<table>
<thead>
<tr>
<th><strong>Legend</strong></th>
</tr>
</thead>
</table>
| **i** | Indicates a hint  
Is used to provide information on how to avoid operating errors or information emphasizing important details |
| **»** | Indicates the solution of a problem  
Is used to provide troubleshooting information or answers to frequently asked questions |
| ■ | Indicates a list item |
| ✔ | Indicates a prerequisite  
Is used for a condition that has to be fulfilled before starting a particular operation |
| ♦ | Indicates a one-step operation |
| 1 2 3 | Indicates steps within operating sequences |
| **Italic** | Is used for references and for table or figure titles |
| ➔ | Is used to identify a link to related information as well as previous or next steps |
| **Bold** | Is used to identify window titles, menu items, function names, buttons, and keys, for example, the Save button |
| **Blue** | Is used to emphasize particularly important sections of the text |
| **Courier** | Is used for on-screen output of the system including code-related elements or commands |
| **Courier** | Is used to identify inputs you need to provide |
| Menu > Menu Item | Is used for the navigation to a certain submenu entry |
| `<variable>` | Is used to identify variables or parameters, for example, within a string |
| **CAUTION** | **CAUTION**  
Used with the safety alert symbol, indicates a hazardous situation which, if not avoided, could result in minor or moderate injury or material damage.  
**CAUTION** consists of the following elements:  
- Information about the nature of a hazardous situation  
- Consequences of not avoiding a hazardous situation  
- Methods of avoiding a hazardous situation |
WARNING
Indicates a hazardous situation which, if not avoided, could result in death or serious injury.

WARNING consists of the following elements:
- Information about the nature of a hazardous situation
- Consequences of not avoiding a hazardous situation
- Methods of avoiding a hazardous situation
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1 Introduction

In order to operate the MR system accurately and safely, the operating personnel must have the necessary expertise as well as knowledge of the complete operator manual. The operator manual must be read carefully prior to using the MR system.

1.1 Layout of the operator manual

Your complete operator manual is split up into several volumes to improve readability. Each of these individual operator manuals covers a specific topic:

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

Another element of the complete operator manual is the information provided for the system owner of the MR system.

The extent of the respective operator manual depends on the system configuration used and may vary.

All components of the complete operator manual may include safety information that needs to be adhered to.

The operator manuals for hardware and software address the authorized user. Basic knowledge in operating PCs and software is a prerequisite.

1.2 The current operator manual

This manual may include descriptions covering standard as well as optional hardware and software. Contact your Siemens Sales Organization with respect to the hardware and software available for your system. The description of an option does not infer a legal requirement to provide it.
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.

Male and female patients are referred to as “the patient” for the sake of simplicity.

1.3 Intended use

Your MAGNETOM MR 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\(^1\) 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.

\(^1\) The drugs mentioned herein shall be used consistent with the approved labeling and/or indications for use of the drug. The treating physician bears the sole responsibility for the diagnosis and treatment of patients, including drugs and doses prescribed in connection with such use.

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

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**i**

The MAGNETOM MR system is not a device with measuring function as defined in the Medical Device Directive (MDD). Quantitative measured values obtained are for informational purposes and cannot be used as the only basis for diagnosis.

**i**

For the USA only: Federal law restricts this device to sale, distribution and use by or on the order of a physician.
Your MR system is a medical device for human use only!

1.4 Authorized operating personnel

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

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

Please contact Siemens Service for more information on available training options and suggested duration and frequency of such training.

1.4.1 Definitions of different persons

<table>
<thead>
<tr>
<th>Term used</th>
<th>Explanation</th>
</tr>
</thead>
<tbody>
<tr>
<td>User/Operator/Operating personnel</td>
<td>Person who operates the system or software, takes care of the patient or reads images</td>
</tr>
<tr>
<td></td>
<td>Typically physicians, trained radiological technicians, or technologists</td>
</tr>
<tr>
<td>System owner</td>
<td>Person who is responsible for the MR environment. This includes legal requirements, emergency plans, employee information and qualifications, as well as maintenance/repair.</td>
</tr>
<tr>
<td>Term used</td>
<td>Explanation</td>
</tr>
<tr>
<td>-------------------------------</td>
<td>---------------------------------------------------------------------------------------------------------------------------------------------</td>
</tr>
<tr>
<td>MR worker</td>
<td>Person who works within the controlled access area or MR environment</td>
</tr>
<tr>
<td></td>
<td>User/Operator as well as further personnel (for example, cleaning staff, facility manager, service personnel)</td>
</tr>
<tr>
<td>Siemens Service/service personnel</td>
<td>Group of specially trained persons who are authorized by Siemens to perform certain maintenance activities</td>
</tr>
<tr>
<td></td>
<td>References to “Siemens Service” include service personnel authorized by Siemens.</td>
</tr>
</tbody>
</table>
2 Preparation

2.1 Preparing and positioning the patient
2.1 Preparing and positioning the patient

2.1.1 Reducing motion artifacts

1. Instruct the patient to remain still during the entire examination.
2. Instruct the patient to take shallow gentle breaths during all free-breathing examinations.
3. Optional: Inject medication for relaxing the intestines.

Breathhold commands

When performing breathhold measurements:

- Ensure that the patient wears the headset so that the breathhold commands can be understood despite the gradient knocking.

2.1.2 Preparing the contrast agent injection

Prior to moving the patient table into the magnet, you must route the tube for the infusion.

1. Insert an intravenous port into the forearm vein of the patient.
2. Connect the port to the extension tube.

3. Connect the tube to the contrast agent injector.

The tube should be long enough so that it can be accessed from the outside when the patient is in the magnet bore.

2.1.3 Preparing ECG-triggered examinations

Positioning the electrodes and PERU

Electrodes: Positioning of the electrodes varies according to the position of the heart. An example is provided in the figure below.

Use only disposable ECG electrodes as released by Siemens.
(→ Page 18 Procurement addresses)
PERU: The ECG sensor in the PERU ensures transfer of the ECG signal. Typically, the PERU is aligned in the direction of the foot end of the patient table even though the patient may be positioned feet first in the direction of the magnet bore.

- Position the PERU in the appropriate support or add absorbent material between the ECG cables, PERU and skin. The distance between PERU and patient should be at least 2 cm.

![Positioning the ECG electrodes (left) and the PERU (right).](image)

- The transmitter unit of the PERU includes three LEDs for signaling the battery status and one LED as fault indicator (e.g. insufficient skin contact of the ECG electrodes).

  Battery status and electrode fault are also indicated on the Dot display above the magnet bore and the Physiological Display dialog window.

- If the red LED Electrode fault on the PERU flashes, the ECG electrodes are not attached correctly. Check to ensure that the electrodes are not falling off.

**Attaching ECG electrodes**

The electrodes must be positioned and attached with care to ensure a sufficient and consistent ECG signal.

Only MR Safe electrodes should be used for ECG monitoring during MR examinations.

1. Discuss the breathholds and respective commands with the patient.
2. Ensure satisfactory contact between the electrodes and the patient's skin.
3 Thoroughly clean the patient’s skin with a dry cloth or NUPREP ECG & EEG Abrasive Skin Prepping Gel. (→ Page 18 Procurement addresses)

4 If the patient is hirsute, shave the location where you want to attach the electrodes.

5 Dry the skin carefully.

6 Check the signal at the Dot display above the magnet bore.

7 If the signal received is not satisfactory and consistent, vary the location of the electrodes. Use new electrodes every single time.

8 If one of the leads does not provide a sufficient signal, change to a single ECG lead in the Physiological Display dialog window.

Procurement addresses

Use MR Safe electrodes only.

Disposable ECG electrodes may be ordered from:

Siemens Commercial goods (Catalog Med & More), CONMED 2700 Cleartrace

- Item no. 07437861 (30 pieces) or
- Item no. 07437598 (600 pieces)

or from:

CONMED CORPORATION, 310 Broad Street, Utica, New York 13501, USA

Cleaning gel: NUPREP ECG & EEG Abrasive Skin Prepping Gel

Weaver and Company, 565 Nucla Way, Unit B, Aurora, Colorado 80011, USA
3 Measurement

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3.1 Lesion evaluation with TimCT Oncology

The TimCT Oncology application package combines transverse 2D multi-slice imaging with continuous table movement. Examinations with different image contrasts (T1/T2) are supported, and can be performed in multi-breathhold mode to avoid motion artifacts.

T1 contrast: The GRE sequence is available for T1 contrast either with spectral fat saturation or as a double-echo sequence with DIXON reconstruction.

T2 contrast: The TSE or HASTE sequences can be used for T2 contrast either with spectral fat saturation or inversion recovery (STIR/TIRM).

⚠️ Caution

When using the DIXON method, water and fat swaps might occur!

Incorrect diagnosis

◆ Diagnosis should be confirmed by a second contrast and/or a different orientation.

For the TSE sequence, the BLADE technique may also be used to reduce motion sensitivity. For a detailed description of BLADE, please refer to: Application Brochure “Pulse Sequences”.

3.1.1 Setting up the measurement range

✓ FastView localizer is available

The size of the measurement range automatically determines the number of slices to be measured.

1 Open the Geometry TimCT parameter card.
2 Select the start position (Range start) and the length of the measurement range (Total FoV). (You may also set the measurement range graphically in the GSP.)

The measurement requires continuous adjustments and an acceleration region for the patient table. For this reason, the table range of the adjustment information should extend approx. 10 cm beyond both ends of the measurement range.

To avoid additional inline adjustments, plan a generous FastView localizer.

Slice groups in the graphic slice positioning (GSP) mode. The blue line shows the start position of the table movement.
Performing multi-breathhold measurements

✓ Measurement range has been set

You can divide the total measurement time into breathhold intervals of arbitrary length using the Inline Display.

1. Open the Physio PACE parameter card.

2. Enter the patient-specific breathhold duration.

3. Start the measurement.

4. Open the Inline Display.

5. Start the measurement of one breathhold duration interval (Scan breathhold icon in the Inline Display).

   After this time the measurement pauses automatically.

6. To toggle between anatomical and projection progress images click the Display Filter icon.

7. To manually start and pause the measurement click the Scan/pause icon. (Also possible while a Scan breathhold is running.) This is useful for measuring regions without respiratory motions.
You may use **Scan/pause** to start the last breathhold of a measurement. Instruct the patient to continue holding his breath as long as possible and then continue with shallow breathing. This avoids automatic pauses during the remainder of the measurement.

In contrast to conventional breathhold measurements, the measurement data are shared between various breathhold intervals (exception: measurements using HASTE). For this reason, ensure the best possible reproducibility of the breathhold status.

### 3.2 Inline Liver registration

Multiple phases are acquired within a contrast-enhanced MR examination of the abdomen:

- Pre-contrast measurement (before administration of contrast media)
- Arterial phase
Portal-venous phase and

Delayed phase

For diagnostic purposes, subtraction series are calculated by subtracting the pre-contrast measurement from the arterial, portal-venous and delayed phase. When viewing original and subtraction images, shifting or misalignment of the anatomy may be observed between the different phases. The more phases, the greater the shifting and misalignment could be.

**Cause:** The same anatomical region is measured at different time points, all within one breathhold. Therefore, the anatomy under examination may shift substantially depending on the depth of the breathhold.

**Remedy:** For best visualization of lesions regarding form, morphological information, or evaluation of the enhancement pattern, a mechanism of automatic registration/alignment (= Liver registration) has been implemented within the VIBE sequence.

Liver registration is performed after enabling the *Liver registration* checkbox on the *Inline* parameter card.
3.2.1 Image examples

The importance of registration/correction can be seen when examining nodular enhancing pathologies. The improvement in subtraction quality between the registered and unregistered exam is self-evident in the images shown below.

Original images: Patient with HCC, misalignment of the anatomy (2, 3, 4 = subtraction images).

(1) Pre-contrast image
(2) Arterial phase
(3) Portal-venous phase
(4) Delayed phase
Corrected images: Patient with HCC, better visualization of pathology after liver registration (see portal-venous and delayed phase; 2, 3, 4 = subtraction images).

1. Pre-contrast image
2. Arterial phase
3. Portal-venous phase
4. Delayed phase

The system checks the quality of the registration. If the quality is not sufficient (e.g., shift between different phases is too large) an error message is displayed and only the original (unregistered) images are saved.
3.3 **TimCT Oncology Dot Engine**

The **TimCT Oncology Dot Engine** provides comprehensive metastasis information for the evaluation from measurement to report covering thorax, abdomen, and pelvis with special focus on the upper abdomen.

The TimCT technology enables multi-slice T1-weighted measurements (with fat saturation or Dixon technique) or T2-weighted measurements (with fat saturation or inversion recovery) acquired with continuous table movement. Therefore it suits best as a complement to the primary tumor diagnosis done by the physician using stationary mode (e.g., for the upper abdomen) by providing comprehensive metastasis and lymph node information for the evaluation of thorax, abdomen, and pelvis.

**Caution**

When using the DIXON method, water and fat swaps might occur!

**Incorrect diagnosis**

- Diagnosis should be confirmed by a second contrast and/or a different orientation.

**Information**

The Dot Engine user interfaces shown in this operator manual are examples only. The actual guidance texts and the design may be slightly different on your system.

3.3.1 **Planning the examination and measuring the localizer**

- Patient has been registered
- **TimCT Oncology Dot Engine** has been selected

**Adapting the examination to the patient**

After registration, the **Patient View** opens automatically. The default examination parameters are loaded.
In the Patient View you activate automatic functionalities and adapt the breathhold parameters to the patient’s need. In addition, you can decide if contrast agent is administered. The pending protocols of the measurement queue are updated upon your selection.

Applies only to protocols within the Focus Upper-Abdomen section.

1. Enter the Breath-hold capability of the patient.
   
   The sequence parameters of the breathhold protocols will be adapted automatically.

2. If you want to use Automatic breath-hold commands throughout the whole examination, activate the checkbox and set the timing and language for the commands.

You are also able to set the breathhold commands individually for each protocol (in the Step properties dialog window).

Setting the breathhold parameters

Calculating the FoV automatically

Activating automatic functionalities

1. Select Auto Coverage in the Protocol Adaption drop-down menu.
   
   In case of breathhold examinations, select Auto Coverage + BH.

2. Activate the automatic functionalities, if necessary.

| Auto ROI | Position of the ROI is suggested by the system. |
**Auto Bolus Detection**

Automatic detection of the contrast bolus arrival in the region of interest and proper start of arterial phase measurement.

**Using contrast agent**

- Select **without Contrast agent** from the drop-down menu, if no contrast agent is to be used.

  All contrast agent protocols will be removed from the measurement queue.

**Accessing the Patient View**

You can access the **Patient View** at any time during the examination.

1. To open the view, click the icon.

2. To confirm the settings and close the view, click the icon.

**Modifying parameters of measured protocols**

Changes in the **Patient View** only apply to pending protocols in the measurement queue.

1. To change the status of a protocol from measured to pending, select the measured protocol.

2. Select **Rerun from here** from the context menu (right-click with the mouse)

3. Open the **Patient View**.
   - or –
   Select **Rerun from here with** from the context menu (right-click with the mouse).

   The **Patient View** opens automatically.

4. Enter the requested modifications.

**Starting the measurement of the FastView localizer**

- Confirm the patient-specific settings.

  The FastView localizer is measured. Coronal and sagittal MPRs are displayed in the GSP.

  A T2-weighted transverse protocol (HASTE with inversion recovery) with continuous table movement opens.
3.3.2 Performing TimCT measurements

The size of the measurement range automatically determines the number of slices to be measured. A guidance text will support you while planning the measurement range.

✓ FastView localizer is available

T2-weighted transverse measurement

1 Specify the measurement range.

2 Start the measurement.

The measurement is performed in multi-breathhold technique in the regions thorax to abdomen and without breathhold technique in the pelvic region.

The T2-weighted result images are displayed. A T1-weighted transverse protocol (FLASH with fat saturation) with continuous table movement opens.

T1-weighted transverse measurement

The measurement range is inherited from the previous TimCT measurement.

◆ Start the measurement.

The measurement is performed in multi-breathhold technique. The result images are displayed. Subsequently, a localizer for AutoFoV calculations in the abdominal region is measured automatically.

Based on the localizer data, the system determines the FoV-Read and FoV-Phase for the transverse measurements.

3.3.3 Planning liver dynamics

✓ TimCT detection scans have been measured

Setting the dynamic parameters

The liver dynamic measurement consists of four T1-weighted transverse 3D measurements with breathhold technique. Within this step, you define the presets for all subsequent dynamic measurements.
Check and adapt the preset delays between the contrast agent phases, if necessary.

Activate or deactivate **Auto Bolus Detection**.

Even while **Auto Bolus Detection** is activated, you can manually start the subsequent arterial phase with **Stop&Continue** in the Inline Display.

If **Automatic breath-hold commands** is deactivated, the user is informed by the system when to give the breathhold commands.

**Starting the dynamic measurements**

1. Start the pre-contrast measurement.

   If **Automatic breath-hold commands** is deactivated, the system waits for the first manual breathhold command to start the dynamic scans. For the following breathhold commands, the system informs the user when to give the breathhold command.

2. Apply the breathhold command and click this icon.
If **Automatic breath-hold commands** is activated, all breathhold commands are given by the system.

The pre-contrast images are measured. The Care Bolus protocol opens.

Monitoring the dynamic measurements: In the monitoring window on the left-hand side of the screen, you can follow the progression of the dynamic measurements.

### 3.3.4 Positioning the slice and ROI for Care Bolus

- **✓ Pre-contrast images have been measured**

You use the Care Bolus protocol to monitor the contrast agent inflow in real time on the **Inline Display**.

1. Check and adapt the suggested ROI, or
2. Select the sagittal slice with the best vessel visualization.
3. Position the ROI in the sagittal slice with a left mouse click (if **Auto Bolus Detection** is on).
4. Adjust slice position for Care Bolus.
5. Start Care Bolus and then start the contrast agent injection.

- or –

Select an adequate sagittal slice for best visualization.
2 Position the ROI on the sagittal slice by clicking in the GSP (Auto Bolus Detection On only).

3 Adjust the slice position for Care Bolus.

3.3.5 Starting dynamic contrast agent measurements

✓ Care bolus slice has been positioned
✓ ROI for bolus detection has been positioned

1 Start the Care Bolus measurement.

The main vessel for bolus monitoring is displayed in the Inline Display at an image rate of approximately 1 image/sec.

2 Begin with the contrast agent injection as soon as images appear in the Inline Display.

The bolus arrival is monitored in the ROI with Auto Bolus Detection On and visualized via a corresponding signal curve.

A Stop&Continue icon is available in the icon bar for manual start or override of the automatic start of arterial phase measurement.

3 With Auto Bolus Detection On, you may check if contrast agent arrival is detected in time.

4 Override with the Stop&Continue icon if the automatic bolus detection fails.
– or –

With **Auto Bolus Detection Off**, manually start the arterial phase measurement with the **Stop&Continue** icon upon the visual detection of bolus arrival in the **Inline Display**.

The consecutive measurement of arterial, venous, and delayed phase is performed automatically. The delay time settings are taken into account. Breathhold commands are output before and after each measurement.

The following image data are generated:

- Series of original data of all phases
- Subtraction series

### 3.3.6 Measuring coronal post-contrast images

✓ Measurement of the delayed phase has been completed

A high-resolution coronal post-contrast measurement with breathhold complements the preceding transverse measurements allowing a detailed analysis of the anatomy in two planes.

1. Position the slices for optimum coverage.

2. Start the measurement.
   
The result images are displayed.

### 3.3.7 Measuring TimCT post-contrast images

✓ Measurement of the delayed phase has been completed

Finally, you measure T1-weighted transverse post-contrast images using multi-breathhold technique and continuous table movement.

- Start the measurement.
  
The result images are displayed.
3.4 1H CSI MRS for the prostate

3.4.1 General information

1H CSI MRS of the prostate can be used to detect changes in signal intensity of the citrate metabolite.

Citrate is an important metabolic product of the tricarboxylic acid cycle (Krebs cycle) in the mitochondria of living cells. Intracellular citrate concentrations are very low. However, citrate can be detected as a secretion from the healthy prostate.

The spectrum of healthy prostate tissue shows a strong citrate signal, which is typically significantly higher than the choline signal. (Examples of spectra: (➔ Page 54 Evaluating voxels of interest).)

However, the citrate/choline signal ratio in the prostate is subject to regional differences. The highest ratios may be found in the peripheral zone; in the area of the ureter, however, the ratio may be reversed even in a healthy prostate. High choline and low citrate signals may be found in cancerous prostate tissue. However, the spatial inhomogeneity must be considered during evaluation.

After a biopsy, four weeks should be waited before a spectroscopy examination.

Due to the strong coupling of the citrate signal, the sequence timing of the RF pulses has to be adjusted as a function of the field strength.

- 1.5 T: TE = 120 ms
- 3 T: TE = 145 ms (plus special timing) (➔ Page 36 Performing 1H CSI MRS of the prostate)

For this reason, the citrate signal will appear differently dependent on field strength.
3.4.2 Performing 1H CSI MRS of the prostate

Planning the examination
✓ Patient has been positioned

1 Use an appropriate coil.

2 During registration, select the Prostate_1H examination (under Study).

Planning the MRS measurement

To cover the whole prostate, the measurement protocols are based on a 3D CSI sequence.

To plan spectroscopy and for post-processing, you need non-distortion corrected images (ND) in the three main orientations. Spectroscopy measurements must be performed at the same table position as the ND images used for planning.

✓ Prostate protocol has been opened

1 Select the images showing the largest diameter of the prostate.

2 Try to maximize the coverage of the prostate, while minimizing inclusion of periprostatic fat.

3 Ensure that reference images are available which are parallel to the defined orientation of the CSI measurement.

Otherwise, the display of metabolite images and spectral maps might not be possible.

4 Adjust the FoV so that at least two voxels of the measurement matrix are outside the VOI in each direction.

Suppressing fat signals

With a combination of the “Outer Volume Suppression” and the spectral signal suppression, you are able to effectively suppress interfering fat signals.

◆ Carefully position the regional saturation pulses for suppressing unwanted signals (especially the fat signal) in the vicinity of the prostate.
Specialities for 3 T

Setting the sequence timing
1. Open the **Contrast Common** parameter card.
2. Select **Prostate** from the **Application** list to activate the correct sequence timing.

Magnetic field homogeneity
At 3 T, expect stronger air-induced susceptibility effects in the vicinity of the prostate.

- If necessary, manually optimize the magnetic field homogeneity with the interactive shim after completion of the automatic adjustments. (→ Page 38 **Shimming interactively (optional)**)

Starting protocol adjustments (optional)

Semi-automatic adjustments are recommended for difficult anatomical regions (e.g., flow, vessels, jumps in susceptibility). You can check the shim status prior to the spectroscopy measurement and improve it, if necessary.

✓ Automatic adjustment is not satisfactory

1. Select **Options > Adjustments** from the main menu.
   - The **Manual Adjustments** dialog window is opened.
2. Select the **Show** subtask card.
3 Start the adjustments with Adjust All.

All protocol adjustments are performed (as displayed in the information window).

Shimming interactively (optional)

The shim quality is particularly important for spectroscopy examinations. Use interactive shimming for checking and improving the examination. By changing the shim currents you are able to optimize the results (FWHM, T2*).

✓ Protocol adjustment has ended

1 In the Manual Adjustments dialog window: Select the Interactive Shim subtask card.
2. Start the shim with **Measure**.

An infinite measurement is performed with the currently set shim parameters.

3. Monitor the results for FWHM and T2*.

**FWHM [Hz]:** as small as possible
- 1.5 T < 20 Hz
- 3 T < 30 Hz

**T2*: as large as possible. Depends on voxel size and the metabolites contained within.
4 End the measurement with **Stop** as soon as you are satisfied with the results. (Otherwise: (→ Page 40 *Improving shim results (optional)*).)

---

**During visual inspection, if the water amplitude is less than twice the fat amplitude, the size and/or position of the voxel should be readjusted.**

5 Apply the shim results to the following spectroscopy measurement with **Apply**.

6 Close the dialog window.

7 Start the spectroscopy measurement.

---

### Improving shim results (optional)

If the results for FWHM and T2* are not satisfactory, you can improve the homogeneity of the magnetic field by changing the shim currents.

- **✓ Interactive Shim** subtask card has been opened
- **✓** Shim results are not satisfactory
- ◆ Change the gradient offset for **one** shim channel.

---

#### Example Channel X

1 Increase the value with the **up** arrow button.

2 Monitor FWHM and T2*.
   
   If the result worsens:

3 Use the best shim results of the current measurement with **Load Best**.

4 Change the gradient offset in the other direction (use the **down** arrow button).
   
   If the results for FWHM and T2* continue to be unsatisfactory:

5 Repeat the steps for the other channels (Y, Z).
   
   As soon as you are satisfied with the results:

6 End the measurement with **Stop**.

7 Apply the shim results to the following spectroscopy measurement with **Apply**.
Adjusting the frequency (optional)

Whenever you change shim currents, a “?” appears in the **Frequency (syst)** field. This means that the frequency still needs to be adjusted (if not performed manually, the system handles it automatically).

✓ Shim currents have been changed

1 In the **Manual Adjustments** dialog window: Select the **Frequency** subtask card.

2 Start the frequency adjustment with **Go**.

3 Monitor the tolerance parameter “Diff [Hz]”.
4 Repeat the adjustment until you obtain a satisfactory value for “Diff [Hz]” and the “Y” in the A. column appears.

5 Transfer the frequency determined to the measurement system with Close.

You can now begin with the spectroscopy measurement.
4 Post-processing

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4.1 Evaluation of dynamic 3D datasets with Tissue 4D

syngo Tissue 4D facilitates the detection of tumors in organs such as the liver and the prostate. It is a task card for visualizing and post-processing dynamic contrast-enhanced 3D datasets.

The software allows the application of non-linear fitting with pharmacokinetic models and the creation of parameter maps as color-coded images. The exchange of contrast agents between blood and tissue is described by the following parameters:

- $K_{\text{trans}}$ (transfer constant)
- $V_e$ (extra-vascular extra-cellular volume fraction)
- $K_{\text{ep}}$ (reflux constant)

Pharmacokinetic modeling is performed pixel-by-pixel using a 2-compartment model. Calculation is based on the Tofts model.

The following example describes how to apply pharmacokinetic modeling to dynamic prostate MR examination data for the calculation of parameter images.

4.1.1 Preparing the data

Loading the data to Tissue 4D

- Dynamic series have been acquired with fixed flip angle
- Pre-contrast series with variable flip angle (i.e. 2°, 15°) are available for T1 map calculation
- Corresponding morphological images are available (recommended)

1. Select the study to be evaluated in the Patient Browser.
2. Click the icon to transfer the data to the Tissue 4D task card.

Pre-contrast data is displayed in the 1st segment. Dynamic data is displayed in the 2nd segment.
MPR images at the positions of the dynamic images are calculated from loaded morphological data. This icon allows toggling between the pre-contrast data (T1 maps) and the morphological view in the 1st segment.

Optimizing the image display
1. Use the **Auto Cine** function to get an overview of the loaded dynamic image data.
2. Activate this function if you want to exclude a certain point in time from subsequent evaluations.
3. Zoom and pan the images to display suspicious enhancing regions.
4. Window the images to optimize their contrast and brightness.

Performing motion correction
1. Select the 2nd segment and activate subtraction mode with the icon.
   The first volume (reference volume) is substracted. The results are displayed as magnitude images in the same segment.
2. Activate 4D scrolling with the icon.
3. Check for motion artifacts in the subtraction images by scrolling in time (move cursor left/right) and in slice direction (move cursor up/down).
4. If necessary, start motion correction with the icon on the **Motion Correction** subtask card.
   The currently displayed volume of the dynamic data is selected as reference for registration. Motion is corrected in all other volumes.

Registering pre-contrast and morphological data
The reference for registration of the data is a volume of the dynamic series at the currently displayed point in time.

Registering pre-contrast data
1. Open the **Registration** subtask card and select the **PreContrast** mode, if necessary.
In the 1st segment, the pre-contrast images are overlaid with dynamic images taking the slice positions into account. The reference volume is shown as colored images.

2 Use the blending slider to visually evaluate the registration quality of the pre-contrast data with the selected dynamic volume.

3 If necessary, adjust the registration with the icon.

Registering morphological data

1 Select the **Morphological** mode in the 2. **Registration** subtask card.

Fused MPR (three orthogonal MPRs) renderings of the morphological and the dynamic data are displayed in segments 1, 2, and 3. The reference volume is shown as colored images.

2 Use the blending slider to visually evaluate the registration quality of the morphological data with the selected dynamic volume.

3 If necessary, adjust the registration with the icon.

### 4.1.2 Evaluating the data

#### Calculating enhancement curves

Curve calculation is performed for up to 4 regions defined by ROIs in the dynamic images.

1 Open the 3. **Curve Calculation** subtask card.
2 Select **ROI1** in the **ROI Selection** list to set the color and the label of the first ROI.

3 Draw the ROI around the lesion in a subtraction image in the 2nd segment.

4 To define additional ROIs, select the corresponding ROI labels in the **ROI Selection** list and draw them in the subtraction image.

If you want to delete a selected ROI, press the **Delete** key on the keyboard.

Starting calculation

- Click the icon to plot the signal enhancement curves.

The calculation results for all defined ROIs are displayed in the 4th segment. The curves are shown as relative enhancement curves, the first volume serves as reference.
Preparing pharmacokinetic modeling

Calculating T1 maps
The T1 map masks define the areas to be adjusted for the pharmacokinetic fit. T1 fitting is restricted to pixels with values above a certain noise level value.

1 Open the 4. Pre Evaluation subtask card.
   The T1 map calculation runs automatically. Once the T1 map has been calculated, the pre-contrast data is replaced.

2 Change the threshold value for masking out noise in the Noise Level selection list, if necessary (default: 20).

3 Select the MR acquisition technique in the MR Protocol selection list (default: T1 + Dynamic).

   If T1 map is not available, dynamic 3D is chosen and an estimated value for T1 can be set.

Setting contrast agent parameters
The contrast agent parameters are used for the application of pharmacokinetic models.

1 Select the contrast agent applied in the Contrast Ag. selection list.
   Molarity, Relaxivity and Volume are automatically selected by the system as a function of the contrast agent entered.

   An application specialist can configure a list of preset contrast agents and assign contrast agent parameters.

2 Adapt the contrast agent parameters in the respective input fields, if necessary.

Defining the fitting volume
By defining a VOI, you restrict the application of pharmacokinetic modeling to a subvolume of the dynamic volume data.

1 Activate VOI drawing mode with the icon.
2 Draw an ellipse around the organ or around a subvolume in the 2nd segment enclosing the lesion. The ellipse is extended to form an ellipsoid in the 3D structure.

3 Scroll through the slices to ensure that the VOI covers the part of the volume relevant for modeling.

4 Modify the VOI, if necessary.

Applying pharmacokinetic modeling
Pharmacokinetic modeling can be applied for the mean curves or voxelwise for the selected ROI/VOI.

Fitting mean ROI curves
1 Open the 5. Evaluation subtask card and select an ROI in the Selector list (e.g. ROI1).

2 Select the pharmacokinetic model to be applied in the Model selection list.

Currently, the two-compartment Tofts model is provided.

3 Select the Model AIF function which provides the applicable information about the concentration of the contrast enhancing media in the blood plasma.

**Fast**: high temporal resolution, high kinetics.

**Intermediate**: moderate temporal resolution, moderate kinetics.

**Slow**: slow temporal resolution, slow kinetics.

4 Check the value in the Contrast Arrival Time field. Adjust the onset time of enhancement with the icon, if necessary.
5 Start pharmacokinetic modeling for mean ROI curves with the icon.

The fitting curve for the selected ROI label is displayed in the 4th segment.
Calculated parameter values for the exchange of contrast agent between blood and tissue are displayed top left in the diagram.

Fitting voxel by voxel

1 In the **Selector** list, select the VOI or the ROI whose parameters should be fitted.

2 Start pharmacokinetic modeling for all voxels of the VOI or ROI with the icon.

Parameter maps describing the contrast media kinetics are calculated for the selected VOI or ROI label. They are displayed as color-coded overlays of the morphological images in the 3rd segment.

Analyzing the results statistically

The parametric data of pharmacokinetic modeling are used to calculate frequency distributions (histograms) and mean values for the ROIs defined in the parameter images.

**Defining ROIs**

1 Open the **6. Results** subtask card.

2 In the **ROI Selection** list, select an already existing ROI (e.g. ROI1).
3 Click the icon to copy the ROI from the 2nd segment to the parameter image of the 3rd segment.

4 To define new ROIs, use the ROI drawing mode.

Displaying a histogram

- Click the icon to calculate the frequency distribution of parameter values inside the ROI.

The histogram is displayed in the 4th segment.

Displaying mean values

- Click the icon to calculate statistical data of parameter values inside the ROI.

The median, mean and standard deviation for the selected ROI are displayed bottom left in the 3rd segment.

4.1.3 Saving parametric data as ASCII files

1 Click the icon to save all parameter values from the 4th segment for the selected ROI.

The values of the Ktrans, Kep, Ve, Chi², FitCode, and iAUC parameters are written to a text file.

2 Click the icon to save the currently displayed curves for the selected ROI to a text file.
4.2 Spectroscopy evaluation

The following example describes some typical procedures in the course of prostate CSI data evaluation.

The evaluation of CSI data results in spectra from the voxels of interest in the CSI slice. The spectra provide information regarding the existence, distribution, and ratio of diagnostically relevant metabolites in the examination region. Spectroscopy evaluation also allows the creation of spectral maps for an overview of spectra of interest as well as displaying the CSI data as colored metabolite images.

⚠️ Caution

Selection of unsuitable evaluation parameters!

Artifacts in the spectrum (additional or covered lines)

- Ensure that interactive evaluations are handled by experts.

4.2.1 Preparing the data

Loading the data

✓ CSI data is available for evaluation

- Load the raw data into the Spectroscopy task card with the icon (double-click).

The reference images from the graphic slice positioning and the CSI slice are displayed. The raw data of a predefined voxel (blue) in the center of the CSI grid are automatically evaluated with the appropriate post-processing protocol. The resulting spectrum is shown together with the associated stamp reference images.
Changing the post-processing protocol

If a suitable protocol is not found, the program reads the standard protocol from the General folder.

1. To assign a different protocol, select **Protocols > Open**.
2. Open the protocol directory in the **Open Protocol** dialog window and select the desired post-processing protocol.
3. Select **Protocols > Keep Common** to evaluate all spectra with the same post-processing protocol.

Adjusting the reference image

The displayed reference image should show the anatomical region of interest.

1. Activate **Image > Auto Selection Mode**.
   - When scrolling through reference images, the most suitable CSI slice is selected.
2. Use the dog ear to look for the reference image that includes the anatomical region of interest.
3 To hide interfering graphics, open the Display Parameters dialog window with the icon and deselect the graphic objects in the Images tab card.

To only display the VOI and voxel for evaluation, hide Saturation regions, Slice intersections and CSI matrix grid.

4.2.2 Evaluating the data

Evaluating voxels of interest

1 Set the Single Dataset Mode with the icon.

2 Click the voxel of interest in the CSI slice.

The associated spectrum is displayed immediately.

(1) Example: spectrum of healthy prostate tissue (3 Tesla)

(2) Example: spectrum of pathological prostate tissue (3 Tesla)

To adjust the signal display, open the Display Parameters dialog window with the Signal > Display Parameters menu entry.
Changing the CSI slice

Instead of the currently displayed CSI slice, you can select another diagnostically relevant slice for evaluation within the CSI 3D slab.

1. Open the 3D CSI Selection dialog window with Postprocessing > 3D CSI Selection.

2. Set the Plane number of the desired CSI slice.
   The spectrum in the active segment is newly calculated. The matching reference image is displayed if Auto selection mode is activated.

3. If required, change the Main orientation of the slice.
   Voxel selection in the reference image remains unchanged.

Displaying spectral maps

The spectral map allows a quick and easy comparison of all spectra in one segment. Changes of choline/citrate ratios can easily be seen.

Spectral maps can be generated only if the reference image lies roughly in parallel to the CSI plane and the projection view includes a complete plane of the CSI grid.

Creating a spectral map

1. Select the segment that will be used for displaying the spectral map.

2. Open the Spectral Map dialog window with the icon in the control area.

3. Activate the Inside VOI option to calculate the spectral map for the entire VOI.
The spectral map is superposed on the reference image and displayed in the selected segment.

4 To improve the visibility of details, zoom and pan the spectral map.

With the **User defined** option, you can restrict the **Calculation region** to an area of interest.

### Enlarging the spectrum of a voxel

1. Select the segment that will be used for displaying the single spectrum.
2. Click the voxel that contains the relevant spectrum in the metabolite image.
   
   The spectrum is enlarged to segment size in the selected segment. The respective voxel in the metabolite image is highlighted in color.

### Displaying metabolite images

Metabolite images allow you to visualize the voxel-dependent intensities of a metabolite or the intensity ratios of two metabolites within the CSI slice.

### Creating intensity ratios of two metabolites

1. Select the segment that will be used for displaying the metabolite image.
2. Open the **Metabolite Image** dialog window with the icon in the control area.
3. Select the **Ratio of metabolites** checkbox to activate the intensity ratio calculation.
4 Enter the desired metabolites (e.g. Cho+Cr/Ci).

Choline and creatine can not be separated in prostate exams. Therefore, the sum of both is used for the calculation of the metabolite ratio with respect to citrate.

5 Generate the metabolite image with OK.

With the User defined option, you can restrict the Calculation region to an area of interest. This can be necessary, for example, to exclude interfering saturation regions.

The metabolite image is superposed on the reference image and displayed in the selected segment.

In this example, the metabolite image shows healthy and pathological tissue.

Metabolite images should be checked against the spectral map to ensure that the fitting process created reasonable values.

Displaying the intensity values

- Select the Peak info map checkbox in the Metabolite Image dialog window.
  
The numerical values of the metabolite intensity ratios are displayed in the image on top of the color shades.
Displaying a metabolite movie

1. Start the movie with the **Metabolite Movie** button in the **Metabolite Image** dialog window.

   The transparency of the overlaid CSI slice graphic is continuously increased and decreased again.

   At 0% transparency, the reference image cannot be seen under the colored regions of the CSI slice graphic. At 100% transparency, however, only the reference image is visible.

2. To stop playing the metabolite movie, click **Cancel** in the movie progress window displayed.

   ![Metabolite Movie Image]

   You can use the transparency slider in the **Metabolite Image** dialog window to set the transparency at a defined value.

4.2.3 Documenting the results

   Generating and saving a result table

   The result table shows the integrals of metabolites and metabolite ratios with respect to a reference metabolite.

   1. Select the segment for displaying the result table of the selected spectrum.

   2. Open the **Result Table Of Current Spectrum** dialog window with **Signal > Result Table**.

   ![Result Table Image]
3. Select the reference metabolite for computation of metabolite ratios.

4. To combine metabolite results, click **Combine**.

5. Select the **Store in text file** checkbox to save the table as a text file.

6. Display the result table in the selected segment with **OK**.

### Result Table of Current Spectrum

<table>
<thead>
<tr>
<th>Metabolite</th>
<th>Pos./ppm</th>
<th>Integral</th>
<th>Ratio</th>
</tr>
</thead>
<tbody>
<tr>
<td>NAA</td>
<td>2.00</td>
<td>7.38</td>
<td>1.83</td>
</tr>
<tr>
<td>Cr</td>
<td>3.03</td>
<td>4.03</td>
<td>1.00</td>
</tr>
<tr>
<td>Cho</td>
<td>3.22</td>
<td>3.03</td>
<td>0.75</td>
</tr>
<tr>
<td>NAA ddi</td>
<td>3.55</td>
<td>1.54</td>
<td>0.38</td>
</tr>
<tr>
<td>Cr2</td>
<td>3.93</td>
<td>1.42</td>
<td>0.35</td>
</tr>
<tr>
<td>NAA ddi</td>
<td>2.46</td>
<td>0.00</td>
<td>0.00</td>
</tr>
<tr>
<td>NAA ddi2</td>
<td>2.66</td>
<td>0.32</td>
<td>0.08</td>
</tr>
</tbody>
</table>

**Saving and filming the results**

1. Select the respective segment for saving or filming.

2. Save the results with the icon.

3. Transfer the result to the film sheet with **Patient > Copy to Film Sheet**.
Saving new post-processing protocol

You can save a changed post-processing protocol, e.g. changes due to phase correction, as a new protocol.

1. Open the **Save Protocol** dialog window with **Protocols > Save As**.
2. Select the directory of the new protocol and enter a suitable name.
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Manufacturer's note:

This product bears a CE marking in accordance with the provisions of regulation 93/42/EEC of June 14, 1993 for medical products.

The CE marking applies only to medico-technical products/medical products introduced in connection with the above-mentioned comprehensive EC regulation.

Global Business Unit
Siemens AG
Medical Solutions
Magnetic Resonance
Henkestr. 127
DE-91052 Erlangen
Germany
Phone: +49913184-0
www.siemens.com/healthcare