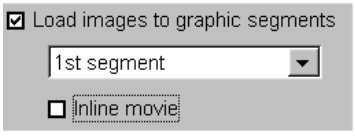
After reconstruction, you are able to load the series measured into the stamp segments of the Maestro layout of the **Examination** task card.
→ Page C.17–2, *Maestro layout*



✧ Select the **Load images to stamp segments** check box.

Loading images into GSP

After reconstruction, you are able to load the series measured into a GSP segment of the **Examination**task card and set the automatic start of movies.
→ Page C.17–13, *Movie display*

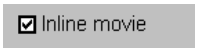


✧ Select the **Load images to graphic segments** check box.

✧ Select the required GSP segment from the selection list.

Activating inline movie

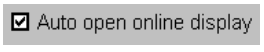
If you want to view the scanned images in movie display, activate inline movie.



✧ Select the **Inline movie** check box.

Opening Inline Display automatically

To check the reconstructed images, you are able to automatically superimpose the **Inline Display** while measuring the protocol.
→ Chapter C 10, *Inline Display*

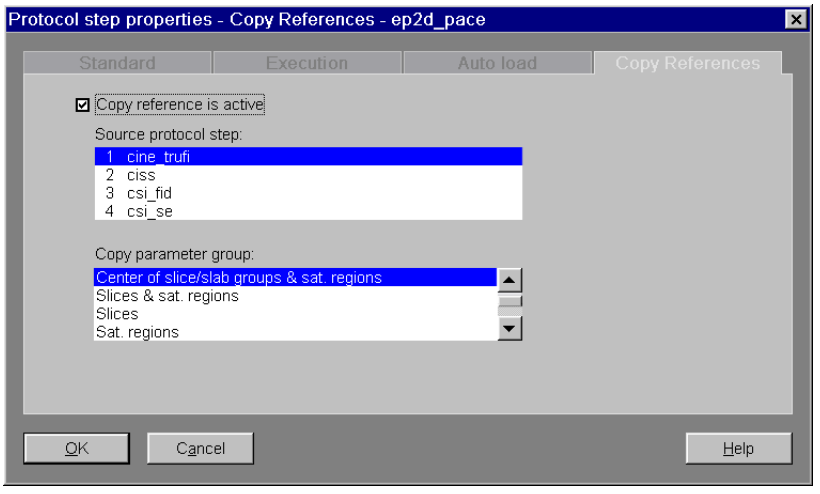


✧ Select the **Auto open Inline Display** check box.

Setting a copy reference

Copy references are used to transfer the parameter settings from a source protocol to a target protocol. Copy references make it easier to define the parameter settings.

✧ Click the **Copy References** card into foreground.



✧ Activate the **Copy reference is active** check box.

Once the copy reference is activated, you can browse the lists below and select the protocol with the parameter settings you want to copy.

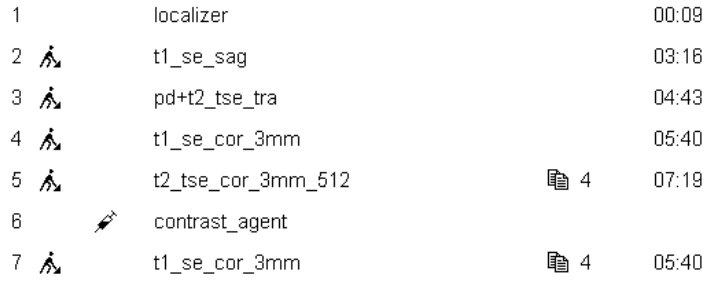
The list of source protocols contains all protocols that are in front of the selected protocol in the scan program and are not already the target of a copy reference.

✧ Select the protocol from the **Source protocol step** list.

✧ In the **Copy parameter group** list, select the parameter settings to be transferred from the source protocol to the target protocol.

➪ You are able to copy *only* the settings of parameter groups, that is, *not* those of individual parameters.
→ Page C.5–87, *Copying measurement parameters*
→ Page C.6–45, *Setting a copy reference*

Scan protocols with a copy reference are marked with a copy reference icon in the job list and in the content area of the **Exam Explorer**. The number after the icon identifies the source protocol with the copied parameters.



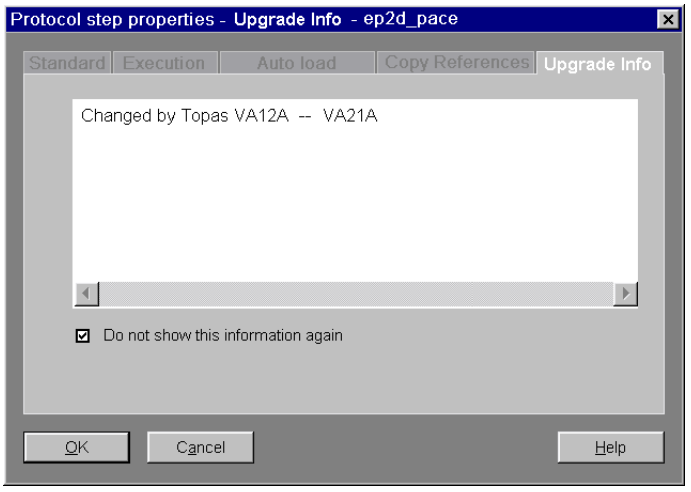
➪ If you position the mouse pointer over the copy reference icon, a tool tip shows the parameter group of the copy reference.

Displaying upgrade info

If a protocol has been modified by a software update, the **Protocol step properties** dialog box will contain the **Upgrade Info** subtask card. This tells you what software update changed the current scan protocol and who made the changes (change information).

➪ Protocols with upgrade information are marked by an underscore under their name in the scan program.

✧ Go to the **Upgrade Info** subtask card to view the change information.



Once you have read the change information, you can tell the system not to display the **Upgrade Info** subtask card for this protocol again.



✧ Activate the **Do not show this information again** check box.

The underscoring of the name disappears.

Applying or rejecting the changed protocol properties

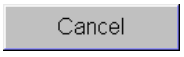
The new settings are applied after you have finished editing protocol properties on all subtask cards.



✧ Click the **OK** button.

The dialog box closes and your changes are applied.

You can also close the **Protocol step properties** dialog box without applying your changes.



✧ Click the **Cancel** button.

➪ If modify the content of any scan programs, a message box will be displayed as you exit the content area. You will be prompted to save the scan program with the changes or in its original state.

Editing pause properties

Scan pauses allow you to plan short interruptions in the examination sequence. You can use scan pauses to administer contrast agent, connect additional coils, or allow the patient to take a short break.

The properties of a pause is changed in the **Pause Step Properties** dialog box. You can call this dialog box from the **Exam Explorer** or from the job list.

➪ The pause properties can only be processed in the part of the job list that has not yet been executed.

Calling from the Exam Explorer

✧ Select a protocol in the **Exam Explorer**.
→ Page C.16–53, *Inserting a scan pause*

✧ Select **Edit > Properties** from the main menu of the **Exam Explorer**.

Or

✧ Select **Properties** from the context menu.

Or



✧ Click this button on the tool bar.

Or

✧ Press the shortcut **Alt + Enter** on your keyboard.

The **Pause Step Properties** dialog box is displayed.

Calling from the job list

✧ Select a pause from the job list.

✧ Select **Edit > Properties** from the main menu.

Or

✧ Select **Properties** from the context menu.

Or

✧ Press the shortcut **Alt + Enter** on your keyboard.

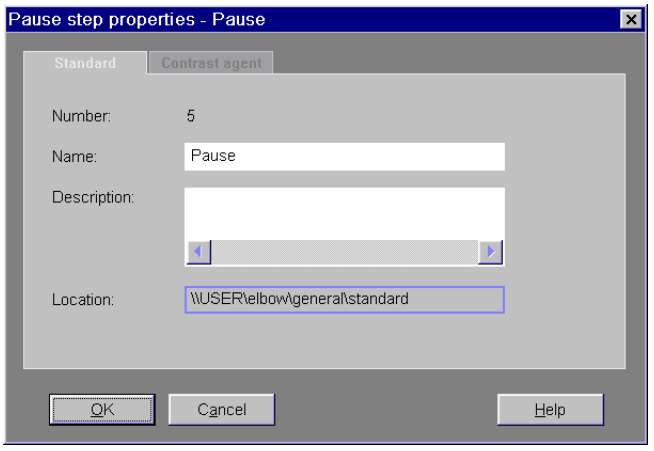
Or

✧ Double-click on this pause.

The **Pause properties** dialog window opens.

Entering the pause name and comment

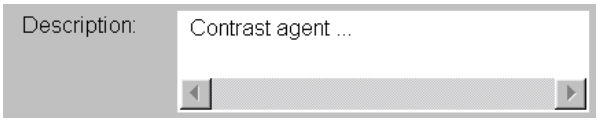
When you first open the **Pause step properties** dialog box, the **Standard** card is on top. You can enter a name and comment for the pause.



The pause name you enter should describe the purpose of the pause in the scan sequence.



✧ Enter a name for the pause.



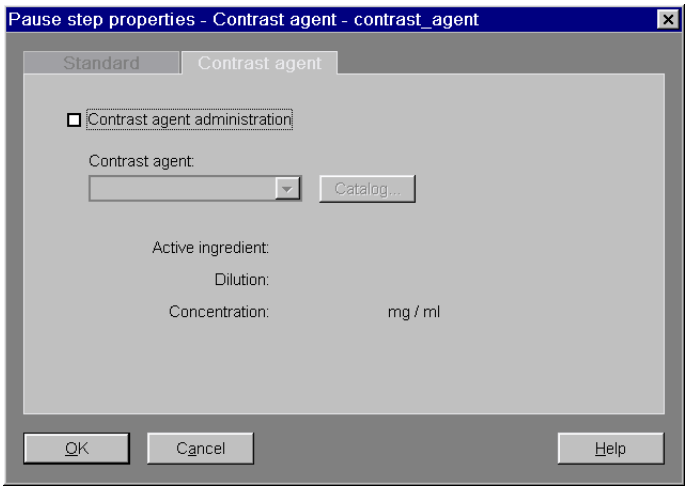
✧ Add a comment, if required.

➪ If you hover the mouse pointer over a pause entry in the **Exam Explorer** or program control, a tool tip displays the pause name and the comment.

Planning contrast agent administration

If you intend to use a pause for contrast administration, enter the type and quantity of contrast agent on the **Contrast agent** card.
→ Chapter C 7, *Using a Contrast Agent*

✧ Click the **Contrast Agent** card into foreground.



Selecting a contrast agent



✧ Click the **Contrast agent administration** option to activate the **Contrast agent** selection list and the **Catalog** button.



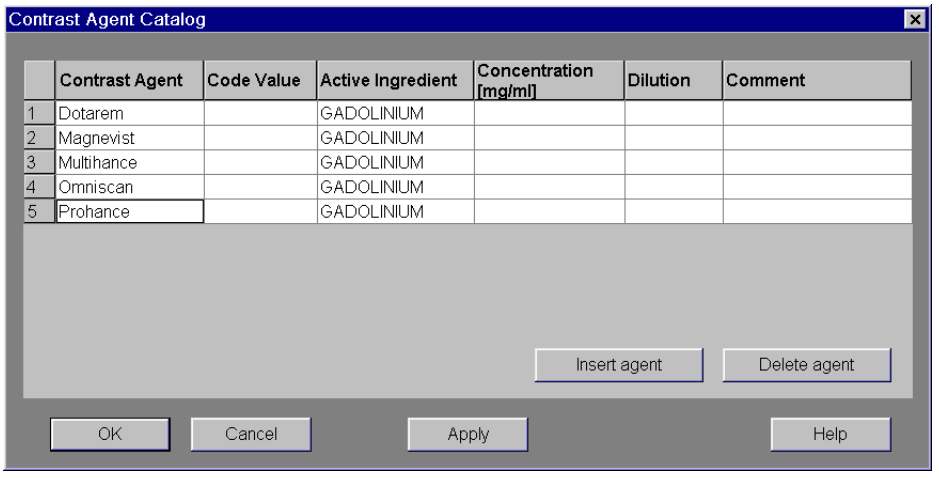
✧ Select the contrast agent to be administered in the selection list.

You can also select the contrast agent from the **Contrast agent catalog**.



✧ Click the **Catalog...** button.

The **Contrast Agent Catalog** dialog box is displayed.



✧ Select a contrast agent.

Entering a new contrast agent

If the contrast agent you want is not listed, you may enter it.



✧ Click the **Insert Agent** button.

A new, blank line will be entered in the list of the contrast agent catalog.

✧ Enter a name for the contrast agent, the code value, the active component, concentration, dilution, and a comment.



✧ Click the **Apply** button.

The newly entered contrast agent is now included in the catalog.

➪ The values entered will be incorporated in the DICOM image information whenever images are acquired with this contrast agent.

Deleting contrast agent

The steps are similar for deleting contrast agents you no longer need.

✧ Select the contrast medium you want to delete.



✧ Click the **Delete agent** button.



Click the **Apply** button.

The selected contrast agent will be deleted from the **Contrast agent catalog**.

Confirming contrast agent selection



✧ Click the **OK** button.

The selected contrast agent is applied and the dialog box closed.

Applying or rejecting modified pause properties

New settings are applied after you have finished editing pause properties.



✧ Click the **OK** button.

The dialog box closes and your changes are applied.

You may also close the **Pause Step Properties** dialog box without applying your changes.



✧ Click the **Cancel** button.



If you have entered settings for contrast administration, the pause instruction in your scan program will now be marked with a syringe, indicating the contrast administration pause.

➪ If modify the content of any scan programs, a message box will be displayed as you exit the content area. You will be prompted to save the scan program with the changes or in its original state.

CHAPTER C.13

Printing Protocols

You are able to either print out the parameter overview of protocols, contents of measurement programs, examinations and regions, or write them to a PDF file (export).

The prerequisite for printing is a printer connected to your system either locally or via the network.

The parameter overview enables you to directly compare the parameters of the protocols.

The lists of contents provide you with an overview of the available examinations and scan programs, making selection easier.

➪ Since printing this data is time-consuming, it is generally not used during clinical examinations.

Printing protocols was implemented with the
Report/print module List & Label® Version 10.0
Copyright *combit*® GmbH 1991-2003.

Printing

This is how you print out protocols:

- ❏ Select the print dialog
- ❏ Set the printer
- ❏ Setting the print range
- ❏ Select Print Preview (optional)
- ❏ Starting to print

Opening the print dialog window

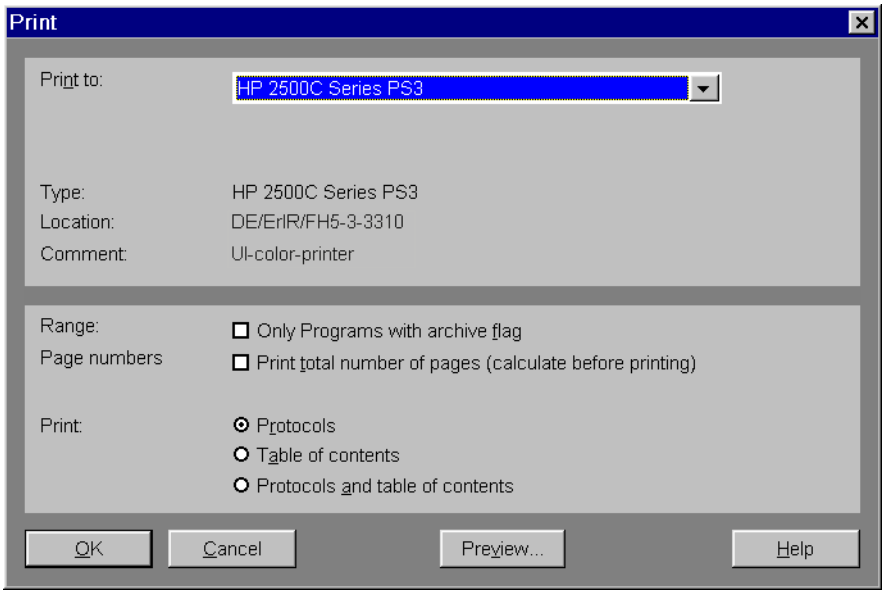
You may select one or more protocols, measurement programs, examinations or regions for printing and then open the print dialog window.

➪ Theoretically, you could print the entire protocol tree in the Exam Explorer. However, preparing such a large volume of data for printing would take a lot of time.

✧ Select the required objects in the **Exam Explorer**.

✧ Select **Object > Print** in the **Exam Explorer**.
- Or -
Select **Print** from the pop-up menu.

The **Print** dialog box opens.



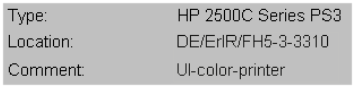
Setting the printer

The **Print to** selection list displays all printers available to your system locally or via the network. The default printer is preselected.

Printing medium Printer



✧ Select the desired printer from the **Print to** selection list.



The **Type**, **Location** and **Comment** fields provide information about the printer.

➪ The default properties of the printers defined in the control panel of the MR system are used for printing.

Setting the print range

You set the print scope and the print options in the lower part of the **Print** dialog window.

Print scope

You can limit the print scope so that only the protocols of *modified* measurement programs are printed.



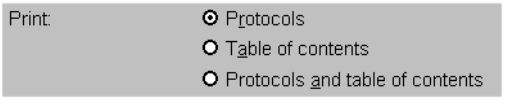
✧ Activate the **Only programs with archive flag** option.
→ Page C.16–29, *"Archive" option*

➪ If you have not selected a measurement program, examinations, or regions, clicking the check box has no effect.

➪ If you do not want to limit the print scope, deactivate the check box.

Setting print options

Using the print options you select the data to be printed.



The print options include the following:

Print option	Effect
Protocols	An overview of the parameter settings is printed for all selected protocols. The settings are listed in the same way as on the parameter cards.
Table of contents	A list of contents is printed for the selected scan programs, examinations, or regions.
Protocols and table of contents	Both the parameter overview and the list of contents are printed.

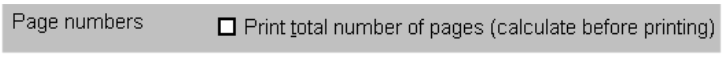
✧ Select the desired print option.

! When setting the print output, remember that printing a large selection of objects can take some time. If necessary, see if you can reduce the number of objects selected.

Setting page numbering

The pages of the printed protocols can be numbered in two ways:

Format	Comment
Page only	Only the page with a plus or minus sign is shown in this format. Example: ***Page 3+*** or ***Page 5-*** The plus sign indicates that there are more pages to follow. The minus sign identifies the last page of the print-out. Advantage of this format: Print data using this page numbering format are prepared much faster than page numbering including the running number of total pages.
Page with total pages	This format prints the current page number with the total number of pages. Example: *Page 5 / 10*.



✧ When the total number of pages is to be printed out, activate the **Print total number of pages (calculate before printing)**.

Looking at data via print preview

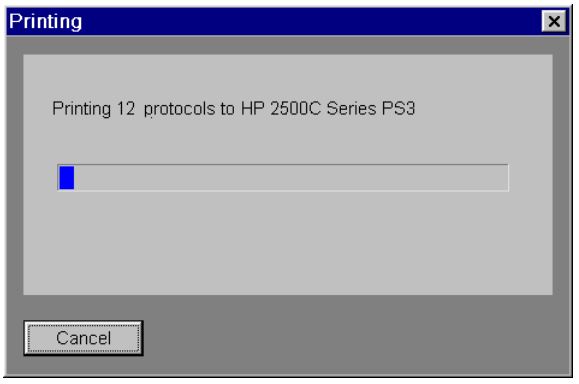
You can check the data to be printed in print preview mode.
→ Page C.13–11, *Print preview of protocols*

Starting to print

✧ Click the **Print** dialog window and then **OK**.

The selected data are sent to the selected printer. The dialog box is closed.

A progress bar is displayed, which you can use, if necessary, to cancel printing.



Exporting data into a file

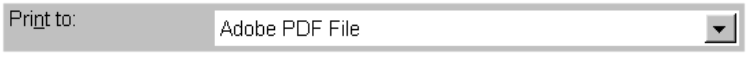
You are able to print protocols and lists of contents directly into a PDF file. This is useful if the system does not have a printer or if you want to take the data to another location for printing.

✧ Open the print dialog window.
→ Page C.13–2, *Opening the print dialog window*

Providing export settings

To export data, the name of the export file and its directory have to be set after the corresponding print medium has been established.

Setting the print medium



✧ Select the **Print to** item from the **Adobe PDF File** selection list.

The **File Name** input box is active. The target directory of the last data export is the default.



As a rule, you can use the following drives:

Drive	Description
T:	This drive corresponds to the local directory **C:\Medcom\User** on your MR system.
A:	Diskette drive
U:	This drive is usually used to temporarily store data you will later burn on CD-ROM.

➪ Other network drives may be accessible depending on your MR system.

You can directly enter the drive, directory, and name of the export file as a path in the **File name** input field. As an alternative, you can enter this information in the **Save As** dialog window.

Entering the file name and path directly

✧ Enter the drive, directory and name of the export file directly into the **File name** input field.

Example: `U:\Protokolle\Protokoll1.pdf`

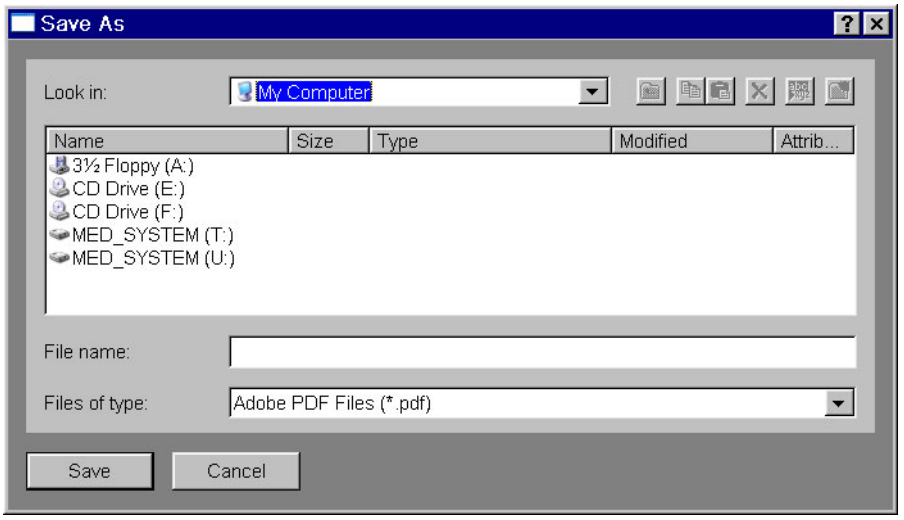
Using the Save As dialog window

Or



✧ To open the **Save As** dialog window, click this button.

In the **Save As** dialog window you can create subdirectories on drives **A:**, **T:** and **U:**, as well as delete subdirectories and files.



✧ Select the target directory for the data export.

✧ Enter a name for the export file in the **File name** field.

Save

✧ Click **Save** to apply the settings made in the **Print** dialog window.

The **Save As** dialog window closes.

The field **File name** under the **Print** dialog window shows the path and name of the export file. Example:



Performing additional settings

✧ Set the print range.
→ Page C.13–4, *Setting the print range*

➪ You can check the data to be printed in print preview mode.
→ Page C.13–11, *Print preview of protocols*

Starting to export

✧ Click the **Print** dialog window and then **OK**.

The selected data are exported to the desired pdf file. The dialog box is closed.

A progress bar is displayed, which you can use, if necessary, to cancel export.

Print preview of protocols

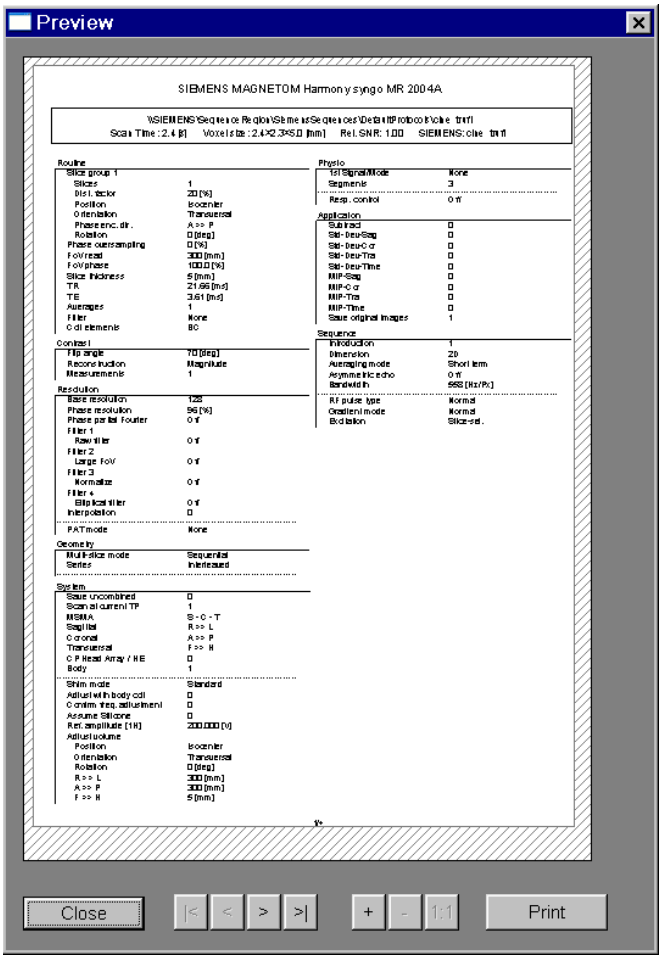
You can check the data under print preview before you start to print or export.

Selecting print preview



✧ Click the **Print** dialog window and then **Preview**.

The print data are prepared and displayed in the **Preview** window.


Preview
SIEMENS MAGNETOM Harmony sygo MR 2004A
Close
Print

Changing the display of the print preview

You can change the display of the print preview via buttons (in the lower part of the dialog box).

Button	Function
< >	Scrolling forward or backward through the pages
|< >|	Scrolling to the first or last page
+ -	Changing the display to twice its size or to half of it
1:1	Returns the display to the default setting

✧ Click the button for the desired function.

Printing from the preview

You can print or export the displayed data directly from the preview.



✧ Click **Print**.

The displayed data is output to the print medium set in the **Print** dialog window.
→ Page C.13–3, *Printing medium Printer*
→ Page C.13–8, *Setting the print medium*

➪ If you did not set an appropriate print medium in the **Print** dialog window, the **Print** button does not work in preview.

Closing the print preview



✧ Click **Close**.

The print preview is closed.

CHAPTER C.14

SAR and Stimulation Monitoring

Examinations with MR systems may trigger physiological effects in patients. These effects are caused by radio-frequency fields or by magnetic fields varying over time.

Temperature rise due to radio frequency

The patient is in a radio-frequency field during the examination. Part of this electromagnetic radiation is absorbed by the patient's body tissue and converted into heat.

The RF power per kg of body mass absorbed by the patient is called the **s**pecific **a**bsorption **r**ate (**SAR**). It is expressed in W/kg. If the SAR exceeds the thermal regulation capacity of the patient, his/her body temperature will rise.

Stimulation due to varying magnetic fields

In addition to the RF field, the patient is also subjected to an electrical field during the examination. The magnetic flux generated by the gradient coil changes over time. This change can be expressed mathematically as **dB/dt**.

Peripheral nerve stimulation may result if dB/dt (and therefore the strength of the electrical field) rises above a certain value that is characteristic for the patient. Nerve stimulation can manifest itself as tingling sensations or slight muscle spasms in the ribs, side, abdomen, hip, buttock, or thorax region, in the upper arms or the back muscles in the shoulder region.

Avoiding physiological effects

Your system automatically monitors the SAR and dB/dt load on the patient. Different operating modes are taken into account to avoid physiological effects.

Operating modes

SAR and stimulation monitoring may be performed in two operating modes. **Normal mode** and **First level** controlled operating mode.

Normal operating mode

During a scan the system observes especially strict limit values so that the patient is not subjected to any special temperature rise and muscle stimulation is prevented.

Normal mode is the default setting at the beginning of an examination.

First level controlled operating mode (first level mode)

The patient may experience a clearly noticeable sensation of warmth if you have activated **first level** mode. If stimulation monitoring is performed in **first level** mode, increased dB/dt values may cause the patient to experience slight peripheral nerve stimulation.

The decision to switch to **first level** mode is the duty of the person with medical responsibility.

→ Page C.14–14, *Switching modes*
→ Page C.14–30, *Stimulation threshold exceeded*

SAR limit values

The specific absorption rate (SAR) is calculated and monitored for the areas **whole body**, **partial body**, and **local** RF stress. The limits applied are set in accordance with the guidelines applicable to your country.

The various regions are defined differently and have different limit values. For example, the permissible SAR limit value for local exposure may be higher than the SAR limit value for the whole body. For this reason, several limits apply to each mode.

Limit values according to stimulation models

Stimulation monitoring is based on stimulation models. These models are used to calculate the threshold values (limit of **normal mode**) and stimulation limits (limit of **first level** mode) depending on the gradient coils.

❏ SAFE model
The thresholds and stimulation limits are determined according to a semi-emperical method by taking into account the results of extensive studies performed with volunteers. At the threshold value, stimulation is possible in no more than 1% of patients. At the stimulation limit, the probability of stimulation is 50%.

❏ dB/dt model
The calculation of threshold values and stimulation limits includes the legally required dB/dt restrictions.

Stimulation monitoring according to the SAFE model is always performed. Depending on country-specific guidelines, the dB/dt model may be additionally applied.

NOTE

SAR and dB/dt monitoring of the limit values is performed automatically by the system software.

Correct automatic monitoring presupposes compliance with the prescribed sequence of operations.

Display of the mode

The status bar shows you the operating mode used for the current sequence.

The abbreviations represent the operating modes for stimulation monitoring (Stimu) and SAR monitoring (SAR):

Stimu=NM SAR=NM

❏ NM (Normal mode)
The limits of the **Normal mode** are observed.

SAR=FL

❏ ES (First level mode)
The **First level** controlled operating mode is activated. The SAR values or dB/dt values can exceed the limits of normal mode.

Stimu= SP

❏ SM (Stimulation possible)
This mode is only possible with stimulation monitoring according to the SAFE model. Stimulations may occur during the scan in progress.

➪ Changing to the **First level** mode is permissible within the framework of automatic SAR and/or stimulation monitoring.
→ Page C.14–14, *Switching modes*
→ Page C.14–31, *Switch to first level mode*

Automatic SAR Monitoring

The weight, age, sex, and position of the registered patient are used directly to calculate the SAR monitoring. For this reason, it is important to enter the patient data correctly during patient registration.

The expected SAR values will be calculated as soon as you load a new protocol. It not possible to start scanning unless all limit values are observed.

During the scan, your system monitors compliance with the limit values using the transmitting power which is measured continuously. If the permissible transmitting power is exceeded, the system will shut down immediately. This eliminates the possibility of exceeding the limit values.

Display of the necessary registration

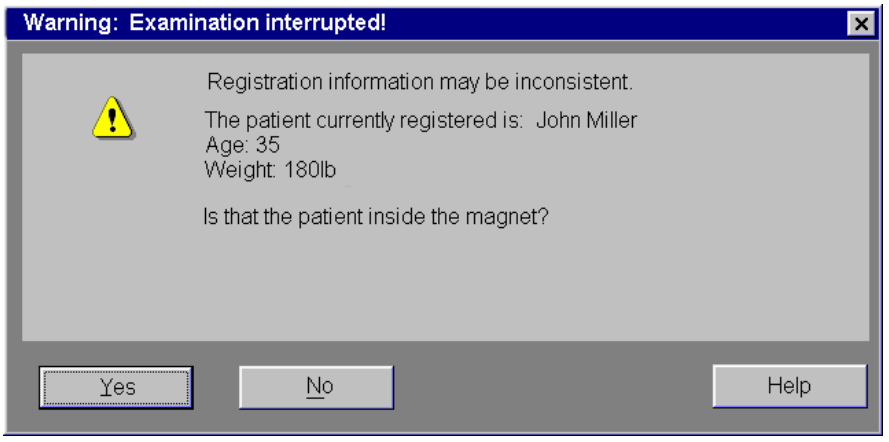
Because correct patient registration is of central importance for SAR monitoring, the system monitors events that indicate a change in patients (patient registration, table movement).

At the beginning of a new examination, the patient table is moved out completely (to the home position) so that you can position the next patient on the table. For this reason, your system assumes that moving to the HOME position and registering a new patient are always associated with a change of patient.

If only one of these two events indicating a change of patient occurs, the system displays a warning.

Moving to the HOME position

The following message is displayed if you load the next protocol after moving the table to the HOME position but do not register another patient first.



If this registered patient is really on the table, you may continue scanning.

Yes

✧ Click **Yes**.

The measurement is started.

If these patient data do not apply to the current patient, cancel the scan.

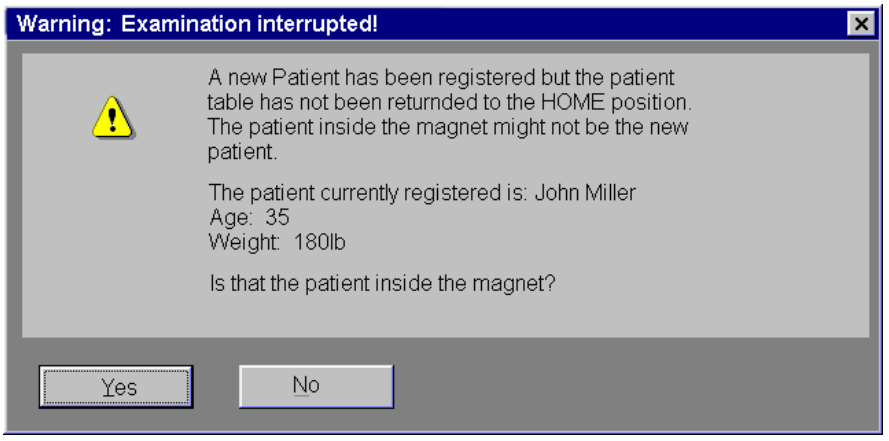
No

✧ Click on **No** or close the dialog box using the **ESC** key or the icon in the top right corner of the window.
→ *syngo* Operator Manual

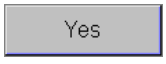
Scanning will be stopped. You are prompted to register a new patient.

Table not moved out during registration

If you have registered a new patient for examination although the patient table has not been moved out completely, your system will display the following warning before the start of the next scan.



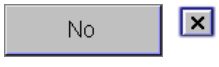
If this registered patient is really on the table, you may continue scanning.



✧ Click **Yes**.

The measurement is started.

If these patient data do not apply to the current patient, cancel the scan.

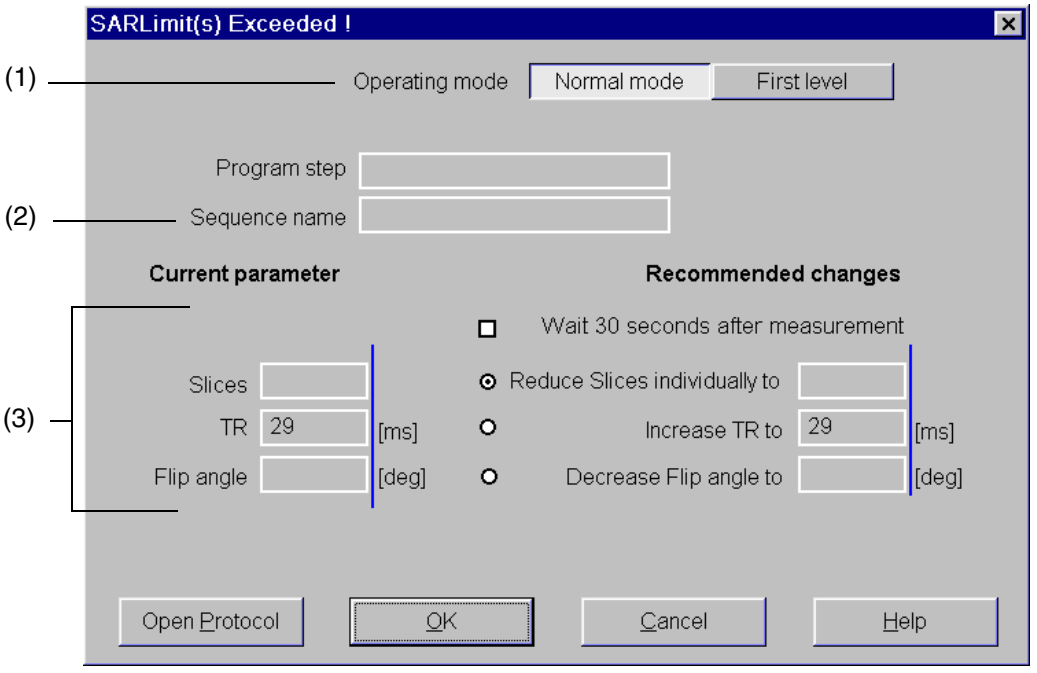


✧ Click on **No** or close the dialog box using the **ESC** key or the icon in the top right corner of the window.
→ *syngo* Operator Manual

Scanning will be stopped. A message on the status bar prompts you to register a new patient.

Calculated SAR higher than the limit value

A protocol will not be loaded if your system has calculated in advance that the SAR limit values would be exceeded for this scan. The **SAR Limit(s) Exceeded** dialog box is displayed on the **Exam** card.



(1) Buttons for selecting the SAR mode
(2) Name of the program step and the sequence
(3) Current and recommended measurement parameters

You may perform one of the following steps to continue the examination:

- ❏ Change one or more of the protocol parameters so that the SAR remains below the limit values.
- ❏ Switch to **first level** mode (only if appropriate for the physical condition of the patient).
- ❏ Skip the planned protocol and continue scanning with the subsequent protocol.

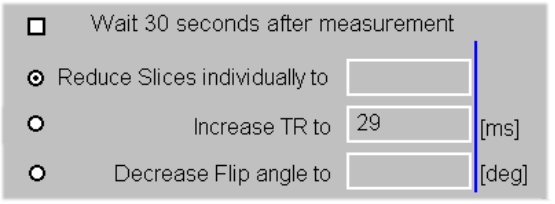
Changing the measurement parameters in the dialog window

The lower part of the **SAR Limit(s) Exceeded!** window recommends parameters you can use to avoid exceeding the SAR limit values.

The suggestions are calculated assuming that the other parameters remain unchanged. Changing two or more parameters at once reduces the amount each parameter has to be changed.

You may insert a pause after the protocol has run.

➪ Remember that any changes you make to the parameters may increase scan time and affect image quality.



✧ Activate the **Wait ... seconds after measurement** option to insert a pause.

✧ Select a suggested change from the **SAR Limit(s) Exceeded!** dialog box.

OK

✧ Click **OK** to confirm your setting.

The scan will then start automatically.

➪ If a change option is dimmed, no change suggestion is available for that particular scan parameter.

Opening a measurement parameter in the protocol

You can open the protocol yourself and make appropriate adjustments to the parameters on the parameter cards.
→ Page C.5–1, *Adjusting Measurement Parameters*

This method is especially useful if all of the recommended changes in the **SAR Limit(s) Exceeded!** dialog box are dimmed.

For example, reducing the number and thickness of saturation slices also decreases the SAR load. You may also set the RF pulse type **Low SAR** on the **Sequence/Part 2**parameter card.



✧ Click **Open Protocol**.

✧ Change the appropriate parameters on the parameter cards.

Switching modes

You can switch from **normal mode** to controlled **first level** mode in the **SAR Limit(s) Exceeded!** dialog box. It is then possible to run the protocol with the intended scan parameters or, at least, the extent of required parameter changes will be reduced.

WARNING

The increased RF load in **first level** mode may pose a hazard to the health of the patient.

- ✧ Always use **normal mode** to examine patients with impaired heat regulation, patients with a higher than normal body temperature or pregnant patients.
- ✧ Always use **normal mode** for examinations of fetuses, testicles, and eyes using local transmitter coils. In addition, please note the special restrictions applying to these coils.

WARNING

The increased RF load in **first level** mode may pose a hazard to the health of the patient.

- ✧ In **first level** mode, you must monitor the patient carefully (e.g. using a squeeze bulb or pulse sensor).

NOTICE

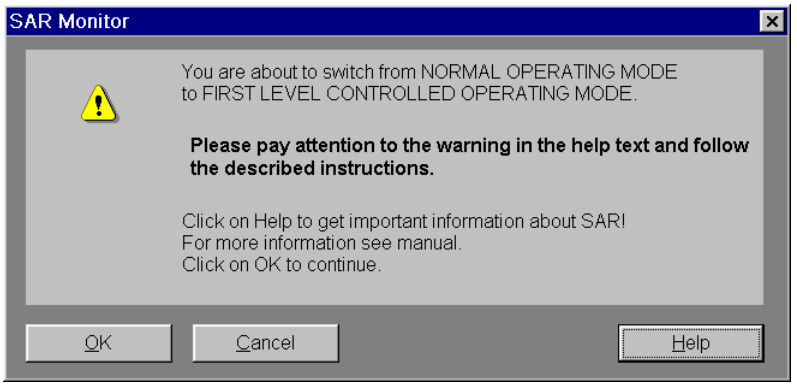
Normal mode is activated automatically as soon as you register a new patient.

First level mode remains active while you are examining *the current* patient until you switch modes manually.

FIRST LEVEL

✧ Click the **First level** button in the **SAR Limit(s) Exceeded!** dialog box.

The **SAR Monitor** dialog box opens.



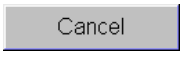


✧ Click **OK** in the **SAR Monitor** dialog box to switch to **first level** mode.

The **SAR Limit(s) Exceeded!** dialog now shows the **FIRST LEVEL** button as depressed, and the recommended parameters are adjusted for this mode.

✧ Click **OK** to run the protocol in **first level** mode.

If you want to return to **normal mode**, close the **SAR Monitor** dialog box.

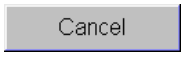


✧ Click either **Cancel** or the **close window icon**, or press the **ESC** key.

All suggestions dimmed

If all suggested changes are dimmed in **first level** mode, try changing the parameters directly in the protocol until you are permitted to scan in **first level** mode.
→ Page C.5–1, *Adjusting Measurement Parameters*

Skipping the measurement



✧ Click **Cancel** in the **SAR Limit(s) Exceeded!** dialog box to skip the scan.

The protocol is marked as canceled in the job list. The next protocol is loaded.

Switching back to normal mode

You can set the operating mode **Normal mode** as follows in the dialog box **SAR limit values exceeded:**

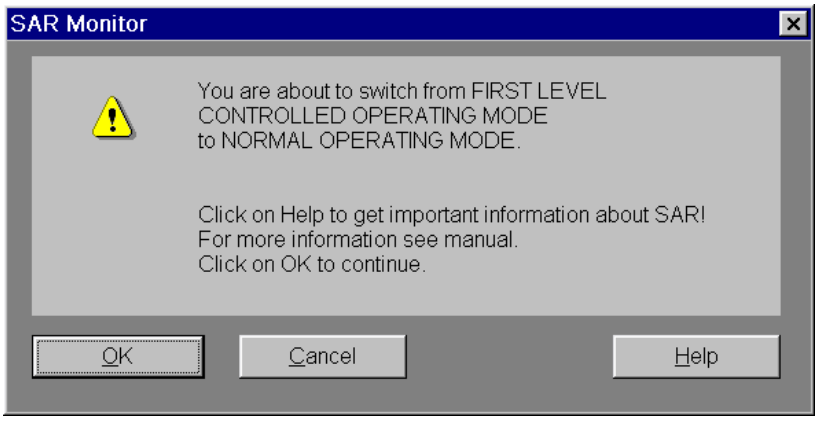


✧ Click the **Normal Mode** button.

NOTICE

The load on the patient may be above the **Normal Mode**. To ensure that the load state of the patient returns to a **Normal Mode** level, a pause of at least 3 minutes must be observed. Otherwise, scanning is shut down by the online monitoring. The online monitoring evaluates the load on the patient and shuts down when a permissible limit is violated.

The **SAR Monitor** dialog box opens.

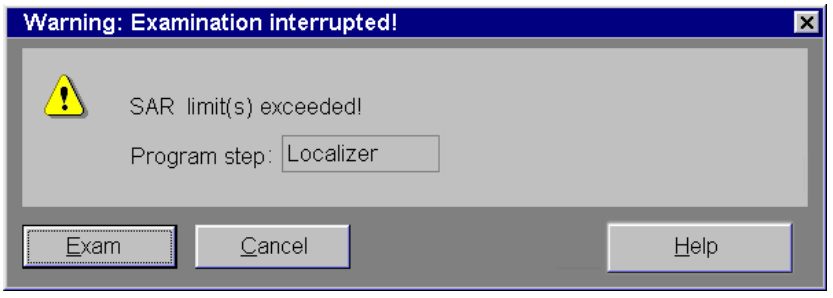


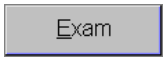
✧ Click the **OK** button.

The system switches to **normal mode**.

SAR message on other task cards

If a task card other than **Exam** is open and the SAR limit is exceeded, the measurement will be cancelled or not even started. The **Warning: Examination interrupted!** window is displayed.





✧ Click the **Exam** button to switch to the **Exam** task card.

The **SAR limits exceeded!** dialog window is displayed and you are able to adjust the parameters
→ Page C.14–10, *Calculated SAR higher than the limit value*

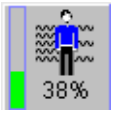


✧ Click **Cancel** if you want to continue working in the current task card and do not want to edit the protocol until later.

Displaying SAR information

Your system allows you to view the data of the *current* protocol that is relevant to SAR monitoring.

SAR display



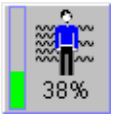
The **SAR** button on the **Exam** card contains a level indicator. It shows you how close you are to the critical SAR limit (as a percentage).

Calling up SAR information

The **SAR Information** window provides detailed information on parameters for SAR monitoring.

✧ Select **System > SAR Information** to query the current SAR values and the information relevant to SAR.

Or



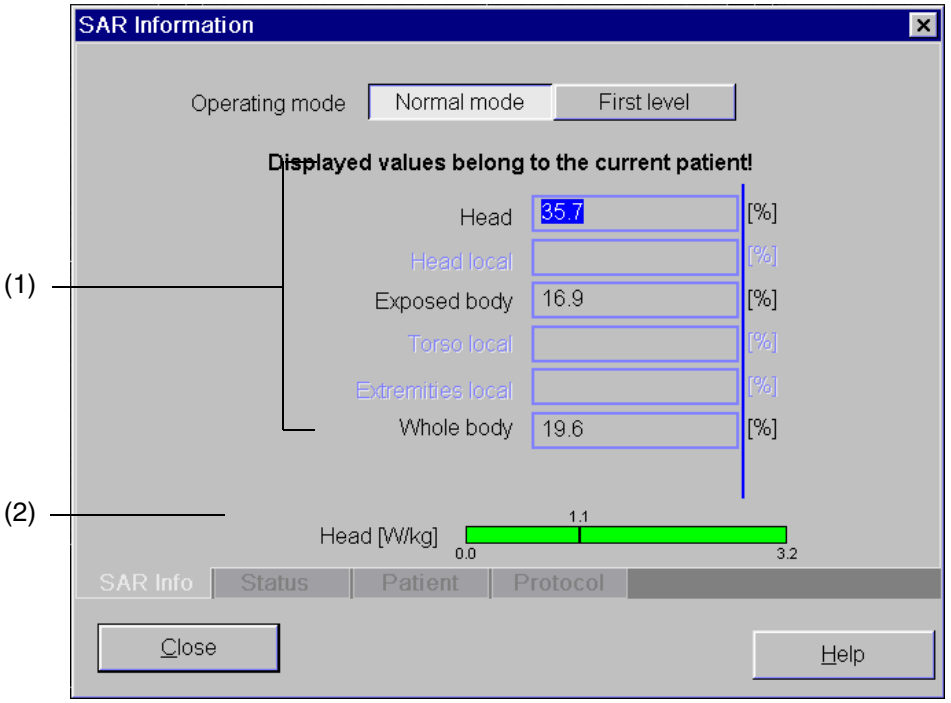
✧ Click the **SAR information** button.

The **SAR Information** window is displayed with the **SAR Info**, **Status**, **Patient**, and **Protocol** subtask cards.

Displaying SAR values

The **SAR Information** subtask card includes a list of SAR values for all the monitored body regions.

✧ Go to the **SAR Information** subtask card.

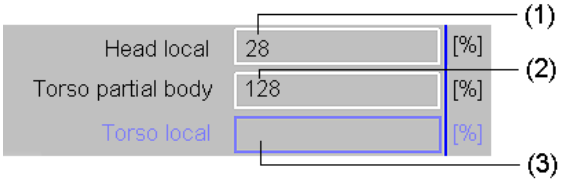


(1) Relative SAR (SAR value with reference to limit value in %)
(2) Bar display for the highest SAR value

Relative SAR values

Within the framework of SAR monitoring, the different limit values for the individual SAR aspects have to be observed.
→ Page C.14–3, *SAR limit values*

The list of the relative SAR (divided into body regions) indicates what percentage of the individual limit values has already been reached. If one of the values is above 100%, this means that the respective SAR limit value is exceeded. This may be the case, e.g. when you select a high-performance RF protocol in the **normal mode**.



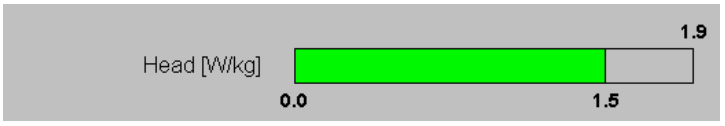
(1) SAR is below the limit value
(2) SAR limit value has been exceeded
(3) For this region, no SAR limit value has been defined in accordance with the valid limit guidelines

Display of the body regions depends on both the transmitter coil used and the SAR guidelines in effect for your system.

Body regions not currently being monitored are either dimmed or not displayed.

Displaying the highest SAR value

A bar displays the SAR value that is currently the highest (the one that should be limited).



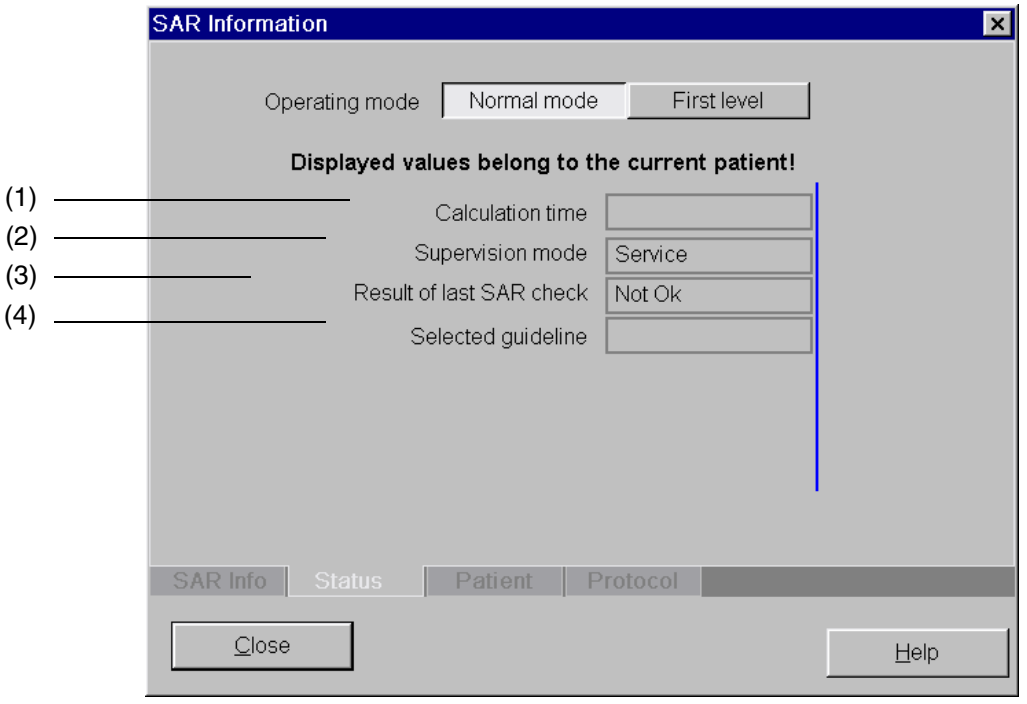
The current SAR value is shown below the bar chart. The permissible limit is shown above it.

If the SAR value is outside the green range, the permissible limit value has been exceeded for the operating mode currently selected.

Displaying the SAR status

The **Status** subtask card provides information regarding the current status of SAR monitoring.

✧ Go to the **Status** subtask card.

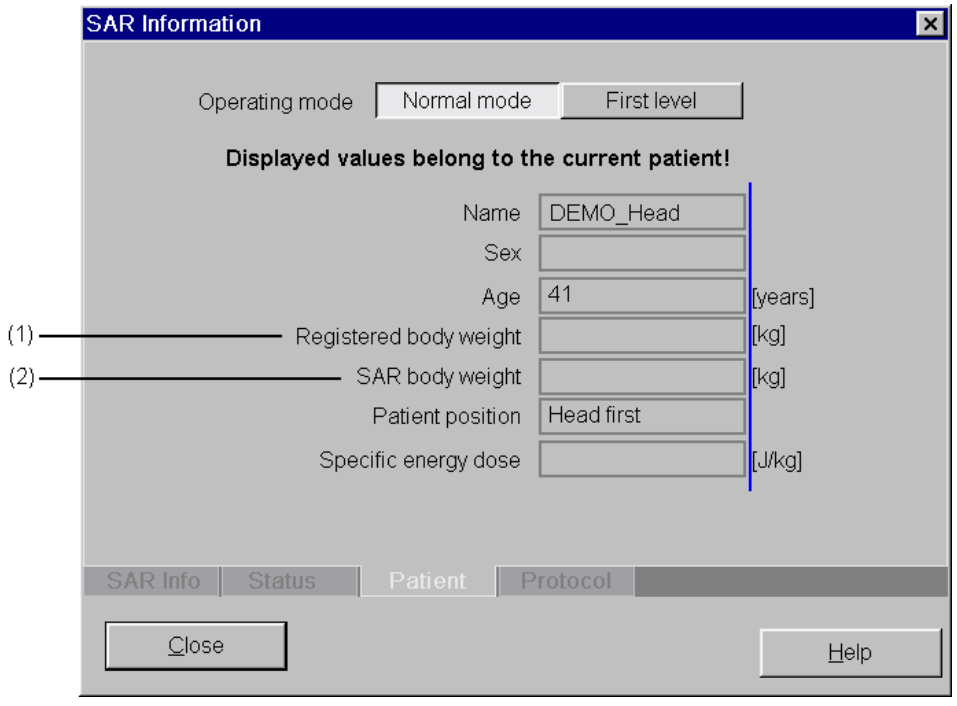


(1) Time at which SAR calculation was last performed
(2) Current mode (patient mode or service)
(3) Result of the last SAR check
(4) Legal guidelines for SAR monitoring

Querying SAR-relevant patient data

Ensure that the patient data are correct before the SAR limits are calculated. You can check the patient data on the **Patient** card. If the data are incorrect, you have to register the patient again.

✧ Go to the **Patient** subtask card to display the patient data relevant to the SAR.



(1) Body weight (entered during patient registration)
(2) Weight actually used for SAR monitoring

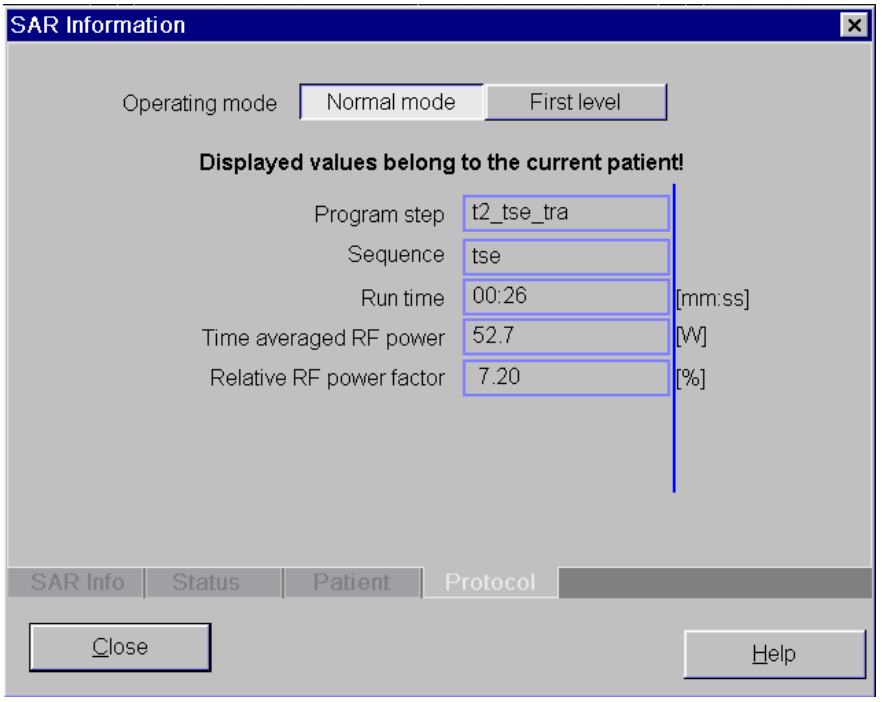
In certain cases, the **SAR weight** may differ from the **registered weight**.

The system calculates the mass actually exposed to the RF transmit power and compares it with the **registered weight**. The **registered weight** will be corrected in case of deviation. The corrected weight is the **SAR body weight**.

Displaying information about the protocol

SAR-relevant information about the current protocol are shown on the **Protocol** subtask card.

✧ Go to the **Protocol** subtask card.



Closing SAR information

You may close the **SAR Information** window again once you have accessed the required information.





✧ Click the **Close** button; click the **close window icon**; or press the **ESC** key.

You return to the application you were using when you called up the **SAR Information**.

Automatic Stimulation Monitoring

MR systems with Quantum, Sonata, or Sprint gradients are equipped with automatic stimulation monitoring.

Every time you load a new protocol, the system uses the stimulation models to check whether stimulation may occur during scanning.

When stimulation monitoring is active in the **normal mode**, it is not possible to start a scan that would exceed the stimulation threshold. Nerve stimulation is not expected in **normal mode**.

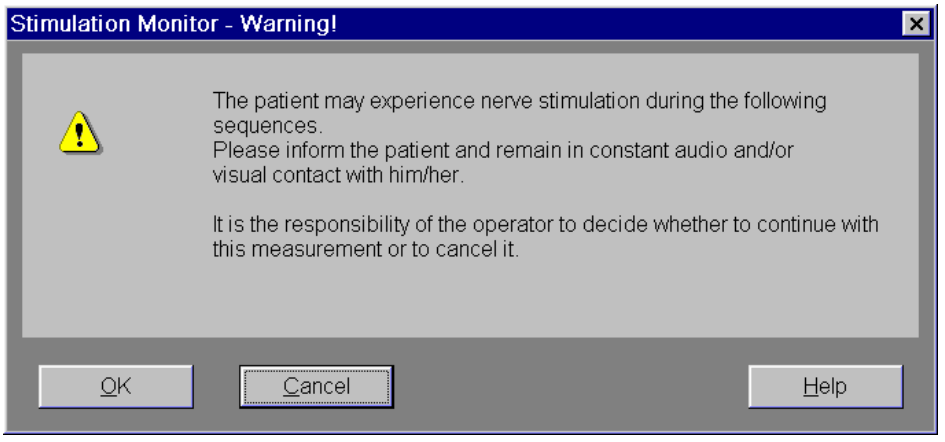
If the system switches to **Stimulation possible** (**SP**) mode, the higher limits will be taken into account. In this case, nerve stimulation may occur during scanning. However, it is not possible to start a protocol if the system precalculates that the stimulation limit would be exceeded. In this case, you have to e.g. lower the dB/dt values by making appropriate changes to the measurement parameters.

Even during scanning, stimulation monitoring is active and controls the actual value gradient signals. If the stimulation limits are exceeded, active scanning is stopped immediately and the gradient currents are reset. This eliminates the possibility of exceeding the limit values.

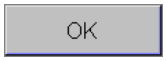
➪ Unlike in SAR monitoring, patient data such as age, weight are not used for the stimulation models. With respect to stimulation monitoring, a protocol may either be run for all or none of the patients.

Stimulation threshold exceeded

The following dialog box will appear if your system detects that the pending scan exceeds the stimulation threshold.



Switch to first level mode



You may start scanning despite possible stimulation.

✧ Click **OK** in the **Stimulation Monitor - Warning!** dialog box.

Stimulation monitoring is now performed in the controlled **first level** operating mode. The status bar shows the abbreviation **SM** whenver the stimulation threshold is exceeded for the current measurement.
→ Page C.14–5, *Display of the mode*

Skipping a scan protocol



You may skip the current protocol.

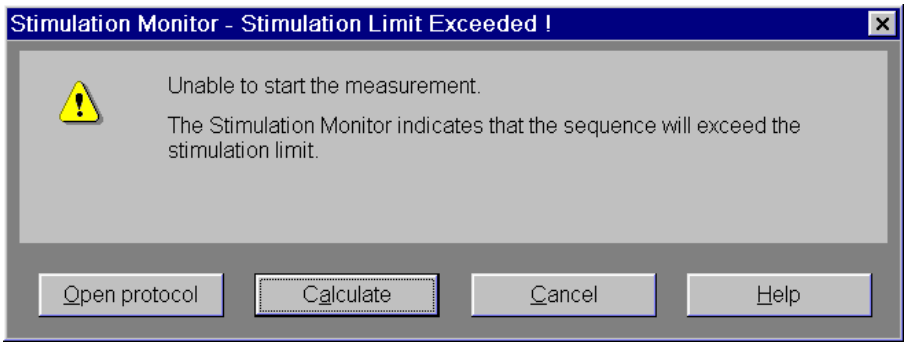
✧ Click **Cancel** in the **Stimulation Monitor - Warning!** dialog box.

The dialog box closes. The next protocol in the job list is loaded.

Stimulation limit reached

A protocol is not loaded if the stimulation limit (**first level** mode limit) would be exceeded during the scan.

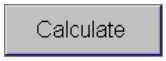
The **Stimulation Monitor - Stimulation Limit Exceeded!** dialog box is displayed on the **Exam** task card.



To continue running the protocol, you can modify the parameters in 3 different ways:

- ❏ Have the system calculate suitable parameter changes and display them in the **Stimulation Monitor - Recommendations** dialog box. Apply these parameter changes.
- ❏ Change the gradient mode of the protocol in the **Stimulation Monitor - Recommendations** dialog box.
- ❏ Open the protocol and change one or more measurement parameters on the parameter cards so that the stimulation limit is no longer exceeded.

Calculating parameter changes

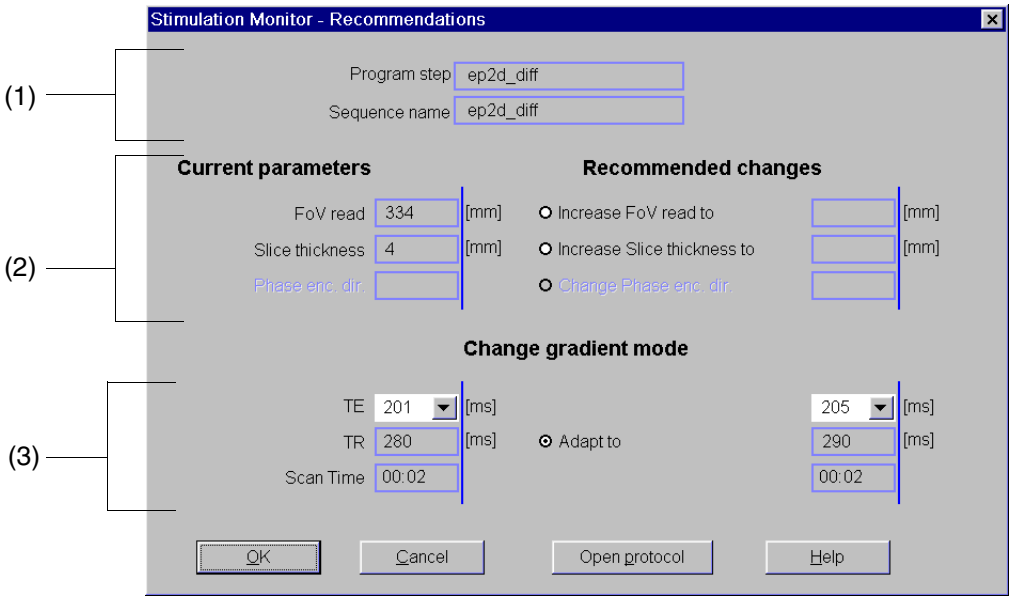


Have the system calculate recommended changes to the measurement parameters that are below the stimulation limit.

✧ Click the **Calculate** button in the **Stimulation Monitor – Stimulation Limit Exceeded!** dialog box.

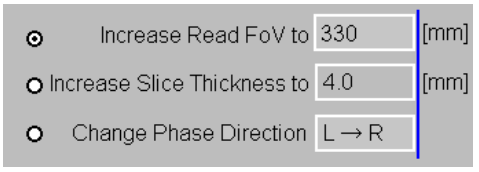
The **Stimulation Monitor - Recommendations** dialog box is displayed.

➪ If the stimulation limit has been exceeded, it is possible that no change recommendations will be displayed. In that case, you cannot make any changes and will have to change the measurement parameters manually.



(1) Name of the protocol and the sequence
(2) Current and recommended measurement parameters
(3) Current parameters modified by changes to the gradient mode

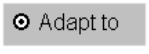
✧ Select one of the recommended changes.



➪ If a change option is dimmed, this means no suggested change is available for that particular scan parameter.

Changing a gradient mode

You may also set a new, slower gradient mode. The system will modify the gradient slope iteratively until the simulation limit is no longer exceeded. As a result, changes are made to the TE, TR, and measurement time.



✧ Change the gradient mode, by switching on the **Adjust to** option.

The modified gradient mode in a protocol is identified by an asterisk on the **Sequence/Part2** parameter card.
→ Page C.5–69, *Sequence-Part 2 parameter card*

✧ Click **OK** to confirm the new setting.

The protocol starts automatically.

Editing the protocol

If suggested changes are not possible for the current protocol, the dialog box **Stimulation Monitor - Recommendations** is displayed along with the message "Measurement not possible! Please change protocol."

You are able to adjust the parameters in the parameter cards only.
→ Page C.5–1, *Adjusting Measurement Parameters*



✧ Click **Open Protocol**.

The parameter cards enable you to combine several parameter changes.
→ Page C.5–1, *Adjusting Measurement Parameters*

Skipping a scan protocol

You can skip the protocol if the system precalculates a violation of the stimulation limit.



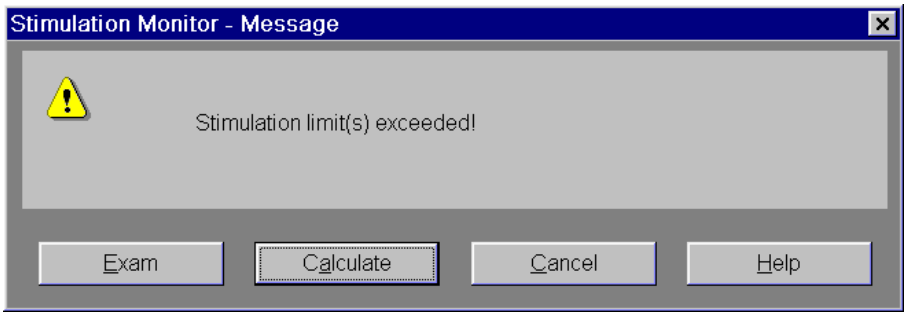
✧ Click **Cancel** in the **Stimulation Monitor – Stimulation Limit Exceeded!** dialog box.

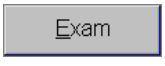
The protocol is marked as canceled in the job list and the next protocol is loaded.

Stimulation message on other task cards

If you are currently working in another task card than **Examination** while your system is predicting that the stimulation limit will be exceeded, the measurement is not started.

The **Stimulation Monitor - Message** window opens. You may continue working on the task card currently open or switch to the **Exam** card, e.g. to edit the protocol.

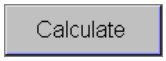




✧ Click the **Exam** button to switch to the **Exam** card.

The **Stimulation Monitor - Stimulation limit exceeded** window opens.
→ Page C.14–32, *Stimulation limit reached*

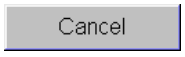
Or



✧ Click **Calculate** if you want your system to calculate suitable parameter changes.

The previous application remains open and a message is displayed as soon as the parameter changes have been calculated. If you switch to the **Exam** card, the **Stimulation Monitor - Recommendations** window will be displayed including the calculated parameter adjustments.

Or



✧ Click **Cancel** to skip the scan.

The protocol is marked as canceled in the job list and the next protocol is loaded.

Information about Stimulation Monitoring

You may query the threshold/limit values and other parameters important for automatic stimulation monitoring of the current protocol.

✧ Select **System > Stimulation Monitor - Information** to display information about stimulation monitoring.

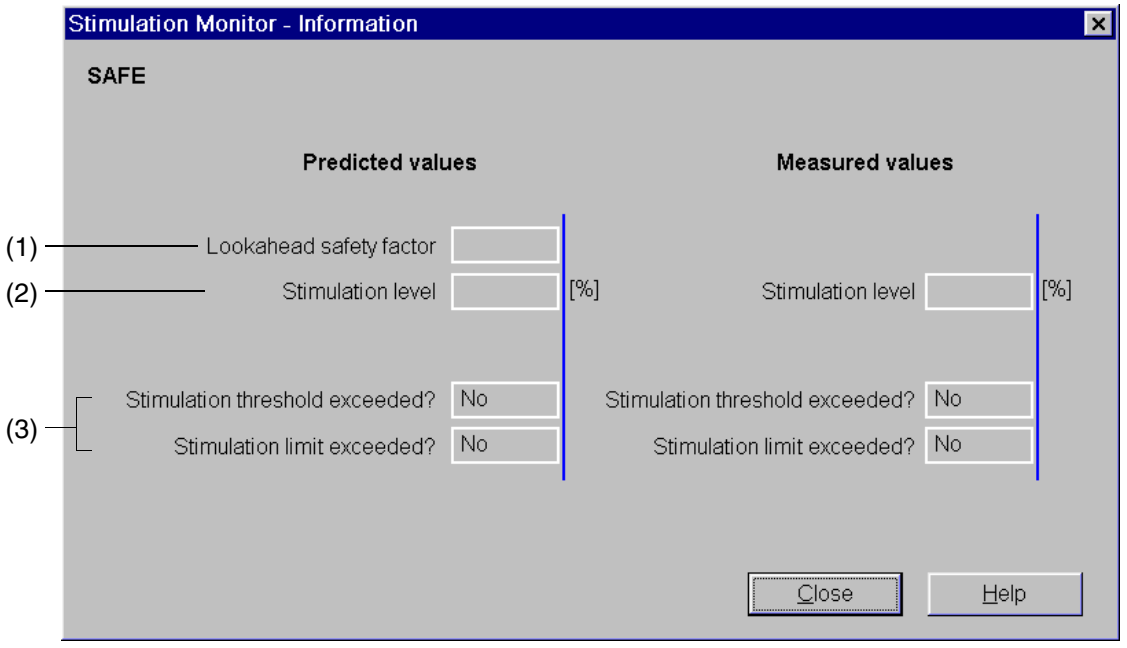
The **Stimulation Monitor - Information** window opens with the **SAFE** subtask card and (depending on country-specific regulations) the **dB/dt** card.

The SAFE subtask card

The **SAFE** subtask card contains a list of the calculated and measured parameters that have to be factord into the SAFE model.
→ Page C.14–3, *Limit values according to stimulation models*

✧ To query the stimulation parameters according to the SAFE model, go to the **SAFE** subtask card.

The left-hand side of the subtask card displays the precalculated parameter values of the stimulation monitoring. The measured data is shown on the right. The data refer to the protocol in progress or just completed.



(1) Safety factors for stimulation predictions
The possibility of stimulation is increased by this factor over the value calculated.

(2) Maximum approximation to the stimulation limit (in %)

(3) Information about whether the stimulation threshold or the stimulation limit has been exceeded.

The dB/dt subtask card

The country-specific regulations determine whether monitoring is performed by taking the statutory dB/dt limit values into account on your system. In this case, you may also select the **dB/dt** subtask card.

CHAPTER C.15

Physiologically Controlled Measurements

Physiological movements in the body, such as heart beats or respiration, can cause motion artifacts. Such artifacts may appear as noise or distortion in the images.

You can avoid these motion artifacts by synchronizing physiological signals (ECG signal, pulse, respiration) with the scans. Physiologically triggered scans also enable you to create cine studies of motion cycles, such as the functioning of a heart valve.

Two scan methods are currently used, namely triggering or retrospective gating.

Triggering involves using a characteristics position in the physiological signal curve as the trigger for scanning. Triggering is possible using ECG signals, pulse signals, respiration signals, and external trigger signals.

Retrospective gating involves retrospectively correlating the acquired image data with the curve of a physiological signal. Retrospective gating can be applied using ECG signals, pulse signals, and external trigger signals.

The **Physiological Display** window lets you track physiological signal curves.

The special parameters for triggering or retrogating scan methods are set on the **Physio** parameter card.

NOTICE

You may perform physiologically controlled scans only if you have the PMU display.

Preparing a physiologically controlled scan

Physiologically triggered scans are performed the same way as regular MR examinations. However, you have to perform a few additional preparations, and there are additional settings as well as control options.

Applying sensors

Position sensors on the patient prior to a physiologically triggered scan. These sensors pick up the signals used for physiologically triggering.
See System Manual

- ❏ ECG electrodes for recording the ECG
- ❏ Pulse sensor for recording the pulse curve
- ❏ Respiratory belt for recording the respiratory curve

PMU display

The signal curves of the sensors are shown on the PMU display integrated in the housing of the magnet. This allows you to check whether the quality of the signals is satisfactory while you are in the examination room.

⇨ The PMU display option is not available on "MAGNETOM Concerto"

You monitor the physiological signals on the **Physiological Display** dialog box in the control room.
→ Page C.15–5, *Monitoring signals on the physiological display*

Trigger indication

You can listen to the trigger signal (a short beep) via the intercom system. Use the slider at the *syngo* Acquisition Workplace to adjust the volume of the beep.
Refer to the System Manual

Loading the Scan Program

Once you have finished the preparation steps, select a scan program for your examination.

✧ Select the required scan program from the **Program** card.

✧ Transfer the scan program into the program control.

On completion of the localizer, the first protocol is opened. Adjust the slices graphically and set the measurement parameters.
→ Page C.4–30, *Graphic slice positioning (GSP)*
→ Chapter C 5, *Adjusting Measurement Parameters*

Monitoring signals on the physiological display

You have attached the sensors to the patient in the examination room and are observing the signals in the **Physiological Display** window. You may also use the **Physiological Display** window to select an ECG lead and to check the long-term statistical values.

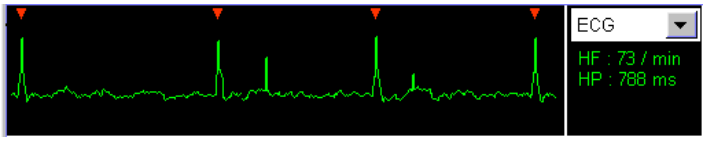
✧ Select **View > Physiological Display**.

Or



✧ Click the button in the toolbar of the **Exam** task card.

The **Physiological Display** window is displayed to the right of the image area. You can resize or move this window around the screen.
→ *syngo* Operator Manual



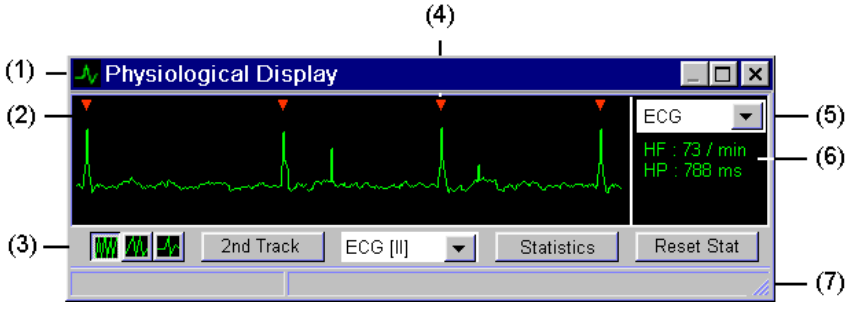
Changing window display

There are two display modes for the **Physiological Display** window.

- ❏ Without a border (default setting)
- ❏ With a border

✧ Select **Border** from the context menu.

The **Physiological Display** window is displayed with its title bar, status bar, and buttons. The size of the physiological signals does not change in the display.

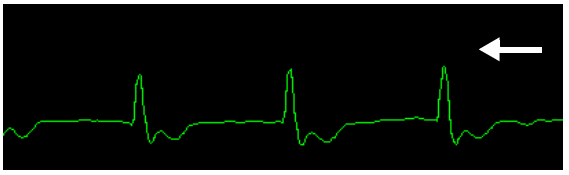


(1) Title bar
(2) Image area for display of signal curves
(3) Buttons for setting the speed and operating the physiological display
(4) Symbol for a standard trigger
(5) List for selecting the physiological signal
(6) Online statistical values
(7) Status bar

➪ If you want to display the **Physiological Display** window without the title bar, status bar, and buttons, deselect **Border** in the context menu.

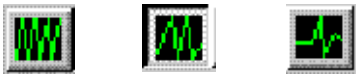
Displaying physiological signals

The physiological signals are displayed in the image area of the window. They move from right to left. If you enlarge or reduce the window, the signals in the image area will be displayed enlarged or reduced accordingly.



Setting the Plotting Speed

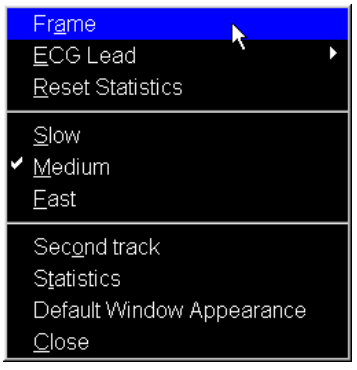
The speed at which the signals move across the image area may be set to one of three levels.



Slow Medi- Fast

✧ Click one of these buttons to select a recording speed.

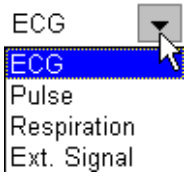
Or



✧ Select **Slow**, **Medium** or **Fast** from the context menu.

Selecting a signal

You may only select up to two signals for display in the **Physiological Display** window, even if more than two sensors are connected.



✧ To display the first signal, select **ECG**, **Pulse**, **Respiration**, or **Ext. Signal**.

The selected signal is displayed in the image area.

Displaying a second signal

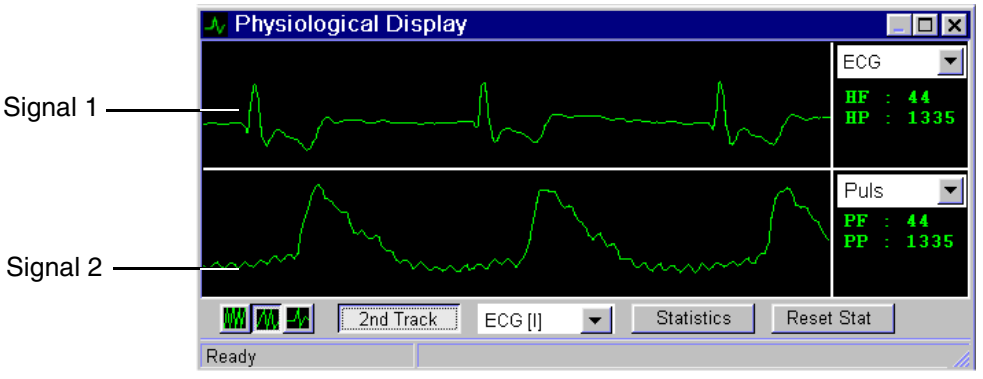
You may have two signals displayed. The tracks for the two signals are synchronized in time.



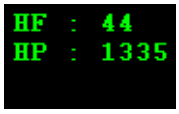
✧ Click the **2nd Track** button.

Or

✧ Select **2nd Track** in the context menu.



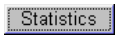
Online statistical values



The online statistical values are displayed to the right of the curve. They show the values currently being measured by the system. For an ECG, for example, the current cardiac rate and cycle are displayed.

Long-term statistics

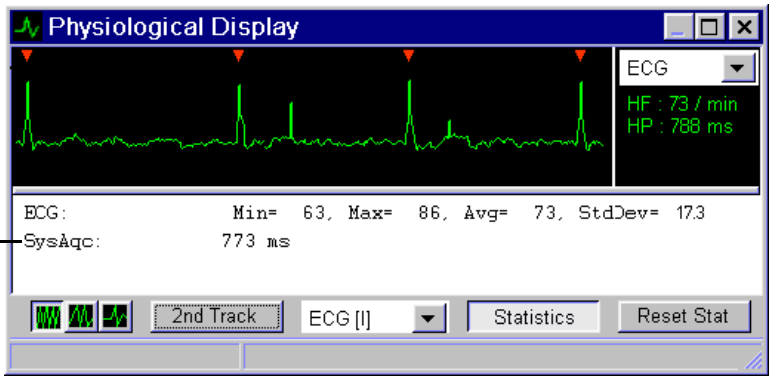
In addition to current data, the system also collects signal data over a longer period to calculate the average value, standard deviation, minimum, maximum, as well as the system acquisition window.



✧ Click the **Statistics** button to display these data.

Or

✧ Select **Statistics** from the context menu.



Long-term statistics

Resetting the long-term statistics

The system calculates the system acquisition window from the long-term statistics. Once the patient has become accustomed to having the measurements taken after a few minutes, their respiration, pulse, or heart rate will become calmer.

You should then reset the long-term statistics to have the system calculate current values again. The system acquisition window will also be updated.



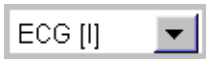
✧ Click the **Reset Stat** button.

Or

✧ Select **Reset Statistics** from the context menu.

Selecting the ECG Signal Lead

You can have one of six leads (three for active ECG electrodes) generated from the four electrodes applied (three if you are using active ECG electrodes). You may select another lead if one of the leads does not provide a satisfactory signal or no signal at all, making triggering impossible.

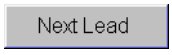


✧ Select a lead that provides a satisfactory signal.

Or

✧ Select **ECG lead** from the context menu and click the required lead.

Or



✧ Click the **Next Lead** button to select the next lead if you are using active ECG electrodes.

Or

✧ Select the lead on the PMU display (option not available on "MAGNETOM Concerto") on the housing of the magnet. *See System Manual*

➪ You may not change a lead if a scan is in progress.

➪ The leads are described in detail in the *System Manual*.

Faulty contact

The system detects poor sensor contact. Relevant error messages are displayed on the status bar of the **Physiological Display** window when **Border** display mode is set:

❏ Lead error (with ECG)
❏ Sensor not connected (with pulse sensor)
❏ Current ECG El. are connected

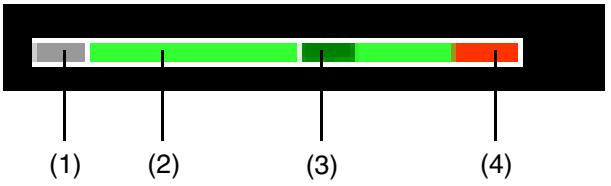
Graphic display of time ranges

The various time ranges of a scan are indicated during scanning in a bar below the *first* signal curve in the **Physiological Display** window.

Each time range is assigned a different color:

(1) Delay time - gray
(2) Scan interval (scan acquisition window) - green
(3) Scan pause (e.g. transmission of saturation pulses) - dark green
(4) Timeout - red

→ Page C.15–25, *Graphic display of the time ranges*



The following restrictions apply to the display of time ranges:

- ❏ No time ranges are displayed for the second track.
- ❏ With display rate **Fast** no time ranges are displayed.
- ❏ With display rate **Medium** time ranges are displayed.
- ❏ With display rate **Slow** time ranges are displayed if the selected signal is a respiratory signal or an external signal.

Display of trigger information

Trigger information is displayed above the physiological curve. Different symbols are used for different types of trigger.



❏ Standard trigger - appears for triggering and for retrogating

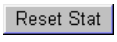


❏ Irregular heart beat

Setting parameters

To perform a physiologically controlled scan, you have to set additional measurement parameters on the **Physio** parameter card.

➪ Before you set the scan parameters, we recommend resetting the long-term statistics using the **Reset Stat** button of the **Physiological Display** dialog box to obtain the most current value for the **Average cycle** parameter.
→ Page C.15–10, *Resetting the long-term statistics*
→ Page C.15–20, *Average cycle*



✧ Click the **Reset Stat** button in the **Physiological Display** window.

Or

✧ Select **Reset statistics** from the context menu.

Displaying the Physio parameter card

✧ Click the **Physio** tab to move the parameter card into foreground.

The **Physio** parameter card is divided into several subtask cards. Different subtask cards are shown depending on the installed and configured PMU and on the sequence the protocol is based on.

❏ **Signal 1**
Use the **Signal 1** subtask card to set the parameters for the 1st physiological signal.

❏ **Cardiac**
Use the **Cardiac** subtask card to set the parameters for cardiological examinations.

❏ **PACE**
This subtask card is used to set additional parameters to correct breath-hold motion and for multiple breath-hold scans.

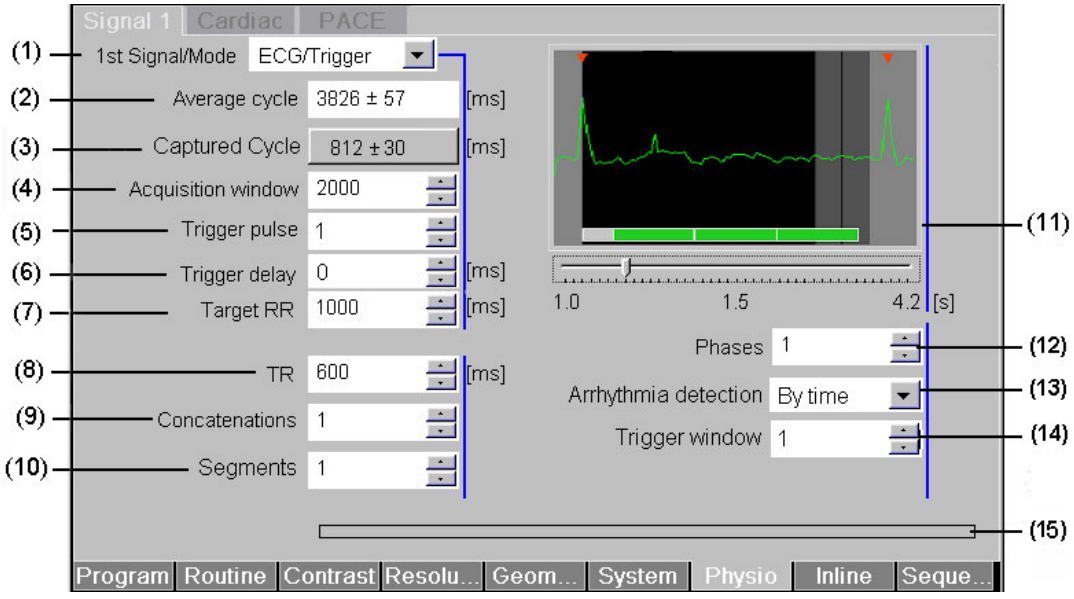
The **Cardiac** and **PACE** subtask cards are described in → Chapter C.5.

Setting ECG triggering

ECG triggering is especially useful for thoracic and cardiac scans to avoid image blurring caused by the heartbeat during regular scans.

Signal 1 subtask card

✧ Click the **Signal 1** subtask card to move it into foreground.



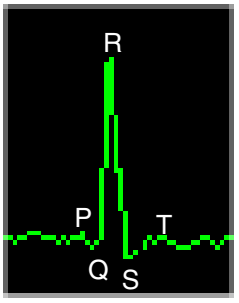
(1) Signal and mode selection
(2) Average time between two trigger events and standard deviation
(3) Current, captured average cycle
(4) Acquisition window
(5) Trigger counter
(6) Delay time
(7) Target RR (average heart rate of the patient)
(8) Repetition time TR
(9) Number of concatenations
(10) Number of segments
(11) Graphic display of scan times
(12) Number of cardiac phases
(13) Arrhythmia detection
(14) Size of acquisition window
(15) Limit display of numeric parameters

The display of the **Signal 1** subtask card depends on the signal setting.

Use the **1st Signal/Mode** selection list to enter the physiological signal to be used for triggering. You may also select the scan mode at this time.



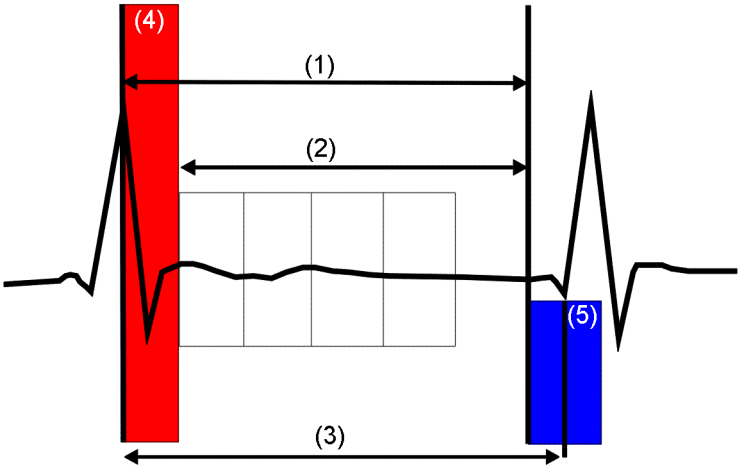
✧ Select **ECG/Trigger** from the selection list.



The **ECG Signal** shows the action potential of the heart in the form of a curve.

The individual curve phases correspond to the respective contraction or relaxation phases of the heart. The R wave in the QRS complex is used as the trigger point for the measurement.

The signal curve for ECG triggering may be illustrated as follows:



(1) System acquisition window
(2) Scan acquisition window
(3) Average interval (average cycle)
(4) Delay time (delay trigger TD)
(5) Standard deviation of the average cycle

Average cycle

Your system calculates the **Average cycle** from statistical values. This value indicates the time that has elapsed between two trigger events.

The average cycle is recalculated and updated continually. You cannot change this value.



If **Average cycle** displays "**No Signal**", then either no sensors are connected or the sensors are not providing a usable signal.

Captured cycle

You can have the acquisition window calculated from the current cycle.



✧ Click the **Captured cycle** contour button.

The value of the current average cycle is displayed on the button and used to calculate the acquisition window. Protocol parameters may have to be adjusted.

The **Captured cycle** parameter is reset as soon as you edit the value for the acquisition window.

Target RR

In some sequences, arrhythmia is detected by the **Target RR** parameter.



✧ Set the **Target RR** parameter to the average heart rate of the patient.

Acquisition window

The **Acquisition window** parameter stands for the time used for data acquisition after a trigger pulse in a physiologically triggered scan.

The delay time, number of phases, and repetition time are proportional to the size of the **Acquisition window**.

➪ Place the mouse pointer over the **Acquisition window** input field for a few seconds to display a tool tip. It shows the value recommended by the system.



✧ Enter a time (in ms) in the spin box.

Please also note the difference in meaning between the terms system acquisition time and scan acquisition time:

❏ **System acquisition time**
Determined by the system; Difference of the average cycle and double standard deviation.
The acquisition window cannot be greater than the system acquisition time.

❏ **Scan acquisition time**
The time actually used by the system for data acquisition.

Number of triggers

In the **Trigger pulse** field you can define which trigger event is to be used for triggering a scan.



✧ Enter a value in the **Trigger pulse** spin box.

✧ Select 1 if you want to use every trigger to start a scan.

✧ Select 2 if you want to use every second trigger to start a scan.

Entering the delay time

You may enter a delay time for the **ECG/Trigger** signal This parameter defines the delay before the system starts the scan after the trigger signal has been received. For example, for an adult patient with a pulse rate of 70/min, you will obtain an image of the systole with a 0 second delay time, and an image of the end diastole with a 250 to 350 ms delay time. This allows you to acquire images at any point in the signal cycle.



✧ Enter a delay time in ms in the **Trigger Delay** spin box.

Repetition time TR

The repetition time TR is set if permitted by the parameters of the protocol. The longer the repetition time TR, the fewer images you will obtain per trigger event.



✧ Enter a value in the **TR** spin box.

If you can enter more than one repetition time, use the spin buttons to scroll through individual times.

Concatenations

With triggered multislice scans ("interleaved" excitation sequence), it is sometimes not possible to acquire all slices in one measurement. The missing slices will then be acquired with the next scan.



✧ Enter the number of scans you want to concatenate in the **Concatenations** spin box.

Segments

With the segments, you may define the number of rows in the k space that are measured for an image during a TR interval.



✧ Enter the number of segments in the **Segments** spin box.

Phases

This parameter defines the number of phases of the heart beat that will be acquired. The number of phases is usually automatically calculated from the acquisition window, TR, and the delay time.



✧ Enter the number of cardiac phases in the **Phases** spin box.

Arrhythmia detection

Some sequences contain automatic detection of rhythm disturbances.

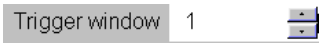
This detection is based either on time-controlled extra systole detection (**By time**) or on pattern detection of the extra systole (**By Pattern**).



✧ Select **Arrhythmia detection** from the selection list.

Trigger window

If you have selected the **By time** entry, another parameter will appear on the parameter card.

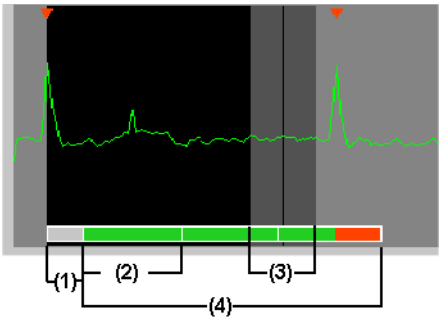


✧ Enter the size of the trigger window for extra systole detection in the **Trigger window** spin box.

Graphic display of the time ranges

The top right area of the parameter card shows the physiological signal and the time domains resulting from the parameters set.
→ Page C.15–12, *Graphic display of time ranges*

Unlike the **Physiological Display** dialog box, a frozen image is displayed on the **Physio** parameter card.



(1) Delay time
(2) Repetition time
(3) Twice the standard deviation
(4) Scan acquisition window

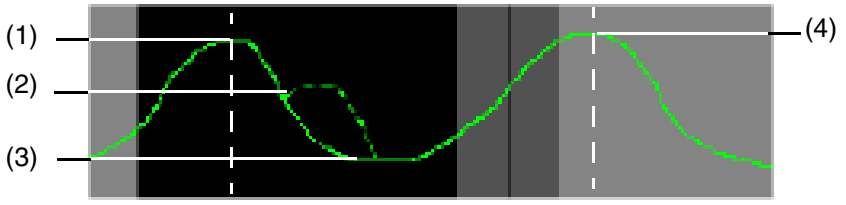
If e.g. the scan acquisition time set is longer than the time between two trigger events, the scan acquisition window will overlap the following trigger section. The time overlap is shown in red.

If the input focus is on the trigger delay or TR, the corresponding time range has a blue border.

Setting pulse triggering

Pulse triggering is especially useful for suppressing motion and flow artifacts caused by pulsating blood or CSF.

The pulse sensor may be attached to the patient's middle finger.



(1) First pulse wave
(2) Second pulse wave
(3) Diastolic blood pressure
(4) Systolic blood pressure

The first pulse wave (premature pulse wave) is used for triggering. This wave corresponds to the systolic blood pressure.



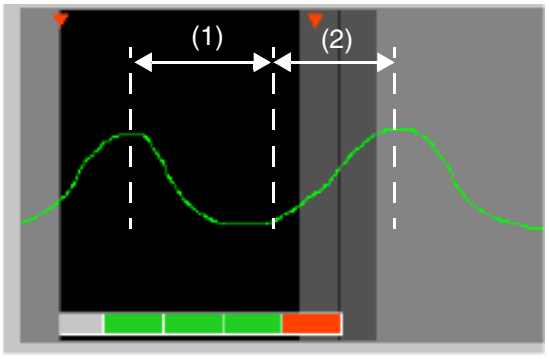
✧ Select **Pulse/Trigger** from the **1st Signal/Mode** subtask card.

You can set the same parameters on the **Signal 1** subtask card as on the **ECG/Trigger** card.

Setting respiratory triggering

Respiratory triggering is used to avoid motion artifacts caused by breathing.

The respiratory signal is obtained e.g. using a respiratory belt. The cyclic expansion and contraction of the thorax generates the respiratory curve.

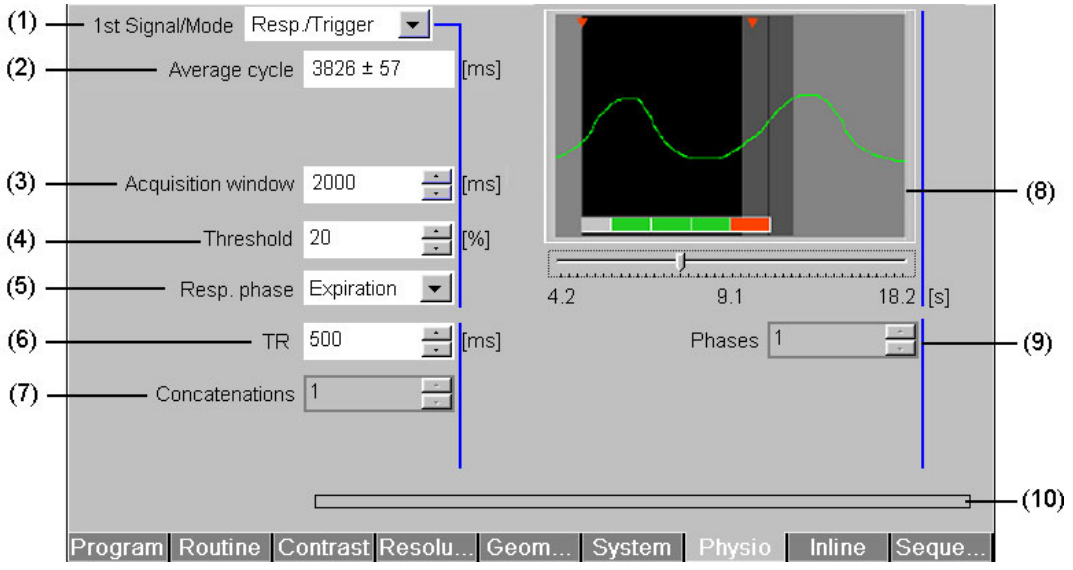


(1) Expiration
(2) Inspiration



✧ Select **Resp./Trigger** under **1st Signal/Mode** in the selection list.

Physio parameter card for respiratory triggering



(1) Signal and mode selection
(2) Average time between two trigger events and standard deviation
(3) Acquisition window
(4) Threshold value for respiration
(5) Respiratory phase (inspiration or expiration)
(6) Repetition time TR
(7) Number of concatenations
(8) Graphic display of scan times
(9) Number of respiratory phases
(10) Limit display of numeric parameters

Average cycle

The value of the **Average cycle** is calculated by the system.

The system acquisition window is calculated as follows for respiratory triggering: Difference between half the average cycle and the standard deviation.

Acquisition window

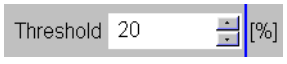


The **Acquisition window** shows the time used for the scan after a trigger pulse in a physiologically triggered scan.

✧ Enter a time in ms in the **Acquisition Window** spin box.

➪ Place the mouse pointer over the **Acquisition window** input field to display a tool tip. It shows the value recommended by the system.

Threshold



The threshold value determines the point of the respiratory cycle where scanning is triggered.

✧ Enter a threshold in the **Threshold** spin box.

When the respiratory curve reaches this value, the signal is triggered. The threshold value is expressed as a percentage of the respiratory curve. 100% is the maximum expansion of the thorax.

Respiratory phases

You may use either inspiration or expiration for triggering.



✧ Select **Inspiration** or **Expiration** from the **Resp. phases** selection list.

Repetition time TR



✧ Enter the repetition time in the **TR** spin box.

Concatenations

You will define the number of scans to be concatenated.



✧ Enter a value in the **Concatenations** spin box.

Phases

This setting determines the number of respiratory phases to be acquired. It is used for e.g. multislice or multiphase cardiac measurements. The number of phases (respiration) depends on the repetition time selected. Please observe the limits.



✧ Enter the number of respiratory phases in the **Phases** spin box.

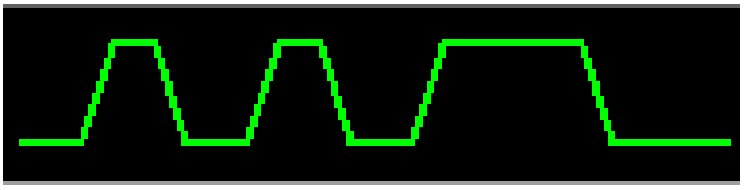
After you have set and checked all parameters, you may start scanning.

→ Page C.15–35, *Starting the measurement*

Setting an external trigger signal

An external signal may be used e.g. for functional scans (BOLD imaging) to trigger scanning of the stimulated series.

The PMU connection at the foot end of the patient table allows you to induce an external *digital* triggering signal.



The rising edge of the signal is used to start the measurement.



✧ Select **Ext./Trigger** under **1st Signal/Mode** in the selection list.

You can set the same parameters on the **Signal 1** subtask card as on the **ECG/Trigger** card.

Setting retrospective gating

Certain sequences support retrospective gating, e.g. cine_trufi.

In this case, the scan is performed without triggering. Instead, the acquired image data are retrospectively correlated with the characteristic of a physiological signal.

Unlike with triggering, with retrospective gating you can measure all cardiac phases including the late diastole.

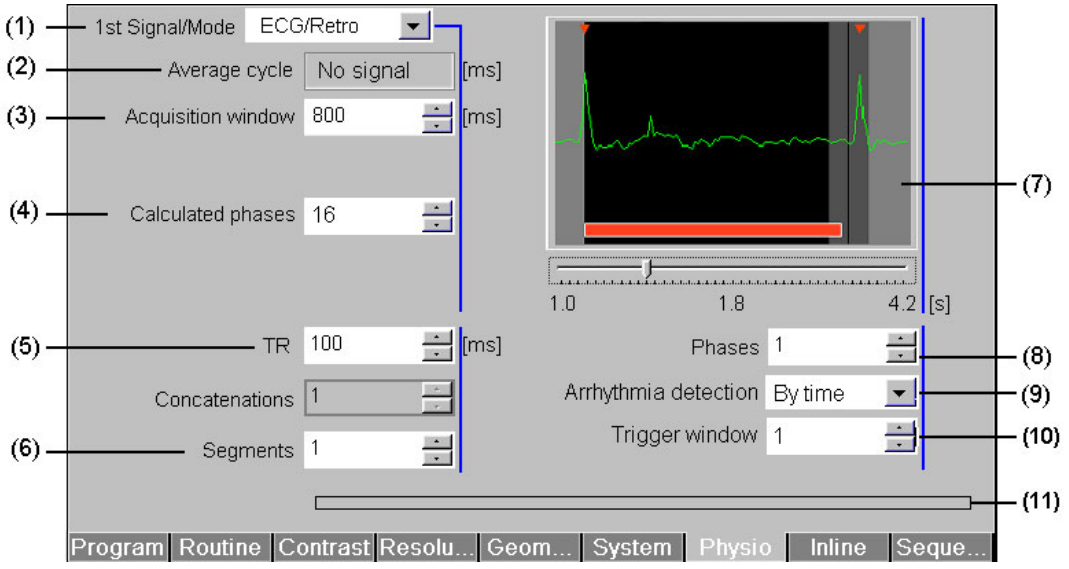
Retrospective gating may be applied to ECG signal curves, pulse signal curves, and external trigger signal curves. The **1st Signal/Mode** selection list on the **Signal 1** subtask card contains the following additional entries:

- ❏ **ECG/Retro**
- ❏ **Pulse/Retro**
- ❏ **Ext/Retro**

Signal 1 subtask card with ECG/Retro



✧ Select **ECG/Retro** from the **1st Signal/Mode** subtask card.



(1) Signal and mode selection
(2) Average time between two trigger events and standard deviation
(3) Acquisition window
(4) Calculated phases
(5) Repetition time TR
(6) Number of segments
(7) Graphic display of scan times
(8) Number of phases
(9) Detection of rhythm disturbances
(10) Trigger window
(11) Limit display of numeric parameters

The **Average cycle** and **Acquisition Window** parameters are set by the system.

⇨ In retrospective gating, the **Acquisition window** should be 20-30% larger than the average cycle.

The **Segments**, **Phases**, **Arrhythmia detection**, and **Trigger window** parameters are the same as for ECG triggering.

Calculated phases

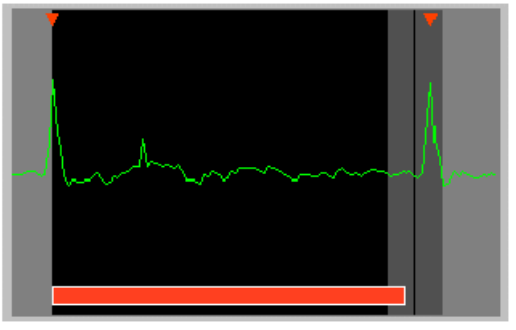
This parameter is used to define the number of images to be reconstructed per cardiac interval.



✧ Enter the number of phases to be calculated in the **Calculated Phases** spin box.

Graphic display of the ECG/ Retro

In retrospective gating, the second trigger must arrive within the scan acquisition time. If this is not the case, the entire scan acquisition range will be displayed in red.



After you have set and checked all parameters, you may start scanning.

→ Page C.15–35, *Starting the measurement*

Starting the measurement

After you have checked all scan parameters on the parameter cards, apply these parameters as usual and start scanning.

Loading parameters



✧ Click the **Apply** button in the program control.

The settings are transferred to the scan system. The protocol is now complete.

Starting the measurement

The complete protocol starts automatically and is processed. If there are still incomplete protocols in the job list (construction-worker icon), open and edit them like the first protocol of the program so that they can be started automatically as well.
→ Page C.6–10, *Scan procedure for a routine examination*

CHAPTER C.16

Organizing Scan Programs

The sequences and parameter settings of frequently performed MR examinations are stored in your system as scan programs. **Exam Explorer** provides an overview of the available scan programs.

The programs are divided into two groups: Siemens programs and customer programs. The Siemens programs are used as a basis for customer programs. Customer programs comprise the directory of scan programs used for your daily work and examinations.

➪ The customer programs are offered for selection on the program card.
→ Page C.2–4, *Selecting a scan program*

The **Exam Explorer** allows you to manage and maintain your scan programs.

For example, the **Exam Explorer** is used for:

❏ Copying scan programs from the Siemens tree into the customer tree. You can then use these programs to perform examinations.

❏ Changing scan programs of the customer tree. For example, you can re-organize, delete, or add new program steps or make permanent changes to the measurement parameters of a protocol.

❏ Exchanging scan programs or protocols with other ***syngo* MR** systems. In an intermediate step, you will be required to use external data media (diskette) or a file system.

➪ You cannot change the existing scan programs in the Siemens tree.

You can only edit entries in the customer tree of the **Exam Explorer** (e.g. delete exams or change scan parameters of a protocol) if you have the appropriate authorization.
Note the information in the Safety Standards book.

You will generally work with the **Exam Explorer** "offline", i.e. not during an examination in progress. In some cases, you may use the **Exam Explorer** to search for scan programs or protocols during an examination and transfer them directly into the queue.

The **Exam Explorer** is primarily a tool for managing and maintaining your scan programs. If you want to change a scan program immediately prior to an examination (and for this particular examination only), use the joblist in the program control instead.

The **Exam Explorer** provides a **print dialog** for you to print protocols with an overview of parameter settings and lists of protocol contents.

Calling up the Exam Explorer

✧ Select **View > Exam Explorer** from the main menu.

Or

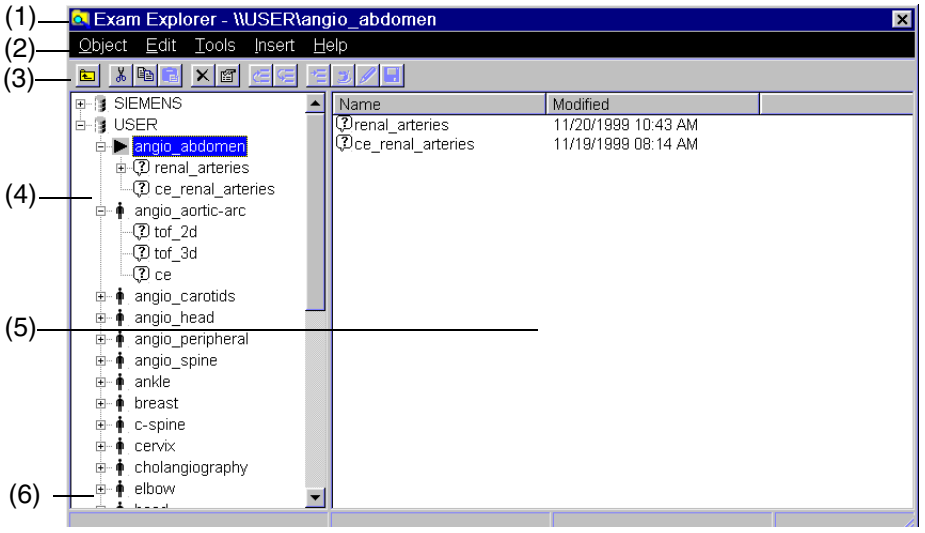


✧ Click this button on the tool bar of the **Exam** task card.

Or

✧ If you are in the **Program** parameter card, select **Explorer** from the context menu.

The **Exam Explorer** window is displayed. You may resize or move this window around the screen.
→ *syngo* Operator Manual



(1) Title bar with path
(2) Menu bar
(3) Tool bar
(4) Navigation area
(5) Content area
(6) Status bar

Layout of the Exam Explorer

The program window of the **Exam Explorer** is similar to Windows Explorer. You will be able to intuitively use the **Exam Explorer** within a short time.

Navigation and content area

The **Exam Explorer** window is divided into two main areas:

❏ **Navigation area** (left)
Here you can navigate through the various data levels with the mouse.
→ Page C.16–6, *Data levels*

❏ **Content area** (right)
Displays the content of the data level selected in the navigation area.

Moving the border line

To optimize the display, you may move the border between the navigation area and content area.



✧ Place the cursor on the border line between the two window areas.

The cursor changes shape.

✧ Hold down the *left* mouse button down and drag the border line left or right.

The size of the content area will increase and the size of the navigation area will be reduced, or vice versa.

Data levels

The examinations and scan programs stored in your system are grouped hierarchically in the **Exam Explorer**:

❑ **Level 1: Customer/Siemens level**

The **Siemens** tree contains a variety of clinically tested, recommended scan programs set up by Siemens customer service during system installation. They are to be used as a basis for preparing your own selection of frequently used scan programs.

You cannot change the Siemens tree You may, however, copy the folders to your customer tree and edit them there. You can always go back and recover the original recommended Siemens scan programs at any time.

❏ **Level 2: Examination region**

All examinations for a certain body region are grouped together in an examination region (**Region**).

❏ **Level 3: Examination**

An **Examination** contains all scan programs for a certain body part or anatomical structure of a body region.

❏ **Level 4: Scan program**

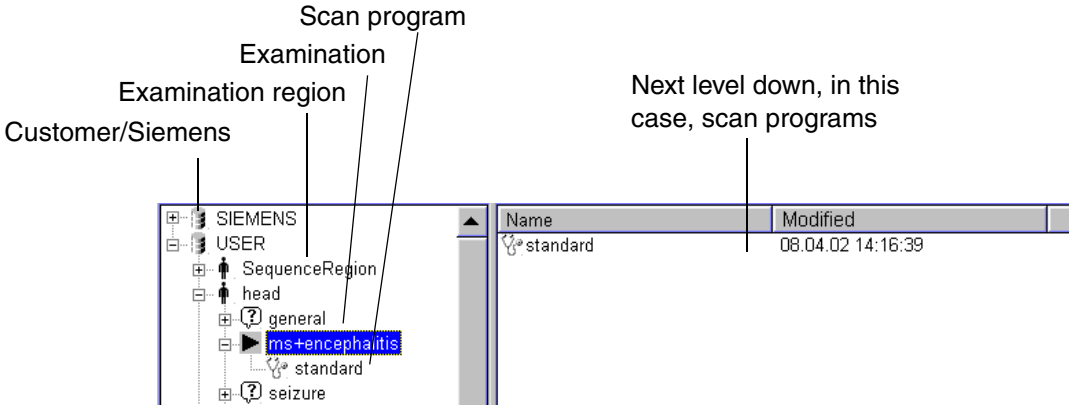
A scan program (**Program**) contains a sequence of optimized program instructions suitable for particular diagnostic problems.

❏ **Level 5: Program instructions**

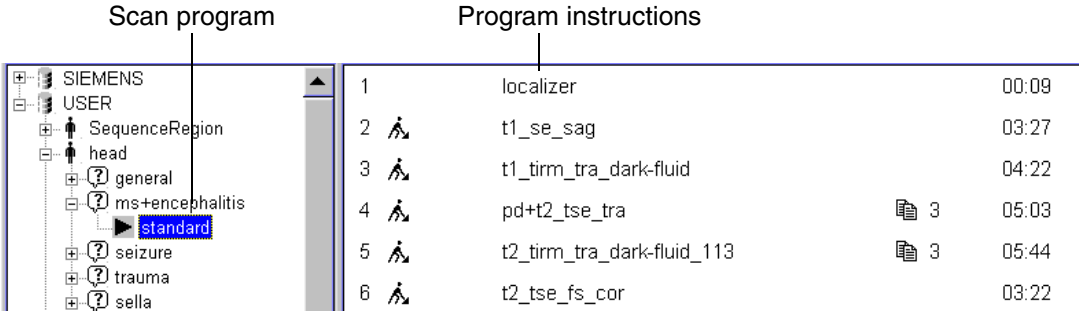
A program instruction may be a scan protocol (**Protocol**) or a scan pause (**Pause**). The sequence of scan protocols/pauses in a scan program determines the course of the examination.

Content of a data level

If you select the customer/Siemens tree, a region, or an examination in the navigation area, its content will be listed in the content area.



Select a scan program to display its program instructions in the content area.



Tool bar

Similar to the Windows Explorer, the **Exam Explorer** also has a toolbar that allows you to perform frequently required operator actions quickly and easily.


Move up one directory level


Cut


Copy


Insert


Delete


Display property window


Move selection up


Move selection down


Insert scan protocol


Inserting a measurement pause


Edit scan protocol


Save scan program in the examination database

Displaying unlicensed scan programs

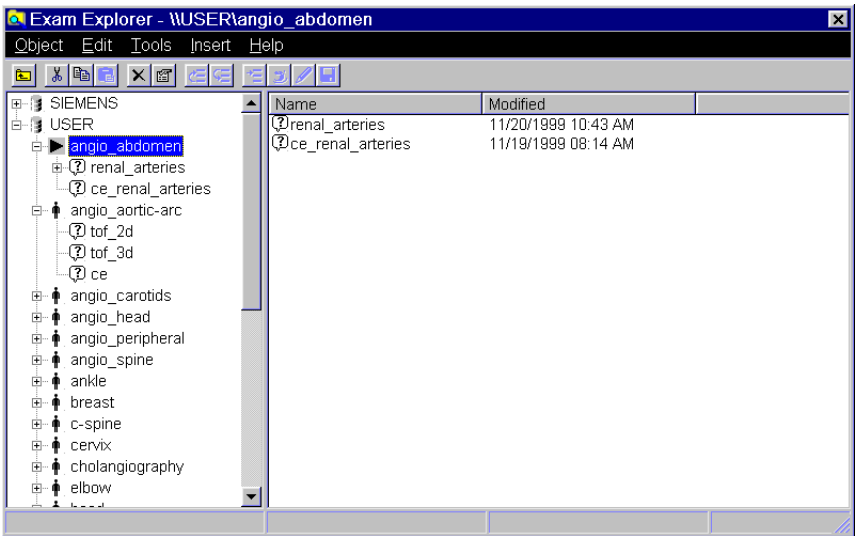
Scan programs that include unlicensed protocols are normally not displayed in the **Exam Explorer**. However, you may display unlicensed scan programs and protocols.

✔ Show Unlicensed Items

✧ Select **Tools > Show Unlicensed Items** from the main menu of the **Exam Explorer**.

A checkmark is placed in front of the menu item.

Unlicensed scan programs and protocols are now shown as additional gray items in the **Exam Explorer**.



You may use the **Protocol View** and the **Protocol Properties** dialog box to obtain information regarding the parameters and properties of the unlicensed protocols.
→ Page C.16–44, *Viewing protocol parameters*
→ Page C.12–2, *Editing protocol properties*

Of course, you may also hide the unlicensed scan programs and protocols again.



✧ Select **Tools > Show Unlicensed Items** from the main menu of the **Exam Explorer**.

The checkmark in front of the menu item will disappear again. The gray items are no longer shown.

⇨ In the **Object Properties** dialog box, you may select a single unlicensed scan program to be always displayed in the folder structure of the **Exam Explorer**, regardless of the setting in the main menu.
→ Page C.16–28, *Editing properties of scan programs*

Finding a scan program

To search for scan programs, click through data levels in the navigation area.

➪ The content of any entry in the navigation area may also be displayed in the content area. For this purpose, select the entry in the navigation area.

Selecting an examination tree

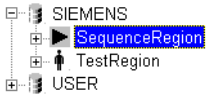


First decide whether you are looking for a scan program in the Siemens tree or in the customer tree.

✧ Click the **+** symbol in front of the entry in the navigation area.

The folder level expands to show the examination region stored in the Siemens or customer tree. The **+** symbol becomes a **-** symbol.

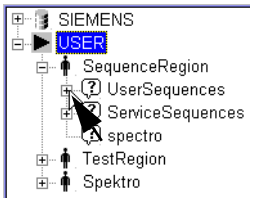
Selecting an examination region



✧ Then click the **+** symbol in front of a region.

The folder level expands to show the examinations stored for this region.

Selecting an examination

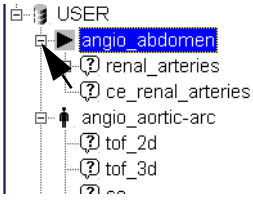


✧ Then click the **+** symbol in front of an examination.

The folder level expands to show the scan programs stored for this examination.

Scan program not found

If the scan program you a looking for is not contained in the open folder, just look in one of the other folders.



✧ First click the **-** symbol in front of the folder.

The directory closes again, keeping the display in the navigation area uncluttered.

✧ Then click the **+** symbol in front of another folder to open it and look for your scan program.

➪ If you know the name of the scan program you are looking for, you can also search for it by name in the examination database.
→ Page C.16–14, *Searching for a name*

Searching for a name

If you know the name of a specific region, examination, scan program, and protocol, you may search for the exact name.

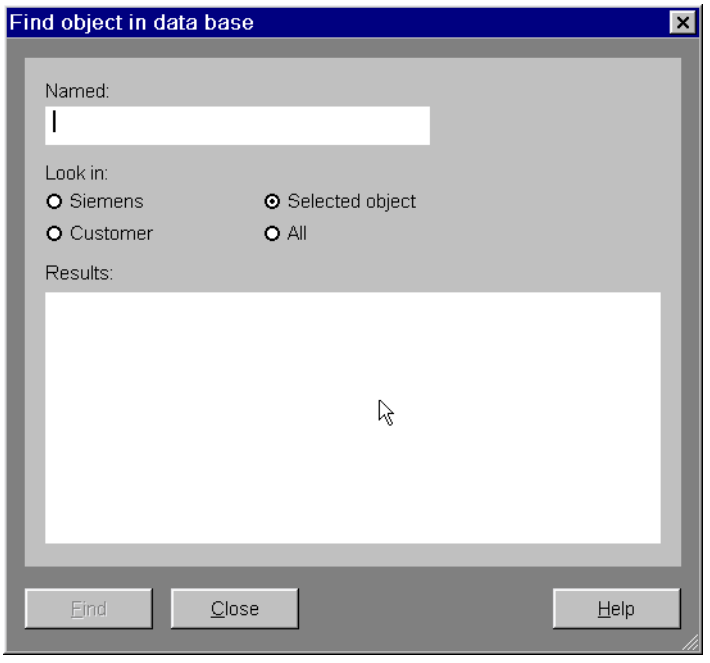
➪ If you do not know the entire name or are not sure of its spelling, you may use wildcards in your search.
→ *syngo* Operator Manual

✧ Select **Tools > Find** from the main menu of the **Exam Explorer**.

Or

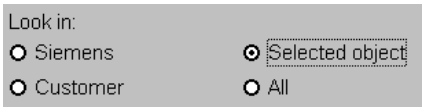
✧ Press the **Ctrl + F** shortcut on your keyboard.

The **Find Object in data base** dialog box opens.





✧ Enter the name of the region, examination, scan program, or protocol.



✧ Select one of the following options under **Look in**:

❑ **Siemens**
Only search the Siemens tree

❑ **Customer**
Only search the customer tree

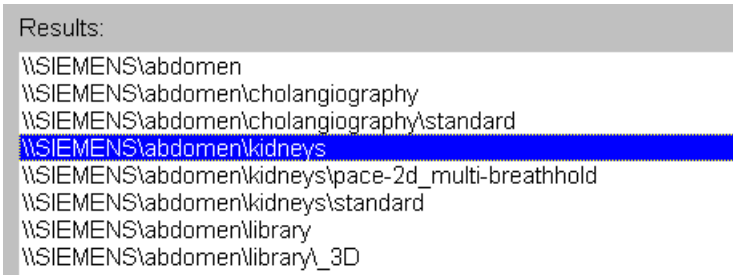
❑ **Selected object**
Only search within the selected entry

❑ **All**
Search the entire examination data base



✧ Click the **Find** button.

The result are all objects found with their paths:

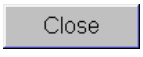


✧ Select the entry you require.

✧ Double-click this path.

The **Find object in data base** dialog box closes and the object found (region, examination, scan program, or protocol) opens in the **Exam Explorer**.

Or



✧ Click the **Close** button to close the dialog box.

✧ After that, click the region, examination, scan program, or protocol you located in the navigation area of the **Exam Explorer**.

Processing entries

You may copy regions, examinations, scan programs and protocols, delete them, or rename them. You can also change the order of the lists.

- You cannot make changes in the Siemens tree. You may only view the objects (regions, examinations, programs, and program steps) and copy them to the customer tree.

- If modify the content of any scan programs, a message box will be displayed as you exit the content area. You will be prompted to save the scan program with the changes or in its original state.

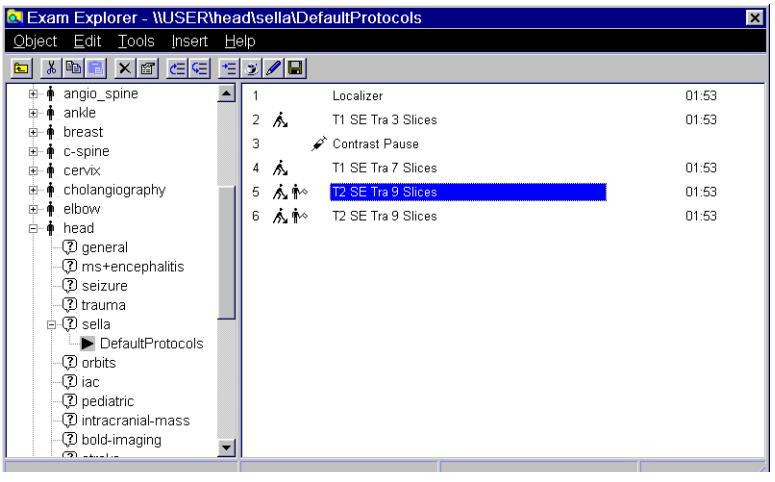
Moving entries

You can define the order of examination regions, examinations, and scan programs displayed in your customer tree. This enables you to place the regions, examinations, and exams frequently used in your daily routine near to the top, making them easily accessible.

You may also relocate individual program instructions within a scan program to modify the program sequence.

✧ First, open the examination tree, examination region, examination, or the program whose content you want to rearrange.

✧ Select the entry that you want to move in the content area.



Moving up

✧ Select **Edit > Move Up** from the main menu of the **Exam Explorer**.

Or

✧ Select **Move Up** from the context menu.

Or



✧ Click this button on the tool bar.

Or

✧ Press the **Alt** + ↑ shortcut on your keyboard.

✧ Repeat this step until the entry has reached the correct position.

Moving down

✧ Select **Edit > Move Down** from the main menu of the **Exam Explorer**.

Or

✧ Select **Move Down** from the context menu.

Or



✧ Click this button on the tool bar.

Or

✧ Press the shortcut **Alt** + ↓ on your keyboard.

✧ Repeat this step until the entry has reached the correct position.

Moving entries via *drag and drop*

✧ Hold down the *left* mouse button down and drag the entry to its new position.

Copying, cutting, and pasting entries

You may transfer examination regions, examinations, scan programs and program instructions from the Siemens tree to your customer tree by copying them.

You can also use the copy function to reorganize the program instructions, scan programs, examinations, and examination regions in your customer tree.

Copy

✧ Select the entry you want to copy in the navigation or content area.

✧ Select **Edit > Copy** from the main menu of the **Exam Explorer**.

Or

✧ Select **Copy** from the context menu.

Or



✧ Click this button on the tool bar.

Or

✧ Press the **Ctrl + C** shortcut on your keyboard.

The selected entry is copied into the clipboard.

Cut

✧ Select the entry you want to cut in the navigation or content area.

✧ Select **Edit > Cut** from the main menu of the **Exam Explorer**.

Or

✧ Select **Cut** from the context menu.

Or



✧ Click this button on the tool bar.

Or

✧ Press the **Ctrl + X** shortcut on your keyboard.

The selected entry will be cut and placed on the clipboard.

Paste

✧ Select the region, the examination, or the scan program to which you want to append a copied or cut entry.

Or (for program instructions)

✧ Select the program instruction *in front* of which you want to paste the cut or copied entry.

✧ Select **Edit > Paste** from the main menu of the **Exam Explorer**.

Or

✧ Select **Paste** from the context menu.

Or



✧ Click this button on the tool bar.

Or

✧ Press the **Ctrl + V** shortcut on your keyboard.

➪ If you had not selected a program step before pasting a program instruction, the program instruction will be appended to the end of the list.

Copying an entry via *drag and drop*

✧ Select the entry you want to copy in the navigation or content area.

✧ Keep the **Ctrl** key and the *left* mouse button pressed and drag the selection to its new position.

Deleting entries

You can delete any examination regions, examinations, scan programs, or program instructions that you do not require for your work.

✧ Select the entry you want to delete.

✧ Select **Edit > Delete** from the main menu of the **Exam Explorer**.

Or

✧ Select **Delete** from the context menu.

Or



✧ Click this button on the tool bar.

Or

✧ Press the **Del** key on your keyboard.

The selected entry is deleted along with its entire contents.

Renaming and annotating entries

Similar to the Windows Explorer, you may also modify the names of entries in the **Exam Explorer**.

✧ Select the entry you want to rename.

✧ Select **Edit > Properties** from the main menu of the **Exam Explorer**.

Or

✧ Select **Properties** from the context menu.

Or

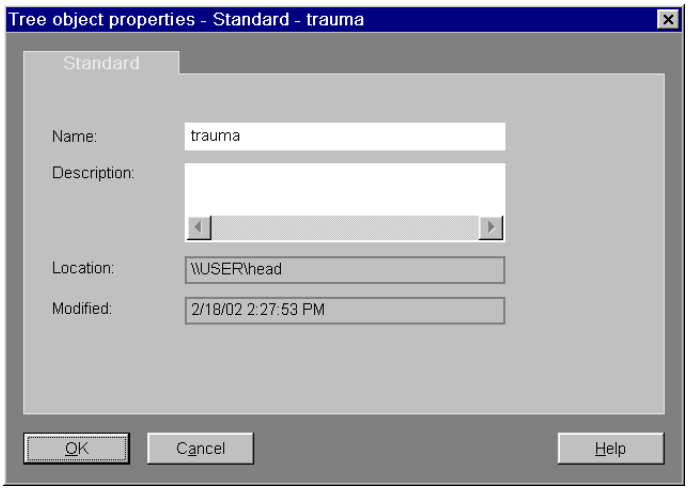


✧ Click this button on the tool bar.

Or

✧ Press the **Alt + Enter** shortcut on your keyboard.

The **Properties** dialog box is displayed with the **Standard** subtask card.



This subtask card shows the name, a brief description, and path of the selected entry. You can also see the date and time of the last changes made to this entry.

➪ The **Standard** subtask card in the **Region properties** dialog box is displayed on the level of examination regions. The **Standard** subtask card in the **Protocol step properties** or **Pause step properties** dialog box is displayed on the level of program instructions.

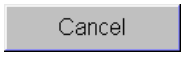
✧ Change the name and/or the short description of the entry.



✧ Click the **OK** button.

Your changes are applied and the dialog box closes.

Or

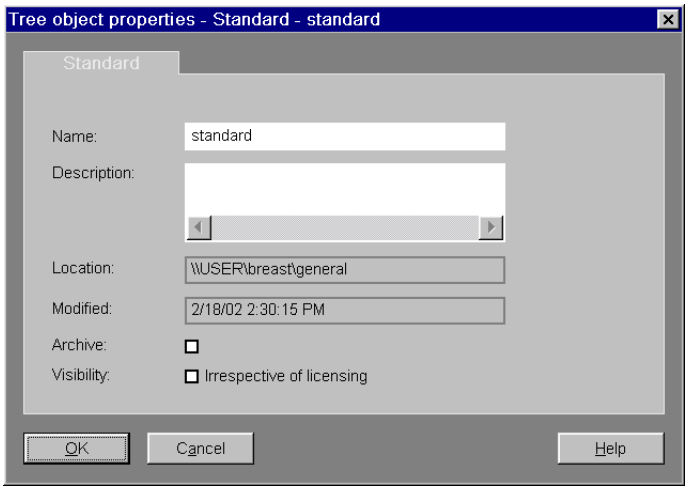


✧ Click the **Cancel** button.

The dialog box closes without applying your changes.

Editing properties of scan programs

If you are working at scan program level, the additional options **Archive** and **Visibility - Irrespective of licensing** will appear on the **Standard** subtask card in the **Properties** dialog box.



"Archive" option



The **Archive** option is automatically enabled for a scan program as soon as you modify it in the **Exam Explorer**.

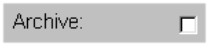
If the **Archive** option is enabled, you may restore scan programs in case of data recovery or software updates.

Scan programs for which the **Archive** option is not enabled will usually be replaced by the original programs from the Siemens tree.

You may also manually activate/deactivate the **Archive** option for a scan program.

✧ Select the scan program.

✧ Open the **Tree object properties** dialog box and move the **Standard** subtask card in to the foreground.
→ Page C.16–28



✧ Click the **Archive** check box to select or deselect it.

"Visibility - Irrespective of licensing" option

When you activate the **Visibility - Irrespective of licensing** option, the scan program is available in the folder structure of the **Exam Explorer**, even if it is an unlicensed scan program.
→ Page C.16–10, *Displaying unlicensed scan programs*

However, before you can activate the **Visibility - Irrespective of licensing** option for an unlicensed scan program, you must first show *all* unlicensed scan programs.



✧ Select **Tools > Show Unlicensed Items** from the main menu of the **Exam Explorer**.

Unlicensed scan programs are now shown as gray items in the **Exam Explorer**.

✧ Select the required unlicensed scan program.

✧ Open the **Properties** dialog box and go to the **Standard** subtask card.



✧ Click the **Visibility - Irrespective of licensing** check box to select it.

Creating a new examination region

You can create new examination regions in your customer tree.

✧ Select the customer tree (**USER)**.

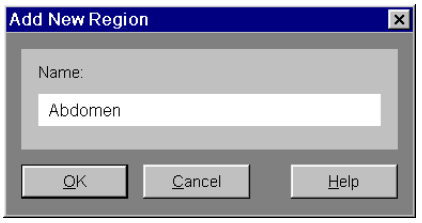
All examination regions in the customer tree are now displayed in the content area.

✧ Select **Object > New** from the main menu of the **Exam Explorer**.

Or

✧ Select **New** from the context menu.

The **Add New Region** dialog box opens.



✧ Enter a name for the new examination region.

✧ Click the **OK** button.

The new region will be appended to the end of the list of examination regions.

Assigning an examination region to a body region

The **Region properties** dialog window allows you to assign a newly created examination region to a body region and to change the assignment of an existing examination region.

✧ Select the examination region.

✧ Select **Edit > Properties** from the main menu of the **Exam Explorer**.

Or

✧ Select **Properties** from the context menu.

Or



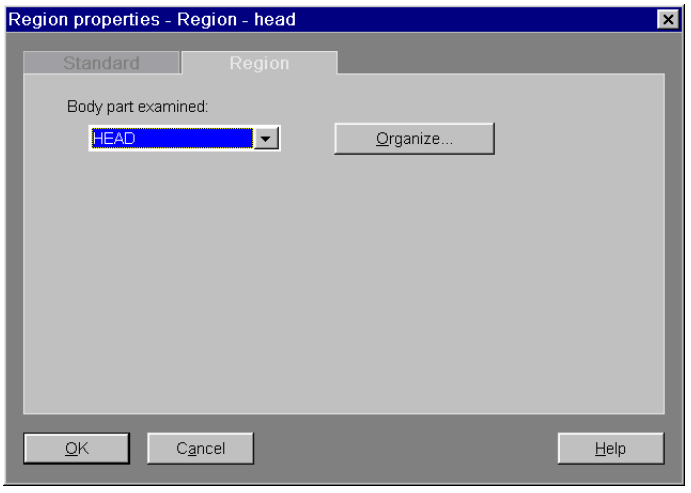
✧ Click this button on the tool bar.

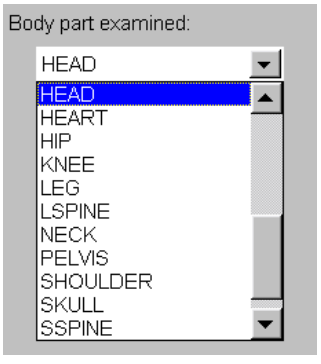
Or

✧ Press the **Alt + Enter** shortcut on your keyboard.

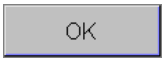
The **Region properties** dialog window opens.

✧ Click the **Region** subtask card to the foreground.





✧ Select the required body region from the **Body part examined** selection list.



✧ Click the **OK** button.

That confirms the assignment and closes the dialog box.

Managing the body regions

The **Body part examined** selection list shows all the body regions of your system.

The regions are grouped as follows:

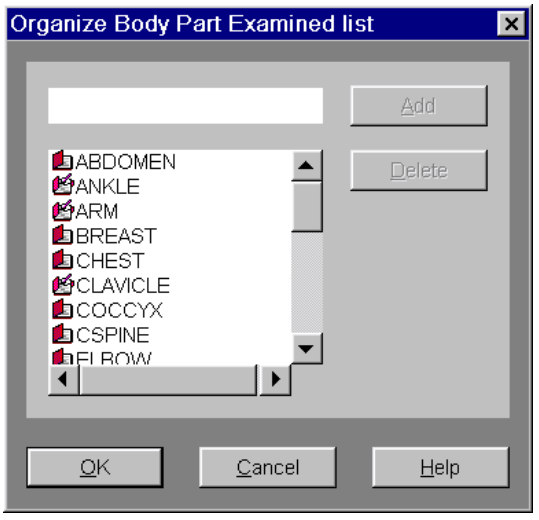
- **DICOM regions**
  DICOM regions are regions defined in the DICOM standard.
- **SIEMENS regions**
  SIEMENS regions are regions defined by SIEMENS and published in compliance with DICOM specifications.
- **Customer regions**
  Customer regions are regions users can define for themselves.

➪ You may *only* edit the customer regions in the list of body regions. DICOM and SIEMENS regions *cannot* be modified.



✧ Click the **Organize** button to edit the list of body regions.

The **Organize body regions examined** dialog box opens.



The icons in the list indicate whether it is an *invariable* DICOM or SIEMENS region or a customer region that you can change:

 DICOM or SIEMENS region

 Customer region

Creating a new customer region

You can add a new customer region to the list of body regions.



✧ Enter a name for the new body region in the input field.

➪ The name must consist of no more than 16 characters. Acceptable characters are capital letters, figures, blanks, and underscores.



✧ Click the **Add** button.

The new customer region will appear as a new entry in the list.

Deleting a customer region

You may remove from the list any customer regions that are no longer required.

✧ Select the customer region in the list.



✧ Click the **Delete** button

The entry will be deleted from the list.

Creating a new examination

You may create new examinations in your customer tree.

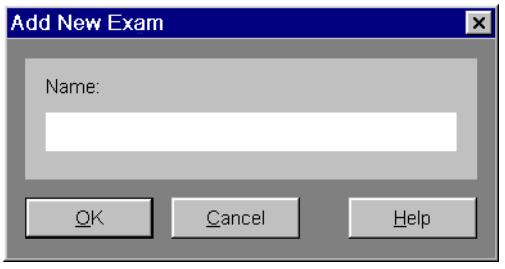
✧ Select the region for which you want to create a new examination.

✧ Select **Object > New** from the main menu of the **Exam Explorer**.

Or

✧ Select **New** from the context menu.

The **Add New Exam** dialog box opens.



✧ Enter a descriptive name in the **Name** field and confirm with **OK**.

The new examination is appended to the end of the examination list of the respective region.

Creating a new program

You may create new scan programs in your customer area.

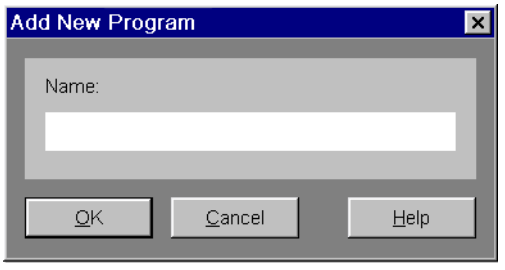
✧ Open the examination for which you want to create a new scan program.

✧ Select **Object > New** from the main menu of the **Exam Explorer**.

Or

✧ Select **New** from the context menu.

The **Add New Program** dialog box opens.



✧ Enter a name for the new scan program and confirm with **OK**.

The new program is appended to the list of scan programs of the open examination.

Inserting program instructions

You may add existing scan protocols and pauses to a scan program.

All steps are performed in the content area of the **Exam Explorer**.

Please note:

❏ If a program instruction in a scan program is already selected, the new instruction will be inserted in front of it.

❏ If no program instruction is selected, the new instruction will be appended to the end of the scan program.

If none of the scan protocols stored in your system are suitable for your new scan program, you can create a new scan protocol from a sequence or a reconstructed image and add it to your scan program.

➪ If modify the content of any scan programs, a message box will be displayed as you exit the content area. You will be prompted to save the scan program with the changes or in its original state.

Finding a protocol

The protocols you insert will usually be from other scan programs. You can make use of any program steps from customer and Siemens programs.

✧ Select **Insert > Program instruction** from the main menu of the **Exam Explorer**.

Or

✧ Select **Insert Program Steps** from the context menu.

➪ The **Insert Program Steps** menu item will only be active when you select the context menu if i) a scan program is open and ii) *no* program step is selected.

Or

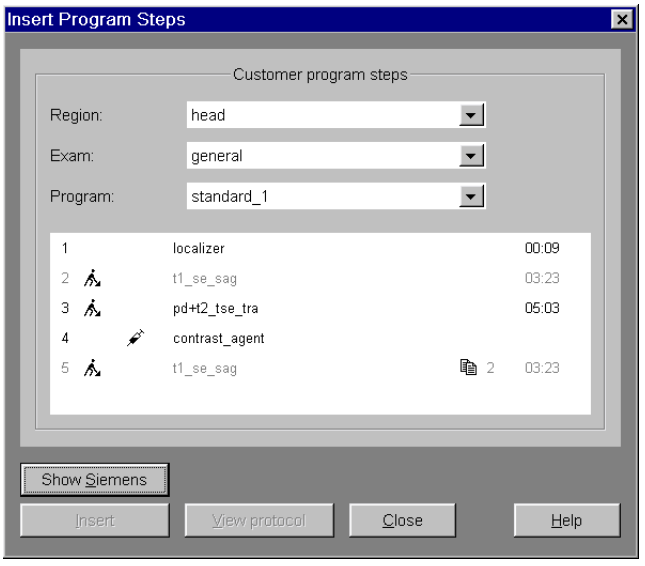


✧ Click this button on the tool bar.

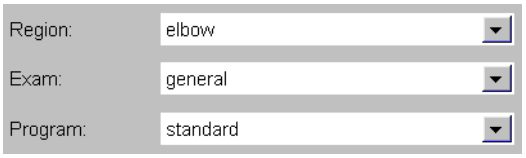
Or

✧ Press the **Ctrl + I** shortcut on your keyboard.

The **Insert Program Steps** dialog box opens.

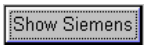


If the open scan program already contains program steps, they will be displayed in the **Insert Program Steps** dialog box.

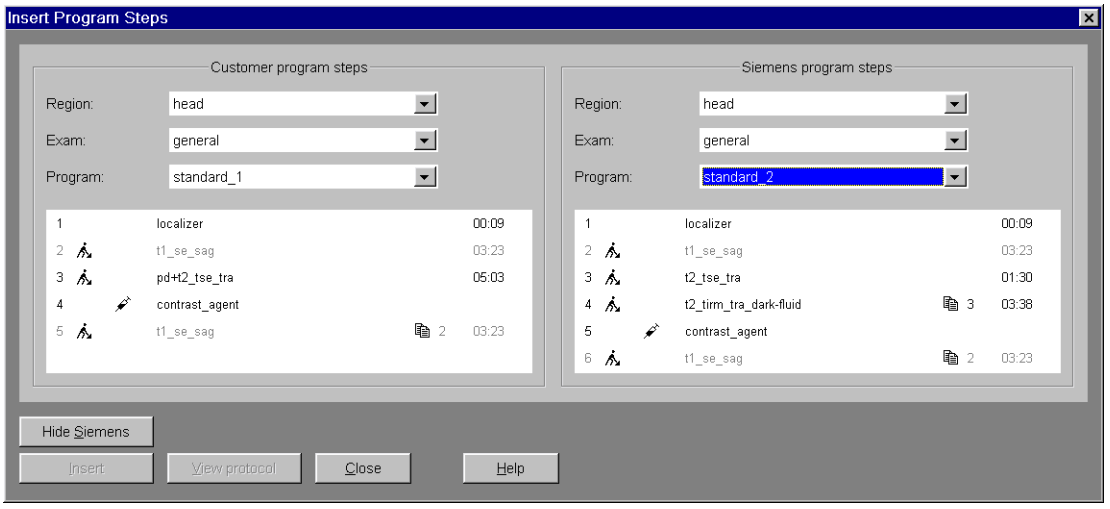


✧ Go to another scan program using the **Region**, **Exam**, and **Program** lists.

Or



✧ Click the **Show Siemens** button to search for program steps in the Siemens tree as well.



Customer program steps Siemens program steps

You can go to other examination regions, examinations, and scan program in the Siemens half of the window as well.

⇨ **<Select Item>** will be displayed in the selection lists if you have created a new region or examination in your customer tree for which there is no equivalent in the Siemens area. You now have to search for a corresponding scan program in the Siemens tree yourself.



✧ Click **Hide Siemens** to hide the Siemens program steps again.

Viewing protocol parameters

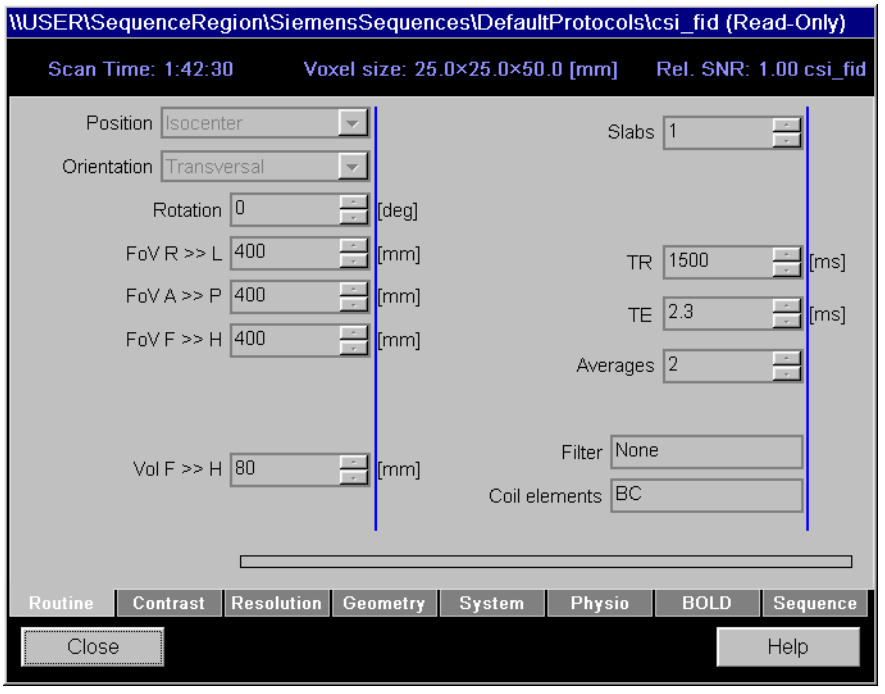
Before you insert a protocol into your scan program, you can review the protocol parameters.

✧ Select a protocol.

View Protocol

✧ Click the **View Protocol** button.

The **View Protocol** window opens.

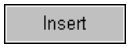


You will find the parameter card stack in the protocol view. You can view all cards and measurement parameters of the protocol, but you may not change them.

Inserting a protocol

✧ Select the protocol that you want to transfer to your scan program.

➪ If you want to transfer two or more protocols from a program, you may extend your selection with the **Ctrl** and **Shift** keys.
→ *syngo* Operator Manual



✧ Click the **Insert** button.

Or

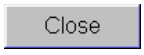
✧ Double-click the protocol item (to select a single protocol).

The selected protocol will be copied into the scan program in the **Exam Explorer**.

➪ If you had not selected a program step before pasting the protocol, the protocol will be appended to the end of the list.

Now you can search for additional protocols and copy them into your scan program.

Close the **Insert Program Steps** dialog box once you have copied all required protocols into your scan program.



✧ Click the **Close** button.

Creating a new protocol from a sequence

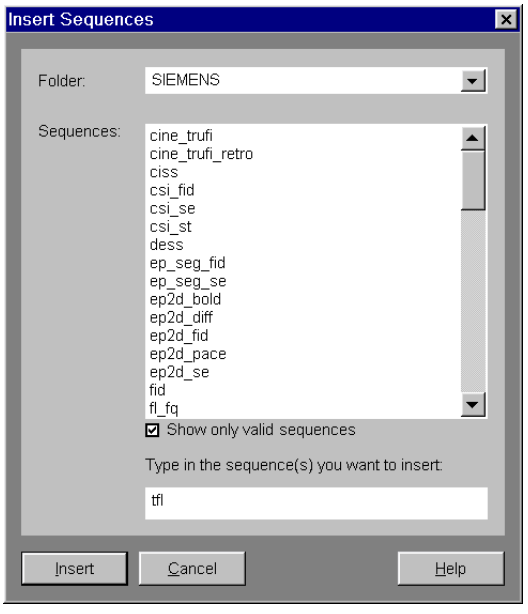
Sequences are sequences of commands for controlling scanning: they control the RF fields (RF pulses), magnetic field gradients, data acquisition, and image reconstruction. Protocols, on the other hand, contain the measurement parameter settings for a sequence.

➪ The applications guide contains a list of all the sequences available on your system.

You can access a sequence and create a new protocol for the current scan program.

✧ Select **Insert > Sequence**.

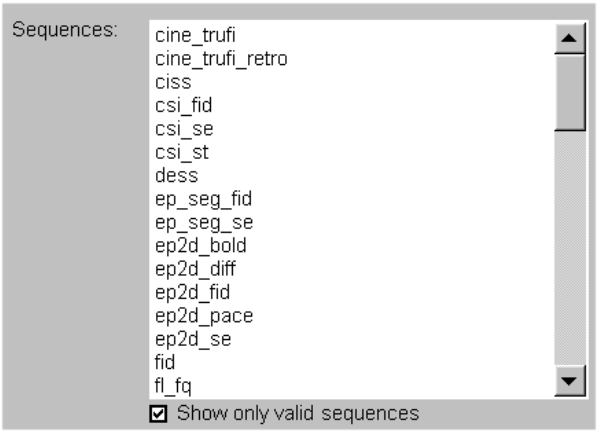
The **Insert Sequences** dialog box opens.





✧ Go to the **Folder** selection list. You may either insert a Siemens sequence or a sequence from the customer tree.

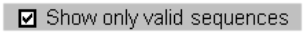
The **Sequences** display field now lists all sequences from the Siemens and customer trees in alphabetical order.



Checking sequences

If the folder contains fewer than 200 sequences, they will be checked automatically and only the sequences licensed and executable on your system will be displayed.

This time-consuming check is not performed automatically if the folder contains more than 200 sequences. In this case, the **show only valid sequences** option will not be dimmed and you may decide yourself whether to perform the check.



✧ Click the **show only valid sequences** check box to display only licensed and executable sequences.

Selecting sequence(s)

You can use the scroll bar (right-hand bar) to scroll to sequences further down in the alphabet.

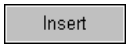
✧ Click on the sequence you are looking for in the list.

➪ Use the **Ctrl** or **Shift** key on your keyboard to make a multiple selection.

Or

✧ Enter the name of the required sequence in the **Type in the sequence(s) you want to insert** field.

➪ For multiple selection, enter the sequences one after the other, with a blank between sequences.



✧ Click the **Insert** button.

Or

✧ Double-click the required sequence (to select a single sequence).

A protocol is created from the selected sequence and transferred to your scan program.

➪ If you selected more than one sequence, a protocol is created for each sequence and added to the scan program.

Creating a new protocol from a series or image (Phoenix)

You may create a new protocol from previously acquired series and images and add them to the scan program.

Select a series or image in the program control, the stamp segments of the Maestro layout, or the **Patient Browser** and *drag & drop* the selection into the **Exam Explorer**.

NOTICE

It is only possible to create a new protocol from a series or image if the series or image was acquired on *your* system or on a system of the *same* type (same hardware configuration, software version ***syngo* MR A30** and higher). A Maestro Class System is also required to use this function.

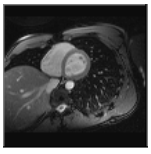
➪ If the system type or software version used to generate the series or image does not match your system, you can try conversion.
→ Page C.16–52, *Reconstructed protocol by conversion*

Creating a new protocol by drag & drop



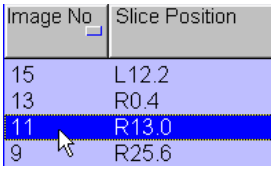
✧ Click the series icon of an acquired series in the program control.

Or



✧ Click a series in a stamp segment.

Or



✧ Display the **Patient Browser** and select an image or a series.
→ *syngo* Operator Manual

✧ Hold down the *left* mouse button and drag the image or series into the **Exam Explorer**.

A scan protocol is created from the image/series and added to the scan program.

➪ An error message is displayed when series or images that do not meet the requirements are rejected .

Reconstructed protocol by conversion

If the images or series were not acquired with the same software version or on the same system type, you can attempt to convert the images.

✧ Select a series or image from the stamp segments of the Maestro layout, from the large image segments, or from the **Patient Browser**.

✧ Press and hold the **Shift** key, press and hold the *left* mouse button and drag the series or image into the **Exam Explorer** (*drag & drop*).

➪ Do not press the **Shift** key too early because then *drag & drop* might not work.

A scan protocol is created from the image/series and added to the scan program, if conversion was possible.

The changes caused by conversion are identified as upgrade info.
→ Page C.12–16, *Displaying upgrade info*

If conversion fails, an error message appears.

Inserting a scan pause

You can insert a pause, for example, to administer contrast agent to a patient prior to a scan.

✧ Select the program step *in front* of where you want to insert the pause.

➪ If you do not select a program step before you insert the pause, the pause will be appended to the end of the list.

✧ Select **Insert > Pause** from the main menu of the **Exam Explorer**.

Or

✧ Select **Insert Pause** from the context menu.

➪ The **Insert Pause** menu item is only available in the context menu, if a scan program is open and *no* program step is selected.

Or



✧ Click this button on the tool bar.

Or

✧ Press the **Ctrl + W** shortcut on your keyboard.

The pause is inserted in the list and the **Pause Step Properties** dialog box opens. Enter a name and comment for the pause in this dialog box. If the pause is for administering contrast agent, you can also enter information regarding the contrast agent.
→ Page C.12–19, *Editing pause properties*

Editing protocol parameters

The **Protocol Editor** is used to view and change protocol parameters. This changes the default settings shown in the parameter card stack of the Exam card, if you access this protocol during a routine examination.

➪ If modify the content of any scan programs, a message box will be displayed as you exit the content area. You will be prompted to save the scan program with the changes or in its original state.

✧ Select a scan protocol.

✧ Select **Edit > Protocol** from the main menu of the **Exam Explorer**.

Or

✧ Select **Edit protocols** from the context menu.

Or



✧ Click this button on the tool bar.

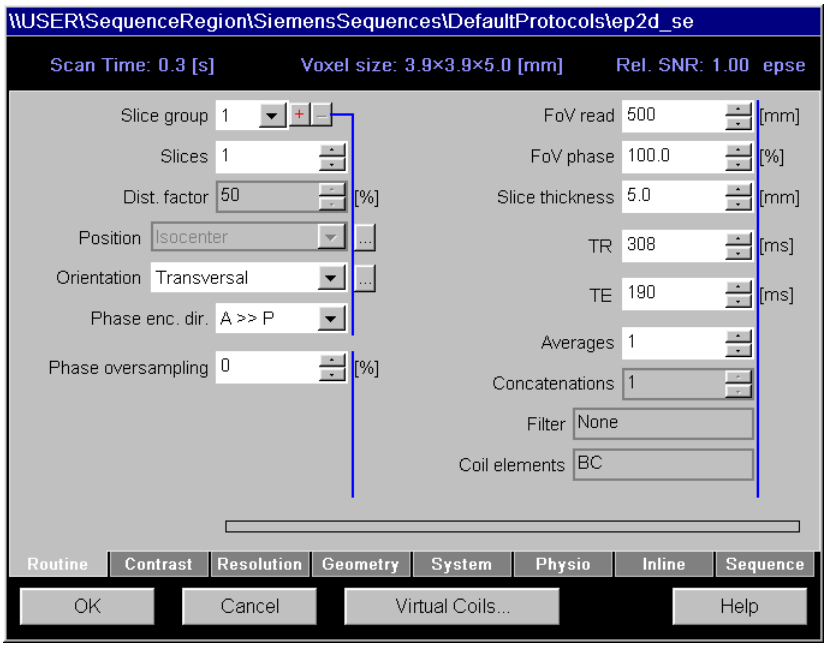
Or

✧ Press the **Enter** key on your keyboard.

Or

✧ Double-click the scan protocol.

The **Protocol Editor** is displayed with the protocol parameters.



Changing parameter settings

The **protocol editor** allows you to modify any of the protocol's parameter settings. The procedure is the same as in the parameter card stack of the **Exam** task card.

→ Page C.5–72, *Working in the parameter card stack*

Changing a coil configuration

Use the **System Common** task card to define the coil elements required for the scan protocol.
→ Page H.1–84, *Coils and coil elements* 🗀 *Routine, System-Common*

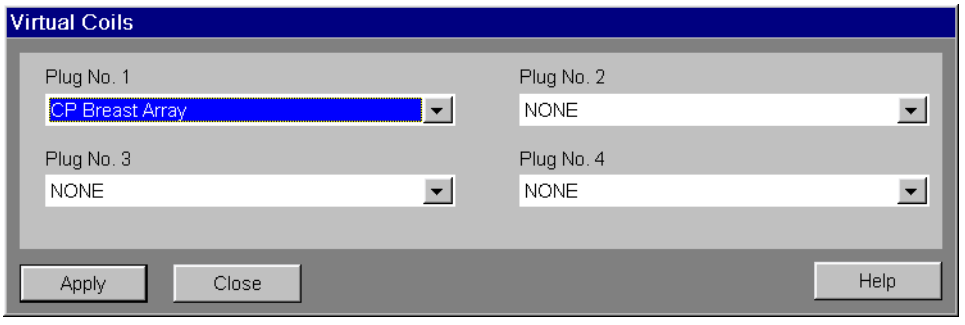
Selecting virtual coils

If you are editing a protocol in the **Protocol Editor** and want to select different coils than the ones stored in the protocol, open the **Virtual Coils** dialog box.



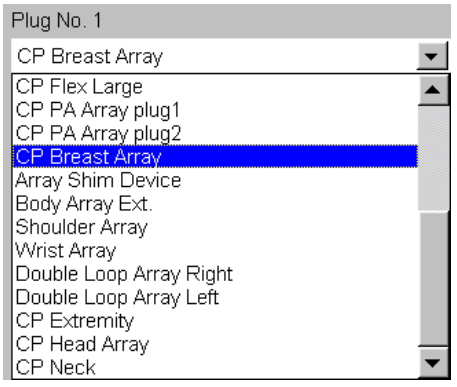
✧ Click the **Virtual Coils** button.

The **Virtual Coils** dialog box opens.



Use the special selection list to set one coil for each of the four coil plug-ins. The list shows only coils that can be connected to the plug.

Example: Selection list for coil plug 1



✧ Set the required coil configuration using the four selection lists.

✧ Click the **Apply** button to confirm.

If you have selected array coils as virtual coils, you still have to set the coil elements on the **System Common** parameter card.
→ Page H.1–84, *Array coils*

Applying or rejecting changes

You can apply the new coil configuration and all other parameter changes to the protocol.



✧ Click the **OK** button.

Your changes are applied and the **Protocol Editor** closes.

You can also close the **Protocol Editor** without applying your changes.



✧ Click the **Cancel** button.

Editing protocol and pause properties

In addition to the measurement parameters that you edit in the **Protocol Editor**, you can set a large number of properties for each protocol and each pause.

You can enter a name and comment for the protocol, define start options for scanning, activate automatic image loading processes, and set a copy reference.

Detailed descriptions of the protocol and pause properties can be found in
→ Chapter C 12, *Protocol and Pause Properties*

Saving scan programs

Once you have inserted all protocols and scan pauses into your scan program, organized them in the desired order, and edited your scan parameters, you can save the result.

Saving the scan program under a new name

Saving a changed scan program under a new name creates a new program.

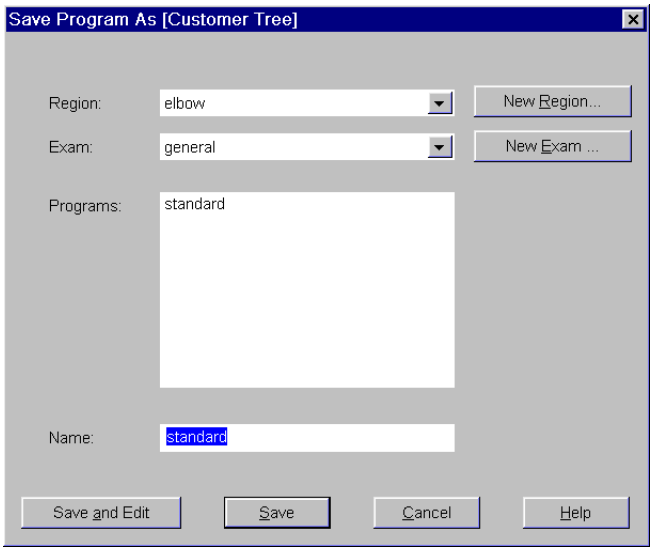
✧ Select the scan program.

✧ Select **Object > Save as** from the main menu of the **Exam Explorer**.

Or

✧ Select **Save as** from the context menu.

The **Save Program As [Customer Tree]** dialog box opens.



It displays the examination region and examination to which the modified scan program belongs. The **Program** list shows all scan programs stored under this examination in the customer tree. The **Name** text input field shows the previous name of the edited scan program.

➪ If you have just created an examination region in the **Exam Explorer**, the entry **<Select Item>** will appear under Exam. You are prompted to assign your new scan program to an examination.

✧ Use the selection list to select a region for your scan program.

You may also create a new region.

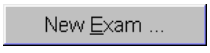


✧ Click the **New region** button.

The **Add New Region** dialog box opens. Here, you can create a new examination region.
→ Page C.16–31, *Creating a new examination region*

✧ Use the selection list to select an examination for your program.

You can create a new examination.



✧ Click the **New Exam** button.

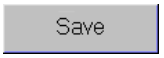
The **Add New Exam** dialog box opens. Create the new examination here.
→ Page C.16–37, *Creating a new examination*



✧ Enter a name for the new scan program.

Or

✧ Click one of the scan program names in the **Programs** list.



✧ Click the **Save** button.

NOTE

If you save your program under an existing name, a message window asks whether you want to overwrite the selected scan program. If you confirm that you do, the previous scan program will be *replaced*. You will no longer be able to access the old version of the program.

The program is saved and the dialog box closes.

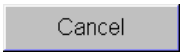


✧ Click the **Save/Edit** button.

NOTE

See notice above.

The program is saved and the dialog box remains open so that you can continue editing.



✧ Click the **Cancel** button.

The dialog box closes without saving the program.

Saving a scan program under the same name

You can also save the changed scan program under the old name.

✧ Select **Object > Save** from the main menu of the **Exam Explorer**.

Or



✧ Click this button on the tool bar.

Or

✧ Press the **Ctrl + S** shortcut on your keyboard.

The program is saved under its old name and path.

Transferring a scan program to the program control

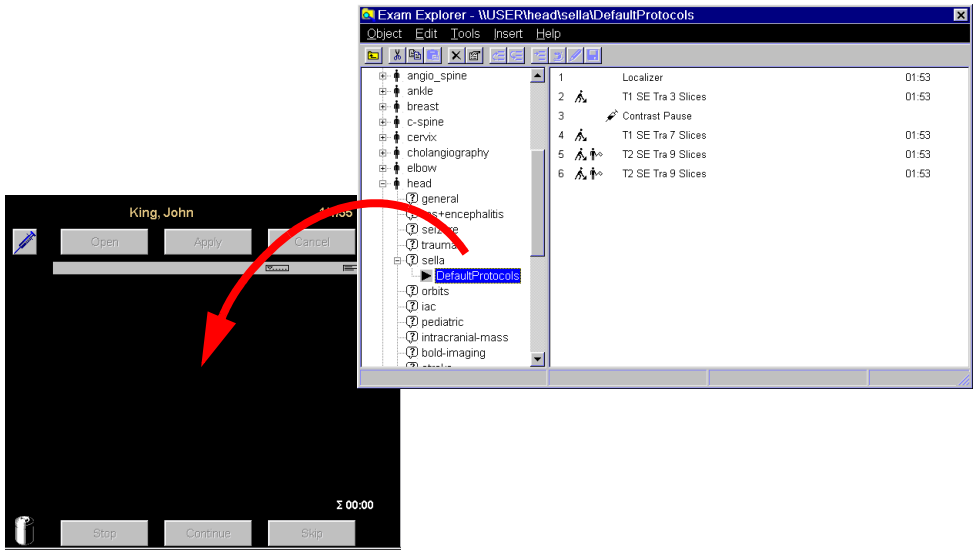
You can also use the **Exam Explorer** to find a scan program and transfer it to the queue.

Transferring a scan program

✧ Open the **Exam Explorer**.
→ Page C.16–3, *Calling up the Exam Explorer*

✧ Click a scan program or a single program step in the navigation or content area.

✧ Hold down the *left* mouse button and drag and drop the selected scan programs or program instructions to the queue.



Or

✧ Select **Tools > Append To Queue** from the main menu of the **Exam Explorer**.

Or

✧ Select **Append To Queue** from the context menu.

Updating filming study layouts

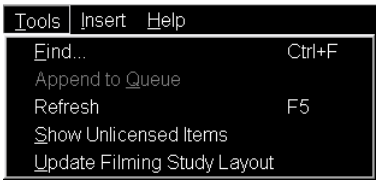
Basics

If you place images or series on the **Filming** task card, you need to select a suitable film layout for these images. You can automate this task by assigning an existing film layout to all series that have a certain study or series description. When you place the images or series on the **Filming** task card, the assigned film layout is then automatically selected.

The film layout assignments are made in the **Filming Study Layouts** configuration dialog box.
→ *syngo* Operator Manual

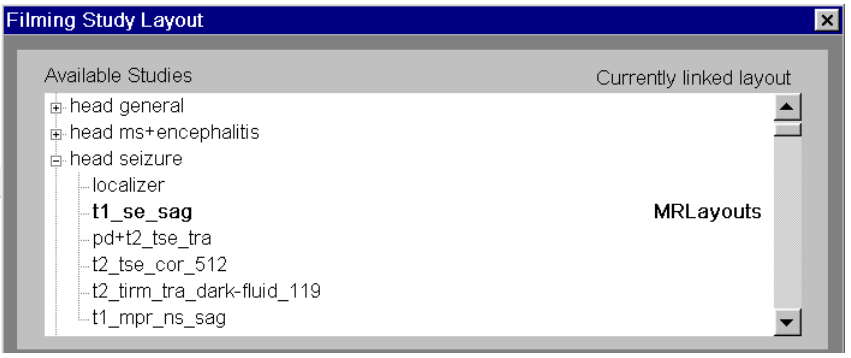
In the **Exam Explorer**, you can automatically update the data contained in the configuration dialog box.

Updating filming study layouts



✧ Select **Tools** > **Filming Study Layouts** from the main menu of the **Exam Explorer**.

The data contained in the customer scan program tree of the Exam Explorer are transferred to the list of available studies and series descriptions of the **Filming Study Layouts** dialog box.



When selecting the update function in the **Exam Explorer** again, the existing list in the **Filming Study Layouts** dialog box is replaced by the data contained in the Examination Explorer.

Existing assignments of filming study layouts to studies and series descriptions are retained, provided that the film layout exists and no other film layout is assigned to these studies and series descriptions.

This means you can make changes in the Exam Explorer at any time and call up the **Update Filming Study Layout** menu item without losing your previous assignments.

⇨ Updating is only possible if the **Filming** task card is configured.

Importing/exporting examination database objects

The Siemens and customer tree is saved in the examination database on the PC of your MR system.

You may also access examination regions, examinations, scan programs, and protocols stored on external data media (CD ROM) or on your hospital-wide data network.

You can also export objects from your database to external data media or network addresses, for example, to make your examinations and scan programs available to other ***syngo*** **MR** users.

Importing objects

You can import examination regions, examinations, and scan programs into your examination database from a network address or from external data media.

✧ In the navigation area, select hierarchy level into which you want to import data.

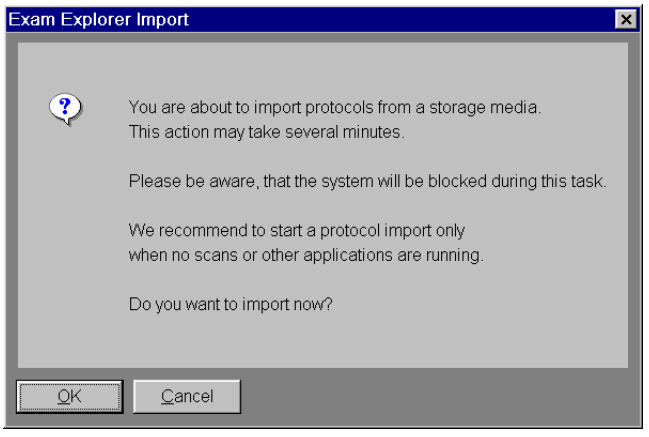
Example: Select an examination to import a scan program into the directory.

✧ Select **Object > Import** from the main menu of the **Exam Explorer**.

Or

✧ Select **Import** from the context menu.

A message window opens.



During an import, your system will check whether the programs are executable, i.e. whether all protocols are licensed and whether the protocol parameters are consistent. For this reason, importing may take some time. Furthermore, it is not possible to perform other actions while an import is in progress. Confirm whether you wish to continue or cancel the import.

OK

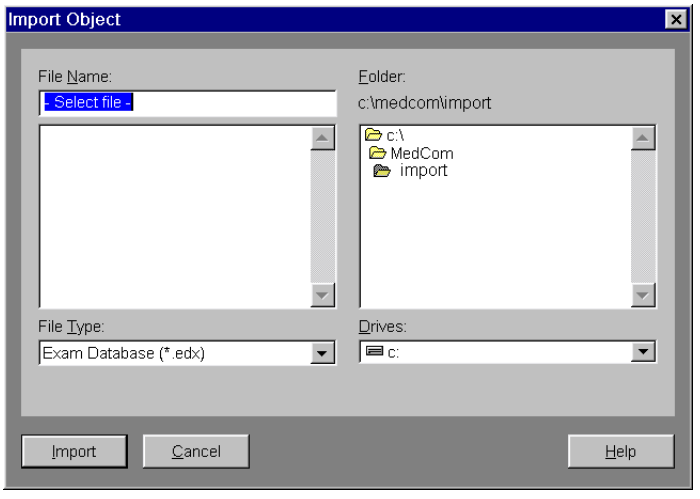
✧ Click the **OK** button if you want to import now.

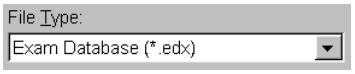
Or

Cancel

✧ Click the **Cancel** button if you want to import later.

If you confirm with **OK**, the **Import Object** dialog box opens.



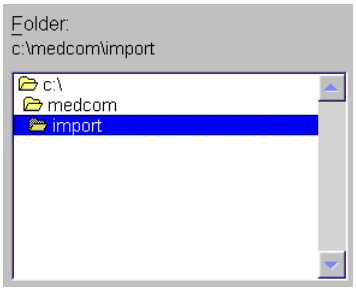


Exam Database (*.edx) is the default setting under **File Type**. No other selection is possible.

➪ The "edx" format is a special file format for the examination database. It is the only format that can be read by the system.



✧ Under **Drives**, select the drive or network address from which you want to import data.



✧ Under **Folder**, select the directory from which you want to import data.

All edx files in the selected folder are now displayed in the content window.

✧ Select the file you want to import.



The name of the selected file is displayed in the **File name** input field.

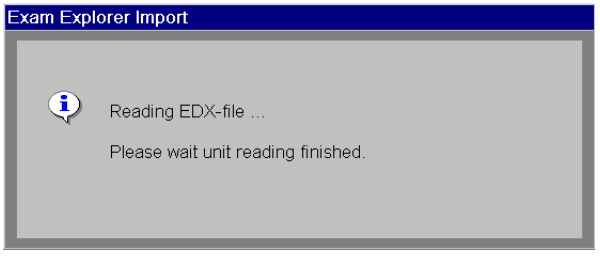


✧ Click the **Import** button.

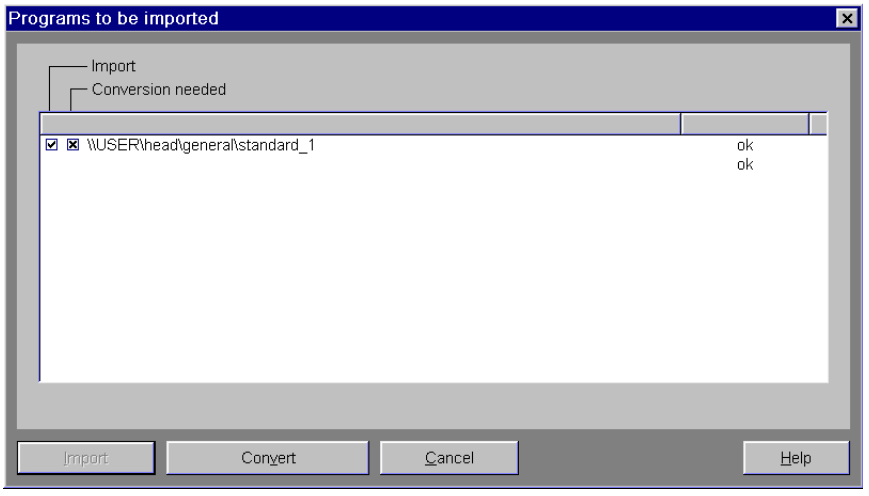
The system will now check whether importing is possible at the selected position in the navigation region of the **Exam Explorer**.

A specific error message will be displayed if it is not possible to import a file at the position you have selected.

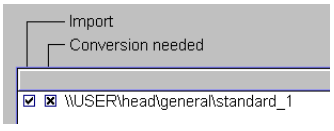
If possible, the edx file is imported and the following message box appears.



The **Program to be imported** dialog box opens after importing has finished.



It shows the scan programs contained in the imported edx file.



The **Conversion needed** check box is active for non-executable scan programs. These programs have to be converted before they can be imported.

To shorten the time required for conversion, exclude the non-executable programs that you do *not* want to import This shortens the time required for the conversion.

✧ Deselect the **Conversion needed** check box in front of these programs.

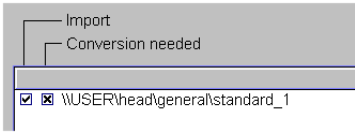


✧ Click the **Convert** button to start conversion.

The selected non-executable programs will now be converted one after the other.

You can see how conversion has progressed from the **Conversion needed** check box. As soon as conversion has been completed, the checkmark disappears.

➪ The **Convert** button also changes to a **Stop conversion** button. This allows you to cancel the conversion after the current scan program in case of, e.g. a patient requiring immediate attention.



Go to **Import** and select the programs to be imported via the check boxes.

✧ Activate the check boxes for the programs you want to import.

✧ Deactivate the check boxes for the programs you do *not* want to import.



✧ Click the **Import** button to import the selected programs.

➪ The **Import** button does not become active until at least one program is ready to be imported, for example, after successful conversion.

The imported scan programs are appended to the end of the directory selected in the **Exam Explorer**.

Exporting objects

You can export examination regions, examinations, and scan programs from your examination database to a network address or to an external data medium.

✧ Select the entry you want to export in the navigation area of the **Exam Explorer**.

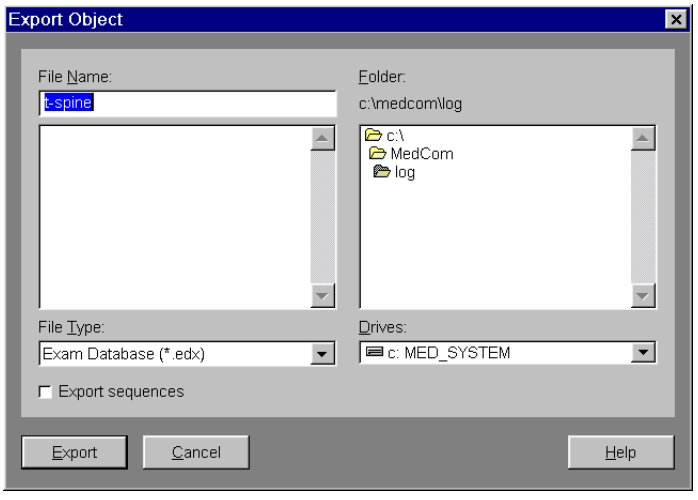
➪ If you select an object in the content area, it is not this object but the object that is opened in the navigation area that will be exported.

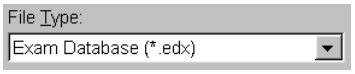
✧ Select **Object > Export** from the main menu of the **Exam Explorer**.

Or

✧ Select **Export** from the context menu.

The **Import Object** dialog box opens.



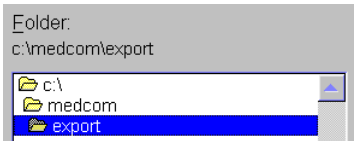


Store objects exported from the examination database as "edx" files in the target directory. This is the only format that the system can read. This is why **Exam Database (*.edx)** is the default setting under **File type**.

⇨ It is not possible to select a file type other than **Exam Database (*.edx)**.



✧ Select the target drive or the network address under **Drives**.



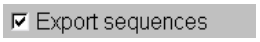
✧ Under **Folder**, select the directory from which you want to export data.

The content window now shows all "edx" files present in the target directory.



✧ Enter a name for the object to be exported in the **Filename** field or accept the name suggested by the system.

⇨ The name suggested by the system is the object name from the **Exam Explorer**.



✧ Click the **Export Sequences** option if you also want to export the associated sequence data.

➪ The **Export Sequences** option is deactivated by default.



✧ Click the **Export** button to export the selected object.

NOTE

The exported objects are retained on your system. The export function only **copies** the objects to the target drive or network address.

Printing protocols

From the **Exam Explorer**, you can print or write to a PDF file (Adobe® Portable Document Format) protocols as an overview of all parameter settings and lists of protocol contents.

The parameter overview enables you to directly compare the parameter settings of the protocols. The lists of contents help you find you way round the numerous available exams and scan programs and make it easier for you to organize and maintain the Exam Explorer.

The print option is based on your object selection. Individual protocols you select are printed. If you have selected an object containing more than one protocol (e.g. a scan program), all protocols are printed.

If a selected object contains more than one scan program, you have the possibility to print only the user-defined programs.
→ Page C.13–1, *Printing Protocols*

Closing the Exam Explorer

Once you have completed all your program management tasks, you can close the **Exam Explorer** again.

✧ Select **Object > Exit** from the main menu of the **Exam Explorer**.

Or



✧ Click the **Close window** button in the upper right of the title bar of the **Exam Explorer**.

CHAPTER C.17

Maestro Layout and Movie Display (Option)

The Maestro layout with the stamp segments is available on the **Exam** task card in addition to the two-segment and three-segment layouts.

The stamp segments help you to orient yourself during examinations and manage the acquired series.

It is *not* possible to perform graphic slice positioning or zooming and panning in the stamp segments. However, it is possible to window the images.

You can load the series from the stamp segments into the large image segments and view them in movie display.

This provides a life-like impression of the morphology and physiology of the examination region and might provide initial diagnostic results even before the examination is completed.

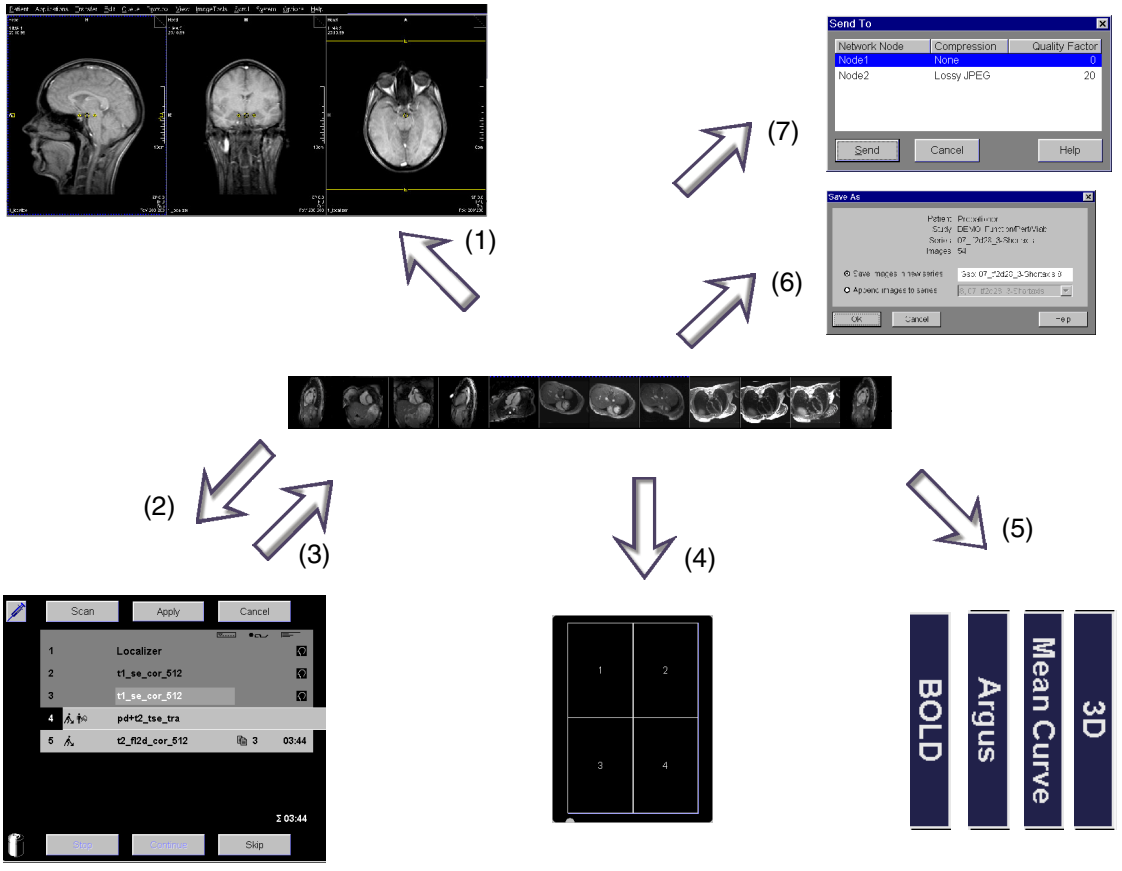
There are numerous ways of configuring and controlling movie display.

NOTICE

Maestro layout and movie display are available only if you have installed a **Maestro Class System** or the **Advanced Workflow Package**.

Maestro layout

This overview shows how to work with stamp segments.



(1) Determine which series are suitable for slice positioning for the following protocols and load them into the large image segments using *Drag & Drop*.
(2) Drag and drop a series into the program control to repeat a scan.
(3) Sort series into the stamp segments.
(4) Transfer the series for filming.
(5) Transfer the series from the stamp segments directly to other task cards for postprocessing.
(6) Save the series together in a new series or append them to an existing series.
(7) Export the series.

Selecting the Maestro layout and loading series

✧ Select **View > Maestro UI** from the main menu.

The **Exam** task card is displayed with the Maestro layout. The stamp segments are still empty.

You can load series manually or automatically.

Loading manually

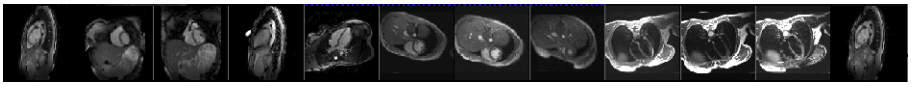
✧ Select the series in the program control or in the **Patient Browser**.

✧ *Drag & drop* your selection into the stamp segments.

Loading automatically

You can set the protocol properties to automatically load the images of a protocol into the stamp segments after scanning. This is the default setting for some protocols.
→ Page C.12–14, *Setting a copy reference*

Once this type of protocol is completed, the series are displayed in the stamp segments immediately following reconstruction.



Each stamp segment represents a series.

You can change the layout of the series in the stamp segments as desired.



➪ If you position and hold the mouse pointer over a stamp segment containing a series, a tool tip displays information about the loaded series.

Transferring series from stamp segments into image segments

You can load series from stamp segments into the large image segments to position slices or start movie display.

✧ Mark the large image segment.

✧ Double-click a stamp segment.

The series in this stamp segment is loaded into the previously selected image segment.

Or

✧ Drag and drop a series from a stamp subsegment into a large segment.

Repeating the measurement of a series

You can repeat scanning of a protocol if you are not satisfied with the image quality.

✧ Drag and drop the series from the stamp segments into the job list.

Or

✧ Select **Append To Queue** from the context menu.

A copy of the protocol with the current slice positions is generated and converted into executable program instructions.

➪ If you select **Append To Queue**, the protocol is appended to the end of the job list. If you use the *drag & drop* method , the protocol will be inserted in the job list where you dropped it.

Saving, filming, exporting, and transferring series for postprocessing

You can save the series to a new series directly from the stamp segments, append them to an existing series, film, export, or load them into other post processing cards.

The procedure is similar to the one described for images and series in the large image segments.
→ Page C.3–45, *Saving, exporting, and transferring images*

Navigating in stamp segments

You may load any number of series into the stamp segments. A maximum of 12 series are displayed.



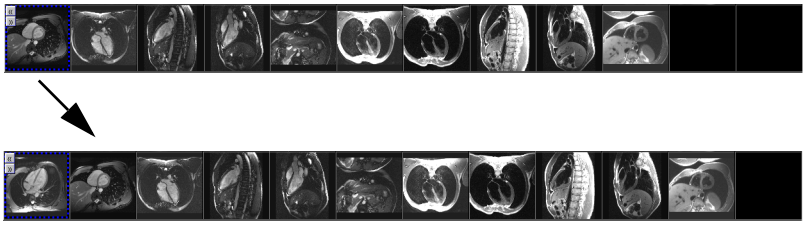
Small arrow buttons are displayed in the far left segment if more than 12 series are loaded.

Navigating between series

You can move the input focus by one segment to the left or right.

✧ Press the left or right arrow key on your keyboard.

➪ If the input focus was on the far left or far right segment, a hidden series will be moved into the visible area.



Shifting series by one segment

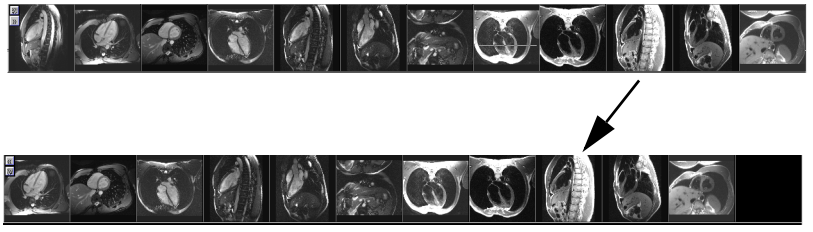
You can move all series by *one* position to the left or right.



✧ Click one of the two arrow buttons in the far left segment.

Or

✧ Press the **Ctrl** + **left arrow** or **Ctrl** + **right arrow** key combination.



Showing the first series in the left stamp segment

You can shift the series in the stamp segments so that the first series is displayed in the far left segment.

✧ Press the **Home** key on your keyboard.

Showing the last series in the right stamp segment

You can shift the series in the stamp segments so that the last series is displayed in the far right segment.

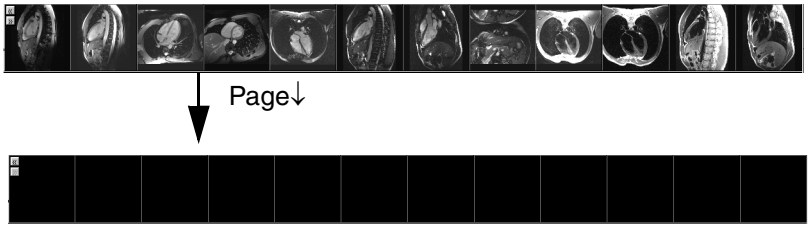
✧ Press the **End** key on your keyboard.

Shifting series by 12 segments



You can shift all series in blocks of 12 segments. This hides all series previously visible.

✧ Press the **Page**↑ or **Page**↓ key on your keyboard.



Scrolling through images in a stamp segment



You can scroll images in a stamp segment just like in a large image segment.

✧ Press the respective key on the symbol keypad of your keyboard.

If you hold the key down, the images will be displayed one after the other like a movie (pseudo movie).

Changing the arrangement of series

Suppose you are viewing the series in the stamp segments and determine that some of the series have to be rescanned. You can remove the faulty series and sort the rescanned series back into the stamp segments.

Removing series

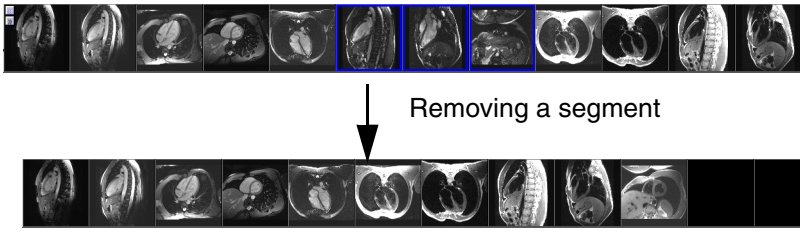
The series are removed from the stamp segments only. They are still available in the **Patient Browser**.

✧ Select the required stamp segments.
→ Page C.3–21, *Selecting images explicitly and implicitly*

➪ Selecting a stamp segment automatically selects the whole series.

✧ Select **Remove Segment** from the context menu.

The selected series will be removed. The adjacent series on the right will be shifted to the left to fill the gap.



You can also remove the series while retaining the empty segments.

✧ Select **Edit > Clear Document(s)** from the main menu.

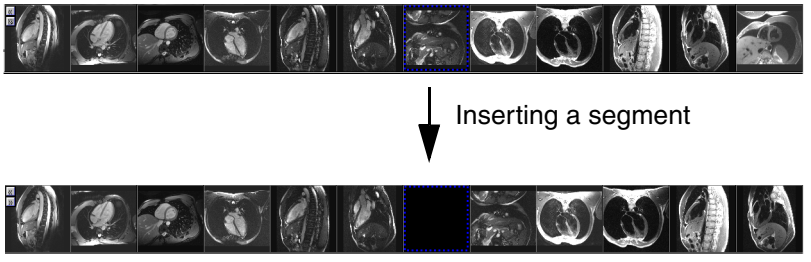
Inserting an empty stamp segment

You can insert an empty stamp segment for positioning series that are loaded using *Drag & Drop*.

✧ Select a segment. The empty segment will be inserted *before* this segment.

✧ Select **Insert Segment** from the context menu.

An empty segment is inserted. The series on the right will be shifted by one position to the right.



If you want to load multiple series requiring several empty segments, you may repeat this step as often as necessary.

Loading series using *Drag & Drop*

You may load series from the program control, the **Patient Browser**, or the large image segments.

✧ Select the series to be loaded.

✧ Drag and drop your selection into an empty stamp segment.

NOTICE

If the target segment is not empty, the existing series will be replaced by the first series loaded using *Drag & Drop*.

Movie display

During a scan or scan pause, you can start the movie display and check the quality of the images being acquired, and gather preliminary diagnostic information.

A large image segment is used for movie display. The images included in a movie are always from *a single* series.

You can optimize the movie display according to your own requirements by:

- ❏ Setting the speed
- ❏ Selecting **Loop** or **Yo-yo** mode
- ❏ Changing the order of the images
- ❏ Jumping to the next group during movie display
- ❏ Setting realtime mode
- ❏ Changing the image display while movie display is paused

➪ Unsatisfactory images (e.g. from breath-hold scans) can be rescanned by dragging and dropping them into the program control during the movie display.

➪ If the series only consists of *one* image, it is *not* possible to start movie mode.

NOTICE

The movie quality may be affected by processes running in background.

Groups within a series

Series are grouped for movie display to provide a better overview. Movies display the images of one group. However, it is possible to jump from group to group.

One series - one group

A series is treated as *one* group if all images in the series differ according to the same sorting criterion.

Example: Single-slice multi-phase series (cardiac imaging)
Sort scheme SP >> TT >> TA
All images of the series have the same slice position. The trigger time, however, is different.

One series - multiple groups

A series is broken down into *multiple* groups if the current display order results in consecutive images with the same primary sort criterion but a different secondary sort criterion.

Example: Multi-slice multi-phase series (cardiac imaging)
Sort scheme SP >> TT >> TA
This series is broken down into *n* groups because they contain images with *n* different slice positions and different trigger times.

The first group contains all images with slice position 1 and different trigger times. The second group contains all images with slice position 2, etc.

Starting the movie display

You can start the movie display manually or automatically.

✧ Place the input focus on the segment you want to use for movie display

✧ Select **Scroll > Movie > Movie ON** from the main menu.

Or

✧ Select **Movie ON** from the context menu.

Or

✧ Make sure the keyboard focus is on the image area and press the spacebar.
→ Page C.3–18, *Keyboard focus*

Movie display starts.

Starting movie display automatically

The protocol properties can be set to start the movie display automatically after scanning. This is the default setting for some protocols.
→ Page C.12–14, *Setting a copy reference*

Once such a protocol has been scanned, the images are displayed in movie display immediately following reconstruction.

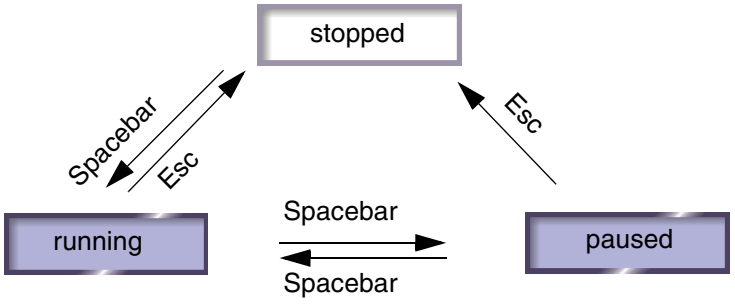
If the protocol generates more that one series, only the first series is shown in movie display. You can display the other series by selecting **Scroll > Series Next**.

Controlling movie display

You can start, pause, and stop the movie display via the keyboard, mouse, main menu or context menu. The **Movie Control** dialog box provides additional features.

Movie display has three statuses:

- **running**
  Movie display is active and running. You can advance to the next group or series.
- **paused**
  Movie display is active but stopped.
  You can look at the image text or scroll from image to image.
- **stopped**
  Movie display is not active. Series divided into groups are ungrouped.



Keyboard or mouse control

You can use the spacebar or mouse to toggle between **running** and **paused** status.

Make sure the keyboard focus is on the image area if you are controlling movie display via the keyboard.

✧ Press the spacebar while movie display is running.

Or

✧ Left-click the movie segment.

Movie display pauses.

✧ Press the spacebar while movie display is paused.

Or

✧ Left-click the movie segment while movie display is paused.

Movie display resumes.

You can switch from **running** or **paused** to **stopped** status using the **Esc** key.

✧ Press the **Esc** key while movie display is running or paused.

Movie display stops.

Menu control

You can control movie display using the menu.

✧ Select **Scroll > Movie > Movie ON** from the main menu or **Movie ON** from the context menu while movie display is running or paused.

Movie display stops. The check mark next to the menu item disappears.

✧ Select **Scroll > Movie > Movie Paused ON** from the main menu while movie display is running.

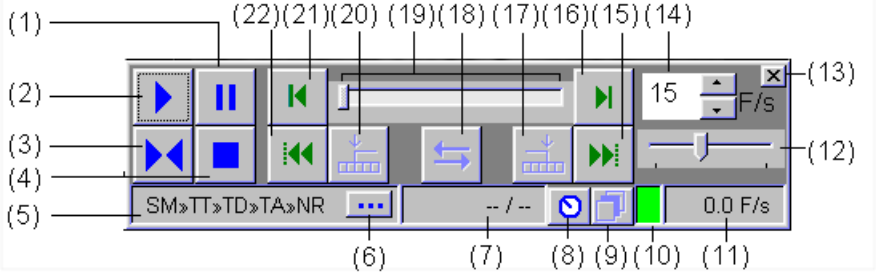
Movie display pauses. A checkmark appears next to the menu item.

Controlling movie display using the dialog box

You can use the **Movie Control** dialog box to define the speed and order of movie display. You can define the range displayed, jump to the next group, and switch to realtime mode.

✧ Select **Scroll > Movie > Movie Control**.

The **Movie Control** dialog box opens.



(1) Pause movie display
(2) **Loop** mode
(3) **Yo-yo** mode
(4) Stop movie display
(5) Current sort order
(6) Open the **Movie Properties** dialog box
(7) Index of the current image/total number of images
(8) Realtime mode
(9) Skip images (realtime mode)
(10) LED display

(11) Display of the current speed in frames per second
(12) Change speed using the slider
(13) Close the **Movie Control** dialog box
(14) Enter speed numerically
(15) **running**/**paused** status: scroll forward by one group
stopped status: scroll forward by one series
(16) Scroll forward by one image, status automatically set to **paused**
(17) Set "to" marker to limit range
(18) Reverse display order (in **paused** status only)
(19) Position of the current image in the series
(20) Set "from" marker to limit range (in **paused** status only)
(21) Scroll back by one image, status automatically set to **paused**
(22) **running**/**paused** status: scroll backward by one group
stopped status: scroll back by one series

➪ The **Movie Properties** dialog box allows you to specify that the **Movie Control** dialog box is to be opened automatically every time movie display is started.
→ Page C.17–32, *Configuring movie display*

Loop mode and yo-yo mode

In **Loop** mode, the images of a series are displayed in a loop. After the last image of the series, the first image is displayed again, etc.

In **Yo-yo** mode, the direction of movie display is reversed after the last image (starting with the second last image, etc.).



✧ Click this button to activate **Loop** mode.



✧ Click this button to activate **Yo-yo** mode.

➪ If you press the **Loop** key a second time and/or **yo-yo**, the movie display is paused while you do so.

➪ If you start or pause movie display from **stopped** status, **Loop** mode is activated in **running** or **paused** status.

Display sequence of images

The sort scheme determines the order of images within a series. The sort scheme is defined in the **Display Order (for Movie)** dialog box.
→ Page C.3–12, *Defining the scroll order*



The current sort scheme is displayed in the bottom left corner of the **Movie Control** dialog box.

You can reverse the image sequence in movie display.



✧ Click this button.

Speed of movie display

You can set the number of images (frames) displayed per second in movie display either numerically or using a slider.



✧ Enter an integer between 1 and 99 and press Enter.

Or



✧ Change the speed using the arrow keys.

Or



✧ Move the slider.

The leftmost position of the slider corresponds to a speed of 1 frame per second. The rightmost position of the slider corresponds to a speed of 30 frames per second by default.

➪ If you enter a higher speed in the input field, the value range of the slider is adjusted accordingly.

➪ When you move the slider, the value in the input field is updated dynamically.

➪ The position of the slider remains unchanged during movie mode, i.e. the slider always indicates the speed set by the user, not the actual speed.



The actual speed is displayed in the bottom right corner of the **Movie Control** dialog box.

Setting realtime mode

Realtime mode can be used to display series of images with different time parameters.

In realtime mode, images are played back in movie display according to the time interval at which they were acquired.

In real-time mode, the movie display speed is determined by this time parameter.



✧ Click this button.

Real-time mode is activated.

If the time interval between images is very short, you may find that the realtime speed is greater than the maximum speed technically possible.

In this case, you can skip images in movie display.



✧ Click this button.

Deactivate this option if you want to view all available images in movie display and are willing to accept a delay in real-time display.

➪ If you manually alter the speed while realtime mode is active, realtime mode will automatically stop.

LED display



The color of the LED indicates the status of the movie display.

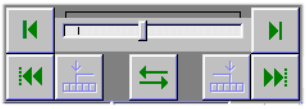
Color	Status
gray	**Stopped** or **paused**
green	**running**, all images are displayed
yellow	**running**, the **Skip images** option is enabled and at least two images are skipped.
rot	**running**, the **Skip images** option is disabled, the actual speed is lower than the set speed.

Editing images during movie display

In movie display, you can window images, zoom in or out, and move image contents.
→ Page C.3–25, *Enlarging, reducing, and panning reference images*

Movie display is paused during image editing while pressing and holding the left mouse button. Movie display resumes when the mouse button is released.

Navigating in movie display



The range display in the center of the **Movie Control** dialog box shows the range of the current group.

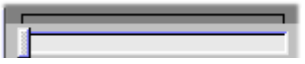
In the **paused** status, the position of the slider indicates the position of the current image within the group.

The position of the current image is also indicated on the status bar of the **Movie Control** dialog box.



The black bracket above the slider indicates the range of the group currently shown in movie display.

You can scroll to the first or last image of the group using the slider.



✧ Drag the slider all the way to the left.

Movie display will pause and the first image of the group will be displayed.

✧ Drag the slider all the way to the right.

Movie display will pause and the last image of the group will be displayed.

➪ You can drag the slider beyond the boundary of the group. If you switch to **running** status afterwards, the movie range will be set to the beginning and end of the group associated with the current image index.

Scrolling from image to image

In the movie segment, you can scroll all images in a series across group boundaries. To do this, use the buttons in the **Movie Control** dialog box, the keys on the symbol keypad, or the dog ears.

→ Page C.3–18, *Scrolling between images*

➪ In **running** or **paused** status, you can use the buttons, menu commands, or symbol keys to scroll.

➪ In **stopped** status, you can only use the menu commands or the keys on the symbol keypad.

The move display has the **running** or **paused** status.



✧ Click this button.

Movie display pauses. You will scroll forward by one image.



✧ Click this button.

Movie display pauses. You will scroll back by one image.

Scrolling from group to group

In **running** or **paused** status, you can use buttons, menu commands or the symbol keys to scroll between groups.

You may also move from the last group of series A to the first group of series B.

➪ If the series in the movie segment contain only one group, you will scroll between series.



✧ Click this button.

Or

✧ Select **Scroll > Series Next**.

Or



✧ Press this symbol key.

You will scroll forward by one group.



✧ Click this button.

Or

✧ Select **Scroll > Series Previous**.

Or



✧ Press this symbol key.

You will scroll back by one group.

Unlike normal scrolling with **Series Next/Previous**, the image of the previous group corresponding to the index is displayed instead of the representative image from the next group.

- If the following series cannot be grouped according to the same criterion as the current series during scrolling, the series will be skipped. This occurs, for instance, if the following series is the localizer series.
- If the series contain multiple groups, but movie display is in **stopped** status, you always scroll between series since the grouping is suspended.

Changing the range of movie display



After you have started the movie display, the "from" marker will be at the beginning and the "to" marker at the end of the group to be displayed.

If a series contains only one group, the "from" marker will be at the leftmost position and the "to" marker at the rightmost position in the range display.

In **running** or **paused** status, you can assign the "from" or "to" marker to the current position of the slider.

✧ Move the slider so that the first image of the new movie sequence is displayed in the movie segment.



✧ Click this button.

The "from" marker will be assigned to this position.

✧ Move the slider so that the last image of the new movie sequence is displayed in the movie segment.



✧ Click this button.

The "to" marker will be assigned to this position.

If you adjust the marker in **running** status, movie display will immediately start within the new range.

➪ If you place a marker at the same position twice, the "from" marker is automatically placed at the beginning and the "to" marker at the end of the group.

Configuring movie display

You can configure movie display according to your individual requirements. Four predefined parameter sets are available for that purpose. You can modify these parameter sets or define your own parameter settings.

Opening the Movie Properties dialog box

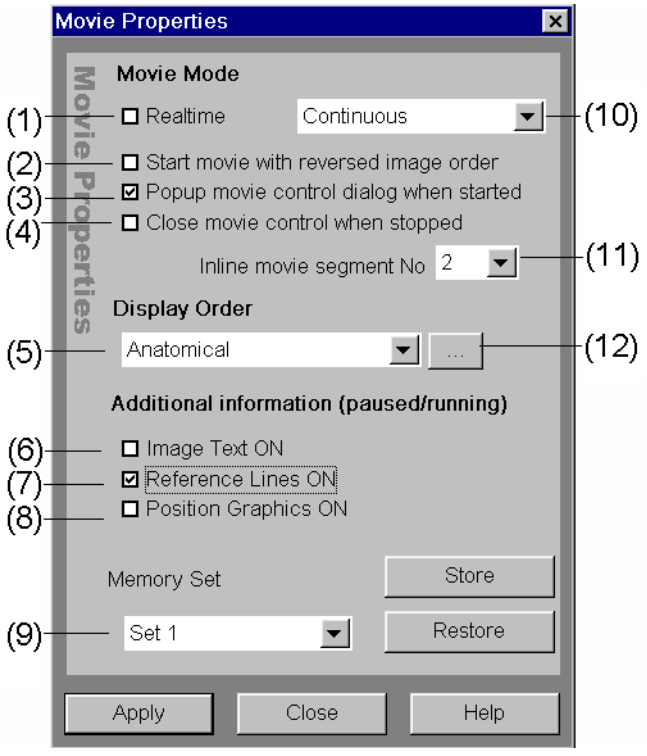
Movie display is configured in the **Movie Properties** dialog box.

✧ Select **Scroll > Movie > Properties**.

Or



✧ Click this button in the **Movie Control** dialog box.



The **Movie Properties** dialog box opens. The current movie display settings and the parameter set last used are displayed.

(1) Setting realtime mode → Page C.17–25
(2) Reverse display order
(3) Open **Movie Control** dialog box automatically on startup
(4) Close **Movie Control** dialog box automatically on stopping
(5) Select sort scheme
(6) Activate or deactivate image text during movie display → Page C.17–35
(7) Activate or deactivate reference lines during movie display, → Page C.17–35
(8) Activate or deactivate GSP objects during movie display, → Page C.17–35
(9) Select predefined parameter sets → Page C.17–36
(10) Select a timeframe for realtime mode
(11) Select a segment for movie display on automatic movie start
(12) Open **Image Order** dialog box, define your own sort scheme → Page C.3–13

➪ All dialog elements have tool tips. Position and hold the mouse pointer over a dialog element to display the corresponding tool tip.

Setting realtime mode



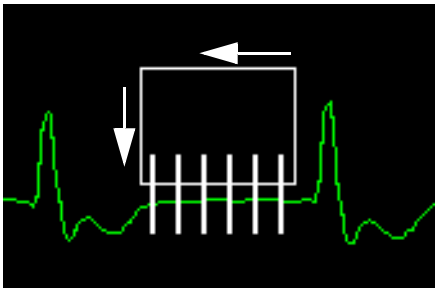
✧ Enable the **Realtime** option.

If the current group is sorted according to trigger time (TT) and you want movie display to run in **Loop** mode, you can also select a time frame for the realtime display.



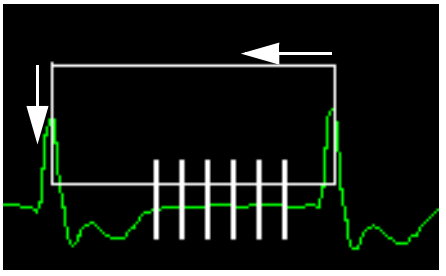
✧ In the list next to **Realtime**, select **Continuous**.

The image sequence will be repeated without delay.



✧ In the list next to **Realtime**, select **R-R Interval**.

A delay will be added between image sequences so that the duration of an image sequence corresponds to the mean R-R interval.

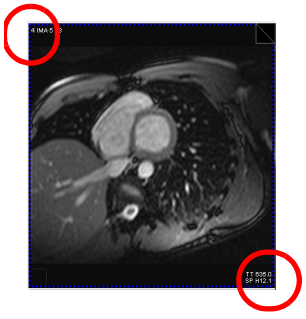


Displaying additional information

In movie display, you can show or hide image text, reference lines, and GSP objects.

➪ For optimal movie quality, we recommend hiding this additional information.

☑ Image Text ON



When image text is activated, the following information is displayed in the movie segment:

- ❏ Image number, top left
- ❏ Slice position SP, bottom right
- ❏ Trigger time TT, bottom right

☑ Reference Lines ON

If the references lines are activated in the menu (**View > Reference Lines ON**) and in the **Movie Properties** dialog box, the position of the current image in the movie segment will be indicated by a reference line in the non-movie segments and continuously updated in **running** or **paused** status.



If this option is activated, all GSP objects and all orientation aids selected via the menu (reference lines, adjustment volume, coil elements, etc.) will be displayed in the movie segment in **running** or **paused** status.
→ Page C.4–31, *Displaying orientation aids*

➪ You can perform graphic slice positioning in the movie display. Movie display is paused while you do so.

Displaying predefined parameter sets

The predefined parameter sets can be selected from the list under **Store Set**.

These parameter sets can be modified, but not renamed.



✧ Select a parameter set.

The **Movie Properties** dialog box shows all the settings of this parameter set.

Applying a parameter set

You check the parameter settings and apply them if they are suitable for the current movie display.



✧ Click **Apply**.

The settings are now applied to the movie display. The **Movie Properties** dialog box remains open.

Changing a predefined parameter set



You can change the parameters sets and store them permanently so that they are available after you reboot the system.

✧ Select a parameter set from the list.

✧ Change the settings in the **Movie Properties** dialog box.



✧ Click **Store**.

The current settings in the **Movie Properties** dialog box are assigned to the selected parameter set. The current movie display is *not* updated.

Applying temporary settings

You can define the parameters and apply them to the current movie display without assigning these settings to a parameter set or saving them.

✧ Define the parameters in the **Movie Properties** dialog box.



✧ Click **Apply**.

The current movie display is updated. The parameter set displayed in the **Memory Set** list is *not* changed.

Canceling the configuration

You can cancel the configuration and close the dialog box without applying the changes.



✧ Click **Close**.

Or

Press the **Esc** key.

Or



✧ Click the **Close window** icon.

CHAPTER C.18

Automatic Position Correction

Together with a standard brain atlas **AutoAlign** enables precise orientation of measurement objects during head examinations independently of the positioning of the head.

The use of **AutoAlign**, requires a license.

For automatic position correction, an AutoAlign head program is available in the Siemens area of the **Exam Explorer**. You can also adapt AutoAlign head programs and save them in your user area.

After a localizing scan has been performed with a standard localizer, a second localizer, or special 3D Scout, is acquired. The volume data obtained from this scan are matched against the atlas with **AutoAlign**. This results in a matrix that describes the offset, translation, and rotation of the measured brain relative to the atlas.

This AutoAlign Matrix (AAM) computed via **AutoAlign** is automatically added to the slices, sats, etc. of the subsequent protocols.

Using statistical images **AutoAlign** allows you to plan slices for certain diagnostic problems. This allows you to create a user-defined scan program for any patient.

Basics

AutoAlign is based on an automatic segmentation algorithm for gray scale values and CSF (cerebral spine fluid) in acquired 3D volume data sets and the use of an atlas.

AutoAlign Scout (AAS)

The AutoAlign scout (AAS) is based on a special 3D flash sequence. The AAS generates the necessary data sets for the AutoAlign calculation.

The AAS records two image data sets with different flip angles:

- ❏ 1. measurement: 2 degrees
- ❏ 2. measurement: 6 degrees

Atlas

The delivery volume of a system with **AutoAlign** includes the appropriate AutoAlign atlas. The atlas is based on a large number of head scans.

AutoAlign matrix (AAM)

The translation and rotation, or AutoAlign matrix (AAM), are calculated from the 3D volume sets generated with the AAS as a function of the atlas of the patient's head.

The AAM is applied to all graphical objects of the following protocols if there is a minimum fit between the patient data and the atlas.

Requirements

Individual anatomical differences may be necessary in applying **AutoAlign**. AutoAlign head programs can be performed under the following conditions:

- ❏ The minimum patient age is 17 years.
- ❏ The patient cannot suffer from certain diseases, such as Alzheimer, does not have a large tumor, nor has had major brain surgery.

Display in the Program Control



A dimmed button below the contrast agent syringe indicates whether the system has an AutoAlign license.

AutoAlign activated



After successful ASS scan, the button is active. It shows that **AutoAlign** is activated.

Until a scan has been successfully completed, the button remains dimmed.

⇨ **AutoAlign** remains active until a patient is newly registered. The function is deactivated by clicking the softkey or selecting the menu item **Queue > Deactivate AutoAlign**.
→ Page C.18–10, *Deactivating AutoAlign*

AutoAlign Scout

The AAS belonging to an AutoAlign scan program is marked with an icon.



The icon appears to the left of the name of the AAS.



A red cross is shown if it was not possible to successfully scan the AAS.

Examination with AutoAlign

Load an AutoAlign program into the Program Control. After measurement of the localizers, the AAS is started automatically. The images are scanned for calculating the AAM. The successfully calculated matrix is then applied to the graphical objects of the following protocols. Thus adapted, the protocols can then be run.

Measuring an AutoAlign Scout

Loading an AutoAlign Scout

The AutoAlign license is available and you registered the patient.

✧ Transfer the AutoAlign program to the Program Control.



➪ When you insert an AAS in the job list, the patient's age is checked automatically. If the patient is too young, a message is displayed.
→ Page C.18–12, *Checking the patient's age*

Scanning a standard localizer

The first localizer starts automatically.

These reference images are loaded into the large image segments of the **Exam** task card once the localizer measurement and image calculation have been completed.

Three reference images are displayed in the sagittal, transverse, and coronal orientation.

Acquiring an AutoAlign Scout

The AAS automatically starts after reconstruction of the reference images. The following protocol opens automatically.

➪ The message "Waiting for slice positioning before ending AutoAlign scan" is shown on the status bar.

Two image data sets are acquired with different flip angles. They are not loaded into the large image segments after calculation. The system calculates the AAM from these data sets.

Adjusting the following protocols

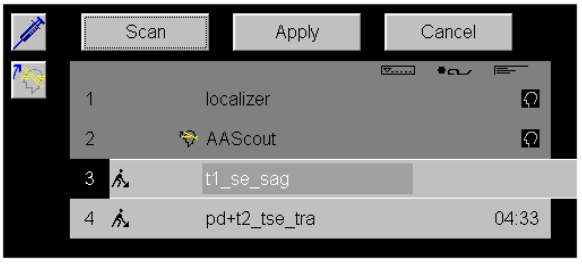
After successfully acquiring the AAS and subsequently calculating the AAM, **AutoAlign** is activated.

AutoAlign active



The **AutoAlign** button and the **Queue > Deactivate AutoAlign** menu item are available again.

The program control shows the series icon to the right of the protocol name.



- If the AAM calculation was not completed before you set protocols in the part of the queue waiting to be executed, this setting will be canceled after the AAM has been successfully calculated.
- If during acquisition of the AAS it is determined that the AAS cannot be calculated or the necessary fit is not obtained, a message is displayed.
  → Page C.18–15, *Canceling an AutoAlign scan*

Applying positioning

After the AAM has been successfully calculated, it is applied to the graphical objects of the subsequent protocols in the job list.

You may be able to observe this: The graphical objects in the GSP segments are rotated immediately after opening a protocol.



✧ Click the **Apply** button.

The protocol is closed and the scan is started with the AAM applied.

NOTE

If you position the graphical objects of the next protocol *during* AAS scanning, these objects will be rotated after the AAM has been calculated.

Not applying slice positioning

If you are not satisfied with the slice positioning corrected by the AAM, you can manually position the slices as usual.
→ Page C.4–1, *Positioning Slices*

Closing the AutoAlign examination

You can close the examination after determining that you do not have to perform additional scans or repeat protocols.

After you have performed the AutoAlign examination and reconstructed the series, **AutoAlign** remains activated.

✧ Move the patient table out of the magnet and allow the patient to leave.

✧ Select **Patient > Close Patient** from the main menu.

Or

✧ Right-click the name of the patient in the program control and select **Close Patient** from the context menu.

AutoAlign is deactivated and the program control is returned to its original state.

Deactivating AutoAlign

After successfully scanning an AAS, it may be necessary to deactivate AutoAlign. This may apply if, e.g., you are not satisfied with the results of the AAS scan and want to continue the examination with manual slice positioning. Another case may be the need for additional body scans after you complete the head examination.

Manually deactivating AutoAlign

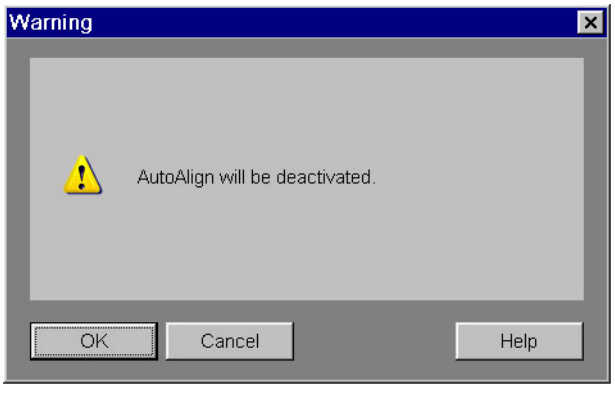


✧ Click the **AutoAlign** button.

Or

✧ Select **Queue > Deactivate AutoAlign** from the main menu.

The following message appears:



✧ Click the **OK** button.



AutoAlign is deactivated. The **AutoAlign** button and the **Queue > Deactivate AutoAlign** menu item are dimmed.

You can now perform additional patient examinations without having to register them again.

Protocols already acquired with **AutoAlign** are not changed by deactivating **AutoAlign**.

New series block

Each table movement deactivates **AutoAlign**, since the calculated AAM refers to a fixed table position.

If the table moves or the light localizer is enabled, e.g., to initiate repositioning, a new series block is started.



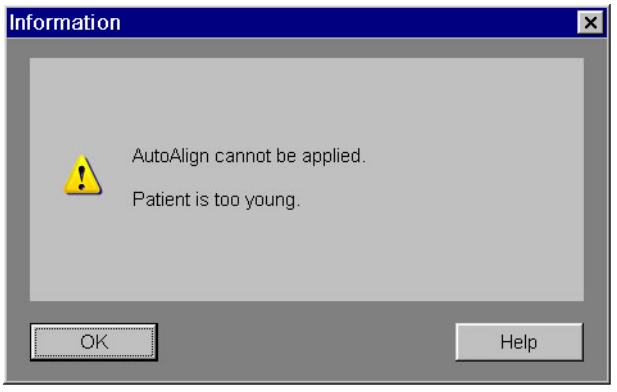
You can see that **AutoAlign** has been deactivated because both the button and **Queue > Deactivate AutoAlign** menu item are dimmed.

Checking the patient's age

As soon as an AutoAlign program is transferred to the job list of the program control, the system checks whether the patient's age meets the requirements for an AAS scan.

Patient too young

If the patient is younger than 17, the program control is blocked and the following message appears.

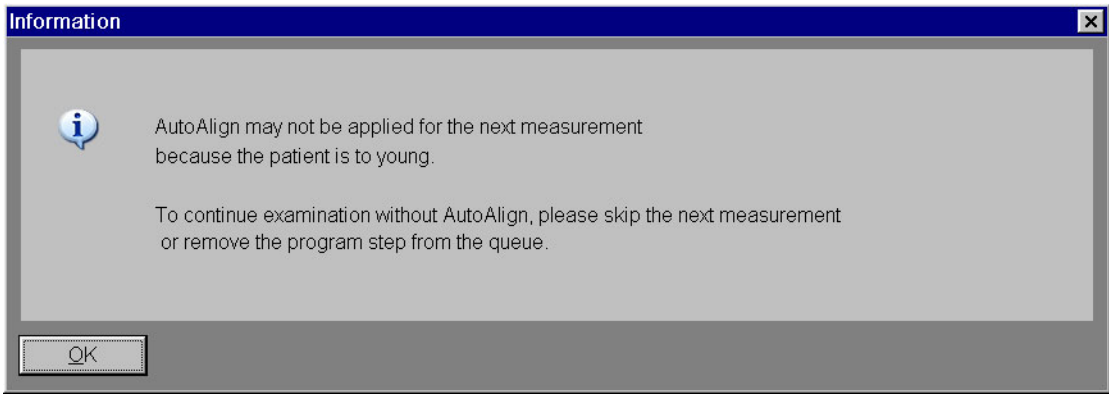


✧ Click the **OK** button.

The window closes.

To continue scanning this patient, select a scan program without **AutoAlign**.

➪ If you attempt to scan the AAS again, a message box appears informing you how to proceed.



Getting the program control ready for scans scan

You can skip or delete the AAS.

✧ Click the **Skip** button.

The AAS is skipped. The next protocol may now be started. Automatic position correction is not used.

✧ Select the AAS in the job list.

✧ Select **Edit > Delete** from the main menu or **Delete** from the context menu.

Or

✧ Use the **Del** key on the keyboard.

Or

✧ Drag the AAS into the wastepaper basket.

The AAS is removed from the job list, and the program control is ready to run again.

Canceling an AutoAlign scan

For an AutoAlign scan to be performed successfully, a given fit has to be obtained to allow for correct application of the AAM to the protocols.

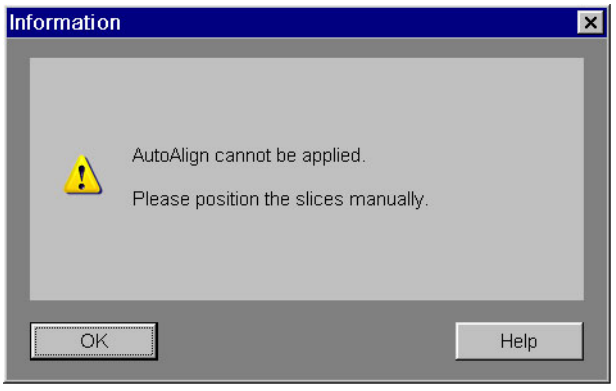
AAS not scanned

If the AAS was not scanned, the message "Scanning of protocol ... has failed" is shown on the status bar.



The AAS is marked as "canceled" by the lightning icon. The series icon next to the protocol indicates that the image data sets have not been calculated.

A message window opens.



✧ Click **OK**.

The protocols of the job list continue to be executable. You may continue scanning as usual.



The **AutoAlign** button and the **Queue > Deactivate AutoAlign** menu item are dimmed.

AAM not usable



If the AAS was scanned successfully, but the defined fit could not be obtained, you will see a line through the icon.

Fit not achieved

The following situations may make it impossible to obtain a defined fit or to calculate the AAM.

❏ Pathological changes to the patient's brain.
→ Page C.18–3, *Requirements*

❏ The head of the patient is offset by > 50 degrees and/or > 50 cm from the atlas.

Repeating the AutoAlign Scout

In some exams, it may be necessary to repeat the AAS, for example, because the patient moved.

✧ Select the AAS from the job list.

✧ Select **Queue > Rerun** from the main menu.

Or

✧ Select **Rerun** from the context menu.

The AAS is started again.



A new AAM is calculated after the AAS scan. It replaces an existing AAM.

Recalculating the AAM automatically resets all subsequent protocols and marks them with a construction worker icon. The protocols must be checked again before they are executed.

Inserting a new AAS

If the patient moved his/her head after the AAS was measured, a second AAS can be inserted in the queue to correct the slice positions again.

✧ Select an AAS on the program card or in the **Exam Explorer** and insert it in the job list.

The new AAS will be started automatically and a new AAM will be calculated.

➪ Inserting the AAS starts a new series block. The following protocols are reset and marked with a construction worker icon.

Editing an AutoAlign scan program

You can modify the AutoAlign scan program in the job list as usual.
→ Page C.6–39, *Processing the job list while scans are being performed*

Inserting programs and protocols

You can transfer program steps or complete scan programs to the job list even if they are for other body regions.

If the protocol requires table movement, a new series block begins and **AutoAlign** is deactivated.
→ Page C.18–11, *New series block*

If the protocols do not include table movement, they are executed and the current AAM as calculated by the AAS is applied.

Setting copy references

You can apply parameter settings of a protocol in the AutoAlign scan program to another protocol by setting a copy reference.
→ Page C.6–45, *Setting a copy reference*

➪ The AAS can be a source protocol but not a target protocol.

NOTICE

The AAM is applied to the target protocol only if the copy reference contains slices.

Creating a protocol from a series or image (Phoenix)

The Phoenix function enables you to reconstruct a protocol from previously acquired images.

It is easy to reconstruct scan protocols for a new examination from images acquired in a previous exam.

The two steps involved are:
- ❏ Transfer the AAS to the job list
- ❏ Transferring the series or image to the job list

Inserting the AAS

To run the reconstructed protocol the AAM has to be recalculated.

✧ Select an AAS on the program card or in the **Exam Explorer** and insert it in the job list.

After the AAS has been successfully scanned, the AAM is calculated. This new AAM is applied to the slices.

Selecting a scanned series or image with AutoAlign

✧ Select a series or image in the **Patient Browser**.

A single image is sufficient for reconstruction.

✧ Press the mouse button and drag your selection into the job list (*drag* & *drop*).

Or

✧ Select **Append To Queue** from the pop-up menu in a GSP segment.

A protocol is generated from the series or image and contains all measurement parameters used to acquire the image. After you have run the protocol, the same slices are scanned as in the previous examination.

NOTE

Phoenix is available for all MAGNETOM systems with ***syngo*** **MR 2002B**. It works with all images that have been generated with this or future software versions.

Phoenix only permits reconstruction of protocols from a MAGNETOM system of the same type for images from MAGNETOM Concerto, MAGNETOM C!.

Reconstructed protocol through conversion

You can attempt to convert images or series that were not acquired on a identical system configuration.

As a prerequisite, the sequence technique for the protocol must be available and licensed for your MAGNETOM system.

✧ Select a series or image in the **Patient Browser**.

✧ Press and hold the **Shift** key, press and hold the *left* mouse button and drag the series or image into the job list (*drag & drop*).

A message box informs you if the conversion was not successful.

Creating new AutoAlign programs

There are various ways of creating a new AutoAlign head program and saving it as a new AutoAlign program in the user area of the **Exam Explorer**.

Creating your own AutoAlign head program in the Exam Explorer

You can create your own AutoAlign head program in the usual way in the **Exam Explorer**.

Insert an AAS into any head scan program or create a head program from selected protocols and add an AAS to it.
→ Page C.16–38, *Creating a new program*

Exporting executed programs to the Exam Explorer

After performing an AutoAlign exam, you can save a changed scan program as a new program and use it for subsequent examinations.

All patient-specific AutoAlign data are removed so that the program can be used just like any other scan program.

✧ Select **Queue > Save As Program** from the main menu or **Save As Program** from the context menu of the program control.

The **Exam Explorer** is opened and displays the **Save Program As [Customer Tree]** dialog box.

Assign your modified scan program to an examination region as well as an examination and enter a name for the scan program.
→ Page C.16–61, *Saving the scan program under a new name*

Planning with atlas images

AutoAlign allows you to plan slices on statistical images for certain diagnostic problems. As a result, you are able to create a user-defined scan program.

This slice positioning using statistical images is not performed for a certain patient but once. You can examine any number of patients with **AutoAlign**.

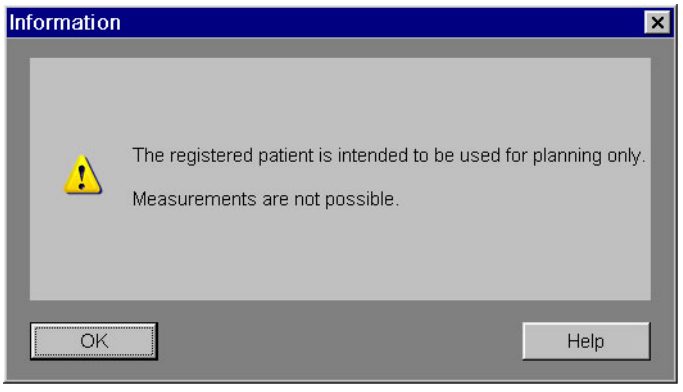
Registering a planning patient

To plan an AutoAlign program, a special planning patient is available in the **Patient Browser**.

✧ Register the **AutoAlign** patient.

✧ Select patient position **Head first - supine**.

A message window opens.

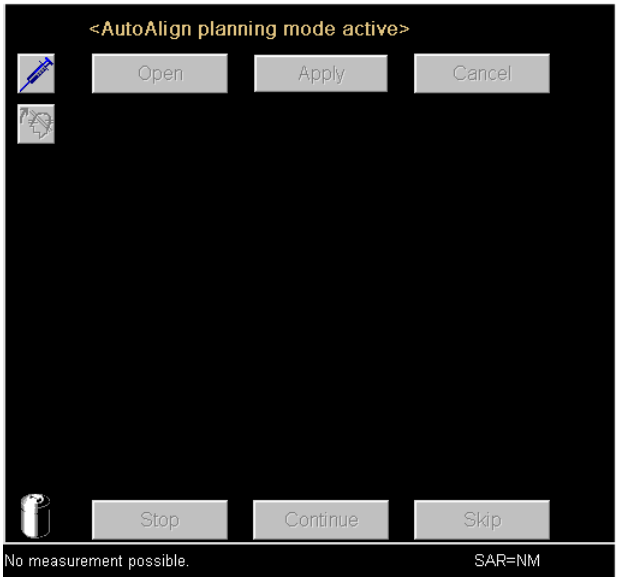


✧ Click **OK**.

The window closes.

Program control in planning mode

The program control indicates planning mode instead of a patient's name. The status bar indicates that scans are not possible.



Loading atlas images in GSP

✧ The images for planning are automatically loaded into the images segments of the **Exam** task card.

The program control is blocked for scans but protocol editing is possible without restriction.

Adjusting AutoAlign protocols

✧ Load, for example, a head program into the job list.

✧ Now open the protocols and position the slices on the atlas images.



✧ Click the **Apply** button.

The changes are applied to the opened protocols.

Saving new protocols

After you have positioned the graphical objects, you can save the edited protocols in the **Exam Explorer**.
→ Page C.18–25, *Exporting executed programs to the Exam Explorer*
→ Page C.6–66, *Saving a job list as a new program*

Quitting planning mode

✧ Register a real patient.

Or

✧ Select **Patient > Close Patient** from the main menu.

Or

✧ Right-click the name of the patient in the program control and select **Close Patient** from the context menu.

CHAPTER C.19

Quality Measurement

You can perform quality checking measurements for each RF coil. This is done with the aid of scan phantoms and the quality program at the *syngo* Acquisition Workplace.

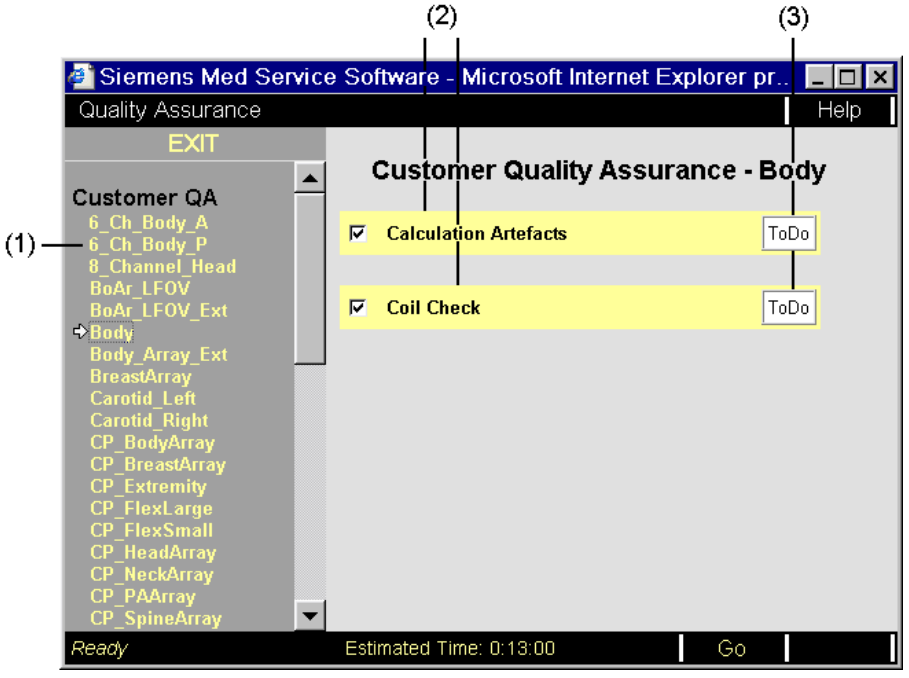
The quality measurement checks the signal-to-noise ratio of the coils. For the body coil (or body spine array with MAGNETOM Concerto, body spine array large with MAGNETOM C!) you can also determine the signal uniformity and check the phantom image for artifacts.

Performing Quality Measurements

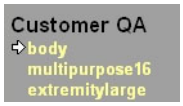
The preparation of quality measurements is performed as described in the "quality assurance" supplement.

✧ At the *syngo* Acquisition Workplace, go to ***syngo* MR** and select **Options > Customer QA**.

✧ The **Quality Assurance** dialog box opens.



(1) List of configured coils
(2) Available quality measurements
(3) Status of quality measurement



✧ Select the correct coil from the list.

➪ This list shows all coils configured by Siemens Service.



✧ Click the **SN DIP** check box if you want to check the signal-to-noise ratio and signal uniformity (DIP).

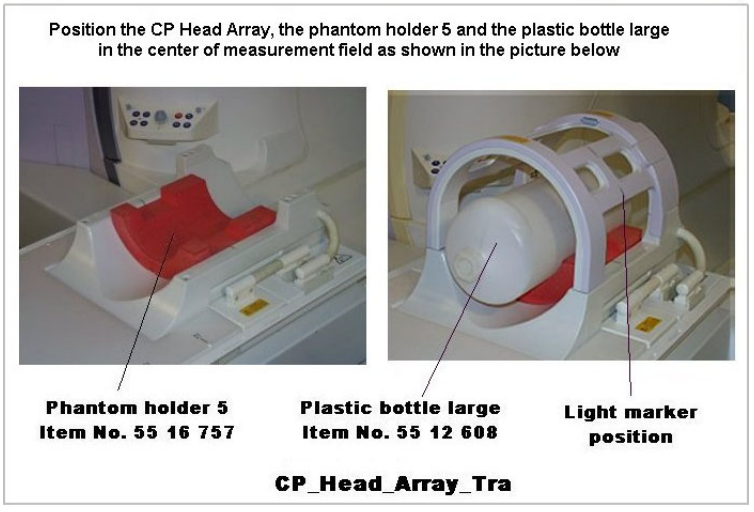


✧ Click the **Calc Artifacts** check box if you want to check the body coil (or the body spine array L or Head_3T) for artifacts.



✧ Click **Go**.

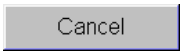
A help window is displayed that describes the position of the phantom holder and phantoms for the selected coil.



✧ Follow all positioning instructions.

✧ Connect the coil to the MR system.

You can still stop the quality measurement at this stage.



✧ Click the **Cancel** button.

The help window closes.



✧ Click the **OK** button.

The help window closes, and the quality measurement starts.

Information regarding the progress of the measurement is displayed in the yellow fields next to **SN DIP** and **Calc Artifacts**.

Message	Explanation
To do	Measurement still has to be performed
Running	Measurement is in progress
Done	Measurement has been performed Parameters correspond to specifications
NotOK	Calculated parameter does *not* correspond to specifications
Error	Measurement cannot be performed

You can stop a quality measurement in progress.

Abort

✧ Click **Abort**.

If the message **Error** or **NotOK** appears, repeat the quality measurement.

✧ Optimize the position of the phantom.

✧ Optimize marking with the laser light localizer.

✧ Repeat the quality measurement.

➪ If the results of the quality measurement are still unsatisfactory, contact Siemens Service.

PART D

Postprocessing Images

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CHAPTER D.1

Dynamic Analysis

Dynamic analysis is used to calculate new evaluations obtained by combining images and series.

You may use a variety of evaluation functions to postprocess images and series that you have obtained, for example, from contrast medium examinations or functional neuro imaging.

For example, you can enhance contrasts by applying arithmetic or statistical functions to the grayscale values. This function is also used to calculate T1 and T2 images.

Dynamic analysis is launched from the **Patient Browser**. You can also start some of its applications from the **Viewing** task card.

A separate dialog box is displayed for each function used to perform evaluation. The procedure for each operation in dynamic analysis is the same. We will begin by describing a few general steps before going into specific aspects of each analysis.

The results images are stored in the database in the usual way. You can load and view them in the **Viewing** task card.

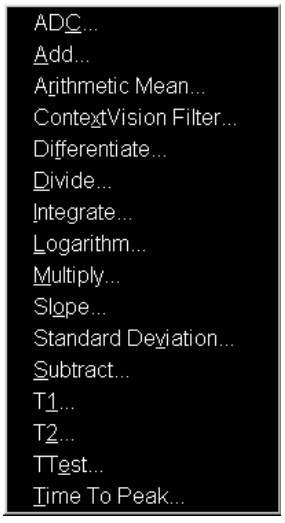
The results obtained from dynamic analysis can be used as input for other evaluations, such as **Mean Curve**.

Access rights for dynamic analysis

Dynamic analysis requires that the user have full access rights to the patient data to be evaluated.

Please observe the information given in the Safety Standards book.

Overview for evaluation



The following functions are available for analysis of dynamic processes and for postprocessing of images:

- ADC - diffusion coefficient
- Addition
- Slope
- Arithmetic mean
- ContextVision filter
  → Page D.3–1, *Image Filtration and Distortion Correction*
- Differentiation
- Division
- Integration
- Logarithm
- Multiplication
- Standard deviation
- Subtraction
- T1-weighted images
- T2-weighted images
- T-test
- Time to peak

Selecting images and starting dynamic analysis

Select the images/series that are of interest to you in the **Patient Browser** or on the **Viewing** task card.

➪ Without selecting an image first, it is not possible to start the **dynamic analysis** function.

Selecting the images from the Patient Browser

The **Patient Browser** allows you to view and process the images and data of all examinations stored in the main database or in an archive.

✧ Open the **Patient Browser**.

✧ Select images/series in the navigation or content area.

Selecting images on the Viewing task card

The **Viewing** task card is used to view and edit images and series.

✧ Go to the **Viewing** task card.

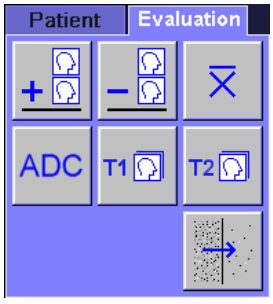
✧ Select the images or series that are relevant to you in the image area of the **Viewing** task card.

Starting Dynamic Analysis

The functions for dynamic analysis are started from the **Patient Browser** and the **Viewing** task card.

✧ Select **Evaluation > Dynamic Analysis > ...** from the **Patient Browser** menu or from the menu of the **Viewing** task card.

Or



✧ Click the relevant icon of the **Evaluation** subtask card on the **Viewing** task card.

Loading Images

The selected images are loaded in the relevant dialog box. It may take several seconds to load the images. A **Progress indicator** on the footer bar shows the current process of the process.

➪ The evaluations are performed similarly to mathematical functions. The series selected first is the first operand of the function, all the series selected after that are the other operands. For some functions, such as division, the result is different depending on the sequence of the operands (= sequence of the series). These are non-commutative functions.



✧ To cancel an operation before it has finished, click the **Cancel** button.

Checking whether images are suitable

Not all images are suitable for dynamic analysis.

Images must fulfill the following conditions to be suitable:

- ❏ They must belong to the same study (and therefore to the same patient).
- ❏ They must have the same FoV.
- ❏ They must have a corresponding matrix size.
- ❏ They must have the same slice orientation.

Some evaluation functions require that other conditions be met as well, for example, the same slice position or slice thickness.

A message box is displayed if images do not fulfill one or more of these conditions.

For functions in which different image positions or slice thicknesses occur, the **Evaluation Check** dialog box will be displayed.

The list shows all images with different image positions or slice positions.

⇨ If more than one series is selected, the images are listed together by their image number.

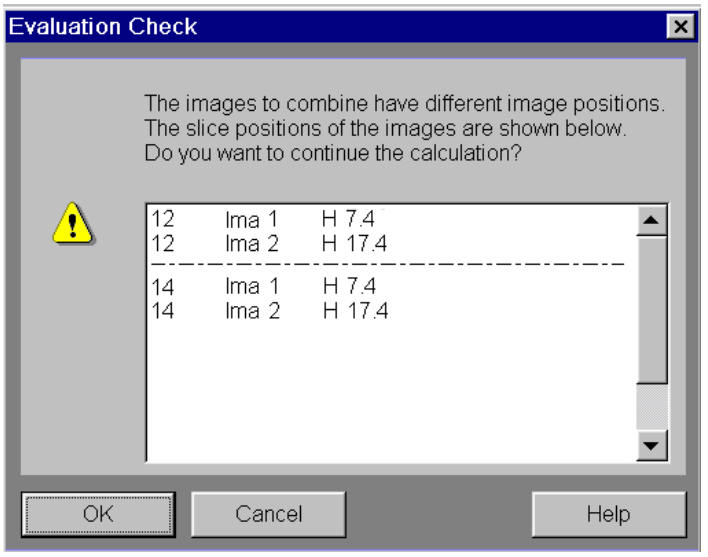
The dialog box appears in two variations for different calculations. Each variation behaves differently.

- **Condition A**: Calculation *does not necessarily* require images with the same image position, slice thickness, etc.
- **Condition B**: Calculation *always* requires images with the same image position, slice thickness, etc.

Here are examples of conditions A and B with the same image position.

Condition A

Calculation *does not necessarily* require images with the same image position or slice thickness, etc. **Example**: Image position





✧ Click the **OK** button if you want to start the evaluation.

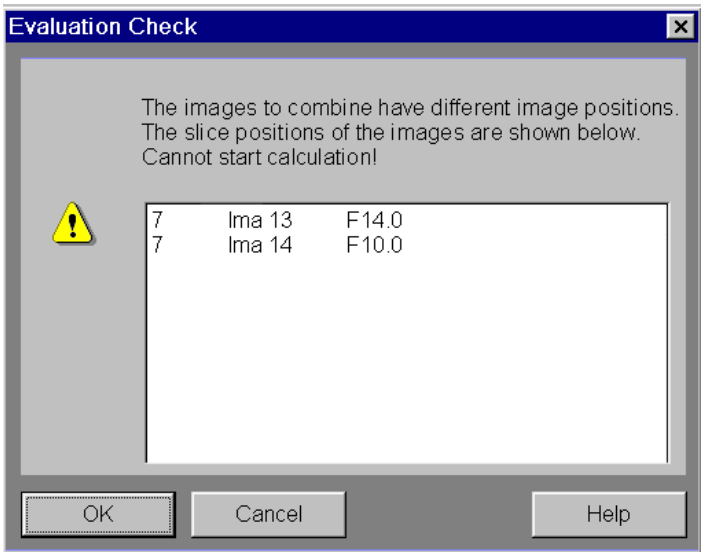
Or

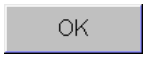


✧ Click the **Cancel** button if you do not want to start evaluation and want to close the function dialog box.

Condition B

Calculation *always* requires images with the same image position or slice thickness, etc. **Example**: Image position





✧ Click the **OK** button if you want to return to the function dialog box.

Or



✧ Click the **Cancel** button if you do not want to start evaluation and want to close the function dialog box.

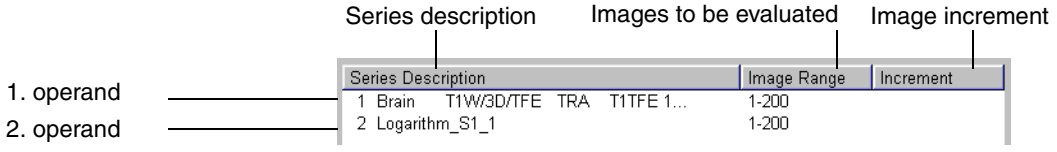
General procedure for dynamic analysis

After you have transferred the selected images and series and have called up an evaluation function, a function-specific dialog box will be displayed.

Displaying and selecting initial images

The selected images and series are listed numerically in the list of operands in the upper part of the dialog box.

➪ The images/series are listed in chronological order of creation when loaded into the evaluation functions **Subtraction** or **Division**.



The **Image Range** column shows the images marked for evaluation.

If you have not transferred all the images of a series, but only every third or fourth one, for example, a display as shown below will indicate the actual images forwarded. It is also possible for you to select and transfer a range of images within a series.

Image range	Selected images
3	Image 3
2-5	Images 2, 3, 4, 5
4-< images. last image >	Image 4 to the end
2, 5, 8	Images 2, 5, 8

Removing series

You can remove series from the list of operands

✧ Select the series in the **Operands** field.

✧ Right-click the series to open the **Deletion of Series** context menu.

Or

✧ Press the **Del** key.

Adding/removing images

You can set image intervals if, for example, you only want to use part of a series for evaluation.

Because direct editing of entries under **Image Range** is not possible, you must set the image intervals like this instead:

✧ First select only some of the images in the **Patient Browser** or on the **Viewing** task card and start evaluation.

The dialog box shows you the selected images under **Operands**.

✧ Select the next images in the **Patient Browser** and drag and drop them into the dialog box of the evaluation function.

The entries under **Image Range** are updated. The series with the appended images from the **Patient Browser** moves to the top of the list of operands.

Entering an increment

You can also set image intervals by entering an increment.

✧ First select the series in the **Operands** field.

✧ Double-click the selected series in the **Increment** column.

A spin box is displayed for entering values.



✧ Enter an increment.

Or

✧ Use the spin buttons to select the value.

✧ Complete your entry by clicking outside the spin box.

➪ Confirm your entry by pressing the **Enter** key. The calculation is started.

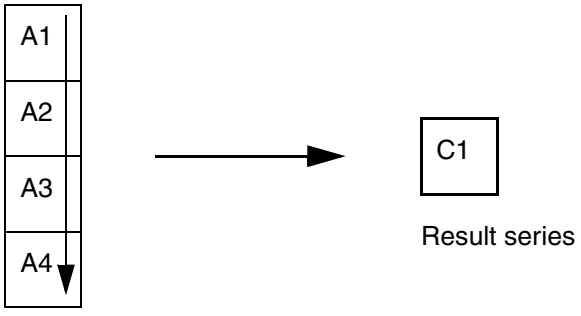
Example:
You want to run a dynamic analysis on every third image in series **6 2_t2_tse_tra**. Enter the value 3 in the **Increment** column.

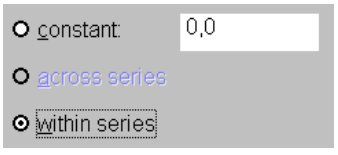
Setting the Operation Mode

Some functions allow you to perform evaluation not only within a series but also across two or more series.

Evaluating images within series

If you evaluate images within series, only the images of the initial series will be used as operands for an evaluation function. In this editing mode, you can generate a series with one or more images from an initial series.



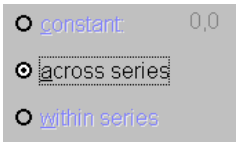


If you have only selected one original series, either **within series** or **constant** mode will be activated, depending on the selected function.

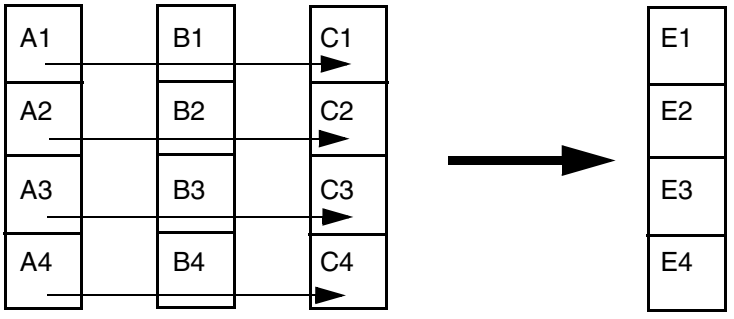
Evaluating images across series

You can evaluate images from different series. In this case, you are generating result series from the individual images of the original series by combining the ith image of each series with the ith images of the other series.

The images in the series are sorted by slice position. If the slice position is the same in several images, they are sorted by image number.



➪ If you have selected more than one original series, **across series** mode will be activated automatically for images with the same slice position.



The result series will contain the same number of images as the smallest initial series.

Applying the constant to images



You can apply an operation with a fixed value to the images of a series by multiplying the images by a constant defined by you.

✧ Select the **constant** option.

✧ Enter a value for the constant in the input field.

➪ You can also edit the entry in this input field via the context menu. To open the context menu, right-click the field.

The operation with the constant is applied to each image in the series.

Depending on which mode is selected, the title bar of the dialog box will show which operation is being performed.



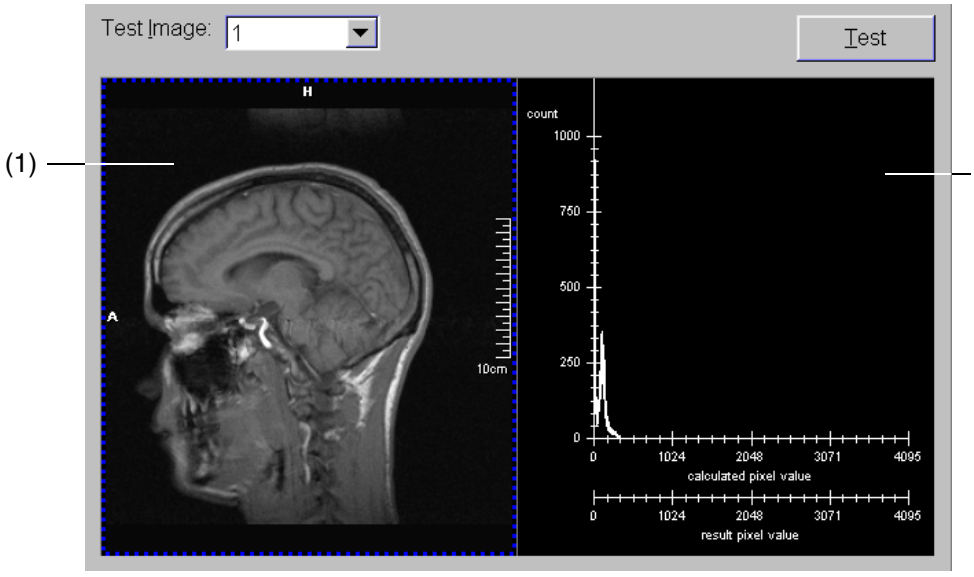
Generating preview images

You can generate preview images for most evaluation functions. These test images are used to decide whether to perform evaluation with these settings for the whole series.

Display in the test area

The test area shows a test image with the associated histogram.

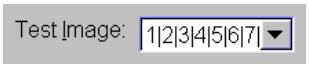
(1) Test image
(2) Histogram of the test image



➪ You can window the test images to optimize display.

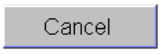
Selecting test images

The **Test Image** selection list shows all possible test combinations of images.



✧ Select a test combination from the selection list.

The image numbers will be separated by vertical lines if two or more images are used for a test evaluation.

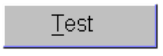


To cancel an operation before it has finished, click the **Cancel** button.

Changing the test image

The test image and histogram do not meet your requirements, you can select another image from the **Test Image** selection list.

✧ Select another test image from the **Test Image** list.



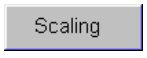
✧ Click the **Test** button to display the new image in the image area with the histogram.

Limiting the display area

You can limit the range displayed in the histogram to the relevant part by defining a lower and an upper threshold value. Only the grayscale values that are within the threshold values will be used for evaluation.

✧ Right-click the histogram window and left-click the only menu item **Properties...**.

Or



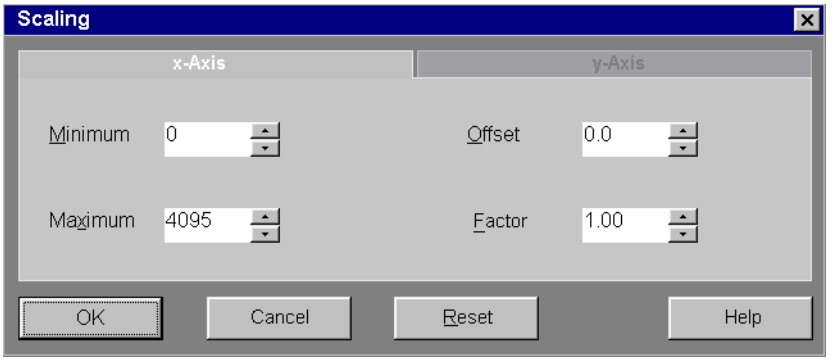
✧ For the **Subtraction** and **Division** functions, click the **Scaling** button.

The **Scaling** dialog box is displayed.

Limiting grayscale ranges

For scaling, select the range of the calculation result data that is mapped onto the grayscale range (0-4095) or onto the range stated on the lower x-axis.

✧ Go to the **x-Axis** subtask card by clicking its tab.



✧ Enter the lower threshold in **Minimum** spin box.

✧ Enter the upper threshold in **Maximum** spin box.

➪ Offset and factor are in a linear relationship with minimum and maximum.

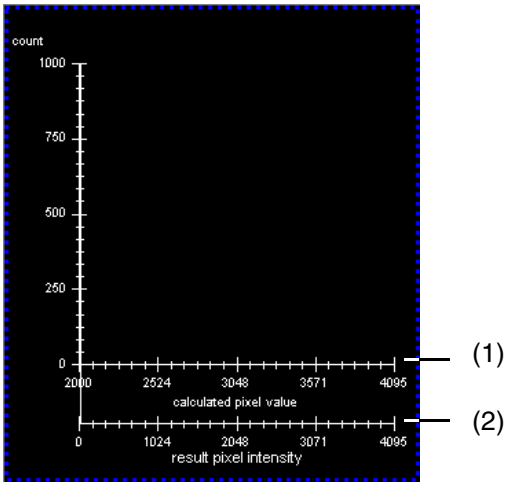
For example, if you have select the value 100 for the offset, minimum and maximum will have the following values:

=> Minimum = -100

=> Maximum = 3995

✧ Click the **Test** button again.

The interval that you define (upper X axis) is then mapped onto the grayscale range of the lower X axis (usually 0 to 4095).



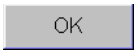
(1) Grayscale range defined by scaling
(2) Grayscale range displayed in the result image

Limiting the number of pixels

- ✧ Now move the **y axis** subtask card to the foreground by clicking on the tab.
- ✧ Enter the lower threshold for the number of pixels in **Minimum** spin box.
- ✧ Enter the upper threshold for the number of pixels in **Maximum** spin box.

NOTE

Changes to the scaling of the histogram's y axis only affect the histogram being displayed, not the results images.



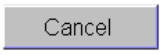
✧ When the scaled image meets your requirements, apply the settings by clicking on **OK**.

Or



✧ Restore the original settings by clicking **Reset**.

Or



✧ Reject the settings by clicking **Cancel**.

Setting a noise level

You can set a noise level for some functions. This threshold value determines the pixels used for evaluation.



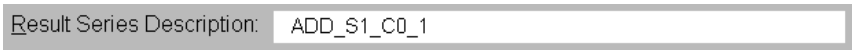
✧ Enter a value in the **Noise Level** input field.

Renaming a results series

A results series is generated for each original image or series.

Name of the result series or image

The **Result Series Description** text input field contains an automatically generated name. However, you are able to modify the name as required.



As the default setting, a name is displayed as follows:

- ❏ First part of the description is the function that was used, e.g., ADD.
- ❏ The different parts are separated by an underscore.
- ❏ The operands are identified with "S" for series, "I" for image, and "C" for constant.
- ❏ This is usually followed by the series number, image number, or the value of the constant.
- ❏ If you are using more than two series or images, the word "various" will be used instead of a series or image number.

Example: You can add the grayscale values of image 34 to those of image 45.
The system then provides the following default description: "ADD_I34_I45_10".

If the name of the result series meets your requirements, you can record the name in the **Result Series Description** field.

Selecting a result series or image

If you have selected more than one series (e.g. **Logarithm**, **Multiplication**, **Subtraction**, and **Division**), you can use the selection list next to the **Result Series Description** input field to select series, check names, or change them, if necessary.

Displaying result images

The results are stored in the database under the name you entered. When you have completed analysis, the results are displayed on the **Viewing** task card in the background. Here, you can further process the images.

Functions for dynamic analysis

This section describes the specific aspects of each function that differ from general procedures applicable to all functions.

Adding images

Image addition is used to add the grayscale values of images or add a constant.

Adding the grayscale values of images is equivalent to image overlay. For example, you can overlay an image with the result image of a T-Test evaluation with exceptional anatomical details.

Adding a constant shifts the entire grayscale range.

You can add:

- ❏ Images from a series with a constant
- ❏ Images within a series
- ❏ A series and one or more series with the same number of images

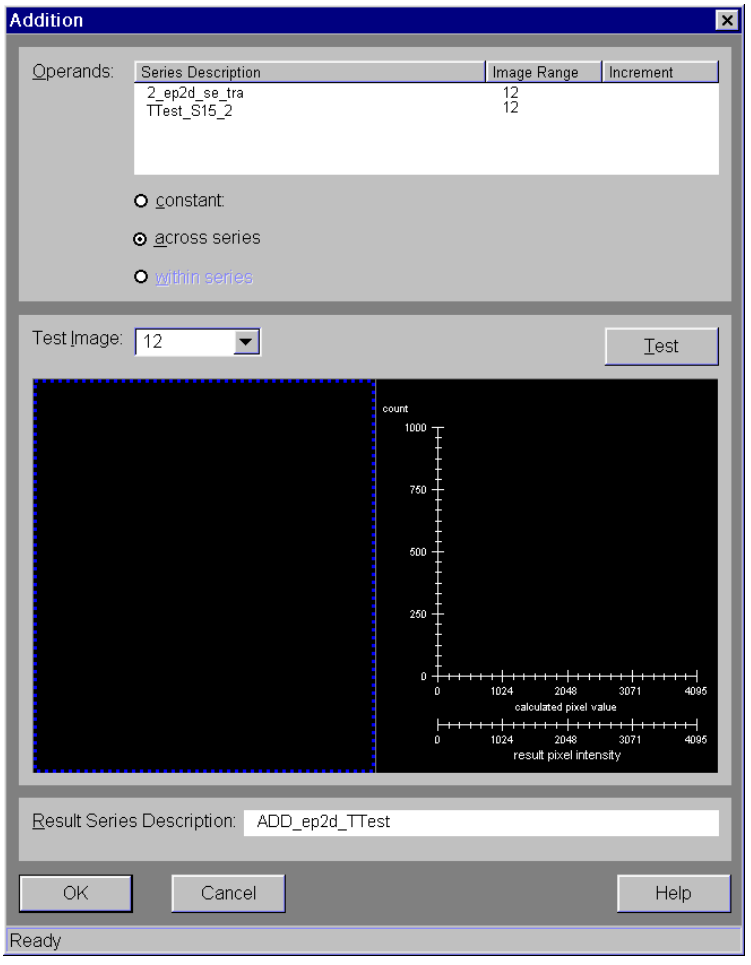
- ✧ Select individual images and/or series in the **Patient Browser** or on the **Viewing** task card.
- ✧ Then select **Evaluation > Dynamic Analysis > Add...**.

Or



✧ Click the **Add** icon on the **Viewing** task card/**Evaluation** subtask card.

The **Addition** dialog box opens.



Operands shows which images or series are selected.

Mode

One of the following modes is already selected depending on whether you have loaded one or more series to the **Addition** dialog box:

- ❏ **with constant** (image, images, series)
- ❏ **across series** (two or more series)
- ❏ **within one series** (a series with two or more images).

✧ Select the mode.

➪ It is not possible to activate **across series** mode if the series selected do not contain the same number of images or if only one series or image is selected.

➪ You cannot select **within series** mode if one series selected contains one image or more than one series is selected.

Start evaluation

✧ If you do not want to use a generated name for the **Result series**, enter a name for the results series now.



✧ Click **OK** to start calculation.

The result will be an image (within series) or a series of images (across series).

Subtracting Images

During subtraction, you subtract the grayscale values of images from other images or subtract a constant from images.

For example, you could use image subtraction to clearly visualize an image after contrast agent application. For this purpose, you subtract the grayscale values of images generated without contrast medium from those generated with contrast medium. The results are images showing only the changes caused by the contrast agent.

You can subtract:

- ❏ Constants from images/series
- ❏ Images/series from constants
- ❏ Series from series
- ❏ Image from image
- ❏ Image from series

Selecting images

Select single images/series in the **Patient Browser** or on the **Viewing** task card.

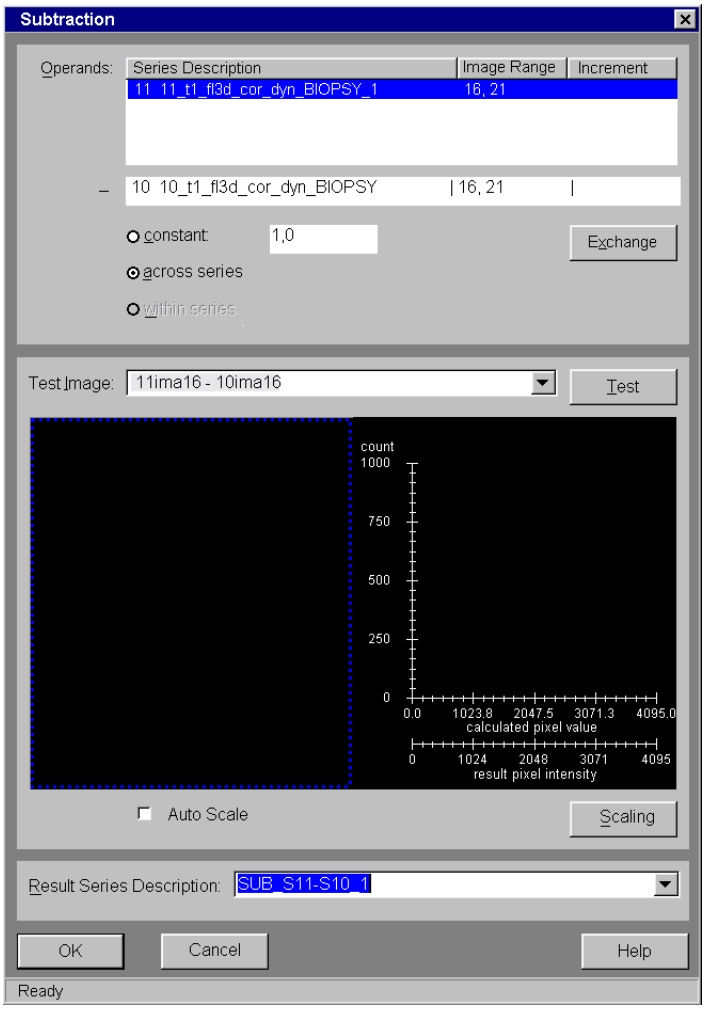
✧ Select **Evaluation > Dynamic Analysis > Subtract...**.

Or



✧ Click the **Subtract** button on the **Viewing** task card/ **Evaluation** subtask card.

The **Subtraction** dialog box opens.



Operands shows which images or series are selected.

Mode

The **constant** (one series) or **across series** (multiple series) option is already selected, depending on whether you have loaded one or more series into the **Subtraction** dialog window.

- If you have selected two images only (two series of one image each or one series with two images), you can only subtract one image from the other or a constant from both images.
- If you have selected two series with the same number of images, you can subtract one image from the corresponding image in the other series or a constant from the images of both series.
- If you have selected two or more series, including one or more with only one image, you can subtract this image from all other images.

Subtraction across series

If you have already selected two or more series, **across series** will be selected automatically.

The **subtrahend** is shown in a separate field below the list of operands.

The series acquired earlier is used as the **subtrahend** default.

- The display field for the subtrahend is not active if the **constant** or **within series** mode is selected.

Subtraction within a series

It is only possible to select the **within a series** option if you have selected a series with only two images.

Changing the sequence

You can change the order of the operands, for example, to subtract image 5 from image 4 instead of image 4 from image 5.



✧ Click the **Exchange** button.

The title bar now shows the new operation.

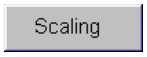
➪ Example: You have loaded 10 series. To replace the subtrahend shown in the field under the list of operands, select the series you want to use as the subtrahend from the list of operands and click the **Exchange** button.

Switching modes

Switching from the **constant** mode to **across series** mode will apply the series selected in the field below. It will then be used as the **subtrahend** if the operation is permissible.

If the selected series is unsuitable, the first series that is suitable for the **across series** option will be selected automatically from the list of operands.

Scaling grayscales



You can scale the grayscale values of the result with the selected values.

✧ Click the **Scaling** button and enter values for the minimum and maximum.

Rescaling images

Negative pixel values can result from subtracting images/ series. Some evaluations, such as mean curve, require the real pixel values as input even if they are negative.

✧ Activate the **Auto Scale** option in the function dialog box.

➪ The grayscale range will now start with the value **-500**.

➪ If you have made any settings in the **Scaling** dialog box, a dialog box will be displayed where you can confirm the settings with **OK** or reject them with **Cancel**.

➪ You can deselect autoscaling by deselecting the **Auto Scale** option or opening the **Scaling** dialog box.

Start evaluation



✧ If you do not want to use a generated name for the **Result series**, enter a name for the results series now.

✧ Click **OK** to start calculation.

The result is an image (within series) or a series of images (across series).

Multiplication

Multiplying the grayscale values by a constant rescales the grayscale values.

You can multiply:

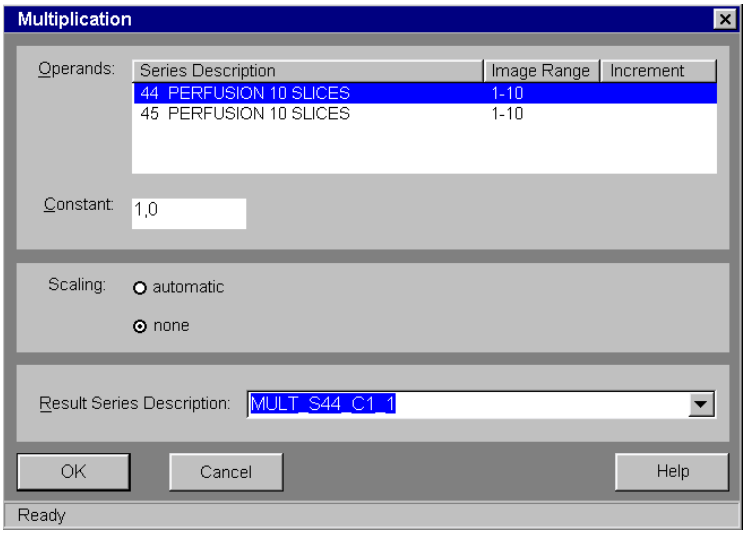
- ❏ Images by a constant
- ❏ A series by a constant
- ❏ Two or more series by a constant

Selecting images

Select single images/series in the **Patient Browser** or on the **Viewing** task card.

✧ Select **Evaluation > Dynamic Analysis > Multiply...**.

The **Multiplication** dialog box opens.



Operands shows which images or series are selected.

Mode



✧ Enter a value for the constant.

Performing grayscale scaling

Because this function does not generate a test image, it provides two options for scaling the result images.



✧ Click the **automatic** option under **Scaling** if you want the grayscale values to be scaled automatically.

Or



✧ Click the **none** option if you want all grayscale values larger than 4095 to be set to this value and the scaling of the result images to correspond to that of the original images.

Start evaluation

✧ If you do not want to use a generated name for the **Result series**, enter a name for the results series now.

✧ Start multiplication by clicking the **OK** button.

Division

You can divide:

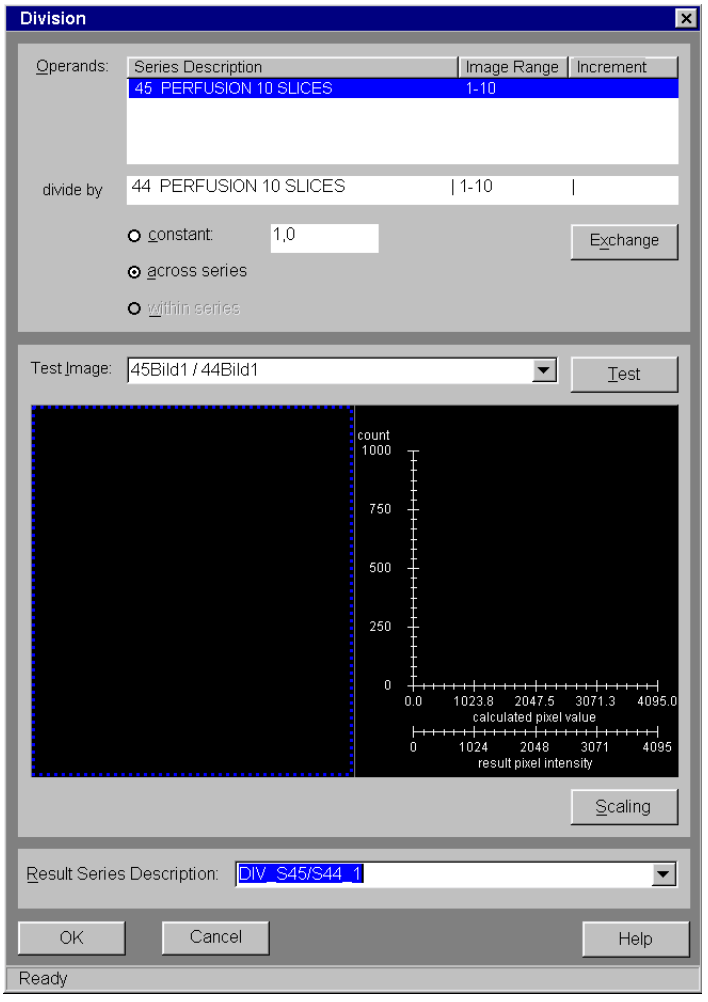
- ❏ A series/images by a constant
- ❏ A series by a second series
- ❏ A series by an image
- ❏ An image by a second image

Selecting images

Select single images/series in the **Patient Browser** or on the **Viewing** task card.

✧ Select **Evaluation > Dynamic Analysis > Divide...**.

The **Division** dialog box opens.



Operands shows which images or series are selected.

Mode

The **constant** (one series) or **across series** (multiple series) option is already selected, depending on whether you have loaded one or more series into the **Division** dialog window.

- If you have selected two images, you can divide one image by the other or both images by a constant.
- If you have selected two series with the same number of images, you can divide the images of one series by the images of the other series, or divide the images of both series by a constant.
- If you have selected two or more series, including one or more with only one image, you can divide all other images by this image.

Division across series

If you have already selected two or more series, **across series** will be selected automatically.

The **divisor** is shown in a separate field below the list of operands.

The series acquired earlier is used as the default **divisor**.

- The display field for the divisor is not active if the **constant** or **within series** mode is selected.

Division within a series

It is only possible to select the **within a series** option if you have selected a series with only two images.

Changing the sequence

You can change the order of the operands, that is, swap round the numerator and denominator of the division.



✧ Click the **Exchange** button.

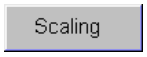
The title bar now shows the new operation.

Switching modes

Switching from **constant** mode to **across series** mode will apply the series selected in the field below. It will then be used as the **divisor** if the operation is permissible.

➪ If the selected series is unsuitable, the first series that is suitable for the **across series** option will automatically be selected as the divisor from the list of operands.

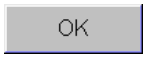
Scaling grayscales



You can scale the grayscale values of the result with the selected values.

✧ Click the **Scaling** button and enter values for the minimum and maximum.

Starting division



✧ If you do not want to use a generated name for the **Result series**, enter a name for the results series now.

✧ Click **OK** to start calculation.

The result is an image or a series of images.

Calculating the Logarithm of Grayscale Values

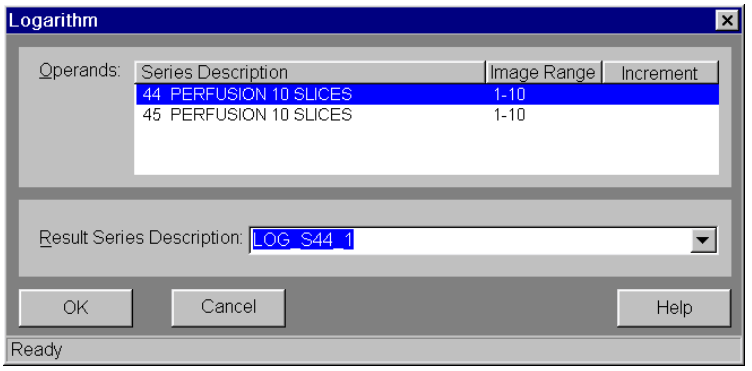
Calculating the logarithm of the grayscale values eliminates large differences in intensity in MR images. Large intensity gradients are common in MR images of the shoulder and the lung, for example.

Selecting images

✧ Select single images/series in the **Patient Browser** or on the **Viewing** task card.

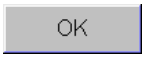
✧ Select **Evaluation > Dynamic Analysis > Logarithm...**.

The **Logarithm** dialog box opens.



Operands shows which images or series are selected.

Start evaluation



✧ If you do not want to use a generated name for the **Result series**, enter a name for the results series now.

✧ Click **OK** to start calculation.

Calculating Differentiation

Differentiation determines the intensity increase (slope) of gray-scale values within a series. For example, it is possible to differentiate inflamed tissue from tumor tissue in mammography by the different enrichment behavior of the contrast agent in the tissue.

➪ You can only ever differentiate one series.

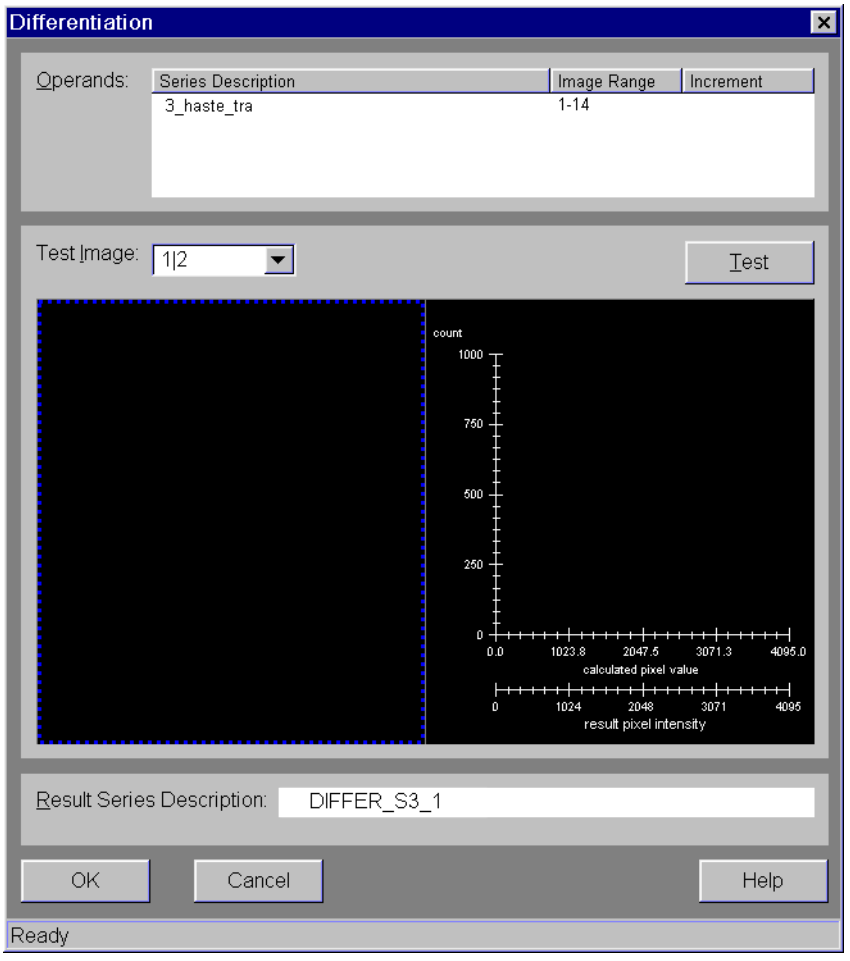
➪ All images of this series must have the same slice position.

Selecting images

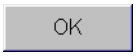
Select a series in the **Patient Browser** or on the **Viewing** task card.

✧ Select **Evaluation > Dynamic Analysis > Differentiate...**.

The **Differentiation** dialog box opens.



Starting differentiation



✧ Enter a name for the result series in the **Result series description** field if you do not want to use the default name.

✧ Click **OK** to start calculation.

The result will be a series that contains one image less than the original series.

The intensity of the grayscales in the images is a direct measure of the differentiation, that is, the tendency of the increase or decrease in grayscale intensity.

Integration of grayscale values

Integration of the grayscale values of a series provides information on enhancement when using contrast agent studies.

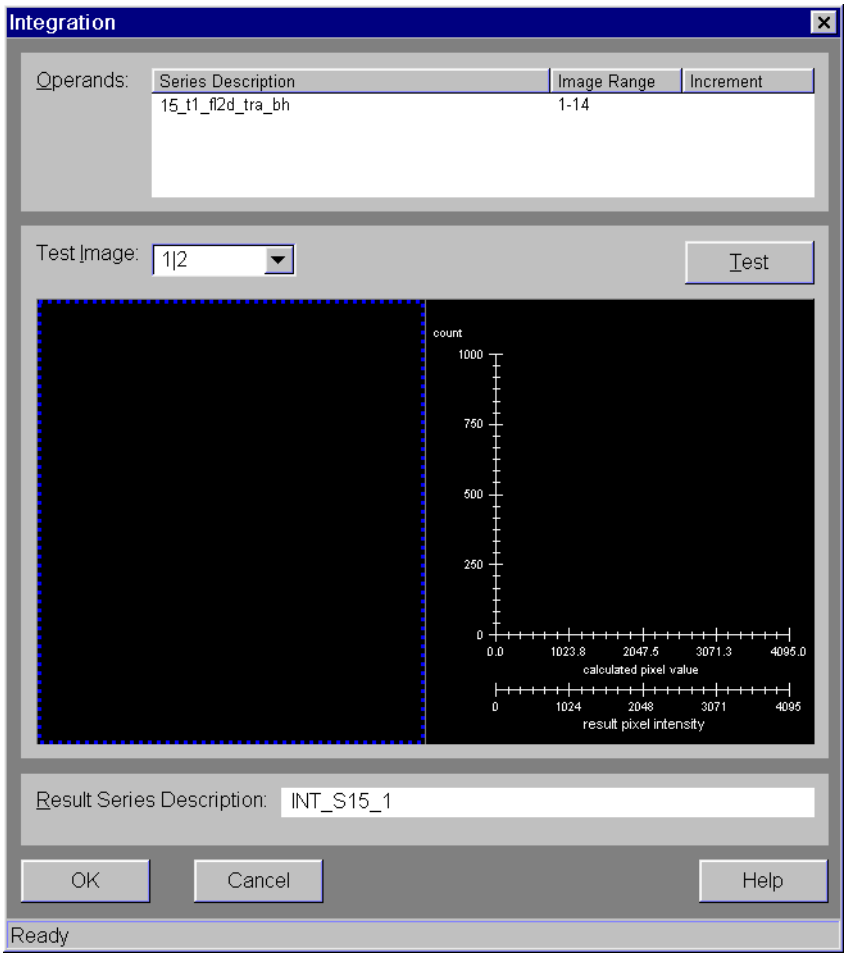
➪ You can only integrate across images of one series. These images must have been scanned at the same slice position.

Selecting images

Select a series in the **Patient Browser** or on the **Viewing** task card.

✧ Select **Evaluation > Dynamic Analysis > Integrate...**.

The **Integration** dialog box opens.



Starting integration



✧ If you do not want to use a generated name for the **Result series**, enter a name for the results series now.

✧ Click **OK** to start calculation.

The result will be a series that contains one image less than the original series.

The intensity of the grayscales in the images corresponds to the integrals of the grayscales.

Arithmetic mean

Calculating the mean value of the grayscales averages large intensity differences in the images. For parallel images with different slice positions this method is equivalent to an MPR Thick display. With a chronological sequence of images, averaging the images improves the signal-to-noise ratio or reduces image artifacts.

It is possible to calculate the arithmetic mean of the grayscale values within or across series.

➪ All images must have the same slice position.

Selecting images

✧ Select a series in the **Patient Browser** or on the **Viewing** task card.

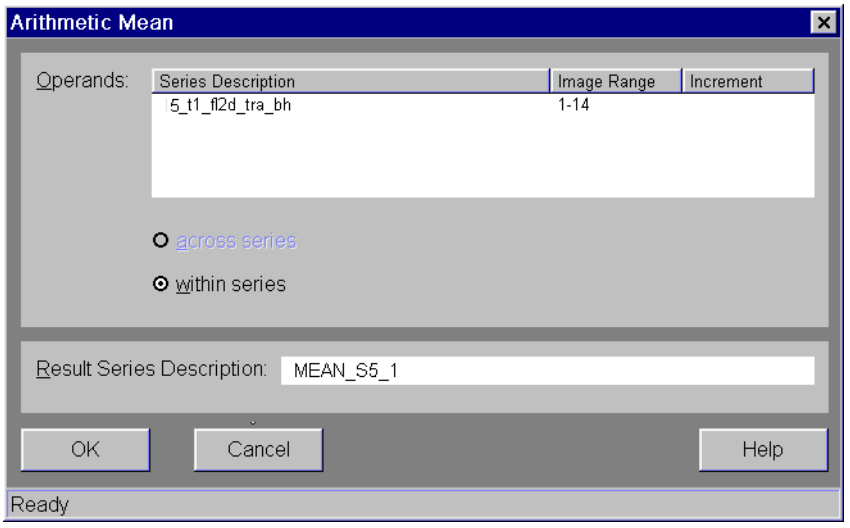
✧ Select **Evaluation > Dynamic Analysis > Arithmetic Mean...**.

Or



✧ Click the **Arithmetic Mean** icon on the **Viewing** task card/ **Evaluation** subtask card.

The **Arithmetic Mean** dialog box opens.



Mode

The **within series** (one series) or **across series** (multiple series) option is already selected, depending on whether you have loaded one or more series into the **Arithmetic Mean** dialog box.

Start evaluation

✧ If you do not want to use a generated name for the **Result series**, enter a name for the results series now.

OK

✧ Click **OK** to start calculation.

The result is an image (within series) or a series of images (across series).

Slope of linear regression

The slope of linear regression describes the rate at which the intensity of the grayscale values increases or decreases within a series. As in the case of differentiation, the different absorption rates of contrast agent in tissue are able to be visualized.

You can obtain the slope of linear regression within series or across series that have the same number of images.

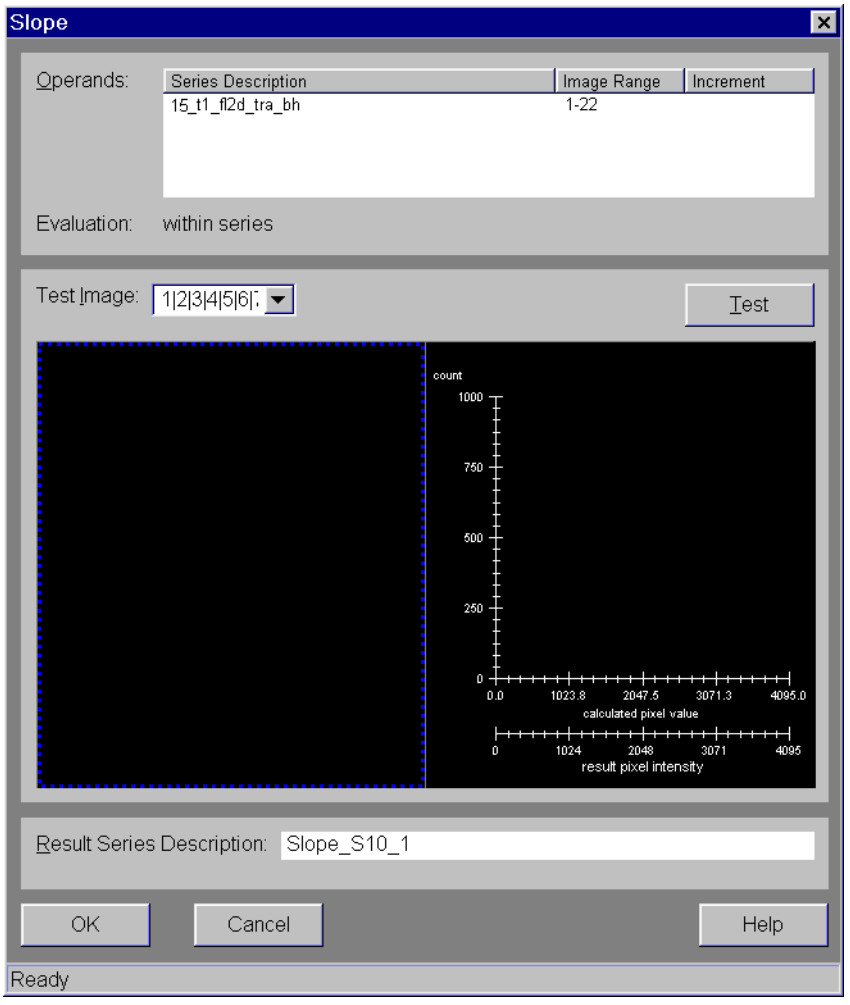
➪ Series must contain at least two images. Otherwise evaluation will not be possible.

Selecting images

✧ Select a series in the **Patient Browser** or on the **Viewing** task card.

✧ Select **Evaluation > Dynamic Analysis > Slope...**.

The **Slope** dialog box opens.

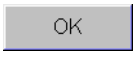


Mode

The **evaluation within series** (one series) or **evaluation across series** (multiple series) option is already selected, depending on whether you have loaded one or more series into the **Slope** dialog window.

Start evaluation

✧ If you do not want to use a generated name for the **Result series**, enter a name for the results series now.



✧ Click **OK** to start calculation.

The result is an image (within series) or a series of images (across series). The intensity of the grayscales corresponds to the gradient of the linear regression. The brighter the grayscale value the greater the gradient.

Determining the Diffusion Coefficient

The diffusion coefficient is a measure of the mobility of water molecules between different types of tissue. The water molecules are sensitized to diffusion measurement by strong gradient pulses. Before you can determine the diffusion coefficients, you require measurements with various diffusion weightings (b values).

You can determine diffusion coefficients for images within series as well as across different series.

Selecting images

✧ Select a series in the **Patient Browser** or on the **Viewing** task card.

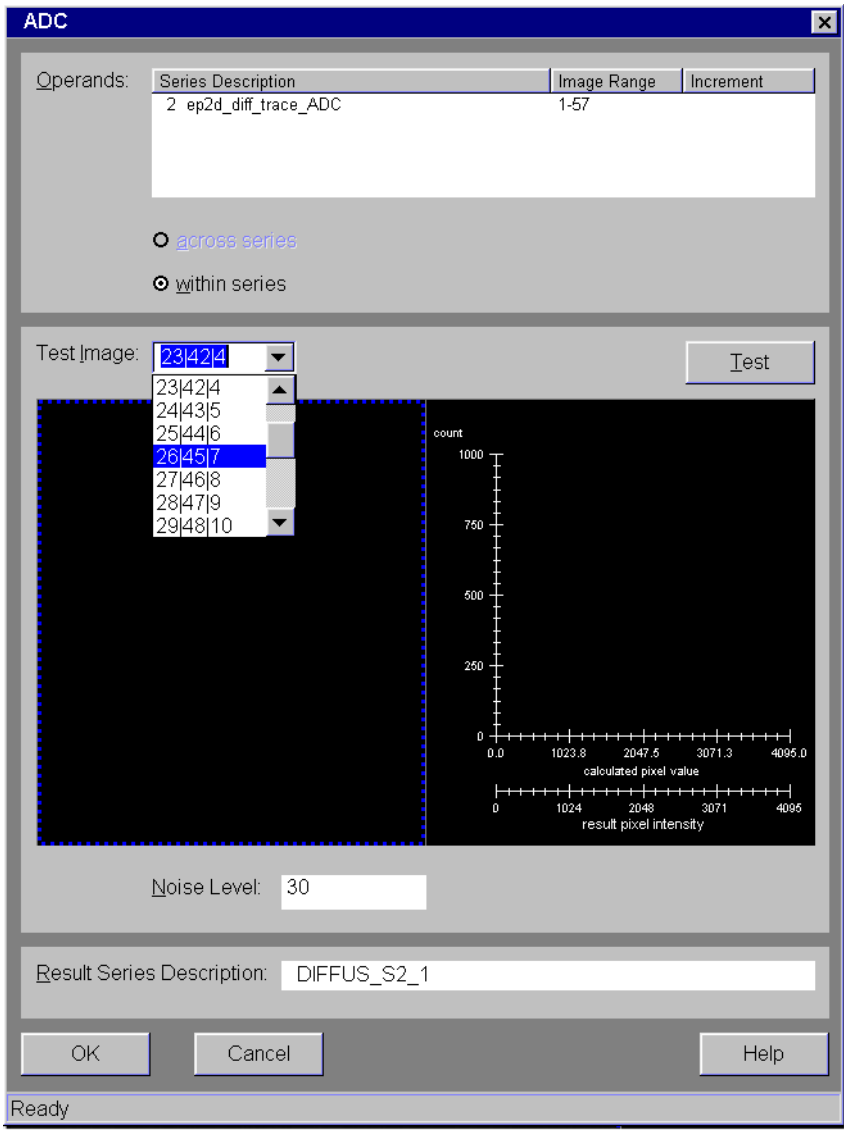
✧ Select **Evaluation > Dynamic Analysis > ADC**.

Or



✧ Click the **Diffusion Coefficient** icon on the **Viewing** task card /**Evaluation** subtask card.

The **ADC** dialog box opens.



Mode

The **within series** (one series) or **across series** (multiple series) option is already selected, depending on whether you have loaded one or more than one series into the **ADC** dialog window.

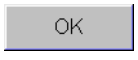
➪ Series have to contain at least two images before you can perform evaluation **within a series**.

❏ If you have selected **within series**, the images of the series are grouped together to form groups with the same slice position. An image with b value = 0 is assigned to all groups. All images of a group must have a different b value (diffusion weighting). A result image is calculated for each group.

❏ If **across series** is selected, all slice positions are expected to have the same b value in each series. A result image is calculated for slice position. In this case, it is not possible to take different diffusion directions into account.

Start evaluation

✧ If you do not want to use a generated name for the **Result series**, enter a name for the results series now.



✧ Click **OK** to start calculation.

The grayscale values correspond to the diffusion coefficient at this point.

T-test evaluation

This special method is used to evaluate examinations performed with functional neuro imaging. These examinations usually consist of a native series (no functional brain activity) and stimulated series (functional brain activity). With the t-test, you can sort the series according to stimulated and non-stimulated series and generate differential images of the mean values. The differential images display only the active areas of the brain.

Selecting images

✧ Select a series in the **Patient Browser**.

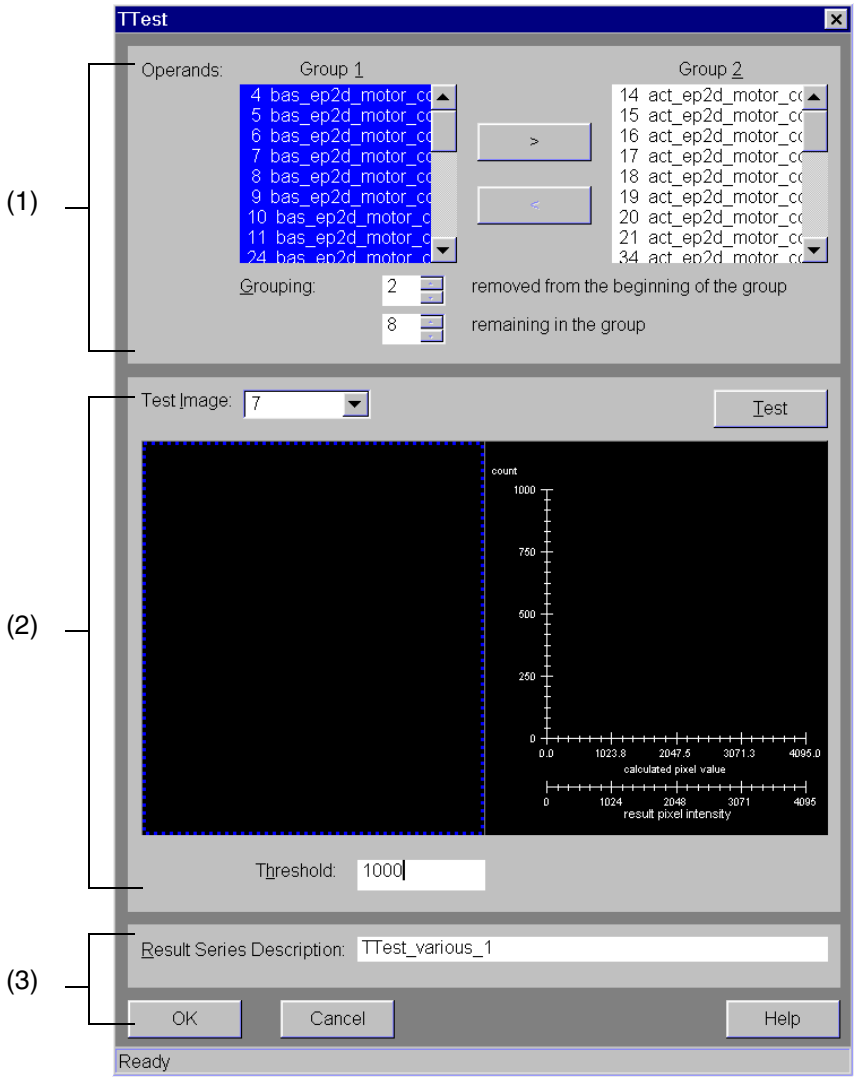
You require the same number of stimulated as non-stimulated series.

✧ Select **Evaluation > Dynamic Analysis > TTest...**.

➪ Always start **t-test** evaluation from the **Patient Browser** and not from the **Viewing** task card.

The **TTest** dialog box opens.

Wait until all the series are displayed under **Group 1**.



(1) Grouping series
(2) Generating a test image
(3) Naming a result series and starting calculation

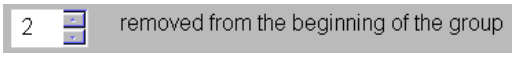
Grouping Series

Grouping of series is explained using the following example of a typical BOLD examination with block paradigms:

The paradigm consists of 10 stimulated and 10 non-stimulated series. The procedure is repeated five times.

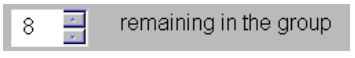
All series initially appear in the **Group 1** list.

You can exclude any series from the evaluation that was acquired at the beginning of the activity or during relaxation, because they only show the time required to reach a steady state (deoxygenation/oxygenation of blood).



✧ Enter **2** in the top spin box to exclude the first two series from evaluation.

You can also define how many series will remain in the groups (**Group 1** - **Group 2**).



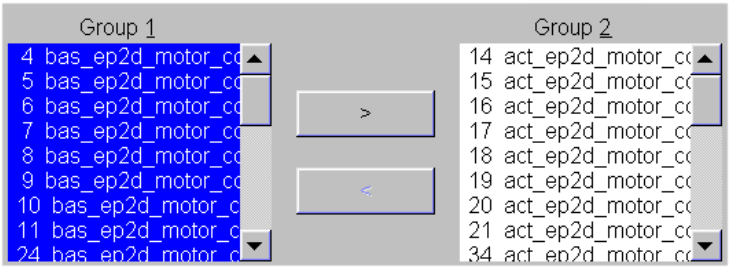
✧ Enter **8** in the bottom spin box.

➪ The contents of the spin boxes are interdependent and always add up to the number of series: **2** + **8** = **10**

✧ Select *all* series under **Group 1**.

✧ Click the **>** button to group the series in **Group 1** and **Group 2**.

After a few seconds the "act" series are moved to the **Group 2** list, the "bas" series remain in the **Group 1** list.

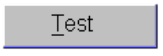


✧ Check the series. Each of the lists should contain the same number of stimulated and non-stimulated series.

Performing the t-Test

The result images show the difference between the mean values of the stimulated and non-stimulated series. The unit of grayscales of these images results from the standard deviation of these mean values. The resulting t-test values are compared with a threshold value. The values below the threshold value appear black in the image. The threshold value is set to 0 by default.

Generating a test image



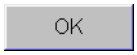


- ✧ Click the **Test** button to reconstruct an image in the test area.
- ✧ Check whether the test image meets your requirements.
- ✧ If it does not, change the threshold value and generate a test image again. The threshold value is expressed in pixels.

Start evaluation



✧ If you do not want to use a generated name for the **result series**, enter a name for the result series now.



✧ Click **OK** to reconstruct the entire series.

Because the t-test images only show the functionally active areas of the brain, you can no longer view any anatomical details.

✧ Overlay these images with images that show the anatomy in question, for example, ep2d.
→ Page D.1–26, *Adding images*

NOTE

If you superimpose t-test images on non-EPI images, compare these images with the superimposed EPI images for safety reasons. Image distortion may occur with EPI scans.

Standard deviation

The standard deviation describes the average deviation of the values from the mean value. This function visualizes changes in images.
The greater the standard deviation, the greater the variance of the grayscale values.

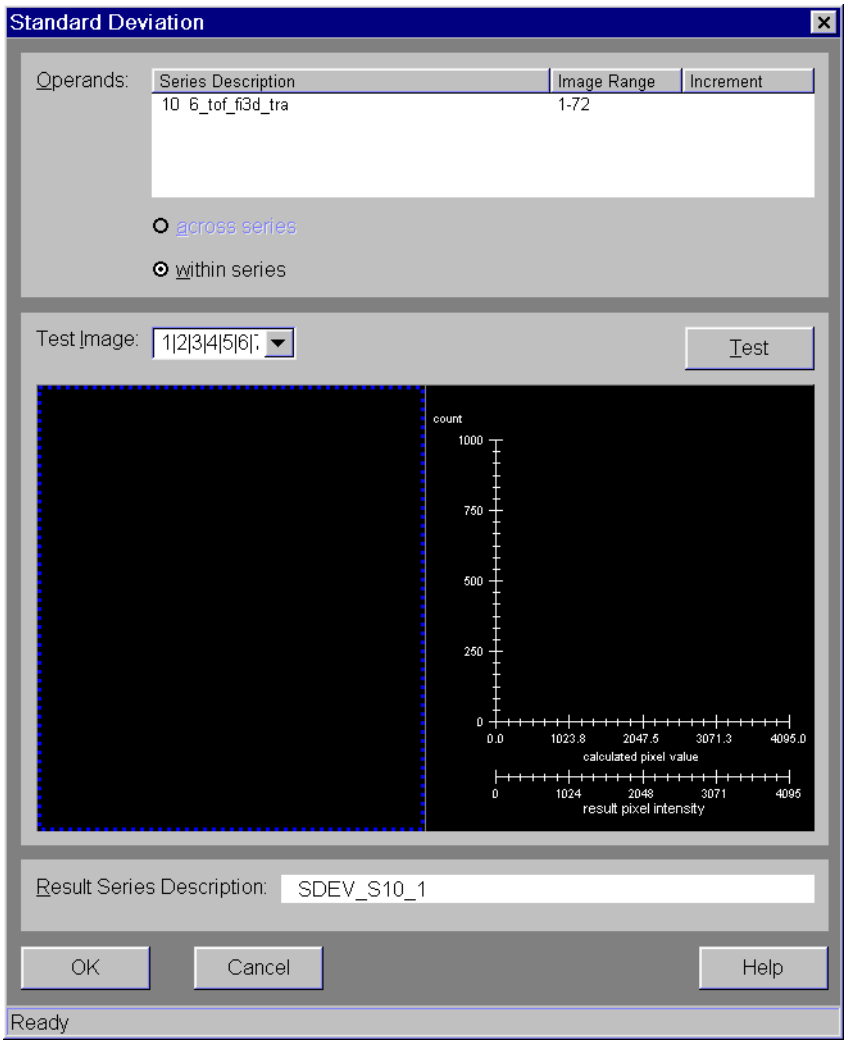
You can calculate the standard deviation within a series or across series.

Selecting images

✧ Select a series in the **Patient Browser** or on the **Viewing** task card.

✧ Select **Evaluation > Dynamic Analysis > Standard Deviation...**.

The **Standard Deviation** dialog box opens.



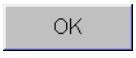
Mode

The **within series** (one series) or **across series** (multiple series) option is already selected, depending on whether you have loaded one or more series into the **Standard Deviation** dialog window.

➪ Series must contain at least two images before you can perform evaluation **within a series**.

Start evaluation

✧ If you do not want to use a generated name for the **Result series**, enter a name for the results series now.



✧ Click **OK** to start calculation.

The result is an image (within series) or a series of images (across series). The grayscales of the images correspond to the standard deviations.

Calculating T1 images

T1-weighted images are suitable for displaying anatomical structures. The system provides you with two ways of calculating T1-weighted images:

- ❏ For the inversion recovery method, you require two images with different inversion times TI. However, the repetition time TR and the echo time TE are the same.
- ❏ For the saturation recovery method, you require two images with a different repetition time TR yet with the same TE.

The result will be a T1 and a T2-weighted image.

Selecting images

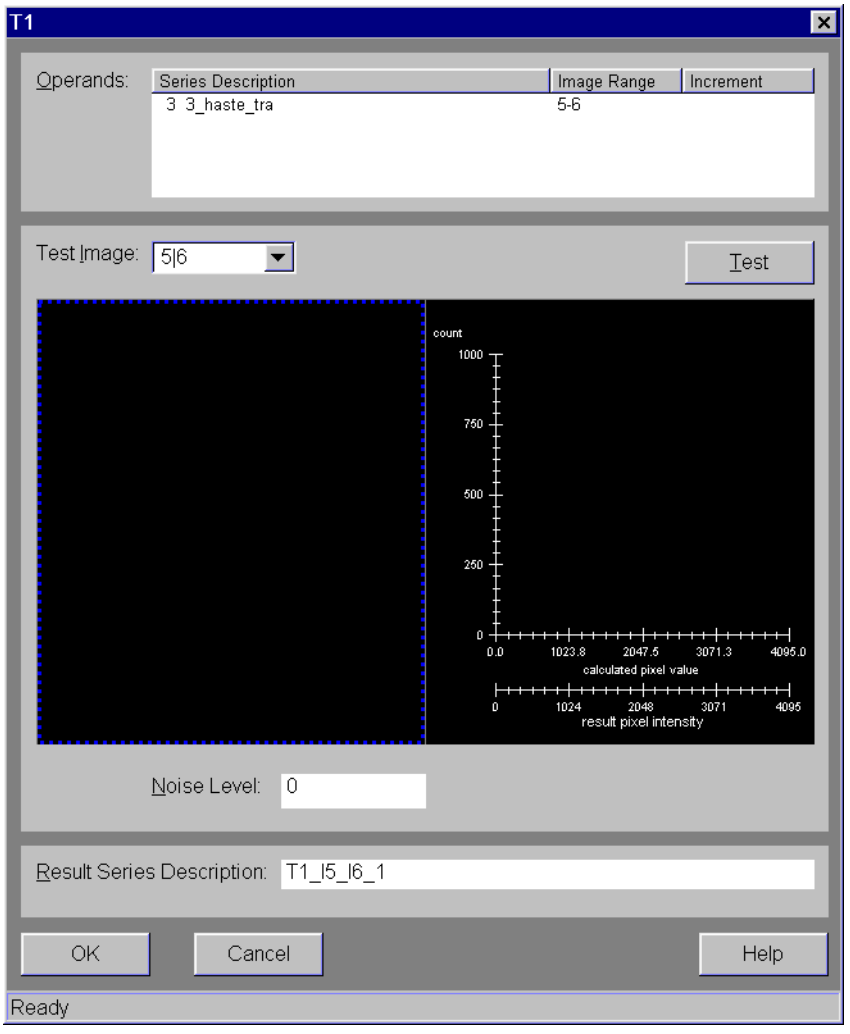
- ✧ Select two images in the **Patient Browser** or on the **Viewing** task card.
- ✧ Select **Evaluation > Dynamic Analysis > T1...**.

Or



- ✧ Click the **T1** button on the **Viewing** task card /**Evaluation** subtask card.

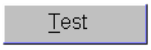
The **T1** dialog box opens.



Generating a test image



✧ First enter a noise level



✧ Click the **Test** button to generate a test image.

✧ Check whether the test image meets your requirements.

✧ Change the noise level, if necessary.

Start evaluation

✧ If you do not want to use a generated name for the **Result series**, enter a name for the results series now.



✧ Click **OK** to reconstruct the images.

The result is two images.

Calculating T2 Images

T2 images are suitable for showing pathological lesions in tissue.

To calculate T2-weighted images, you require images with the same repetition time TR, however a different echo time TE generated with multi-echo sequences. These images must have the same slice position. The multi-echo protocol is located under **head > add_on** in the **Exam Explorer**.

The result will be a T2- and a T1-weighted image.

Selecting images

✧ Select the images or the series in the **Patient Browser** or on the **Viewing** task card.

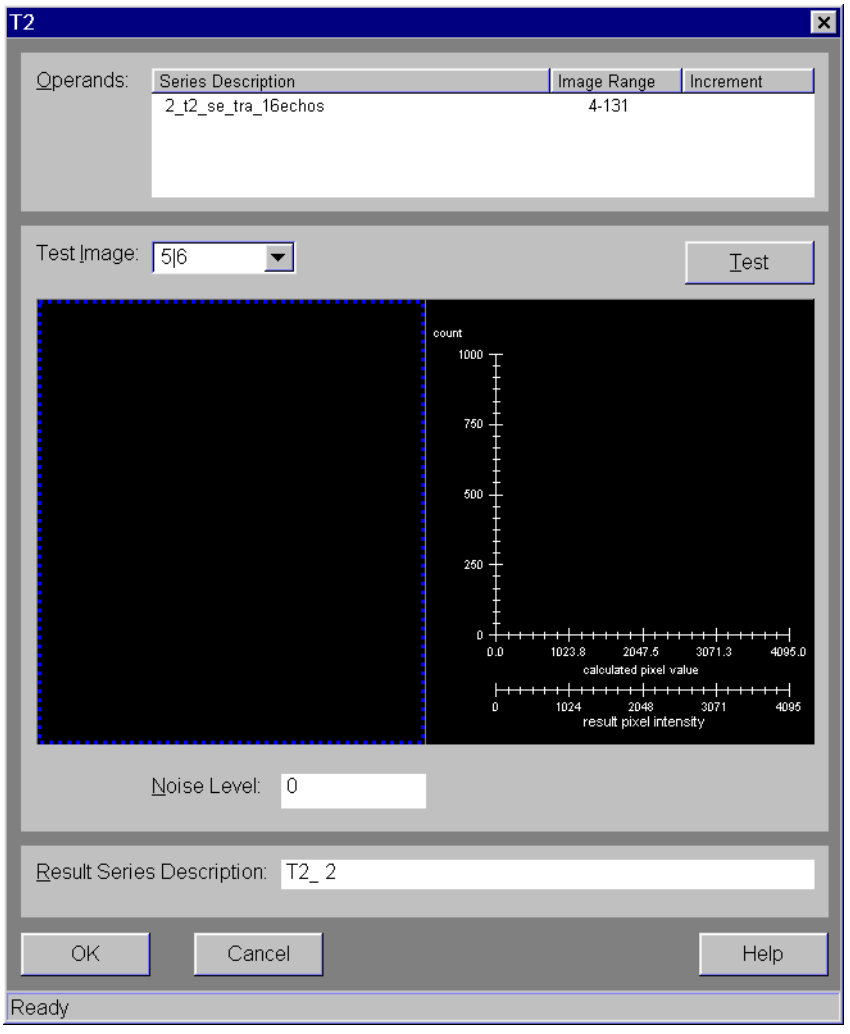
✧ Select **Evaluation > Dynamic Analysis > T2...**.

Or



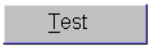
✧ Click the **T2** icon on the **Viewing** task card/**Evaluation** subtask card.

The **T2** dialog box opens.



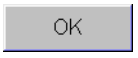
Generating a test image





- ✧ Select a test image.
- ✧ First enter a noise level.
- ✧ Click the **Test** button to generate a test image.
- ✧ Check whether the test image meets your requirements.
- ✧ Change the noise level, if necessary.

Start evaluation



- ✧ If you do not want to use a generated name for the **Result series**, enter a name for the results series now.
- ✧ Click **OK** to reconstruct the images.

The result is two images.

Time-to-peak evaluation

Time to peak evaluation shows the time up to maximum contrast agent enhancement.

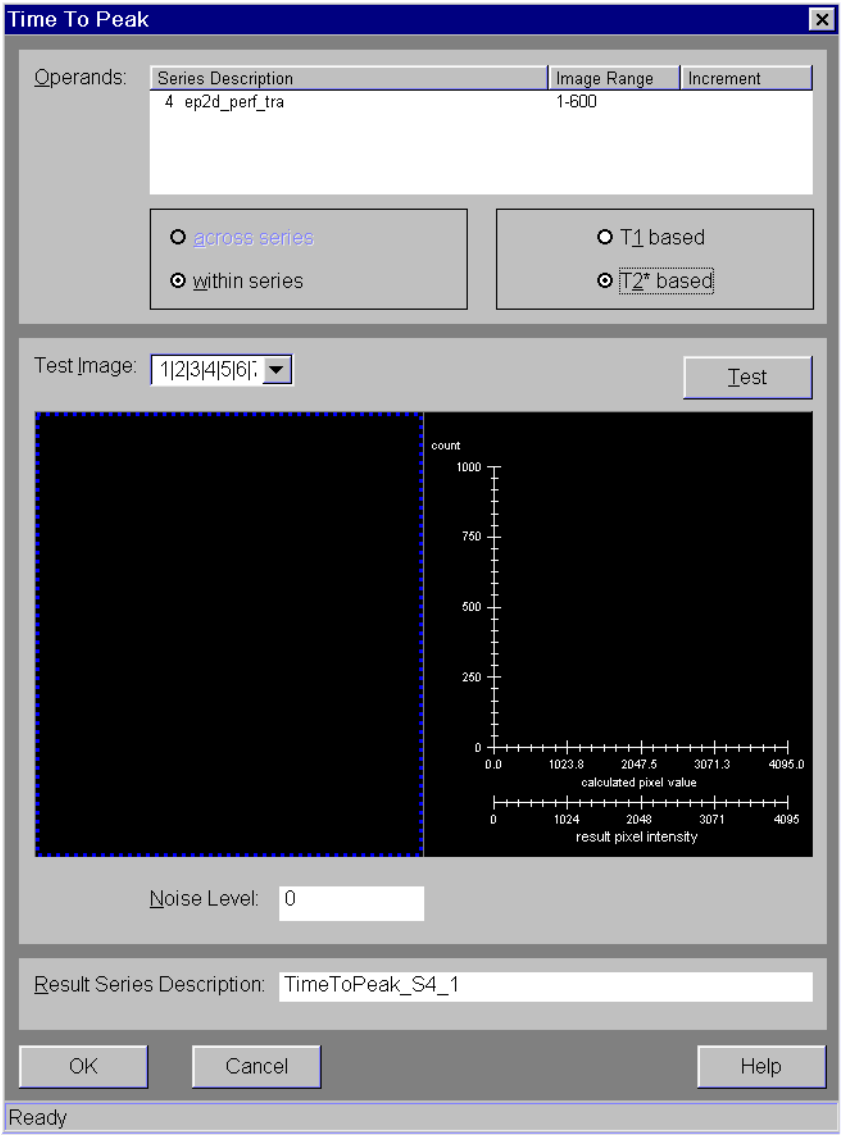
You can either calculate a grayscale value minimum based on T2-weighted EPI images or a grayscale value maximum based on T1-weighted images.

Selecting images

✧ Select the images or the series in the **Patient Browser** or on the **Viewing** task card.

✧ Select **Evaluation > Dynamic Analysis > Time To Peak...**.

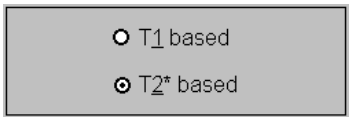
The **Time To Peak** dialog box opens.



Mode

The **within series** (one series) or **across series** (several series) option is already selected, depending on whether you have loaded one or more series into the **Time To Peak** dialog box.

Selecting the evaluation mode



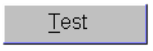
✧ Select whether you want to work on the basis of T1 or on the basis of T2-weighted images (EPI).

Generating a test image

✧ Select a test image.



✧ First enter a noise level

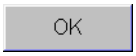


✧ Click the **Test** button to generate a test image.

✧ Check whether the test image meets your requirements.

✧ Change the noise level, if necessary.

Start evaluation



✧ If you do not want to use a generated name for the **Result series**, enter a name for the results series now.

✧ Click **OK** to reconstruct the images.

The result is an image (one slice position) or a series of images (various slice positions). The gray-scale values on the images correspond to the uptake times starting with the first image.

The *later* tissue is enriched with contrast agent, the *brighter* it appears in the image.

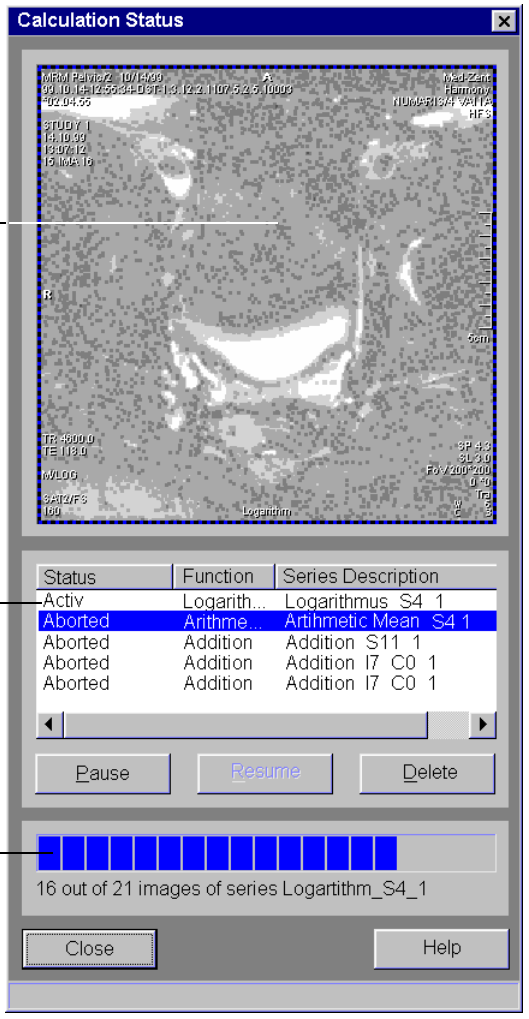
Tracing the progress of evaluation

If you are evaluating a large number of series or very large series, you can trace the progress of evaluation, and pause, resume, or cancel evaluation.



✧ Click the icon for dynamic analysis on the status bar.

The **Calculation Status** dialog box opens.



(1) Image area
(2) Status display of the evaluation jobs
(3) Progress indicator

Status display

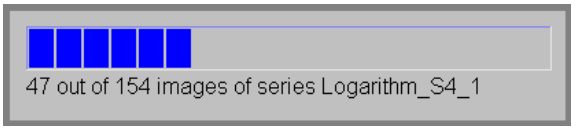
The evaluation jobs can have the following processing statuses:

- **Active**, the job is being processed
- **Paused**, the job has been interrupted
- **Aborted**, the job has been canceled
- **Waiting**, the job is still waiting for evaluation

⇨ Jobs with the status "Aborted" have been terminated by the system because of some calculation error.

Progress indicator

The progress indicator shows the progress of the evaluation in progress. It does not show the status of the selected job in the list.



NOTE

If there is a change of operators in the status dialog during evaluation and the new operator has no access to the data of the image being calculated, the data will be hidden.

The series name is replaced by the name of the user who generated the image.

The new user can stop or resume evaluation but not delete the job.

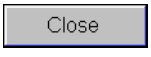
Starting the next job

Once a job has been processed, the images will be displayed on the **Viewing** task card.

The next job with the "Waiting" status (top of the list) is started automatically.

Closing the dialog box

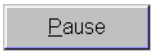
To close the dialog box:



✧ Click the **Close** button.

Pausing evaluation

You can pause evaluation at any time, for example, to view an evaluated image and to check whether the evaluation meets your requirements.



✧ Click the **Pause** button to pause evaluation.

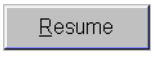
Calculation of the current image will be completed and the image will be displayed in the image area.

The **Resume** button is activated, and the status of the evaluation set to "Paused".

If the list contains a job with the "Waiting" status, this job will be started automatically.

Resuming evaluation

To resume evaluation:



✧ Click the **Resume** button.

If you have activated a further job, this job will go into the queue.

Cancelling and Deleting the Evaluation

You can stop evaluation from the joblist, for example, if you find that the evaluation does not meet your requirements.

However, you cannot delete the active evaluation. You must stop it first.

✧ Select the active evaluation from the list.

✧ Click the **Pause** button to pause evaluation.



✧ Click the **Delete** button to delete the selected jobs from the list.

➪ Jobs with "Aborted", "Waiting", or "Paused" status can be deleted directly.

The canceled job is then deleted from the job list.

➪ The images already calculated are stored and may be displayed on the **Viewing** task card.

CHAPTER D.2

Evaluating Images with Mean Curve

The **Mean Curve** task card allows for statistical evaluation of signal changes as a function of time and place. This evaluation is frequently performed for perfusion measurements, flow measurements, or angiography measurements.

Both acquired series and postprocessing result series, e.g. MPR/MIP or Dynamic Analysis, can be evaluated. However, this does not apply to radial series.

For example, you may want to use Mean Curve to examine how the mean grayscale value in an image section (**Region of Interest, ROI**) varies as a function of the slice position, trigger time, or image number. The result of a **Mean Curve** evaluation appears as a curve that plots the mean grayscale value against a selectable second variable (x axis).

You can evaluate the dependency of the grayscale values on various values *within* a series or *across* the images of more than one series. Before evaluation, define the sort criteria for images within the series or across series.

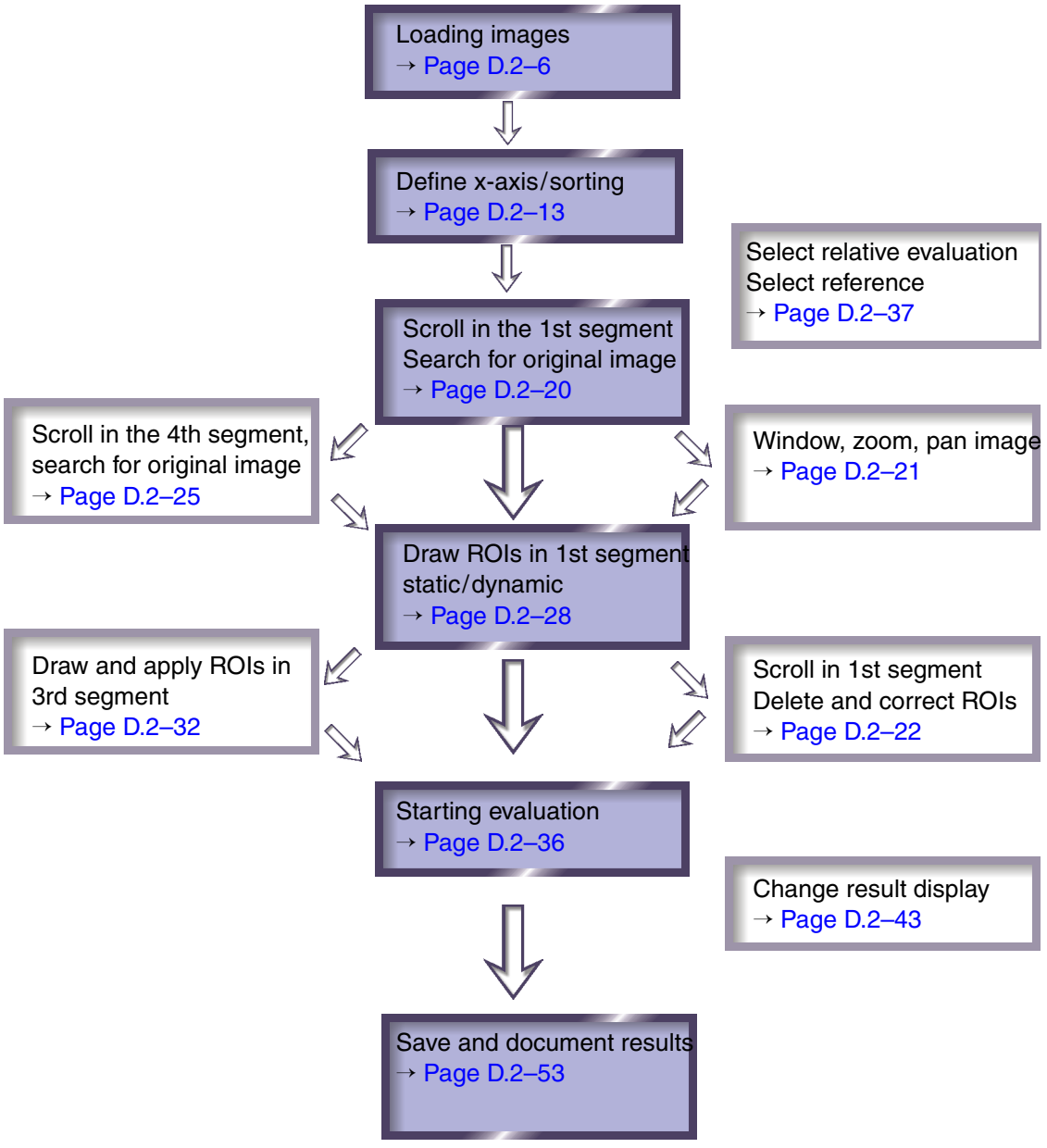
You are able to scroll through the loaded images and look for an initial image suitable for drawing ROIs. If necessary, you may load additional series with a different image orientation to locate the image with the anatomy to be evaluated.

In some cases, it is easier to draw the ROIs in subtraction images and then to apply them to the images to be evaluated.

As you scroll, the ROIs drawn in one image will be applied to the loaded images. You can select whether you want the ROIs to be applied unchanged (static ROI) or changed in each image (dynamic ROI).

You may select a reference image or a reference series if you want to evaluate the change in grayscale values with respect to a reference.

The evaluation results will be displayed as curves or tables. You can scale the curves, insert comments, save, as well as film the results.

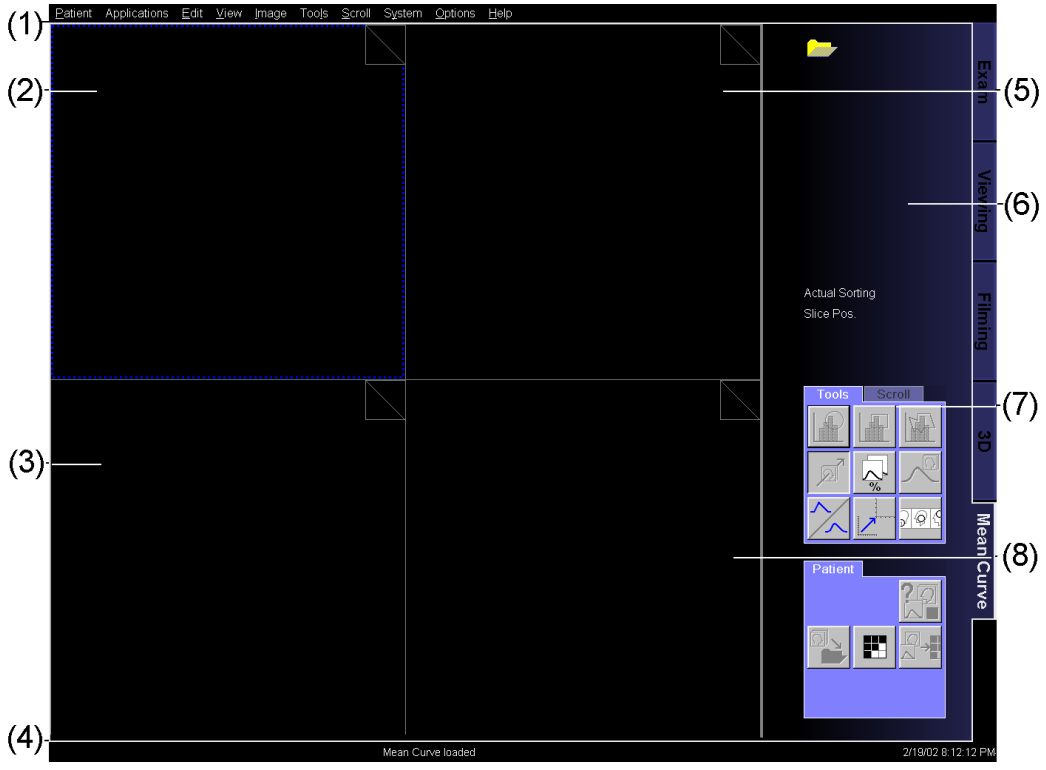

Loading images
→ Page D.2–6
Define x-axis/sorting
→ Page D.2–13
Select relative evaluation
Select reference
→ Page D.2–37
Scroll in the 1st segment
Search for original image
→ Page D.2–20
Scroll in the 4th segment, search for original image
→ Page D.2–25
Window, zoom, pan image
→ Page D.2–21
Draw ROIs in 1st segment static/dynamic
→ Page D.2–28
Draw and apply ROIs in 3rd segment
→ Page D.2–32
Scroll in 1st segment
Delete and correct ROIs
→ Page D.2–22
Starting evaluation
→ Page D.2–36
Change result display
→ Page D.2–43
Save and document results
→ Page D.2–53

Starting Mean Curve

You can open the **Mean Curve** task card from any other task card or from the **Patient Browser**.

✧ Select **Applications > Mean Curve** from a task card or **Applications > Mean Curve** from the **Patient Browser**.

The **Mean Curve** task card opens and is initially empty.



(1) Menu bar
(2) First segment (evaluation segment)
(3) Third segment
(4) Status bar
(5) Second segment (result segment)
(6) Display of sort criteria
(7) Control area with subtask cards
(8) Fourth segment

Loading images

You can load images and series of a patient examination on the **Mean Curve** task card. It is not possible to load a complete examination or patient on the **Mean Curve** task card.

You may load images into the first, third, and fourth segments. The second segment is reserved for displaying the results.

NOTICE

For **Mean Curve** evaluation the user has to have full access rights to the patient data to be evaluated. You also require the data save privilege.

Please observe the information given in the Safety Standards book.

Loading images of the first segment

Select the images and series in the **Patient Browser** or on the **Viewing** task card and load them into the **Mean Curve** task card.

Requirements

The images in the first segment must meet the following criteria prior to mean curve evaluation.

- ❏ same matrix size
- ❏ same field of view (FoV)
- ❏ same orientation
- ❏ same series block and same table position
  → Page C.3–38, *Series block*

If images do not meet one of these criteria, the images will not be loaded into the task card.

The following criteria have to be met:

- ❏ same slice position
- ❏ same slice thickness

A dialog box is displayed if the images do not meet the criteria. You may then decide whether or not to continue loading the images.

Loading from the Patient Browser

You can load images and start the **Mean Curve** task card in one step.

✧ Open the **Patient Browser** and select one or more series.

✧ Select **Applications > Mean Curve**.

Once the **Mean Curve** task card has been opened and is in foreground:

✧ Open the **Patient Browser** and select one or more series.

✧ Select **Applications > Mean Curve**.

Or

✧ Drag and drop the selected series into the first segment.

Or

✧ Double-click the selected series.

Loading from the Viewer task card

The **Viewer** task card is in foreground. You can load images and start the **Mean Curve** task card in one step.

✧ Explicitly select images or series for the mean curve evaluation.

✧ Select **Applications > Mean Curve**.

The **Mean Curve** task card opens.

Displaying the loaded images

The images and series loaded are always displayed as an image stack.

❏ You will see the center image of the series in the first segment if you have loaded one series only.

❏ You will see the center image of the middle series in the first segment if you have loaded more than one series.

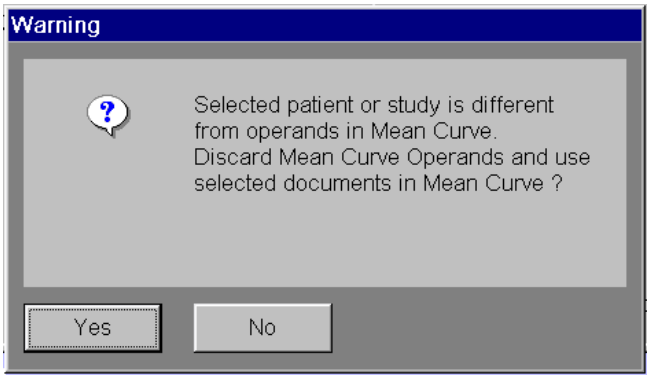
The images are initially sorted according to the preset sorting rules.
→ Page D.2–13, *Defining sorting*

Graphic objects, e.g. from a previous Mean Curve evaluation, will be deleted when loading the images.

Adding images

You may load additional images into the first segment at any time. All images in the first segment are sorted according to the preset sort.

A **Warning** box will be displayed if you select images or series from another examination or another patient and add them to **Mean Curve**.



You may load "new" images and remove "old" images from segments at any time.

✧ Simply click the **Yes** button.

You can stop loading new images.

✧ Simply click the **No** button.

Loading images into the third and fourth segments

The images in the third and fourth segment will *not* be taken into account in the actual evaluation. However, the images have to belong to the same patient and to the same examination as the images in the first segment.

➪ Images are always loaded into the third and fourth segment using *drag and drop*.

Requirements

Images in the fourth segment may have a different orientation from the images in the first segment. For example, you can load reference images of the exam or images showing the lesion in a different orientation into the fourth segment.
→ Page D.2–25, *Searching for an original image by scrolling through the fourth segment*

You may load, for example, the subtraction series or the MIP series of the examination into the third segment. If you want to copy ROIs from the third segment to the first segment, the images in the third segment must meet the same conditions as the images in the first segment.
→ Page D.2–32, *Drawing ROIs in the third segment*

✧ Open the **Patient Browser** and select the series.

✧ *Drag and drop* the selected series into the third or fourth segment.

Displaying the loaded images

The same display rules apply to the loaded images as in the first segment.

Exception:
You have already loaded images or series into the first segment and you are now in the process of loading another series into the third segment. The third segment shows *the* image with the same preset sort criteria as the current image in the first segment.

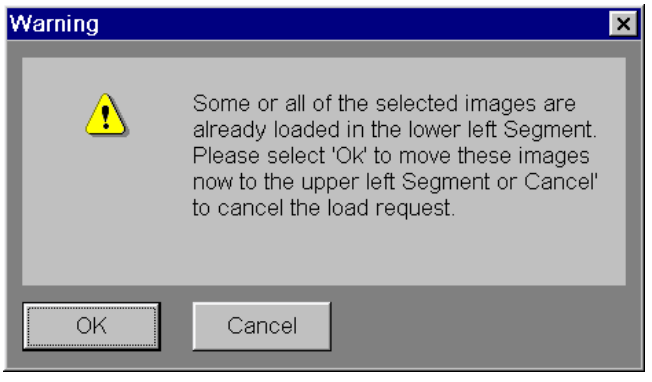
Moving images to another segment

You have loaded images into a segment of the **Mean Curve** task card and now want to move those images to another segment.

✧ Select the same images again in the **Patient Browser**.

✧ Drag the selected images to the mean curve segment.

The **Warning** message box appears.



✧ Click **OK**.

Defining sorting

When sorting loaded images, you may set the scrolling sequence in the first and third segments and define the x axis of the mean curve evaluation.

In the fourth segment, the images are always sorted by image number and series.

The difference between evaluation *within* a series and evaluation *across* the images of more than one series is as follows.

Evaluation within the series

The mode is automatically set to **Within** if you have loaded only *one* series into the first segment.



The **Within** button then appears pressed.

The sort order of the loaded images is defined by selecting the x axis.

Evaluation across series

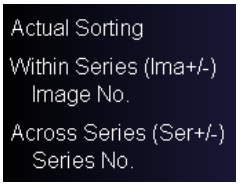
The mode will automatically be set to **Across** if you have loaded *multiple* series into the first segment.



The **Across** button then appears pressed.

You define the sort order of the loaded images *across* the series by selecting the x axis. The sort order *within* the loaded series is defined with a second sort criterion.

The images are initially ordered as defined by the preset sort:



- ❏ **Within: Sorted by slice position**
- ❏ **Across: Sorted by series number**

The current sort order is displayed in the control area.

Defining the x axis



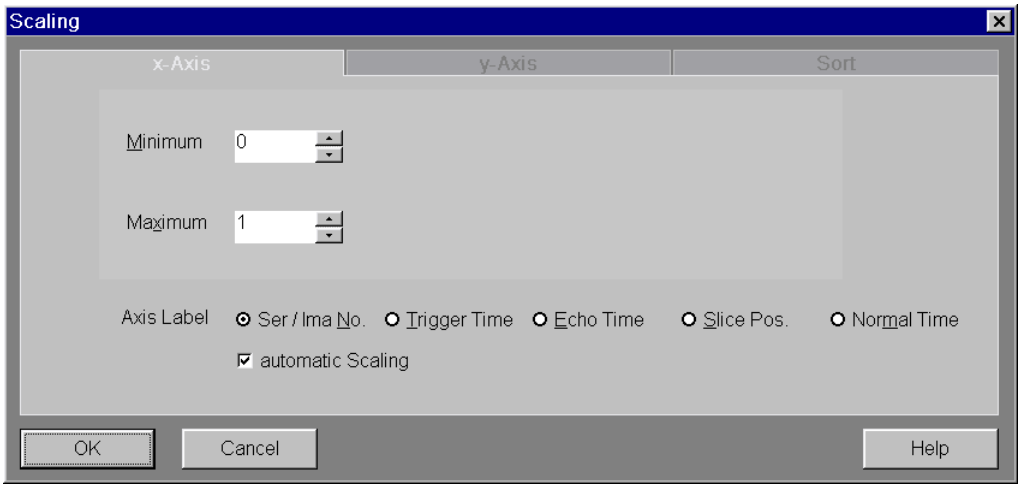
✧ Select **Tools > Scaling/Sorting**.

Or

✧ Click the **Scaling/Sorting** button in the control area of the **Mean Curve** card.

The **Scaling** dialog box is displayed.

✧ Move the **X-Axis** subtask card in foreground.



✧ Select one of the following parameters as the x axis by clicking on the appropriate option.

❏ **Ser / Ima No.**
Image and series number

❏ **Trigger delay**
Suitable for displaying physiologically triggered scans, e.g., cardiac series.

❏ **Echo time**
Suitable for displaying multi-echo sequences, e.g., multi-echo spin echo sequences.

❏ **Slice pos.** default

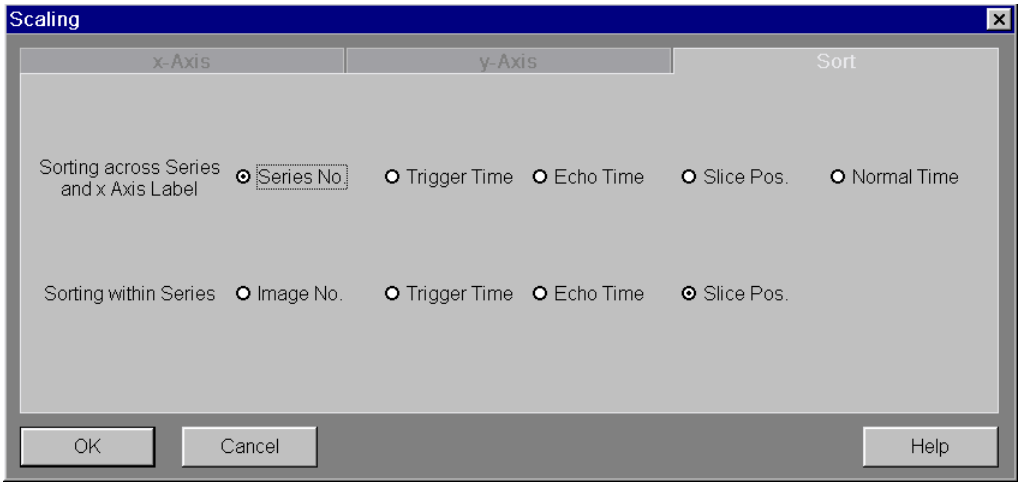
❏ **Normal time**
Excitation time, suitable for dynamic and motion studies
When evaluating **Within**, the **Normal time** of an image is the difference between the acquisition time of the image and the shortest acquisition time in the series.

Sorting in Across mode

The sort criteria for Mean Curve evaluation *across* the series is defined in the **Scaling** dialog box on the **Sorting** card.

✧ Select the **Sorting** subtask card in the **Scaling** dialog box.

The **Sort** card is displayed only if you are evaluating *across* series.



With **Sorting across series**, you define the parameters used as the x axis and the order used for evaluating corresponding images.

You may define the sort parameters used for images within a series (**Sorting within series**). Additionally, the images corresponding during the sort across series are determined (**evaluation across series**).

➪ The criteria for sorting across series and sorting within series have to be different.

✧ Choose an option for sorting within a series and one for across series.

✧ Click **OK**.

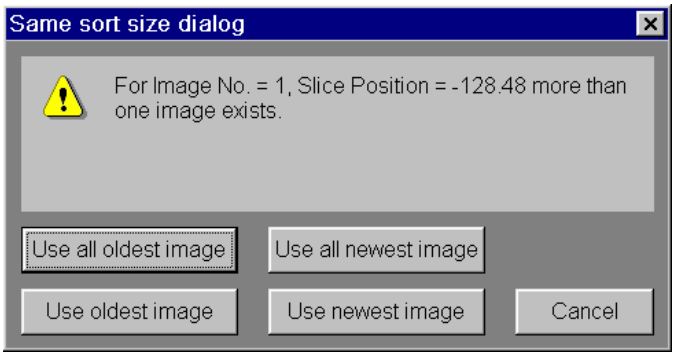
The sort criteria are applied and the **Scaling** dialog box closes.

Images with the same sort criterion

The sort order of images in the first segment is checked and updated every time images are loaded, deleted, or the sort criterion is switched.

The **Same sort size** dialog box will be displayed if more than one image has the same value for one or both sort criteria.

Example: Mode **Across**, x axis = normal.time



For *each* x value, you can decide whether the newest or oldest image will be used for evaluation.

✧ Click the **All newest** or **All oldest** button.

In general, the newest or oldest of *all* the images with the same sort criterion can be used for evaluation.

✧ Click the **Use all newest images** or **Use all oldest images** button.

You can undo the action for locating images with the same sort size.



✧ Just click **Cancel**.

Example:
You have loaded additional images into the first segment.
If you click **Cancel** in the **Same sort size** dialog box, the loaded images will be deleted again.

Searching for an original image for evaluation

You can scroll through the loaded images and series to look for a suitable image.

You can also load the reference images of the same examination into the fourth segment and scroll through them until you find the optimal original image for evaluation.

You may change the way the loaded images are displayed.

Modifying image display

You can use the following methods:

- ❏ Changing brightness and contrast (windowing)
- ❏ Zooming/panning
- ❏ Fit to segment size
- ❏ Inverting grayscale values

These actions are described in detail in the **Viewing** chapter.
→ *syngo* Operator Manual

NOTICE

During scrolling, the **Mean Curve** task card, unlike the **Viewer** task card, automatically transfers each change to *all* images of the respective segment.



✧ Select a method for changing the image display under **Image** in the main menu.

Or

✧ Place the mouse pointer on the first, third, or fourth segment and select a method for changing the image display from the context menu.

Scrolling within a series

There are several ways of scrolling image by image through a series.



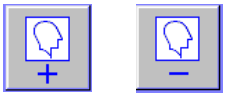
✧ For scrolling, use the dog ears in the top right-hand corner of the image segments.
→ *syngo* Operator Manual

Or



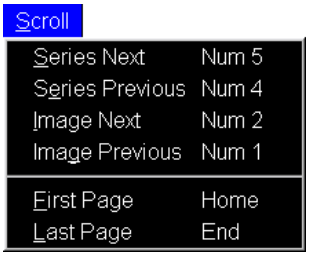
✧ Use the symbol keys on the symbol keypad for scrolling.
→ *syngo* Operator Manual

Or



✧ Click the **Next image** or **Previous image** button on the **Scroll** card in the control area.

Or



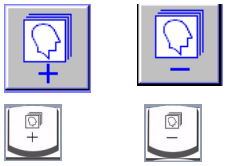
✧ Select **Scroll > Image Next** or **Scroll > Image Previous** from the main menu.

Images not used for evaluation because of the same sort criterion will not be displayed as you scroll.

Once you have loaded a series into the first as well as third segments and are scrolling through one of them, the other segment will look for and display the corresponding image (identical to *within* sort criterion).

Scrolling across series

There are two ways of scrolling across series in a segment.

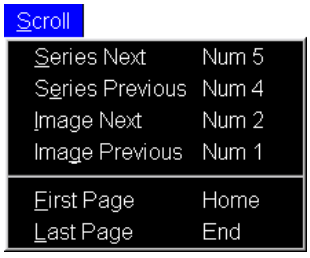


✧ Click the **Series+** or **Series-** buttons on the **Scroll** card.

Or

✧ Use the symbol keys on the symbol keypad for scrolling.
→ *syngo* Operator Manual

Or



✧ Select **Scroll > Series Next** or **Series Previous** from the main menu.

Images that have the same *within* criterion will be displayed as you scroll across series.

Example

If the preset sort applies, images with the same slice position will be displayed as you scroll across series.

A series is placed last in the scrolling order and an empty segment is displayed along with a message, if an image with the corresponding *within* sort criterion is missing in a series. This series will then be ignored during evaluation.

➪ Images of the series not used for evaluation because of the same sort criterion will not be displayed as you scroll.

Searching for an original image by scrolling through the fourth segment

In some cases it is simpler to look for the most suitable image in the first segment using the reference images.

Mean Curve therefore provides a way of loading the reference images of the images loaded in the first segment into the fourth segment.
→ Page D.2–11, *Requirements*

In the reference images loaded, shift the cut line that represents the position of the current image in the first segment.

✧ Load the reference images of the examination into the fourth segment.
→ Page D.2–7, *Requirements*

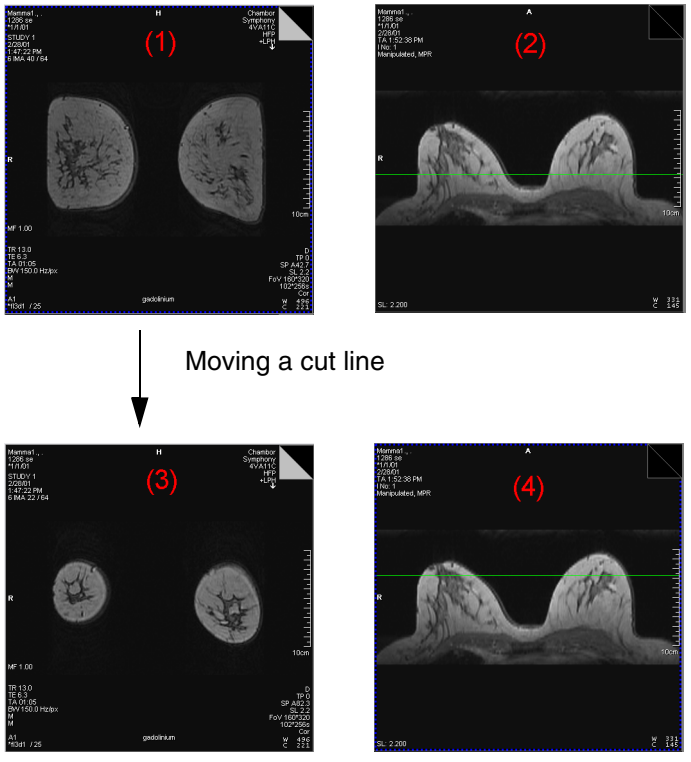
✧ Look for the reference image that best represents the anatomy to be evaluated.

✧ Click the reference image with the left mouse button. Hold the mouse button down and drag the cut line to the anatomy to be evaluated.

✧ Release the mouse button.

The first segment displays the image whose position best matches the position of the cut line.

➪ Scroll through the stack and look for another reference image if the fourth segment does not show a cut line in the reference image.



(1) Current image in the first segment
(2) Reference image in the fourth segment
(3) Original image in the first segment after moving the cut line
(4) Reference image in the fourth segment after moving the cut line

Drawing in ROIs (regions of interest)

You can draw ROIs after you have optimized image display and located the image for evaluation in the first segment. ROIs delineate the part of the image that will be evaluated.

You can draw ROIs in the first and third segment.

➪ The **Mean Curve** task card can manage up to four ROIs simultaneously per evaluation.

Drawing ROIs in the first segment

The following tools are available on the **Mean Curve** task card for drawing ROIs:



❏ Rectangle



❏ Circle



❏ Freehand ROI

Drawing and editing ROIs is described in detail in the **Viewing** chapter.
→ *syngo* Operator Manual

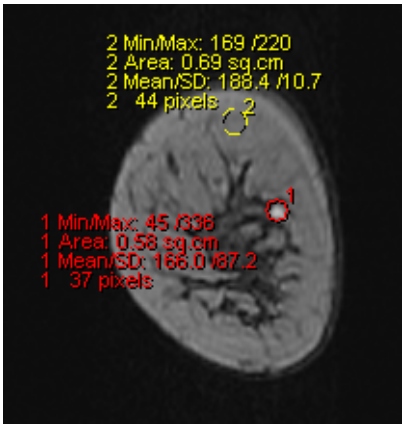
NOTE

Ensure that the ROIs do *not* extend beyond the edge of the image. If they do, you will not be able to perform calculations.

If the ROI extends over the edge of the image, '"**???**'" appears instead of numbers after Min/Max, Area, Mean/SD.

✧ Draw one or more ROIs in the original image in the first segment.

The ROIs in the first segment have different colors and line styles. Each ROI is also identified by a number.



Static or dynamic transfer of the ROIs to other images

You may select whether the ROIs drawn in the image will apply to all other images in the first segment (**Static ROI**) or whether you want to adjust the ROIs for each image (**Dynamic ROI**).

✧ Select **Tools > Static ROI** or **Dynamic ROI** from the main menu.



✧ Click the **Dynamic ROI** button in the control area on the **Tools** card.

Static ROI is the active default setting when you start **Mean Curve**.

Scrolling with static ROIs

As you scroll, the ROIs drawn in the initial image will be applied to *all* other images in the first segment.

If ROIs had already been defined in some images, they will be overwritten by the static ROIs.

Scrolling with dynamic ROIs

The ROIs drawn in the initial image will be copied to the next, current image as you scroll. Existing ROIs will not be overwritten.

At this point, you can check how well ROIs match the anatomy to be evaluated and change the ROIs, if necessary.

Example:
You have drawn four ROIs in the initial image. The next image already contains regions 1 and 2. As you scroll, the image contains only regions 3 and 4 from the initial image.

Adjust region 2 to match the anatomy to be evaluated in the next image. The next image does not include any ROIs. As you continue scrolling, this image will contain all four ROIs from the previous image and not from the initial image.

Deleting ROIs

✧ Select the ROI that you want to delete.

✧ Select **Edit > Delete Graphics** from the main menu or **Delete** from the context menu.

Or

✧ Press the **Del** key on your keyboard.

The selected ROIs are deleted from all images.

Filling in missing ROIs

All images required for the current evaluation must have the same number of ROIs.

Mean Curve adds missing ROIs automatically by copying them from the nearest images.

Example:
If you have loaded additional images into the first segment after drawing the ROIs, the ROIs of the respective previous images will be copied.

Drawing ROIs in the third segment

In some cases, it is easier to position the ROIs in the images of the third segment.

For this reason, **Mean Curve** allows you to load additional series, e.g. subtraction series or the MIP series of the examination into the third segment. These images frequently allow for easier anatomic evaluations and a more accurate drawing of ROIs . Subsequently, you apply the ROIs to the images in the first segment.

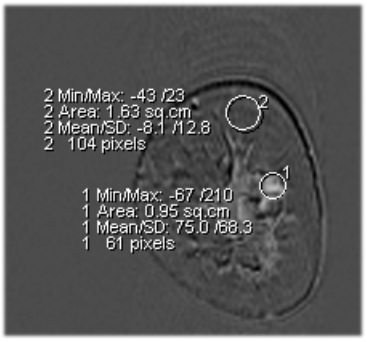
✧ Load suitable images into the third segment.
→ Page D.2–11, *Requirements*

The third segment shows *the* image that has the same sort criterion (*within*) as the current image in the first segment.

✧ Select the initial image for drawing in the third segment.

✧ Draw the ROIs in the third segment

Unlike the first segment, all ROIs are displayed in white and annotated.



Transferring ROIs to the first segment

You may *individually* select and apply the ROIs in the third segment or apply all ROIs *together* to the first segment.

✧ Explicitly select an ROI in the third segment.

Or

✧ Put the input focus on the third segment and select **Edit > Select All Graphics** from the main menu or **Select All Graphics** from the context menu.

The ROIs in the third segment are then selected.

✧ Select **Edit > Apply ROI** from the main menu or **Apply ROI** from the context menu.

The ROIs will be applied to the first segment.

If the slice positions of the current images in the first and third segment do not match, a message box appears.

✧ Click **Yes** in the message box to transfer the ROIs.

✧ Click **No** in the message box to cancel transfer.

NOTICE

Please ensure that you do not exceed the maximum number of four ROIs.

If two ROIs have already been defined in the first segment, you can transfer up to two ROIs from the third segment to the first segment.

NOTICE

If the matrix size of the images in the third segment differs from that in the first segment, you *are not able* transfer ROIs from the third segment to the first segment.

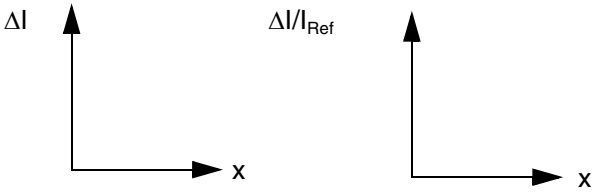
An error message is displayed.

Setting and starting the evaluation

Before you start the evaluation, define whether you want to perform an absolute or relative evaluation.

The signal intensity is assigned to the X-axis during absolute evaluation.

Relative evaluation generates two curves for each ROI. The difference between the signal intensity and a reference value as well as the ratio of the difference to the reference value are applied to the x axis.



- ❏ Select a single image as the reference if you are evaluating within a series.
- ❏ Select a whole series as the reference if you are evaluating across series.

Set relative evaluation

Absolute evaluation is the default setting when you start **Mean Curve**.

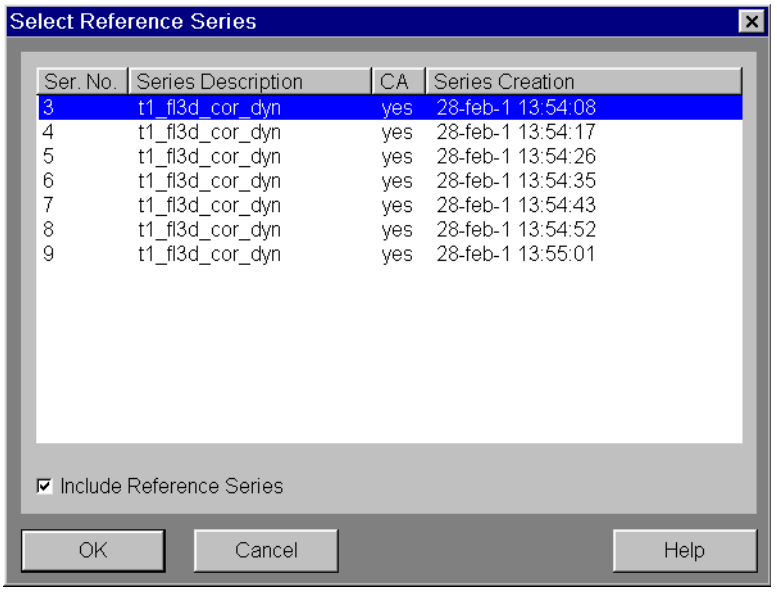
✧ Select the **Tools > Evaluation mode: relative**.

Or



✧ Click this button in the control area of the **Tools** card.

The **Select Reference Image** (*within* mode) or **Select Reference Series** (*across* mode) dialog box opens.



You can also call up this dialog box explicitly.

✧ Select **Tools > Select Reference Image/Series**.

The list contains the images or series loaded in the first segment. These are sorted according to the *within* or *across* sorting criterion.

The oldest image or the oldest series is preselected as the reference.

Select a reference image or reference series from this list. You will also set the reference image or the reference series to be used during evaluation

For example, for a contrast agent series you are able to select the series without contrast agent as a reference series.

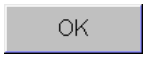
✧ Select a reference image or a reference series.



✧ Activate or deactivate the **Include Reference Series** option.

❏ Activate this option when evaluating the inflow of contrast agent in a mammo series.

❏ Deactivate this option when evaluating cardiac images dependent on the trigger time.



✧ Click **OK**.

The dialog box closes.

➪ The selected reference is used for all subsequent evaluations. As soon as you switch evaluation modes (*within* or *across*), the selected series is no longer valid.

Starting evaluation



✧ Click the **Start Evaluation** button in the control area on the **Mean Curve** card.

Or

✧ Select **Tools > Start Evaluation**.

The results of mean curve evaluation will be displayed as a curve and table in the top right segment (result segment).

Automatic recalculation

The results will be rejected and cleared from the second segment as soon as you add new images, delete images, manipulate ROIs, or change the sort criterion.

Go to the menu and



✧ select the **Auto Recalculation** option under **Tools**.

TIP

You should deactivate the **Auto Recalculation** option if you have loaded a large number of series into **Mean Curve**.

If not, you will find that recalculation is too time consuming.

➪ If you switch from **Dynamic ROI** to **Static ROI** after a **Mean Curve** evaluation, the evaluation is recalculated.

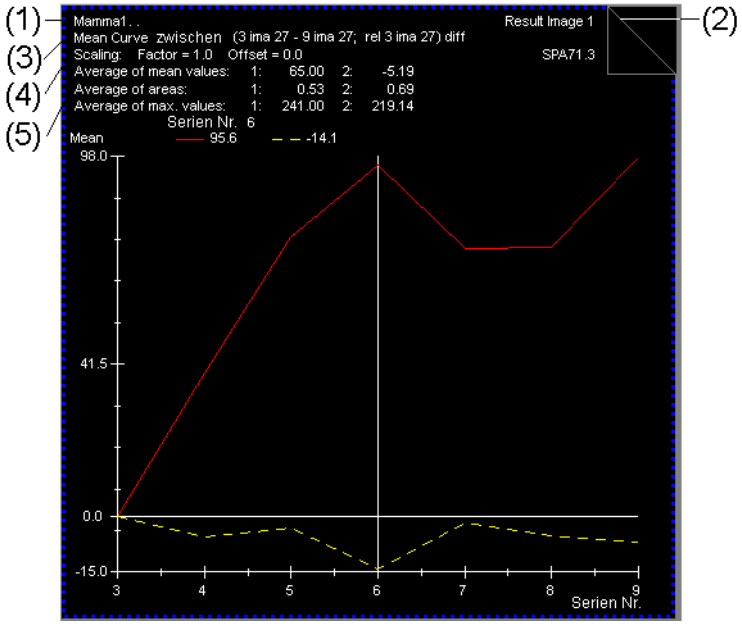
Scroll in the second segment

When you scroll in the second segment, the graphics are displayed first and then the tables.

If you scroll to a table in the second segment, this table is displayed first after re-evaluation.

Result display in the diagram

The diagram shows a curve for each ROI. Using the color and line style, you can assign the ROIs in the first segment to the corresponding curves in the diagram.

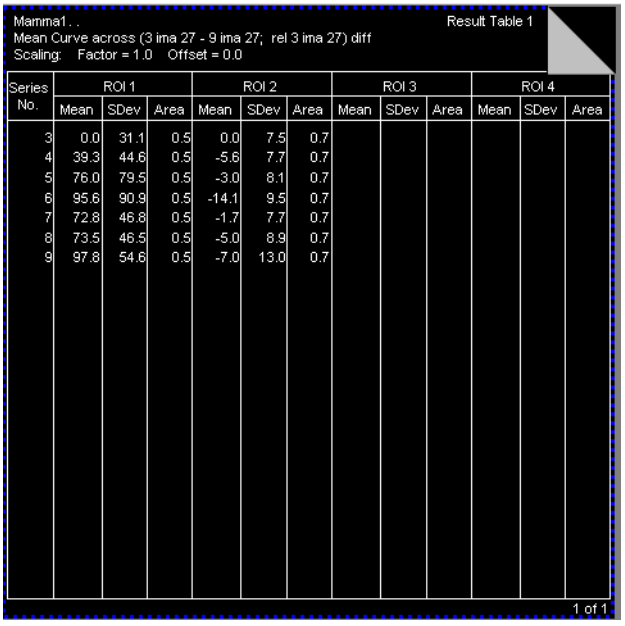


(1) Patient name
(2) Number of the table or diagram
(3) Comment line (can be changed)
(4) Information about scaling
(5) Mean values or the maximum values (for absolute evaluation only)

Result display in the table

A table is generated for each diagram.

✧ Scroll in through result segment until you come across a table.



Mamma1. .
Result Table 1
Mean Curve across (3 ima 27 - 9 ima 27; rel 3 ima 27) diff
Scaling: Factor = 1.0 Offset = 0.0

Series No.	ROI 1			ROI 2			ROI 3			ROI 4		
	Mean	SDev	Area	Mean	SDev	Area	Mean	SDev	Area	Mean	SDev	Area
3	0.0	31.1	0.5	0.0	7.5	0.7						
4	39.3	44.6	0.5	-5.6	7.7	0.7						
5	76.0	79.5	0.5	-3.0	8.1	0.7						
6	95.6	90.9	0.5	-14.1	9.5	0.7						
7	72.8	46.8	0.5	-1.7	7.7	0.7						
8	73.5	46.5	0.5	-5.0	8.9	0.7						
9	97.8	54.6	0.5	-7.0	13.0	0.7						

1 of 1

The far left column lists the values on the x axis, e.g. the serial numbers.

Next to that you will find the mean value, standard deviation, and area content of each ROI.

Changing the display of the results

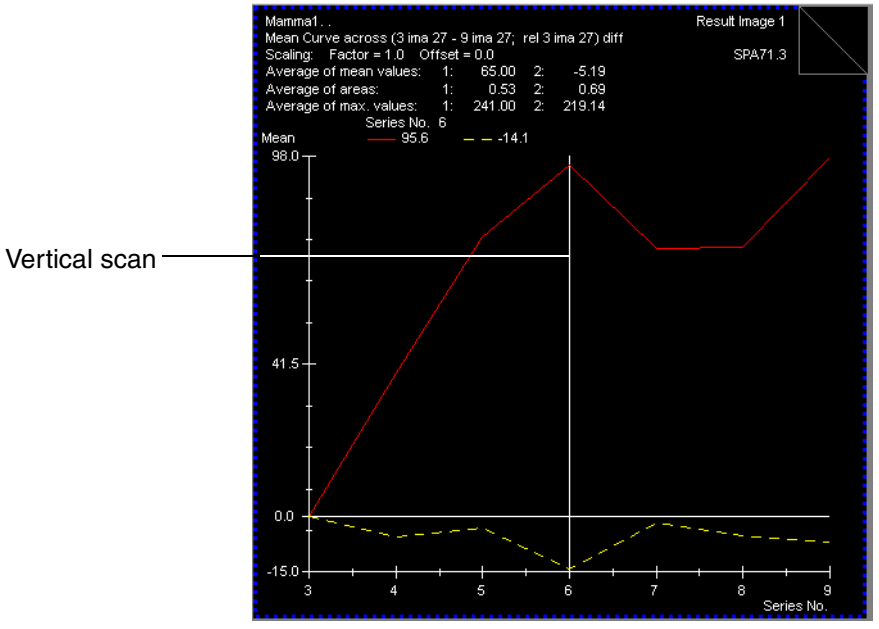
You can use the following options for changing the display of the results in the diagram:

- ❏ Using vertical scan line
- ❏ Scaling the x axis and y axis
- ❏ Smoothing curves
- ❏ Using an image from the first segment as background
- ❏ Changing the comment line in the image text

Using vertical scan line

For more precise evaluation of the curve, you can have the intensity of the signal displayed for a defined x value.

For this purpose, you can shift the vertical line in the image.



✧ Click on the line and move it by holding down the left mouse button.

The X value (**Series No. 6** in the figure) and the mean values of the intensities for each ROI are displayed above the curves.

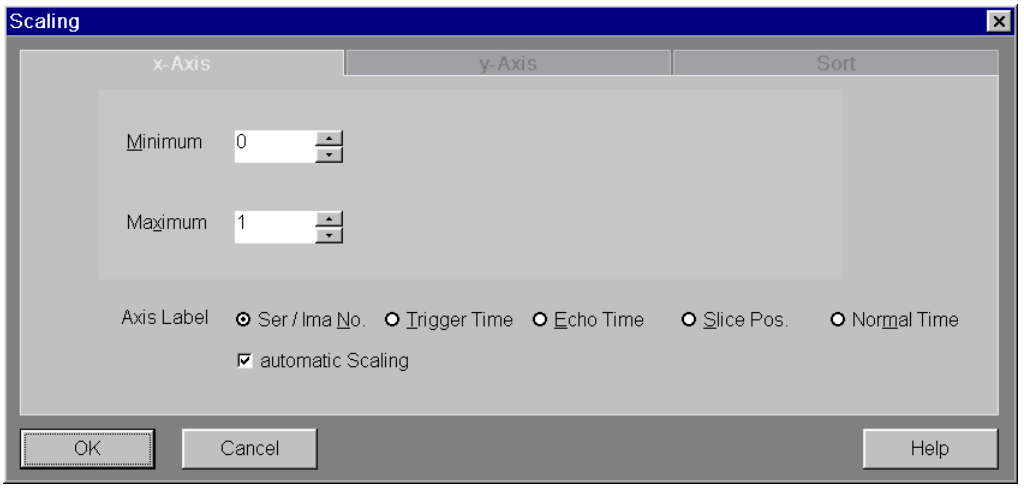
➪ If it is not visible, the vertical line is located directly on top of the Y-axis. You can shift it in this position.

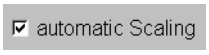
Scaling the x axis

The definition range of the selected parameter is displayed on the x axis. You can limit this range so that only the section of interest will be displayed.

✧ Select the **Scaling** dialog box and go to the **X-Axis** subtask card.
→ Page D.2–15, *Defining the x axis*

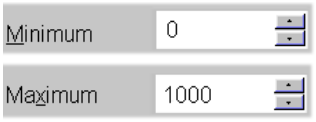
➪ You can also call up the **Scaling** dialog box by selecting **Scaling/Sorting** in the result menu on the context menu.





When you call Mean Curve, the **Auto Scale** option is activated. The X-axis is scaled in accordance with the input data.

You are also able to scale the X-axis manually to focus on areas of interest.



✧ Change the value in the two input fields **Minimum** and **Maximum**.

The **Auto Scale** option is deactivated for the x axis and the y axis.

➪ If the **Auto Scale** option is inactive, the current scaling will be applied to all subsequent evaluations.



✧ Click the **OK** button to apply your changes.

The curves and tables will be adjusted accordingly.

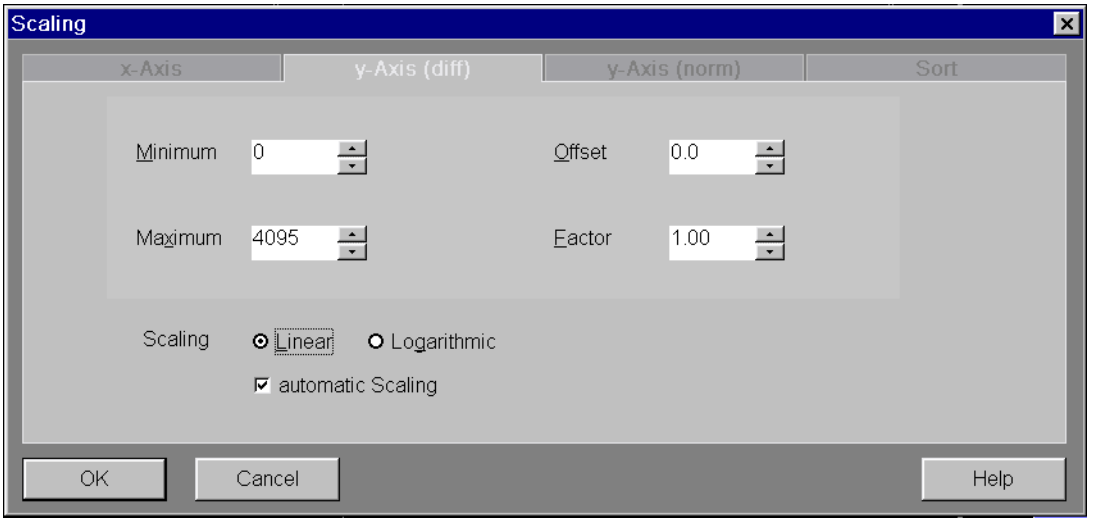
Scaling the y Axis

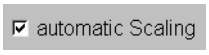
Different cards will be displayed in the **Scaling** dialog box depending on the type of evaluation used.

Only the **Y-Axis** card will be displayed for absolute evaluation. For relative evaluation, a card for differential signal curves with a **Y-Axis (diff)** and a card for normalized curves with a **Y-Axis (norm)** is displayed.

✧ Select the **Scaling** dialog box and go to the **Y-Axis** card.
→ Page D.2–15

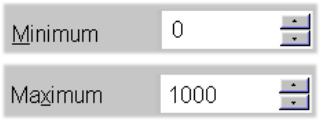
➪ You can also call up the **Scaling** dialog box by selecting **Scaling/Sorting** in the result menu on the context menu.





When you call Mean Curve, the **Auto Scale** option is activated. The y axes are scaled in accordance with the result data.

You are also able to scale the axes manually to focus on areas of interest. The measured grayscale values will *not* be changed.



✧ Change the value in the two input fields **Minimum** and **Maximum**.

The **Auto Scale** option is deactivated for both the x axis and the y axis.

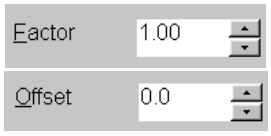
➪ If the **Auto Scale** option is inactive, the current scaling will be applied to all subsequent evaluations.

You can set the scaling of the y axis to be either linear or logarithmic.



✧ Click the **Linear** or **Logarithmic** option.

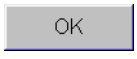
You are able to scale the grayscale values. The grayscale values will be changed. This function is useful if the grayscale values are proportional to a physiologically relevant value and the proportionality factor is known (e.g. flow velocity of the blood).



Example: Factor 2, **Offset** 20
All Y values are multiplied by 2 and shifted towards the positive Y axis by 20 units.

✧ Enter suitable values in the **Factor** and **Offset** input fields.

➪ The **Minimum/Maximum** and **Factor/Offset** parameters are mutually independent.



✧ Click the **OK** button to apply your changes.

The curves and tables will be adjusted accordingly.

Smoothing curves



The individual measurement points can either be connected by straight lines or by a smooth curve.

✧ Click the **Smoothing** button on the **Mean Curve** card in the control area.

Or

✧ Select **View > Smoothing On**.

Or

✧ Select **Smoothing** from the context menu.

The curve is smoothed. The results in the table are not affected.

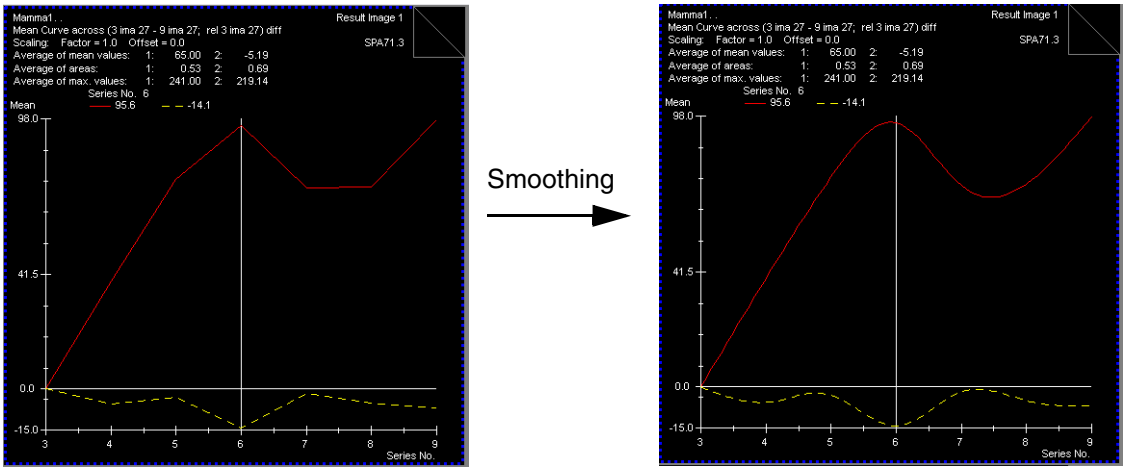


Image text and comments

You are able to change a comment line in the image text of the curves and tables.

✧ Double-click this line.

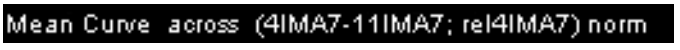
The comment line is selected.

✧ Enter the new comment.

✧ Confirm the new comment line by pressing the **Enter** or **Esc** key or by calling up an ROI tool.

The modified text is updated in all result images.

Example of an automatically generated comment line:



❏ Evaluation of image 7 across series 4 to 11
❏ **rel 4ima 7**: relative evaluation with image 7 from series 4 as the reference
❏ **norm**: Normalized curve
(or **diff**: ratio of the signal difference to the reference image)

Image as a background for the diagram

Instead of the default black background, you may use the current image in the first segment as a background for diagrams.

✧ Select the **Image with Graphics** option under **View**.

✧ If necessary, adjust the contrast and brightness in the second segment for an optimally visible curve.

✧ Select the **Graphics only** option under **View** if you want to reset to a black background.

Storing, filming and deleting results

You may save the results of the Mean Curve evaluation as images or as an ASCII file and send them to a camera for filming.

NOTE

When a user logs off, unsaved data are irretrievably lost.

Check whether data still needs to be saved and save any data you want to keep before you log off.

Saving results as images

The results are saved as separate images in the database as follows:

(1) Explicitly select the initial images and results images and select **Save as**

✧ Explicitly select the images, curves, and tables in all segments that you want to save.

✧ Select **Patient > Save As...** to display the **Save As** dialog box.

You may save the result images in the same way as on the **Viewing** task card.
→ *syngo* Operator Manual

(2) Save all results images and all relevant initial images without making a selection



✧ Click the **Save Evaluation** button on the **Patient** card in the control area.

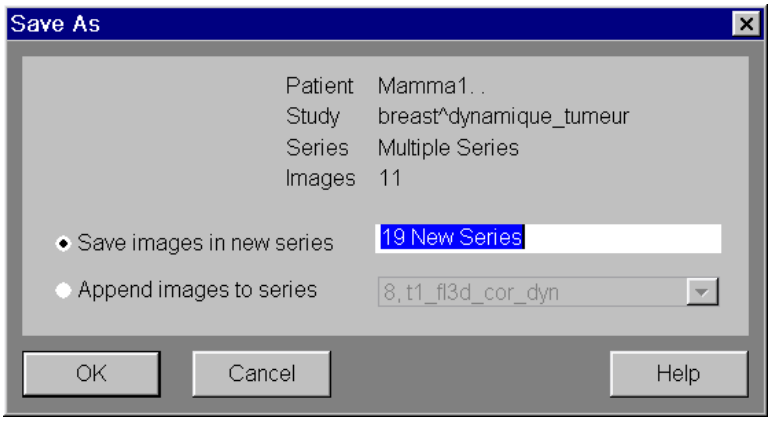
Or

✧ Select **Patient > Save Evaluation As**.

Or

✧ **Select Save As ASCII** from the context menu in the second segment.

The first and second segments are selected explicitly. The **Save As** dialog box is displayed.



A new series is created. This series contains all relevant initial images with ROIs and the window and zoom/pan values from the first segment and the results images from the second segment.

You can archive and send these series automatically.
→ *syngo* Operator Manual

➪ If you have not performed any calculations and the second segment is empty, the **Save Evaluation As** menu item will be dimmed.

➪ The ROIs of images stored in **Mean Curve** can no longer be processed on the **Viewing** task card.

Saving results as an ASCII file

You may save data from the evaluation in an ASCII file.

You may only store ASCII data onto diskette (diskette drive A:) or in directories especially created by Siemens Service for import/export.

NOTICE

The **Save As ASCII** menu item is dimmed if you do not have the necessary EXPORT rights.

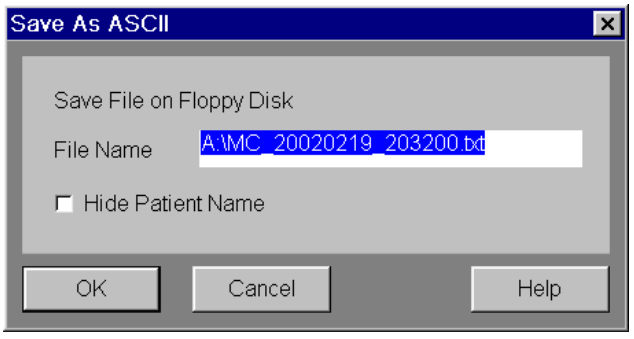
Please observe the information given in the Safety Standards book.

✧ Select **Patient > Save As ASCII**.

Or

✧ Select **Save As ASCII** from the context menu in the second segment.

The **Save in ASCII format** dialog box opens.



You can save the ASCII file on diskette or in directories especially set up for import/export by Siemens Service.

File Name

✧ Choose a directory or diskette under **Filename**.

For security reasons, you are able to deactivate display of the patient name in the first line of the ASCII file.

Hide Patient Name

✧ Select the **Hide Patient Name** option.

The ASCII data now no longer contain any reference to the patient.

After relative evaluation, tables for differential signals end with **_diff**, and tables for normalized values **_norm**. If needed, you may change the file name.

Reading an ASCII file into Excel

The ASCII data from the mean curve evaluation could be imported into Microsoft Excel, for example.

➪ Ensure that you set a decimal point under the **Regional Settings/Numbers** on your PC.

✧ Launch *Microsoft Excel*.

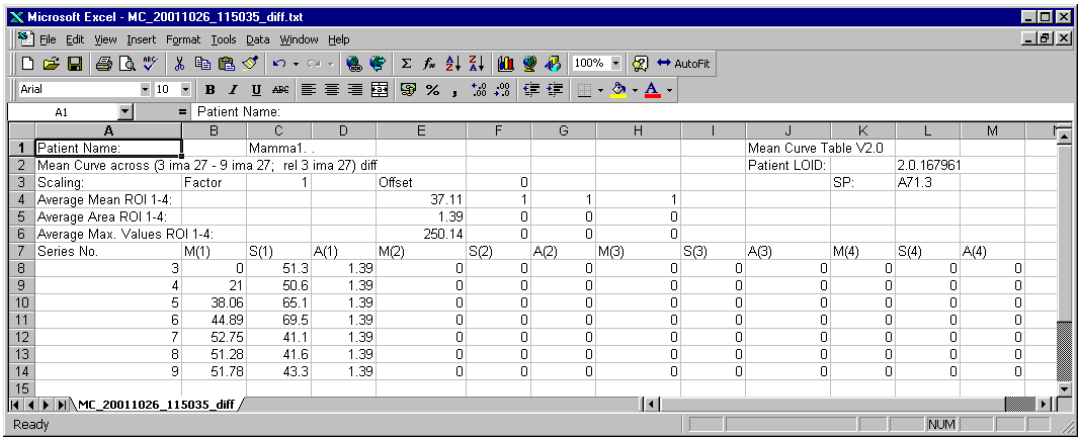
✧ Select **File > Open** in *Microsoft Excel*.

✧ Select drive **A:** under **File type text files (*.txt)**. Under **Look in** Drive A: Click the **Open** button.

The **Convert Text to Columns Wizard** (Text Assistant) dialog box then opens.

✧ Click the **End** button.

You can now use *Microsoft Excel* to continue processing the curve results.



	A	B	C	D	E	F	G	H	I	J	K	L	M
1	Patient Name:		Mamma1. .							Mean Curve Table V2.0			
2	Mean Curve across (3 ima 27 - 9 ima 27; rel 3 ima 27) diff									Patient LOID:		2.0.167961	
3	Scaling:	Factor	1		Offset	0					SP:	A71.3	
4	Average Mean ROI 1-4:				37.11	1	1	1					
5	Average Area ROI 1-4:				1.39	0	0	0					
6	Average Max. Values ROI 1-4:				250.14	0	0	0					
7	Series No.	M(1)	S(1)	A(1)	M(2)	S(2)	A(2)	M(3)	S(3)	A(3)	M(4)	S(4)	A(4)
8	3	0	51.3	1.39	0	0	0	0	0	0	0	0	0
9	4	21	50.6	1.39	0	0	0	0	0	0	0	0	0
10	5	38.06	65.1	1.39	0	0	0	0	0	0	0	0	0
11	6	44.89	69.5	1.39	0	0	0	0	0	0	0	0	0
12	7	52.75	41.1	1.39	0	0	0	0	0	0	0	0	0
13	8	51.28	41.6	1.39	0	0	0	0	0	0	0	0	0
14	9	51.78	43.3	1.39	0	0	0	0	0	0	0	0	0
15													

Filming images

You can transfer the images, curves, and table of the mean curve evaluation to the virtual film sheet for filming or printing as follows:

(1) Select the images and results explicitly and transfer them to film sheet

✧ Explicitly select the images and results from all four segments.

✧ Select **Patient > Copy to Film Sheet**.

(2) Transfer the two current images from the first and second segment to the film sheet without making a selection



✧ Select **Patient > Film Evaluation** or click the **Film Evaluation** button in the control area of the **Patient** card.

The images are transferred to the virtual film sheet and from there they are sent to the camera either immediately or after a delay depending on the setting (**Auto Expose on/off**).

For a detailed description of the film function refer to:
→ *syngo* Operator Manual

Deleting images and results

You can either delete images or results in *one* segment or delete *all* the images loaded in **Mean Curve**.

✧ Put the input focus on a segment.

✧ Select **Edit > Delete document(s)** or select **Delete documents** from the context menu.

The corresponding document is deleted.



✧ Select **Patient > Close Patient** or click the **Close Patient** button in the control area on the **Patient** card.

All segments are cleared.

Ending mean curve

✧ Select **Applications > Close Mean Curve**.

Or

✧ Start another dynamic application function such as **Argus**.

The **Mean Curve** task card closes.

➪ Up to six task cards may be active. You have to close one active task before opening another task card.

NOTICE

If you close the patient but not **MeanCurve**, all settings, e.g. evaluation mode or scaling, are retained.

CHAPTER D.3

Image Filtration and Distortion Correction

You can use an **offline image filter** to postprocess blurred or noisy images. These are adaptive filters that search for conspicuous structures in the image. Subsequently, the filter checks if these are either random or part of other structures. Filters take into account the local distribution of signal intensity and the course of local tissue structures.

The images selected in the **Patient Browser** or the **Viewing** task card are used for calculation.

Siemens provides three default filters and three freely definable filters.

Geometric distortions (barrel/pin cushion) may occur at the edge of images with a large FoV. These image errors can be eliminated using the **distortion correction** postprocessing function.

Editing Images with Image Filters

Images or series that you want to postprocess with an **offline image filter** must not have already been processed with another filter.

Selecting images

Select the images or the series in the **Patient Browser** or in the **Viewing** task card.

❏ Advantages of **Patient Browser**:
Fast image selection

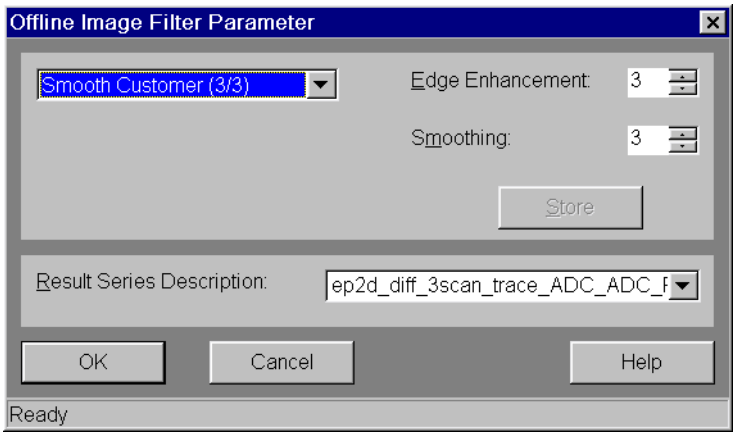
❏ Advantages of **Viewing**:
You can look at the images prior to filtering and edit them, if necessary.

✧ Select all series and images that you want to filter in the **Patient Browser** or **Viewing**.

✧ Select **Evaluation > Dynamic Analysis > Image Filter** to start the filter.
- Or -
Click this button on the tool bar of the **Patient Browser** or in the **Evaluation** subtask card in the **Viewing**.



The **Offline Image Filter Parameter** dialog window opens.



Setting the filters

Select the image filter you want to use in the **Offline Image Filter Parameter** dialog window.

In the case of a customer filter, define the following properties:

- **Edge enhancement:**
  Degree of edge and line enhancement
- **Smoothing:**
  Degree of smoothing

Selecting a filter

Three default Siemens filters are available: **Smooth**, **Medium** and **Sharp**. In addition, there are three freely-selectable customer filters: **Smooth Customer**, **Medium Customer** and **Sharp Customer**.

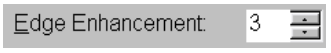
➪ The actual filter properties are displayed in parentheses after the name:

```
Filter name (edge enhancement/smoothing)
```



✧ Select a filter in the upper selection list.

Defining customer filters



✧ Enter a whole number between 1 and 5 in the **Edge Enhancement** input field.



✧ Enter a whole number between 1 and 5 in the **Smoothing** input field.



✧ Click **Store**.

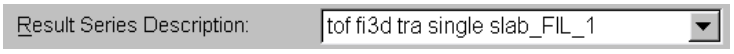
➪ The values cannot be changed when using a Siemens filter.

Renaming a results series

A result image or result series is generated for each original image or series.

Name of the results series

An automatically generated name for the **Result Series Description** is entered in the result series field. You can accept this name or change it as desired.



The suggested name comprises the following sections, separated by underscores:

- ❏ Name of the initial series
- ❏ The abbreviation “FIL” for image filter
- ❏ A running number

➪ The result series name may only contain valid characters and may not exceed 64 characters in length. If necessary, the name of the initial series is truncated automatically.

Renaming

✧ If the name suggested does not meet your expectations, enter the description preferred by you.

Selecting result series

If you loaded several series, the **Result Series Description** input field functions as a selection list as well. This allows you to check and/or change the names for the result series that have been loaded.

Starting filtering

After you have selected your filter, you can start image processing.

✧ Click **OK**.

The dialog box closes.



This icon in the status bar indicates that a filtering process is running in background.

Monitoring filtering

You can monitor the progress of filtering in the **Calculation Status** dialog window. You can also interrupt or cancel filtering and delete filter jobs from the list.



✧ Click the icon on the status bar.

The **Calculation Status** dialog window opens.

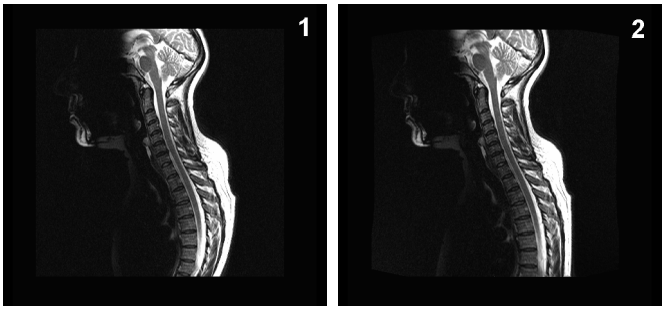
Displaying the results

Once the jobs have been processed, the images will be displayed on the **Viewing** task card.
The following image types indicate filtered images; the values displayed in the user-defined filters correspond to the values set for edge enhancement and smoothing:

Filter (Edge enhancement/ Smoothing)	Image type
Smooth (3/3)	**FSM** (Filter Smooth)
Medium (3/3)	**FM** (Filter Medium)
Sharp (3/3)	**FSH** (Filter Sharp)
Smooth Customer (1/4)	**FSM1_4**
Medium Customer (2/5)	**FM2_5**
Sharp Customer (3/2)	**FSH3_2**

Correcting Distortion Artifacts

Geometric distortions (barrel/pin cushion) may occur at the edge of images with a large FoV or with off-center slices.



(1) Image with distortion artifacts
(2) Image after distortion correction

Cause

Gradient coils are used to encode spatial information whose gradient field ideally rises linearly. In reality, however, deviations from linearity may occur at the edge of the image.

Remedies

If you are planning quantitative evaluations for images, it is essential to correct distortion artifacts

as follows:

(1) Before scanning switch on the FoV compensation filter. The images resulting from this measurement are distortion-corrected.
→ Page H.1–69, *FoV compensation filter (large FoV)*

(2) You can also correct images after scanning. Call distortion correction from the Patient Browser. This method is described on the next pages.

Distortion correction after scanning generates a new series. The uncorrected original images are retained and can be used for slice positioning additional scans.

Selecting images and starting calculation

Requirements

The images have to meet the following conditions for distortion correction:

❏ The images have been acquired with ***syngo*** **MR**
❏ The images have not been distortion corrected before

Selecting images

You may select individual images, one or more series or single images of different series.

✧ Select **Patient > Browser**.

✧ Select the images or series in the Patient Browser.

Starting calculation

✧ Select **Evaluation > Distortion Correction** from the Patient List.

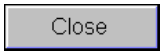
 

Calculation of the distortion correction starts. The status bar shows the icon of the image postprocessing jobs. If calculation fails, the icon appears crossed out.
→ Page D.4–39, *Tracking post-processing*



✧ Click the icon on the status bar.

The **Postprocessing Queue** dialog box is displayed. You are able to monitor progress of the image postprocessing job.



✧ Click the **Close** button in the **Postprocessing Queue** dialog box when the postprocessing job has been completed.

Results

New series are generated as a result of the distortion correction.

Example

You have selected three images from series S1, four images from series S2, and two images from series S3 for distortion correction.

Three new result series are created: Series E1 with three images, series E2 with four images, and series E3 with two images.

Distortion corrected images are identified by image type DIS2D.
→ Page H.2–14, *List of image types*

CHAPTER D.4

Viewing and Evaluating BOLD Images

The **BOLD** task card enables you to create alpha images by combining anatomical images with parameter images as well as to retroactively calculate parameter images.

The various image types are defined as follows:

Parameter images

Post-processed images with functional information. In this case, t-test images.

t-test images

Parameter images that originate from an online or offline BOLD calculation or have been generated by statistical analysis with the **Dynamic analysis > TTest...** function The pixels contain functional information.

⇨ It is not possible to window t-test images on the **BOLD** task card.

Alpha image

Overlay image (magnitude image) created by combining a currently displayed anatomical image with a currently displayed parameter image. This requires an identical slice position.

⇨ It is not possible to window alpha images or to use them for additional analysis.

Access authorization to the task card

Detailed information about access authorization is available in the *Safety Standards* book.

You require access authorization for the **BOLD** task card. If you log on without this access authorization, you will not be able to perform the protected functions.

If you do not have access to a certain patient, his data will not be shown in the **Patient Browser** when you are logged into the system.

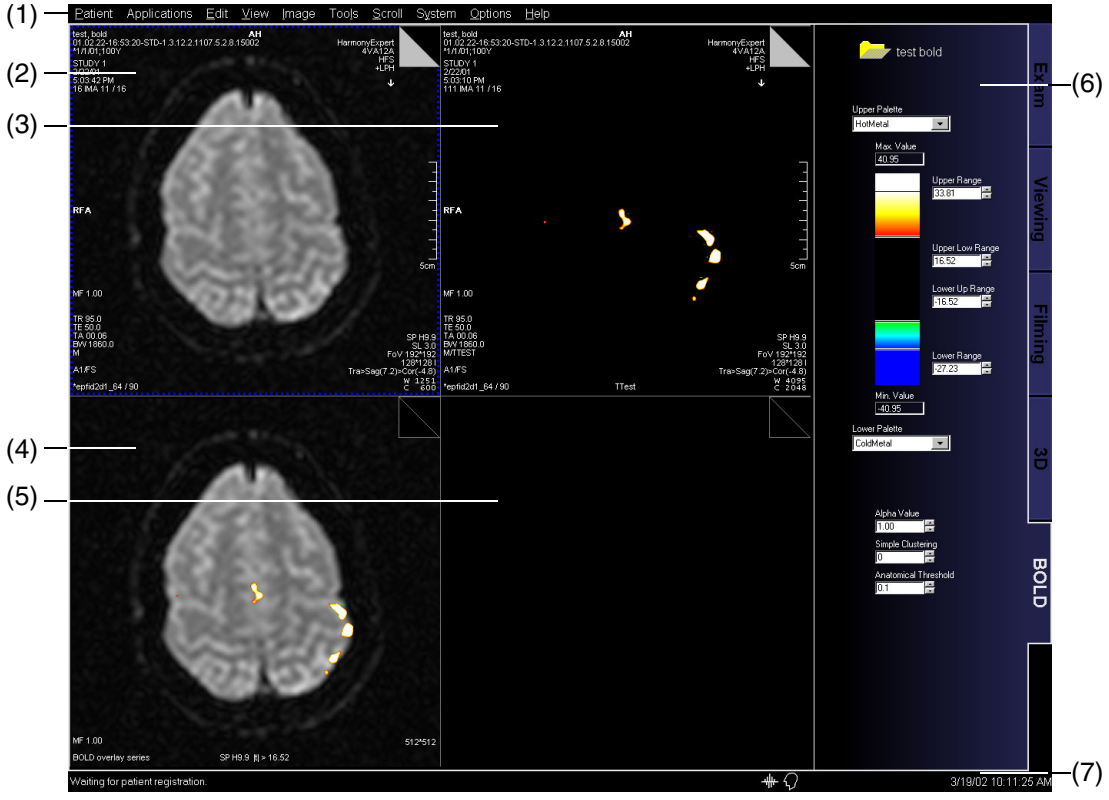
NOTE

When a user logs off, unsaved data are irretrievably lost.

Check whether data still needs to be saved and save any data you want to keep before you log off.

The BOLD task card

The **BOLD** task card is divided into the following areas:



(1) Menu bar
(2) Segment 1 (anatomical segment)
(3) Segment 2 (parameter image segment)
(4) Segment 3 (alpha image segment) contains only one image
(5) Segment 4 (currently not used)
(6) Control area
(7) Status bar

Loading Images

You are transferring anatomical images and parameter images to the **BOLD** task card. The sequence is not important.

This automatically creates overlay images, known as alpha images.
→ Page D.4–11, *Automatic calculation of the alpha images*

You can choose single images as well as series or complete studies.

Restrictions

- ❏ You can *not* transfer the complete images set of a patient to the **BOLD** task card.
- ❏ Anatomical images that include distortion correction through remapping with the **Large FOV filter** can *not* be transferred to the **BOLD** task card.
- ❏ The images can only be loaded from the local database. During direct loading from CD-ROM, loading will be canceled followed by a message appearing on-screen.

NOTE

A message appears when an operator without access authorization to the data currently loaded takes over.

You can then decide whether to continue or cancel log-on of the new operator. If you choose to continue, the current data will be unloaded without saving. The task card is then closed.

Initially loading series

Anatomical series and parameter image series are transferred to the empty **BOLD** task card as follows.

Opening the Patient Browser

✧ Open the **Patient > Browser** from the main menu.

The **Patient Browser** dialog box opens.

Selecting images/series

✧ Select the required study, series, or single images.
→ *syngo* Operator Manual

Transferring images

✧ Open **Applications > BOLD** from the main menu.

Or

✧ Drag and drop the required anatomical series into the image area of the *BOLD* task card.

Or

✧ Double-click the required series.

The anatomical series will be transferred to the *anatomical segment* of the **BOLD** task card. The parameter image series will be transferred to the *parameter image segment*.

- If the series contains images without a clearly defined slice plane, these images will also be loaded into the first segment and appended to the end of the series.
- If the anatomical images are not from EPI measurements, certain restrictions apply.
  → Page D.4–24, *Activating/Deactivating blocking areas*

The segments show the first image of the first series. If the conditions for an alpha image are met, the alpha image segment will show a single alpha image.

Loading additional series

You have already transferred several series to the **BOLD** task card and would like to load additional series.

✧ Select the required study, series, or single images.
→ *syngo* Operator Manual

✧ Open **Applications > BOLD** from the main menu.

Or

✧ Drag and drop the required anatomical series into the image area of the *BOLD* task card.

Or

✧ Double-click the required series.

If the selected series consist of anatomical images, they will be transferred to the *anatomical segment*. Additionally, the first image of the first new series you have loaded will be displayed.

If the new series originated from the same study, they will be stored on the **BOLD** task card according to their series number. In this case, you can scroll between series,
→ Page D.4–15, *Scrolling from series to series*

If you have selected series from another study, a dialog box will be displayed. The dialog box gives you the choice of transferring the new series to the **BOLD** task card.

If yes, the series currently on the **BOLD** task card will be deleted.

Loading mosaic images

You are able to transfer mosaic images to the **BOLD** task card as well.

NOTICE

BOLD imaging generates thousands of images. For simpler handling and to maintain performance, there are special sequences that create mosaic images.

A mosaic image combines the slices scanned within a TR interval. The matrix of the mosaic is defined by the number of slices.

The images are sorted in anatomical order starting top left in the matrix.
→ *syngo* Operator Manual

Automatic calculation of the alpha images

Ensure that the source images loaded meet the following requirements prior to your calculating alpha images:

- ❏ at least one slice position of the anatomical series and parameter image series has to match
- ❏ the parameter image must cover at least half the anatomical image at the matching slice position

If yes, the alpha images are calculated automatically and displayed on the **BOLD** task card in the *alpha image segment*. The image section that does not correspond to the anatomical image, will be shown in turquoise color in the alpha image.

If the parameter image covers less than half the anatomical image, it is not possible to calculate the alpha image. The *alpha image segment* remains black.

- ➪ The alpha images are displayed *singly* rather than as an image stack because only the alpha image for the currently displayed anatomical image and parameter image are calculated.
- ➪ Image numbers are not displayed in the alpha image.

The image text of the alpha text provides the slice position and the magnitude of the threshold value (**upper low range**, **lower up range**) from the color scale, e.g. SP H 29.7 |t| > 4.0. This also applies to mosaic images. In this case, the slice position of the first mosaic image is used.

Rules for mosaic images

- ❏ If both source images (anatomical image and parameter image) are in mosaic format, the alpha image is displayed in mosaic format as well. For this purpose, the slice positions have to match.
- ❏ If only one source images is in mosaic format, (for example, the anatomical image is a single slice image while the parameter image is in mosaic format) BOLD will search for a slice position in the mosaic image that matches the anatomical image. If the search is successful, the alpha image will be calculated and displayed.
- ❏ Anatomical mosaic images that are not available in EPI format cannot be superimposed.

Scrolling images and series

Series and images are displayed as a stack of images in the *anatomical segment* or *parameter images segment* of the **BOLD** task card. This means that you can scroll through the images separately in each segment.

⇨ It is *not* possible to scroll through alpha images because only one alpha image at a time is shown.

Scrolling between images

The **BOLD** task card provides options for scrolling image-by-image through the series:

✧ Use the dog ears in the top right-hand corner of the image segments.
→ *syngo* Operator Manual

Or

✧ Select **Scroll > Image Next** or **Scroll > Image Previous**.

Or

✧ Scroll using the **Image-** or **Image+** key on the symbol keypad.

When you select a slice position while scrolling through the anatomical series that matches an image in the parameter image series, the image will be displayed, and the program calculates the associated alpha image.

➪ If the anatomical series contains images without a clearly defined slice plane, these images will be appended to the end of the series.

If several anatomical series are loaded, it is possible to scroll through image-by-image from one series to another.

When you select a slice position while scrolling through the parameter image series that matches an image in the anatomical series, the image will be displayed, and the program calculates the associated alpha image.

Otherwise, a message will appear informing you that it is not possible to calculate an alpha image from the source images. In this case, the *alpha image segment* remains black.

Scrolling from series to series

You can scroll series-by-series both in the *anatomical segment* as well as the *parameter image segment*.

✧ Select **Scroll > Series next** or **Scroll > Series prev**.

Or

✧ Scroll using the **Series-** or **Series+** key on the symbol keypad.

If at least *one* slice position of the anatomical series and the parameter images series matches, the alpha image will be automatically calculated for the first matching slice position and displayed on the *alpha image segment* on the **BOLD** task card. The associated anatomical images and parameter images will be displayed as well.

Otherwise, a message appears informing you that it is not possible to calculate an alpha image from either of the two source images. Additionally, the *alpha image segment* remains black.

Edit images

The **BOLD** task card lets you edit images and change image display. A number of functions is available, depending on the type of image.

Image type	Editing/display change
Anatomical image	Windowing images
Parameter image	Deactivating interpolation Editing a color scale
Alpha image	Changing the anatomical threshold Activating/deactivating blocking areas Changing the alpha value Changing the cluster size

Windowing anatomical images

You can *only* window anatomical images. It is not possible to window color images (parameter image and alpha image).

✧ Set the required window values in the anatomical image.
→ *syngo* Operator Manual

The alpha image is recalculated and displayed.

Deactivating interpolation in parameter images

The pixels of images from EPI scans are clearly visible due to the small image matrix used. To improve image impression, these images are interpolated by default with a bicubic algorithm.

This interpolation can be deactivated if necessary.

✧ Scroll to the image you require in the image segment for the parameter images.

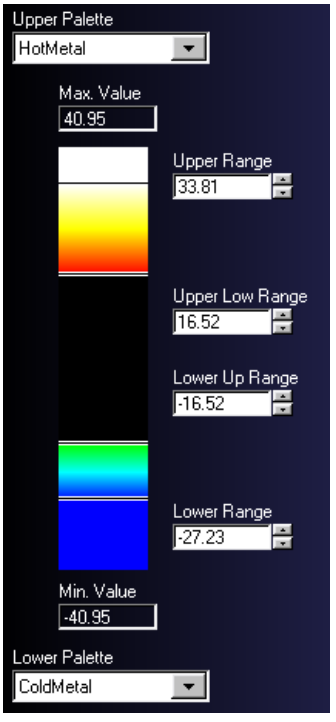
✧ Deactivate the function **View > Interpolation On** in the main menu.

Both the alpha image and the parameter image are displayed without the bicubic algorithm. The pixels are clearly visible.

Editing a color scale

The pixels of the parameter images contain functional information only. A value of the color scale is assigned to each pixel.

You may change the color display of the parameter and alpha images.



Selecting a color scale

If the parameter image has positive and negative values, you can change the color scale in the upper and lower palette.

✧ Select the desired color scale from the **Lower Palette** and/or **Upper Palette** selection list.

The color display of the parameter and alpha image is adjusted to the new color scale.

Deselect the lower color palette

If the parameter image has positive values only, the lower color palette is not required for display. You can therefore deselect this color palette.



✧ Select the **none** setting from the **Lower Palette** selection list.

The lower color scale is hidden.



✧ Select the desired color scale from the **Upper Palette** selection list.

The color display of the parameter and alpha image is adjusted to the new color scale. Only positive correlates (0 to 40.95) will be taken into account.

Deselecting the upper color palette





If the parameter image has negative values only, the upper color palette is not required for display. You can deselect this color palette.

✧ Select the **none** setting from the **Upper Palette** selection list.

The upper color scale is hidden.

✧ Select the desired color scale from the **Lower Palette** selection list.

The color display of the parameter and alpha image is adjusted to the new color scale. Only negative values (–40.95 to 0) will be taken into account.

TIP

If you want to expose alpha images and have a black-and-white printer,
select **Grayscale** as the color scale
(black-and-white scale).

To rule out possible ambiguities in grayscale values,
window the grayscales values in the *anatomical segment*.

Changing the color range

You may define the range of the color scale for displaying parameter images.

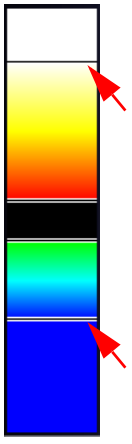
✧ Select the desired color scale from the **Lower Palette** and/or **Upper Palette** selection list.





✧ Enter the new values in the **Lower Range** and/or **Upper Range** spin boxes.

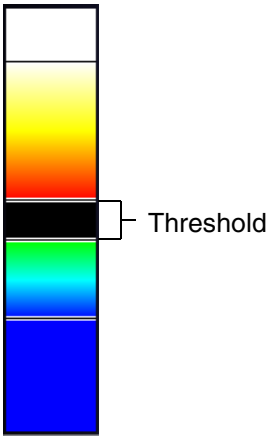
Or



✧ Move the lines in the scale using the mouse.

The color display of the parameter image is adjusted to the new values. The alpha image is recalculated and displayed.

Excluding a color range



You are able to define an intensity threshold for the parameter images that also suppresses noise. For this purpose, set a symmetrical range around zero that will be ignored in the color assignment and displayed as a black area in the parameter images.

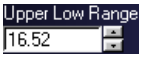
The selected threshold values is displayed as a black area between the color scales on the **BOLD** task card.

If you are only using *one* color scale, you may exclude a range – either ascending (for positive correlates) or descending (for negative correlates).

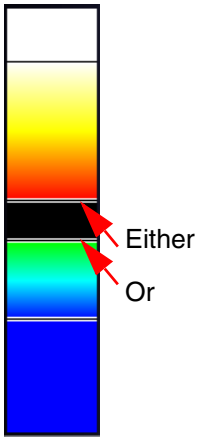
✧ Select the desired color scale from the **Lower Palette** and/or **Upper Palette** selection list.

The color range to be excluded is selected as follows:





✧ Enter a new value in the **Lower Up Range** or **Upper Low Range** spin-box.



Or

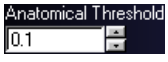
✧ Use the mouse to move a line at the end of the scale.

The other threshold value will change symmetrically.

The color display of the parameter image is adjusted to the new values. The alpha image is recalculated and displayed.

Changing the anatomical threshold

You can define the threshold value for pixel intensity in the anatomical image. As a result, you are able to hide alpha image pixels below a certain threshold. The default threshold is 0.10. This corresponds to 10% of the mean value of all pixels in the anatomical image.



✧ Enter the desired threshold value in the **Anatomical Threshold** spin-box.

The alpha image is recalculated and shown in the bottom left image segment.

➪ The setting is retained when scrolling from image to image.

Activating/Deactivating blocking areas

If you have transferred parameter images and anatomical images of different resolution to the **BOLD** task card (e.g. anatomical spin-echo images), the alpha image is adjusted in size to the anatomical image.

EPI images are prone to artifacts due to the acquisition method used. Distortions and signal losses can occur in images. At times areas may not be allocated correctly when overlaying parameter images that are based on EPI images.

Areas that contain non-defined or incorrect information are shown in color in the alpha images. For this purpose, a field map is superimposed on the alpha image (field map displays the local B0 field).

If the program is not able to find a valid field map, a message appears informing you that the alpha image may be misinterpreted.

Deactivating blocking areas

✧ Deactivate the function **View > Show Fieldmap** in the main menu.

A message appears informing you that the alpha image may be misinterpreted.

➪ The message appears only once per series.

✧ Acknowledge the warning with **OK**.

The message will appear as a comment text in the alpha image. It is *not* possible to hide this message. The alpha image is recalculated and displayed *without* blocking areas.

Activating blocking areas

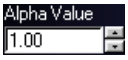
✧ Activate the function **View > Show Fieldmap** in the main menu.

The comment text in the alpha image is deleted. The alpha image is recalculated and displayed *with* blocking areas.

Changing the alpha value

The alpha value defines the degree of overlay, i.e. the weighting used to overlay the anatomical image with the parameter image. The higher the alpha value, the greater the number of brightness values taken from the parameter image. At an alpha value of zero, the alpha image will only show the anatomical image.

The default value is 1.00.



✧ Enter the desired value in the **Alpha Value** spin-box.

The alpha image is recalculated and displayed.

➪ The setting is retained when scrolling from image to image.

Changing the cluster size

To eliminate random pixels from the alpha image, you may change the size of the clusters that should not be displayed for the parameter image. The default cluster size is 1 pixel.



✧ Enter the desired cluster size in the **Simple Clustering** spinbox.

For example, if you select cluster size 3, all pixel clusters smaller than 3 pixels in the parameter image will be hidden in the alpha image.

The alpha image is recalculated and displayed.

➪ The setting is retained when scrolling from image to image.

Saving images

You can save new or changed images on the **BOLD** task card. The following images may be stored:

- ❏ whenever their slice positions match, all alpha images of the anatomical and parameter images are loaded
- ❏ current parameter image with associated color palette
- ❏ current alpha image as a color image

The above save options let you decide whether to append the saved images to an existing series or to save them as a new series.

Saving all alpha images

You can have all alpha images of the loaded anatomical images and parameter images calculated and saved with or without a superimposed field map.

Opening the save dialog box

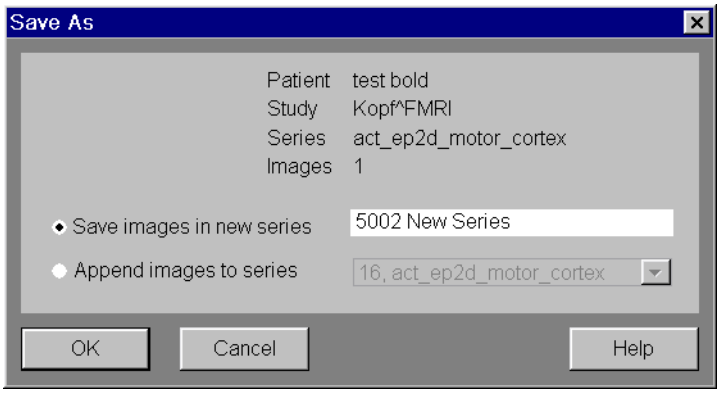
✧ Select **Patient > Save All Alpha As...** from the main menu.

Or

✧ Select **Save All Alpha As...** from the context menu.

➪ When you select saving, the number of alpha images is determined that have to be calculated. If the number is greater than 30, you will be asked whether you want to continue saving. If necessary, you can cancel saving the alpha images by clicking the **No** button. Saving is continued by clicking on the **Yes** button.

The **Save As...** dialog box opens.



The save dialog lets you define how the calculated alpha images will be saved:

❏ You can save the images as a new series.
❏ You can append the images to an existing series.

Saving images as a new series

✧ Select the **Save images in new series** option in the **Save As** dialog box.

The automatically generated series number is displayed in the name field.

✧ Enter a new name for the series if necessary.

✧ Confirm your settings with **OK**.

For all series selected on the **BOLD** task card, all alpha images are calculated and saved in which a suitable parameter image has been found for an anatomical image. Each newly calculated alpha images is displayed in the *alpha images segment*.

You are able to monitor image calculation as well image storage on the progress indicator. These activities may be stopped with **Cancel**.

All alpha images are saved with the color palette and settings selected at the time.

After the alpha images have been saved, the original state is restored on the **BOLD** task card as it was before saving.

NOTE

If an operator without access authorization to the program or the loaded data takes over during saving the data will be hidden on the task card.

Saving is completed in the background. All data are then unloaded from the task card and the task card is closed.

Appending images to an existing series

To append the calculated alpha images to an existing series, proceed as follows:

- ✧ Select the **Append images to series** option in the **Save As** dialog box.
- ✧ Subsequently select the required series from the selection list using the serial number and series description.
- ✧ Confirm your settings with **OK**.

Calculation is performed like for saving as a new series. The alpha images calculated are appended to the selected series.

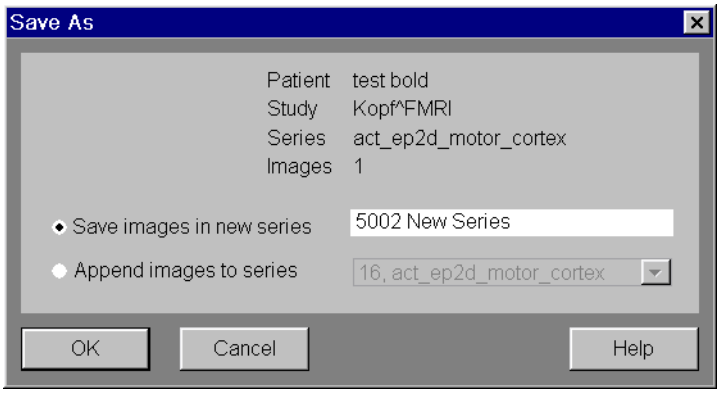
Saving single parameter images or alpha images

You can save both a selected parameter image with the associated color palette and a selected alpha image.

✧ Select the required parameter image or alpha image in the 2nd or 3rd image segment.

✧ Select **Patient > Save As...** from the main menu.

The **Save As** dialog box is displayed.



The saving dialog lets you set whether the image will be appended to an existing series or saved as a new series.

✧ Select the required option and assign a name for a new series, if necessary.
→ Page D.4–28, *Saving all alpha images*

✧ Confirm your settings with **OK**.

The currently selected image (parameter image or alpha image) is saved.

Retroactively Calculating Parameter Images

You can retroactively calculate parameter images on the **BOLD** task card.

The t-test images are saved in mosaic format and are automatically displayed on the **BOLD** task card.

Preparing for postprocessing

✧ Select **Patient > Browser** from the main menu.

✧ Select the anatomical series (EPI measurements).

Suitable series

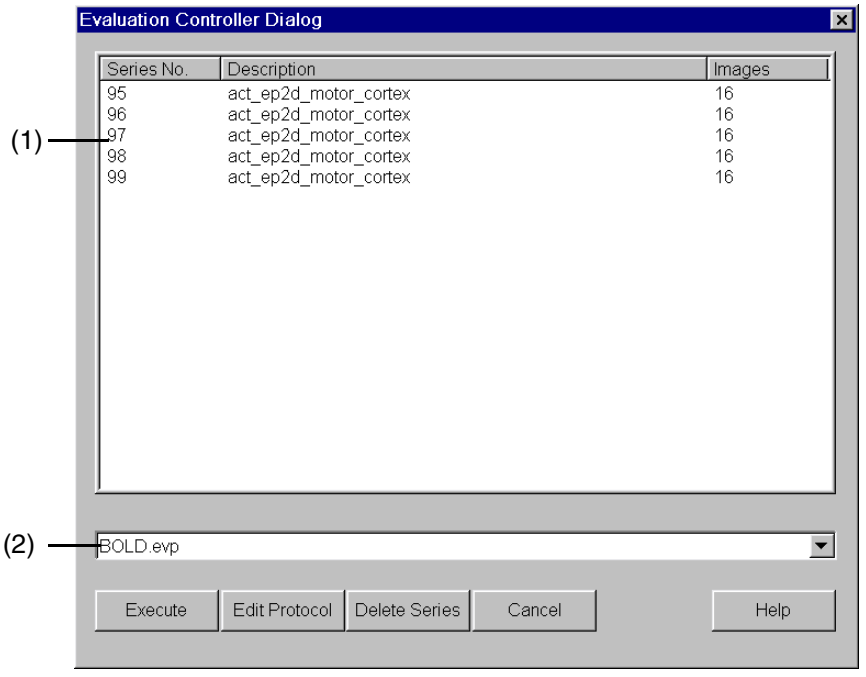
The series must meet the following criteria before they can be post-processed:

❏ same study
❏ same slice position
❏ same table position
❏ same number of images

✧ Select **Applications > Start BOLD calculation** from the main menu.

The **BOLD** task card is displayed or started.

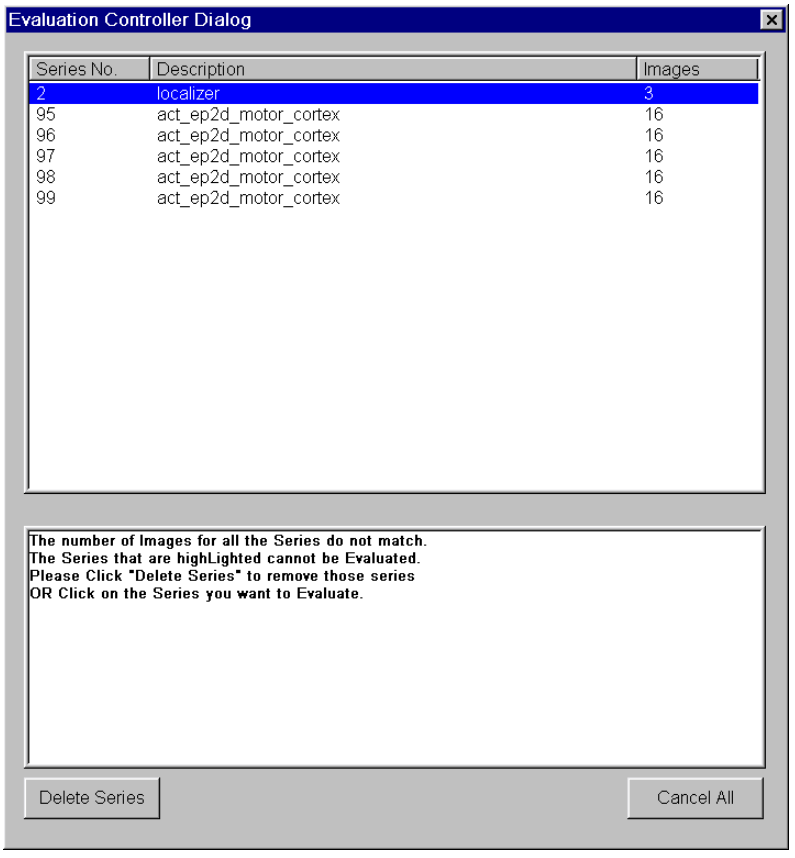
At the same time, the **Evaluation Controller Dialog** box is displayed.



(1) Selected series
(2) Postprocessing protocol last used

The selected series are checked to see whether they fulfill the above criteria.
→ Page D.4–34, *Suitable series*

The **Evaluation Controller Dialog** will indicate if they do not meet the criteria. Unsuitable series will be highlighted in color and have to be removed from the list.



Deleting additional series



✧ Go to the list and select the series to be deleted (multiple selections are possible).

✧ Click the **Delete Series** button.

The series is deleted from the list.

Selecting another postprocessing protocol



✧ Select the required postprocessing protocol from the selection list.

You may also edit the postprocessing protocol.
→ Page D.4–40, *Editing a post-processing protocol*

Starting post-processing



✧ Click the **Execute** button.

Postprocessing starts.

The first image is transferred to the **BOLD** task card. The **Evaluation Controller Dialog** box will be closed. The calculation runs in background.



The icon for image postprocessing jobs in the status bar shows you the calculation in progress.

After calculation has been successfully completed, the calculated parameter images are displayed as mosaic images in the *parameter image segment* of the **BOLD** task card.

Additionally, the alpha image is calculated and displayed. Calculation is identified as "completed" in the **Postprocessing Queue** dialog box.

Unsuccessful calculations are identified as "failed" in the **Postprocessing Queue** dialog box.

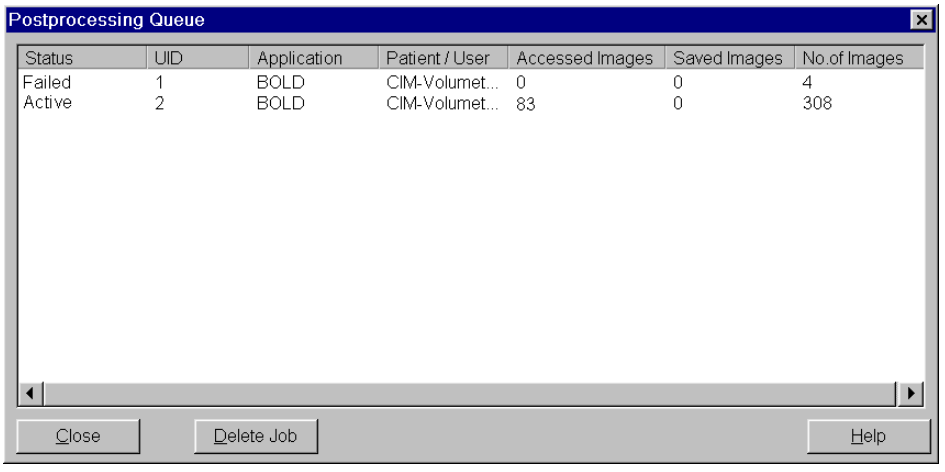
Tracking post-processing

You are able to track image calculations in the **Postprocessing Queue** dialog box.



✧ Click the icon on the status bar.

The **Postprocessing Queue** dialog window is displayed.



You can stop the calculation of individual series if they are identified with the "active" status.

✧ Select a calculation.



✧ Click the **Delete Job** button.

Calculation will be stopped and deleted from the job list. No images will be calculated.

Editing a post-processing protocol

The postprocessing protocol contains the following postprocessing algorithms:

- ❏ Spatial filtering
- ❏ 3D motion correction
- ❏ t-test

Spatial filtering

Low-pass filtering is used to soften images. A Gaussian filter is used. You can choose one of several filter strengths.

3D motion correction

Various interpolation methods (linear, sinc, k space) and their parameters are available. In addition you can save the motion parameters detected (3 translations and 3 rotations).

t-test

You may choose from various algorithms and their parameters (e.g. type of paradigm).

NOTICE

Only experienced users should edit the postprocessing protocol.

The postprocessing protocol itself contains instructions on how to edit.

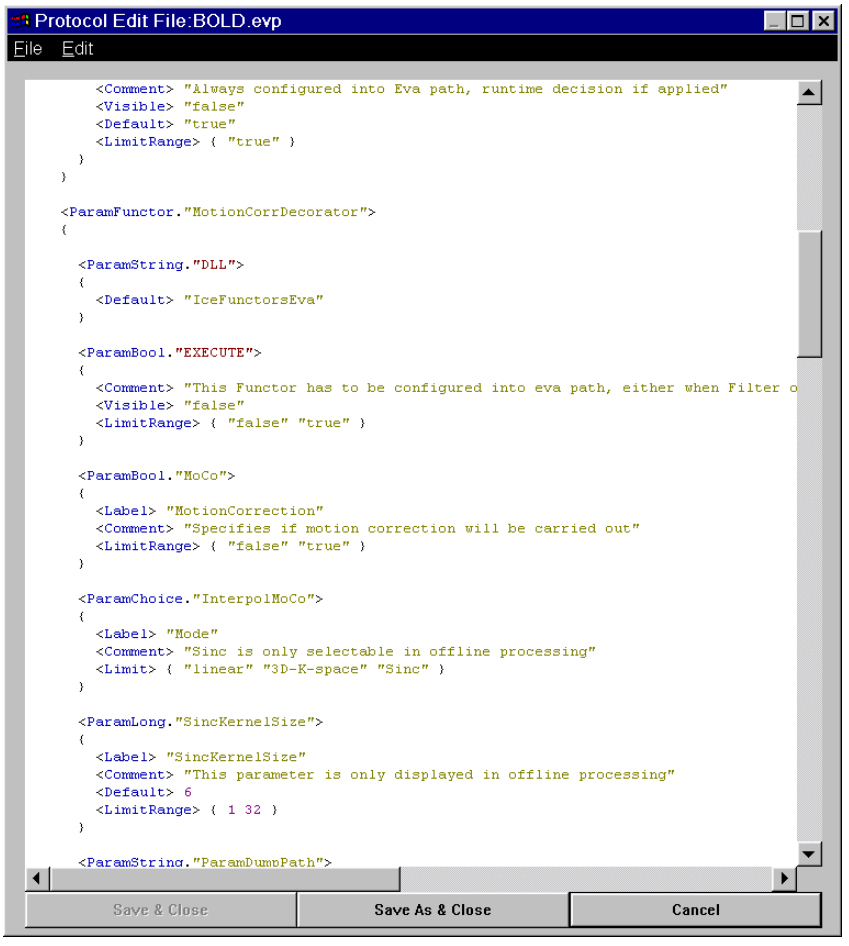
Starting the protocol editor

You can edit a postprocessing protocol in the **Protocol Editor**.



✧ Click the **Edit Protocol** button in the **Evaluation Controller Dialog** dialog box.

The **Edit Protocol** dialog box opens.



Saving a change under the same name

You can quickly save user-defined postprocessing protocols (but *not* Siemens postprocessing protocols).



✧ Click the **Save & Close** button.

The selected post-processing protocol will be overwritten with the new settings.

The **Edit Protocol** dialog box is closed.

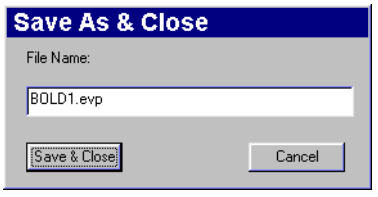
Saving changes under a new name

You can save changed postprocessing protocols under a new name. This makes it possible to change Siemens postprocessing protocols.

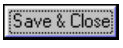


✧ Click the **Save As & Close** button.

The **Save As & Close** dialog box opens.



✧ Enter a file name.



✧ Click the **Save & Close** button.

A new post-processing protocol is created. The **Edit Protocol** dialog box is closed.

Closing BOLD

✧ Select **Applications > Close BOLD** from the main menu.

Or

✧ Start another application function.

The **BOLD** task card is closed.



CHAPTER D.5

Evaluating Perfusion-Weighted Images

The **Perfusion** evaluation function allows the display and evaluation of perfusion-weighted images, for example, for tumor diagnosis.

The following parameters can be calculated on the **Perf MR** task card:

- ❏ time to bolus maximum (time-to-peak, TTP)
- ❏ relative mean transit time (relMTT)

The use of such parameter maps has been shown to be highly beneficial in a number of perfusion studies. Nevertheless, you should only attempt it if you have sufficient experience in interpreting parameter images and take into account possible limitations.

The Perf MR task card

Calling up the task card

You can open the **Perf MR** task card from any other task card or from the **Patient Browser**.

✧ Select **Applications > Perfusion (MR)** from a task card or **Applications > Perfusion (MR)** from the **Patient Browser**.

The **Perf MR** task card opens.

If images, series, or a study are selected in the **Patient Browser**, they will automatically be loaded into **Perf MR**.

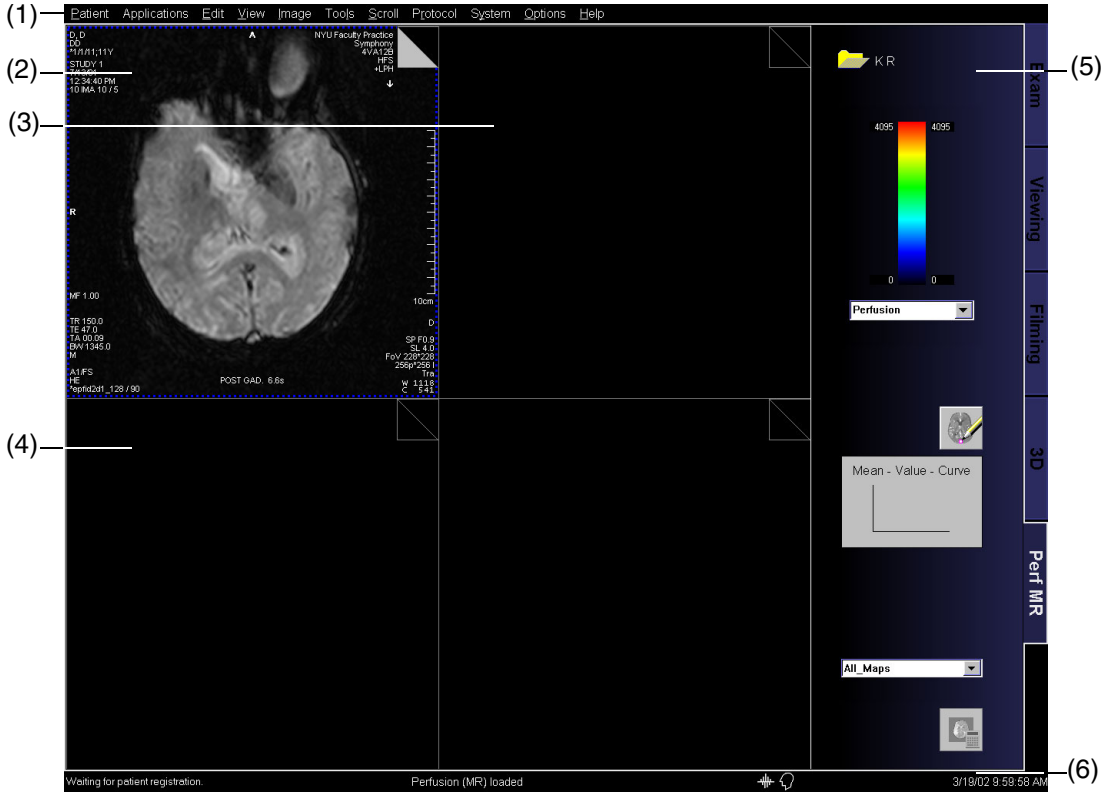
Closing the task card

✧ Select **Applications > Close Perfusion (MR)**.

The **Perf MR** task card is closed.

Task card layout

The **Perf MR** task card is divided into the following areas:



(1) Menu bar
(2) Base image segment
(3) Viewing area
(4) Parameter map segment (TTP and relMTT)
(5) Control area
(6) Status bar

(2) and (4) are the processing area.

Loading Images

You will select images and series in the **Patient Browser** that you want to display or evaluate on the **Perf MR** task card.

You can choose single images as well as a series or complete studies.

It is *not* possible to load images of different studies onto the **Perf MR** task card.

NOTICE

Perfusion analysis requires that the user have full access rights to the patient data to be evaluated.

Please observe the information given in the Safety Standards book.

Loading images for evaluation

The analysis is typically performed using time-series of T_2*-weighted or T_2-weighted single-shot echo-planar images. These base image series may contain several hundred images acquired in quick succession to provide a dynamic display (1 scan every 1 to 2 seconds over 1 to 2 minutes).

Requirements

For calculation of parameter images, suitable basic images are grouped into a "volume block" and evaluated. These basic images have to meet the following criteria:

- ❏ same series block and table position
- ❏ same FOV
- ❏ same slice orientation
- ❏ same matrix size
- ❏ the slice position should not differ by more than one vector orthogonal to the slice plane
- ❏ same number of images for a slice position

➪ Several "volume blocks" can be loaded in the basic image segment. However, the only the volume block evaluated is the one that contains the current image in the base image segment.

✧ Open the **Patient Browser**.

✧ Select the series.

✧ Select **Applications > Perfusion (MR)**.

Or

✧ Drag and drop the required series into the processing area of the *Perf MR* task card.

Or

✧ Double-click the required series.

The images are transferred to the **Perf MR** task card and automatically sorted into the segments of the processing area.

❏ Top left segment (basic image segment)
anatomical images
❏ Bottom left segment (parameter image segment)
TTP images und relMTT images

➪ If you have already loaded these images into the viewing area, a dialog box will let you decide whether to move these images into the processing area.

Loading images for viewing

For example, you can load the diffusion images of the study into the top right segment to view and compare the anatomy being evaluated.

✧ Open the **Patient Browser**.

✧ Select the series and images you want to view.

✧ *Drag and drop* the required series into the top right segment (viewing area) of the *Perf MR* task card.

➪ If you have already loaded these images into the processing area, a dialog box will let you decide whether to move these images into the viewing area.

Viewing images

Series and images are always displayed as an image stack in every segment of the **Perf MR** task card. You may scroll image by image or series by series separately in each segment.

Scrolling gives you a general view of the scan, allowing you to find a suitable basic image for positioning the "Region of Interest" (ROI).

You can optimize image display by various methods.

Automatic sorting of images

The image sort that applies in the **Patient Browser** does *not* apply on the **Perf MR** task card.

On the **Perf MR** task card, images in the basic image segment are sorted differently than in the other three segments.

Sorting in the basic image segment

In the basic image segment, images are sorted independently of series and image numbers. (The series and image numbering can be set by the user.)

The following applies to image-by-image scrolling:

❏ The images are displayed in anatomical sequence. Exception: If image copies are loaded, these will be displayed one after the other before reaching the anatomically closest image.

The following applies to series-by-series scrolling:

❏ The images of a slice position are displayed in the order of their scan times.

Sorting in all the other segments

The other segments sort the images by series or image numbers.

The following applies to image-by-image scrolling:

❏ Series number
❏ Image number
❏ Time of image generation for image copies

The following applies to series-by-series scrolling:

❏ Image number
❏ Series number
❏ Time of image generation for image copies

Automatic sorting when loading more images

You can load additional images onto the **Perf MR** task card even though it already contains images.

These images will be correctly sorted into the segments by image type, series, and image number.

Scrolling images and series

Scrolling between images

Scrolling image by image allows you to look for the slice position that provides the best view of the anatomy to be evaluated.

✧ Use the dog ears in the top right-hand corner of the image segments.
→ *syngo* Operator Manual

Or

✧ Select **Scroll > Image Next** or **Scroll > Image Previous**.

Or

✧ Scroll using the **Image-** or **Image+** key on the symbol keypad.

Scrolling series by series

The image with the "best" slice position is in foreground. Scrolling series by series always shows the image with this slice position.

Scrolling series by series allows you to look for the scan time with maximum vessel contrast in the bolus (vessel is dark).

✧ Select **Scroll > Series next** or **Scroll > Series prev**.

Or

✧ Scroll using the **Series-** or **Series+** key on the symbol keypad.

The series are displayed in the order of the scan times. The images shown all have the same slice position.

Optimizing image display

You can use the following methods:

- ❏ Changing brightness and contrast (windowing)
- ❏ Zooming/panning
- ❏ Fit to segment size
- ❏ Inverting grayscale values
- ❏ Showing/hiding image text
- ❏ Inserting an annotation

These actions are described in detail in the **Viewing** chapters.
→ *syngo* Operator Manual

Calculating parameter images

The following parameter images may be calculated offline via post-processing protocols:

- ❏ TTP image
- ❏ relMTT image

Select a post-processing protocol.

You determine the arterial input function (AIF) and set the time ranges for evaluation.

You start the post-processing protocol.

You can assign suitable color coding to the calculated parameter images and optimize the window values.

Experienced users can edit the postprocessing protocols.

Selecting a post-processing protocol

The last post-processing protocol to have been used is shown in a selection list in the lower part of the control area.



✧ Select the required postprocessing protocol from the selection list.

Calculating mean AIF

Arterial Input Function (AIF)

The AIF is calculated from the time curve of the CA concentration. The measurement method used is the same as for the CA concentration in tissue. The AIF is measured simultaneously with the tissue concentration. It is calculated either in the same slice as the CA concentration in the tissue or in a certain slice of the block if two or more slices are used. This slice should contain sufficiently large vessels to prevent partial volume effects.

Calculation of the relMTT involves deconvolution with the signal time curve selected for the AIF. This slice should contain sufficiently large vessels to prevent partial volume effects. This means that the quality of these parameter maps deteriorates with a reduced signal-to-noise ratio of the basic images that were used for calculating the parameter maps and determining the AIF.

RECOMMENDATION

Please do not use the
relMTT images,
if the SNR in the basic images is too low and/or head movements of the patient are clearly visible.

You determine the mean AIF curve from the individual AIF curves within an ROI (region of interest).

✧ Look for a suitable basic image for positioning the AIF-ROI in the top left segment.
→ Page D.5–10, *Scrolling images and series*

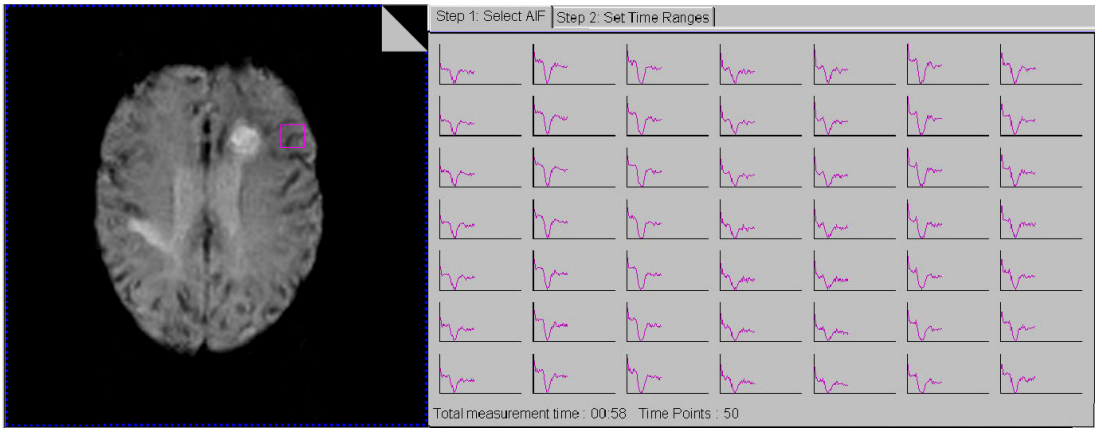


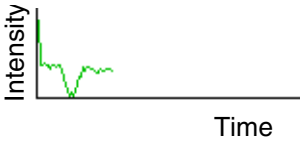
✧ Click the **Define AIF** button in the control area.

Or

✧ Select **Tools > AIF**.

An AIF-ROI is drawn in the basic image. The AIF curves are shown for all pixels within the AIF-ROI above the top right segment (viewing area).





The AIF curves represent the change over time in the signal intensity for each pixel in the AIF ROI. All AIF curves have the same scaling and are therefore comparable.

The position and number of AIF curves shown matches the position and number of pixels in the AIF ROI.



The footer of the **Step 1: Select AIF** subtask card shows the number of images used for determining the AIF.

Positioning an AIF ROI

To calculate the mean AIF, select pixels exhibiting a signal over time curve that is typical of healthy arteries.

NOTICE

Only personnel trained in perfusion diagnostics should position the AIF ROI and select suitable AIF curves to calculate the mean AIF.

The AIF ROI should be located close to the profusion anomaly.

Position the AIF ROI with great care;

over healthy arteries, such as the A. cerebri media, but also over smaller arteries that are not explicitly recognizable as vessels in the basic image.

✧ Left-click the AIF ROI and drag it to its new position in the basic image.

The associated AIF curves are displayed in the viewing area when you release the mouse button.

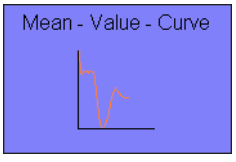
Selecting AIF curves

Select suitable AIF curves for determining the mean AIF.

AIF curves with a very low signal minimum may have a distorted shape if the SNR of the associated pixel in the basic image is too low. Do *not* use such AIF curves for evaluation.

✧ Select the AIF curves in **Step 1: Select AIF** subtask card (press the **Ctrl** or **Shift** key to select multiple items).

The selected AIF curves are displayed with a white background.



The mean AIF curve in the control area is refreshed. It indicates the arithmetic mean of the selected AIF curves.

➪ The selection of AIF curves is retained until you move the AIF ROI to another point in the basic image or until you select an image outside the time series displayed.

Setting the time range

It is mandatory to set the time range for perfusion analysis.

✧ Move **Step 2: Set time ranges** in foreground.



The mean AIF is enlarged. The Global Bolus Plot (GBP) is also displayed.

You define the time range to be used for perfusion analysis. The image range corresponds to the basic images to be used.

✧ *Left*-click on the right line and drag it to the end of the first pass.

✧ *Left*-click on the center line and drag it to the end of the base line.

✧ *Left*-click on the left line and drag it to the beginning of the base line.

➪ Observe the GBP curve. The bolus arrives in the tissue later than in the vessel. Do not define the end of the first pass to far left. Otherwise the bolus in the tissue could be cut off.



✧ Select the **Confirm time ranges** check box to confirm the time range.

The **Run protocol** button in the lower control area is activated. You are now ready to start the post-processing protocol.

Starting calculation

You have selected a post-processing protocol, calculated the mean AIF, and set the time range. You are now ready to start the calculation.



✧ Click the **Run protocol** button in the lower control area.

Or

✧ Select **Protocol > Execute**.

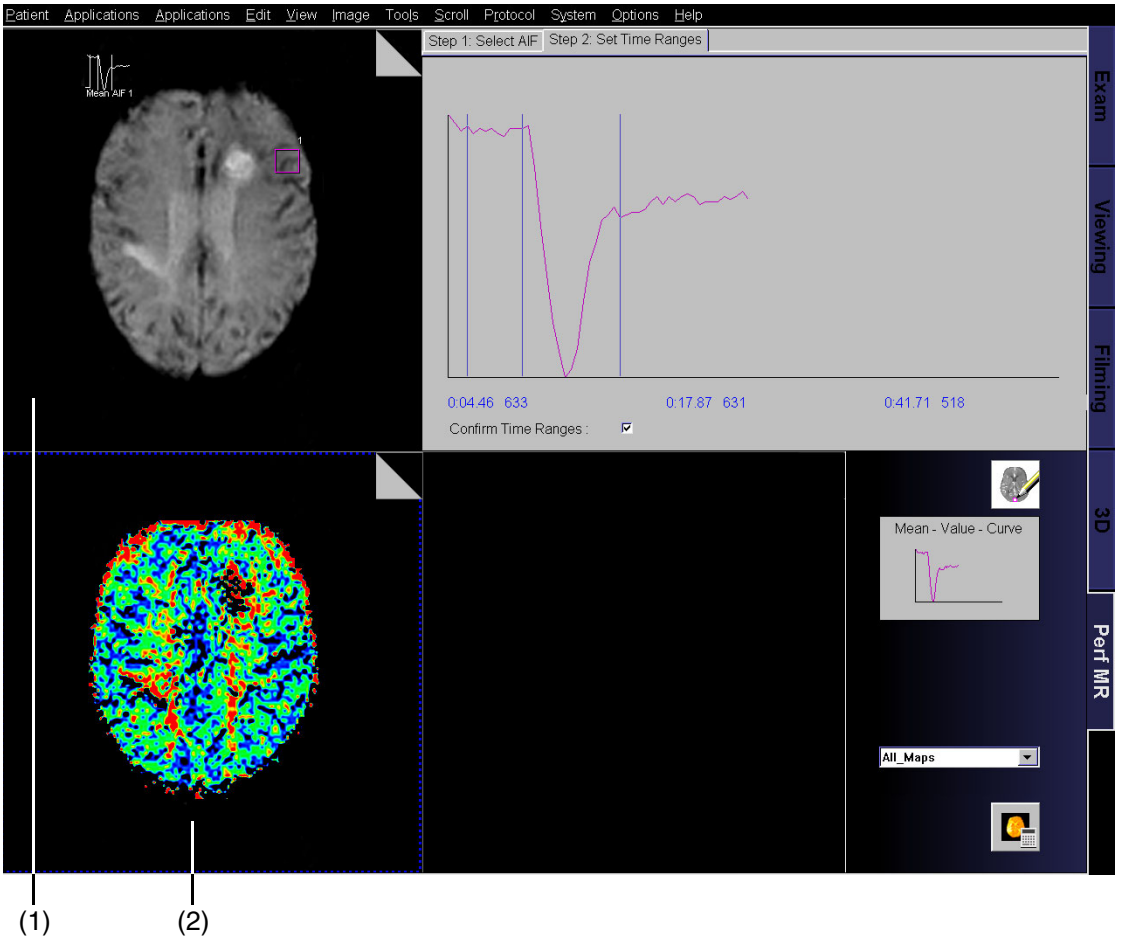


The post-processing protocol starts. The calculation runs in background. The image post-processing job icon appears on the status bar. The message "Calculation in progress - please wait" is also shown.

Upon completion of the calculation, the parameter images calculated are displayed in lower left segment.

Images already loaded in the lower left segment are retained and can be viewed via scrolling.

The top left segment shows the mean AIF with the time range set in the basic image in addition to the AIF-ROI (reference image).



(1) Reference image
(2) relMTT image

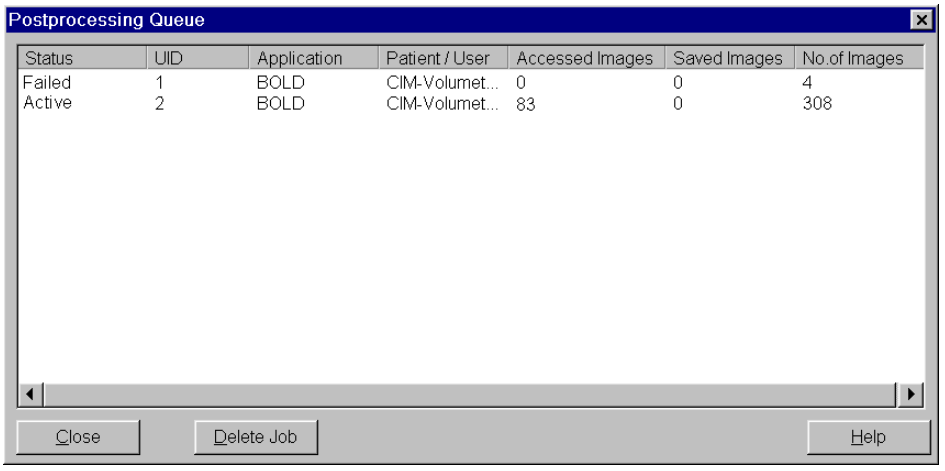
Tracking postprocessing

You can track image calculations in the **Postprocessing Queue** dialog box.



✧ Click the icon on the status bar.

The **Postprocessing Queue** dialog window is displayed.



You can stop the calculation of individual series if they are identified with the "active" status.

✧ Select a job.



✧ Click the **Delete Job** button.

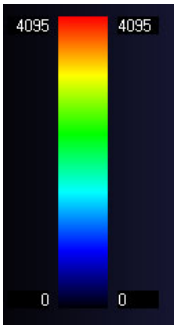
Calculation will be stopped and deleted from the job list. No images will be calculated.

Changing the color display

The color display of parameter images may be defined via the color palette. The color settings apply to all images loaded in the parameter image segments.



✧ Select the required color scheme from the selection list.



The color palette shows the selected color scheme. The color display in the two lower parameter image segments is updated to the color palette selected.

Windowing color parameter images

✧ Window the images in the parameter map segments using the center mouse button.

The minimum and maximum values in the color palette are adjusted to the current window values.

TIP

If optimal windowing is a problem in color parameter images:

✧ Display the parameter images first in black-and-white.

✧ Window the black-and-white parameter images.

✧ Subsequently display the parameter images in color again.

Storing and filming results

The calculated parameter images are automatically stored in the database without a color palette.

You can recognize the automatically stored parameter image series in the **Patient Browser** by the following designation: **[Series number] ep2d_perf_parameter image type**.

The image type of the parameter images is shown in the image text at the bottom left.
→ Page H.2–1, *Text Annotations in Medical Images*

Storing selected images

You can store the reference image and select additional parameter images.

✧ Select the images explicitly.
→ *syngo* Operator Manual

✧ Select **Patient > Save As...**.

The **Save As** dialog box is displayed.

The selected images are stored with the color palette in a new series or appended to an existing series.
→ *syngo* Operator Manual

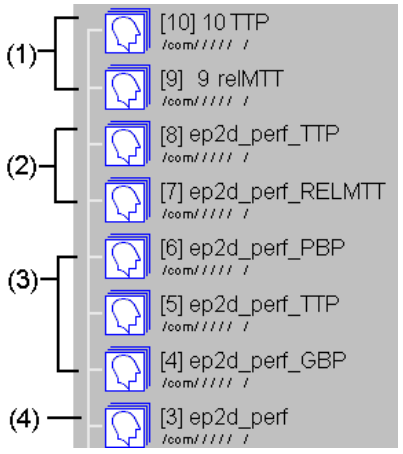
✧ Enter a unique name for the new series.

NOTE

When a user logs off, unsaved data are irretrievably lost.

Check whether data still needs to be saved and save any data you want to keep before you log off.

Parameter image series in the Patient Browser



(1) Parameter images obtained "offline"; explicitly stored with the color palette
(2) Parameter images obtained "offline"; automatically stored without the color palette
(3) Parameter images obtained "inline"
(4) Original series; input for post-processing

Filming results

You may copy images to the film sheet, define film layouts, start filming, and organize film jobs on the **Perf MR** task card.
→ *syngo* Operator Manual

✧ Select the images you would like to transfer to the film sheet.

✧ Select **Patient > Copy to Film Sheet**.

Editing the postprocessing protocol

A post-processing protocol contains a certain sequence of post-processing steps. You can activate, deactivate, and configure the post-processing steps.

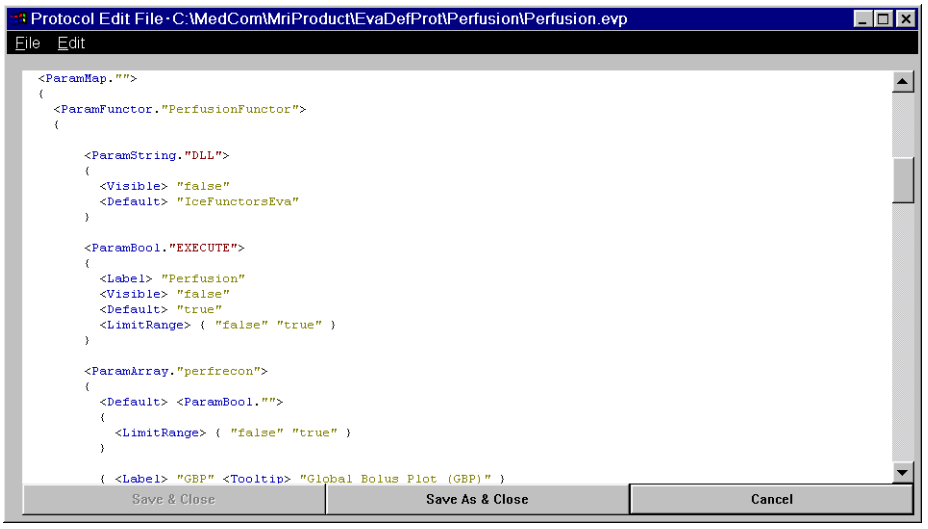
NOTICE

Only experienced users should edit the post-processing protocol.

✧ Select the required post-processing protocol from the selection list.

✧ Select **Protocol > Edit**.

The **Edit Protocol** dialog box opens.



The protocol displayed itself contains instructions on how to edit.

Saving changes under the same name

User-defined post-processing protocols can be changed and stored.



✧ Click the **Save & Close** button.

The selected post-processing protocol will be overwritten with the new settings.

The **Edit Protocol** dialog box is closed.

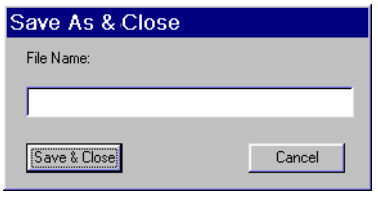
Saving changes under a new name

You can save changed Siemens post-processing protocols under a different name. It is not possible to overwrite Siemens postprocessing protocols.

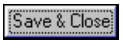


✧ Click the **Save As & Close** button.

The **Save As & Close** dialog box opens.



✧ Enter a file name.



✧ Click the **Save & Close** button.

A new post-processing protocol is created. The **Edit Protocol** dialog box is closed.

CHAPTER D.6

Breast Evaluation MR

The **Breast Evaluation MR** dialog box provides the following options:

- ❏ You can calculate new result images by combining loaded images. This allows you to generate parameter images or combined images.
- ❏ You can edit the protocol parameters to suit your needs and save them in the protocols used to calculate the parameter images and combined images.

Introduction

The result images are calculated in the **Breast Evaluation MR** dialog box, selectable via the Patient Browser.

➪ The **Breast Evaluation** can only process images from the same series block acquired at the same table position. It is only possible to load images of one study, i.e. of one patient.

The following result images can be calculated:

❏ Parameter images
❏ Combined images

Definitions

The image types used in **Breast Evaluation** are defined as follows:

❏ **Anatomical image**
An anatomical image is obtained during a patient exam. This is then used as the basis for calculating parameter images.

❏ **Parameter image**
Instead of anatomical information, a parameter image contains functional information. Using algorithms, it is generally calculated based on anatomical images from several scans.

❏ **Combined image**
This image is calculated by combining several parameter images.

Access authorization to the evaluation dialog box

Detailed information about access authorization is available in the *Safety Standards* book.

If you do not have access to the data of a specific patient, that patient's data will not be shown in the Patient Browser when you are logged onto the system.

The following rules apply to activities in this dialog box:

- ❏ The evaluation dialog box closes automatically on system log-off. Any unsaved changes in a postprocessing protocol are lost.
- ❏ A query appears when changing the operator to one that does not have access authorization to patient data, prompting you to terminate the operator change. If you do not want to cancel the operator change, the activity will be terminated and all data unloaded. The dialog box closes.
  The dialog box remains open and changes to an operator with access authorization to the data.

NOTE

When a user logs off, unsaved data are irretrievably lost.

Check whether data still needs to be saved and save any data you want to keep before you log off.

Selecting the evaluation dialog window

The **Breast Evaluation MR** dialog box is opened from the Patient Browser.

➪ The dialog box will open only if at least one series containing anatomical images and/or parameter images is selected in the Patient Browser.

Procedure for selecting the evaluation dialog box:

❏ Opening the Patient Browser

❏ Select exam, series, or images

❏ Opening the dialog

Opening the Patient Browser

✧ Select **Patient > Browser** from the main menu.

The **Patient Browser** dialog box appears.

Selecting data

The required exam, series, or images are selected just as they are when loading them onto a task card.

In this case, however, the calculations performed in the **Breast Evaluation MR** dialog box depend on the data selected.

❏ Anatomical images in examinations or series are required to calculate parameter images.

❏ Parameter images in exams or series are used to calculate combined images.

✧ Select the required exam, series, or individual images.
→ *syngo* Operator Manual

Opening the dialog

If the selected examinations or series contain anatomical images or parameter images, you may select the evaluation dialog box.

✧ Select **Applications > Breast (MR)** in the Patient Browser.

Only one image type is available

If the examinations or series contain only images of one type (anatomical images or parameter images), the dialog box opens automatically. This also activates the subtask card relevant for evaluation of the loaded image type.

Image type	Associated evaluation/subtask card
Anatomical images	Calculate parameter map
Parameter images	Calculate combined images

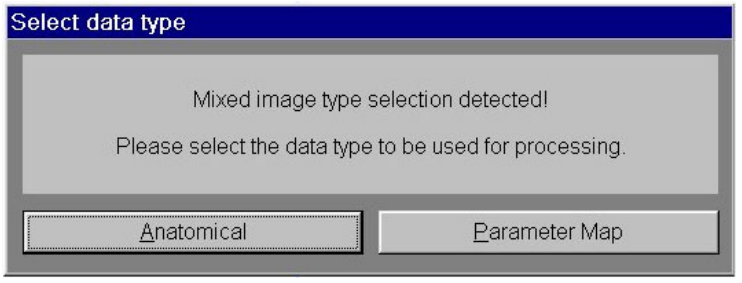
NOTE

Only series containing magnitude images are taken into account in anatomical series. Other series (e.g. other modalities or compressed images) are automatically filtered out when the dialog box starts.

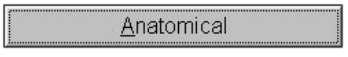
They are not displayed in the list of anatomical series of the **Calculate Parameter Map** subtask card. A message indicates this when the dialog box starts.

Both image types available

If the series contains both anatomical images and parameter images, the **Select Data Type** dialog box appears with a warning that mixed data selection has been detected:



Because only one image type can be calculated in the evaluation dialog box, you have to decide which evaluation you want to give priority to. Load the images with the **Anatomical** or **Parameter Map** buttons.



❏ Loads anatomical images into the evaluation dialog; the **Calculate Parameter Map** subtask card is active.



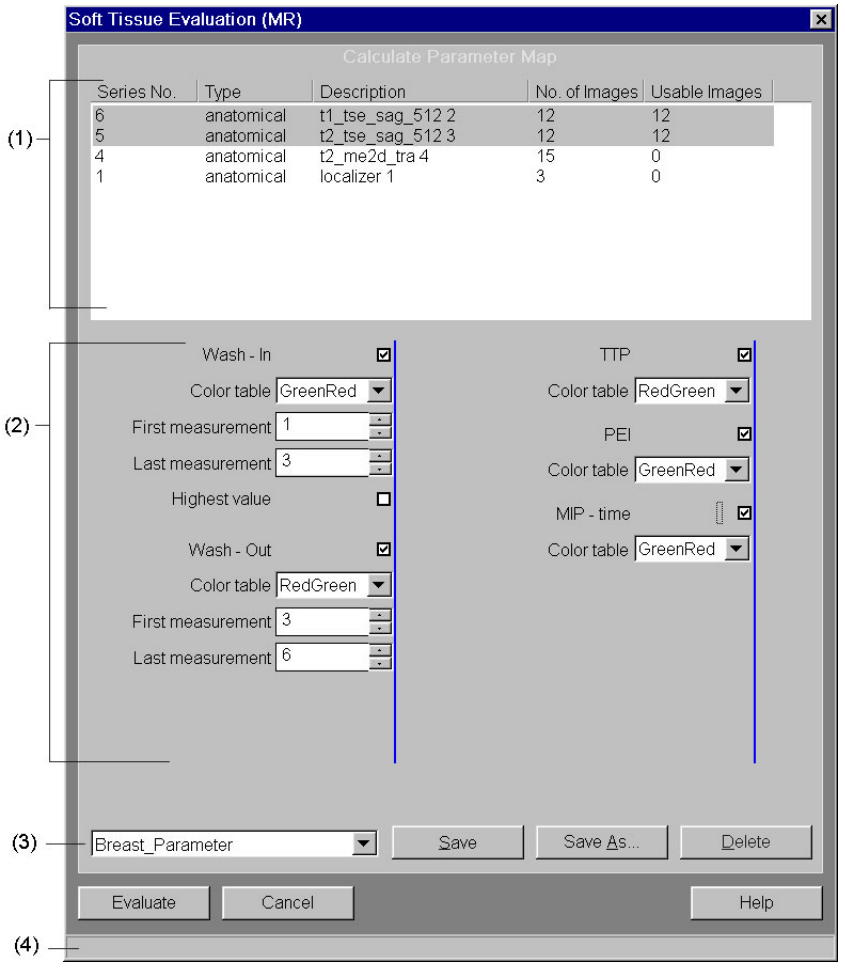
❏ Loads parameter images into the evaluation dialog; the **Calculate Combined Image** subtask card is active.

✧ Click the button to start the required evaluation.

The evaluation dialog box opens; the subtask card for the selected evaluation is automatically active.

Layout of subtask cards

The layout of the two subtask cards in the evaluation dialog is identical. Example: *Calculate Parameter Map* subtask card.



(1) List of all anatomical series or parameter series available in the currently loaded study.
For each series the list shows the **Series No.**, the **Series Type**, the **Series Description**, and the **Number of images contained** and **used**.
(2) Display of the parameters of the selected postprocessing protocol.
(3) Toolbar for selecting, storing, or deleting postprocessing protocols.
(4) Status line for warnings about images not loaded

Calculating parameter images

Parameter images are obtained by selecting and running a parameter image postprocessing protocol if the images meet the following conditions:

Requirements

- ❏ all slice positions and orientations are identical
- ❏ all fields of view (FOV) are identical
- ❏ all slice thicknesses are identical
- ❏ all numbers of columns and lines (matrix) are identical

Additionally, several series of anatomical images have to be loaded on the **Calculate Parameter Map** subtask card.

If all requirements are met, the parameter images are calculated.

Procedure for calculating parameter images:

- ❏ Selecting/Unselecting anatomical image series
- ❏ Selecting postprocessing protocol
- ❏ Editing protocol (optional)
- ❏ Saving protocol data (optional)
- ❏ Deleting customer protocols (optional)
- ❏ Performing reconstructions

Selecting anatomical series

When you open the evaluation dialog box, the preselected series are shown on the **Calculate Parameter Map** subtask card.

The program compares the series previously selected in the Patient Browser with other series of the same examination for an identical number of "usable images".

All series that meet this condition are shown marked together with the original series in the list of series in the dialog box.

➪ Series that do not meet this condition cannot be selected later either.
The first image of the first selected series is the comparison reference for usable images.

Series No.	Type	Description	No. of Images	Usable Images
6	anatomical	t1_tse_sag_512 2	12	12
5	anatomical	t2_tse_sag_512 3	12	12
4	anatomical	t2_me2d_tra 4	15	0
1	anatomical	localizer 1	3	0

You can use the preselected images for calculation. You also have the following options:

❏ You can deselect single series out of a preselection if you do not want to include them in the calculation.

❏ You can select completely new series. These have to have the same number of usable images.

Unselecting series from the preselection

✧ Hold the **Ctrl** key down and unselect series you do not require by clicking them.

The series no longer needed are shown marked in the list of series.

Making a new selection

✧ Click the required series in the list.

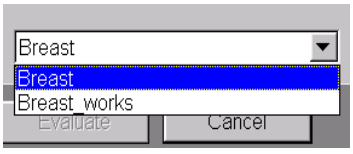
The previous preselection is now canceled. All series in the list of anatomical series having the same number of "usable image" as the selected series are automatically preselected.

➪ You can also deselect unneeded series from this new preselection.

Selecting a postprocessing protocol

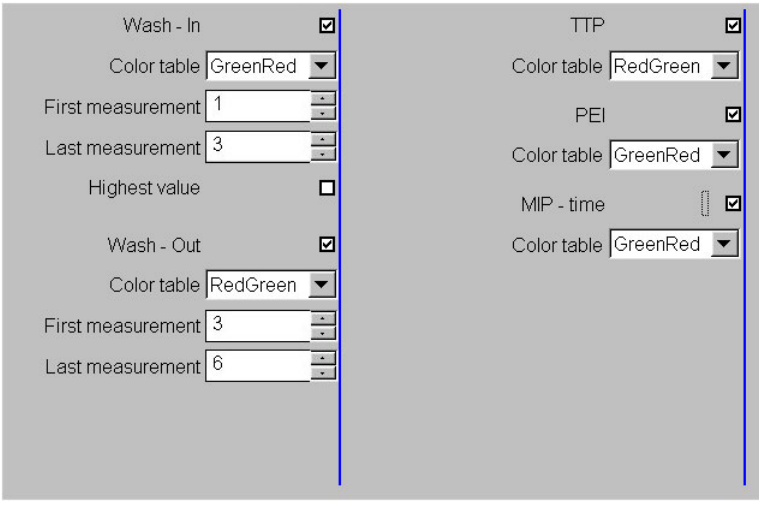
You require a postprocessing protocol for image calculation. You can select the postprocessing protocol from the selection list on the toolbar.

Both Siemens and user-defined customer protocols can be organized in the selection.



✧ Select the required post-processing protocol from the selection list.

The protocol parameters are displayed on the subtask card. If necessary, you may change them prior to the calculation.



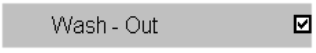
Editing protocol parameters (optional)

For calculating parameter images the system organizes both Siemens and user-defined customer protocols.

You can set the following evaluations in the protocols:

- ❏ **Wash-In** – Signal change in the starting range of the dynamic measurement series
- ❏ **Wash-Out** – Signal change in the end range of the dynamic measurement series
- ❏ **TTP** – Time to peak – time elapsed before reaching the signal peak
- ❏ **PEI** – Positive enhancement integral – area under a signal intensity - time curve
- ❏ **MIP time** – Maximum intensity projection – highest pixel value in the measurement interval

The listed evaluations can be activated in check boxes. These evaluations are either activated or not depending on the protocol selected.



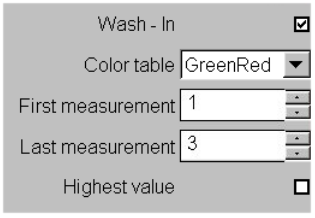
✧ Select or deselect the evaluation.

➪ If an evaluation is deactivated in the protocol, the corresponding parameter image is *not* calculated in the evaluation.

Wash-In

In the **Wash-In** setting area, you may change the parameters for signal change in the starting range of the dynamic measurement series.

Parameters	Comment
Color table	Color table assigned to the wash-in image obtained.
First measurement	First measurement that is used for calculation of the wash-in image.
Last measurement	Last measurement that is used for calculation of the wash-in image.
Highest value	Defines whether the highest value of the input images should be considered in the "First measurement - last measurement" interval for calculating the parameter image instead of the value from "Last measurement".

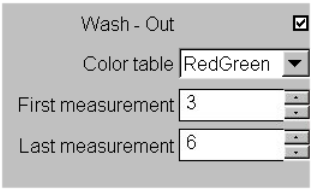


- ✧ Set the **Color table** parameter in the combo box.
- ✧ Set the **First measurement** and **Last measurement** in the appropriate spin box.
- ✧ Select or deselect the **Highest value** option.

Wash-Out

In the **Wash-Out** setting area, you can change the parameters for signal change in the end range of the dynamic measurement series.

Parameters	Comment
Color table	Color table assigned to the wash-out image obtained.
First measurement	First measurement that is used for calculation of the wash-out image.
Last measurement	Last measurement that is used for calculation of the wash-out image.

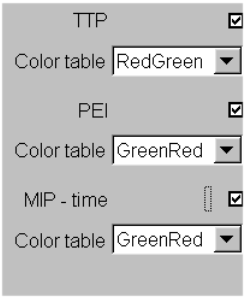


✧ Set the **Color table** parameter in the combo box.

✧ Set the **First measurement** and **Last measurement** in the appropriate spin box.

TTP, PEI, MIP time

In the **TTP**, **PEI**, and **MIP time** setting areas, you can assign color tables to the appropriate TTP, PEI, or MIP images.



✧ Set a color table in the above setting areas using the corresponding combo box.

Saving protocol data (optional)

When saving protocols you have to differentiate between:

- ❏ **Siemens protocols**:
  Changes may only be saved as new customer protocols.
- ❏ **Customer protocols**:
  Changes may be saved in the current protocol. The previous settings are overwritten. You may also save the changes in new customer protocols.

NOTE

If you do not save the data before a change in operators, a message indicating that data have not been saved will appear if the new user does not have the required read rights. You may then decide whether to continue or cancel the action.

Caution: If you go through with the action, the evaluation dialog box will close and all settings made so far will be lost.

NOTE

When a user logs off, unsaved data are irretrievably lost.

Check whether data still needs to be saved and save any data you want to keep before you log off.

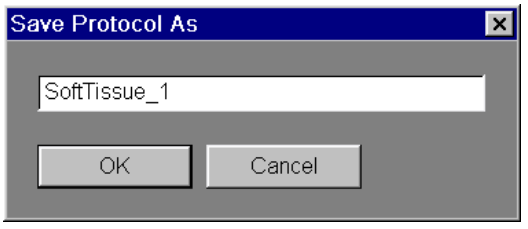
Saving a new customer protocol

You can save a postprocessing protocol that you have changed as a new customer protocol at any time. If you change a write-protected Siemens protocol, you must create a new customer protocol. In this case, the **Save** button is deactivated.

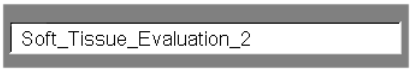


✧ Click the **Save As** button.

The **Save Protocol as** dialog box opens.



➪ For changed Siemens protocols, a new name is automatically suggested for the protocol in the text input box. You can either accept this name or overwrite it with a new name.



✧ Enter a name in the text input field or overwrite the suggested name.



✧ Click the **Save** button.

The postprocessing protocol is saved as a new customer protocol.

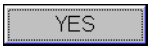
Overwriting an existing customer protocol

If you do not want to create a new protocol having changed a customer protocol, you can save the changes in an existing protocol.



✧ Click the **Save** button.

A message window opens.



✧ Click the **Yes** button.

The existing customer protocol is overwritten.

NOTE

If you do not want to start calculation with the set protocol parameters, you can close the dialog box with **Cancel**.

Deleting a customer protocol (optional)

Unlike Siemens protocols, customer protocols may be deleted at any time.

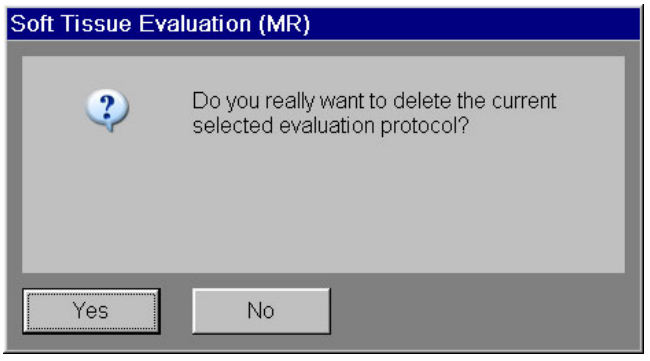
➪ Only a customer protocol that is currently active may be deleted.

✧ Mark the protocol to be deleted in the selection list.

Delete

✧ Click the **Delete** button

A query is displayed:



YES

✧ Click the **Yes** button.

The protocol is deleted from the list of parameter image protocols.

Performing a calculation

After you have made all the necessary settings on the **Calculate Parameter Map** subtask card, you may start with the calculation.



✧ Click the **Evaluate** button.

➪ With the **Cancel** button, you can reject the changes made in the dialog box and close the dialog box.

Calculation starts and the evaluation dialog box closes. The status of postprocessing is indicated on the status bar.

➪ If protocol data are still unsaved when you start calculation, a query asks if you want to save these data before the dialog box closes.

TIP

While image calculation is in progress, you may define and start further calculations. This requires selection in the Patient Browser again. The individual calculations are processed sequentially.

After completing the calculations, the result images are automatically stored in the database and loaded onto the **Viewing** task card.

Calculating Combined Images

Combined images are obtained from combining previously selected parameter images.

Requirements

The loaded images must meet the following conditions:

- ❏ all slice positions and orientations are identical
- ❏ all fields of view (FOV) are identical
- ❏ all slice thicknesses are identical
- ❏ all numbers of columns and lines (matrix) are identical

NOTE

Combinations are based on **Wash-In**, **Wash-Out**, **TTP**, **MIP**, and **PEI** parameter images only.

If all requirements are met, the combined images are calculated.

Procedure for calculating combined images:

- ❏ Selecting parameter image series
- ❏ Selecting a combined protocol
- ❏ Editing protocol (optional)
- ❏ Saving a protocol (optional)
- ❏ Deleting a customer protocols (optional)
- ❏ Performing a calculation

Selecting parameter image series

When you open the evaluation dialog box, the preselected series are shown on the **Calculate Combined Image** subtask card.

The program compares the series previously selected in the Patient Browser with other series of the same examination for an identical number of "usable images".

All series that meet this condition are shown marked together with the original series in the list of series in the dialog box.

➪ Series that do not meet this condition cannot be selected later either.
The first selected series is the comparison reference for usable series.

Series No.	Type	Description	No. of Images	Usable Images
7	wash-in	t1_tse_sag_512 2_Washin	12	12
8	wash-out	t1_tse_sag_512 2_Wash...	12	12
9	TTP	t1_tse_sag_512 2_TTP	12	12
10	MIP-time	t1_tse_sag_512 2_MIP	12	12
11	PEI	t1_tse_sag_512 2_PEI	12	12

You can, of course, use the preselected images for calculation. You also have the following options:

❏ You can deselect single series out of a preselection if you do not want to include them in the calculation.

❏ You can select completely new series, which must then also have the same number of usable images.

➪ It is not possible to select several series of the same type. Selecting a further series of the same type cancels the previous selection.

Unselecting series from the preselection

✧ Hold the **Ctrl** key down and unselect series you do not require by clicking them.

The series no longer needed are shown marked in the list of series.

Making a new selection

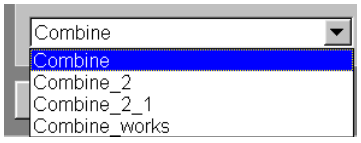
✧ Click the required series in the list.

The previous preselection is canceled. All series in the list of anatomical series having the same number of "usable image" as the selected series are automatically preselected.

➪ You can also deselect unneeded series from this new preselection.

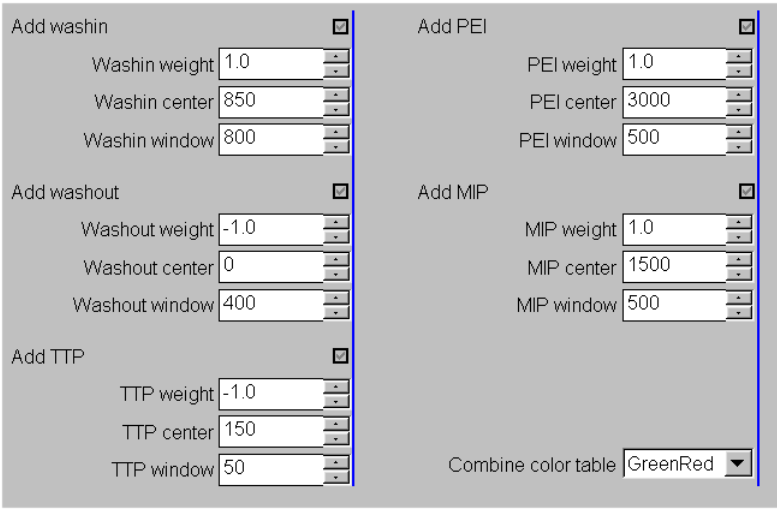
Selecting a combined protocol

You require a combined protocol for image calculation. You can select the protocol from the selection list on the toolbar. Both Siemens and user-defined customer protocols can be organized in the selection.



✧ Select the required post-processing protocol from the selection list.

The protocol parameters are then displayed on the subtask card. If necessary, you may change them prior to the calculation.



Editing protocol parameters (optional)

For calculations of combined images the system organizes both Siemens and user-defined customer protocols. You may modify the parameters of these protocols at any time.

The parameters of a combined protocol are divided into:

- ❏ Parameters for weighting the original images on generating combined images.
- ❏ Color palette that is appended to the combined image generated.

Correcting weighting parameters

You may change the following main parameters after selecting the corresponding series in the preselection:

- ❏ **Add Wash-In**
- ❏ **Add Wash-Out**
- ❏ **Add TTP**
- ❏ **Add PEI**
- ❏ **Add MIP**

NOTE

You may only change main parameters whose image series is marked in the list of series.

Example: If no TTP image series is selected in the list, the main parameter **Add TTP** is not shown on the parameter card and settings are not possible.

For each main parameter you can set the following single parameters separately:

Parameters	Effect on combined images
Weight	Weighting factor for a parameter image on combining the images
Center	Contrast value with which the parameter image is to be windowed for calculation.
Window	Brightness value with which the parameter image is to be windowed for calculation.



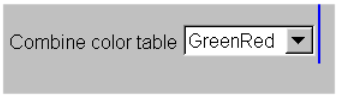
✧ Enter the new values in the spin box.

Or

✧ Click with the left mouse button on the arrows of the spin box to increase the value (up-arrow) or decrease the value (down-arrow).

Assigning a color table

The lower part of the setting area contains the **Combine Color table** selection list. This selection list is used to select the color table to assign to the combined image.



✧ Select the color table.

Saving protocol data (optional)

When saving protocols you have to differentiate between:

- ❏ **Siemens protocols**:
  Changes may only be saved as new customer protocols.
- ❏ **Customer protocols**:
  Changes may be saved in the current protocol. The previous settings are overwritten. You may also save the changes in new customer protocols.

NOTE

If you do not save the data before a change in operators, a message indicating that data have not been saved will appear if the new user does not have the required read rights. You may then decide whether to continue or cancel the action.

Caution: If you go through with the action, the evaluation dialog box will close and all settings made so far will be lost.

NOTE

When a user logs off, unsaved data are irretrievably lost.

Check whether data still needs to be saved and save any data you want to keep before you log off.

✧ Save the changed protocol as a new customer protocol.
→ Page D.6–18, *Saving a new customer protocol*

Or

✧ Overwrite the changed customer protocol.
→ Page D.6–19, *Overwriting an existing customer protocol*

Deleting a customer protocol (optional)

Unlike Siemens protocols, customer protocols may be deleted at any time.

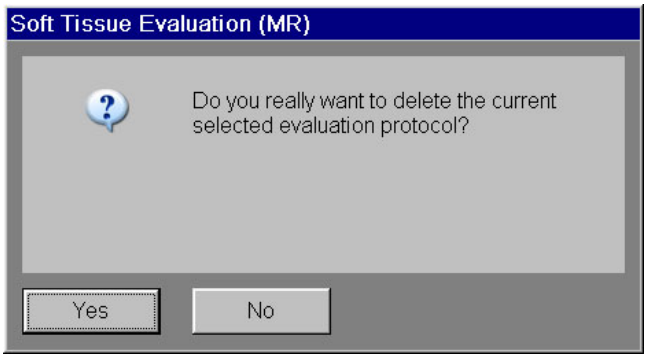
➪ Only a customer protocol that is currently active may be deleted.

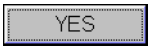
✧ Mark the protocol to be deleted in the selection list.



✧ Click the **Delete** button

A query is displayed:





✧ Click the **Yes** button.

The protocol is deleted from the list of combined image protocols.

Performing a calculation

After you have made all the necessary settings on the **Calculate Combined Image** subtask card, you may start with the calculation.



✧ Click the **Evaluate** button.

➪ With the **Cancel** button, you can reject the changes made in the dialog box and close the dialog box.

Calculation starts and the evaluation dialog box closes. The status of postprocessing is indicated on the status bar.

➪ If protocol data are still unsaved when you start calculation, a query asks if you want to save these data before the dialog box closes.

TIP

While image calculation is in progress, you may define and start further calculations. This requires selection in the Patient Browser again. The individual calculations are processed sequentially.

After calculations have been completed, the result images (combined images) are automatically stored in the database and loaded onto the **Viewing** task card.



PART
E

Vessel View

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E.5 *Saving and Documenting Evaluations*

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CHAPTER E.1

Introduction

After generating volume data during an examination, you would like to review and evaluate the blood vessels. In this case use the **Vessel View** program.

How to proceed

Loading and displaying images:
- ❏ Start **Vessel View**
- ❏ Load 3D image data
- ❏ Optimize volume image display
- ❏ Optimize slice image display

Removing unwanted parts of the image:
- ❏ Crop the Volume of Interest (VOI)
- ❏ Use the clip plane

Highlighting blood vessels:
- ❏ Separate arteries from veins
- ❏ Establish the path of the blood vessels
- ❏ Hide the area surrounding the blood vessels (segmentation)

Evaluating blood vessels:
- ❏ Display slice images through vessels (vascular navigator)
- ❏ Determine and evaluate stenoses (vascular navigator)
- ❏ Prepare series of axial vessel slice images
- ❏ Measure distances, areas, volumes, and angles

Saving and documenting evaluations:
- ❏ Saving and restoring the session
- ❏ Saving images
- ❏ Generating an overview in table format
- ❏ Filming images
- ❏ Send images to the **Viewing** task card
- ❏ Send image data for graphical slice positioning
- ❏ Export path for evaluation with **3D Fly**
- ❏ Save the rotation of the view as a movie

Starting and ending Vessel View

Starting Vessel View

You can start the **Vessel View** task card from any other task card.

✧ Select **Applications > Vessel View**.

The empty **Vessel View** task card opens.

➪ You can also load images from the **Patient Browser** when the task card is not yet opened.
→ Page E.2–1, *Loading images*

➪ Sometimes it may not be possible to use **Vessel View** while another task card is open. You are asked if you want to close the other application.

Ending Vessel View

✧ Select **Applications > Close Vessel View**.

A system message asks whether you still have data to save. This message always appears whether you have saved data or not.

✧ Click **No** if you do not want to save data.

The **Vessel View** task card closes and another task card moves into foreground.

Vessel View task card



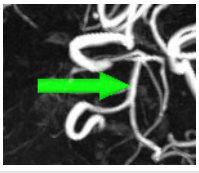
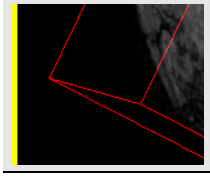
(1) Slice image segments
(2) Volume image segment
(3) Control area
(4) Evaluation area

Volume image segment

The volume image segment shows the data in VRT or MIP display.

VRT display The volume rendering technique (VRT) shows the volume data set as a 3D data set with transparency and color.

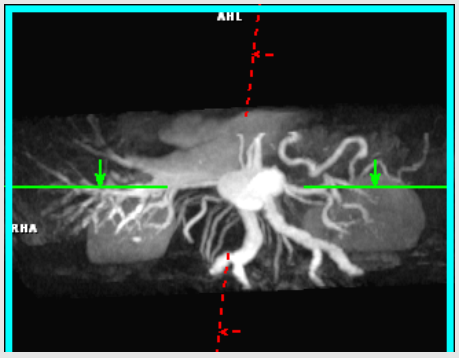
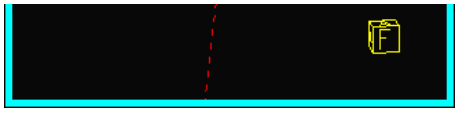
MIP display Maximum Intensity Projection (MIP) is suited to the enhancement of diagnostically relevant volumes of interest (VOIs).

Orientation aids in the volume image	Comment
 Orientation cube	Shows the current orientation of the volume image. Enables fast orientation of the volume in the standard view directions. Is used to initiate automatic rotation of the volume.
 Marking arrow	Marks the object or position last selected in the volume. You can use the **Configure** menu to set the size of the marking arrow.
 Limiting	Edges of the loaded volume data set. You can use the **Configure** menu to show and hide the delimitation.

➪ If necessary, you can temporarily magnify the volume image segment to full screen height.
→ Page E.2–8, *Enlarging the window*

Slice image segments

The three slice image segments to the left in the task card show slice images in the MPR display. As an alternative, you may switch the display to MIP, MIP thin slice, and MPR thick slice. In the standard orientation, you will find the sagittal view in the upper segment, the coronal view in the center segment, and the axial view in the lower segment.

Orientation aids in the slice image		Comment
	Reference lines	Show the position and viewing direction of the other two slice images. → Page E.2–13, *Showing/hiding reference lines*.
	Orientation cube	Shows the current orientation of the respective slice in the volume. The orientation cannot be changed using this cube.

➪ As an alternative, you may want to temporarily display a magnified slice image segment instead of the volume image segment.
→ Page E.2–8, *Enlarging the window*

Evaluation area

The lower part of the task card contains two subtask cards with tools for defining and evaluating vessels.

- The **Measurement** subtask card includes the object list.
- The **Vessel Navigator** subtask card provides special sectional image views of a vessel.

CHAPTER E.2

Loading and Displaying Images

Loading images

How to load images in the open **Vessel View** task card:

✧ Select the images desired from the **Patient Browser**.

✧ Move your selections with the mouse to the **Vessel View** window.

How to load images, regardless of whether **Vessel View** is open or not:

✧ Select the images desired from the **Patient Browser**.



✧ Click this button on the toolbar of the **Patient Browser**.
- Or -
Select **Applications > Vessel View** in the menu of the **Patient Browser**.

The **Vessel View** task card opens and the images are loaded.

➪ If you have completed evaluation, close the data set again with **Patient > Close**.

Requirements

Prior to loading images, the system checks their suitability for 3D evaluation with **Vessel View**. The following requirements have to be met:

- ❏ Only one series at a time may be loaded.
- ❏ This series must contain a minimum of three images.
- ❏ All images have to be from the same patient.
- ❏ All images must be parallel and acquired along one axis.
- ❏ Each image must have a different slice position.
- ❏ The distance between two adjacent slices must be less than 2 times the average slice distance.
- ❏ All images have to have been acquired within a period of 30 minutes.

If you have selected an unsuitable series or multiple series for loading, the **Series List** window opens with the test results.

Volume display

If you have loaded images into the **Vessel View** task card, the complete data set is initially shown as a 3D volume image in the VRT display. You can modify this view as required by assigning different VRT parameter sets.

You can also show the MIP display in the volume image segment instead of the VRT display.

Modifying the VRT display

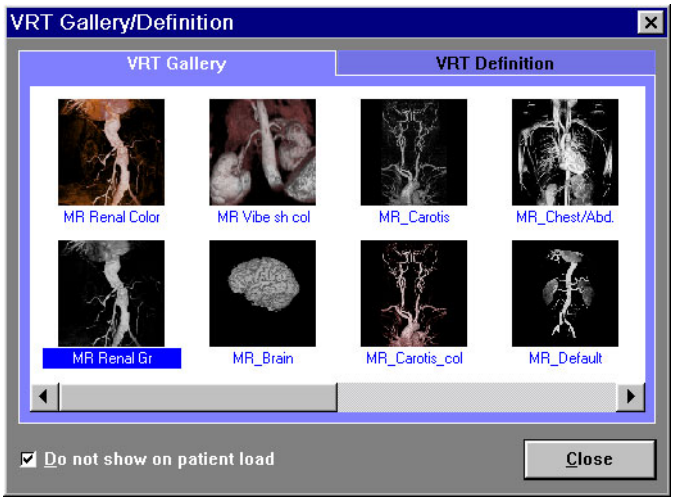
The VRT gallery provides various parameter sets with settings for color, brightness, and transparency. You select a parameter set best suited for the volume display of the data set loaded.

Assigning the parameter set



✧ Select **Image Type > VRT Gallery**.
- Or -
Right-click this button on the **Type** subtask card.

The **VRT Gallery/Definition** dialog window opens with the **VRT Gallery** subtask card.



✧ Click the desired parameter set.

The VRT volume image is displayed including the respective tissue class parameters.

Edit the parameter set

If the existing parameter sets do not meet your requirements, you can individually set the properties of the VRT view in the **VRT Definition** dialog window. For a detailed description on changing and saving parameter sets, refer to
→ *syngo* Operator Manual.

Switching display modes

Maximum intensity projection (MIP) is used for displaying the course of a vessel or the inflow of contrast agent. You can switch the volume image segment from VRT mode to MIP mode and vice versa.

✧ Select the volume image segment.



✧ To set the MIP mode, click this button on the **Type** subtask card.

Or



✧ To return to VRT mode, click this button on the **Type** subtask card.

➪ You can also switch display modes via the **Image Type** menu.

Rotating a volume image

To set a suitable volume image for evaluation, manually rotate the volume into position.

To obtain an overview of the entire volume, start automatic rotation.

Manual rotation

✧ You can rotate the volume image to the desired position using the mouse.

Automatic rotation



How to initiate automatic rotation:

✧ Drag the orientation cube in the desired direction using the mouse and release the mouse button during movement.

The view continually rotates. The direction and speed of rotation corresponds to the mouse movement.

✧ To stop rotation, click in the segment background.

The view last set remains on display.

➪ You can save the image sequence from a 360° rotation as a movie file.
→ Page E.5–8, *Saving rotation of the view as a movie*

Orienting the volume image



How to use the orientation cube to orient the volume image:

✧ To set the volume image to one of the standard view directions, click the corresponding side of the orientation cube.

✧ To set the volume image to front view and original size, double click anywhere in the orientation cube.

You can also orient the volume image using the menu functions or **Orientation** subtask card.
→ Page E.2–11, *Orienting the image segment individually*

Slice images

The following functions are available to optimize the views in the slice image segments:

- ❏ Switching display modes
- ❏ Enlarging a segment
- ❏ Scrolling the slice image stack
- ❏ Rotating image planes
- ❏ Orienting image planes
- ❏ Zooming images
  → *syngo* Operator Manual
- ❏ Panning images
  → *syngo* Operator Manual
- ❏ Windowing images

Switching display modes

In addition to MPR display (standard) modes, MPR thick, MIP, and MIP thin are available for slice image segments.

✧ Select the slice image segment where you want to change the display mode.

✧ Select the required display mode in the main menu under **Image Type**.
- Or -
Click the corresponding button in the **Type** subtask card.

MPR MPR Thick MIP MIP Thin






Slice thickness

The default values of the basic settings of **Vessel View** are used as the slice thickness for display types MPR thick and MIP thin.

You can change the slice thickness in the **MPR Thick** or **MIP Thin** dialog window.




✧ *Right-click* the corresponding button on the **Type** subtask card.

The dialog window opens.

Refer to the *syngo* Operator Manual for detailed instructions.

Enlarging the window

For detailed evaluation, you can display each image segment in full-screen mode.

✧ Select the image segment to be enlarged.



✧ Click this button.
- Or -
Double-click the image segment.

Type of image segment	Result
Small image segment	The segment changes places with the largest image segment at the center of the task card.
Large image segment	The segment is enlarged to full screen size.
Full screen segment	The segment is reduced to a large screen segment of normal size.

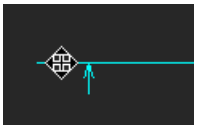
Scrolling through the slice image stacks

For MPR, MPR thick slice, and MIP thin slice display, the slice image segments contain image stacks. You can scroll through these using the dog-ears or icons.
→ *syngo* Operator Manual

Additionally, in **Vessel View** you can shift the image planes using the reference lines or offset them by clicking the mouse.

➪ In the vessel orthogonal orientation, special conditions apply for changing the image plane.
→ Page E.4–2, *Setting vessel orthogonal orientation*

Moving reference lines



✧ Click the reference line with the mouse *near the image center* and then move the line to the desired slice position.

The view in the associated slice image segment will be updated.

Moving a plane of intersection

A point of interest in the volume may be simultaneously displayed in all three slice planes by moving the plane of intersection to this position.

✧ Click the position desired in the slice image or volume image.

The slice image view will be updated. The seed point is at the selected position in the volume image.

➪ Two or three parallel slice image planes do not intersect.

Rotating the slice image plane

You can rotate or tilt the image planes away from the standard orientations.

➪ In the vessel orthogonal orientation, special conditions apply for changing the image plane.
→ Page E.4–2, *Setting vessel orthogonal orientation*

Checking the preferred orientation

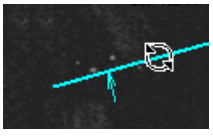
You can ensure that the preferred orientation does not change when you rotate the slice image planes.
→ *syngo* Operator Manual



✧ Click this button on the **Orientation** subtask card to activate the orientation check.

Tilting

You can tilt the image plane of a slice image segment by rotating the corresponding reference line(s).



✧ Click the reference line *at the edge of the image* with the mouse and rotate the line to the desired position.

The view in the associated image segment will be updated.

Rotating freely



✧ Select **Orientation > Rotate images**.

Rotation mode is now active.

✧ You can rotate the view to the desired position using the mouse.

✧ Deselect **Orientation > Rotate images** to switch off rotation mode.

Orienting the slice image planes

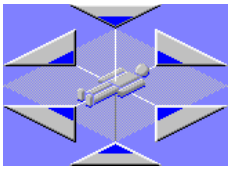
You may return all three slice image planes to standard orientations (sagittal, coronal, axial) via the mouse; you may also return the images to standard orientation one at a time.

Returning to standard orientation



✧ Select **Orientation > Default Orientation**.
- Or -
Click this button on the **Orientation** subtask card.

Orienting the image segment individually



✧ Select the desired slice image segment.

✧ Select the required view orientation under **Orientation** in the main menu.
- Or -
Select the **Orientation** subtask card and click the respective triangle.

Windowing images

Optimize the brightness and contrast windowing values to improve the display of structures.

Single windowing

If you want to change the window values of a single segment, just switch to the Single Windowing mode:

✧ Select **Image > Single Windowing**.

You can deactivate the mode at any time.

Automatic windowing

How to automatically optimize window values:

✧ Select **Image > Auto Window**.

Windowing using the mouse or keyboard

For details on manual windowing, refer to the *syngo* Operator Manual.

➪ When you window the VRT volume image with the mouse, you change the individual parameters of the VRT settings.
→ Page E.2–4, *Edit the parameter set*

Displaying graphics elements

The **Vessel View** image segments contain a variety of graphics elements that support you in the evaluation and illustrate the evaluation results. You can activate or deactivate these graphics elements as needed or change their properties.

Showing/hiding reference lines



✧ To display (hide) the reference lines, select (deselect) this button in the control area.

Showing/hiding measurements



✧ To display (hide) paths and measurements, select (deselect) this button in the control area.

Configuring an image view

In the **Configure** menu, you define which additional elements are displayed in the image segments.

Menu item / Option	Comment
Show Magnifier Window	If this option is activated, the area surrounding the mouse pointer is significantly enlarged at the lower right in a separate window.
Show Bounding Box	If this option is activated, the red boundary lines are visible in the VRT volume image.
Show MPR in VRT	If this option is activated, the three MPR slice images are displayed at the appropriate positions in the VRT volume image.

Menu item / Option	Comment
Show ribbons in VRT	If this option is activated, a flat ribbon MPR is displayed for each path in the VRT volume image.
Focus Pointer Size> Large / Medium / Small / Tiny / Off	Select the size of the focus pointer in the volume image or hide it. The focus pointer in the vessel navigator is not affected by this setting.
Show Image Text	If this option is activated, any existing image texts will be displayed in the image segments.
Show Profile Curve	If this option is activated, you can display the profile in the axial image when working with the Vessel Navigator. For a detailed description of the profile curve, refer to → Page E.4–20, *Displaying profile curves*
Vessel Navigator Curves > Area curve / Min/Max/Equiv. diameter curve	Select the type of stenosis curve in the vessel navigator. The stenosis curve is hidden if both options are deactivated. → Page E.4–21, *Setting stenotic curves*

✧ Make the desired settings in the **Configure** menu.

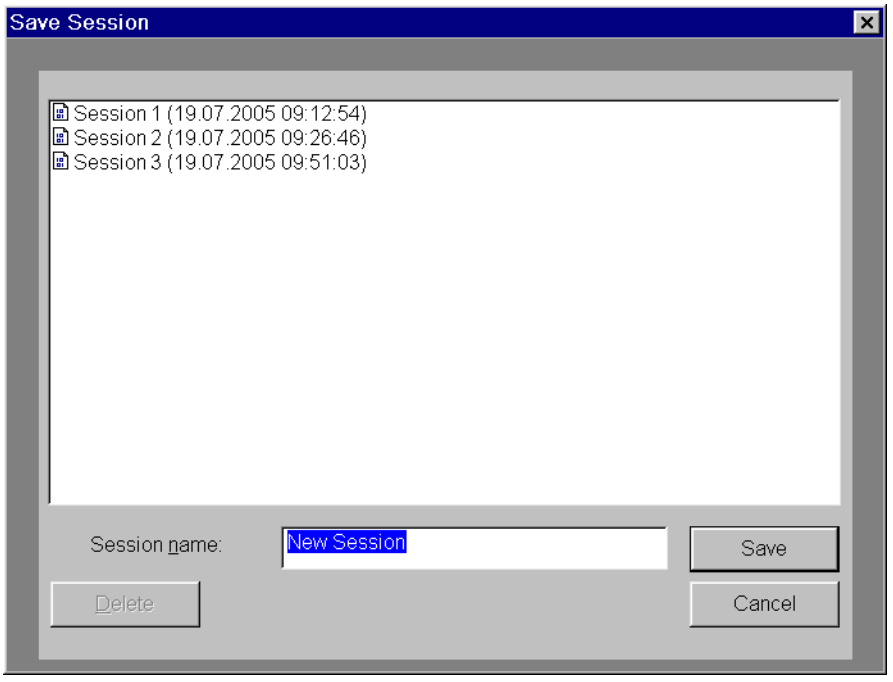
Saving the session

You can save the current status of the image series you have been working on in the database and restore it later.

Saving the session

✧ Select **File > Save Session** from the main menu.

The **Save Session** dialog window opens.



✧ Enter a name for the session in the lower input field.
- Or -
Select the session in the upper field to overwrite a stored session.



✧ Click **Save**.

The session data for the image series will be stored in the database.

Restoring a session

✧ Select **File > Load Session**.

The **Load Session** dialog window opens.



✧ Select the session you want to restore from the list and click **Load**.

Vessel View returns to the status when the session was saved.

➪ Session data are restored only by loading the corresponding image series.

Deleting a session

✧ Open the **Save Session** or **Load Session** dialog window.

✧ Select the session from the list.



✧ Click Delete.

The session is deleted.

CHAPTER E.3

Defining Vessels

Vessel View provides tools that allow you to either remove unwanted parts or enhance vessels. The resulting image information provides for efficient and reliable diagnosis.

Removing unwanted parts of the image

Use the following tools to limit the displayed volume to a volume of interest (VOI).

- ❏ VOI cropping tool to remove unwanted parts from the volume image (freehand VOI)
- ❏ Clip plane to hide outer volume slices

➪ Cropping or hiding volume parts has no effect on the slice plane view.

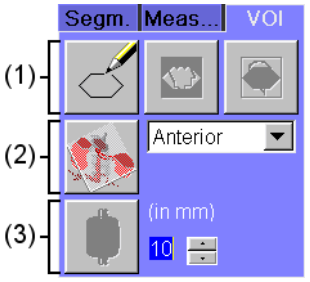
Punching a freehand VOI

For a freehand VOI, draw a contour in the volume image and then crop it in the view direction through the volume.

➪ The MIP mode is especially suitable for defining VOIs.

VOI subtask card

✧ Superpose the **VOI** subtask card in the control area.



(1) Operating element for freehand VOI
(2) Operating element for slice plane
(3) Operating element for tube-shaped VOI

Drawing a VOI contour

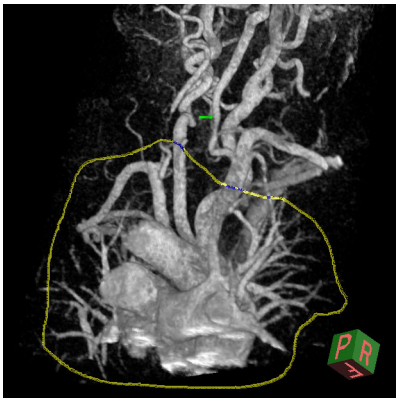


✧ Orient the volume image for easiest tracing.

✧ To switch on the drawing mode, click this button.

✧ Draw the boundaries of the desired volume with the mouse.

✧ Double-click to complete the contour.



➪ To discard the contour drawn by you, simply switch off the drawing mode. The contour will then be deleted.

Cutting out VOIs



✧ Click this button to delete all voxels outside the contour.

Or



✧ Click this button to delete all voxels inside the contour.

The VOI is cut out and the drawing mode is deactivated.

➪ To define more complex VOIs, draw several contours one after the other, hiding the unwanted areas each time.

Undo

You can cancel the last cutting process.

✧ Select **Undo last VOI** from the context menu.

Use the clip plane

You can use the clip plane by moving it between the areas to be evaluated and the hidden areas. The volume outside the clip plane will be hidden. The interior, however, will be visible.

➪ The clip plane is only active in the volume image.

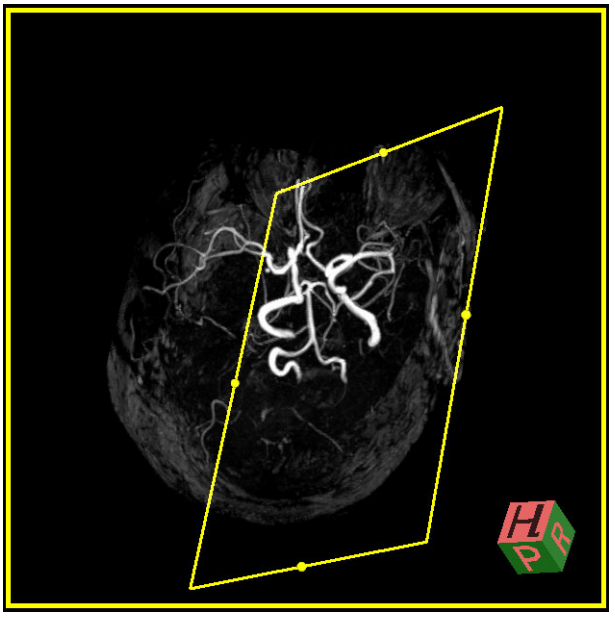
Displaying

You display clip planes to move them in the volume image segment.



✧ Click the **VOI** subtask card and select this button.

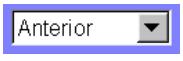
The clip plane is now marked with a color frame.



! The effect of clip planes on the volume image depends on their position only, not on whether they are visible or not.

Align/reset

Before manually moving the clip plane, set it at a suitable starting position.



✧ Select the desired orientation in the selection list of the **VOI** subtask card.

The clip plane is now at the edge of the volume in the orientation desired.

➪ If the clip plane is positioned inside the volume, use this procedure to reset it. You will again see the entire volume.

Panning

This is how you shift the clip plane perpendicular to the plane:

✧ To shift the clip plane away from you, use the mouse and drag it *upward* in the volume image.

Or

✧ To shift the clip plane toward the plane, use the mouse and drag it *downward* in the volume image.

Tilting

You can use the four edge points to tilt a clip plane about its center.

✧ Drag the edge point selected to tilt the plane in the desired direction.

Rotating

This is how you freely rotate the clip plane in the volume:

✧ Press and hold the **Ctrl** key.

✧ Rotate the clip plane with the mouse

Separating arteries from veins (AVS)

Both arteries and veins are displayed in many data sets and difficult to differentiate. For example, this makes reliable time planning for contrast agent measurements difficult. For data sets such as this, **Vessel View** enables you to classify tissue by vessel type prior to subsequent evaluation. You can then separately display and evaluate arteries and veins.

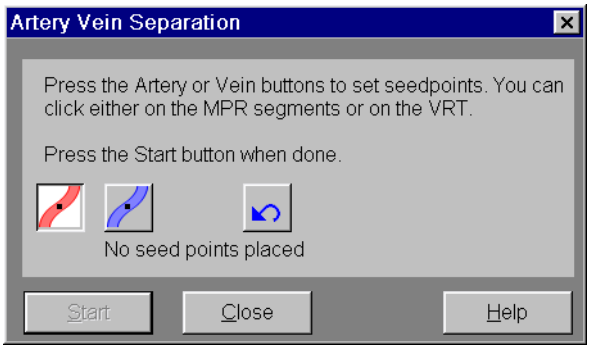
Opening the dialog window



✧ Select **Segmentation > Artery Vein Separation**.
- Or -
Click this button on the **Segmentation** subtask card.

The axial slice image segment becomes the large image segment.

The **Artery Vein Separation** dialog window opens.



Setting seed points

The algorithm expects the marking of the two tissue types. Set seed points in the slice images at a minimum of two locations each (beginning and end of vessel) for an artery and a vein. You set additional pairs at locations where the artery and vein are particularly close to one another.

This is how you set the artery seed points (red):



✧ Click the button.

✧ Use the left mouse button to set seed points in typical arterial tissue.

This is how you set the vein seed points (blue):



✧ Click the button.

✧ Use the left mouse button to set seed points in typical venous tissue.

Notes:

❏ When you are not setting points, you are free to scroll through the views, and rotate or enlarge them.

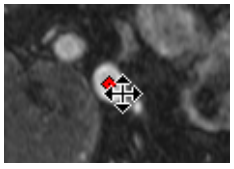
❏ You can set the artery and vein seed points in any sequence.

❏ Seed points cannot be set or moved in the volume image.



✧ To delete the last seed point set, click this button.

Moving the seed point



✧ Move a slice image plane to the seed point location desired.
- Or -
Click the seed point in the volume image.

The seed point is visible in the slice image.

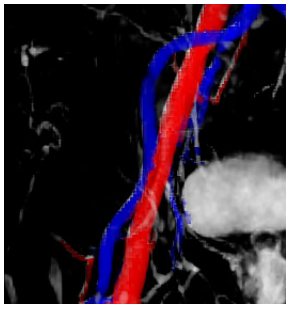
✧ Drag the seed point in the slice image to the position desired with the mouse.

Separation



✧ To start the separation, click **Start**.

A progress bar is displayed, which you can use, if necessary, to cancel the procedure.



After separation has been completed, the view in the volume segment is updated.

❏ Arteries are displayed in red
❏ Veins are displayed in blue.
❏ Other tissue is displayed according to the current VRT parameters.

➪ The fader is automatically set to a suitable value.
→ Page E.3–19, *Fader*

Renewing separation

You can update a completed separation at any time using new or modified seed points.

✧ Open the **Artery Vein Separation**.
→ Page E.3–7 dialog window

All existing seed points are displayed.

✧ Set new seed points.
→ Page E.3–8

✧ Correct the seed points, as required.
→ Page E.3–9



✧ Click **Start**.

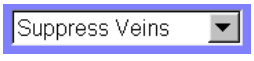
The marked tissue is reclassified.

➪ Before starting a new separation, you can temporarily close the dialog window without losing the newly set seed points.

Selecting the display mode

Once artery – vein separation is complete, the following display types are available for the volume image:

Display mode	Features
Normal	The volume is displayed without Artery Vein Separation.
Color Arteries/Veins	Arteries are displayed in red Veins are displayed in blue. Other tissue is displayed according to the current VRT parameters.
Suppress Veins	Arteries are displayed according to the current VRT parameters. Veins are hidden or are subject to the fader. → Page E.2–3, *Modifying the VRT display* → Page E.3–19, *Fader*
Suppress Arteries	Veins are displayed according to the current VRT parameters. Arteries are hidden or are subject to the fader



✧ Select the desired display mode in the selection list of the **Segmentation** subtask card.

The view is updated. If you select a display type other than **Normal**, corresponding image text is displayed at the lower left in the segment.

➪ The **Color Arteries/Veins** display mode is without effect in the MIP mode.

Creating paths

Lines, known as paths, trace the blood vessels for display and evaluation.

There are two ways to create paths:

- **Semi-automatic path creation**
  Mark the start, end and branching points of the vessel to be defined and start the semi-automatic segmentation algorithm. Additional control points are set automatically.
- **Manual path creation**
  Manually position all control points for a blood vessel and let the system calculate the smoothed connection line.

The paths created are shown in the object list on the **Measurement** subtask card.

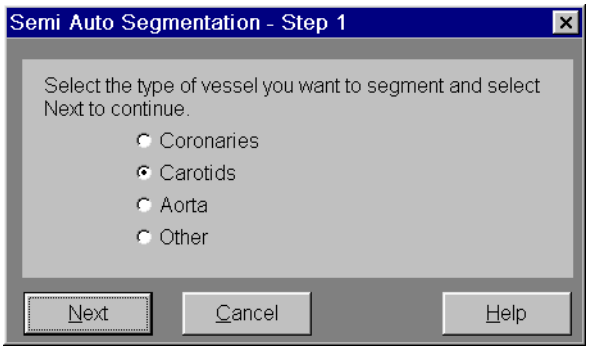
Semi Automatic Path Planning (CT)

Semi-automatic path planning is as follows for CT data sets:



✧ Click this button on the **Segmentation** subtask card.
- Or -
Select **Segmentation > Semi-Auto Segmentation**.

The dialog window for controlling semi-automatic path planning opens (step 1).



Selecting the vessel type

✧ Select the type of vessel you want to segment.

The segmentation algorithm is adapted to the selected vessel type.



✧ Click **Next**.

The dialog window for setting the center and end points (step 2) opens.

Setting seed points



✧ Click the button.

The mode for setting center points is active.

✧ Set center points in the vessel to be segmented via mouse click.



✧ When you want to limit the segmentation algorithm, click this button.

The mode for setting end points is active.

✧ Set end points in the vessel to be segmented via mouse click.

Notes:

❏ You can set seed points in all segments.

❏ You can set any number of center and/or end points.

❏ Two end points have to be set when segmenting the coronary arteries. Set the end points in the aorta above and below the coronary branch.

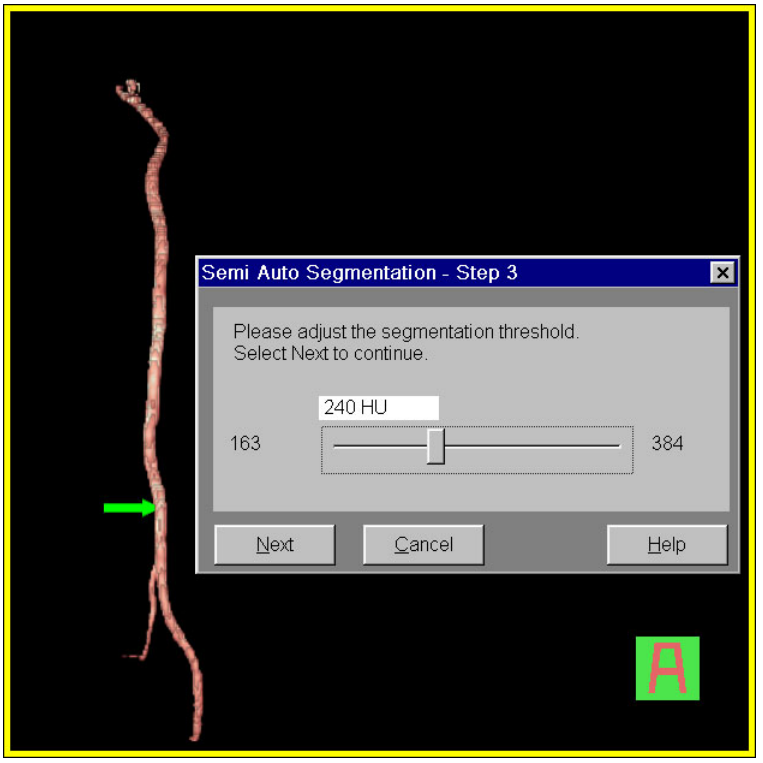


❏ Delete the seed point last set with the button.



✧ Click **Next**.

The dialog window for defining the segmentation threshold (step 3) opens.



Set the segmentation threshold

You can adapt the segmentation threshold to maintain more or less of the structure.

✧ Set the threshold with the slide control.

Voxels whose intensity lies below the segmentation threshold are elmininated from the image segment.
Check your view and correct the settings, as required.



✧ Click **Next**.

Segmentation is performed and the dialog window for creating vessel paths (step 4) opens.

Creating paths

Create a path for every vessel section you want to evaluate separately:

✧ Click first on the starting point and then on the end point of the vessel section.

The new path is transferred to the object list and you can then create the next path.



✧ Click **Done** after you have generated all requested paths.

Semiautomatic segmentation ends and the dialog window closes.

After segmentation, the translucent mode is active to facilitate viewing the paths in the volume image.
→ Page E.3–22, *Translucent*

Additional information

You can set the transparency of the volume sections blanked out by segmentation:
→ Page E.3–19, *Fader*

You may apply semi-automatic path planning several times to a data set:
→ Page E.3–19, *Repeated segmentation*

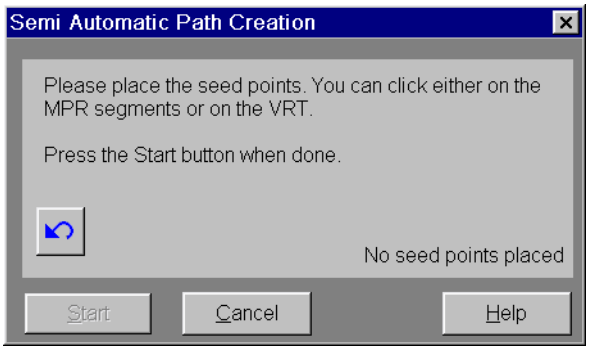
Semi-automatic path planning (MR)

Semi-automatic path planning is as follows for MR data sets:



✧ Click this button on the **Segmentation** subtask card.
- Or -
Select **Segmentation > Semi-Auto Segmentation**.

The dialog window for controlling semi-automatic path creation opens.



Setting seed points

The algorithm now expects input of at least two seed points.

✧ If you have performed artery-vein separation and only want to perform semi-automatic segmentation on one of the two vessel types, select the corresponding display in the **Segmentation** subtask card.
→ Page E.3–11, *Selecting the display mode*

✧ Position a seed point at the beginning and end of the path via the left mouse button.

➪ Position the individual seed points in the most suitable image segment. In many cases this will be the volume image rather than one of the slice images. When you are not setting points, you are free to scroll through the views, and rotate or enlarge them.

✧ If you want to identify branched vessels, position a seed point where the branches join.

Correcting seed points

✧ To correct the position of a seed point, drag it to its new position with the mouse.



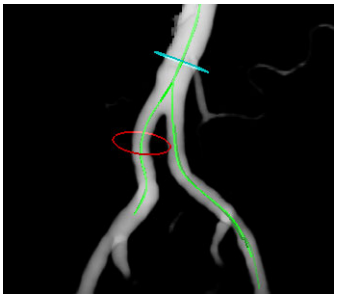
✧ To delete the last seed point set, click this button.

Segmentation



✧ To start the segmentation, click **Start**.

The segmentation algorithm automatically finds the vessel limits and determines the vessel centerline (path).



➪ When you segment branched vessels, a separate path will be created for each branch.

After segmentation, the translucent mode is active to facilitate viewing the paths in the volume image.
→ Page E.3–22, *Translucent*

Fader

The volume parts hidden by the segmentation are not removed from the data record. With the **fader**, you may modify the transparency between 0 (= hidden completely) and 100 (= shown completely).



✧ On the **Segmentation** subtask card drag the slider to the *right* to increase the visibility of hidden areas.

Repeated segmentation

You are able to perform semi-automatic path creation even if the data record has been segmented already. In that case, the volume defined by the latest segmentation is added to the volume parts already defined. All volume parts hidden by vessel segmentation are temporarily re-shown while you set the seed points.

Manual path planning

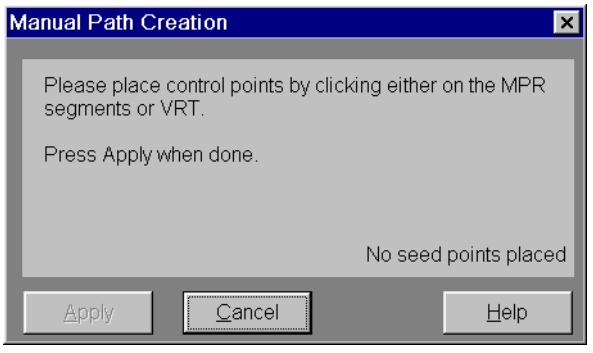
For manual path creation, you need to set all control points by hand. How well the path represents the actual course of the blood vessel depends on the number as well as accuracy used in positioning the control points.

➪ Manual path creation is not connected with a segmentation algorithm. No volume parts are hidden.



✧ Click this button on the **Segmentation** subtask card.
- Or -
Select **Segmentation > Manual Path Creation**.

The dialog window for controlling manual path creation opens.



➪ All image segments are available for setting the control points. Ensure that the control points are set as close to the center of the vessel as possible.

✧ Set a control point at the beginning of the vessel.

✧ Set additional control points at all locations where the vessel changes direction.

The path line will be drawn in immediately. Based on the characteristics of the tissue, the program automatically calculates the depth of a point set in the volume.

✧ Set the last control point at the end of the vessel.

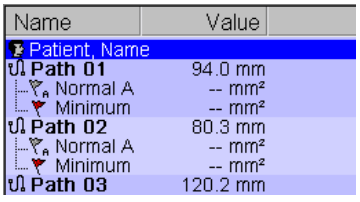


✧ Click **Apply**.

➪ Create a tube-shaped VOI to expose the vessel with the path.
→ Page E.3–26, *Defining vessels*

➪ Switch to translucent mode to make the path more visible in the volume image.
→ Page E.3–22, *Translucent*

Managing paths



The object list on the **Measurement** subtask card of the evaluation area shows each path with a unique name. You can change the name of a path, store notes for each path, or delete paths you no longer need.
→ Page E.4–14, *Object list*

Processing paths

You can change the course of a path as well as merge paths.

Translucent



If you have created paths with a segmentation algorithm, the transparency is automatically set to 85% in the VRT settings (translucent mode). In that way, the paths in the volume image are easily visible because they are no longer hidden by the surrounding contrast agent. If this mode is no longer active or if you want to edit a manually created path, activate it manually:

✧ Select the **Translucent** option in the context menu.

Changing the course of a path

Activate the editing mode when you want to change the course of a path. You can change the position of the path by moving, inserting, or removing control points.

Activating the editing mode

✧ Select the path to be edited in the volume image or object list.

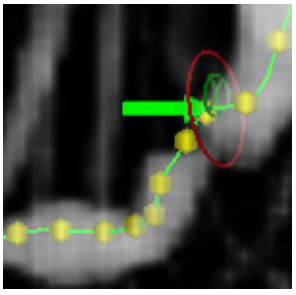
The selected path will be shown in color.

In the slice image, the closer the path line is to the image plane, the brighter it appears.

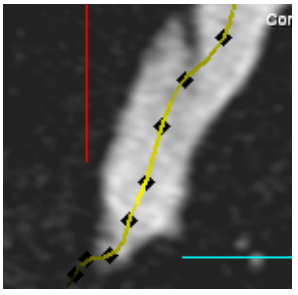


✧ Click the **Segmentation** subtask card and select this button.

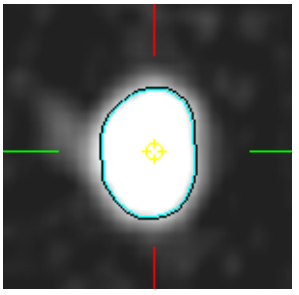
The control points are now visible.



Volume image view



Slice image view
non-vessel orthogonal



Slice image view
Vessel orthogonal

Slice image true orthogonal

If the lower slice image is perpendicular to the path (vessel orthogonal orientation), only the intersection of the path with the image plane is shown as a small cross. You can move this intersection point with the mouse. The path is updated automatically:

❏ the path lines go through the new intersection point,
❏ the position of neighboring control points is adjusted,
❏ a new control point is inserted if necessary.

Direct movement, insertion, or deletion of control points is not possible in the true orthogonal slice image.

For a description of the vessel-orthogonal orientation, see also → Page E.4–2, *Setting vessel orthogonal orientation*.

Inserting control points

By adding control points you facilitate an even more accurate adjustment to vessel curves.

✧ Set a new control point at the appropriate position in the image with a mouse click.

The path line opens between the two closest points and is recalculated accordingly.

Moving control points

✧ Click directly on the control point in the volume image and drag it to the desired position using the mouse.
- Or -
Move the mouse pointer *up to* the required point in a slice image.



The mouse cursor changes shape.

✧ Drag the point to the position desired with the mouse.

The path line will be adjusted automatically.

Deleting control points

✧ Click the control point you want to delete in the volume image or one of the slice images.

The selected control point changes color in all image segments.

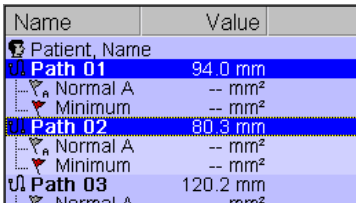
✧ Press **Del.**

The control point will be deleted and the path line is recalculated.

Connecting paths

You first have to link the paths before you can evaluate a vessel comprising different paths. The result is a new continuous path that does not affect the original paths.

Selecting paths



✧ Click the first path to be merged in the object list.

✧ Keep the **Ctrl** button pressed and click the second path to be merged in the object list.

➪ You can only merge two paths with one merging operation.

Merging

✧ Click **Merge** in the footer of the object list.

A new, continuous path will be created from the two marked paths and entered in the object list.

Defining vessels

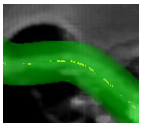
You can crop or remove a vessel as a tube-shaped VOI using the path.

Displaying a vessel tube



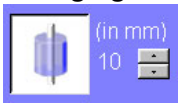
✧ Mark the path in the object list or volume image.

✧ Click this button on the **VOI** subtask card to display the tube-shaped vessel.



The vessel tube will be displayed with a semi-transparent surface in the volume image. The tube is not visible in the slice image segments.

Changing the tube radius



You can select any radius between 0 and 50 mm for the vessel tube.

✧ Set the required radius using the arrow buttons.

Exposing / removing



✧ Click this button to make the vessel tube available.

Or



✧ Click this button to remove the vessel tube.

CHAPTER E.4

Evaluating Vessels

Vessels are evaluated on the basis of diagnostically useful images. You can use the vessel orthogonal orientation of the slice image segments to navigate through the vessel and document vessels with series of axial slice images.

Measurements

Various measurement tools are provided for quantitative image evaluations.

The following measurements are possible:

- ❏ Distances from the image structures in the plane and in space
- ❏ Lengths of vessels (curve lengths)
- ❏ Cross-sections of vessels
- ❏ Volume of vessels
- ❏ Angle

You may perform measurements in all image segments or in the Vessel Navigator.

Annotations

You provide annotations for interesting or notable image areas. Annotations, together with paths and measurements, are managed in the object list.

Vessel navigator

Special image sections of blood vessels can be displayed and evaluated in the vessel navigator.

Setting vessel orthogonal orientation

By setting the vessel orthogonal orientation, you are aligning the slice plane automatically along the vessel path. The lower slice plane is then located vertically to the vessel path and shows the vessel cross-section. The center and upper image planes are perpendicular to the lower image and to each other.

If you scroll the lower slice image stack with the dog-ears in this orientation, you will move backward or forward along the blood vessel.

➪ It is not possible to scroll through the upper image stack in the vessel orthogonal orientation.

✧ Select the path of the vessel from the object list or the volume image.



✧ Click the button in the control area.

➪ If you have created a new path, the slice image segments are automatically set in the vessel orthogonal orientation.

Generating axial vessel images

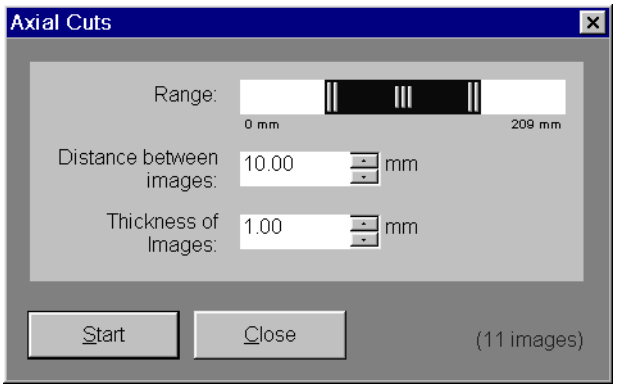
You can document a defined vessel with a series of axial vessel section images in MPR format. The first image is placed perpendicular to the vessel axis at a freely selectable path point. All other images are generated at defined intervals along the vessel axis. The images are saved in a new series.

✧ Select the path of the vessel from the object list or the volume image.



✧ Click this button in the lower section of the control area.

The **Axial Cuts** dialog window is opened with default settings.



A symbolic preview of the section image series is shown in the volume image and vessel navigator: Small borders or white lines along the vessel path identify the positions of each section image.

Changing the settings

This is how you adjust the settings to your question:

✧ Drag the left (right) slider handle to the start (end) of the desired area.

➪ If you want to change the starting and end position by the same amount, move the slider using the middle handle.



✧ Type the distance between images.

The symbolic preview in the volume image will be updated. The number of images depends on the length of the area and the images distance.

✧ Check the section image positions and correct the settings as necessary.



✧ Enter the desired slice thickness.

Generating axial images



✧ Click **Start**.

The axial MPR images are reconstructed and saved. The dialog window is closed and the symbolic preview is hidden.

Creating annotations

You provide annotations for interesting or notable image areas.

✧ Position the section of the volume segment or one of the slice image segments to receive the annotation in foreground.



✧ Click this button in the **Meas...** subtask card of the control area.

Annotation mode is now active.

✧ Click the part of the image you want to annotate.

The position is marked and the annotation entered.

➪ The annotations are now displayed in the volume image.

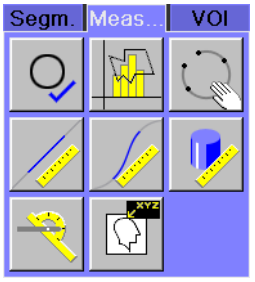
✧ To change the automatically-assigned text, enter the annotation text desired.

✧ Deselect this button to end the annotation mode.

You manage all annotations together with all other objects created in the object list.
→ Page E.4–14, *Object list*

Performing measurements

The measurement tools are located on the **Meas...** subtask card in the control area.



Completed measurements are shown in the object list on the **Meas...** subtask card of the evaluation area.
→ Page E.4–14, *Object list*

Measuring distances

As a first step, set the start and end points of the distance to be measured in a slice image or in the volume image.

➪ The vessel navigator is especially suitable for measuring vessel diameters.
→ Page E.4–25, *Measuring vessel diameter*





✧ Click this button in the **Meas...** subtask card of the control area.

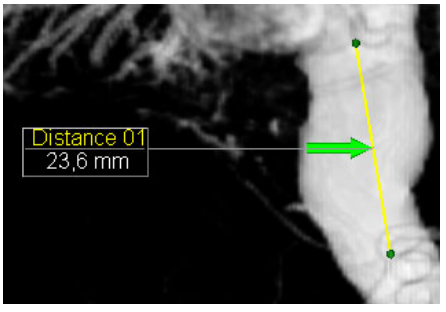
The mouse pointer changes shape. The distance measurement mode is now active.

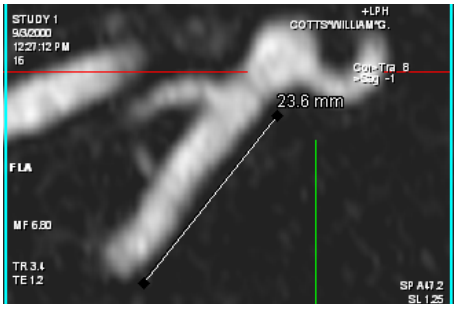
Setting measurement points

✧ Set a suitable view in a three slice image segment or in the volume segment.

✧ Click the starting point and then the end point of the distance to be measured.
- Or -
Use the mouse and draw the line to be measured in the image.

The measured section and the measurement value are displayed.





Post-processing a distance measurement

If necessary, you can post-process a distance measurement.

✧ Select the measurement from the object list.

The image views switch to the position of the measurement.

✧ Move the measurement points to be corrected to the required position with the mouse.

The measurement is updated.

Measuring curves

Use the curve measurement to determine the length of a path section.

➪ Refer to the object list for the complete length of the path.

In general, you use the vessel navigator for a curve measurement. In flat ribbon mode, the measurement points can be set easily.
→ Page E.4–26, *Measuring the length of a vessel segment*

However, you can also make curve measurements in the volume image. Proceed in the same manner in Curved MPR mode at the vessel navigator.

Activating curve measurement





✧ Click this button in the **Meas...** subtask card of the control area.

The mouse pointer changes shape. The curve measurement mode is now active.

Setting measurement points

✧ Click the starting point of the curved distance measurement in the volume image.

✧ Click the end point of the curved distance measurement.

The shortest distance between the two points is calculated. The curve measurement is put in the object list and shown in the volume image. The measurement mode remains active for a follow-up curve measurement.

Continuous curve measurement

You can continue the curve measurement from the measurement point last entered:

✧ Click the end point for the next measurement.

The new section of the path is measured.

Ending curve measurement



✧ Deselect this button to end the curve measurement.

Post-processing a curve measurement

If necessary, you can post-process a curve measurement.

✧ Select the measurement from the object list.

The image views switch to the position of the measurement.

✧ Move the measurement points to be corrected to the required position with the mouse.

The measurement is updated.

Measuring areas

You evaluate diagnostically relevant areas using a contour in the lower slice image.

Use the vessel navigator to measure vascular cross-sections.
→ Page E.4–27, *Measuring cross-sections*

Alternately, you can make an area measurement without using a path. Manually draw a contour in the lower slice image and have the area measured.

Measured values



The following measurement values are displayed in the image together with the contour:

- ❏ Area content
- ❏ Minimum diameter
- ❏ Maximum diameter
- ❏ Average intensity

The object list also includes the average diameter.

Draw contour



✧ Set a view suitable for the intended area measurement in the lower image segment.

✧ Click this button in the **Meas...** subtask card of the control area.



The mouse pointer changes shape. Drawing mode is now active.

✧ Draw the contour in the slice image using the mouse.

✧ Double-click to complete the contour.

The contour is evaluated and the area measurement is entered in the object list.

Post-processing a contour

When required, you can edit an existing contour.



✧ Click this button in the **Meas...** subtask card of the control area.



The mouse pointer changes shape. Contour editing mode is now active.

✧ Click *next* to the contour (inside or outside) and move the line to the desired position with the tool.
- Or -
Move the desired contour points to the desired position using the mouse.



✧ To complete editing, click this button in the **Meas...** subtask card of the control area.

The measured values are updated and editing mode is deactivated.

➪ If you deactivated the contour edit mode manually, editing is canceled and changes are not accepted.

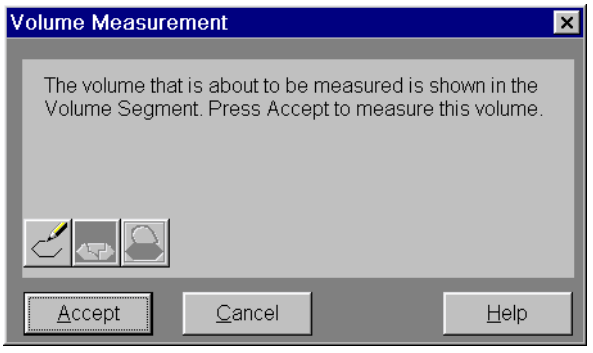
Measuring volumes



✧ Click this button in the **Meas...** subtask card of the control area.

The volume to be acquired by the measurement plan is shown in red in the volume segment.

The **Volume Measurement** dialog window opens.



✧ Review the highlighted volume.

✧ If needed, crop the highlighted volume for the measurement using the buttons.
→ Page E.3–2, *Punching a freehand VOI*.

➪ Once the volume measurement is completed, volume sections removed in this manner are redisplayed.

✧ Click **Accept**.

The highlighted volume is measured and the volume measurement is transferred to the object list. The dialog box is closed.

As long as the volume measurement is selected in the object list, the measured volume remains highlighted.

Measuring an angle

For an angle measurement set three measurement points in the image segment: the apex and one point for each leg of the angle.





✧ Click this button in the **Meas...** subtask card of the control area.

The mouse pointer changes shape. The angle measurement mode is now active.

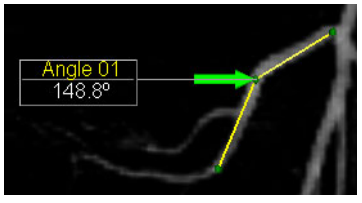
Setting measurement points

You can set the measurement points in different image segments.

✧ Click the end point for the first side.

✧ Click the apex.

✧ Click the end point for the second side.



The angle is calculated and the angle measurement is put in the object list. The legs and the angle measurements are displayed in the VRT volume image.

Post-processing angle measurement

If necessary, you can post-process an angle measurement.

✧ Select the measurement from the object list.

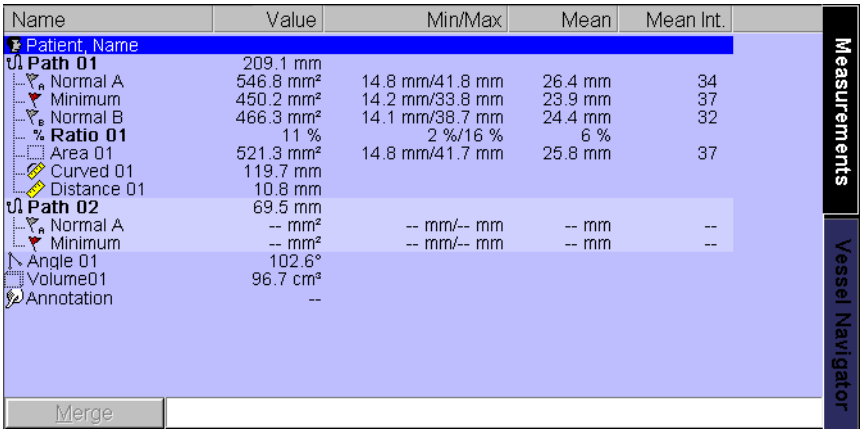
The image views switch to the position of the measurement.

✧ Move the measurement points to be corrected to the required position with the mouse.

The measurement is updated.

Object list

The paths, measurements, and annotations created during a session are entered in the object list in the **Measurements** subtask card.



➪ You can change the column width of the measurement list using the mouse.

Object hierarchy

Indented list items are not independent objects but flags or measurements that are linked to a higher-level path. The measured values refer to a certain point on the associated vessel.

➪ When you change the course of a path, measurements linked to the path are no longer up-to-date and are deleted automatically.

Object types

Newly created objects are put in the object list with an object-type identifying symbol and name.

Symbol + autom. generated name	Object type	Meas. value(s)
Path XY	Path	Path length in mm
Normal A, Minimum Normal B	Flag	Vessel cross-sectional area in mm², Min./max. vessel diameter in mm Average vessel diameter in mm, Average intensity
Ratio XY	Degree of stenosis	Meas. value ratio(s) of the minimum flag to the normal flag according to NASCET criteria
Distance XY	Distance measurement	Distance in mm
Curved XY	Curve measurement	Curve length in mm
Area XY	Area measurement	Area in mm², Min./max. area diameter in mm, Average area diameter in mm, Average intensity
Angle XY	Angle measurement	Angle size in degrees
Volume XY	Volume measurement	Volume in cm³
Annotation XY	Annotation text	–

Displaying an object

If you select a measurement from the object list, the image views automatically switch to the position of this object (only the volume view switches in curve measurement). The object is highlighted in the view.

Renaming an object



✧ Click the object you want to rename in the object list.

✧ Click the object name.

The object name is now shown in color and you can change it.

✧ Enter the new object name and then press **ENTER**.

Storing notes

This is how you store notes in connection with an object:

✧ In the object list, mark the object for which you want to add a note.

✧ Enter the new text in the input field at the footer of the object list and press **ENTER**.

A paper clip symbol in the last column of the object list indicates a note.

Deleting an object

✧ Click the object to be deleted from the object list.

✧ Press **Del.**

The object is deleted from the data set and the object list with all the elements linked to it when you confirm the safety query.

Vessel navigator

The Vessel Navigator enables you to display and evaluate slices along blood vessels. You can use the vessel navigator in two different modes:

(1) Flat Ribbon Mode
(2) Curved MPR Mode

Displaying the vessel navigator

Flat Ribbon Mode displays automatically the first time you open the vessel navigator. You can switch back and forth to Curved MPR mode at any time.

✧ Select the path of the vessel from the object list or the volume image.

✧ Display the **Vessel Navigator** subtask card in the evaluation area.

The flat ribbon MPR will be calculated and displayed.



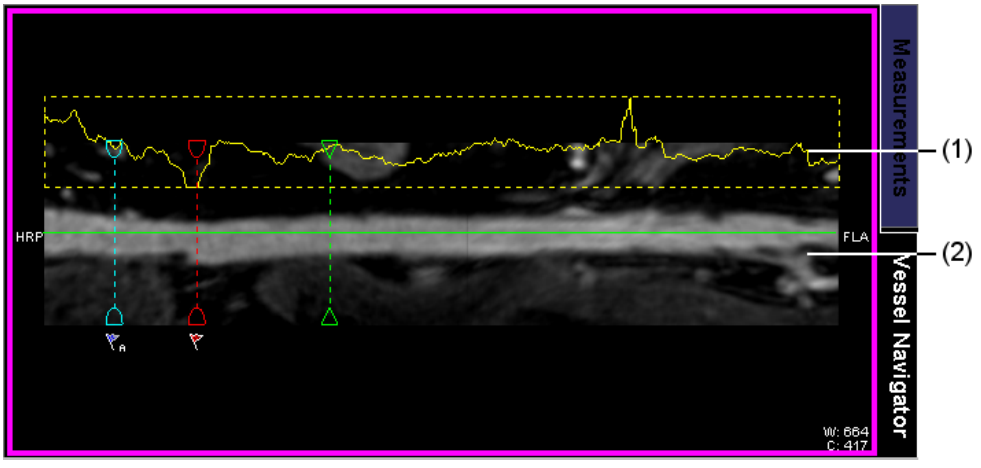
✧ To change to the Curved MPR Mode, click this button in the **Type** subtask card.

The vessel navigator changes places with the volume segment. The curved MPR is calculated and displayed.

✧ To return to flat ribbon mode, deselect this button.

Flat Ribbon Mode

The vessel navigator calculates the slice image in Flat Ribbon Mode (standard view) using a special procedure that reconstructs both curvature of the vessel as well as rotation of the vessel about its own axis. The result is a so-called *flat ribbon MPR* - the display of a longitudinal cut in the form of a flat, straight ribbon.

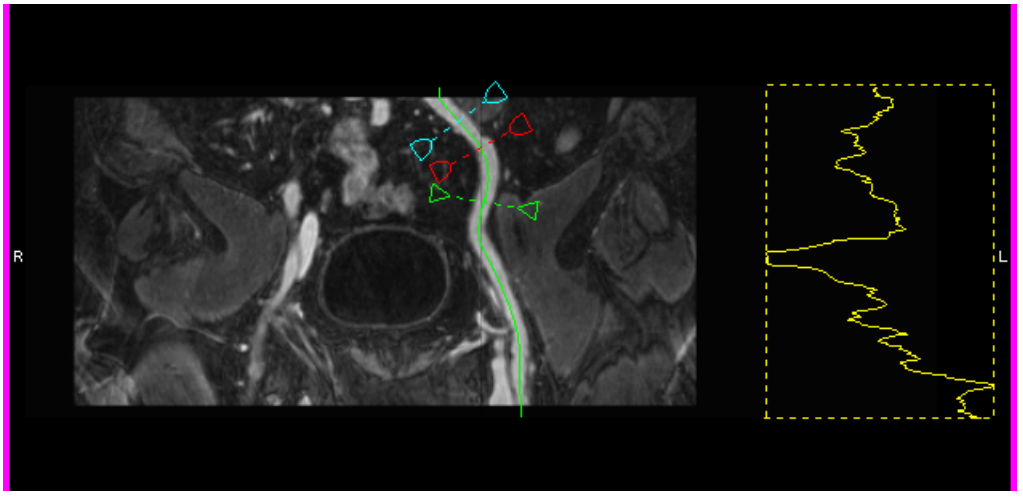


(1) Stenosis curve
(2) Flat ribbon

Instead of the flat ribbon MPR, you can also display an MIP image of the vessel. This MIP image is acquired perpendicularly to the flat ribbon to provide a view that takes the curvature and torsion of the vessel into account.

Curved MPR Mode

The curved image in the Curved-MPR mode can be seen as the result of a measurement whereby a measurement line oriented perpendicularly to the path passes through the path.

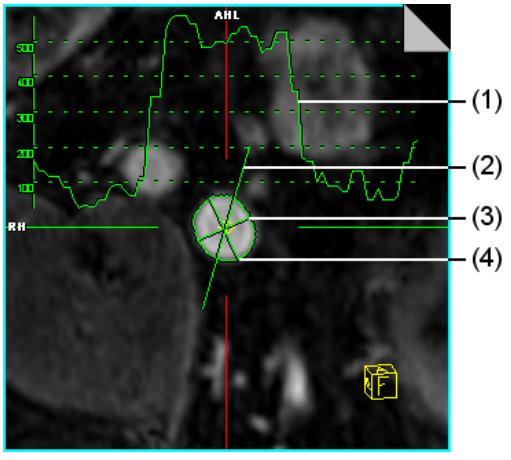


Instead of the curved MPR, you can also display a curved MIP image.

Displaying profile curves

When working with the Vessel Navigator, you can display the profile curve in the lower slice image.

✧ Select the **Show Profile Curve** option in the **Configure** menu.

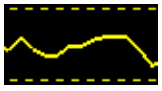


(1) Profile curve
(2) Intersecting line of the flat ribbon
(3) Minimum diameter
(4) Maximum diameter

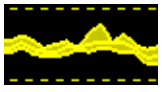
The position of the flat ribbon intersection with the image plane is displayed in the vessel. The profile curve represents the signal intensity along this intersecting line. The larger the interval between the curve point and the baseline, the greater the signal intensity.

Setting stenotic curves

The stenosis curve in the flat ribbon mode provides an overview of the shape of the vessel to help you find medically relevant locations along the vessel. Two different types of display are available.



❑ **Cross-sectional area display** (1 curve)
The stenosis curve is the cross-sectional area along the vessel. With stenoses, the curve is extremely low, with aneurysms it is extremely high.



❑ **Diameter display** (3 curves)
Three different diameter curves are displayed:
Curve of the vessel diameter maxima (top),
Curve of the equivalent diameter (center),
Curve of the vessel diameter minima (bottom).
The less the three curves differ at a point along the vessel, the more the vessel cross-section resembles a circle.

➪ The equivalent diameter is the diameter of a circle covering the same area as the vascular cross-section.

How to set the display type desired:

✧ Select the **Configure > Vessel Navigator Curves** and the required setting in the submenu.

➪ The stenotic curve is not displayed if both submenu items are deactivated.

Optimizing display

To optimize display in the vessel navigator, you can:

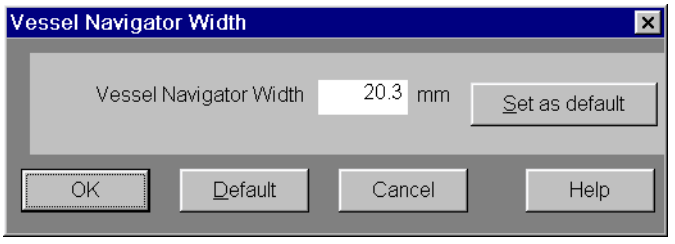
- ❏ Zoom the view
  → *syngo* Operator Manual
- ❏ Pan the view
  → *syngo* Operator Manual
- ❏ Window the view
  → Page E.2–12
- ❏ Change the display mode
  → Page E.2–7
- ❏ Set the width of the vessel navigator
- ❏ Rotate the view about the vessel axis

Setting the width of the vessel navigator

To hide unnecessary areas around the vessel, reduce the width of the vessel navigator image. If less than the full vessel width or not enough of the vessel surroundings are shown, increase the width.

✧ In the vessel navigator context menu, select **Set Ribbon Width**.

The following dialog window will be displayed:



✧ Overwrite the current width in the input field with the value desired.

Or

✧ Click **Default** to set the standard width.

✧ If you want to save the entered value as the standard value, click **Set as Default**.

✧ Click **OK**.

The dialog window closes and the view updates.

The current width is displayed in the image text in the lower left corner of the vessel navigator.

Rotating the view about the vessel axis

You can manually rotate the view in the vessel navigator, or rotate it in 90° increments.

The current rotation angle is displayed as image text in the lower left corner of the vessel navigator.

This is how you rotate the view manually:

✧ Using the mouse, move the image perpendicular to the vascular axis until the desired view is set.

This is how you rotate the view in 90° increments:

✧ Select **Orientation > Rotate forward 90°** or **Rotate backward 90°**.

➪ You can export the image sequence in a 360° turn.
→ Page E.5–8, *Saving rotation of the view as a movie*

Evaluating images

In the vessel navigator you can track the path and take measurements at the vessel.

Tracking the path

You track the vessel path by moving the marking arrow.

✧ Drag the focus pointer in the desired direction using the mouse or click the desired position in the vessel navigator view.
- Or -
Scroll the lower slice image in the required direction.

➪ If you have activated a measurement mode, you will not be able to move the marking arrow.

Measuring vessel diameter

The Flat Ribbon Mode of the vessel navigator allows you to measure distances perpendicularly to the vessel axis, for example, the diameter of a vessel. This type of measurement is not possible in Curved MPR mode.



✧ Click this button in the **Meas...** subtask card of the control area.

The mouse pointer changes shape. The distance measurement mode is now active.

✧ Drag a line from the starting point to the end point of the measured section with the mouse.

A perpendicular line will be drawn. The measured value is displayed next to the line and entered in the object list.

Measuring the length of a vessel segment

The length of the vessel between two measurement points along the path is determined by curve measurements.





✧ Click this button in the **Meas...** subtask card of the control area.

The mouse pointer changes shape. The curve measurement mode is now active.

✧ Click the starting point of the measurement.

✧ Click the end point of the measurement.

The length of the corresponding path segment is calculated and put in the object list as a curve measurement.

➪ In flat ribbon mode, you can also drag a line from the starting point to the end point of the measurement with the mouse.

Measuring cross-sections

If you move slice image views orthogonally to the vessel, a vessel contour is drawn in the lower segment. You can apply this automatically generated contour to area measurements in the vessel navigator.



✧ Switch to vessel orthogonal orientation, if not already active.

✧ Move the marking arrow to the point to be measured on the vessel.

The lower slice image is updated.

➪ If the suggested contour does not meet your requirements, redraw or edit the contour.
→ Page E.4–10, *Draw contour*

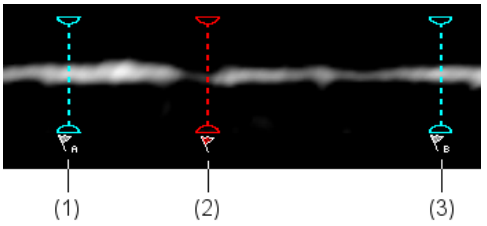


✧ Click this button on the **Meas...** subtask card of the control area.

An area measurement is created and linked to the path. In the vessel navigator view, the area measurement is displayed as a perpendicular line.

Stenosis evaluation with flags

To evaluate stenoses, measure the cross-sectional area of the vessel within and behind the stenosis and compare the values. The vessel navigator automatically prepares a stenosis evaluation by calculating the suitable measurement points and marking them with flags.



(1) Normal A: Healthy reference proximal to the stenosis
(2) Minimum: Possible stenosis
(3) Normal B: Healthy reference, distal to stenosis (visible only when three flags have been selected)

Determining the number of flags

The vessel navigator lets you define how many flags will be set on the path:

❏ No flags,
❏ Two flags (minimum and Normal A) or
❏ Three flags.

✧ Select the appropriate entry from the context menu for the vessel navigator.

Evaluating a stenosis

Once you have created a path, a contour suggestion for the vascular cross-section is displayed in the lower slice image at the position of the minimum flag.

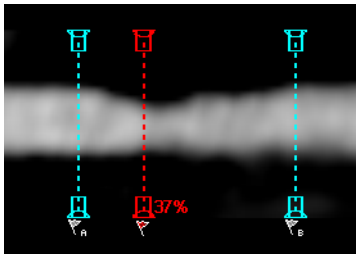


✧ Click this button in the vessel navigator.

The contour is evaluated and the measurement value for the minimum flag is entered in the object list. At the same time, the marking arrow changes to a comparison flag.

✧ Repeat the contour transfer for flag Normal A and Normal B, if necessary.

The cross-sectional area of the flags is compared and the result is shown as the degree of stenosis in the object list. The value will be between 0% (vessel not occluded) and 100% (vessel shows maximum occlusion).



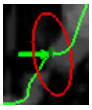
In the vessel navigator view, you can recognize the evaluated flags by their rectangular marking. The degree of stenosis is shown at the stenosis.

➪ When you use two normal flags, the degree of stenosis is calculated using the average of the two comparison measurements.

Manual adjustments

❏ If the contour at a flag position does not meet your requirements, redraw or edit the contour.
→ Page E.4–10, *Draw contour*
Please note that contour suggestions are displayed only when vessel orthogonal orientation is active.

❏ If a flag is positioned incorrectly, drag it with the mouse to the location for the evaluation.
To move a flag in the volume image, click the flag ring directly and drag it to the desired position using the mouse.



Displaying stenoses

If you select a degree of stenosis in the object list, the flags return to their position at the time of measurement. This allows you to re-display the measured values on which the degree of stenosis is based.

CHAPTER E.5

Saving and Documenting Evaluations

Vessel View allows you to store images and evaluation results and export them for further use at any stage.

The following functions are available:

- ❏ Saving the session → Page E.2–15
- ❏ Generating axial vessel images → Page E.4–3
- ❏ Saving images
- ❏ Generating an overview in table format
- ❏ Filming images
- ❏ Transferring images to the **Viewing** task card
- ❏ Send image data for graphical slice positioning
- ❏ Exporting path for evaluation with **3D Fly**
- ❏ Save the rotation of the view as a movie

Saving images

You can save the views from **Vessel View** according to image group (one series per image type) or ungrouped (one series with all image types).



This button displays the type of save setting selected prior to saving so that you can edit or confirm it.
→ *syngo* Operator Manual



This button saves images with the last settings used without checking them.
→ *syngo* Operator Manual

Generating an overview in table format



✧ Select **File > Create Report**.
- Or -
Click this button in the control area.

A list is created of all measurements performed sorted by type.

The list is automatically saved in the local database under the name <REPORTS Collection>.

You can display or print the list via the Patient Browser:

✧ To display the list, load the <REPORTS Collection> series into the **Viewing** task card.

✧ To print the list, load the <REPORTS Collection> series into the **Filming** task card.

Filming images

You can copy views from **Vessel View** to the virtual film sheet at any time or have them forwarded to a printer.

✧ Select the respective segment (slice image, volume image, or vessel navigator view).

✧ Select **Patient > Copy to Film Sheet**.
- Or -
Click this button in the control area.



The view is transferred and simultaneously stored in the database.

➪ If you want to film or print images of a measurement, select the measurement from the object list. It will then be displayed in all image segments.

Sending images to the Viewing task card

After Vessel View, you can transfer images to the **Viewing** task card for 2D-processing or evaluation.

✧ Select the respective segment (slice image, volume image, or vessel navigator view).



✧ Click this button in the control area.

The images are transferred and simultaneously stored in the database.

Sending images to graphical slice positioning

In **Vessel View** you are able to transfer image data to the **Exam** task card for graphical slice positioning (GSP). The transferred coordinates are then automatically used for scanning the next slice.

➪ It is only possible to transfer coordinates of MPR images.

Sample

For example, to evaluate a stenosis, you can set the vessel orthogonal MPR view at the stenosis position and transfer the image to the GSP. On the **Exam** task card, you can then immediately start plaque or flow measurements without having to plan, orient, and position the slice first.

Transferring image data

✧ Select the slice image segment with the image data to be transferred.

✧ Select **Send to GSP**.

The image coordinates are transmitted.

Exporting a path for evaluation with 3D-Fly

You can save path data in **Vessel View** that can be read by the **3D** task card and displayed with the **Fly** function.

✧ Select the path from the object list or the volume image.

✧ Select **Send Path to 3D Fly** from the context menu.

The path data are stored in the database and can be loaded via **3D Fly**.

Saving rotation of the view as a movie

You can store automatic rotation of the vessel navigator view and automatic rotation of the volume as an image sequence. You can define whether to save the images in a new series in the database or in an avi movie file on the hard disk.

➪ An avi movie file can be replayed on other systems using any multimedia software.

The image sequence in the vessel navigator is obtained by rotating the image plane about the vessel axis.
→ Page E.4–24, *Rotating the view about the vessel axis*

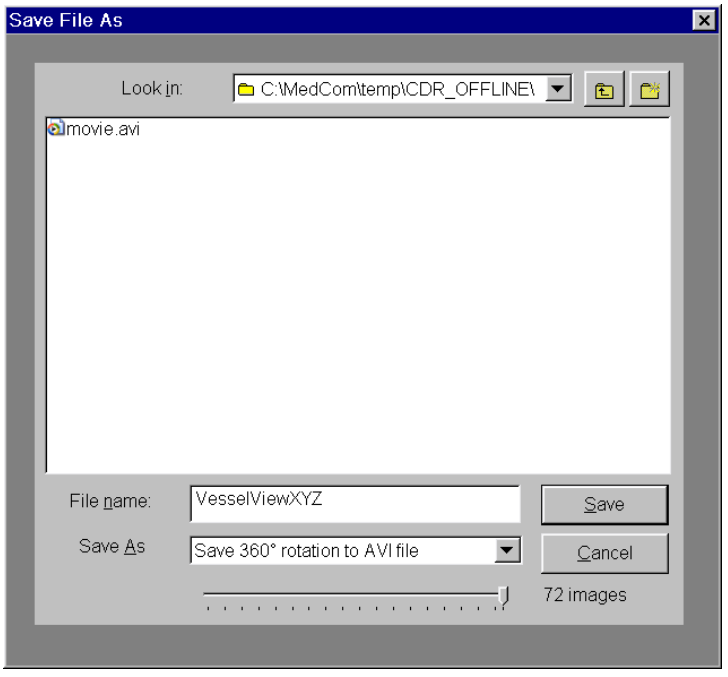
The image sequence in the volume segment is created by rotating the volume about its vertical axis.
→ Page E.2–5, *Rotating a volume image*

✧ Select the volume segment (vessel navigator) if you want to save the vessel view rotation (vessel view).



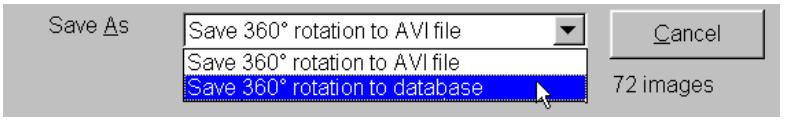
✧ Click this button in the control area.

The **Save As** dialog window opens.



✧ Enter a name for the image sequence in the **File name** input field.

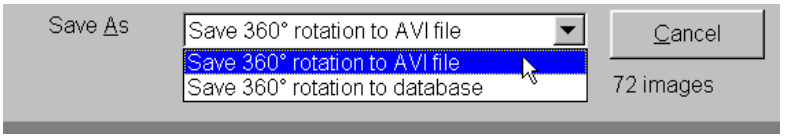
Storing in the database



✧ Go to the selection list **Save As** and select the entry **Save 360° rotation to database**.

Or

Saving to a movie file



✧ Go to the selection list **Save As** and select the entry **Save 360° rotation to AVI file**.



✧ Select the number of images with the slider.

➪ The maximum number of 72 images results in the smallest viewing angle interval of 5° between two consecutive images.



✧ Click **Save**.

The dialog window closes and the image sequence is stored.

PART
F

Composing

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CHAPTER F.1

Introduction

You have obtained several *overlapping* volume data sets from a tomographic examination and want to combine them into overview images. For this purpose, you are using the **Composing** task card.

Use

You are generating overviews of the spinal column.

Reconstruction

Once you have started **Composing**, load the series with the **Patient Browser**. The overview images are reconstructed (composed).

Visualization

The **Composing** task card allows you to display the original, detail and reconstruction images in various layouts, compare two reconstruction images for evaluation of dynamic processes and film the results in various layouts.

Measurements

Subsequently, you can perform measurements:

- ❏ Basic functions: circle, distance, angle, freehand ROI, arrow
- ❏ Orthopedic functions: scoliosis angle according to Cobb, kyphosis angle, vertical distance measurement, difference in height

Hardcopy

The overview images as well as individual images can be shown via hardcopy cameras (film sheet) or paper printers using the **Filming** task card.

Restrictions

- ❏ The **Composing** application is not available for MAGNETOM Concerto.
- ❏ For MAGNETOM C! the **Composing** application is available only with the **Spine** algorithm.

The overview images taken with the **Composing** task card *cannot* be used for therapy planning (e.g. surgical invasion) or diagnosing purposes (e.g. segmental instabilities).

Danger of incorrect diagnoses

✧ Diagnose using original images.

As the user you are responsible for accurately selecting original images for reconstruction as well as manual adjustment of the image margins.

Reconstructed images differ from original images with respect to image information, especially at the image transitions. For this reason, reconstructed images of bones and vascular structures are not always suitable for diagnosis.

When transmitting one or several reconstructed images through the network or on a data medium, please inform the recipients of the above facts.

Starting and ending Composing

Selecting Composing

You are able to start the **Composing** task card from any of the other task cards or from the **Patient Browser**.

➪ **Composing** can be started only if you have obtained and installed the license.

✧ Select **Applications** > **Composing**.

The **Composing** task card is opened.

➪ If too many task cards are active, please close one of them.

Closing Composing

✧ Select **Applications** > **Close Composing**.

The **Composing** task card will be closed. Another task card is moved into the foreground.

CHAPTER F.2

Image Selection and Reconstruction

Start reconstruction by selecting a series in the **Patient Browser**.

Reconstruction

When you load images to the **Composing** task card, they are checked by a number of criteria and then combined into overview images. Depending on the type of images, the reconstruction algorithm is set automatically or selected by you.

Manual correction

You can manually juxtapose images in a slice or slices.

Selecting series and starting reconstruction

Select suitable series of images for reconstruction in your local database using the **Patient Browser**.
→ *syngo* Operator Manual

Selecting studies/series

✧ Open a study and click a range of suitable series.

➪ Press and hold **Shift** while you select several consecutive studies or press and hold **Ctrl** to select several individual series.

➪ Select only matching individual *Series*, because in practical application, a study always includes additional series/images that could cause a complete study to cancel while you are loading it.

Loading the selection

✧ Select **Applications > Composing** in the menu of the **Patient Browser**.
- Or -
Use the mouse to drag the selection to the image area of the **Composing** task card.

➪ To load multiple selections via double-click, keep the **Shift** or **Ctrl** key pressed as well.

Reconstruction

MIP and subtraction images can be composed, in addition to original images measured.

➪ You can only compose MIP images that were measured inline. You cannot use MIP images generated with 3D *syngo*.

Requirements

The images selected for reconstruction via **Composing** have to meet the following prerequisites:

Criterion	Description
Image type	Only MR images acquired with ***syngo* MR** are acceptable.
Image matrix	All images of a volume must have the same matrix.
Image layout	All images of a volume have to form a cuboid.
Database storage	All images (or series of images) must belong to one study. All images of a volume must come from one series.
Series block	All images must be part of the same series block.
Slice thickness	All images of a volume have to have the same slice thickness.
Pixel spacing	All images of a volume have to have the same pixel spacing. Pixel spacing = FoV / image matrix

Criterion	Description
Distortion correction	The same distortion correction procedure will be/was used for all images. Corrected images cannot be mixed in with uncorrected images.
Slice distance	The images within a volume must have the same slice distance.
Slice orientation	The images within a volume must have the same slice orientation.
Slice inclination (based on the first volume)	If the slices were acquired in coronal direction (primary direction), only an inclination from coronal to axial is permitted (max. ±45°). Inclinations in other directions are not permitted (tolerance max. ±1°).
	If the slices were acquired in sagittal direction (primary direction), only an inclination from sagittal to axial is permitted (max. ±45°). Inclinations in other directions are not permitted (tolerance max. ±1°).
	Images acquired in axial direction cannot be composed.

If the input data does not meet one of these criteria, the data is rejected and a corresponding message is displayed.

➪ The prerequisites that have to be identical within a volume according to the list above, may differ from volume to volume.

Distortion correction

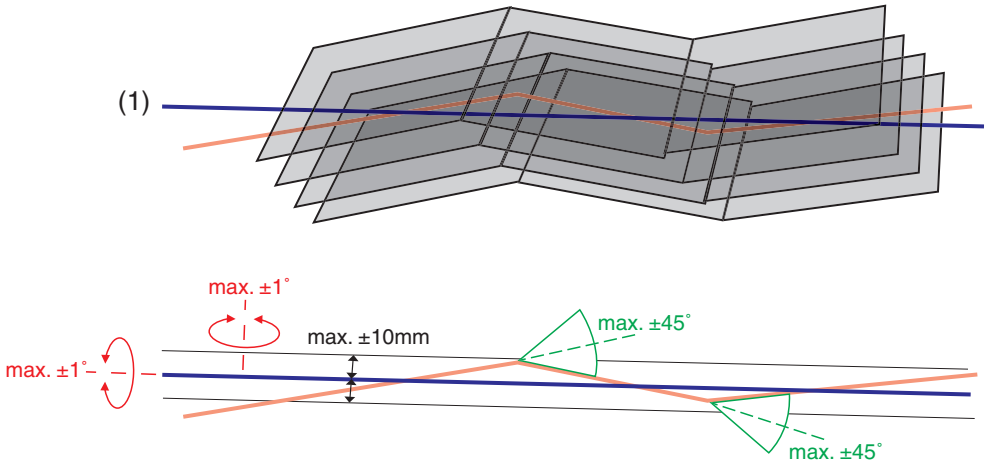
Before images are composed, they may have to be geometrically corrected. The images are first checked to see if they are already corrected.

If they are not, they are corrected now. In this case, a relevant message is shown in the status bar.

The corrected images are stored each time in a new series.

Resulting data

The spatial deviation of a pixel in the composed image may deviate by max. 10 mm from the resulting slice plane. The resulting slice plane is corrected for small differences in the orientations of the slabs.



(1) resulting slice plane

❏ MR images are generated if this criterion is met. The composed images may be used to plan additional measurements.

❏ If this criterion is not met, SC (Secondary Capture) images are created. SC images may not be used to plan additional measurements.

➪ Due to the modified criterion for generating MR images, a data set used to compose MR images with ***syngo* MR** 2004A, 2004V, 2005E, 2006T, or LEONARDO 2004, may only result in the generation of SC images with ***syngo* MR** A40.

Process of reconstruction

When images have been selected for reconstruction, the software of the **Composing** task card "searches" for similar structures in the overlapping areas of single images.

Automatic alignment

Individual images are shifted until the best alignment is obtained.

Manual alignment

In cases where transition areas have not been optimally reconstructed by the computer, you can adjust them manually. Proceed by shifting the image part below the transition edge relative to the image part above the transition edge until the best alignment is achieved in the overlapping area.

➪ The first time you perform manual alignment, a dialog window appears with a warning.

Original images

In certain cases, for example, when diagnosing bone structures, it will be necessary to use the original image information. To this end, you can use individual images, or as an alternative, a special display mode, the Cut mode (**Hard Image Transitions**).

In Cut mode, the images are joined at the cut lines without overlapping. This displays an overall image with the unchanged information of the individual images.
→ Page F.3–15, *Switching between blend mode and cut mode*

Important notes

The reconstruction algorithms detect similar prominent features in the images to be joined and match them to one another.

!

Before using a composed image to support a diagnosis, visually verify the image match using the original images with an appropriate resolution.

Independent of how reliable the transitions between individual images may appear, only a physician can ensure diagnostic accuracy using the image margins of the original image for visual inspection.

✧ Use the **View > Single with Original** function to compare the composite image with the original images.

Same volume position

If volumes are selected that were acquired at the same position, reconstruction will not be performed.

Volumes that do not overlap

If selecting volumes that do not overlap, "holes" will be present during reconstruction. Reconstruction is performed. Missing areas are shown in black in the composed images.

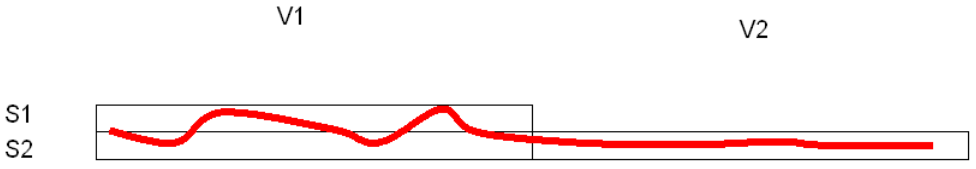
➪ Image margins cannot be manually adjusted.

Incomplete slices

During distortion correction, areas in which no data were measured may be shown in the image.

Reconstruction with the **Spine** algorithm does *not* use such incomplete slices.

However, reconstruction with the **Angio** algorithm uses incomplete slices. This is demonstrated by the following graph:



A blood vessel runs through the two volumes V1 and V2. V1 contains the two slices S1 and S2. V2 only contains S2. Slice S1 is incomplete, since it is missing in V2. If the **Angio** algorithm was using only the complete slice S2 verwenden, the information from S1 would be missing.

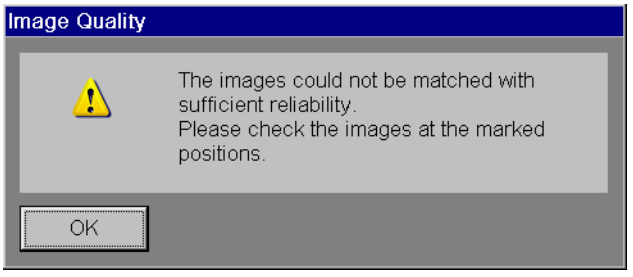
Too many images

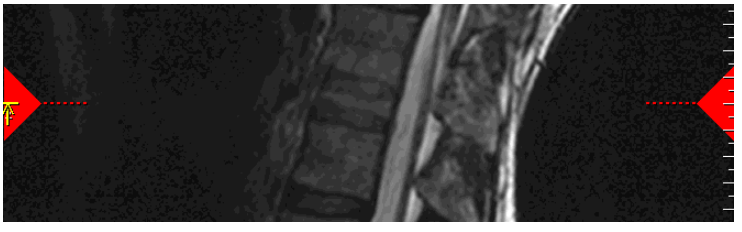
If you select volumes with too many images, reconstruction will not be performed.

➪ Depending on the quantity of images, some of the images that were loaded may have to be unloaded before a new data set can be composed.

Transition does not match

If one or more transition areas between images are not recognized properly by the reconstruction algorithm, a message appears after reconstruction.





➪ Transition areas that do not match exactly are marked with a red triangle to the left and right. In addition, the text "image sections do not match" is shown at the bottom of the image.

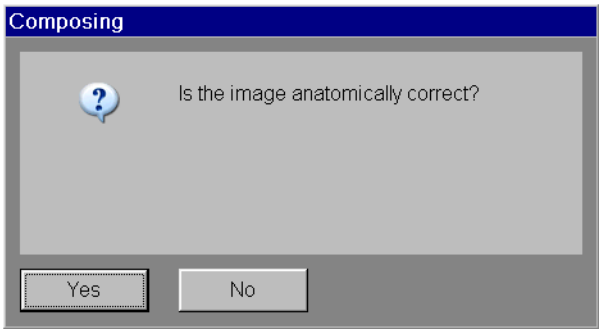
✧ Check the transition areas marked.

The note "image sections do not match!" is an image text that can be blanked out.

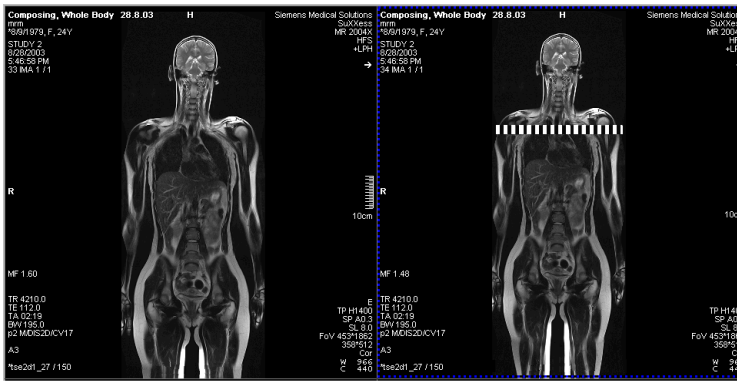
✧ Ensure that the image text is displayed for diagnoses.
→ Page F.3–22, *Switching image text on/off*

Anatomically correct?

If it was not possible to match the image sections correctly (red triangles), or the image margin was manually corrected (**M**), a query appears prior to storage asking if the composition is anatomically correct.



✧ Click **Yes** or **No**.



(1) (2)

(1) When you click **Yes**, the red triangles and the note "Image sections do not match!" or the markers for manual adjustments (**M**) are removed.

(2) In case of **No** the transition areas are marked with black and white stripes.

! As the user, you are responsible for correct evaluation of the reconstruction and the diagnostic conclusions drawn from it.

Change in users

If the new user has access rights to the images loaded with **Composing**, the function remains available for use.

If a reconstruction is in progress at the time the users change places, **Composing** is blocked for the new user until reconstruction is ended.

If the new user does not have rights for the current patient, the images are automatically unloaded.

If **Composing** is blocked for the new user while reconstruction is in progress, the contents of the **Composing** task card are deleted.

The new user must close **Composing** and start it again to continue working.
For further information, refer to the *syngo* Security Package brochure.

Reconstruction

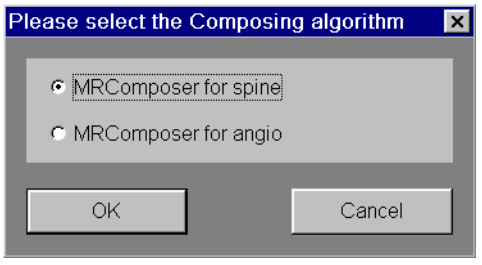
By accepting the series, the **Composing** task card moves into the foreground.

If the input images are of the Inline MIP type, reconstruction will start automatically using the MIP algorithm.

Selecting the algorithm

Otherwise a dialog window for selecting the algorithm appears. You can then select one of the following two composing algorithms:

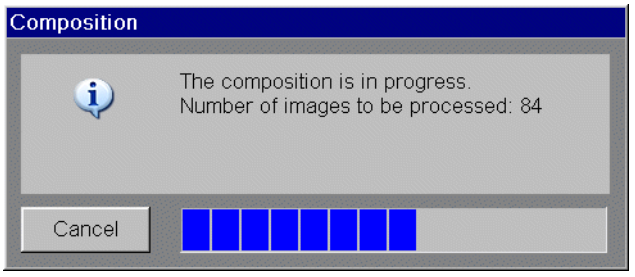
- ❏ The **Spine** algorithm is based on the bone structure of the images. Composed images of this kind may be measured and evaluated, e.g. scoliosis, kyphosis, pelvic obliquity.
- ❏ The **Angio** algorithm is based on the vessel structure in the images. This allows for overall display of the vessels.



✧ Click the required algorithm and confirm with **OK**.

Reconstruction starts.

The **Composing** window shows the reconstruction process.



Canceling reconstruction

Reconstruction can be canceled if, for example, you have selected a series with a large number of images and the reconstruction process is taking too long:

✧ Click **Cancel**.

Reconstruction stops within the current process.

The images composed so far are displayed.

Adjusting reconstruction manually

Normally, all parameters required for image reconstruction are determined automatically.

Occasionally, the automatic algorithm does not provide optimum results. In this case, you may manually determine the position of the images relative to one another (pixel-by-pixel shifting).

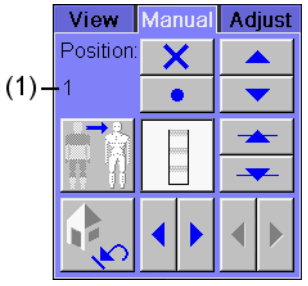
! By changing the reference parameters, the graphics shown in the composite image are no longer valid following manual adjustment. They have to be redrawn accordingly.

➪ In the case of a saved and reloaded composed image, the position of the single images may be changed only if the original images are still available in the local database.

! As the user, you are responsible for correct evaluation of the reconstruction and the diagnostic conclusions drawn from it.

Tools

The tools for manual positioning are located under the **Manual** subtask card of the **Composing** task card.



(1) Position number (position of the orientation label)

Selecting the image position to be shifted

First, select the image in the series you want to pan:

✧ Double-click the required position in the *overview image* (on the right).



The position of the image margin to be corrected is shown via an orientation label in the left margin of the *detail image* (on the left).

The position number is displayed.
→ Page F.3–4, *Displays in images*

Setting the number of pixels to be shifted

For subsequent corrections you can set the number of pixels per mouse click in the **Image** menu.

You can use one of the following values: 1, 3, 5, 10, 15, 20, 30, 40, 50, 100, 200 pixels

When you start the system, 3 pixels per mouse click is the default setting.

✧ Select the required number of pixels in **Image > Manual Adjustment**.

The setting remains the same until you change it again or restart the application.

Shifting the Images Relative to Each Other in a Slice

You can now pan the image identified with the orientation mark. This image as well as all subsequent images are panned relative to the images above the marked image.

➪ The top image cannot be panned.

! The shift should be performed in Cut mode (**hard image transitions**) because pixel-by-pixel shifting is easier to see in this mode.
→ Page F.3–15, *Switching between blend mode and cut mode*

Moving up/down



✧ Click the up or down arrow.

The images below are moved up or down by the set number of pixels.

Moving left/right



✧ Click the right or left arrow.

The images below are moved to the right or left by the set number of pixels.

Moving a cut line



✧ Click the up or down arrow with the line symbol.

The cut-line (image margin) is moved up or down by the set number of pixels.

Shifting Slices Relative to Each Other

You can move from slice to slice in the composed volume, maintaining the composition.

Selecting a slice

✧ Use the dog-ears and scroll to the required slice.
- Or -
Press the **Image -** (**Num 1**) or **Image +** (**Num 2**) on the keyboard.

Shifting the image



✧ Click the end of the arrow (cross) or arrowhead (circle) once or repeatedly.

The slice is shifted to the front or the back.

The composed slice images affected are recalculated. Composed slice images that are not affected remain unchanged.

Normalizing Image Brightness

You can normalize the brightness impression of image sections for volumes included in the composite volume (caused by measurements performed with different coils).

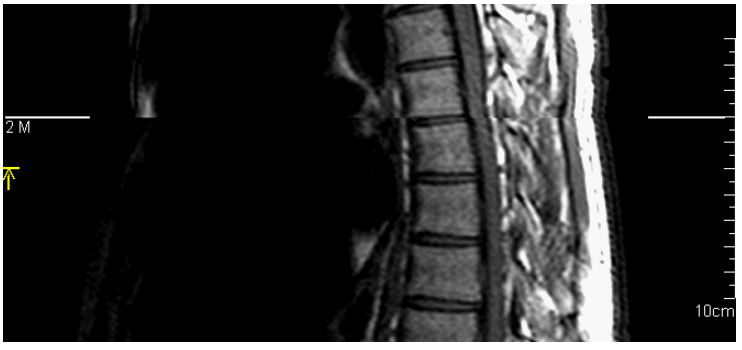


✧ Click this button.
Or
Select **Image > Normalize.**

Brightness of the individual image sections is normalized for the current composite volume.

➪ During manual correction **Normalize** is automatically switched off again.

Display



When a single image has been panned manually, it is identified with an "M" as a composite image. At the bottom of the image "Performed manual adjustment" is superposed.

! When defining the film layout after manual correction in **Composing**, make sure that **All text** is selected for the **Image Text** selection so that the message "Manual adjustment performed!" is exposed onto the film.
→ *syngo* Operator Manual

Returning to Automatic Positioning



✧ Select **Auto Adjustment** from the context menu.
- Or -
Click this button.

All manual positioning is canceled and the status after automatic reconstruction is restored.

CHAPTER F.3

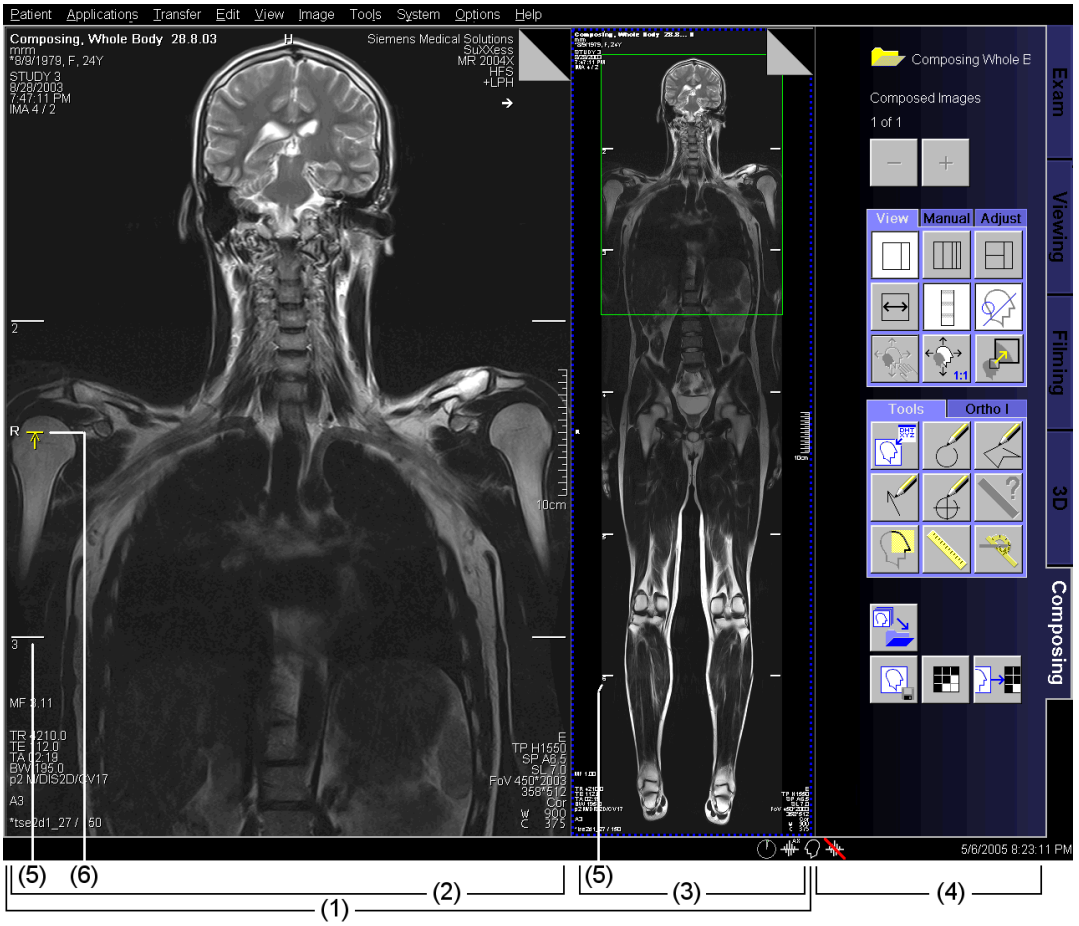
Viewing Images

The **Composing** task card allows you to view and post-process *composite images* after reconstruction.

You can switch between different layouts and scroll among several composed images and slices.

You can load and view images that have already been composed and stored. (Manual alignment is possible only if all original images are available.)

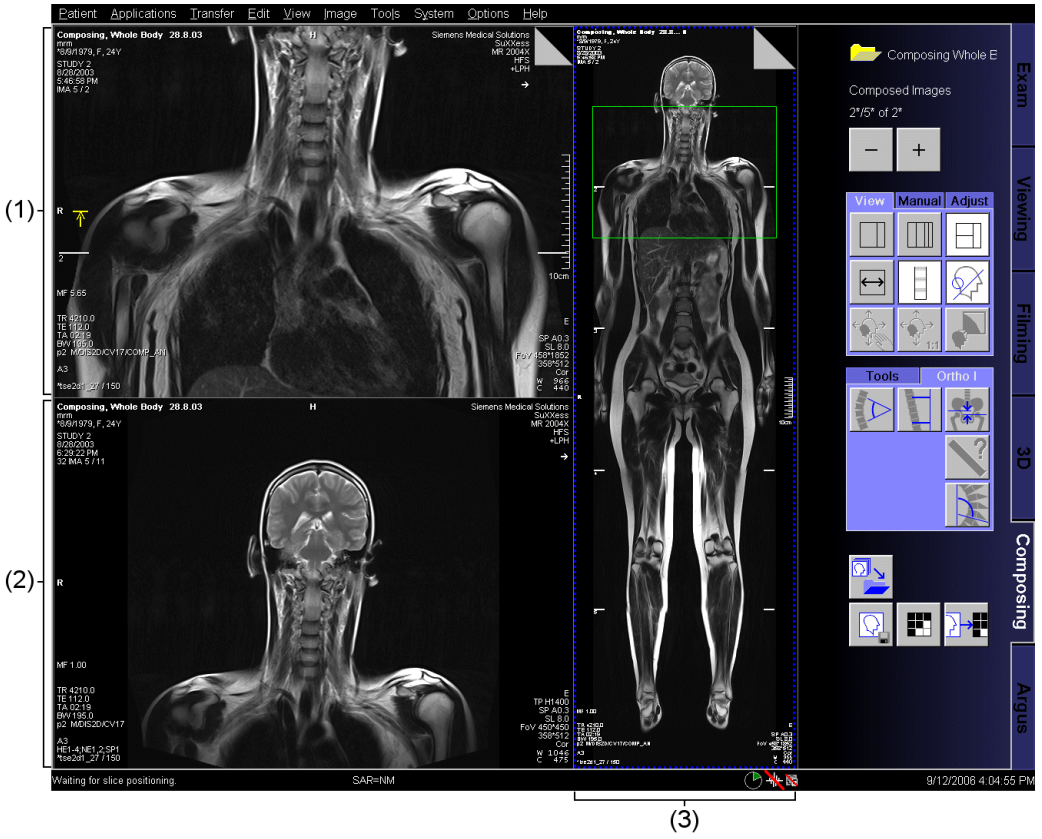
The Composing task card



(1) Image area
(2) Detailed image
(3) Overview image
(4) Control area
(5) Section markers and image position numbers
(6) Orientation mark

Image segments

The image area of the **Composing** task card can be divided into different segments which can be switched on or off.



(1) Detail image segment: Display of the composed image
(2) Original image segment: Display of the corresponding original image
(3) Overview image segment: Overview of the entire composed image

Displays in images

The following special displays appear in the image area for the **Composing** task card:



Dog ears for scrolling through the slice image stack



Image position numbers



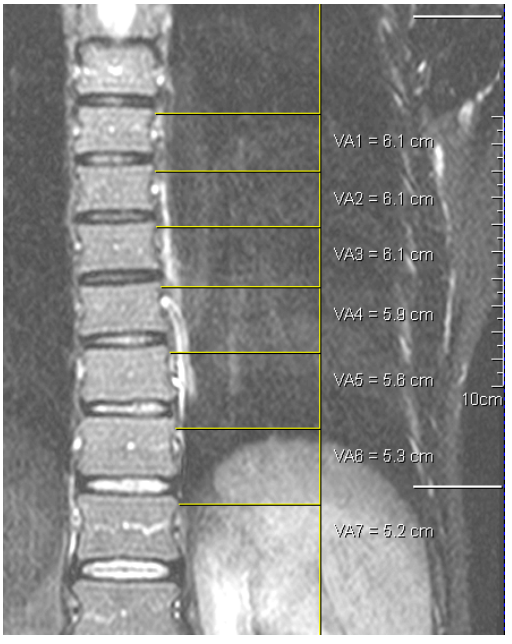
Image position number with orientation mark



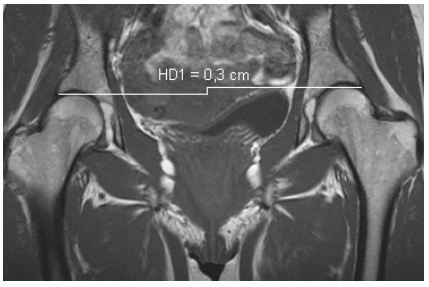
Image position number identified with "**M**anual"



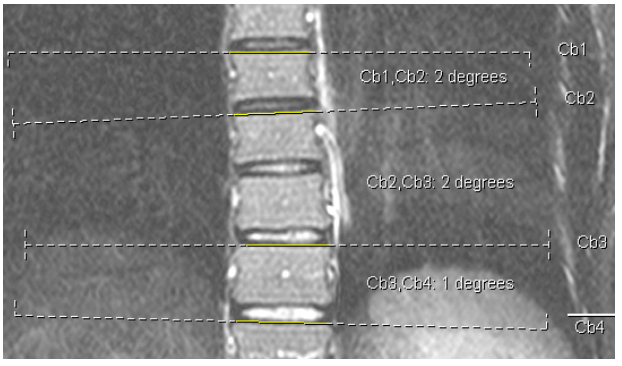
Image position number with identification "image segments do not match!"



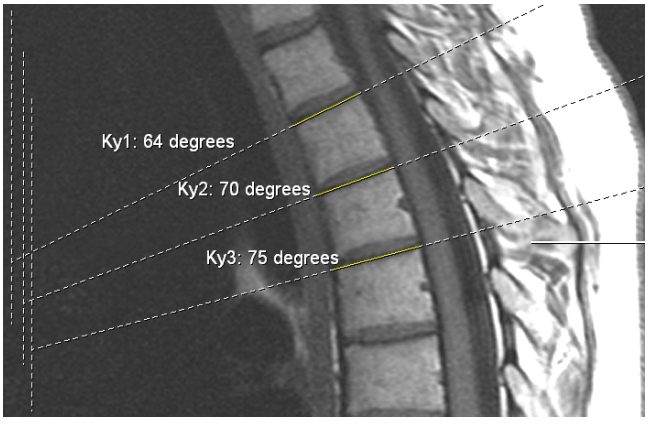
Vertical **D**istance measurement



Height **D**ifference

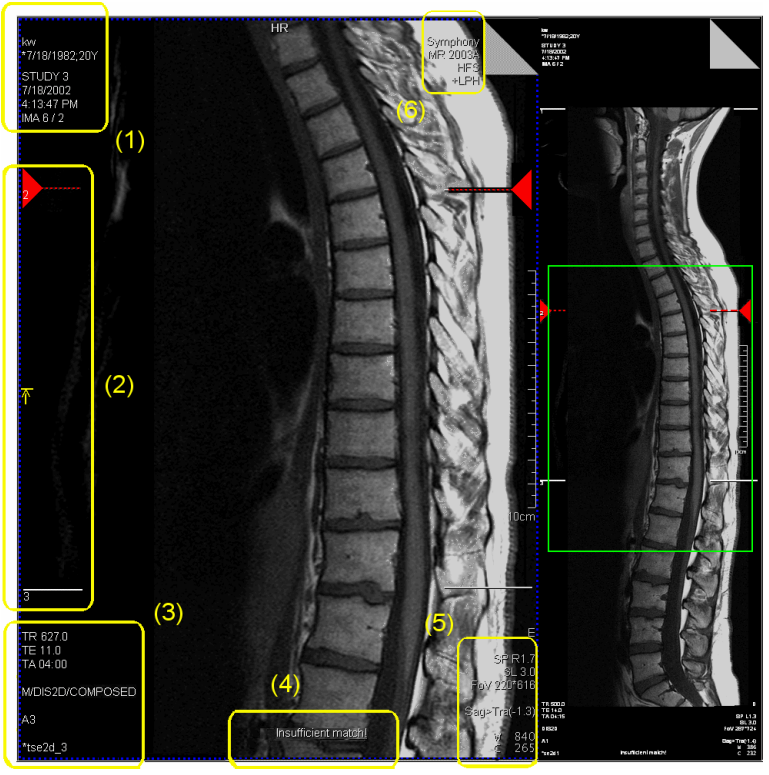


Co**b**b angle



Kyphosis angle

Text Information in Images



(1) Patient and examination data
(2) Image position numbers with orientation mark and identification
(3) Examination and image parameters
(4) Notes
(5) Slice information and window values
(6) System-specific information

Loading and Displaying Images

For viewing and post-processing, load the series and images into the **Composing** task card.

✧ Select **Patient > Browser**.

✧ Select the requested patient/requested study
→ *syngo* Operator Manual

✧ Click the tab of the **Composing** task card.

The **Composing** task card is placed in foreground.

!

You can only load images of *one* patient into the **Composing** task card.

Images of *one* series block only may be loaded per load operation (same frame of reference).

If you load images of another patient, the current patient is automatically closed if you confirmed the message accordingly.

Loading images for reconstruction

✧ Select the series in the navigation or content area of the **Patient Browser**.
→ Page F.2–1, *Selecting series and starting reconstruction*

Loading a composite image/volume or single images/volumes

You are able to load a composed as well as saved image/volume or just individual images/volumes in the **Composing** task card.

!

In the case of a composed image/volume that has been stored and reloaded, you can change the position of single images relative to each other *only if*:

- ❏ All original images are available
- ❏ The images are not the result of a canceled reconstruction
- ❏ The composed image or the original images were not changed outside **Composing** or provided with an electronic shutter.

Loading a volume

✧ Select the required series in the content area of the **Patient Browser** which already contains composed images.

✧ Select **Applications > Composing** in the menu of the **Patient Browser**.
- Or, in case **Composing** is open -
Double-click the series containing composed images.

The composed volume is loaded into the **Composing** task card.

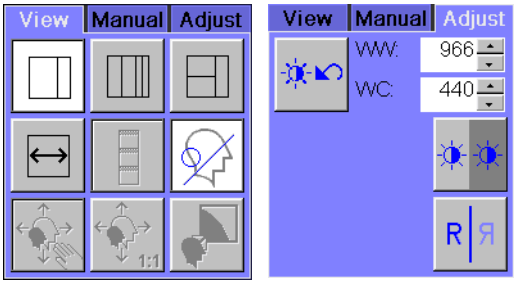
➪ If you double-click a series that does not contain composed images, only this particular series is loaded.

Display after loading

For a volume that has just been composed, the center image of the result volume is shown. The focus is on the center volume.

An already composed image is displayed as it was when it was last saved.

Changing image display



The tools are located in the **View** and **Window** subtask cards as well as in the **View** menu.

→ Page F.2–5, *Process of reconstruction*
→ Page F.2–6, *Important notes*

Effect of functions

Some functions affect the selected image segment (focus) only, in particular in the **Single with original image view**; other functions affect all image segments.

Function	Only affects the selected image segment	Affects all image segments
Windowing	x	
Reset window values		x
Inverting grayscale values		x
Mirroring vertically		x
Zoom/Pan	x	
Zoom factor 2.0 or **Zoom factor 0.5**	x	
Acquired image size	x	
Determining the area	x	
Home Zoom/Pan		x

Views

Detailed image or comparison



The **Composing** task card provides you with three different kinds of image displays (no film layouts):

❑ **Single layout** (default setting)
Only the composed image is displayed. In this display you will see a composed image, if necessary, with an overview reduced in size.
→ Page F.3–12, *Selecting single layout*



❏ **Single with original**
The composed image and the original image with the original image information (if available) are displayed one below the other. This display mode can be used for checking reconstruction and performing diagnoses.
→ Page F.3–13, *Select Single with original image view*



❏ **Double layout**
Two composed images are displayed next to each other. This display can be used to compare composed images/volume, for example, to assess the course of an illness.
→ Page F.3–14, *Selecting double layout*

Full image or overview

In each case you can switch between:



❏ **Full image display**
Only the detailed image or the detailed image with the original image at maximum width are shown. The overview is hidden.



❏ **Overview** (default setting)
In addition to the detailed/original image(s), one or two overviews of the composed images is/are displayed. In this display you can navigate easily with the support of the overviews.

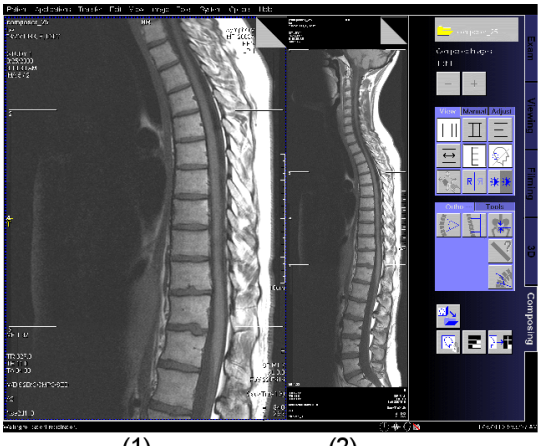
Switching between full image and overview

✧ To display (hide) the overview image, deselect/select **View > Hide overview**.
- Or -
Click the **View** subtask card and select/deselect this button.



Selecting single layout

If you just want to view only one composed image of a volume, select **Single Layout**.



(1) (2)



(1)

Single layout with/without overview display

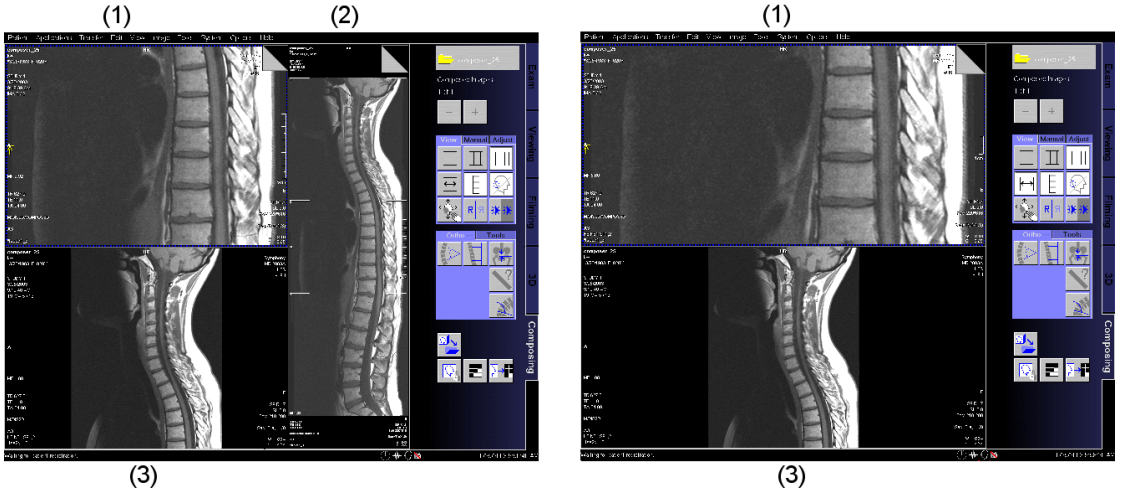
(1) Detailed image
(2) Overview image

✧ Select **View > Single layout...**.
- Or -
Click this button on the **View** subtask card.



Select Single with original image view

The original image should be used for diagnosis. For this purpose the composed image and an original image can be displayed simultaneously and compared. Select **Single with original image view**.



Single with original image view with/without overview display

(1) Detailed image
(2) Overview image
(3) Original image

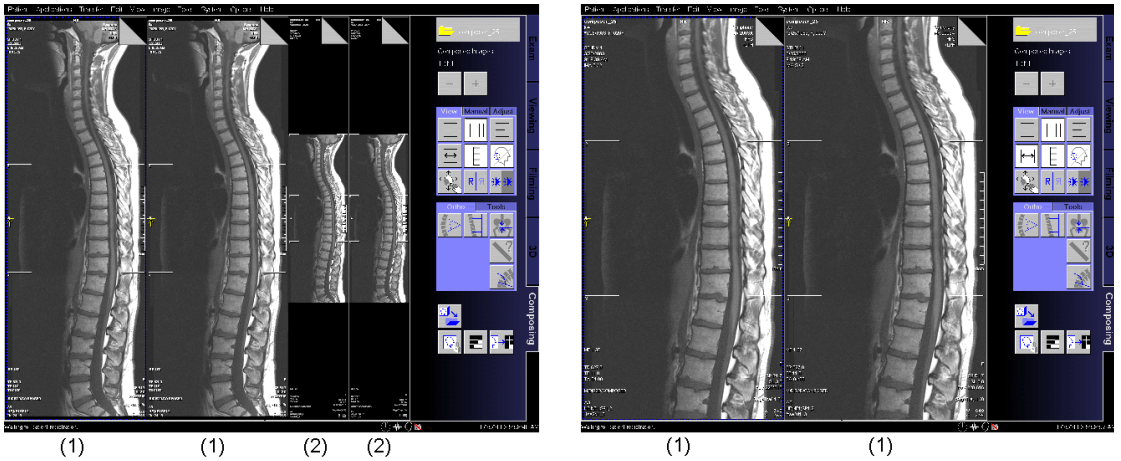
✧ Select **View > Single with original image view**.
- Or -
Click this button on the **View** subtask card.



Selecting double layout

When you want to compare two composed images (of two volumes), select **Double Layout**.

Prerequisite: Several volumes have been composed and loaded.



Double layout with/without overview display

(1) Detailed image
(2) Overview image

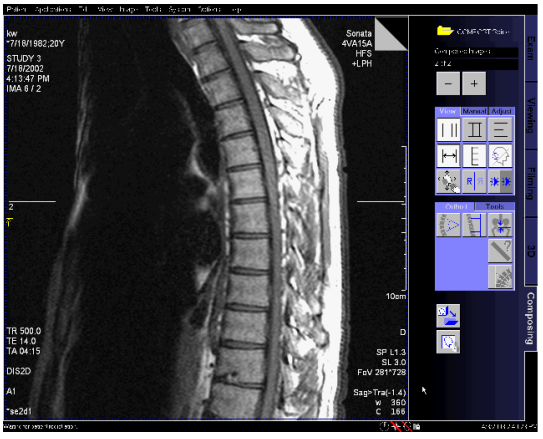
✧ Select **View > Double Layout...**.
- Or -
Click this button on the **View** subtask card.

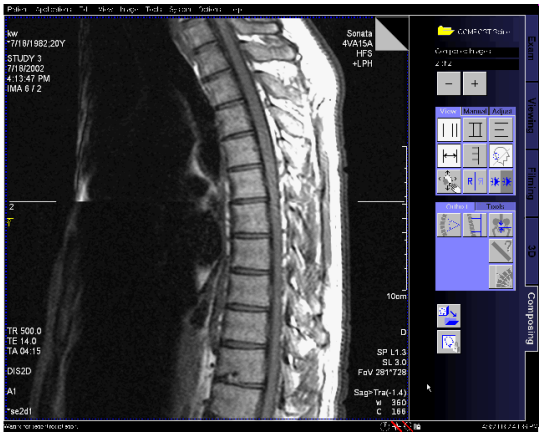


➪ If only one composed volume is loaded, a composed image is displayed twice. In this case, you cannot use all functions in the right image.

Switching between blend mode and cut mode

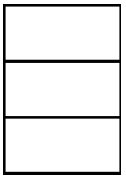
Usually, composed images are shown with "soft" transitions. For diagnostic purposes you can use images with "hard" cuts and display the original image information as well:





Blend mode (**soft image transitions**; default): The single images are blended at the transitions between each pair of images.





Cut (**hard image transitions**): The single images are joined without blending.

Switching blend mode on/ off



➪ Image transitions for a saved and reloaded composed image can be changed only if the original images are still available.

✧ To switch on (off) soft image transitions, select/deselect **View > Blend/Cut Mode**.
- Or -
Click the **View** subtask card and select/deselect this button.

The display changes.

➪ If the reconstruction algorithm does not identify sufficiently similar features at an image transition, a warning will be displayed, and the image transition will be marked.

➪ The images can be repositioned manually.

! When **Blend mode** is used, there are transition areas between the single images that were interpolated from two images. Although an image in the **Soft Transition display** appears more pleasant to the eye, *only* original images (**single images with original image view** or **hard transitions** may be used for*diagnosing* bone and vessel structures.

Scrolling through composite volumes

If several volumes have been composed and loaded, you can scroll through them one by one.

✧ Select the required image segment in the **double layout**.






✧ Click **–** or **+**.
- Or -

Press the **Study -** (**Num 7**) or **Study +** (**Num 8**) on the keyboard.

The images of the previous or next composed volume are displayed.

➪ In overview mode, the overview also changes.

Scrolling through a single volume

You can also "scroll" among single volumes within a reconstructed volume.

✧ Click the required image segment.

This segment is identified with a blue (light) border.




✧ Press the **Series -** (**Num 4**) or **Series +** (**Num 5**) on the keyboard.

The displayed image is moved to the next/previous partial image/volume.

➪ In overview mode, the overview also changes.

Scrolling through the image stack

You can scroll through the image stack of composed images using the dog ears or icons.
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Selecting an image section / navigating in the detailed image

There are several ways of navigating in the composed detailed image:

- ❏ Shifting the image position
- ❏ Selecting / changing an image section
- ❏ Continuously zooming/panning an image
  → *syngo* Operator Manual
- ❏ Enlarging or reducing the image by a factor of 2
- ❏ Setting 1:1 pixel display

Shifting the image position



You determine the image position by setting an orientation marker in the detailed image.

✧ Double-click the required position *in the overview image*.

The position is marked on the left with the orientation marker in the *detailed image*.

The detailed image is shifted so that the marked position is in the center in the vertical direction.

If applicable, the corresponding original image is displayed in the lower part.

Or

✧ Press one of the following keys on the keyboard.

Image ↑: The orientation marker is moved to the next lower image number.

Image ↓: The orientation marker is moved to the next higher image number.

Pos1: The orientation marker is moved to the first image number.

End: The orientation marker is moved to the last image number.

The detailed image is shifted accordingly.

Selecting an image section



You can also select an image section (ROI).

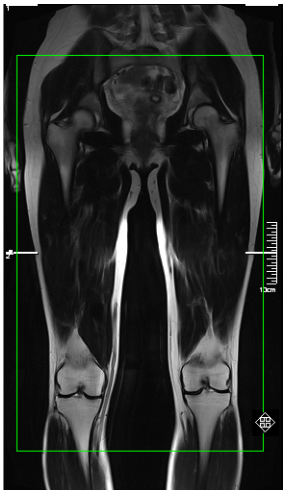
✧ Click this button.
Or
Select **Tools > Capture Area** in the main menu.

✧ Click and draw a frame in the detailed image.

The *detailed image* is enlarged according to the image section and centered.

The image section is shown in the *Overview Image*.

Modifying the image section



In the *Overview image* (right), the portion of the image shown in the detailed image (left) is marked with a green border.

You can change this border and therefore the image section.

Moving an image section:

✧ Move the mouse pointer to one of the four sides of the green border.

✧ Drag the green border to the desired position.

Resizing the image segment:

✧ Move the mouse pointer to one of the four corners of the green border.

✧ Enlarge or reduce the size of the green border.

The image section shown in the detailed image is modified accordingly.

Enlarging or reducing the image by a factor of 2

You can also enlarge or reduce the image step-by-step (each time by a factor of two).

✧ Go to the main menu and select **Image > Zoom in by 2.0** or **Zoom in by 0.5** in the main menu.

The *detailed image* is enlarged/reduced by a factor of 2.

The *overview image* does not change.

Setting 1:1 pixel display

To achieve optimal image display without interpolation, you can define that each image pixel is assigned a monitor pixel.



✧ Click this button.

The *Detailed Image* is magnified or reduced so that every image pixel corresponds to a monitor pixel.

Resetting the image display

You can reset the image to the default setting for zoom and position.

✧ Select **Image > Home Zoom/Pan** in the main menu.

The original image display is restored.

Switching image text on/off

The *image text* contains the following information:

- ❏ Text input at the four corners of the image (patient data, etc.)
- ❏ System messages at the bottom in the image center (for example, “Insufficient match!“)

This text can be hidden if, for example, you want to film an image anonymously.

! If you film a composed image with the image text and/or graphics switched off, non-matching or manually adjusted transitions between the individual images cannot be identified as such!

✧ Switch on image text and graphics for diagnostic applications.

✧ Select/deselect **View > Image Text ON**.

The image text is switched on or off accordingly.

Activating/deactivating graphic elements

You are able to temporarily hide graphic elements (lines, circles...), if e.g. you would like to view details underneath them.

This includes:

- ❏ All graphic elements drawn (lines, circles...)
- ❏ The image segment markings and image position numbers
- ❏ Special identifications for transitions (e.g. red triangles for non-matching transitions or "M" for manually set transitions)

Activating/deactivating graphic elements



✧ To switch on (off) graphic elements, select **View > Image Graphics On**.
- Or -
Click the **View** subtask card and select/deselect this button.

Image display/Windowing

Set the windowing values in the **Composing** task card.

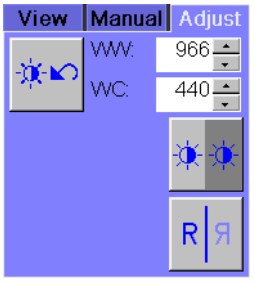
➪ During scrolling, windowing values are automatically applied to other composed images.

Windowing with the mouse or keyboard

Details for windowing with the mouse or the keyboard are included in the *syngo* Operator Manual.

Setting the windowing values numerically

Set the window values numerically by using the **Window** subtask card:



✧ Enter the desired window values with the keyboard into the **WW** (= window width) and **WC** (= window center) fields.
- Or -
Set the required values using the arrow keys.

Resetting the window values



✧ Click this button to reset the window values to the values last saved.

Additional display modes

Function	Button	Description
Mirroring an image		→ *syngo* Operator Manual
Inverting grayscale values		→ *syngo* Operator Manual
Editing graphics	→ *syngo* Operator Manual	



Image is mirrored

Confusing left/right leads to incorrect diagnosis!

The examiner is responsible for correct application of functions and/or interpretation of the images as well as the consequences resulting from his actions.

✧ Minimize the risk of incorrect interpretations by e.g. providing notes/comments.

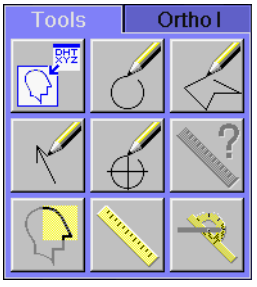
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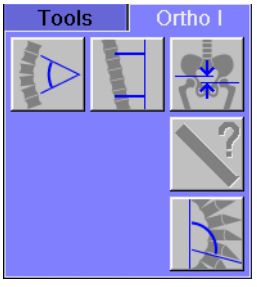
Evaluations

The **Composing** task card allows you to perform evaluations and apply post-processing functions.

Tools

The tools are located on the **Tools** and **Ortho I** subtask card as well as in the **Tools** menu.





Important notes

Distance measurements

When performing distance measurements, please keep the following in mind:

- ❏ Distance measurements made across image boundaries in composed images (in the vertical direction on the monitor) are inaccurate. This error is additive across the sum of the original images.
- ❏ Digits appearing after the decimal point in the measurement results are *not* representative of the accuracy of the measurement taken. When using a measurement to support diagnosis, the physician has to consider all sources of errors.

Image sections do not match

Risk of incorrect measurements

✧ Only measure within each image (between the transitions), if possible.

✧ Do not perform measurements across edges that are identified as "image sections do not match!".

Angle measurements

When performing angle measurements, please keep the following in mind:

❏ The main sources for error when determining Cobb and Kyphosis angles are the *subjective positioning of the tangent* to the vertebrae and the *position* of the patient's body.

❏ Digits appearing after the decimal point in the measurement results are *not* representative of the accuracy of the measurement taken.

❏ The accuracy of Cobb angle or kyphosis angle measurements is comparable with that of measurements made by hand on film images.

❏ In the case of angle measurements on projection images, the projected plane must be parallel to the angle plane.

Graphics functions

Availability of graphics functions

Graphics functions are also available if red triangles are displayed in the images.
→ Page F.2–8, *Transition does not match*

However, measurements across image transitions (e.g. distance measurements) should be performed only when all image sections fit together (no red triangles).

! Graphic elements may be drawn in the detailed image only, not in the overview.

The functions described in what follows can be selected via the buttons on the **Measure** subtask card as well as via the **Measurement** menu.

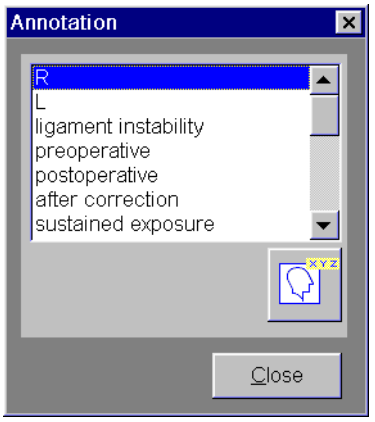
Annotating images (annotation)

You can enter predefined text or freely formulated texts on the **Composing** task card.



✧ Click this button on the **Measure** subtask card.

The **Annotation** dialog window opens.



Using a predefined text

✧ Mark the desired sequence in the list.

✧ Click the required position in the image.

The text is inserted immediately.

Entering free text



✧ Click this key in the **Annotation** dialog window.

✧ Click the required position in the image.

A text field is displayed.



✧ Enter the text.

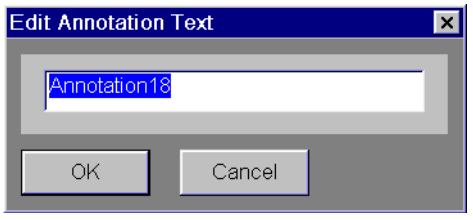
✧ Press the **Enter** key.

Defining text

20 predefined texts are available. You can change the texts at any time:

✧ Double-click the entry you want to change in the **Remark** dialog window.

The **Edit Annotation Text** dialog window opens.



✧ Overwrite the text as required.

✧ To apply new text, click **OK**.

Positioning text



✧ Click the text.

The text is marked with small squares.

✧ Move the text to the desired position.

Editing text



✧ Double-click the text.

The text is transferred to an input field.

✧ Change or supplement the text.

✧ Press the **Enter** key.

Deleting text



✧ Click the text.

The text is marked with small squares.

✧ To remove the text, press **Del**.

→ *syngo* Operator Manual

Ending text input, switching to another image

✧ When you have completed adding remarks, close the **Annotation** dialog window.

Or

✧ Select the next image where you would like to add annotations and continue with your work.

Switching text on/off

→ Page F.3–22, *Switching image text on/off*

Drawing circles and lines/polygons

The **Composing** task card lets you draw lines/polygons such as circular and free hand ROIs identically to the **Viewing** task card. However, it is not associated with statistical evaluation.

Drawing function	Button	Description / cross-reference
Drawing circles		→ *syngo* Operator Manual
Drawing circles with a center		You draw circles with a center the same as other circles. Using this method you can easily perform distance measurements starting from the center of the circle, e.g. the center of a ball-and-socket joint. As compared to the circle line, you are not able to select the "crosshair" in the circle.
Drawing lines/polygons		→ *syngo* Operator Manual

Drawing arrows

You can emphasize image details with arrows:



✧ Click the button.

✧ Click the point in the image where you want to position the arrowhead, and drag the mouse to the end point of the arrow to create the line.

The arrow is drawn.

Changing the size

✧ To change the size of the arrow, drag one of the two arrow end points with the mouse.

Additional graphics functions

Graphics function	Button	Description / cross-reference
Shutter		→ *syngo* Operator Manual
Distance line		→ *syngo* Operator Manual
Angle		→ *syngo* Operator Manual
Switching graphics on/off		→ Page F.3–23, *Activating/deactivating graphic elements*
Editing graphics	→ *syngo* Operator Manual	

Evaluations for the Spine and Pelvis

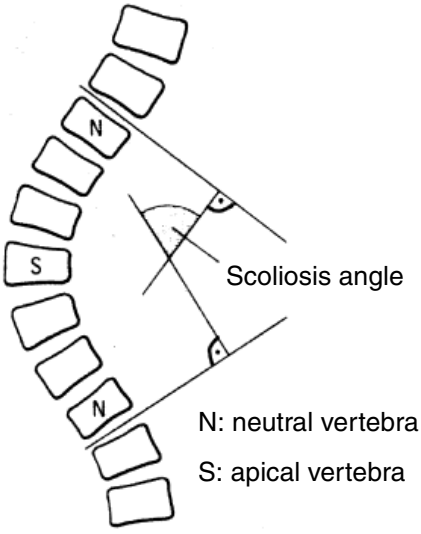
Depending on the reconstruction used, you are able to perform the following evaluation with composed images:

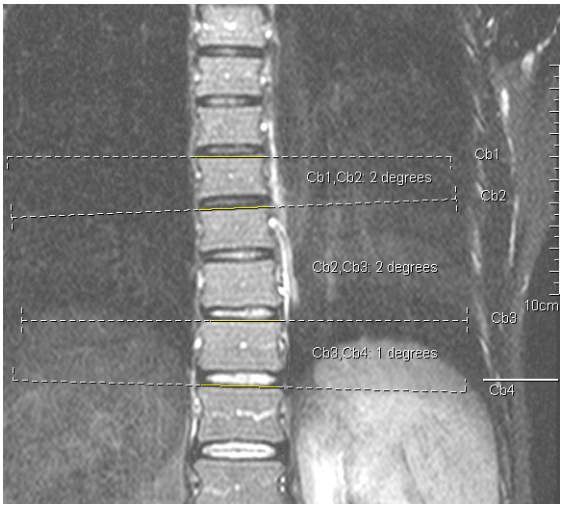
Tools	Evaluation
	Scoliosis angle according to Cobb: Measuring one or several curvatures of the spine. → Page F.4–10, *Determining the curvature of the spine (scoliosis angle according to Cobb)*.
	Kyphosis angle: Measuring the angle of the basic spine tangent relative to the vertical. → Page F.4–14, *Determining kyphosis angles of vertebrae*
	Vertical distance measurement: Measuring the spine's deviation from the vertical. → Page F.4–16, *Measuring the deviation of the spine from the vertical*
	Difference in height: Measuring the difference in height, e.g. between the left and right side of the pelvis. → Page F.4–20, *Measuring the difference in height*

Determining the curvature of the spine (scoliosis angle according to Cobb)

There are different methods for determining the scoliosis angle of the spine. The most widely accepted is the method according to Cobb.

This method involves drawing the tangent to the dorsal plate of the upper neutral vertebra and to the basal plate of the lower neutral vertebra. From these, the system calculates the scoliosis angle:





Scoliosis angle: schematic representation[1] (left), example (right)

1. Zilch, H.; Weber, U.: Orthopädie mit Repetitorium. Berlin: de Gruyter, 1989

Drawing the scoliosis angle

One or several scoliosis angles may be drawn:

✧ Select the required image.
→ Page F.3–7, *Loading and Displaying Images*

✧ Select a detailed image display.
→ Page F.3–9, *Changing image display*

➪ You can only draw the angle tangents in a detailed image; however, the results are also displayed in the overview image.

✧ Select **Measure > COBB angle**.
- Or -
Click the button.





✧ Move the mouse pointer into the detailed image.

The mouse pointer changes shape.

First tangent

✧ Drag a line from the starting point to the end point of the first tangent with the mouse.

The tangent is drawn.

Second tangent

✧ If necessary, move the image area by double-clicking in the overview (new position of the orientation mark).

✧ Draw the second tangent in the same way.

The tangents are marked according to their position, for example, **Cb1**, **Cb2**, etc.

The scoliosis angle is drawn in the vicinity of the apical vertebra.

Additional tangents

If there are additional curvatures, more angles can be defined:

✧ Draw additional tangents in the same way.

In each case, scoliosis angles are drawn in the vicinity of the apical vertebrae.

Changing the scoliosis angle drawn

Previously drawn angles can be changed at any time:

Changing angles or tangents

✧ Click on the required tangent.

The tangent is marked with small squares at the corner points.

✧ Drag an end point to the new position with the mouse.

The relevant scoliosis angles are updated.

Moving the annotation

✧ Click the annotation to be moved.

The characters are marked with a small square.

✧ Drag the annotation to the desired new position.

Removing angles

To remove an angle, delete a tangent:

✧ Click on the required tangent.

The tangent is marked with small squares at the corner points.

✧ Select **Edit > Delete Selected Graphics**.
- Or -
Press the **Del** key.

If it was the lowest or topmost tangent, the lowest or topmost scoliosis angle is deleted.

If it was the middle tangent, the scoliosis angles above and below it are deleted and a new angle is drawn instead.

If it was one of two tangents, both tangents including the angle will be deleted.

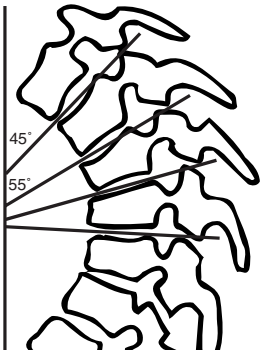
Ending editing

✧ Select another function.

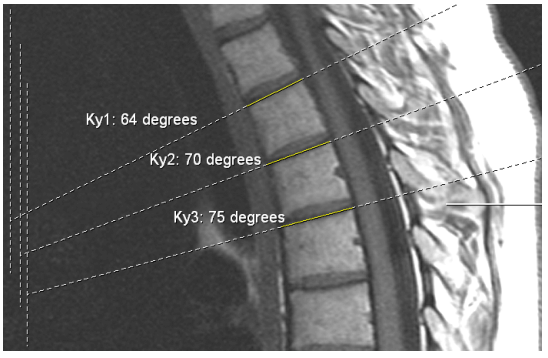
If only one tangent (but no angle) is drawn, it is deleted.

Determining kyphosis angles of vertebrae

A kyphosis angle is the angle between a vertebra and the vertical in a lateral acquisition:



Kyphosis angle: schematic representation



Sample

Drawing kyphosis angles

You can draw one or several kyphosis angles:

✧ Select the required image (lateral acquisition!).
→ Page F.3–7, *Loading and Displaying Images*

✧ Select a detailed image display.
→ Page F.3–9, *Changing image display*

➪ You can only draw the angle tangents in a detailed image; however, the results are also displayed in the overview image.



✧ Select **Measure > Kyphosis**.
- Or -
Click this button.

Drawing an angle

✧ Drag a line from the first point to the second point on the vertebra with the mouse.

The line is extended. A vertical line and the kyphosis angle are drawn.

Changing the scoliosis angle drawn

Changing angles or lines

✧ Click on the required line.

The line is marked with small squares at the end points.

✧ Drag one of the end points to the position desired.

The relevant kyphosis angle is updated.

Removing angles

To remove an angle, delete the associated line:

✧ Click on the required line.

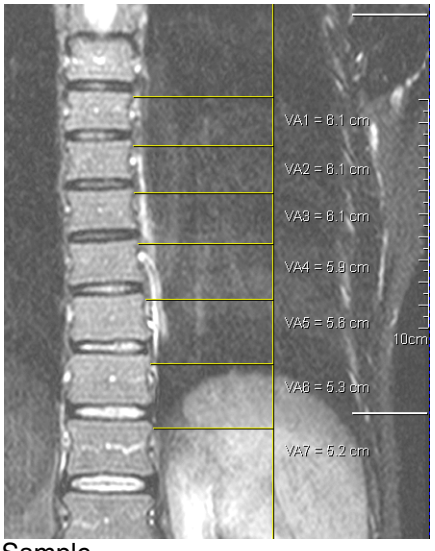
The line is marked with small squares at the end points.

✧ Select **Edit > Delete Selected Graphics**.
- Or -
Press the **Del** key.

The line and the associated kyphosis angle are deleted.

Measuring the deviation of the spine from the vertical

An additional tool for evaluating scoliosis is to determine the deviation of the spine from an imaginary vertical line.



Sample

Drawing lines

✧ Select the required image.
→ Page F.3–7, *Loading and Displaying Images*

✧ Select a detailed image display.
→ Page F.3–9, *Changing image display*

✧ Select **Measure > Vertical Alignment**.
- Or -
Click the button.



Vertical line

As a first step, determine the line to be used for measuring the deviation from the vertical line:



✧ Move the mouse pointer into the detailed image.

The mouse pointer changes shape.

✧ Click the image and drag a short line up or down with the mouse.

As soon as you move the mouse, a line is displayed.

✧ Release the mouse button.

A vertical line is drawn through the entire image.

Reference point

As soon as you have drawn the vertical line, draw distances to this line:

✧ Use the mouse to draw a short line from the desired point toward the vertical line.

A plumb line is dropped to the vertical line and the length of the plumb line is shown in cm.

Changing drawn lines

Changing a line

✧ Click on the required line.

The line is marked with a small square at the end point.

✧ Drag the end point to the new position.

The distances are updated accordingly.

Removing a line

✧ Click on the required line.

The line is marked with small squares at the end points.

✧ Select **Edit > Delete Selected Graphics**.
- Or -
Press the **Del** key.

The line and the given distance are deleted.

Moving the annotation

The annotation displayed (distance) can be moved if, for example, it hides important details:

✧ Click the annotation to be moved.

The characters are marked with a small square.

✧ Drag the annotation to the desired new position.

Moving a vertical line

✧ Click the line.

The line is marked with small squares at the end points.

✧ Drag the line to the desired position.

All distances are updated.

Removing entire graphics

✧ Click the vertical line.

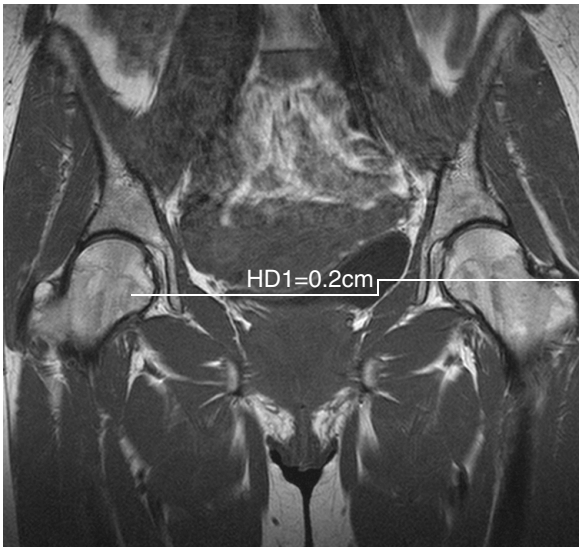
The vertical line is marked with small squares at the end points.

✧ Select **Edit > Delete Selected Graphics**.
- Or -
Press the **Del** key.

The lines as well as all distances are deleted.

Measuring the difference in height

The system offers a difference in height measurement which can be used for measuring the difference in height between two points.



Example of difference in height measurement

Drawing the difference in height

You can draw one or several difference(s) in height:

✧ Select the required image.
→ Page F.3–7, *Loading and Displaying Images*

✧ Select a detailed image display.
→ Page F.3–9, *Changing image display*

✧ Select **Measure > Height Difference**.
- Or -
Click this button.





✧ Move the mouse pointer into the detailed image.

The mouse pointer changes shape.

✧ Position the mouse pointer on the first reference point.

✧ Drag a line from the first reference point to the second reference point with the mouse.

The line indicating the difference in height as well as the actual difference in cm are displayed.

Changing the drawn differences in height

Modifying the line indicating the difference in height

✧ Click on the required line.

The line is marked with small squares at the end points.

✧ Drag one of the end points to the position desired.

The relevant line is updated.

Moving the annotation

You can move the displayed annotation (height difference):

✧ Click the annotation to be moved.

The characters are marked with a small square.

✧ Drag the annotation to the desired new position.

Removing difference in height

✧ Click the required line indicating the difference in height.

The line is marked with small squares at the end points.

✧ Select **Edit > Delete Selected Graphics**.
- Or -
Press the **Del** key.

The line and the given difference in height are deleted.

CHAPTER F.5

Saving and Documenting Images

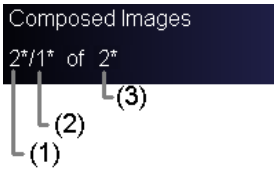
The following functions are available under **Composing** for documenting composed images:

- ❏ Save to database
- ❏ Transfer to the virtual film sheet
- ❏ Sending to other workstations

➪ The **Copy Image to Clipboard** function cannot be used at a *syngo* Acquisition Workplace or a *syngo* MR Workplace. It is reserved for the **Composing** version at the *syngo* MultiModality Workplace.

Display of changes

If an image was newly composed or composed images were changed, this is indicated by an asterisk * above the – and + keys.



(1) Current volume
* means: At least one image of the current volume was changed.

(2) Current image
* means: The image currently displayed was changed.

(3) Total number of the composed volume loaded
* means: At least one image of all volumes loaded was changed.

The following changes are taken into account:

- ❏ After a new composition
- ❏ Manual adjustment, including resetting the manual adjustment
- ❏ Mirroring
- ❏ Inverting
- ❏ Changes in the image text
- ❏ Changing graphic elements

➪ When performing **Save**, **Save As ...** or **Save All As ...**, the display is reset.

Saving images

To keep composed images with the graphics, they have to be *saved before* you select a new patient.

➪ When **Composing** is to be closed and data are still loaded that have not been saved, a query appears asking the user whether the respective images should be stored or scrapped.

Saving all

To save all composed images of the volume currently being displayed:

✧ Select **Patient > Save All As ...**.

Saving individually

If you only want to save the composed image currently being displayed:

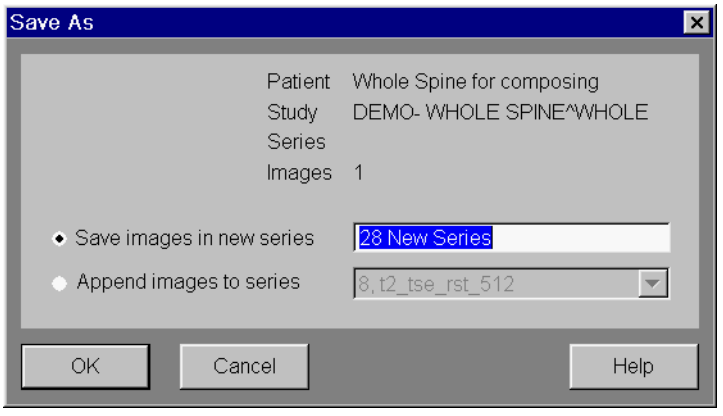
✧ Select the requested image of the volume.
→ Page F.3–17, *Scrolling through composite volumes*
→ Page F.3–17, *Scrolling through a single volume*

✧ Select **Patient > Save**.

Only the currently displayed composed image is saved as a new series under the name **SPINE** and/or **ANGIO**.

Or

✧ Select **Patient > Save As ...**.



✧ Select the requested save option and the name of the series.
→ *syngo* Operator Manual

✧ Click **OK**.

The composed image currently displayed is saved with the defined properties.

Filming images

The complete overview image (unzoomed) is always sent or filmed from the **Composing** task card.



➪ The 2x1 layout is very suitable for filming composed images.

For additional information, refer to the *syngo* Operator Manual.

Filming volumes

✧ Select the required volume.
→ Page F.3–17, *Scrolling through composite volumes*

✧ Select **Patient > Copy to Film Sheet**.

Filming a single image

✧ Select the required image.
→ Page F.3–18, *Scrolling through the image stack*

The image segment is given a colored (bright) border.

✧ Select **Patient > Copy to Film Sheet**.
- Or -
Click this button.



Only the currently displayed composed image is copied to the virtual filmsheet (copied with the **Fit to Segment** setting).

Filming all composed images

✧ Select **Patient > Film all...**.

All composed images are copied to the virtual filmsheet (copied with the **Fit to Segment** setting).

Sending images

You are able to send composed images as you do with other applications.

Note

When the receiving system is equipped with an older ***syngo* MR** version or a different software platform, the following needs to be considered:

❏ Annotations cannot be changed after transmission.
❏ However, new annotations can be added.

!

When you loaded composed images into the **Viewing** task card, only the visible section is transmitted for non-square, zoomed images.

Complete images are sent from the **Composing** task card.

✧ Scroll to the required image.
→ Page F.3–17, *Scrolling through composite volumes*
→ Page F.3–18, *Scrolling through the image stack*



✧ To start the measurement, click this button.

For additional information, refer to the *syngo* Operator Manual.

Closing the patient



✧ Select **Patient > Close Patient**.
- Or -
Click this button.

➪ If you want to load images of another patient, the current patient is automatically closed if you confirm the message accordingly.

PART G

Expert-i/RemoteAssist

G.1 *Expert-i*

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CHAPTER G.1

Expert-i

Safety

General safety information

! During examinations, you are required to adhere to the safety measures as described in the “Safety” chapter of the system manual.



CAUTION

Insuffienct image quality of the remote computer!

Incorrect interpretation of the MR images

✧ Do not use the remote computer for diagnoses or reports.



CAUTION

Remote user does not adhere to the currently valid safety guidelines!

Hazard. Patient injury due to uncontrolled actions of the remote user.

Possible injury to patient due to missing control or absence of local user.

- ✧ As the local user, you are responsible for the patient during the entire examination.
- ✧ Remain continuously at the MR console and monitor the actions of the remote user.
- ✧ Remain continuously in touch with the remote user via telephone.
- ✧ Stop the patient table if hazardous conditions are present for the patient or terminate the entire measurement sequence (e.g. via the **table STOP /sequence termination** at the intercom).
- ✧ Interrupt the remote connection in case of uncontrolled actions by the remote user.

Description

The *syngo* Expert-i software supports local users at the MR console via experts (e.g. physicians) outside the examination room (for example, at a remote networked PC).

Functionality

Remote access is handled via a suitable computer (remote computer) connected to the local network.

For remote access, the remote user has to register at the MR console. For this purpose, he needs a password.

This password is generated by the *syngo* Expert-i software and is only applicable for the registration planned.

In this case, the system can be operated at the MR console as well as the romeote computer.

HIPAA audit trail

Each time you use the *syngo* Expert-i software, the protocol inputs are entered into the HIPAA audit trail.

- ❏ The local user *syngo* Expert–i activates the software.
- ❏ The remote user successfully established the remote connection.
- ❏ The remote connection was not established within the time reserved for this purpose.
- ❏ The local user or the remote user disconnected the remote connection.

Software installation

The *syngo* Expert-i software can only be used in conjunction with the released versions of the *syngo* software.

The released versions are listed on the front page of this document.

The *syngo* Expert-i software needs to be installed and configured by Siemens Service on the MR system as well as the designated remote computer. The *syngo* Expert-i software is integrated in the MR system by Numaris/4 installation.

Minimum requirements

The following minimum requirements must be met for the remote computer and the local network.

Computer hardware	Current standard hardware
Processor	850 MHz
Operating system	Windows NT4.0, XP
Primary storage	256 MB
Network card	100 Mbit/s
Graphic card, monitor	1280x1024
Color	32 bit
Local network	100 Mbit/s or higher
Min. transfer rate	> 600 kB/s
Response time	<30 ms

! When falling beyond the minimum requirements, the performance and display of the remote computer may be adversely affected.

Operation

Perform the following steps to access the MR console: *syngo* Expert-i

- ❏ Activate the *syngo* Expert-i software at the MR console
- ❏ Transfer the password to the remote user
- ❏ Establish a connection at the remote computer.

!

As the local user, you are responsible for the patient during the entire examination.

Do not leave the MR console at any time during remote connection and monitor the actions of the remote user.

Local user: Activate

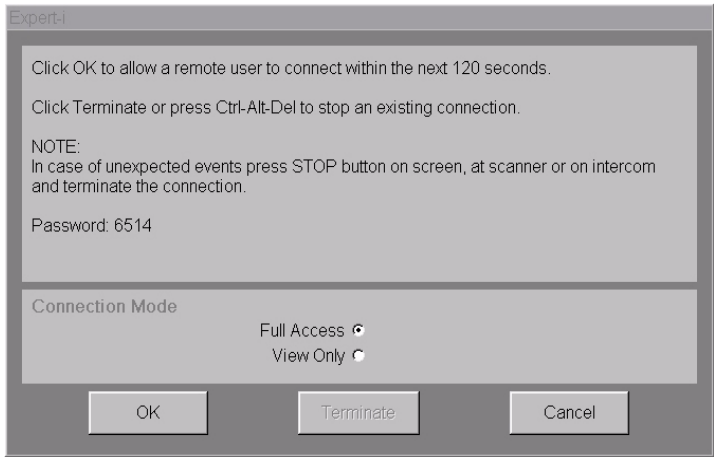
To ensure that the remote user can access the MR console, the local user must first activate the *syngo* Expert-i software at the MR console.

Prerequisite: The *syngo* Expert-i software is installed on the MR system.

✧ Call the remote user to request the initiation of a remote connection.

✧ Activate the *syngo* Expert-i software by clicking the tray icon.

The "*syngo* Expert-i" dialog window is opened; a four-digit password is displayed.



Dialog window of the MR console

! The password displayed is only valid once - for the next registration. The *syngo* Expert-i software generates a new password for every registration.

Local user: Transferring the password

✧ Confirm the message with **OK** and activate the *syngo* Expert-i software with this message.

✧ Communicate the generated password to the remote user. While the local user is waiting for registration of the remote



While the local user is waiting for registration of the remote user, the tray icon is changing.

Local user: Establishing the connection

After the local user has activated the *syngo* Expert-i software at the MR console, the local user has 2 minutes to establish the remote connection.

The local user must select whether the remote user should have **Full Access** or **View Only** access to the MR console.

! If he exceeds the allocated time, the local user has to request a new password. In this case, you have to start the *syngo* Expert–i software again.

Prerequisites:

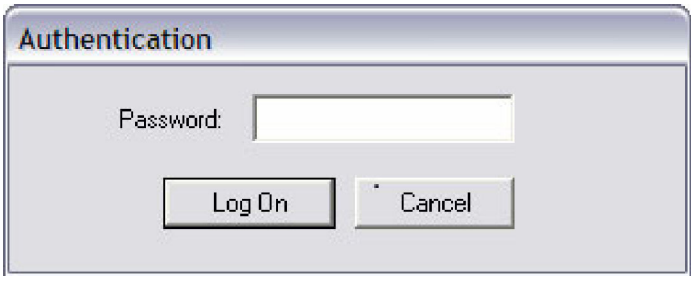
❏ The *syngo* Expert-i software is installed at the remote com puter.

❏ You received the password from the local user.

✧ Start the *syngo* Expert-i software via the program icon or a link at the remote computer.

! The location of the link depends on the installation of the software on the remote computer.

Remote user: Entering a password and registering at the MR system



Entering the password at the remote computer

✧ Enter the password and click **Log On.**

The active connection is shown by the tray icon of the *syngo* Expert-i software at the MR console.



The screen of the remote computer shows the user interface of the MR console. The remote user is now able to access the MR console.

Local user: Disconnecting the remote connection

The local user can disconnect the remote connection at any time.

✧ Press the key combination **Ctrl+Alt+Del** to disconnect the remote connection immediately.

- Or -

Click the tray icon of the *syngo* Expert-i software to display the dialog window.

✧ Click "*syngo* Expert -i" in the dialog window and press **Terminate**.

The remote connection is disconnected. The tray icon shows that the connection is down.

Remote user: Disconnecting the active connection

The remote user can disconnect the active connection at any time.

✧ Click the symbol to close the window which is shown when you move the mouse in the upper right corner of the screen.
-Or-

Click the tray icon of the *syngo* Expert-i software to display the dialog window.

✧ Click "*syngo* Expert-i" in the dialog window and press **Terminate**.

The remote connection is disconnected.



Local user: Installing Expert-i Viewer

The local user can also install the **Expert-i Viewer**.

✧ Click the Expert-i client link in the Expert-i entry in the **programs** menu.

The **installation** dialog windows opens.

✧ Click **Next.**

The dialog window for the user opens. You can browse to the right directory or type into the entry field.

✧ Click **Next** after the configuration.

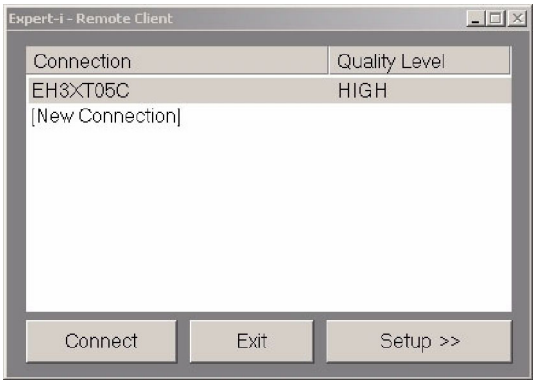
The installation is done.

Remote user: Using the Expert-i Remote Client

The remote user can use the **Expert-i Remote Client** to connect to a specific workplace.

✧ Click the Expert-i client link in the startup menu.

The ***syngo*** **Expert-i - Remote Client** dialog window opens.



✧ Select New Connection and click Setup to create a new connection.

- Or -

Select an existing connection and click **Setup** to edit an existing connection.

If you have problems connecting

If the connection on the remote computer fails, the reasons for it may be as follows:

❏ The local user did not activate the *syngo* Expert-i software at the MR console.

The following message appears at the remote computer:

"Your connection has been rejected. Please contact local user first."

❏ The remote user entered the wrong password or the time allowed for entering the password exceeded:

The following message appears at the remote computer:

"**Authentication failed!"**

❏ The remote computer is unable to establish a connection to the MR console.

The following message appears at the remote computer:

"Failed to connect to server."

✧ Check the error sources described and repeat the registration.

Establishing a connection at the remote computer failed.

The remote user entered the wrong password or he exceeded the time for registration:

- ✧ Get in touch with the local user and request a new password.
- ✧ Repeat your registration.

Establishing a connection at the remote computer failed.

The local user did not activate the *syngo* Expert-i software at the MR console.

- ✧ Ensure that the local user activated access to the *syngo* Expert-i sowftware.
- ✧ Request that the local user provide you with a new password.
- ✧ Repeat your registration.

Establishing a connection at the remote computer failed.

The remote computer is unable to establish a connection to the MR console.

- ✧ Check the network connection from the remote computer to the MR console
- ✧ Get in touch with your system administrtor.

If it is still not possible to establish a connection, get in touch with your system administrator or Siemens Service.

CHAPTER G.2

RemoteAssist

Description

The *syngo* RemoteAssist software supports local users at the MR console via Siemens Customer Service.

!

Do not use the *syngo* RemoteAssist software function **Take over remote control** during patient examination!

During patient clinical routine it is not allowed to let 3rd persons take over control via the *syngo* RemoteAssist software.

Functionality

Remote access is handled via a suitable computer (remote computer) connected to the local network.

For remote access, the remote user has to register at the MR console. For this purpose, he needs a password.

This password is generated by the *syngo* RemoteAssist software and is only applicable for the registration planned.

In this case, the system can be operated at the MR console as well as the remote computer.

HIPAA audit trail

Each time you use the *syngo* RemoteAssist software, the protocol inputs are entered into the HIPAA audit trail.

The inputs are generated when you perform the following actions:

- ❏ The local user *syngo* RemoteAssist activates the software.
- ❏ The remote user successfully established the remote connection.
- ❏ The remote connection was not established within the time reserved for this purpose.
- ❏ The local user or the remote user disconnected the remote connection.

Software installation

The *syngo* RemoteAssist software can only be used in conjunction with the released versions of the *syngo* software.

The released versions are listed on the front page of this document.

The *syngo* RemoteAssist software is installed and configured by Siemens Service on the MR system as well as the respective remote computer.

Minimum requirements

The following minimum requirements must be met for the remote computer and the local network:

Computer hardware	Current standard hardware
Processor	850 MHz
Operating system	Windows NT4.0, XP
Primary storage	256 MB
Network card	100 Mbit/s
Graphic card, monitor	1280x1024
Color	32 bit
Local network	100 Mbit/s or higher
Min. transfer rate	> 600 kB/s
Response time	<30 ms

! When falling beyond the minimum requirements, the performance and display of the remote computer may be adversely affected.

! The Remote Assistance Software must be installed on your MR system.

Siemens service technicians can support the local user at the MR system e.g. if problems arise or new software has to be installed.

A service technician can access your system only if you enable him to do so.Unauthorized access is blocked.

Operation

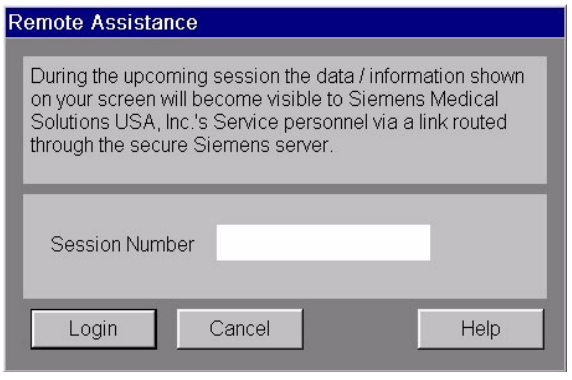
Usually your service technician informs you if he wants to access your MR system.

You can activate a single connection with a service technician via a menu.

Activating a single connection

✧ Call up **Options > Service > Remote Assistance**

The following dialog window is displayed.



In this dialog window, you enter a non-assigned session number.

✧ Enter the session number in the input field.

If there are sensitive data on your system, a corresponding message is displayed, referring to privacy rules for these data.

✧ Click the Logon button to activate the connection.

If remote assistance has been successfully started, the icon (**single connection**) appears in the status bar. Remote user access to your MR system is in **View Only** mode with another cursor.The remote user cannot operate your MR system.

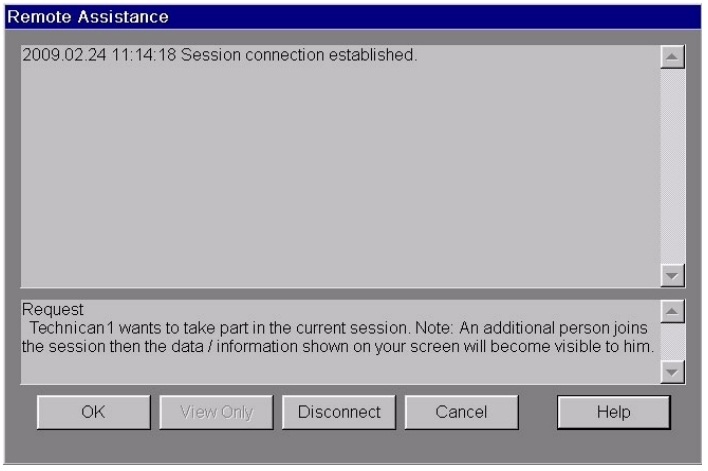
! If a remote connection could not be established, a corresponding message is displayed on your screen. In this case, contact your service technician.

Activate third-party access

If another service technician wants to access your MR system, the remote assistance icon in the status bar blinks.

✧ Click the **Remote Assistance** icon.

A corresponding request appears in this dialog window.



✧ If you agree to further access, click **OK**.

-Or-

Click **Cancel** to cancel the dialog and refuse the request.

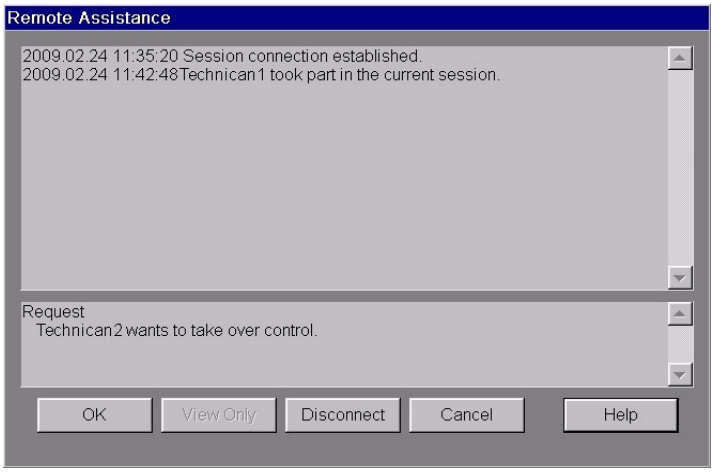
If remote assistance is started successfully, an icon (**multiple connections**) is displayed in the status bar. A third party can access your MR system in **View Only** mode with another cursor and cannot operate your MR system.

Transferring Remote Assistance

Even if several service technicians can access your workstation, there are - at most - two remote users who can access your MR system and you can control the system all the time. If any technician wants to take control of your system, the **Remote Assistance** icon in the status bar blinks.

✧ Click the **Remote Assistance** icon in the status bar.

The following request is displayed in this dialog window:



✧ If you agree to transfer control, click **OK**.

-Or-

Click **Cancel** to cancel the dialog and refuse the request.

If transferring control access is started successfully, the remote user can operate on the MR system. At the same time, there is only one remote user who can operate the MR system. If one remote user is allowed to operate the MR system, another remote user who is operating the MR system will lose control automatically.

Restricting access

If necessary, you can restrict the access of the service technician to your workstation. For instance, if you switch to **View Only** mode, you can call functions by yourself. In the meantime the service technician is restricted to View Only mode.





- ✧ Click the **Remote Assistance** icon to open the **Remote Assistance** dialog window.
- ✧ Click the **View Only** button.

  The service technician has **View Only** access to your workstation.

Disconnecting Remote Assistance

You can disconnect the Remote Assistance at any time.





- ✧ Click the **Remote Assistance** icon to open the **Remote Assistance** dialog window.
- ✧ Click the **Disconnect** button.

  The connection to the service technician is disconnected.

PART H

Appendix

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🗀 *Inline-Common, Angio-Inline* H.1–135

Std-Dev-Tra
🗀 *Inline-Common, Angio-Inline* H.1–136

Std-Dev-Time
🗀 *Inline-Common, Angio-Inline* H.1–136

MIP-Sag
🗀 *Inline-Common, Angio-Inline* H.1–137

MIP-Cor
🗀 *Inline-Common, Angio-Inline* H.1–137

MIP-Tra
🗀 *Inline-Common, Angio-Inline* H.1–138

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APPENDIX
H.1 Scan Parameters

This section provides a detailed description of the scan parameters that allow value modifications within various scan protocols in ***syngo* MR**.

These scan parameters are combined into comprehensive groups of topics.

Each parameter description includes a reference to the parameter cards of the exam task card where the parameter may be entered or modified.

The **Examination** volume of this Operator Manual provides instructions on how to work with parameter cards including the input tools available.
→ Page C.5–1, *Adjusting Measurement Parameters*

The **System Manager** volume of this Operator Manual contains a detailed description of the parameters used for system adjustment.
→ Page B.2–1, *Adjusting the System*

The Spectroscopy Manual provides information regarding scan parameters relevant only for spectroscopy scans.

Slice parameters

By entering slice parameters, you control the position, orientation, and extent of the slice to be measured.

The parameters available for editing in the parameter cards vary depending on whether the current scan protocol is used for a 2D or 3D scan. Scan parameters with the same name may have different characteristics for 2D and 3D scans.

➪ During routine scan operation, the slices and slabs to be measured are normally planned graphically in the reference images using the toolbar for graphic slice positioning and the mouse. The parameter cards are rarely used for this purpose.
→ Page C.4–1, *Positioning Slices*

Slice group/Slab group

Routine, Geometry-Common

The slices or slabs to be scanned within a protocol are combined into groups.

The number of the slice group currently displayed is indicated. All slice parameters currently shown on the **Routine** or **Geometry** card refer to this slice or slab group.

Displaying parameters of another group





The selection list of the **Slice group** or **Slab group** field shows how many slice or slab groups are planned in the current scan protocol.

This list allows you to select another group and check and change its parameters.

Creating new groups



The **Plus** button next to the **Slice or Slab group** selection list lets you create a new group.

The new slice/slab group is added to the selected reference image. To avoid overlapping, it is slightly offset in relation to the existing group to the far side.

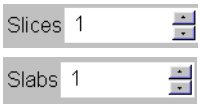
Deleting a group



You can use the **Minus** button to delete the current group.

Slices/Slabs

Routine, Geometry-Common



The number of slices or slabs defines the extent of the examination region in the slice selection direction.

The larger the number of slices to be scanned, the longer the scanning time for sequential multislice scans.

The number of slices or slabs possible with interleaved multiple slice measurements depends on the repetition time TR. Therefore, the number of slices or slabs for a constant repetition time can be increased only within the range limits. If the limit is exceeded, the TR is automatically adjusted by the system. The **Confirm Parameter Changes** message box notifies you of parameter adjustments.
→ Page C.5–74

If you hover the mouse pointer over the **Slices** or **Slabs** field, a tool tip displays the number of slices or slabs planned in the scan protocol.

Distance factor

🗀 *Routine, Geometry-Common*



The gap between the slices of a slice group or the slabs of a slab group is indicated as a percentage of the slice thickness or slab thickness.

At 100%, the gap between the slices/slabs is exactly one slice/slab thickness. Negative values cause the slices/slabs to overlap.

➪ If you hover the mouse pointer over the spin box, a tool tip displays the gap between the slices/slabs in millimeters.

Slice thickness

Routine, Geometry-Common, Resolution-Common



Together with the number of slices, the slice thickness determines the extent of the scan region in the slice selection direction.

2D scans

In the case of 2D scans, the slice thickness corresponds to the thickness of a slice within a slice group.

Changing the slice thickness will also change the distance between slices, because the distance is calculated from the distance factor entered as a percentage of the slice thickness.

3D scans

In case of 3D scans, the slice thickness corresponds to the effective thickness of the individual slices of the slabs (partitions).

Increasing the slice thickness in 3D scans increases the slab thickness as well because the slab thickness is calculated from the number of slices and the slice thickness.

➪ Increasing the slice thickness improves the signal-to-noise ratio, but degrades spatial resolution in the slice selection direction.

Slices per slab

🗀 *Routine, Geometry-Common*



The **Slices per slab** parameter shows the number of slices per slab. The slab thickness is adjusted after each change because the thickness is calculated from the number of slices and the slice thickness. In addition, the absolute slice oversampling changes since it is defined as a percentage of the slab thickness.

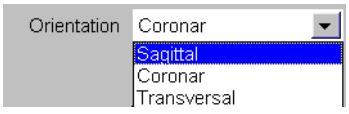
➪ If you hover the mouse pointer over the spin box, a tool tip displays the resulting slab thickness in millimeters.

Orientation

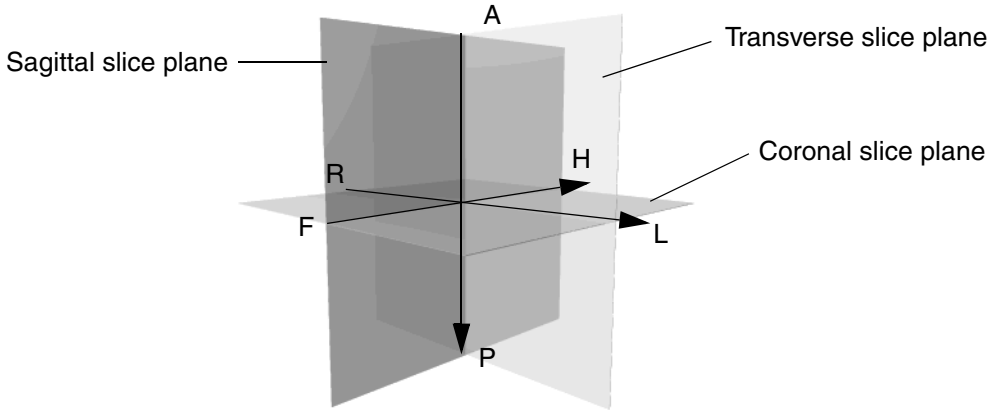
Routine, Geometry-Common

The orientation indicates the position of the slice or slab group in space based on the patient coordinate system.

Selecting a main orientation



The **Orientation** selection list allows you to orient the current slice/slab group on one of the main orientations of the patient coordinate system.

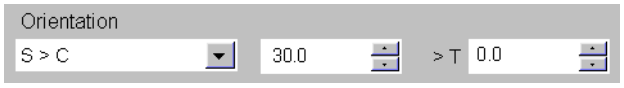


Planning oblique and double-oblique slices

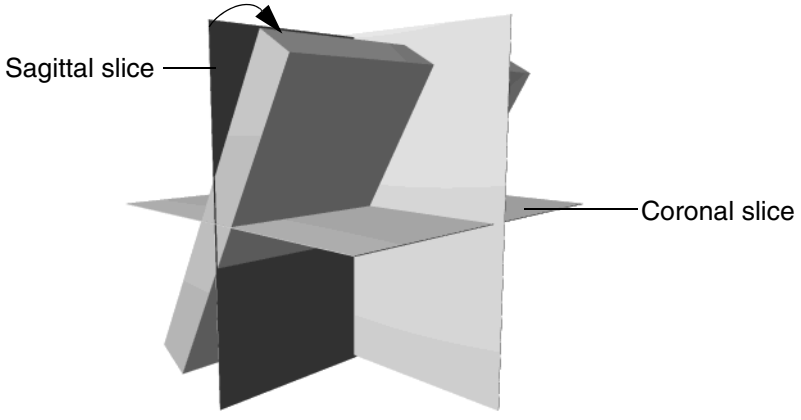


Clicking this button next to the selection list opens the **Orientation** dialog box where you can select oblique or double-oblique orientation for your current slice/slab group.

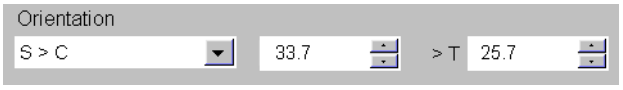
Example of oblique slice orientation:



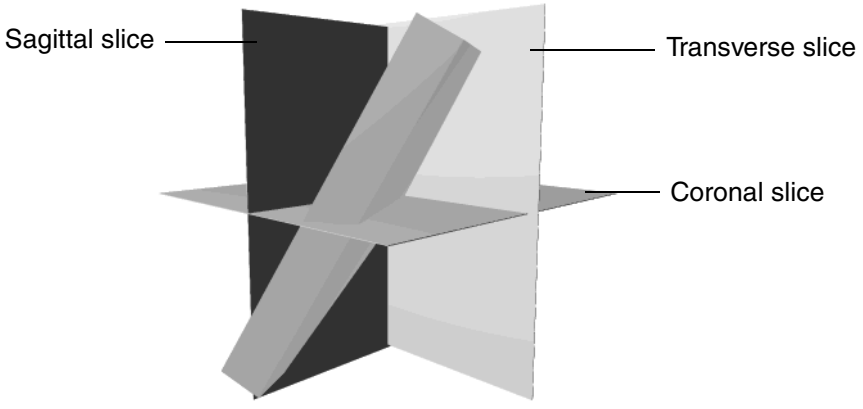
S > C30 corresponds to a sagittal slice tilted by 30° toward the coronal slice.



Example of double-oblique slice orientation:



S > C33.7 > T25.7 corresponds to a sagittal slice tilted by 33.7° in the coronal direction followed by another 25.7° in the transverse direction.



Flip and rotation angles are normally indicated in the following order:

- ❏ Larger angles of rotation are preferred (not S > C10 > T30 but S > T30 > C10).
- ❏ The angles are always indicated in the main orientation of the slice (not T > S46 but S > T44).

If your entries do not follow these conventions, the system will rearrange the values accordingly.

Position

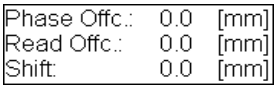
🗀 *Routine, Geometry-Common*



The **Position** field shows the position of the center of the slice or slab group.

➪ If the position matches the isocenter, the input field is grayed out.

Displaying the slice position



If you position and hold the mouse pointer over the **Position** field, a tool tip indicates the slice position.

❏ **Phase Offcenter**
shows the offset in the phase-encoding direction

❏ **Read Offcenter**
shows the offset in the readout direction

❏ **Slice Offset**
shows the offset in the slice selection direction

Changing the slice position

The **Position** selection list lets you move the current slice and slab group into the magnet isocenter.

Or



✧ Click this button next to the selection list to display the **Position** dialog box.

This window allows you to position your slice/slab group with a precision of 0.1 mm.

✧ If necessary, select the **Position mode**.

❏ **L - P - H**
In this mode you enter the offset based on the patient coordinate system.
L - to the left (negative value: offset to the right),
P - to posterior (negative value: to anterior),
H - in the direction of the head (negative value: in direction of the feet).

❏ **Offcenter-Shift**
In this mode you enter the shift in the gradient directions:
Phase - Offcenter in phase-encoding direction
Read - Offcenter in the readout direction
Shift - Shift in the slice selection direction

➪ The selected **Position mode** is maintained after the current slice positioning procedure. When you open the **Position** dialog box the next time (even from another protocol), the position mode previously selected continues to apply.

Phase enc. dir.

Routine, Geometry-Common

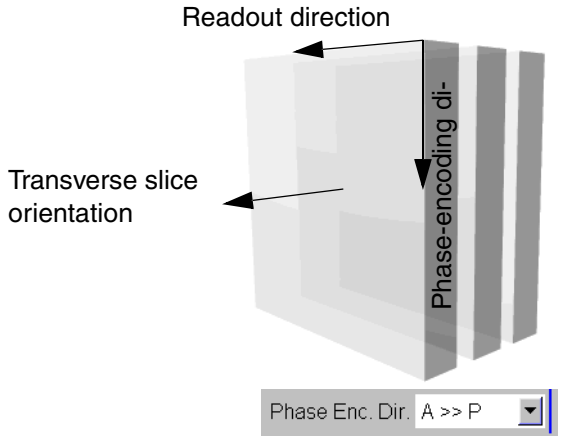


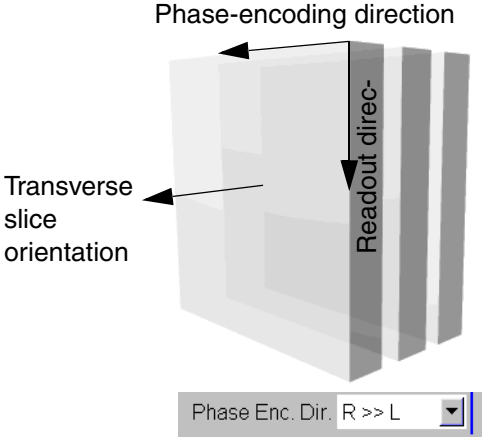
The current phase-encoding direction (direction of the phase-encoding gradient) is indicated in the main orientations of the patient coordinate system.

You can change the phase-encoding direction. This will swap the phase-encoding and readout direction.

Using this method allows you to prevent aliasing artifacts in the phase-encoding direction or change the direction of flow and motion artifacts.

The selection list **Phase enc. dir.** on the parameter cards contains only options relevant to the current slice/3D slab orientation.





Phase oversampling

Routine, Geometry-Common



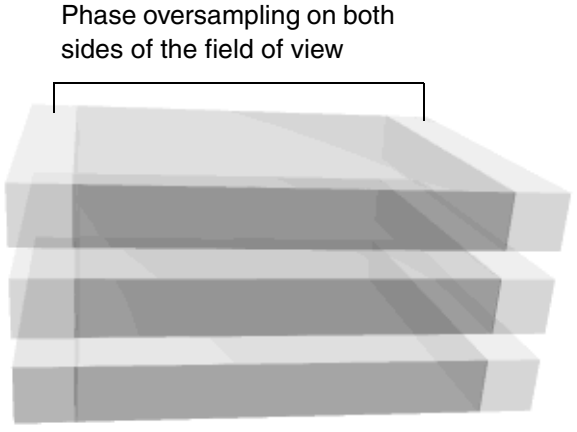
Phase oversampling increases the phase-encoded area symmetrically on both sides of the field of view (FoV). This extended FoV area is not displayed in the reconstructed image.

Phase oversampling is used to prevent overfolding artifacts. Aliasing artifacts occur when the excited body regions are larger than the field of view (FoV) in the phase-encoding direction. These regions are visibly "folded" on the opposite side of the image.

Phase oversampling increases the scan time. The signal-to-noise ratio is improved.

Phase oversampling is indicated as a percentage of the field of view (FoV) in the phase-encoding direction.

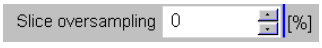
Example: with 30% phase oversampling, the scan region increases by 15% on both sides of the phase-encoding direction.



➪ Oversampling is automatically applied in the readout direction, because it does not increase the scan time.

Slice oversampling

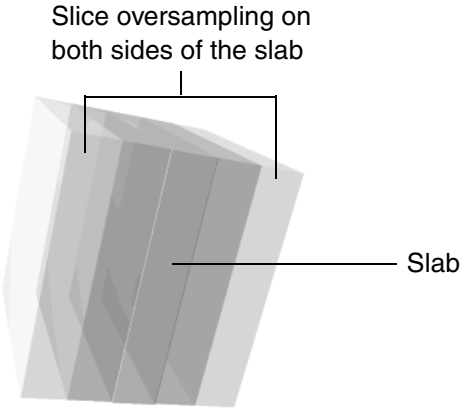
Routine, Geometry-Common



Slice oversampling increases the phase-encoded area symmetrically on both sides of the slab in the slice selection direction.

This creates slices that are reconstructed but not displayed in the image. Using this method allows you to prevent aliasing artifacts in the slice-selection direction for 3D scans.

Slice oversampling is indicated as a percentage of the slab thickness.



➪ Similar to phase oversampling, slice oversampling increases the scan time while improving the signal-to-noise ratio.

Saturation

Saturation regions are areas where the signal is saturated using special RF pulses. You can use saturation regions to avoid motion artifacts.

Depending on the scan protocol and the slice or slab groups planned, you can define standard, parallel, or tracking saturation regions.

Saturation mode

🗀 *Geometry-Saturation*



The **Saturation mode** selection list allows you to select the frequency for transmitting saturation pulses.

❏ **Standard**
Saturation pulses are transmitted before each scan.

❏ **Quick**
Saturation pulses are *not* transmitted before each scan.

Selecting the **Quick** saturation mode lets you reduce the scan time with fat/water saturation and regional saturation (regular and parallel saturation regions). During runtime, the sequence calculates the frequency for transmitting the saturation pulses.

⇨ **Quick** mode can be used e.g. for breath-hold studies to reduce scan time.

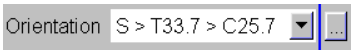
Regular saturation regions

🗀 *Geometry-Saturation*



Standard saturation regions are numbered and may be positioned as required.

You may:





- ❏ freely position regular saturation regions via their **Orientation** and **Position**.
  To do this, proceed in the same way as for positioning slice and slab groups.
  → Page H.1–8 and → Page H.1–11



- ❏ change the **Thickness** of regular saturation regions.

New saturation region



The **Plus** button next to the saturation region field lets you add new saturation regions to the scan protocol.

Deleting a saturation region



The **Minus** button lets you delete the current saturation region.

Parallel and tracking saturation regions

🗀 *Geometry-Saturation*

Parallel or tracking saturation regions are always linked to a slice or slab group.

As a result, it is not possible to change the position and orientation of these saturation regions. Instead, the position of these regions is automatically adjusted by the system whenever you move or rotate the slice or slab group.



The **Special sat.** selection list lets you select a parallel or tracking saturation region.
Special saturators can be applied only if there is just one slice/slab.

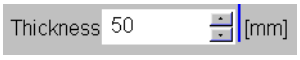
Tracking saturation regions are excited before the scanning of each slice at the specified distance either "before" or "after" the slice and in the specified thickness. In this way, they are tracking the slice currently scanned within the slice group.

Parallel saturation regions are positioned either on one side or on both sides parallel to the slice group. These saturation regions do not move along with the slice, but rather remain at the specified distance ”before” or ”after” or on both sides of the slice group.

The setting "before" or "after" the slice or slice group is displayed in the main orientation of the slice group:

- For **transverse** main orientation: **H** ("before")/**F** ("behind")
- For **sagittal** main orientation: **L** ("before")/**R** ("behind")
- For **coronal** main orientation: **P** ("before")/**A** ("behind")

"Before" means that the saturation region tracks ahead and "behind" that the saturation region tracks behind.



The **Thickness** spin box allows you to enter the slice thickness of the saturation regions.



The **Gap** spin box allows you to enter the distance from the corresponding slice or slab group.

⇨ Use of special RF pulses allows for saturation of the water proton or fat proton signals. For information on how to set the parameters for fat and water saturation, refer to
→ Page H.1–44, *Fat suppression* 🗀 *Contrast-Common, Geometry-Saturation, Physio-Cardiac*
→ Page H.1–46, *Water suppression* 🗀 *Contrast-Common, Geometry-Saturation*.

Navigator Objects

You can define navigator objects for special navigator sequences, for example, to measure respiratory movement.

NOTICE
Refer to the *Application Manual* for important information about setting navigator parameters for cardiac imaging.

Navigator

🗀 *Geometry-Navigator*



This is where you select the type of the navigator object currently displayed. All parameters currently displayed on the **Geometry Navigator** card refer to this navigator object.

The navigator is positioned precisely on the edge of the diaphragm.

Position

🗀 *Geometry-Navigator*



The **Position** field shows the position of the center of the selected navigator object.

➪ If the position matches the isocenter, the input field is grayed out.

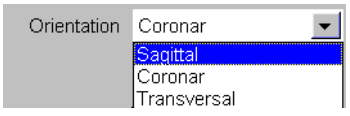
Changing the position of the navigator object

The procedure is similar to changing the slice position.
→ Page H.1–12, *Changing the slice position*



Orientation

🗀 *Geometry-Navigator*



The **Orientation** field lets you select the position of the navigator object in the patient coordinate system.
→ Page H.1–8, *Selecting a main orientation*

Changing the orientation of the navigator object

The procedure is similar to changing the slice orientation.
→ Page H.1–9, *Planning oblique and double-oblique slices*



Rotation

🗀 *Geometry-Navigator*



Only 90° or 0° angles are supported for the rotation of navigator objects. This is equivalent to swapping the readout and phase-encoding directions.

FoV phase

🗀 *Geometry-Navigator*



The **FoV phase** field lets you enter the extent of the navigator object in the phase-encoding direction in millimeters.

FoV read

🗀 *Geometry-Navigator*



The **FoV read** field lets you enter the extent of the navigator object in the readout direction in millimeters.

Thickness

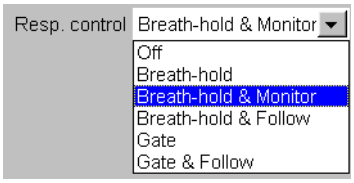
🗀 *Geometry-Navigator*



The **Thickness** field allows you to enter the extent of the navigator slice in millimeters.

Resp. control

🗀 *Physio-PACE*



The **Resp. control** field lets you select a method for suppressing respiratory artifacts.

❏ **Off**
Navigator control is switched off.

❏ **Breath-hold**
The slices of a concatenation will be scanned as soon as you press the **Scan Breath-hold** button on the Inline Display. The number of manual starts required for the complete scan is the number of set concatenations times the number of scans.

❏ **Breath-hold & Monitor**
Identical to **Breath-hold**. However, in addition, the respiratory curve of the patient is monitored before the first breath-holding and during pauses between breath-hold intervals using the Navigator.

❏ **Breath-hold & Follow**
Identical to **Breath-hold & Monitor**. However, in addition, the calculated offset of the diaphragm position between breath-hold intervals is used to adjust the positions of the slices to be scanned in real time.

❏ **Gate**
The image data are only accepted if the diaphragm position is within the acceptance window.

❏ **Gate & Follow**
If the navigator result is within the acceptance window, the positions of the slices to be scanned are offset in accordance with the navigator result and scanning is resumed with the next iteration of the loop structure. Otherwise, the current loop is repeated.

❏ **Trigger**
Respiratory triggering reduces motion artifacts since the acquisition of image data is synchronized with the patient's respiratory cycle.
A set of image data is acquired as soon as the sequence of scanned diaphragm positions shows the end of the expiratory phase.

❏ **Trigger & Follow**
Identical to **Trigger**. However, in addition, the positions of the slices to be scanned are offset in accordance with the navigator result.

❏ **Monitor only**
The navigator signals are calculated and displayed in the usual way but they are not used for controlling the scan.

Scout mode

🗀 *Physio-PACE*



Scout mode is used to plan a preparation phase for measuring only the Navigator signal. In this way you can check whether or not the navigator records the respiratory signal as required.

Scout duration

🗀 *Physio-PACE*



If you select the **Scout mode** check box, you can enter the duration of the preparation phase under **Scout duration**.

Scout TR

🗀 *Physio-PACE*



The **Scout TR** field allows you to enter the repetition time for the navigator pulses.

Accept window ±

Physio-PACE



This parameter is available if you select the **Breath-hold & Follow**, **Gate**, **Gate & Follow**, **Trigger**, or **Trigger & Follow** option under **Resp. control**.

Breath-hold & Follow:
The deviation of the diaphragm position from the position immediately before the first breath-hold is determined. If the deviation is greater than the value specified in the **Acceptance window ±**, the slice positions are not changed for safety reasons. If the diaphragm deviation is greater than the limit value, the result is implausible.

Gate, **Gate & Follow**:
The image data are acquired as soon as the deviation of the diaphragm position (relative to the reference position) is less than the value specified in the **Accept window ±**.

Trigger, **Trigger & Follow**:
Determines the vertical width of the yellow acceptance window shown in the Inline Display. The trigger algorithm ascertains the end of expiration as soon as the sequence of measured diaphragm positions (green curve) falls within the acceptance window. The acceptance window is not displayed while the patient is breathing in.

Position accept window

🗀 *Physio-PACE*



If the respiratory control is set to **Trigger** or **Trigger & Follow**, the **Position accept window** appears.

This parameter determines whether the system will set the center of the acceptance window "automatically" during the learning phase or whether you will set it "manually" as a percentage in the **Accept. Position** field.

Accept position (green)

🗀 *Physio-PACE*



This parameter only appears during **Gate** or **Gate & Follow** respiratory control.

The **Accept position (green)** field allows you to enter the centering position of the accept window.

Accept position

🗀 *Physio-PACE*



This parameter allows you to set the center of the acceptance window with **Trigger** and **Trigger & Follow**.
0% corresponds to the center position at the end of expiration during the learning phase, and 100% corresponds to the center position at the end of inspiration during the learning phase.

Search window ±

🗀 *Physio-PACE*



For **Gate** or **Gate & Follow**, you can enter the size of the window in millimeters in the **Search window ±** field.

The search window is displayed as a red box surrounding the tolerance center in the **Inline Display**.

Search position (red)

🗀 *Physio-PACE*



For **Gate** or **Gate & Follow**, you can enter the centering position of the search window in millimeters in the **Search window (red)** field.

Store profile images

🗀 *Physio-PACE*



The temporal change of the navigator signal is displayed graphically in the **Inline Display**. These images can be saved in a separate series.

Tracking factor

🗀 *Physio-PACE*



This parameter is available if you select the **Breath-hold & Follow**, **Trigger & Follow**,or **Gate & Follow** option under **Resp. control**.

The **Tracking factor** establishes the correlation between the movement of the diaphragm and the resulting shift of the anatomy to be measured.

Chronologic position

🗀 *Physio-PACE*



The **Chronological Position** field lets you select the time for triggering the navigator signal (with **Gate** or **Gate & Follow**).

- ❏ **Before the echo train of the image**
- ❏ **After the echo train of the image**
  If you have selected **Gate & Follow** in the respiratory control, the **After the echo train of the image** mode is not possible.
- ❏ **Before and after the echo train of the image**
  If you have selected **Gate & Follow** in the respiratory control, the slice sequence algorithm based on the first navigator signal and the gating algorithm based on the second navigator signal will change.

Excitation sequence of slices

For multi-slice scans, the sequence of excitation can be defined according to various criteria.

Multi-slice mode

🗀 *Geometry-Common, Sequence-Part 1*



This parameter allows you to select a scan method for multi-slice scanning:

- **Sequential** - scanning slice by slice
  All lines (phase-encoding steps) of the first slice are scanned, followed by all lines of the second slice etc.
- **Interleaved** - scanning line by line
  All first lines (phase-encoding steps) of all slices within a concatenation are first measured in sequence in one repetition time TR, followed by all second lines, etc.
- **Single shot -** Special mode for fast sequences
  All lines (phase encoding steps) of one slice are scanned in one go after excitation. Then all lines of the second slice in one go etc.

The **Sequential** multislice mode is necessary for a tracking saturation region. If you are planning a tracking saturation region while **Interleaved** mode is set, the system automatically switches to **Sequential** mode. The **Confirm Parameter Changes** message box notifies you of parameter adjustment.

The **Interleaved** multislice mode lets you reduce the scan time. The individual lines of different slices can be excited in quicker succession within a repetition time TR without affecting the signals of adjacent lines.

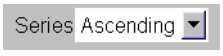
The **Single shot** multislice mode is available for very fast sequences only (e.g. epi, haste, Turboflash). These sequences do not offer any other modes.

Series

🗀 *Geometry-Common*

The **Series** scan parameter lets you define the sequence for slice processing.

The images are displayed in ascending order according to the image numbers after reconstruction, irrespective of the sequence for slice processing.

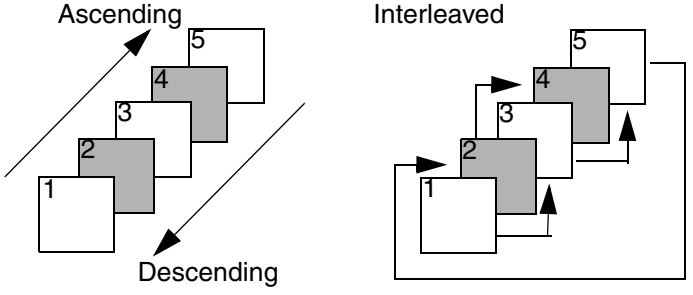


The following excitation sequences are available:

❏ **Ascending**
The slices are excited starting at the beginning of the slice or slab group (start -> end).

❏ **Descending**
The slices are excited starting at the end of the slice or slab group (end -> start).

❏ **Interleaved**



➪ You can combine the **Multi-slice mode Interleaved** and **Series Interleaved** settings for a very short TR and small slice distance to avoid cross-talk.

❏ **Interl. in B.-h**
If you set **Interl. in B.-h** (interleaved in breath-hold interval), the slices are scanned separately for each breath-hold interval of a multiple breath-hold scan, similar to **Interleaved** mode (see *Application Manual*).

➪ The **Interl. in B.-h.** option is available only if you are planning a scan in multiple breath-hold mode after selecting either **Breath-hold**, **Breath-hold & Monitor**, or **Breath-hold & Follow** under **Resp. control** on the **Physio-PACE** parameter card.

Concatenations

🗀 *Routine, Geometry-Common, Physio-Signal1, Physio-PACE*



After selecting the **Interleaved** or **Single shot** option in the **Multi-slice mode** field, you can use the **Concatenations** field to specify across how many TRs the scanning of the planned slices should be distributed.

The system then determines across how many single sequential measurements the slices will be distributed.

This method lets you acquire a large number of slices with a short repetition time TR (T1-weighted imaging). Additionally, slice cross-talk is reduced.

If you select the **Breath-hold**, **Breath-hold & Monitor**, or **Breath-hold & Follow** option under **Resp. control** for a scan in multiple breath-hold mode, the **Concatenations** parameter also determines the number of breath-hold intervals:

- In **Interleaved** multi-slice mode, the number of breath-hold intervals is the product of the **Measurements** and **Concatenations** parameter values.
- In the **Single shot** multi-slice mode, the number of breath-hold intervals is the product of the parameter values **Measurements**, **Concatenations** and **Averages**.

Simult. excit.

Geometry-Common

To reduce the scan time, slices or slabs of a scan protocol may be excited simultaneously.



Via the selection list **Simult. Excit.** you can set the following:

- **Off**
  No simultaneous excitation.
- **2 slices** or **2 slabs**
  Simultaneous excitation of two slices (for 2D scans) or two slabs (for 3D scans).

Image Numbering

🗀 *System-Common*

The **System Common** card allows you to define the image numbering.

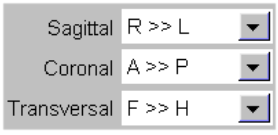


The **MSMA** selection list lets you set the primary order for image numbering.

Example: S - C - T

The reconstructed images are numbered as follows:

- ❏ All sagittal images
- ❏ All coronal images
- ❏ All transverse images



The **Sagittal**, **Coronal**, and **Transverse** selection lists let you set the secondary order for image numbering.
The conventions of the DICOM patient coordinate system apply (→ Page A.1–3).

- **Sagittal R >> L** or **L >> R, Med >> Lat** or **Lat >> Med**
  Sagittal images are numbered in ascending (**R >> L** from right to left) or descending (**L >> R** from left to right) order with regard to their position.
  They can also be numbered with respect to their distance from the isocenter (**Med >> Lat** or **Lat >> Med**). Sorting is performed according to the sagittal position of the slice in the LPH patient coordinate system.
- **Coronal A >> P** or **P>> A**
  Coronal images are numbered in ascending order (from anterior to posterior) or descending order (from posterior to anterior) with respect to their position.
- **Transverse F >> H** or **H >> F**
  Transverse images are numbered in ascending order (from foot to head) or in descending order (from head to foot) with respect to their position.

Image contrast and resolution

Among other factors, image contrast is critical for correct diagnosis.

The **Contrast** and **Resolution** cards as well as application-specific parameter cards are the primary tools for setting image contrast and resolution parameters.

Repetition Time (TR)

🗀 *Routine, Contrast-Common, Geometry-Common, Physio-Signal1*



The repetition time is the time that elapses between two consecutive excitations.

Changing the repetition time affects the image contrast:

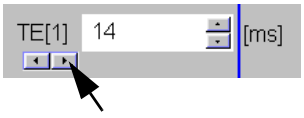
- ❏ Short repetition times of about 400 ms produce good T1 contrast for spin-echo sequences.
- ❏ Long repetition times of about 2000 ms produce good T2 contrast for spin-echo sequences.

Echo Time (TE)

🗀 *Routine, Contrast-Common*

The echo time is the time between the RF excitation pulse and the resulting echo that is measured.

For some sequences, the echo time cannot be changed. In this case, the input field is grayed out.



You may enter several echo times for multi-echo sequences. You can then scroll through the echo times using the arrow keys. When you change a given echo time, the following echo times will be adjusted accordingly.

➪ For gradient echo sequences, a tool tip indicates the in-phase and opposed-phase condition of the fat/water spin.

Inversion Time (TI)

Contrast-Common, Physio-Cardiac



The spins are inverted with a 180° RF pulse (inversion pulse). The spins relax during an inversion time TI according to their T1 relaxation time. This spin preparation applies additional T1 contrast to the image.

In case of inversion recovery sequences, TI is the time that elapses between transmission of the inversion pulse and transmission of the excitation pulse of the subsequent scan (e.g., a spin echo pulse sequence). Depending on the TI, certain signals are suppressed (e.g., fat) and additional T1 contrast is applied to the signal.

In case of turbo FLASH sequences, TI describes the time that elapses between transmission of the inversion pulse and readout of the echo signal which is sorted into the center of the raw data matrix (this echo determines the contrast).

Delay Time (TD)

Contrast-Common



Using the delay time, you can insert a pause between concatenations, for example, to give breath-holding instructions during breath-hold scans.

Averages

🗀 *Routine, Contrast Dynamic*

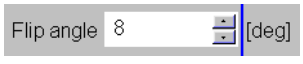


Performing a measurement several times improves the signal-to-noise ratio. The results of repeat scans are averaged by the system.

➪ Please note that the greater the number of scans, the longer the scan time.

Flip angle

🗀 *Contrast-Common, ToF*



The flip angle specifies by what angle the longitudinal (z) magnetization should be rotated into the xy plane by the RF pulse.

The flip angle directly affects image contrast.

With a 90° excitation pulse, for example, the longitudinal magnetization is rotated completely out of the z direction. If a smaller flip angle is used, the magnetization returns to equilibrium more quickly, allowing you to reduce the repetition time TR (for gradient echo sequences).

For spin echo sequences, you can enhance the T1 contrast by reducing the flip angle.

Magn. preparation

🗀 *Contrast-Common, Physio-Cardiac*



You can affect the contrast by transmitting an RF pulse before every scan.

The inversion pulse can be slice-selective or non-selective.

Consider whether your current sequence is an inversion recovery sequence (IR) or a saturation recovery sequence (SR).

The following options are available in the **Magn. preparation** selection list:

❏ **Slice-sel./Slab-sel.** (**IR** or **SR**)
The scans are performed slice by slice.

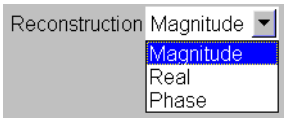
❏ **Non-sel.**(**IR** or **SR**)
The RF pulses excite the entire volume irrespective of the current slice position of the scan sequence.

❏ **None**
No inversion pulse is transmitted.

➪ If you select the **None** option from the **Magn. preparation** list, the **TI** parameter is not available on the **Contrast** card.

Reconstruction

🗀 *Contrast Dynamic*



MR images are usually **magnitude images**. The MR signal intensity is displayed directly in these images.

In **phase images**, however, the grayscales correspond to the phase positions of the spins (between -180° and +180°). They depend on the velocity of the spins as they move in the body (e.g., velocity of blood flow). Spins with the same phase position (i.e., velocity) have the same grayscale value in this type of image.

In **real images**, the grayscale distribution indicates the real orientation of the longitudinal magnetization following an inversion pulse.

You can select the image type(s) for reconstruction from the **Reconstruction** selection list:

- ❏ **Magnitude** - magnitude images
- ❏ **Phase** - phase images
- ❏ **Real** - real images
- ❏ **Magnitude/Phase** - magnitude and phase images
- ❏ **Real/Phase** - real and phase images

⇨ Real images can be selected only if an inversion pulse is selected.

Fat suppression

🗀 *Contrast-Common, Geometry-Saturation, Physio-Cardiac*



This parameter suppresses the signal from fat protons in a targeted way.

The following settings are available:

Adjustment	Description
Fat sat.	Suppresses the fat signal and has no effect on TE, TR is greatly prolonged. This extends the measurement time as well.
Water excit. normal	Suppresses the fat signal, effects moderate extension of TE and TR.
Water excit. fast	Suppresses the fat signal and causes slight extension of TE and TR. The effect on fat saturation is slightly less than in **Water excit. normal** mode.
Q-fat sat.	Suppresses the fat signal. This mode is only available when selecting **Quick** mode in the **Saturation mode**.
SPAIR	Prior to image saturation, the fat signal is suppressed via a frequency-selective adiabatic inversion pulse. However, this option is only available with certain sequences for 1.5 T and 3 T systems.
None	Does not suppress the fat portion in the MR signal.

➪ To shorten the measurement time in connection with fat sat, select **Quick** Mode in the **Saturation Mode** parameter.

Fat saturation

You can reduce the scan time by selecting the **Quick** saturation mode when applying fat saturation. Please note that not all sequences support the **Quick** saturation mode.
→ Page H.1–17

Water excit. Offset (only with MAGNETOM Concerto and MAGNETOM C!)

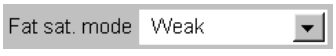
If you select water excitation (**Water excit.**) to suppress the fat signal, the **WE Offset** parameter is available on the **Contrast** parameter card for special sequences:



This spin box is used to enter a frequency shift for the RF pulse for water excitation (in Hertz).

Fatsat mode

🗀 *Contrast-Common, Geometry-Saturation*



Via the selection list **FatSat. mode** you can set the type of fat suppression.

❏ **Weak**
Weak saturation

❏ **Strong**
Strong saturation

Water suppression

🗀 *Contrast-Common, Geometry-Saturation*



The **Water suppr.** selection list contains the following options:

- **Water sat.**
  Suppresses the water signal and does not effect TE. However, TR is increased greatly.
- **Fat excit.**
  Suppresses the water signal; has only a moderate effect on TE and TR, resulting in a slight increase in scan time.
- **None**
  Does not suppress the water component in the MR signal.

Fat saturation

You can reduce the scan time by selecting the **Quick** saturation mode when applying fat saturation. Please note that not all sequences support the **Quick** saturation mode.
→ Page H.1–17

Restore magn.

🗀 *Contrast-Common, Geometry-Saturation*



You can use the **Restore magn.** option to speed up longitudinal magnetization. As a result, the signal for T2-weighed acquisitions will increase (even for short repetition times).

Magnetization transfer (MTC)

🗀 *Contrast-Common, Angio-Common*



In addition to the saturation of water or fat protons, another type of presaturation may be applied.

Applying a special RF pulse causes magnetization transfer to weaken the signal from tissue with a high macro molecular content (e.g., white/gray brain tissue). This effect is hardly noticeable in blood, so that the contrast between blood and white/gray brain tissue is increased.

➪ The **MTC** option is therefore used to obtain greater contrast in images for vascular examinations.

SWI

🗀 *Contrast-Common*



The parameter activates reconstruction of susceptibility-weighted images.

Dixon

🗀 *Contrast-Common*



This parameter determines whether the fat and water signal are displayed separately. For this purpose, the Dixon method separates the MR signal into a fat and water signal.

The following settings are available:

Adjustment	Description
No Dixon	The Dixon method for separation of the MR signal is *not* applied.
Water image	The Dixon method is performed and an image is reconstructed that contains the water signal only.
Fat image	The Dixon method is performed and an image is reconstructed that contains the fat signal only.
Water + fat image	The Dixon method is performed and two images are reconstructed: one image contains only the water signal, the other only the fat signal.



CAUTION

Magnet field inhomogeneity

Wrong separation of water and fat in the images

✧ Check 3D shim

✧ Increase slice thickness and image SNR

✧ Change slice position

Lines per shot

🗀 *Contrast-Common*

This parameter defines the number of slices to be measured with one shot. For example, the number of lines that are acquired after a fat sat pulse.

➪ This parameter is available only, when the **Q-fat sat.** or **SPAIR** mode has been selected under the **Fat suppr.** parameter.

FoV read, FoV phase

Routine, Geometry-Common, Resolution-Common



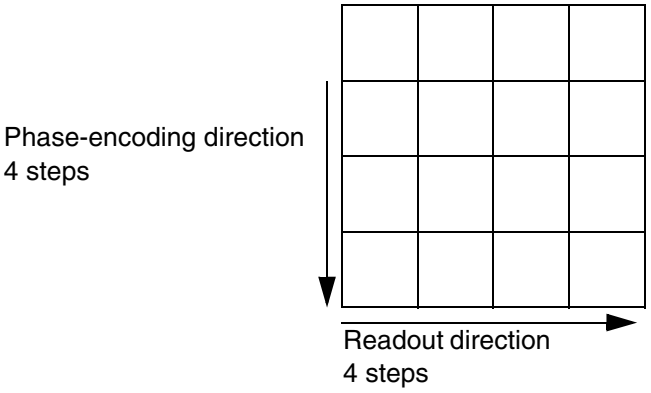
The field of view (FoV) defines the anatomical region to be displayed (extent of scan in the readout and phase-encoding direction) and its resolution (pixel size).



The FoV in the phase-encoding direction (**FoV phase**) is defined as a percentage ratio to the FoV in the readout direction (**FoV read**).

Square field of view (FoV)

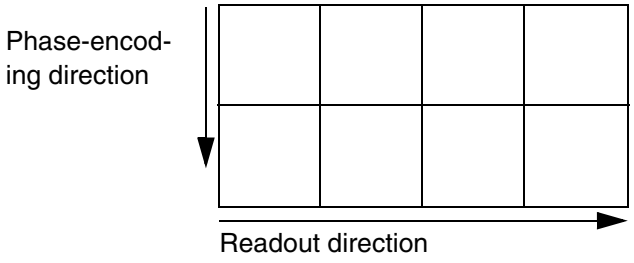
With the **FoV phase** set to 100 %, the system will scan a square FoV. In other words, the same number of pixels is scanned in the readout direction as in the phase-encoding direction.



Rectangular field of view (FoV)

When examining elongated parts of the body, it can helpful to work with a rectangular field of view to reduce the scan time.

In order to obtain a rectangular FoV, you must set the parameter **FoV phase** to a value less than 100%.



Changing the field of view in the readout direction

Changing the FoV in the readout direction also changes the FoV in the phase-encoding direction. This changes the pixel size.

Changing the field of view in the phase-encoding direction

The gradients for encoding the phases are switched in the phase-encoding direction (**FoV phase**).

You can only set the extent in the phase-encoding direction to be less than or equal to the extent in the readout direction. If you change the FoV in the phase-encoding direction, the number of phase-encoding steps is always adapted to keep the resolution ratio constant.

➪ If you increase the number of phase-encoding steps, the scanning time will be adjusted accordingly.

The phase-encoding direction is indicated by an arrow in the image.

Base resolution

🗀 *Resolution-Common*



Base Resolution is used to specify the number of pixels in the readout direction. This determines the spatial resolution in the readout direction.

The base resolution is also the reference value for specifying the percentage of resolution in the phase-encoding direction.

➪ The base resolution also determines the image matrix size, which can be doubled by selecting interpolation.

Changing the number of readout steps (example)

Enter the value 256 for the number of readout steps.

With phase resolution of 100% and a square FoV (FoV Phase = 100%), the matrix is then 256 × 256.

The size of the pixels depends on the size of the field of view (FoV) you have entered in the readout direction.

For an FoV of 256 mm in the readout direction, the pixels are 1 × 1 mm in size, and for an FoV of 396 mm in the readout direction, the pixels are 1.5 × 1.5 mm.

Phase resolution

🗀 *Resolution-Common*



Phase resolution is the resolution of slices in the phase-encoding direction expressed as a percentage value of the base resolution.

If phase resolution is 100%, the resolution in the readout and phase-encoding directions will have the same value and the pixels are square. At 75%, the pixels are oblong and the resolution decreases.

If you reduce the FoV in the phase-encoding direction, the number of pixels has to be reduced as well to keep the resolution ratio constant. As a result, the number of phase-encoding steps are reduced.

⇨ If you hold the mouse pointer over the **Phase resolution** parameter, a tool tip will be displayed together with the matrix.

Examples for image resolutions

Field of view read (mm)	Field of view phase (%)	Phase resolution (%)	Matrix size	Pixels (mm)
256	100	100	256 × 256	1 × 1
256	75	100	192 × 256	1 × 1
256	100	75	192 × 256	1,33 × 1
256	75	75	144 × 256	1,33 × 1

The pixel size is determined by both the base resolution and the phase resolution, as well as by the FoV in the readout direction. The base resolution determines the number of pixels in the readout direction, and the phase resolution determines the aspect ratio of the pixels (square or rectangular).

Changing the FoV in the readout direction changes the pixel size, but not the aspect ratio. For very large pixels, the resolution of the reconstructed images decreases because the signal is averaged across a larger area.

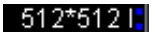
Interpolation

🗀 *Resolution-Common*



Interpolation increases the image matrix to twice its size without increasing the scanning time (for example, from 256 × 256 to 512 × 512 matrix).

After interpolation, the transitions in the image will be softer because the pixels are now smaller. You will need four times the memory to store the image in the database.



➪ In an interpolated image, the interpolated matrix, *not* the scan matrix, is shown bottom right in the image text. Interpolation is indicated by an **I** after the matrix.

NOTE

Interpolation doubles the size of the image matrix in the readout and phase-encoding directions. *No* interpolation is performed in the slice-selection direction.

If you increase the base resolution, interpolation is automatically switched off.
Otherwise the reconstruction time would increase considerably.

You can deactivate interpolation at any time.

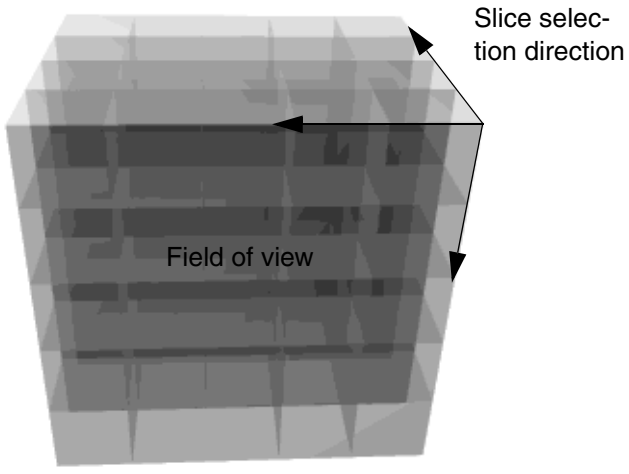
Slice resolution

Resolution-Common



In 3D scans, phase-encoding is performed in addition to the readout and phase-encoding directions.

The **Slice resolution** parameter defines the resolution in the slice-selection direction. The resolution ratio is expressed as a percentage of the readout steps.



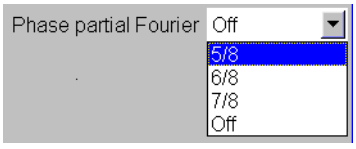
With slice resolution at 100%, the phase-encoding table in the slice-selection direction has as many steps as the number of slices (partitions) to be reconstructed.

With slice resolution < 100%, fewer phase-encoded steps are scanned in the slice-selection direction (resulting in a reduction of the scan time). Additional slices are subsequently calculated using interpolation. The slice thickness displayed in the image text does not change. An "i" is simply appended to its numeric value to identify it (e.g. **SL 2.0i**).

Example:
To obtain 32 slices, 24 slices are scanned with a slice resolution of 75% and 32 slices calculated from them. The resolution in the slice selection direction is reduced accordingly.

Phasen partial Fourier

🗀 *Resolution-Common*



If partial Fourier matrices are used for 2D scans, only part (at least half) of the phase-encoding steps are acquired.

Phase partial Fourier allows you to reduce the scanning time while maintaining the spatial resolution via asymmetric sampling of the k space in the phase-encoding direction.

This reduces the scan time and worsens the signal-to-noise ratio.

Possible settings:

- ❏ **4/8** (half Fourier)
- ❏ **5/8**
- ❏ **6/8**
- ❏ **7/8**
- ❏ **Off** (use whole image matrix)

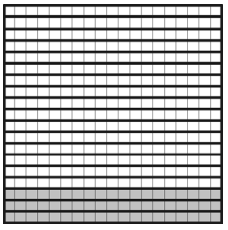
Trajectory

Resolution-Common



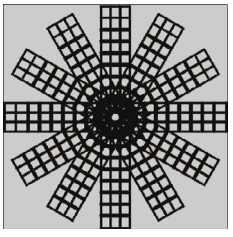
This parameter defines the geometric shape to be sampled in the k-space.

The following shapes are possible:



Cartesian

The k-space is sampled as a matrix of rows and columns. The k-space is built up line by line, for example, from the bottom left to the top right.



BLADE

Data are acquired in blades. Every blade comprises parallel phase-encoding lines. The individual blades are rotated in order to cover a circle in the raw data space.

➪ The number of lines per blade is determined in the **Turbo Factor** parameter on the **Sequence part 2** parameter card.

BLADE coverage

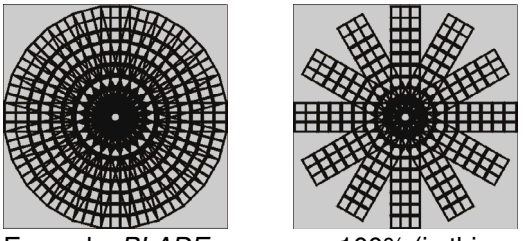
🗀 *Resolution-Common*



This parameter calculates the number of blades of varying rotation angles for k-space sampling.

The value is indicated as a percentage.

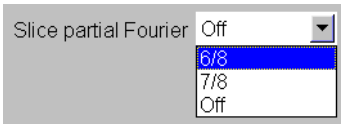
- **100%**
  The number of blades is selected so that a circle is fully covered in the k-space.
- **larger 100%**
  More blades are measured than required for complete coverage. The measurement time increases and the signal-to-noise ratio improves.
- **smaller 100%**
  Less blades are measured than required for complete coverage. Measurement time is reduced and image quality degraded.



Example: *BLADE coverage*=100% (in this case 12 blades) and *BLADE coverage*=50% (in this case 6 blades)

Slice partial Fourier

🗀 *Routine, Resolution-Common*



With 3D scans, you can change the image matrix and therefore the scan time not only via the phase-encoding direction and readout direction but also via the slice-selection direction.

Identical to phase partial Fourier, slice partial Fourier only acquires a part of the raw data space acquired in the slice-selection direction (asymmetric sampling of the k space in slice-selection direction).

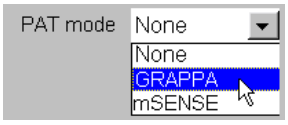
The signal-to-noise ratio decreases, however, resolution in the slice-selection direction remains the same.

Possible settings:

- ❏ **4/8** (half Fourier)
- ❏ **5/8**
- ❏ **6/8**
- ❏ **7/8**
- ❏ **Off** (use whole image matrix)

PAT mode

🗀 *Resolution-iPAT*



The **PAT mode** selection list allows you to choose a PAT reconstruction mode to shorten the scan time.

➪ This parameter is dimmed and the **None** option is the default setting, if only one coil element is selected. A tooltip informs the user.
If not iPAT coils are connected to the system when an iPAT protocol is opened, iPAT mode is set to **None**.

The following options are available:

❏ **None**
The PAT reconstruction method is not used.

❏ **GRAPPA**
PAT reconstruction mode based on the GRAPPA algorithm.

❏ **mSENSE**
PAT reconstruction mode based on the mSENSE algorithm.

Accel. factor PE

🗀 *Resolution-iPAT*



Via the spin box **Accel. factor PE** the acceleration factor is set in phase encoding direction for PAT reconstruction.

➪ The acceleration factor in the phase-encoding direction cannot exceed the number of coils selected.

Ref. lines PE

🗀 *Resolution-iPAT*



The **Ref. lines PE** spin box allows you to set the number of reference lines in the phase-encoding direction for a PAT reconstruction. The **Ref. lines PE** parameter is only displayed if the **Accel. factor PE** parameter is greater than 1.

➪ The number of reference lines in the phase-encoding direction cannot exceed the number of lines in the phase-encoding direction.

Accel. factor 3D

🗀 *Resolution-iPAT*



The parameter **Accel. factor 3D** parameter is displayed only if the protocol is based on a 3D sequence that supports PAT in 3D. Use the associated spin box to set the acceleration factor in the slice-selection direction for a PAT reconstruction.

➪ The acceleration factor in the slice selection direction cannot exceed the number of coil elements selected.

Ref. lines 3D

🗀 *Resolution-iPAT*

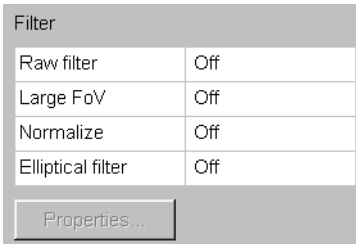


The **Ref. lines 3D** parameter is only displayed if the protocol is based on a 3D sequence that supports PAT in 3D and the **Accel. factor 3D** is greater than 1. Use the associated spin box to set the number of reference lines in the slice-selection direction for a PAT reconstruction.

➪ The number of reference lines in the slice-selection direction cannot exceed the number of slices in the slabs.

Filter

🗀 *Routine, Resolution-Common*



To improve image quality, you can use filters for image reconstruction.

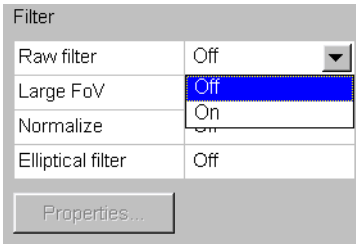
You can select any of the following filters:

- ❏ Raw data (Hanning filter)
- ❏ FoV compensation filter (large FoV)
- ❏ Normalization filter
- ❏ Elliptical filter
- ❏ Image filter

You can either use just one filter or combine two or more filters and apply them at the same time.

Raw filter (Hanning filter)

The outer rows of the raw data matrix contain the edge information (i.e. high spatial frequency) of an image. You can weight specific lines with the raw data filter, for example, to suppress edge oscillation.



✧ Click the field to the right of the **Raw data** entry.

A selection list is displayed.

✧ Select **On**.

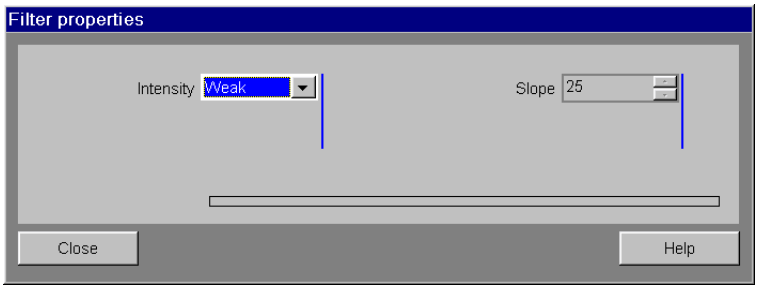
The raw data filter is now active.

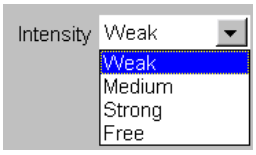
The **Properties...** button is no longer grayed out. You can use those button to open the **Filter properties** dialog box and set specific settings for the raw data filter.



✧ Click the **Properties...** button.

The **Filter properties** dialog box is displayed.



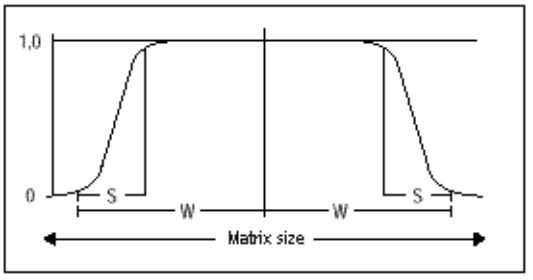


✧ Select a filter strength from the **Intensity** selection list (**Weak**, **Medium**, **Strong**, or **Free**).

➪ The image will be more homogeneous by increasing the filter intensity. However, image contrast may be compromised at the same time. This means that weak filters should be used whenever possible.

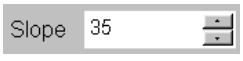


Slope shows the slope at the edges of the filter for the selected filter intensity.



S: slope at the edges of the filter
W: filter width

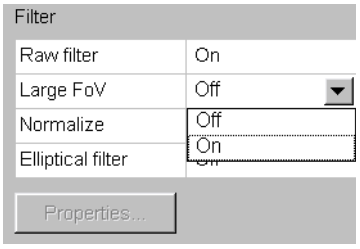
If you have selected **Free** from the **Intensity** selection list, you are able to define the slope yourself.



✧ Enter a value for the slope in the **Slope** spin box.

FoV compensation filter (large FoV)

The FoV compensation filter helps to correct geometric (e.g. pincushion) distortions at the image edge.



✧ Click the field to the right of the **Large FoV** entry.

A selection list is displayed.

✧ Select **On**.

The FoV compensation filter is now active.

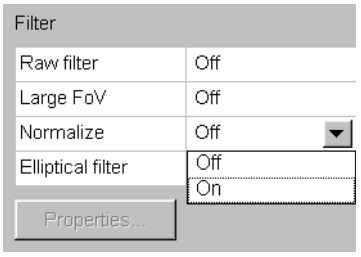
NOTICE

If you use the FoV compensation filter, you are no longer able to use the reconstructed images as reference images for graphic slice positioning in a new examination.

Normalization filter

If you are using surface coils, the area in the vicinity of the coil will appear lighter in the images and darker the areas farther from the coil. The signal intensity is greater in the vicinity of the coil.

Use the normalization filter to reduce the brightness of areas in the vicinity of the coil and increase the brightness in areas farther away from the coil.



✧ Click the field to the right of the **Normalization** entry.

A selection list is displayed.

✧ Select **On**.

The normalization filter is now active.

The **Properties...** button is no longer grayed out. You can use this button to open the **Filter properties** dialog box and make specific settings for the normalization filter.

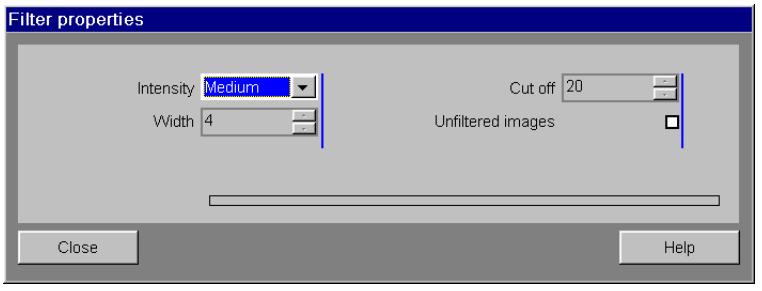
NOTICE

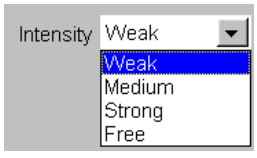
The **Filter properties** dialog box is *not* available for the normalization filter if you are planning a scan with the **body array coil**.



✧ Click the **Properties...** button.

The **Filter properties** dialog box is displayed.





✧ Select a filter strength from the **Intensity** selection list (**Weak**, **Medium**, **Strong**, or **Free**).

➪ The image will be more homogeneous by increasing the filter intensity. However, image contrast may be compromised at the same time. This means that weak filters should be used whenever possible.



Width shows the bandwidth of the filter for the selected filter intensity



Cut off shows the level of pixel brightness that excludes pixels from image reconstruction.

➪ This limit is expressed as a percentage of the maximum intensity profile. If you set **20**, for example, pixels whose intensity profile is below 20% of the maximum value will only be corrected by a factor of 5 (=1/20%).

If you have selected **Free** from the **Intensity** selection list, you can define the bandwidth of the filter and the limit for pixel brightness yourself.



✧ Enter a bandwidth for the filter in the **Width** spin box.



✧ Enter a limit value for the pixel brightness in the **Cut off** spin box.

If you want to save both the images reconstructed with the normalization filter and the unfiltered images, activate the **Unfiltered images** option.



✧ Click the **Unfiltered images** check box.

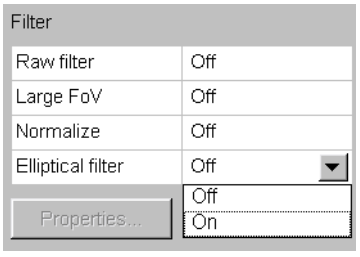
NOTE

Use of the normalization filter may lead to a loss of contrast and an increase in background noise.

Elliptical filter

With the elliptical filter, you will only use the center of the raw data space (the corners are set to 0).

This improves the signal-to-noise ratio up to 10% (without loss of resolution).



✧ Click the field to the right of the **Elliptical filter** entry.

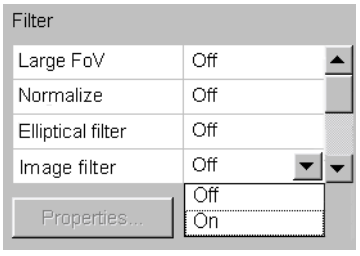
A selection list is displayed.

✧ Select **On**.

The elliptical filter is now active.

Image filter

The image filter is used to set the intensity, edge enhancement, and smoothing.



✧ Click the field to the right of the **Image filter** entry.

A selection list is displayed.

✧ Select **On**.

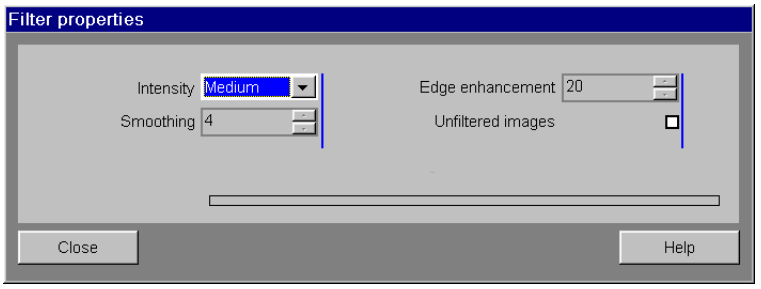
The image filter is now active.

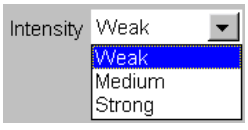
The **Properties...** button is no longer grayed out. You can use the button to open the **Filter properties** dialog box and make specific settings for the image filter.



✧ Click the **Properties...** button.

The **Filter properties** dialog box is displayed.





✧ Select a filter strength from the **Intensity** selection list (**Strong**, **Medium** or **Weak**.

You can define edge enhancement and smoothing of the filter yourself.



✧ Enter an edge enhancement value for the filter in the **Edge enhancement** spin box.



✧ Enter a smoothing limit for the filter in the **Smoothing** spin box.

➪ An exclamation mark in front of **Intensity** indicates that you have changed the default values for **Edge enhancement** and/or **Smoothing**. If you select a new intensity, the default edge enhancement and smoothing values are set for the new intensity, and the exclamation mark disappears.

If you want to save both the images reconstructed with the image filter and the unfiltered images, activate the **Unfiltered images** option.



✧ Click the **Unfiltered images** check box.

Applying filter settings



✧ Click the **Close** button.

The filter settings are applied and the **Filter properties** dialog box closes.

Parameters for dynamic scanning

In dynamic studies with contrast agent or in movement studies (e.g. joints), you can repeat the scans at regular intervals. You can thus track, for example, the inflow of contrast agent, the activation of a region of the brain (e.g. due to finger movement), or display a joint in various phases of a movement.

Infinite Measurement

🗀 *Contrast Dynamic, BOLD*



The **Infinite measurement** option sets the number of scans to the maximum value.

If the **Infinite measurement** option is active, the **Measurements** parameter will not be displayed.

Measurements

🗀 *Contrast-Dynamic, BOLD, Perf, Inline-Breast, Inline-Common*



You set the number of measurements with the **Measurement** parameters.

➪ If you set fewer than 15 measurements, the **GBP**, **PBP**, and **TTP** parameters on the **Perf** parameter card cannot be selected. On the **Inline-Mamma** parameter card, the **TTP** parameter is not activated if you select less than 2 measurements.

Pause after meas.

🗀 *Contrast-Dynamic, BOLD, Inline-Breast*



The **Pause after meas.** field is used for defining pauses (in seconds) for dynamic scans between individual scans. You are able to enter individual pauses after each scan.

✧ Click the horizontal arrow buttons below the input field of the spin box to access a specific pause parameter.

✧ Enter a value for the pause time in the spin box and change the displayed value with the vertical spin buttons on the right of the spin box.

➪ If you hover the mouse pointer over the **Pause after Meas.** parameter name, a tool tip will be displayed with the pause time.

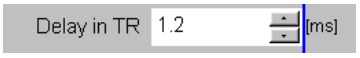
➪ If you hold the mouse pointer over an input field of the spin box, a tool tip will appear stating the starting and ending time of the first 10 scans.

NOTE

In theory, you may define up to 64 separate pauses. However, in most cases you are going to set a pause time that is the same between all measurements or you set the pause time to zero. When you increase the number of measurements to 66, you are automatically limited to setting one and the same pause time.

Delay in TR

🗀 *Contrast Dynamic, BOLD*



This spin box is used to set the time between consecutive scans. The parameter appears in all ep2d sequences. The delay in TR is shown in milliseconds.

✧ Enter a value for the delay in the spin box and change the displayed value with the vertical spin buttons on the right of the spin box.

NOTE

You can only set one delay time which is the same for all scans.

Multiple series

🗀 *Contrast Dynamic, BOLD, Perf.*

Multiple Series ☐

When you have planned several scan runs, you have a choice to:

✧ Click the **Multiple series** option to save the generated images in separate series for each scan.

Or

✧ Deselect **Multiple Series** to save all images acquired in multiple scans in one series.

Position of the scan region

At the beginning of an examination, you will mark the center of the examination region on the patient using the laser light localizer. Subsequently, you move the patient into the magnet. The position marked has to align with the magnet isocenter (center position).

After you have defined a home table position (original table position), all subsequent table movements for this examination refer to it if the position of the scan region is changed.

In most examinations, you will run all protocols of your scan program at the home table position. In a few cases, the examination range may be so large that you have to move the patient table and run protocols at different table positions. This means that the positions of the scan regions are changed as well.

You can set the position of the scan region for a protocol as follows:

❏ Load reference images with the required scan region position into the image area.
→ Page C.3–4, *Using reconstructed images as reference images*

❏ Change the parameters for the scan region position on the **System-Common** parameter card.

Scan at current TP

System-Common

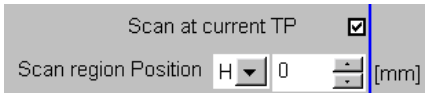


The **Scan at current TP** option specifies whether the protocol will be run at the current table position.

Scan region position

System-Common

The **Scan region position** parameter is only displayed if the **Scan at current TP** option is not active. This parameter is used for defining the position of the scan region by setting an offset between the patient table and the home position (original table position).



The Scan region position selection list allows you to set the direction of the patient table: "Head" (**H**) or "Feet" (**F**).

Enter the distance of table movement in mm.

NOTICE

If you have loaded images into the image area of the **Exam** task card while setting the position of the scan region and these images have a different position, a message box will appear.

You must then decide whether the loaded images will be removed from the image area so that you can apply the newly defined scan region position or whether the scan region position of the loaded images will be retained.

Scan region memory

🗀 *System-Common*



The selection list **Scan Region Memory** is visible only when the parameter **Scan at current TP** is deactivated.

The list displays all scan region positions of the current series block. You may select a scan region position from the list and apply it to your protocol.

NOTICE

When the image area of the task card **Exam** includes images, all positions in the selection list **Scan Region Memory** that do not correspond to the position of the scan region of the loaded images, are set in square brackets.

If you select one of these positions, a message box appears.
You must then decide whether the loaded images will be removed from the image area so that you can apply the selected scan region position or whether the scan region position of the loaded images will be retained.

Coils and coil elements

Routine, System-Common

You can select the coils that you want to use for your examination in the right half of the **System-Common** parameter card.
→ Page C.5–40, *Selecting coils*

You can use two types of surface coils on your system: Coils with a fixed position on the patient table (array coils) or flexible coils (flex coils).

Array coils

Array coils consist of several elements you may select independently of one another.

Depending on the examination region relevant to your diagnostic problem, you may activate different numbers of coil elements.



✧ Select the elements of an array coil you need for your examination by clicking the appropriate buttons.

The button of a selected coil element appears pressed.

Or

✧ Click the coil element in the reference image.
→ Page C.4–34, *Coil elements*

Combining array images

The image generated by an array coil is composed of images from different array elements.

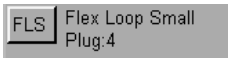


The **Save uncombined** option allows you to additionally save the output images of individual coil elements.

Flex coils

On coils with a flexible position, the plug is also indicated.

You can use several CP flex coils at the same time.



✧ For example, click FS to select CP Flex Small with plug four.

Body coil

All local coils will be deactivated if you want to perform a scan with the body coil.



✧ Click the **Body** button.

Deselecting the body coil reactivates all local coils and coil elements that were previously active.

Sequence-specific parameters

Your system provides various different sequence types for your scans.

As a function of the type of sequence associated with the scan protocol, different display and input fields will be appearing on the sub-cards of the **Sequence** parameter card.

Introduction

Sequence-Part 1

Introduction

You may want to alert the patient to the start of the scan by short knocking noises from the gradient system. These noises inform the patient that the scan is about to begin.

Dimension

🗀 *Sequence-Part 1*



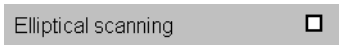
The **Dimension** field allows you to specify whether the scan protocol is to execute 2D or 3D scanning.

➪ Switching from 2D to 3D changes the entries on various parameter cards. They now contain slab group parameters instead of slice group parameters.

NOTE
You cannot switch the dimension for all sequences. In such cases this parameter is displayed dimmed or is not offered.

Elliptical scanning

🗀 *Sequence-Part 1*



In 3D sequences you can reduce the scanning time by up to 25% with elliptical k space scanning (no loss of resolution).

The edges of the k-space (with minimal contribution to resolution) are not included in data acquisition.

Phase stabilization

Sequence-Part 1

Phase stabilize ☐

Phase stabilization prevents phase errors caused, for example, by respiration.

The **Phase stabilization** option is especially advisable for gradient echo sequences with a long echo time (TE) to improve image quality.

Compensation T2 decay

Sequence-Part 1

Compensate T2 decay ☐

This compensation for T2 decay is a procedure for avoiding negative effects of the T2 decay during acquisition of long echo trains.

➪ Can be selected for turbo echo sequences, for example.

Averaging mode

🗀 *Contrast Dynamic, Sequence-Part 1*



If you are performing several scans, you can select a method for averaging the scans:

❏ **Short term**
gives a better signal-to-noise ratio while maintaining the best resolution.

❏ **Long term**
gives a better signal-to-noise ratio with optimized suppression of motion artifacts.

Reordering

🗀 *Sequence-Part 1*



Reordering defines the acquisition sequence of the raw data lines.

❏ **Linear**
The k-space is stepped through linearly.

❏ **Centric**
The first measured raw data lines are sorted into the center of the k-space. This improves the fat saturation in single shot sequences since the center of the k-space is scanned immediately after the fat saturation pulse.

Asymmetric echo

Sequence-Part 1



To reduce the echo time, an asymmetrical echo may be used in the readout direction. The maximum asymmetry not to be exceeded is defined in the sequence.

If the echo time is long enough, the echo is centered even if the asymmetrical echo is permitted.

- Echo asymmetry may lead to cut-off artifacts.
- The asymmetry of the echo is shown as a tool tip.

Contrasts

Sequence-Part 1



This parameter is used to define the number of image contrasts. In this way, you can specify the number of images to be acquired with different T2- (for example, se-tse sequences) or T2* weightings (gre sequences) in one scan.

- The **Contrasts** parameter is available only for a few sequences.
- You have to define an echo time for each contrast.

Bandwidth

🗀 *Sequence-Part 1*



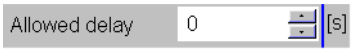
The readout bandwidth determines the fat-water pixel offset and the signal-to-noise ratio.

In some sequences, it is possible to assign a readout bandwidth to each contrast.

➪ If you keep the mouse pointer over the entry, a tooltip will be displayed. The positional shift between fat and water is displayed in pixels.

Allowed delay

🗀 *Sequence-Part 1*



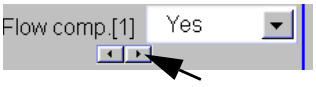
Here you can define a *maximum* delay time after the end of measurement. This parameter defines the earliest time you may restart scanning.

The delay time is used to reduce the specific absorption rate (SAR). The required delay time is automatically calculated by the system and ranges between 0 seconds and the maximum delay time.

Flow compensation

🗀 *Sequence-Part 1*

Flow compensation (gradient motion reduction) is used to avoid signal loss and signal smearing due to moving spins. For this purpose, additional gradient pulses are switched with a suitable time duration and amplitude. Flow compensation can be performed in the readout *and* slice-selection direction, or just in the readout *or* slice-selection direction (for example, for tse).



Some sequences enable you to specify flow compensation separately for each contrast. Use the arrow buttons under the input field to scroll through the flow compensation.

The following settings are possible for each contrast:

- ❏ **Yes**
  compensation in readout and in slice-encoding direction
- ❏ **Read**
  in readout direction only
- ❏ **Slice**
  in slice-encoding direction only
- ❏ **No**
  no flow compensation

Echo spacing

Sequence-Part 1

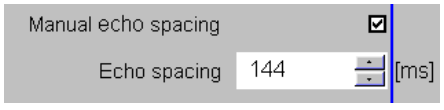


This is the distance between two echoes for turbospin echo sequences or epi sequences.

Smaller echo spacing results in more compact sequence timing and reduces image artifacts (improved resolution in the phase-encoding direction with turbospin echo sequences, reduced distortion through susceptibility with EPI).

Manual echo spacing

Sequence-Part 1



If the **Manual echo spacing** option is active, the **Echo spacing** display field changes into a spin box and you can enter a value for the echo spacing.

NOTE

Excessive echo spacing may cause increased distortion in EPI sequences due to susceptibility.

Readout mode

Sequence-Part 1



This parameter determines the read-out mode for gradient echo sequences (GRE).

The following modes are available:

Mode	Description
Bipolar	In this mode, the MR signals of the different contrasts are alternately read out with a positive or negative gradient. This enables narrower echo spacing than in the monopolar mode. However, the fat-water shift alternates from contrast to contrast.
Monopolar	In this mode, the MR signals of all contrasts are read out with a positive gradient. Echo spacing is greater than in the bipolar mode. The fat-water shift is identical in all contrasts.

Turbo factor

🗀 *Sequence-Part 2*



This parameter determines the number of refocused spin echoes per RF excitation pulse that contribute to an image. It therefore determines the gain in measurement time as compared to a conventional spin echo sequence with comparable parameters.

➪ When the **BLADE** mode is selected in the parameter card **Resolution - Common** or **Physio - Cardiac** in the **Trajectory** parameter, the turbo factor determines the lines per blade.

Echo train duration

🗀 *Sequence-Part 2*



In this display field you check whether the echo train is long enough for a sensible measurement.

EPI factor

🗀 *Sequence-Part 2*



The EPI factor specifies the number of refocused gradient echoes per RF excitation that help generate an image.

➪ In single-shot EPI sequences, the number of lines to be measured is used as the EPI factor.

Segments

🗀 *Sequence-Part 2, Physio-Signal1*



With the segments, you may define the number of rows in the k space that are measured for an image during a TR interval.

⇨ The **Segments** parameter is especially suitable for physiological imaging.

Combined echoes

🗀 *Sequence-Part 2*



The number of echoes acquired during a single measurement may be combined to form an image (for example, MEDIC sequences).

This method produces flow-compensated T2* images with a high signal-to-noise ratio.

RF Pulse Type

🗀 *Sequence-Part 2*



RF Pulse Type defines the length and the envelope of the radio frequency pulses.

The following settings are possible:

- **Fast**
  short RF pulse, which may cause cross-talk between the slices/slabs. This setting is therefore only recommended for fast scans with medium distance factors (for example, breath-holding techniques)
- **Normal**
  RF pulse with a good slice profile, allowing for scans with a small distance factor and little "cross-talk"
- **Low SAR**
  extended RF pulse with a good slice profile and reduced specific absorption rate;
  This setting can be selected to reduce the SAR. This adversely affects scan performance.
- **Optimized**
  optimized RF pulse for reducing slice cross-talk

Gradient mode

🗀 *Sequence-Part 2*



Here you define the rise time and maximum gradient strength the gradients can be switched during the sequence.

The possible settings depend on the gradient system:

❏ **Fast**
The gradient rise time and strength are utilized to the full. This mode may cause peripheral nerve stimulation in the patient. The **fast** option is only available on Quantum and Sonata systems.

❏ **Normal**
For many sequences this setting is a good compromise between performance and noise.

❏ **Whisper**
Guarantees the quietest possible gradients at an acceptable performance level.

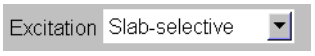
A high gradient rise time can lead to an exceeded stimulation threshold and as a result to peripheral nerve stimulation in the patient.

If the gradient mode is adjusted by the stimulation monitor, the setting is marked by an asterisk * , e.g. **Fast***. This means the gradient rise times have been adjusted automatically to prevent them from exceeding the stimulation limit.
→ Page C.14–32, *Stimulation limit reached*

You can change the mode from **Fast*** to **Fast**. To reverse the mode, you need the stimulation monitor to ensure an optimal adjusted sequence.

Excitation

🗀 *Sequence-Part 2*



This parameter defines how the RF excitation pulse is to be transmitted.

Possible settings:

- ❏ **slice-selective** or **slab-selective**
- ❏ **non-selective**

➪ If you have selected the **non-sel.** option, aliasing artifacts may occur in the slice selection direction.

RF Spoiler

🗀 *Sequence-Part 2*



The RF spoiler is used to destroy residual phase coherence of spins and is used in gradient echo sequences to generate FLASH contrast.

Motion correction

🗀 *Sequence-Part 2*



The parameter indicates whether a BLADE motion correction is performed. The motion correction corrects for patient movement in the image plane that occurs between the acquisition of two echo trains.

The following settings are available:

Options	Description
On	Patient motions in the image plane are corrected.
Off	Motion correction is not performed.
On+Off	Two image series are reconstructed, one with motion correction and one without motion correction.

➪ This parameter is active only if you go to the **Resolution-Common** parameter card and select the **BLADE** mode in the **Trajectory** field.

Flip angle mode

🗀 *Sequence-Part2*



This parameter more precisely defines the flip angle of the refocusing pulse in the echo train.

The following settings are available:

Options	Description
Constant	The flip angle of the refocusing pulse remains constant across the entire echo train. You set it here: → Page H.1–41, *Flip angle* 🗀 *Contrast-Common, ToF*
T2 var	The flip angles of the refocusing pulse vary across the echo train. This mode enables very long echo trains for fast T2 weighted measurements, and is optimized for SAR.
PD var	The flip angles of the refocusing pulse vary across the echo train. This mode is particularly suited to proton density measurements, and is optimized for SAR.

Fluid enhancement

Sequence-Part 2



This parameter is used to improve the image contrast for self-weighted DESS images.

An increase in this value, however, leads to a reduced signal-to-noise ratio.

SNR optimization

Sequence-Part 2



This value improves the signal-to-noise ratio for self-weighted DESS images.

➪ **Fluid enhancement = 1** and **SNR optimization = 0** generates the image contrast and the signal-to-noise ratio of a standard DESS sequence.

Parameter for multi-nuclear scan

It is possible to excite nuclei other than protons and receive signals from them (e.g. ^{31}P). However, the sensitivity of these nuclei is lower than that of protons.

It is possible to increase the signal intensity of such nuclei using the double resonance method. This method involves transmitting saturation pulses to excite a secondary nucleus during signal acquisition. This eliminates the dipole-dipole coupling between the primary and the secondary nucleus and therefore provides a stronger signal from the primary nucleus.

TX/RX Nucleus

🗀 *Sequence-Nuclei*



The **TX/RX Nucleus** selection list is used for selecting the primary nucleus in multinuclear scanning. RF pulses are transmitted and signals received for this type of nucleus.

➪ The selection options in the **TX/RX Nucleus** list depend on the coil configuration set.

TX/RX delta frequency

🗀 *Sequence-Nuclei*



The **TX/RX delta frequency** spin box allows you to enter the frequency shift for the primary nucleus. The shift refers to the adjustment frequency for the primary nucleus and is expressed in hertz [Hz]. Exact slice-selection is achieved for the resulting frequency.

NOTICE

The **TX/RX delta frequency** parameter can only be edited in spectroscopy protocols.

TX Nucleus

🗀 *Sequence-Nuclei*



The **TX Nucleus** selection list is used for selecting the secondary nucleus in multinuclear scanning. RF pulses are transmitted but no signals received for this type of nucleus.

➪ The selection options in the **TX Nucleus** list depend on the coil configuration set.

TX delta frequency

Sequence-Nuclei



The **TX delta frequency** spin box allows you to enter the frequency shift for the secondary nucleus. The shift refers to the adjustment frequency for the secondary nucleus and is expressed in hertz [Hz]. Exact slice-selection is achieved for the resulting frequency.

NOTICE

The **TX delta frequency** parameter can only be edited in spectroscopy protocols.

Application-specific parameters

Depending on the sequence selected, the parameter card stack might contain an additional card for application-specific settings.

The following application cards might be displayed:

- ❏ Angio (**T**ime-**o**f-**F**light angiography, contrast agent enhanced angiography, phase contrast angiography, flow quantification)
- ❏ Diff (diffusion-weighted imaging)
- ❏ Perf (perfusion scans)
- ❏ BOLD (**B**lood **O**xygenation **L**evel **D**ependent imaging)
- ❏ Physio-Cardiac (cardiac imaging)
- ❏ Inline-Mamma
- ❏ Inline-Common

➪ The application-specific parameter cards contain a number of parameters that are described on the preceding pages.

Inflow

🗀 *Angio-Common*



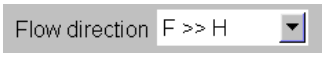
The shape of the RF pulse is adapted to the velocity and direction of the blood flow (slow, medium, fast) to prevent saturation effects of the blood when it passes through a slice or slab.

In this way, even signal distribution of the blood vessels of a slab is achieved.

➪ TONE method = **T**ilted, **O**ptimized, **N**on-saturating **E**xcitation

Flow direction

🗀 *Angio-Common*



Flow direction defines which direction of blood flow will be displayed.

The direction always refers to the patient coordinate system.

For example, in a mainly transverse slice you can select the Head-Feet or Feet-Head direction.

➪ As you change the flow direction, the tracking saturation region automatically moves to the outflow side of the slab.

3D centric reordering

🗀 *Angio-Common*



The **3D centric reordering** option causes quickest possible scanning of the center of the raw data space in contrast agent enhanced 3D angiography after contrast agent inflow.

This ensures optimal contrast enhancement of the arterial vessels.

Time to center

🗀 *Angio-Common*



The **Time to Center** field shows the scan time required until the scan has reached the k space center.

This information is required for timing the contrast agent bolus in contrast-enhanced angiography.

Flow mode

🗀 *Angio-Common*



Here you can define the flow encoding mode:

- **Single vel.** - one flow sensitivity (flow velocity encoding)
  Measures the velocity of blood flow in 3 spatial directions, with reference to a flow sensitivity. This mode provides vessel display independent of the direction of flow.
- **Single dir.** - one direction for several flow sensitivities
  Measures the blood flow with reference to several flow sensitivities, but only in one spatial direction.
  This mode is used for recording large variations of flow velocities (e.g. in the area of peripheral arteries).
- **Free**
  Permits free selection of the flow sensitivities and spatial directions.

➪ The input options for the following parameters depend on the flow mode selected.

Encodings

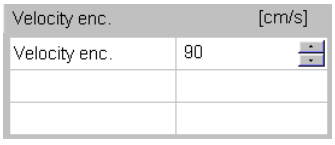
🗀 *Angio-Common*



Number of flow sensitivities to be set.

Velocity enc.

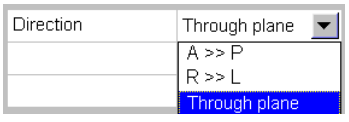
🗀 *Angio-Common*



Determines the flow sensitivities in cm/s.

Direction

🗀 *Angio-Common*



Flow-sensitive axis for each flow sensitivity entered.

❑ **Through plane**
The flow-sensitive axis is perpendicular to the image plane. Only flow moving perpendicular to the image plane is detected.

Rephased images

🗀 *Angio-Common*

Rephased images ☑

Reconstruction of a flow-rephased image (magnitude image).

Magnitude images

🗀 *Angio-Common*

Magnitude images ☑

Reconstruction of a set of magnitude images (1 image per flow direction and flow sensitivity).

Magnitude sum

🗀 *Angio-Common*

Magnitude sum ☑

Reconstruction of a magnitude sum image from the magnitude images of a slice.

Phase images

🗀 *Angio-Common*

Phase images ☑

Reconstruction of a set of phase images (1 image per flow direction and flow sensitivity).

Diffusion mode

🗀 *Diff*



The **Diffusion Mode** describes the measurement method and the diffusion-sensitive direction.

❏ **1-Scan Trace**
Only one scan is required per image.
Advantage: Shorter acquisition time than in **3-Scan Trace** mode

❏ **3-Scan Trace**
Three scans are required per image.
Advantage: Shorter echo time and better SNR than in **1-Scan Trace** mode

One diffusion-weighted image per slice position and b-value is calculated. The diffusion weighting depends on the trace of the diffusion sensor (mean value of the diagonal elements Dxx, Dyy, and Dzz).

❏ **Orthogonal**
Three images are acquired per slice position and b-value (if $b \neq 0$), one image with diffusion weighting each for the read, phase, and slice directions.
For b-value b = 0, only one image per slice position is acquired.

❏ **Slice**
One image is acquired per slice position and b-value, the diffusion weighting is in the slice selection direction.

❏ **Phase**
One image is acquired per slice position and b-value, the diffusion weighting is in the phase-encoding direction.

❏ **Read**
One image is acquired per slice position and b-value, the diffusion weighting is in the readout direction.

❏ **Diagonal**
In the HASTE sequence with diffusion weighting, the diffusion weighting points in the direction of the spatial diagonal.

❏ **MDDW**
MDDW stands for multi-directional diffusion weighting. One diffusion-weighted images is acquired per slice position, per b-value, and (for b > 0) per diffusion encoding direction. The number of directions is defined with the **Diff. Directions** parameter.

➪ In **MDDW** mode it is *not* possible to calculate ADC maps or other parameter images. This mode is mainly for customers who have their own image post-processing system.

Diff. weightings

🗀 *Diff*



Number of diffusion weightings included in a scan. Individual weightings have to be defined before measurement in the **b value** field. You can enter up to 16 b values.

b-value

Diff

b-value	
b-value[1]	0
b-value[2]	500
b-value[3]	1000

The nominal b value is a measure of diffusion weighting. It is expressed in s/mm^2.

The number of possible b values is defined by the **Diffusion Weighting** parameter.

The greater the value, the stronger the diffusion weighting. The b-value increases with the intensity, duration, and time interval of the diffusion-sensitive gradient pulses.

b-value = 0 corresponds to one T2*-weighted image.

Diff.-weighted images

Diff

Here you can define the reconstruction settings for inline reconstruction of the diffusion:



When you click **Diff. weighted images**, you obtain original images with diffusion weighting. These images contain T1, T2, and diffusion-weighted portions.

Diffusion weighting is performed in the direction set with the **Diffusion mode** parameter (e.g. with **Slice**, in the slice selection direction).

Trace-weighted images

🗀 *Diff*

Trace weighted images ☐

This option calculates an isotropically diffusion-weighted image, i.e. all spatial directions are averaged. This eliminates signal variations in healthy tissue caused by anisotropic effects. As a result, it is easier to identify abnormal areas with restricted diffusion.

This option can be selected both in 1-scan trace mode and in 3-scan trace (diffusion mode).

Average ADC maps

🗀 *Diff*

The ADC maps (**A**pparent **D**iffusion **C**oefficient) indicated the grayscale values of the diffusion coefficients. The grayscales are derived from scans with different diffusion weighting (b values).
ADC maps contain no T1 or T2 components.

Average ADC maps ☐

The **Averaged ADC maps** option provides an ADC image in which averaging has been performed over the different spatial directions and b-values used.

➪ The option can only be selected if at least two b-values are set.

Individual ADC maps

🗀 *Diff*



Individual ADC maps show the ADC along the gradient axis.

➪ The option can only be selected if at least two b-values are set.

Noise level

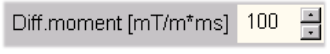
🗀 *Diff*



The noise level is a threshold value used to determine the pixel intensity from which ADC maps are calculated.

Diff. moment

🗀 *Diff*



This parameter is *only* displayed for the **psif** sequence.

The **diffusion moment** is a measure of the strength of diffusion weighting. It is the amplitude multiplied by the duration of the diffusion gradient.

Diff. directions

🗀 *Diff*



If you have selected the **MDDW** mode, you can enter the number of diffusion encoding directions under **Diff. directions**.

You can set **6** or **12** directions.

The b-value and the diffusion direction are displayed to you in the image text of the diffusion-weighted images acquired.

Example:
b1000#3 – b=1000s/mm2, third direction of 6 or 12

⇨ For a precise definition of the individual directions refer to the Application Manual, Chapter *Multidirectional diffusion weighting*.

Original images

🗀 *Perf*



In perfusion scans, the original images are *always* reconstructed and stored. You can use them for additional postprocessing functions.

Time-to-Peak map (TTP)

🗀 *Perf, Inline-Breast*



If the **TTP** option is activated, a time-to-peak image will be calculated for each slice. The pixel intensity value in the image shows the time (in seconds) that elapsed before the signal peak was reached.

The *brighter* the areas in the grayscale image, the *longer* the time until signal peak. For this reason, arrival of the contrast agent is delayed.

If you have set fewer than 15 measurements, you cannot activate the **TTP** option. On the **Inline-Mamma** card, the option is not activated for fewer than 2 measurements.

➪ In color perfusion images, the TTP display depends on the selected color scale.

Percentage of Baseline at Peak map (PBP)

🗀 *Perf*



If the **PBP** option is activated, a percentage signal image will be calculated for each slice. This image shows the signal change of the bolus peak relative to the base line.

The *lighter* the regions are displayed in the image, the *less* contrast agent has arrived there.

If you have set fewer than 15 measurements, you cannot activate the **PBP** option.

Global Bolus Plot (GBP)

🗀 *Perf*



With the **GBP** option activated, a global time-density curve is calculated to assess the bolus passage that has just occurred.

If you have set fewer than 15 measurements, you cannot activate the **GBP** option.

Wash-In

🗀 *Inline-Breast*



Here you can define whether the parameters for signal change in the starting range of the dynamic measurement series will be enabled.

Color table

🗀 *Inline-Breast*



You can define color palettes for individual images.

First measurement

🗀 *Inline-Breast*



For a Wash - In / Wash - Out calculation, you can define the measurement to be used first within a measurement series.

Last measurement

🗀 *Inline-Breast*



For a Wash - In / Wash - Out calculation, you can define the measurement to be used last within a measurement series.

Highest value

🗀 *Inline-Breast*



You are not using the value of the last measurement but rather the highest value in the range between the first and last measurement for calculating the Wash – In parameter image.

Wash-Out

🗀 *Inline-Breast*



You are defining that the parameter card for signal change will be calculated in the end range of the dynamic measurement series and that the parameters are enabled.

PEI

🗀 *Inline-Breast*



Positive enhancement integral

Starting ignore meas.

🗀 *Perf, BOLD*



The **Starting ignore meas** spin box is used to define the number of first scans that are not used for evaluation (contrast has stabilized).

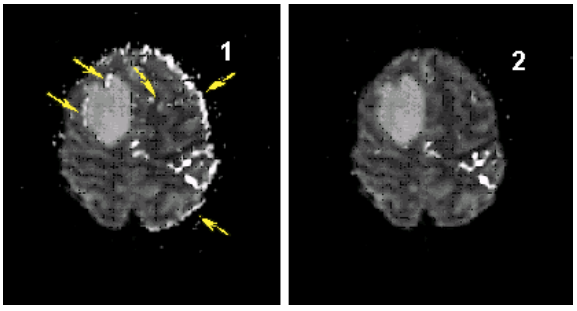
Motion correction

🗀 *Perf, BOLD*

Motion correction ☑

If this option is activated, motion correction will be performed during image calculation.

Small patient movements (0.3 mm) may cause significant artifacts in the functional information. In Fig. 1 these apparent instances of activation are marked yellow. Using the 3D motion correction, you can reduce the relative motion (translation and rotation) between measured volume data sets (Fig. 2).



The motion correction is displayed in the image text.
→ Page H.2–1, *Text Annotations in Medical Images*



Image type **MOCO** applies.

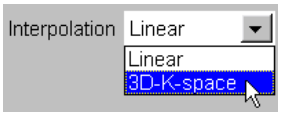


The comment line shows the correction parameters. The images of the first repetition have only the comment "Reference volume for motion correction".

Example: Motion: -3.98, -0.27, 4.04, -2.48, 3.12, -0.35
The first three values show the translation in the x, y, z direction (in millimeters) and the following three values show the rotation about the x, y, z axis (degrees).

Interpolation

🗀 *Perf, BOLD*



If the **Motion correction** option is activated, you can select an interpolation method for motion correction in the **Interpolation** selection list:

- ❏ **Linear** - Linear interpolation
  Fastest method for realtime postprocessing
- ❏ **3D-k-Space** - Interpolation in the Fourier space
  Best quality method for realtime postprocessing

Spatial filter

🗀 *Perf, BOLD*



If you have selected the **Motion correction** option, you can select low-pass filtering for softening the images under **Spatial filter**.

The spatial filter increases the signal-to-noise ratio, but reduces spatial resolution.

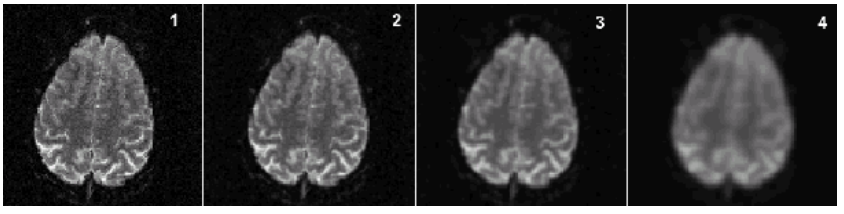
Filter setting

🗀 *Perf, BOLD*



If the **Spatial filter** option is activated, you can use the **Filter Setting** spin box to set the width of the Gaussian filter used. It defines the filter strength.

Example:



(1) No filtering
(2) Weak (2.0)
(3) Medium (1.0)
(4) Strong (0.5)

t-Test

BOLD

t-Test ☐

The **t-test** option provides a student's t-test evaluation. A parameter map of the t values is calculated to locate the cerebral regions exhibiting significant signal differences between the resting and active states.

- The **t-test** option can *not* be selected if the number of scans is less than 15. Neither can the associated parameters **Threshold**, **Window**, and **Starting ignore meas.**
- The t-test calculation is saved as an additional series.

Dynamic t-maps

BOLD

If the **Dynamic t-cards** option is activated, the t-cards generated during scanning are stored. This permits real-time operation of the 3D neuro task card.

A "StartFMRI" series is also created at the start of scanning.

Threshold

🗀 *BOLD*

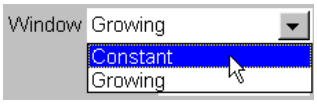


The **Threshold** spin box is used for entering a threshold value for the t-test evaluation. At a certain level of intensity, pixels from the t-test images will be used to calculate overlaid images.

➪ This threshold does *not* apply for the calculation of pure t-test images.

Window

🗀 *BOLD*



The **Window** selection list is used to set the t-test calculation window.

❏ **Constant**
Only the BOLD images of a paradigm cycle are used to calculate the t-test images. Previously acquired series are excluded.

❏ **Growing**
All acquired series are included in the calculation of the t-test images. Signal differences are summed up to improve the statistics.

Paradigm size

🗀 *BOLD*



The **Paradigm size** spin box is used to determine the number of entries in the paradigm table.

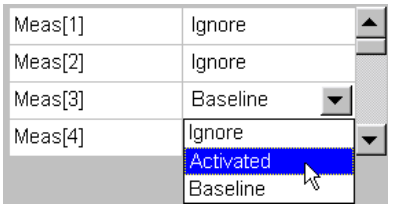
Paradigm table

🗀 *BOLD*

This table can only be edited if **t-test** is selected. You can make one of the following settings for each scan here:

- ❏ **Baseline**
  The scan is performed as a functional measurement *without* stimulation.
- ❏ **Active**
  The scan is performed as a functional measurement *with* stimulation.
- ❏ **Ignore**
  The scan is not used for evaluation.

You may edit the cells in the right column of the paradigm table. Just click them with the mouse. The selection list appears and you can select one of the three settings listed above:



Dark Blood

Physio-Cardiac



This option is used to transmit a special preparation pulse to saturate the blood in cardiac sequences. The cardiac muscle is then displayed especially well.

Blood will then appear dark in the image, hence the name "dark blood".

Tagging

Physio-Cardiac



It is possible to excite tagging lines in the image plane. This provides for clearly visible differences in heart wall thickness.

Possible settings:

- **Grid tag**
  Grid of lines as an orientation aid. For visualizing regional and global heart wall movements.
- **Line tag**
  Parallel lines as an orientation aid. For visualizing heart wall movements in the long main axis view or four-chamber view.
- **None**
  No orientation aids

Distance

🗀 *Physio-Cardiac*



The **Distance** parameter allows you to select the distance between orientation aids (tags).

Angle

🗀 *Physio-Cardiac*



If you have selected **Line tag** as auxiliary lines, you can also enter the angle between the orientation lines (tags) and the phase-encoding direction.

Parameters for image evaluation

Suitable series, e.g. from a contrast agent examination, can be postprocessed on the **Viewing** or **3D** task cards with different evaluation functions.
→ Page D.1–1
→ *syngo* Operator Manual

You can set protocol parameters for the evaluation functions **Subtraction** and **Standard deviation** and for the **MIP projection** on the **Inline-Common** or **Angio-Inline** parameter cards (for angiography examinations).

Subtract

🗀 *Inline-Common, Angio-Inline*



If the **Subtract** option is activated, subtraction evaluation is performed with a series of current scans.

This generates images showing, for example, changes after contrast agent administration.

Saving images

🗀 *Inline-Common, Angio-Inline*



If the **Save Images** option is activated, the result images of the subtraction will be saved automatically.

➪ The **Save images** parameter is displayed only if the **Subtract** option is activated.

Autoscaling

🗀 *Inline-Common, Angio-Inline*



If the **Autoscaling** option is activated, the subtraction result images are scaled automatically, that is, the display area of the calculated values is adjusted automatically.

➪ The **Autoscaling** parameter is displayed only if the **Subtract** option is activated.

Scaling factor

🗀 *Inline-Common, Angio-Inline*



The **Scaling factor** spin box is used for entering an individual factor for scaling the display area of the calculated subtraction values.

➪ The **Scaling factor** parameter is displayed only if the **Subtract** option is activated and the **Autoscaling** option is deactivated.

Offset

🗀 *Inline-Common, Angio-Inline*



The **Offset** spin box is used for entering an offset for the lower and upper threshold of the display area of the calculated subtraction values.

➪ The **Offset** parameter is displayed only if the **Subtract** option is activated and the **Autoscaling** option is deactivated.

Subtrahend

🗀 *Inline-Common, Angio-Inline*



If multiple scans are set in the current protocol, the **Subtrahend** spin box is used to define the acquired series that will be subtracted from all following series (**subtraction within a protocol**).

If only one scan is set, the acquired series for a subtraction evaluation will be used with the acquired series of another protocol (**subtraction across protocols**)



In this case, it is not possible to edit the **Subtrahend** spin box, and the selection of the subtrahend depends on whether the protocol is identified as a contrast agent scan in the program control.

- ❏ If the protocol is marked as a contrast agent scan with a syringe icon, the series last buffered on the image reconstruction system will be subtracted from the current series.
- ❏ If the protocol is *not* marked with the syringe icon, the current series will be loaded into the buffer of the image reconstruction system and subtracted from the series of a following protocol.

⇨ The **Subtrahend** parameter is displayed only if the **Subtract** option is activated.

Std-Dev-Sag

🗀 *Inline-Common, Angio-Inline*

Std-Dev-Sag ☐

If the **Std-Dev-Sag** option is activated, standard deviation result images with sagittal orientation are calculated from the acquired slabs of the current protocol. You can see variances in pixel values in the sagittal direction.

➪ The **Std-Dev-Sag** parameter can be edited only if the measurement is a 3D scan and the number of slices in the slabs is at least 4.

Std-Dev-Cor

🗀 *Inline-Common, Angio-Inline*

Std-Dev-Cor ☐

If the **Std-Dev-Cor** option is activated, standard deviation result images with coronal orientation are calculated from the acquired slabs of the current protocol. You can see the variance of the pixel values in the coronal direction.

➪ The **Std-Dev-Cor** parameter can be edited only if the measurement is a 3D scan and the number of slices in the slabs is at least 4.

Std-Dev-Tra

🗀 *Inline-Common, Angio-Inline*

Std-Dev-Tra ☐

If the **Std-Dev-Tra** option is activated, standard deviation result images with transverse orientation are calculated from the acquired slabs of the current protocol. You can see the variance of the pixel values in the transverse direction.

➪ The **Std-Dev-Tra** parameter can be edited only if the measurement is a 3D scan and the number of slices in the slabs is at least 4.

Std-Dev-Time

🗀 *Inline-Common, Angio-Inline*

Std-Dev-Time ☐

If the **Std-Dev-Time** option is activated, standard deviation result images with the orientation of the acquired slice groups or slabs are calculated from the acquired slice groups or slabs of the current protocol. You can see the variance of the pixel values within the scan period. Both multiple phases and multiple scans can be evaluated.

MIP-Sag

🗀 *Inline-Common, Angio-Inline*



If the **MIP-Sag** option is activated, MIP images with sagittal orientation are calculated from the acquired slabs of the current protocol.

➪ The **MIP-Sag** parameter can be edited only if the measurement is a 3D scan and the number of slices in the slabs is at least 4.

MIP-Cor

🗀 *Inline-Common, Angio-Inline*



If the **MIP-Cor** option is activated, MIP images with coronal orientation are calculated from the acquired slabs of the current protocol.

➪ The **MIP-Cor** parameter can be edited only if the measurement is a 3D scan and the number of slices in the slabs is at least 4.

MIP-Tra

🗀 *Inline-Common, Angio-Inline*

MIP-Tra ☐

If the **MIP-Tra** option is activated, MIP images with transverse orientation are calculated from the acquired slabs of the current protocol.

➪ The **MIP-Tra** parameter can be edited only if the measurement is a 3D scan and the number of slices in the slabs is at least 4.

MIP-Time

🗀 *Inline-Common, Angio-Inline, Inline-Breast*

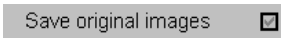
MIP-Time ☐

If the **MIP-Time** option is activated, MIP images with the orientation of the acquired slice groups or slabs are calculated from the acquired slice groups or slabs of the current protocol. In the calculation, the highest pixel value along the time axis is taken into account.

➪ It is only possible to edit the **MIP-Time** option if there is at least one scan repetition or, in the case of triggered scans, at least 2 phases are scanned.

Save original images

🗀 *Inline-Common, Angio-Inline*



The **Save original images** option is normally activated and can not be edited. It is therefore possible to use the original images for other post-processing functions.

Only if an option for standard deviation or for MIP project is activated, can you deactivate the **Save original images** option.

Parameters for physiologically triggered scanning

Physiologically triggered scan synchronize physiological signals sensed on the patient's body with scans. This avoids motion artifacts caused by the heartbeat or respiration.

You may also retrospectively assign acquired image data to physiological signal curves.

Scan parameters specifically for physiologically triggered scans can be found on the **Physio** parameter card.

1st Signal/Mode

🗀 *Physio-Signal 1*



The **1st Signal/Mode** selection list allows you to select a physiological signal and a scan mode.

Selectable physiological trigger signals:

ECG signal

The ECG signal is detected on the skin surface with electrodes. The signal shows the action potential of the heart as a curve.

The individual curve phases correspond to the respective contraction or relaxation phases of the heart. The R wave in the QRS complex is used as triggering point for the scan.

ECG triggering is especially suitable for scans of the chest and heart, because such images would be blurred by the heartbeat with the normal scanning method.

Pulse signal

Pulse triggering is especially suitable for suppressing motion and flow artifacts that result from pulsating blood or CSF.

You can take the pulse signal, for example, from the middle finger of the patient with the pulse sensor.

The first pulse wave ("premature pulse wave") is used for triggering. This wave corresponds to the systolic blood pressure.

External signal

You can input an external, digital triggering signal via the PMU strip at the foot end of the patient table.

You use an external triggering signal, for example, for functional scans (bold imaging) to trigger scanning of a series.

The rising edge of the signal is used to start the scan.

Respiratory signal

The respiratory signal is obtained with the respiratory belt. The cyclic expansion and contraction of the thorax generates the respiratory curve.

With respiratory triggering you can avoid motion artifacts caused by the patient breathing.

ECG/Retro, Pulse/Retro, Ext/Retro

Some special sequences allow **retrospective gating**. In this case, the scan is performed without triggering. Instead, the acquired image data are retrospectively correlated with the characteristic of a physiological signal.

Retrospective gating may be applied to ECG signal curves, pulse signal curves, and external trigger signal curves.

Average cycle

🗀 *Physio-Signal 1*



Your system derives the **Average Cycle** from statistical values. This value indicates the time that has elapsed between two trigger events.

The standard deviation is subtracted from this value to calculate the system acquisition window:

❏ For the **ECG**, **Pulse**, and **External** signals, the system acquisition window is the **Average cycle** minus twice the standard deviation.

❏ For the **Resp signal**, the system acquisition window is **average cycle**/2 minus the standard deviation.

Acquisition window

🗀 *Physio-Signal 1*



In the field **Acquisition window** you can enter the data acquisition time, that is, the time that is used for the scan after a trigger pulse in the physiologically triggered scan.

In this way you define the scan acquisition window.

You should choose an acquisition window that is approximately 10% shorter than the average signal period (average cycle).

➪ If you hover the mouse pointer over the **Acquisition window** input field, a tool tip will be displayed. It shows the acquisition time recommended by the system.

Trigger pulse

🗀 *Physio-Signal 1, Physio-PACE*



In the **Trigger pulse** field, you define whether you want to use every trigger event or only every nth event to trigger scanning.

The value 1 means that every trigger signal starts a scan.

➪ For ECG, pulse, or external trigger signals only.

Trigger delay

🗀 *Physio-Signal 1*



After the trigger signal, the system waits for the time specified here before scanning starts.

For an adult patient with a pulse frequency of 70/min you will obtain, for example, an image of the end diastole with a 0 second delay time, and an image of the systole with a 250 to 350 ms delay time.

This allows you to acquire images at any point in the signal cycle.

➪ For ECG, pulse, or external trigger signal only.

Phases

🗀 *Physio-Signal 1*



The **Phases** field defines how many phases of the heartbeat or how many respiratory phases you want to include.

You can use this, for example, for multislice/multiphase scans of the heart.

➪ The number of heart phases or respiratory phases depends on the selected repetition time TR. Please observe the limits.

Calculated phases

🗀 *Physio-Signal 1*

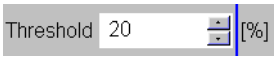


This parameter is displayed if you have selected a **Retro** mode from the **1st Signal/Mode** selection list.

The **Calculated phases** parameter is used to define the number of reconstructed images per heart interval.

Threshold

🗀 *Physio-Signal 1*



Here, you select at which point of the respiratory cycle scanning is to be triggered.

When the respiratory curve reaches this threshold value, the signal is triggered.

The threshold value is stated as a percentage of the respiratory curve. 100% corresponds to the maximum expansion of the rib cage.

➪ Respiratory triggering only.

Resp. phase

🗀 *Physio-Signal 1*



Here, you select whether **Inspiration** (breathing in) or **Expiration** (breathing out) will be used for triggering.

Slices per resp. cycle

🗀 *Physio-PACE*



Number of slices acquired during a respiratory cycle. Only available for HASTE, trufi, and tfl sequences.

Card. trig. per resp. cycle

🗀 *Physio-PACE*



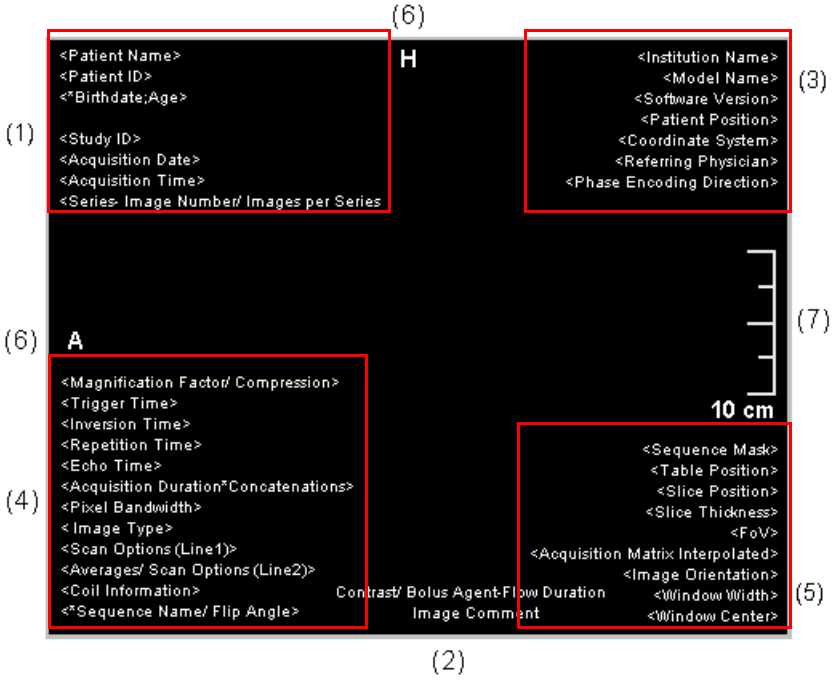
Number of cardiac trigger pulses per respiratory cycle. Replaces **Slices per resp. cycle** for double triggering.

APPENDIX H.2

Text Annotations in Medical Images

Various information is shown as image text on medical images. This information is used to identify the patient and to document scan and image parameters.

The image text is sorted by topic and positioned in the four corners of the image.



(1) Patient and examination data
(2) Comment lines
(3) Mainly system-specific information
(4) Examination and image parameters
(5) Data about the MR image
(6) Orientation mark
(7) Scale bar

Content of the image text components

Here is a list of the individual items of information in the image text components.

(1) Patient and examination data

The top left corner shows the patient and examination data.

Image text	Example	Description
Patient name	Peter Patient	
Patient ID	02081948	
Date of birth, age	*11.11.1970; 30Y	
Examination number	STUDY 1	
Date acquired	17.10.01	
Time acquired	13:47:46.78	
Series and image number and total number of images	2 IMA 5/7	Series 2, a total of 7 images in series 2 image 5 is displayed

(2) Comment lines

At the lower edge next to the scan and image parameters, the data about contrast medium administration as well as an image comment are provided.

Image text	Example	Description
Contrast agent/time after injection in sec	GADOLINIUM 1.1	1.1 s after administration of GADOLINIUM
Image comment	Motion: 0.27, -0.07, 1.29, -0.47, 0.11, -0.01	Motion correction parameters for BOLD images

(3) Plant-specific information and patient position

The top right corner contains the name of your hospital or practice, the system name, the software version, patient position, and direction of viewing.

Image text	Abbreviation	Example
Institution	-	St. Mary´s, New York
System name	-	Magnetom Harmony
Software version	-	MR A30
Patient position (orientation and position) and viewing orientation	HFS (Head First Supine) HFP (Head First Prone) HFDR (Head First Decubitus Right) HFDL (Head First Decubitus Left) FFS (Feet First Supine) FFP (Feet First Prone) FFDR (Feet First Decubitus Right) FFDL (Head First Decubitus Left)	
Coordinate system	LPH (patient coordinate system left-posterior-head)	+LPH
Referring physician		Dr. Mustermann
Phase-encoding direction		→

(4) Scan and image parameters

In the bottom left corner you can see the parameters used to generate the image.

Image text	Abbreviation	Example
Magnification factor/compression	MF CQ as a percentage	MF 1.51/CQ 80
Trigger time	TT in msec	TT 50
Inversion time	TI in msec	TI 50
Repetition time	TR in msec	TR 600
Echo time	TE in msec	TE 30
Scan duration * concatenations	TA HH:MM:SS (hours range); MM:SS (minutes range); SS.HS (seconds range)	TA 02:36*4
Pixel bandwidth	BW in hertz/pixels	BW 1000.0
Image type	→ Page H.2–14, *List of image types* px - Grappa with acceleration factor x Px - Sense with acceleration factor x	 p2 M/MIP
Scan options (1st line)	RG - Respiratory Gating CG - Cardiac Gating RT - Respiratory Trigger CT - Cardiac Trigger EXT - External trigger	RG/CT

Image text	Abbreviation	Example
Averages/scan options (2nd line)	A (y) - number of averages FS - Fat Saturation SFS - Fat Saturation with SPAIR WS - Water Saturation WE - Water Excitation SAT(y) - Number of Saturation Regions DB - Dark blood IR - Inversion Recovery SR - Saturation Recovery G (x) - Grid tag with x mm grid distance or L(x) - Line tag with x mm line distance MT - MTC pulse	A4/FS/SAT1/MT
Coil information	→ Page H.2–7, *List of Coil Abbreviations in the Image Text*	NE1;SP1
Sequence name/flip angle	A * in front of the sequence name means that an original Siemens sequence was used.	*TS2_23 80

(5) Data about the MR image

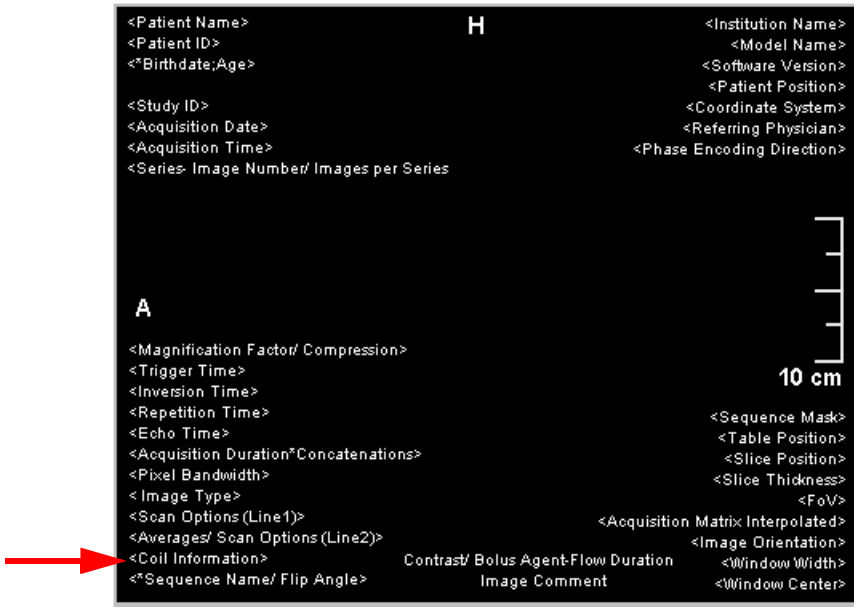
The bottom right corner shows data about the position, orientation, and thickness of the acquired slice, about the extent (FoV), and about the window values.

Image text	Abbreviation	Example
Sequence mask	D - Door open I - Interpolation R - Raw data filter E - Elliptical filter	D\I
Table position (H,F)	TP H/F in mm	TP H300
Slice position (+LPH)	SP in mm	SP L8.7

Image text	Abbreviation	Example
Slice thickness/slice gap Slice thickness interpolated	SL in mm/slice gap in mm SL i in mm	SL 4.0/2.0 SL 4.0 i
FoV (Field of View)	FoV in mm	FoV 230 × 230
Acquisition matrix interpolated Acquisition matrix not interpolated	p - partial fourier s - swap I - interpolation	192p × 256s I 192p × 256s
Image orientation with inplane rotation	Sag, Tra, Cor	Tra>Cor(-20)>Sag(-30)
Flow-encoding direction	vXXX_inplane_xy - in-plane flow encoding vXXX_through - through-plane flow encoding XXX - flow velocity in cm/sec xy - direction, e.g. fh (feet to head)	v150_inplane_fh
Window width (contrast)	W	W -100
Window center (brightness)	C	C -200

List of Coil Abbreviations in the Image Text

The coils and coil elements used are shown in in the lower left image text.



MAGNETOM Harmony and Harmony Expert

Image text	Coil name
AS	Array Shim Device
BC	Body
BO1, BO2	CP Body Array
BO3, BO4	CP Body Array Extender
BRL, BRR	CP Breast Array
DLL	Double Loop Array Left
DLR	Double Loop Array Right
EN	Endorectal
EX	CP Extremity
FL	CP Flex Large
FLL	Flex Loop Large
FLS	Flex Loop Small
FS	CP Flex Small
HE	CP Head Array
NE1, NE2	CP Neck Array
PL1, ..., PL4 PR1, ... , PR4	CP PA Array
SH1, ..., SH4	Shoulder Array
SP1, ..., SP6	CP Spine Array
SP1, ..., SP6	CP Spine Array + LFOV
WR1, ..., WR4	Wrist Array
XX1, ..., XX4	Service Plug

MAGNETOM Symphony, Symphony P, Sonata, Symphony/Sonata Vision and Novus 1.5

Image text	Coil name
AS	Array Shim Device
BC	Body
BL1, BL2, BR1, BR2	Breast Array
BL, BR	4 Channel Breast Confirma
BL, BR	4 Channel Breast_Machet
BO1, BO2	CP Body Array
BO3, BO4	CP Body Array Extender
BRL, BRR	CP Breast Array
CL1, CL2	Carotid Array Left
CR1, CR2	Carotid Array Right
DLL	Double Loop Array Left
DLR	Double Loop Array Right
EN	Endorectal
EX	CP Extremity
EX	Extremity MAI
FA	8 Ch Foot Ankle
FL	CP Flex Large
FLL	Flex Loop Large
FLS	Flex Loop Small
FS	CP Flex Small
HB1, ..., HB4	High Resolution Head

Image text	Coil name
HE	CP Head Array
HE	Tx Rx Head
HU1, HU2	Not for Humans
ICC	Incomplete Coil
KN	HR Knee
LBR, MBR, RBR	7 Channel Breast
LE1,..., LE4	Lower Extremity Flex
NB	Neonate Body
NE1, NE2	CP Neck Array
NH	Neonate Head
OT	Coil Overtemp.
PA1, ..., PA6	6 Channel Body Anterior
PH1, ..., PH8	8 Channel Head
PH1, PL1, PL2, PL3	Large Pediatric Array
PH1, PS1, PS2, PS3	Small Pediatric Array
PL1, ..., PL4 PR1, ... , PR4	CP PA Array
PP1, ... , PP4	6 Channel Body Posterior
SE1, ..., SE4	Small Extremity
SH1, ..., SH4	Shoulder Array
SP1, ..., SP6	Spine Array + LFOV
UE1, UE2, UE3	Upper Extremity Flex
WR1, ..., WR4	Wrist Array
WT1, ..., WT4	Wrist Array MAI

Image text	Coil name
XX1, ..., XX4	Service Plug
1H, 31P	Heart/Liver 31P
8WR	8 Channel Wrist

MAGNETOM Concerto

Image text	Coil name
AS	Array Shim Device
BC	Body
BS 1, BS2, BS3, BS4	Body Spine Array S, M, L, XL
EX1, EX2	Extremity S, L
HE1, HE2	Head Array
LCC	Cordless
M11, M16, M21, M35, M45	Multi Purpose 11, 16, 21, 35, 45
NL	Neck Large
NM	Neck Medium
SH1, SH2	Shoulder
WR1, WR2	Wrist
XXL	XXL Coil
1, 2, 3, 4	Service Probe

MAGNETOM C!

Image text	Coil name
BS1, BS2, BS3, BS4	Body Spine Array S, M, L, XL
BS1, BS2	Body Spine Array XXL
BL1, BL2, BR1, BR2	CPMamma
EX1, EX2, CA1, CA2	Extremity S, L, XL
HL1, HL2, HS1,HS2	Head Array
HL1, HL2 HS2, NM	Head Neck M
HL1, HL2 HS2, NL	Head Neck L
LCC	Cordless
M16, M21	Multi Purpose 16, 21
NL	Neck Large
NM	Neck Medium
SH1, SH2	Shoulder
WR1, WR2	Wrist
WR1, WR2, WR3, WR4	Wrist 4CH

iPat Imaging

MAGNETOM C

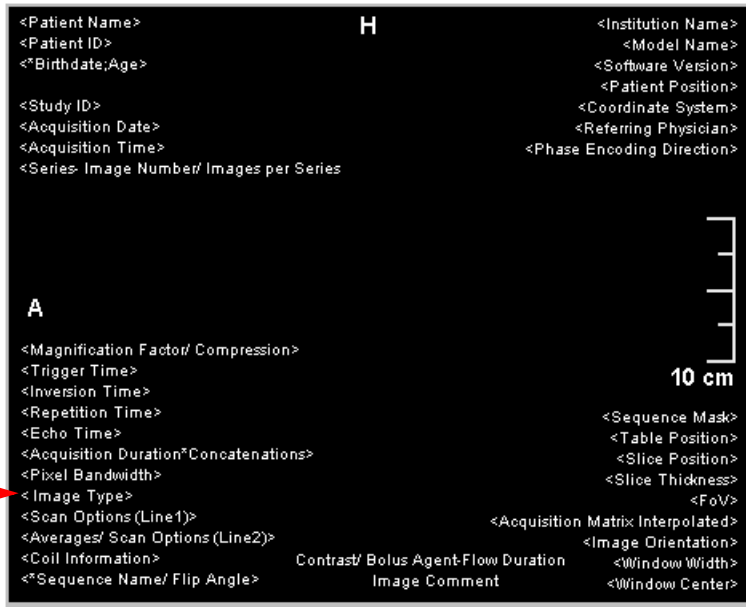
Coil/Orientation	Coronal	Axial	Sagittal
CP Head/Neck Array	Y	N	Y
Neck (M,L) + CP Head/Neck Array	Y	N	Y
Body/Spine Array (S, M, L, XL)	Y	N	Y
Body/Spine Array XXL	N	N	N
Shoulder Array	N	N	N
Extremity Array (S, L, XL)	Y	N	Y
Wrist Array	N	N	N
Multi Purpose 16	N	N	N
Multi Purpose 21	N	N	N

Y = Yes; N = No

Note: For iPAT the phase encoding direction must be H – F (Head to Feed).

List of image types

The image type is shown in the lower left image text.



An image may include more than one image type, e.g. after several post-processing steps. These are concatenated, and separated by a slash (/). If the maximum line length is exceeded, the last image types are omitted.

Example

Assuming the defined maximum length is 18 characters:

TYP1/TYP2/TYP3/TYP4 (19 characters)

will be truncated to **TYP1/TYP2/TYP3** (14 characters).

Inline reconstruction

Flow quantification

Abbreviation	Image type
R	Real image
M	Rephased image (magnitude image)
P	Phase contrast image

Diffusion, Perfusion

Abbreviation	Image type
ADC	Apparent Diffusion Coefficient, diffusion-weighted image (b-values)
TTP	Time To Peak image
SCM	Signal Change image
TCS	Time Course of Signal
PBP	Percentage signal image (Percent-of-Base-line at Peak; bolus peak relative to baseline).
GBP	Global time-density curve (Global Average Bolus Curve Plotted; passage of bolus)
RELMTT	Relative MTT image (relat. average transit time)
WI	Wash In image
WO	Wash Out image
PEI	Positive Enhancement Integral image
MITP	Maximum Intensity Time Projection image
COMB	Combination image

Phase contrast Angio

Abbreviation	Image type
MAG	Magnitude image
MSUM	Sum image from magnitude images of a slice

Graphic slice position

Abbreviation	Image type
GSP	Reference image with graphic objects

Functional imaging

Abbreviation	Image type
MEAN	Mean value image
TTEST	Result image of volunteer's t-test
MOSAIC	Mosaic image
COR	Correlation image

Inline post-processing

Abbreviation	Image type
MIP	Maximum Intensity Projection image
MIP_SAG	Sagittal image from MIP reconstruction
MIP_COR	Coronal image from MIP reconstruction
MIP_TRA	Transverse image from MIP reconstruction
TMIP	Temporal MIP, MIP reconstruction of time sequence of images
TMIP_SAG	Sagittal TMIP image
TMIP_COR	Coronal TMIP image
TMIP_TRA	Transverse TMIP image
TSTDDEV	Temporary standard deviation image

Abbreviation	Image type
STDDEV_SAG	Sagittal standard deviation image
STDDEV_COR	Coronal standard deviation image
STDDEV_TRA	Transverse standard deviation image
DIS2D	2D distortion corrected image
DIS2D*	2D distortion corrected image that cannot be used as reference image for positioning, because it was scanned too far off-center.
DIS3D	3D distortion corrected image
ND	Not distortion corrected image
RETRO	Retro-Gating image
NORM	Image after normalization algorithm
PROJECTION IMAGE	Projection image
FIL	Inline Image Filter
MOCO	BOLD or perfusion image with motion correction
FILTERED	BOLD or perfusion image with spatial filtering

Import/export

Abbreviation	Image type
OTHER	Converted N3/3.5 image or SC (secondary captured) image

Post-processing

3D reconstruction

Abbreviation	Image type
MPR	Multiplanar reconstruction image (MPR)
MPR THIN	MPR Thin image
MPR THICK	MPR Thick image
MPR CURVED	Curved MPR image
MIP	MIP reconstruction image
MIP THIN	MIP Thin image
SSD	SSD reconstruction (Shaded Surface Display)
SUBTRACT	Subtraction image
3D EDITOR	3D editor processing image
3D FUSION	Fusion image
VRT	VRT (Volume Rendering Technique) image
AVERAGE	VRT image
RESAMPLED	Zooming/panning image
BLACK IMAGE	Graphic image

Dynamic analysis

Abbreviation	Image type
ADD	An addition
MEAN	Mean value image
COR	Correlation image
DIFFER	Differentiation image
DIFFUS	Diffusion weighted image

Abbreviation	Image type
DIV	Division image
SDEV	Standard deviation image
INT	Integration image
MULT	Multiplication image
SLOPE	SLOPE evaluation contrast imagery
SUB	Subtraction image
T1	T1 image
T2	T2 image
PDT1	T1-weighted proton density image
PDT2	T2-weighted proton density image
TTP	Time To Peak image
TTEST	Statistical analysis method for BOLD images
LOG	Logarithm function image
CVxx	Image with Context Vision filter (xx stands for filter strength; integer value)

Mean Curve

Abbreviation	Image type
CSA BLACK IMAGE	Graphics and table image

Position display

Abbreviation	Image type
POSDISP	Position display image

Image composing

Abbreviation	Image type
COMPOSED	Composed images

Spectroscopy

Abbreviation	Image type
SPEC	Spectrum

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