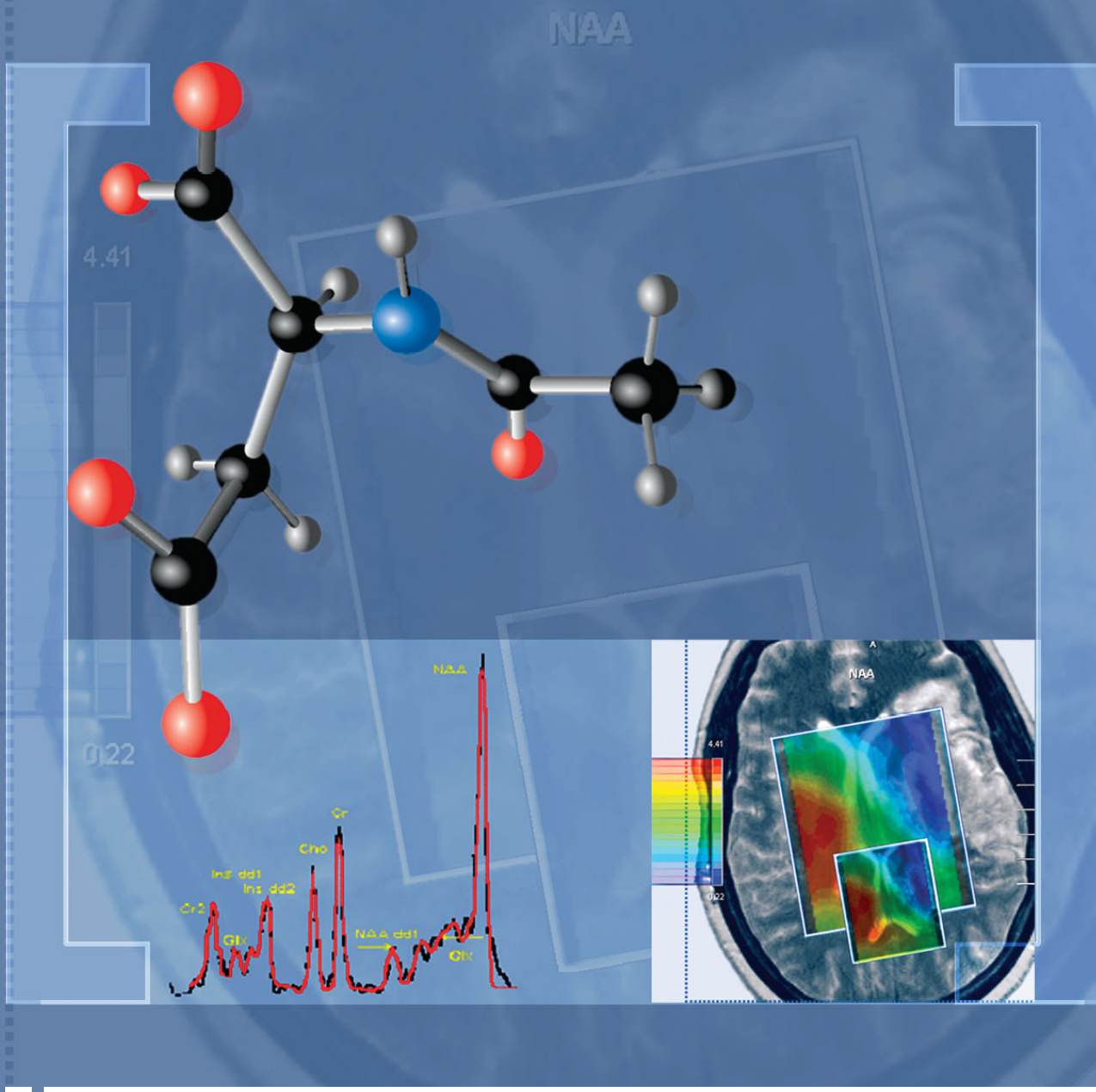


syngo MR D13

Basic Manual – Spectroscopy

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Manufacturer's note:

Products, that are bearing a CE mark fulfill the provisions of the Council Directive 93/42/EEC of 14 June 1993 concerning medical devices.

The CE mark applies exclusively to medical equipment and products that are released under the relevant EU guidelines mentioned above.

Table of Contents

A *Spectroscopy Basics*

A.1 Introduction to MR Spectroscopy

A.2 Techniques

A.3 Applications

B *Spectroscopy Measurements*

B.1 Licenses

B.2 Procedure for Spectroscopy Measurements

B.3 Preparing the Measurement

B.4 Preparing the Measurement Program

B.5 Reference Images

B.6 Graphic Display of Measurement Objects

B.7 Adapting the Parameters for an SVS Measurement

B.8 Adapting the Parameters for a CSI Measurement

B.9 Configuring Adjustments

B.10 Measuring

B.11 Interactive Adjustment

B.12 Performing Quality Assurance

B.13 Measurement Protocols

C *Spectroscopy Evaluation*

C.1 Spectroscopy Task Card

C.2 Loading Raw Data and Reference Images

C.3 Editing the Display of Reference Images

C.4 Editing the Display of the Spectrum

C.5 Evaluating Data Using a Different Protocol

C.6 Displaying Evaluation Results in Table Format

C.7 Evaluating CSI Data

C.8 Evaluating Data Interactively

C.9 Editing Peaks and Peak Lists

C.10 Saving and Documenting Results

C.11 Managing Post-processing Protocols

C.12 Exporting Raw Data

C.13 Ending a Spectroscopy Evaluation

C.14 Post-processing Protocols for ^{1}H MRS

Index

Notes on the Basic Manual

This documentation describes MR spectroscopy for software version ***syngo* MR D13**.

This Basic Manual includes a complete description of the optional **Spectroscopy** functionality associated with the software. In addition, the software also contains an Online Help package derived from the Operator Manual. A license is required for using the optional **Spectroscopy** functionality.

For questions, please contact the respective Siemens sales organization.

The changes and functionality enhancements compared to the previous version are described below.

Spectroscopy measurement

- ***syngo* GRACE at 3 T**
  ^{1}H SVS measurement protocols for breast spectroscopy to detect choline and a reference signal (internal or external).
- **prostate spectroscopy at 3 T**
  ^{1}H 3D CSI measurement protocols for prostate spectroscopy at 3 T.

Spectroscopy license

- **new license for 3D CSI measurements**

PART
A

Spectroscopy Basics

A.1 *Introduction to MR Spectroscopy*

The MRS experiment A.1–2

The most important atomic nuclei for MR Spectroscopy A.1–5

From MRS signal to spectrum A.1–7

Characteristics of a peak A.1–8

Chemical shift A.1–9

Fine Splitting of the Resonance Lines via J Coupling A.1–11

Spectral resolution A.1–13

The relative nuclear ratio A.1–14

Quantification of the MRS signals A.1–15

Signal-to-noise ratio (SNR) A.1–16

Important MRS Signals A.1–19

- The most important signals of ^{1}H MRS A.1–20
- The Most Important Signals of ^{31}P MRS A.1–23

Spectroscopy at 3 Tesla A.1–26

A.2 *Techniques*

Sequences A.2–1

- Spin echo sequence A.2–1
- STEAM sequence A.2–2
- Comparison of SE and STEAM sequences A.2–3

Suppressing the water signal A.2–3

Single Voxel Spectroscopy (SVS) A.2–4

- Echo times for SVS measurements A.2–5

Chemical Shift Imaging (CSI) A.2–6
Hybrid CSI technique A.2–6
Localization using phase-encoding A.2–10
Phase-encoding and Hamming filter A.2–18
Signal-to-noise ratio with phase-encoding A.2–21
Chemical shift artifact in Hybrid CSI A.2–22
Outer Volume Suppression (OVS) – CSI A.2–24
Saturation regions – SVS A.2–27
Spectral signal suppression A.2–27
Techniques with ^{31}P MRS A.2–27
Nuclear Overhauser Effect (NOE) A.2–28
Decoupling A.2–31

A.3 *Applications*

SVS technique applications A.3–1
^{1}H SVS measurement of the head A.3–1
^{1}H SVS measurement of the breast (syngo GRACE) A.3–2
CSI technique applications A.3–3
^{1}H Hybrid CSI measurement of the brain A.3–3
^{1}H Hybrid CSI measurement of the prostate A.3–4
^{31}P CSI measurement of muscle, heart, liver A.3–7

CHAPTER A.1

Introduction to MR Spectroscopy

MR Spectroscopy (MRS) determines the presence of specific chemical compounds selectively, non-invasively, and non-destructively. This makes MR spectroscopy an important method for *in-vitro* and *in-vivo* examinations of the cell metabolism of tissue and organs.

In healthy tissue, the metabolic products (metabolites) as determined with MR spectroscopy are present in concentrations characteristic of specific tissues. However, stress, functional disorders, or diseases may shift the concentration of metabolites. These changes in concentration may be displayed with MR spectroscopy.

Low sensitivity, caused by low concentration of metabolites, is characteristic of this method. Metabolite signals typically have intensities 10000 times lower than the water signal used for MR imaging. For this reason, signals are accumulated via repeated measurements, typically over several minutes.

MR spectroscopy is primarily used for evaluating the status of cell metabolism. This method is also suitable for monitoring slow reactions, e.g. the effects of therapy over a longer period of time.

The MRS experiment

As with MR imaging, MR spectroscopy is based on the magnetism of atomic nuclei.

Atomic nuclei in the magnetic field

Certain atomic nuclei possess a magnetic moment. In quantum mechanics, the magnetic moment of the nucleus is known as the “nuclear spin”.

The nuclear spins are aligned in an external magnetic field. Depending on the type of nucleus, each individual nuclear spin may be aligned differently. For example, there are only two types of alignment for protons. Without the effects of additional forces, nuclear spins prefer to align themselves in the orientation having the lower energy state.

Since magnetic resonance techniques detect a large number of spins collectively (i.e. the nuclei of a macroscopic specimen, magnitude 10^{23}), the individual alignments of the spins are never observed directly.

Deflection of the nuclear magnetization by the RF pulse

The overall magnetization observed is a directional variable (vector) that is aligned in parallel to the magnetic field in the absence of additional forces.

Within the scope of MR experiments, nuclear magnetization is deflected from this state of equilibrium. The deflection may be anti-parallel (inversion) or perpendicular to the external magnetic field. When returning to its state of equilibrium, the deflection may point to a continuum of intermediate direction. It is described according to the Bloch equations and does not require quantum mechanics.

Resonance frequency

Electromagnetic waves are used to deflect the magnetization from its state of equilibrium. The energy required, that is, the frequency of the waves, is different for each nucleus. It is determined by one of the characteristics of the nucleus, the gyromagnetic ratio γ, and by the strength of the magnetic field B_0 applied:

$$\omega_0 = \gamma B_0$$

Excitation is not possible if the Larmor frequency condition is not met. The nuclei in an MR probe precess at slightly different resonance frequencies 1) due to the unavoidable inhomogeneity of the B_0field and 2) due to the chemical shift. To stimulate as many nuclei of interest as possible, broadband excitation is selected by applying a short excitation pulse. The MR resonance frequencies are typically in the radio wave range. For example, the resonance frequency 63.6 MHz is obtained for protons at B_0= 1.5 T.

MRS signal

Radio frequency excitation aligns the nuclei such that there is a net magnetic moment perpendicular (transverse) to the main magnetic field. This moment precesses about the axis of the main field at the resonance (“Larmor”) frequency. Just as a rotating magnet creates an alternating current in the coil of a power generator, the rotating nuclear magnetization generates radio frequency signals in the MR receiving coil.

The radio waves are generated by nuclear magnetization components precessing across the main magnetic field (“transverse magnetization”) with resonance frequency (“Larmor frequency”). The frequency is detected using an antenna (“coil”).

The decay of the transverse magnetization and the MR signal takes place over several hundred milliseconds. The decay rate is quantitatively expressed as the relaxation time “T_2”.

Chemical shift

The spectroscopic MR experiment utilizes the effect that different chemical connections create different shielding of the main magnetic field at the location of the nucleus. For this reason, the same nuclear spins, e.g. protons, precess at different resonance frequencies in different chemical environments. This resonance frequency shift effect is termed *chemical shift*.

MR spectrum

The Fourier Transform of the acquired time signal creates a graph of its frequency components. This “MR line spectrum” is therefore interpreted as the weighted concentration of the nuclear spins precessing at a certain Larmor frequency (chemical shift).

In the most favorable case, a resonance line can be clearly associated with a metabolite. Under worst case conditions, the lines of several metabolites either overlap or cover one another. Frequently, a metabolic product contains several nuclei detectable by MR with different resonance frequencies. As a result, this metabolic product generates a multi-line spectrum.

Prerequisites: Homogeneous magnetic field

Good spectroscopic results require both an especially high homogeneity of the B_0 field across the specimen volume of interest (to avoid line widening due to field inhomogeneity) and a satisfactory separation of the metabolite signals.

For this reason, homogenization of the main magnetic field using relatively weak additional fields (called “shimming”) is especially important in MRS experiments.

Localizing the measured area

The spectroscopy sequences included in the attached documentation differ from the simple experiment described. They additionally allow for localizing the area to be measured within the coil volume.

The most important atomic nuclei for MR Spectroscopy

Magnetic spin

Atomic nuclei detectable with MR have to possess a magnetic spin. The overall nuclear spin comprises spins of the components of the nucleus, namely protons and neutrons. For a nucleus with an even number of protons and neutrons (i.e. an even atomic and mass number), the individual moments cancel out. These types of nuclei are not detectable with MR.

The magnitude of the magnetic spin is directly proportional to the gyromagnetic ratio which in turn determines the Larmor frequency at a specific magnetic field strength.

The Larmor frequencies for 1.5 T and 3.0 T are shown in the table below. As the Larmor frequencies change with the magnetic field strength, the frequency of other field strengths can be determined by performing a simple calculation.

Spin quantum number

The alignment possibilities of the magnetic nuclear spin in the magnetic field and the number of possible states of energy are characterized by the spin quantum number I. The value of I may be zero or a multiple of ½. The number of energy states is computed as (2I+1).

The spin quantum number of hydrogen nuclei (protons) is I = ½, resulting in two energy states.

Atomic nuclei with I = ½ result in narrow lines. At higher spin quantum numbers, broader signals are generated.

Sensitivity

MRS experiments are used to determine metabolite concentrations. The sensitivity of the measurement depends on two factors:

- ❏ the natural isotopic abundance of the MR active nucleus
- ❏ a sensitivity specific to the nucleus determined by the magnetic moment (here, specified relative to the sensitivity of protons.)

Isotope table

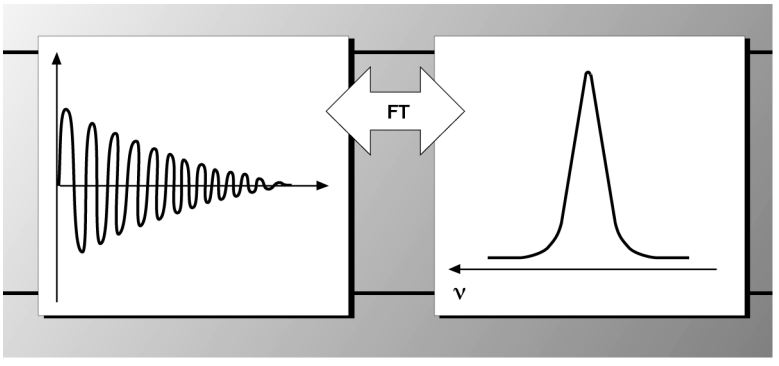
The following table list the atomic nuclei for MR spectroscopy that are supported by the system, including important MR-relevant properties.

Isotope	Number of spin quanta I	Larmor frequency at 1.5 T [MHz]	Larmor frequency at 3 T [MHz]	Natural abundance [%]	Absolute sensitivity [%]
^{1}H	1/2	63.6	123.2	99.9	100
^{3}He	1/2	48.5	93.9	0.0001	0.00006
^{7}Li	3/2	24.7	47.9	92.6	27
^{13}C	1/2	16.0	31.0	1.1	0.017
^{17}O	5/2	–	16.7	0.04	0.001
^{19}F	1/2	59.8	115.9	100	83
^{23}Na	3/2	16.9	32.6	100	9.3
^{31}P	1/2	25.7	49.9	100	6.6
^{129}Xe	1/2	17.6	34.1	26.2	0.56

➪ The absolute sensitivity corresponds to the product: relative sensitivity x natural abundance.

From MRS signal to spectrum

In MR spectroscopy, the MR signal is measured as a function of time. The signal is a rapidly decaying high-frequency oscillation. Via Fourier Transformation (FT), this oscillation is displayed as a plot of frequency components, the so-called spectrum.

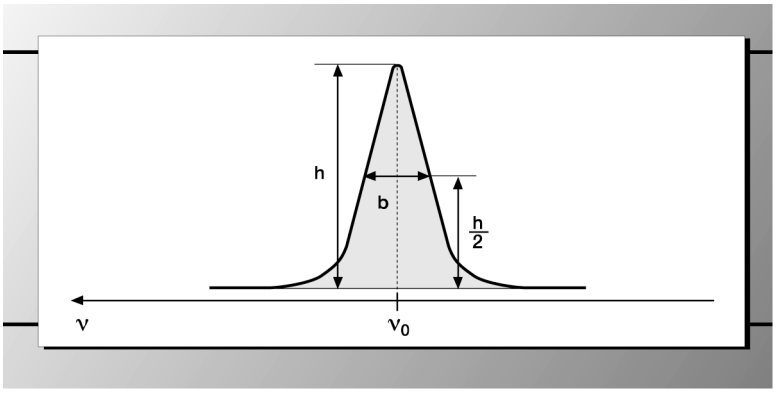


Time representation (MR signal) Frequency representation (spectrum)

➪ The high-frequency oscillation is shown in the time domain, the frequency components are shown in the frequency domain.

Characteristics of a peak

Theoretically, the frequency display of a pure oscillation is a spectral line in place of the resonance frequency ν_0. In reality, however, the time limit for data acquisition and the signal decay caused by T_2^* change the line into a broadened peak.



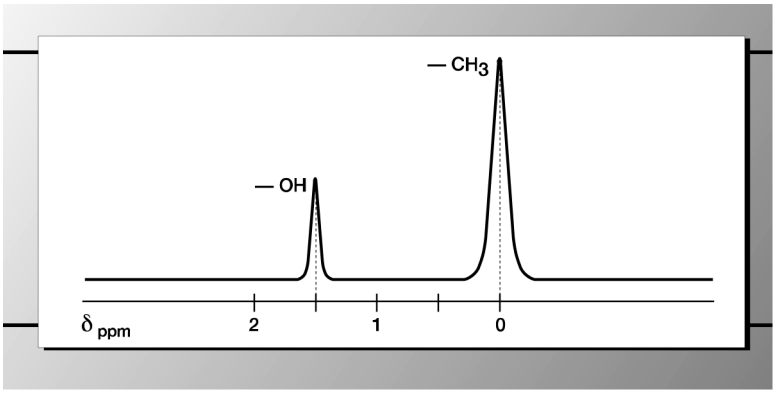
A peak is characterized by:

- ❏ the resonance frequency (ν_0)
- ❏ the height of the peak (*h*) (amplitude)
- ❏ full width of peak at half maximum (*b*) (Full Width Half Maximum, FWHM)
- ❏ the area contained in it (integral)

The spectral display for MR shows the frequency axis from right to left (ν).

Chemical shift

In different chemical connections, the atomic nuclei under examination are shielded at different levels by the electronic envelope surrounding them. Due to the different resonance frequencies, signals of the same nuclei, as e.g. protons which are bonded to different elements or molecular components, appear at different positions within the MR spectrum. As a result, molecular components as well as entire molecules or substance classes can be differentiated as well as identified.



Dependence on the magnetic field strength

Quantitatively, the shift in resonance frequency caused by shielding σ can be expressed as:

$$\omega = (1 - \sigma)\, \gamma\, B_0$$

As can be seen, the frequency shift increases with the field strength. To compare spectra measured on different systems, the frequency shift is defined relative to a reference signal with a known frequency shift:

$$\delta - \delta_{ref} = (\omega_{ref} - \omega)\, 10^6 / \omega_{ref}$$

By dividing with the reference frequency, the dependency of the chemical shift on the magnetic field strength is eliminated. In other words, each spectral peak is then expressed as a shift in parts per million from the reference signal, thus standardizing the chemical shift axis.

By convention, the spectral axis measures the shielding:

- ❏ Signals from nuclei with weaker shielding and higher resonance frequency are located to the left.
- ❏ Signals from nuclei with stronger shielding and lower resonance frequencies are located to the right.

As compared to the reference frequency, chemical shifts are usually so small that the number δ is expressed in parts per million (ppm).

Point of Origin

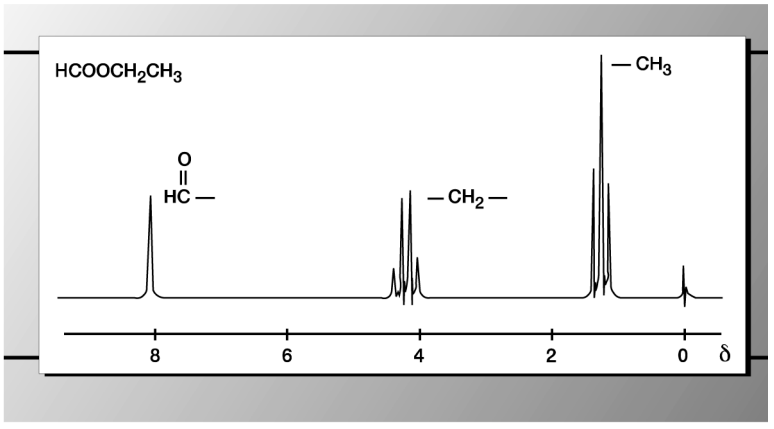
In analytical chemistry, the point of origin of the chemical shift is determined on a signal of a standard (in ^{1}H and ^{13}C spectra, the signal of Tetramethylsilane).

However, this substance is not observed in *in-vivo* spectroscopy. In this case, the origin of the spectral axis is defined by assigning a δ-value (in ppm) for a peak that is visible. Subsequently, a check is made to determine if this reference signal appears at the expected location.

When the water signal is used for this purpose, its dependence on the temperature is considered: At room temperature the chemical shift of the water signal is 4.9 ppm, at body temperature, 4.7 ppm. For other metabolites detected via proton spectroscopy, the dependency of the chemical shift on the temperature is negligible.

Fine Splitting of the Resonance Lines via J Coupling

Reciprocal effects between the nuclei may lead to a split in energy level. The spectrum shows multiplet lines. In the case of *in vivo* proton spectroscopy at 1.5 T, the spectral resolution may not suffice to display fine structures. However, when using phantoms highly suitable for shimming, the resolution of fine structures reaches a satisfactory level.



For nuclei with half-integer spin quantum numbers in the liquid phase, the intra-molecular, scalar J coupling is the dominant reciprocal spin-spin effect. As compared to the chemical shift, J coupling does not depend on the strength of the external magnetic field.

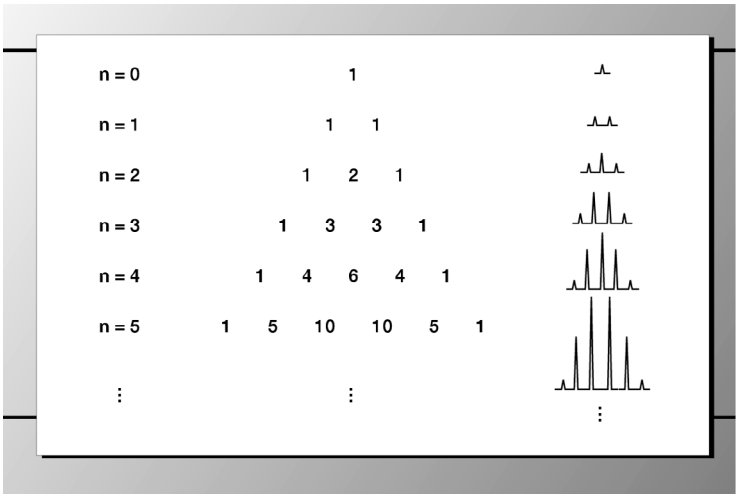
Coupling constant J

A measure of the strength of coupling is the coupling constant J expressed in Hz. A distinction between weak and strong coupling is made. In the case of weak coupling, J is at least one order of magnitude smaller than the chemical shift, expressed in Hz, of the coupled nuclei.

Since coupling constant J is independent from B_0, while the difference in chemical shift in Hz between two nuclei is not, the condition of weak coupling at higher fields is met. This can simplify the spectra, if the difference between the chemical shifts is only slightly greater than J.

Weak coupling

In the case of weak coupling, the rather simple rules for multiplicity and intensity ratios apply. The relative line intensities of doublets, triplets, quartets etc. act like binomial coefficients and can be read as Pascal's triangle.



Strong coupling

Strong coupling shows more lines than expected with weak coupling. The intensity distribution in signal groups changes as well.

TE echo time

The echo time considerably affects the coupling behavior and, as a result, the fine structure of the spectrum. An echo time should be selected that allows for a phase-coherent superposition of the multiplet signals. Otherwise, signal portions will be cancelled out.

Select an echo time that is an integer multiple of the reciprocal value of the corresponding coupling constant. For lactate where J = 7.3 Hz, select either 136 ms or 272 ms.

Recent measurements have yielded a coupling constant of J = 6.9 Hz, 1/J = 144 ms for the lactate doublet.

Spectral resolution

In addition to the dependency of the spectral resolution on the magnetic field strength, the resolution is additionally limited by the field homogeneity that can be achieved across the measurement volume. Quantitatively, the homogeneity determines the T_2^* decay of the time signal or the line width of the spectral signals. Occasionally, the spectral resolution at B_0 = 1.5 T is not sufficient, e.g. for complete resolution of the lactate doublet.

Susceptibility effects that widen the lines and reduce the T_2^* increase with magnetic field strength B_0 and present a greater problem with higher fields.

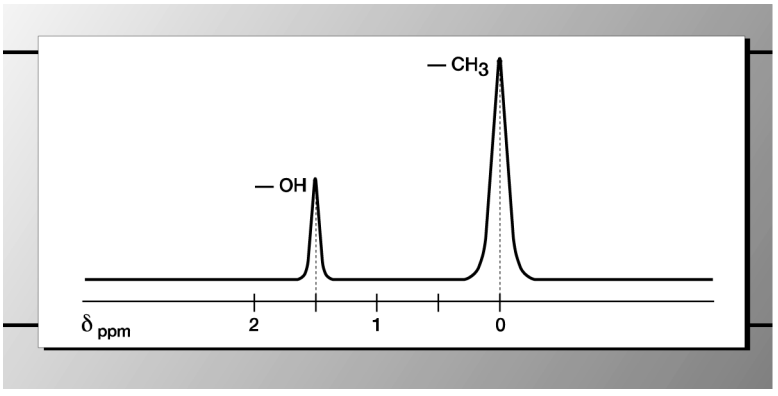
Besides technical factors, the ability to resolve metabolite signals is ultimately limited by the mobility of the molecules.

- ❏ Small molecules in solutions provide narrow, well-defined signals.
- ❏ Macromolecules, or molecules that are bound to membranes result in broadened signals.

The relative nuclear ratio

The integral under an NMR signal is proportional to the number of nuclei contributing to the signal.

The above is demonstrated by way of example using the ^{1}H spectrum of methanol. The protons of the methyl groups (CH_3) provide a signal with an area three times larger than the protons of the hydroxyl groups (OH).



Peak integration allows you to estimate the relative nuclear ratio (the relative proton ratio in the example shown) from the spectrum.

Quantification of the MRS signals

For spectral quantification, the **peak area** variable (integral) is preferred over the **peak amplitude** variable, because the area is independent of the field inhomogeneity and less sensitive to noise.

Absolute quantification

Absolute quantification of the spectra, i.e. interpretation of the peak areas as metabolite concentrations is not easy. Simple calibration of peak areas using phantom solutions of known concentration is made especially difficult by the fact that the sensitivity of the coil changes with the coil load.

Moreover, the T_2 dependency of the metabolite signals would have to be taken into account for absolute quantification.

Simple assignment of the peak area to a metabolite concentration is also hindered by the possibility that signals may overlap and that metabolite pools do not contribute to the signal because of their low mobility.

Relative signal intensities

For this reason, relative signal intensities are used for comparing spectra. Using relative signal intensities, spectra measured in both healthy and pathological tissue may be compared.

If it is possible to assume that the pathology is not going to affect the peak (e.g. creatine), ratios of the integrals (e.g. lactate/creatine area ratio) allow for comparison between patients.

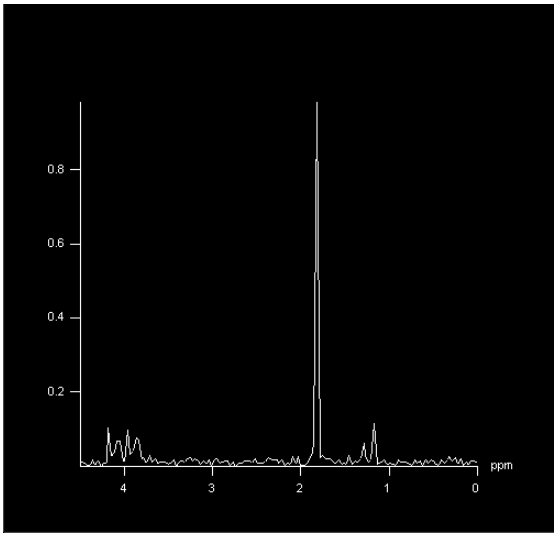
Signal-to-noise ratio (SNR)

The spectrum quality is largely determined by the signal-to-noise ratio (SNR). As a user you can decide on the trade off between the SNR achieved in relation to the time or spatial resolution of the experiment.

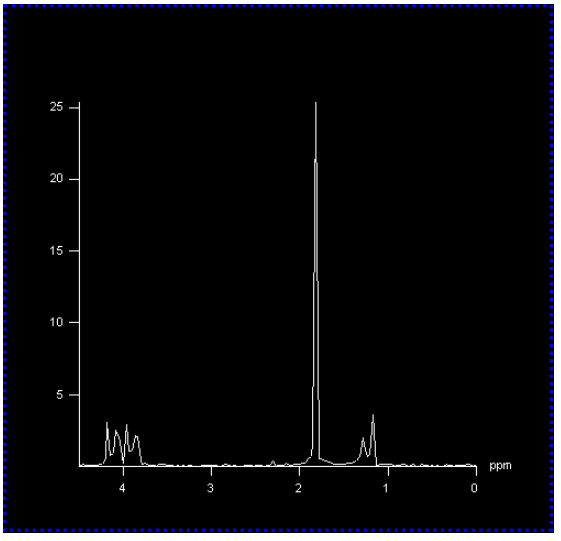
Averaging

Since noise adds incoherently, while signals add coherently, the signal-to-noise ratio (SNR) increases through averaging.

During non-correlated noise, the SNR increases with the square root of the number of acquisitions. Multiplying the number of acquisitions by 4 results in double the signal-to-noise ratio SNR. The temporal resolution of the experiment decreases.



Phantom measurement with 2 averagings



Phantom measurement with 64 averagings (the gain in SNR is 5.8)

For a typical *in-vivo* ^{1}H measurement, for example, 256 acquisitions are generated at a repetition time of TR = 1.5 s. This results in a total measurement duration of approximately 6 minutes. The repetition time is a decisive factor because it defines the equilibrium magnetization determining the signal.

Optimal repetition time

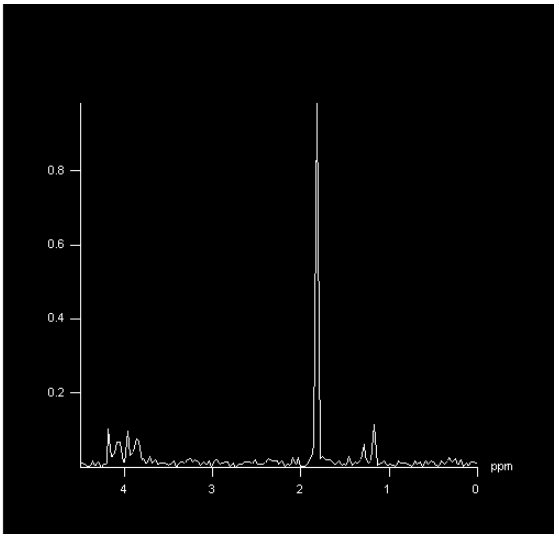
Longer repetition times permit greater longitudinal relaxation (determined by the relaxation time T_1) and yield a higher equilibrium magnetization. An optimum SNR per unit of measurement time is obtained if the repetition time approximately corresponds to the T_1 values of the metabolites to be examined. In ^{1}H spectroscopy, a TR of approximately 1.5 s proved to be an optimum value in this respect.

- ^{31}P signals might have significantly longer T1 values in the range of a few seconds. Instead of prolonging TR, an optimal SNR can also be obtained by setting an optimal excitation angle smaller than 90 degrees (Ernst angle).

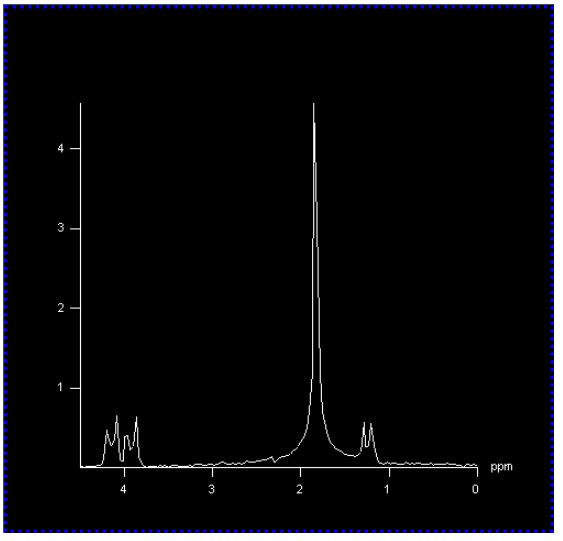
Increasing the specimen volume

The greater the measurement volume, the more nuclei can be excited, producing higher SNR.

However, this gain in SNR degrades spatial resolution. The line width increases as well.



Phantom measurement with a voxel size of 20×20×20 mm



Phantom measurement with a voxel size of 40×40×40 mm (the gain in SNR is 8)

Important MRS Signals

The following tables provide an overview of the most important signals of *in-vivo* proton and phosphorous spectroscopy. These signals are characterized as follows:

Metabolite

The **Metabolite** column includes the name of the chemical compound (the abbreviation is provided in brackets).

The color image shows a model of its chemical structure. The various types of atoms are color-coded:

- ❏ Carbon - black
- ❏ Hydrogen - white
- ❏ Oxygen - red
- ❏ Nitrogen - blue
- ❏ Sulfur - yellow
- ❏ Phosphorous - green

Signals

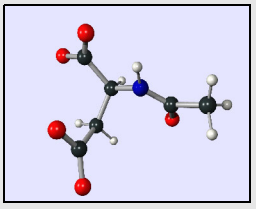
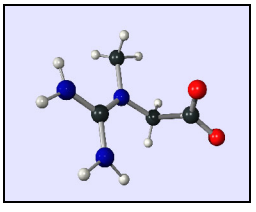
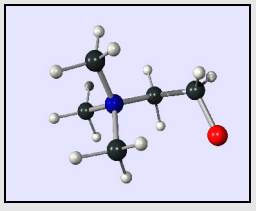
The **Signals** column lists the characteristic values of the signals allocated to the metabolite:

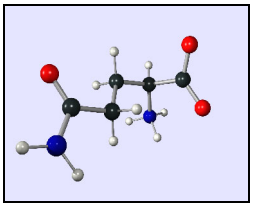
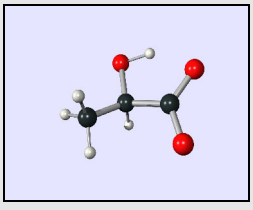
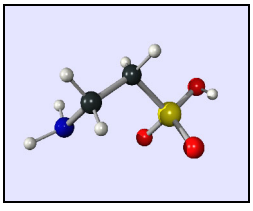
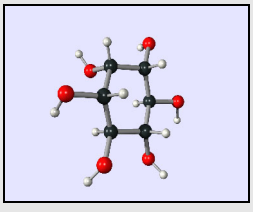
- ❏ Chemical shift in parts per million [ppm]
- ❏ Group name of the nucleus producing the signal
- ❏ Fine splitting
  (s = singlet, d = doublet, t = triplet, q = quadruplet, dd = doublet of the doublet, m = multiplet) An asterisk indicates strongly coupled signals that generally can only be detected with short echo times.
- ❏ Coupling constants in Hertz [Hz]

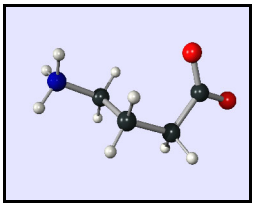
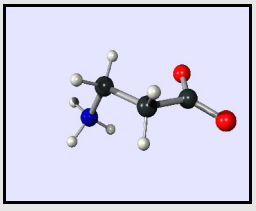
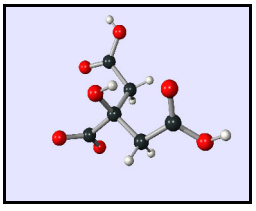
Comment

The **Comment** column lists important information about the metabolite, e.g. regarding its biochemical function. Please note that the functions of MR active metabolites are subject to continuous research. As a result, it is not possible to provide definitive and complete information.

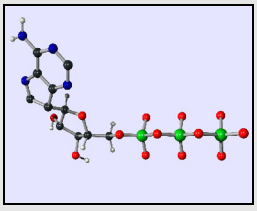
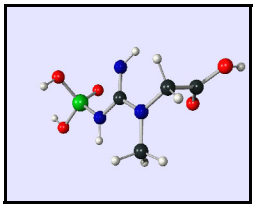
The most important signals of ^1H MRS

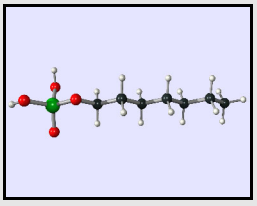
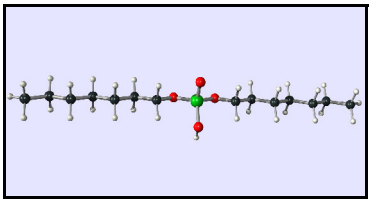
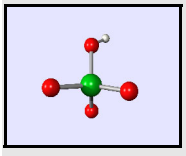
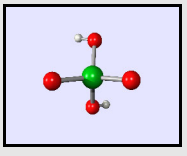
Metabolite	Signals	Comment
N-Acetylaspartate (NAA) 	2.02, CH_3, s, -- 2.52, CH_2, dd, 3.7 2.70; CH_2; dd*; 9.8, 15.9 4.40, CH, dd, 3.7, 9.8	NAA is often cited as a phenomenological indicator for the functionality of neuronal tissue. A decrease in NAA signal is frequently observed in tumors.
Creatine (Cr), phosphocreatine (PCr), other creatine compounds 	3.93, CH_2, s, -- 3.04, CH_3, s, --	When converting the high-energy compound ATP from ADP, PCr is converted to Cr. In brain tissue the signal intensity remains largely constant even in case of pathological changes. However, isolated cases of creatine deficiency may occur in children.
Choline (Cho), choline compounds 	3.24, CH_3, s, -- 3.56, CH_2, t. 7.0 4.07, CH_2, t. 7.0	Choline compounds are present, for example, in the cell membrane and in the synaptic ends of cholinergic neurons. They are part of the lipid metabolism. Increased choline concentrations may mark tumor tissue or multiple sclerosis plaques.

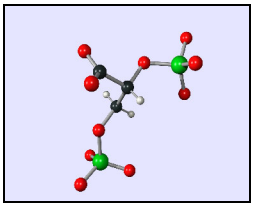
Metabolite	Signals	Comment
Glutamate (Glu), Glutamine (Gln) 	3.76; Glu, CH; dd; 7.3, 4.9 3.78; Gln, CH; t; -- 2.36, Glu, CH_2, m*, -- 2.46, Gln, CH_2, m*, -- 2.10, Glu, CH_2, m*, -- 2.14, Gln, CH_2, m*, --	Glu is a neurotransmitter, Gln a regulator of the Glu metabolism. It is hardly possible to detect the signals separately. As a result, the combined signals are often labeled “Glx.”
Lactate (Lac) 	4.12, CH, q, 7.3 1.33, CH_3, d, 7.3	Lactate plays an important role in the assessment of ischemic tissue and tumors as the final product of the anaerobic glycolysis cycle.
Taurine (Tau) 	3.44, SCH_2, t*, 6.7 3.27, NCH_2, t, 6.7	Cell examinations indicate taurine synthesis in astrocytes.
Myo-inositol (Ins) 	3.54; CH; dd*; 2.7, 9.9 4.06, CH, t*, 3.0 3.62; CH; dd*; 9.8, 9.8 3.28, CH, t*, 9.2	Ins marks glia cells in brain tissue.

Metabolite	Signals	Comment
γ amino butyrate (GABA) 	2.25, CH_2, m*, -- 3.00, CH_2, m*, --	GABA is an inhibitory neurotransmitter.
Alanine (Ala) 	3.78, CH, q, -- 1.48, CH_3, d, 7.3	Increased Ala concentrations have been found in meningioma.
Citrate 	2.60, CH_2, dd, --	Citrate is an important metabolic product of the tricarboxolic acid cycle in the mitochondria of living cells. Intracellular citrate concentrations are low. Citrate can be detected as a secretion product in a normal prostate. A missing citrate signal in prostate tissue might indicate a carcinoma.

The Most Important Signals of ^{31}P MRS

Metabolite	Signals	Comment
Adenosine triphosphate (ATP) 	-2.7; γ-ATP; d; -- -7.8; α-ATP; d; -- -16.5; β-ATP; t; --	ATP is the most important energy carrier in all living systems. In a ^{31}P spectrum, the resolution of α-, β and γ of ATP phosphate groups is excellent. The resonances of ADP overlap the γ and α signals of ATP.
Phosphocreatine (PCr) 	0; PCr; s; --	Phosphocreatine is the most important storage molecule for chemical energy in muscle tissue. It can rapidly transmit its high-energy phosphate group to ADP. Phosphocreatine is not present in the liver. A PCr signal in the liver is therefore indicative of pathological changes. Phosphocreatine is used as internal reference for the scale of the chemical shift.

Metabolite	Signals	Comment
Phosphomonoester (PME) 	6 - 2, PMe, variable, --	PME are characteristic components of the cellular membrane. Only minute amounts occur elsewhere in the cell. For tumors, increased PME concentrations can be determined frequently.
Phosphodiester (PDE) 	2 -0; PDE; variable; --	PDE are characteristic components of the cellular membrane. They are only present in very small quantities in other parts of the cell.
Inorganic phosphate (P_i)  	5.0 (depend. on pH value); P_i; s; --	Inorganic phosphate exists in two forms $H_2PO_4^-$ and HPO_4^{2-} in the physiological pH range. Both forms are in a pH dependent equilibrium via a dissociation reaction. As a result, instead of two separate peaks for $H_2PO_4^-$ and HPO_4^{2-}, only one sharp pH-dependent peak is generated whose chemical shift is dependent on the concentration of both molecules. The location of the inorganic phosphate signal depends on the pH value (with increasing pH value, the chemical shift decreases). Using the chemical shift of the P_i signal as compared to the PCr resonance, the pH value can be determined in a non-invasive manner.

Metabolite	Signals	Comment
2,3-Diphosphoglycerate (DPG) 	5.6; 2-DPG 6.7; 3-DPG	2,3-DPG is present in large quantities in the red blood cells (erythrocytes). This molecule has an important support function in the transport of oxygen via hemoglobin. The signal consists of a multiplet structure. The structure is simplified to two lines during proton decoupling with resonances at 5.6 and 6.7 ppm. During *in vivo* spectroscopy of the myocardium, large DPG peaks are typically obtained through contamination with ventricular blood. As a result, these broad DPG lines overlap the P_i and PME peaks.

Spectroscopy at 3 Tesla

The MAGNETOM Skyra and MAGNETOM Verio allow for MR spectroscopy at 3 Tesla. These systems provide a better signal-to-noise ratio and a greater spectral resolution than 1.5 T systems.

As a result, 3 Tmeasurements enable detection of metabolites in smaller concentrations. In addition, measurement times can be reduced, and a more accurate quantification is possible.

In addition to these advantages, there are also several disadvantages which are described below.

Signal-to-noise ratio (SNR)

Due to the magnetic field increase from 1.5T to 3T, both the magnetization of the specimen and the induced signal increase; however, the noise increases as well.

If the influences on the signal from T1 and T2 effects are not taken into consideration, the following applies:

$S \sim \omega_0^2$
$R \sim \omega_0$
$SNR \sim \omega_0$

Theoretically, the SNR at 3T is double the SNR at 1.5T.

Chemical shift and spectral resolution

The chemical shift in Hz increases in proportion to the magnetic field strength, providing for a better separation of the singlet signals in the spectrum. The multiplet signals of nuclei with strong J-coupling are simplified.
→ Page A.1–9, *Chemical shift*

One negative effect of the increased magnetic field strength involves an undesirable increase in line width caused by the increased spin-spin relaxation and magnetic field inhomogeneities in tissue.
→ Page A.1–27, *Susceptibility effects*

In many cases, the influence of the chemical shift outweighs the negative effects, and an overall improved better spectral resolution can be observed.

Chemical shift artifact

The increased chemical shift at 3 T also results in a correspondingly large chemical shift artifact.
→ Page A.2–22, *Chemical shift artifact in Hybrid CSI*

You can minimize this artifact by specifying a delta frequency or through Outer Volume Suppression.
→ Page A.2–22, *Delta frequency*
→ Page A.2–24, *Outer Volume Suppression (OVS) – CSI*

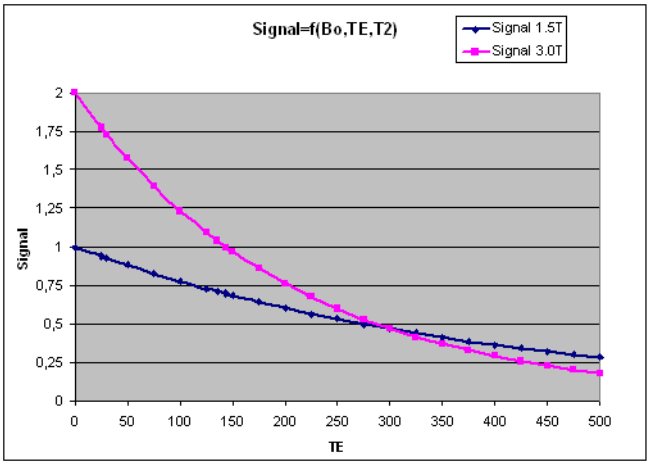
Susceptibility effects

If matter is introduced to a magnetic field, the magnetic induction B in the matter changes as compared with B_0 outside the magnetic field. Susceptibility describes the ability of a substance to influence the strength of an external magnetic field. Changes in susceptibility during the transition from one tissue to another lead to changes in the magnetic field and compromise field homogeneity. The lines in the spectrum grow wider and, in extreme cases, result in signal loss. This effect is particularly strong at the borders between tissue/air and grows more pronounced at increasing magnetic field strengths.

Short T2 relaxation time

Since spin-spin interactions increase with higher magnetic field strengths, T2 times are reduced accordingly. The signal decays faster with an increased echo time for a 3 T acquisition than for a 1.5 T acquisition.

The following figure shows the theoretical signal strength for choline at 1.5 T and 3 T as a function of the echo time. The T2 time at 1.5 T is 330 ms, and at 3T, 187 ms.



To take advantage of the stronger signal at 3T, select short echo times.

The T1 relaxation times for the important metabolites do not show a significant dependency on the magnetic field strength.

High RF power

The required RF power is proportional to the square of the Larmor frequency. This places great demands on the RF amplifier, coils, and cables.

As a result, the RF load for the patient increases as well. However, the SAR threshold values are not reached during ^{1}H spectroscopy (3 T). In the future, however, it is possible that the permissible threshold values may be reached during measurements of nuclei other than ^{1}H (e.g. ^{31}P with proton decoupling). The SAR is therefore the limiting factor for TR during these measurements.

RF penetration

Reduced RF penetration depths and dielectrical properties, possibly resulting in standing waves, change the local field strengths of the RF field should the magnetic field strength increase. This should be considered especially during measurements of the torso.

Summary

The following table provides a short overview of possible effects during 3 T measurements as well as appropriate corrective actions.

Effect	Corrective step
Chemical shift artifact	Suppression through delta frequency or Outer Volume Suppression.
Susceptibility effects	Do not position the VOI in the vicinity of air-filled cavities. If possible, reduce the VOI.
Short T2 time	Select short echo times.
Short T2* time (magnetic field inhomogeneities)	Increase filtering during post-processing (smaller filter widths).
RF power	No action required.
RF penetration	Only compare metabolic ratios between different voxels; do not directly compare integral values.

CHAPTER A.2

Techniques

You may use one of two methods for spectroscopy examinations with ***syngo* MR**:

- **Single Voxel Spectroscopy (SVS)**
- **Chemical Shift Imaging (CSI)**

These methods differ in their localization properties:

- With an SVS measurement, you acquire the MR spectrum of a small volume of interest (VOI).
- With a CSI measurement, you acquire several spectra arranged in a matrix in the volume of interest (VOI).

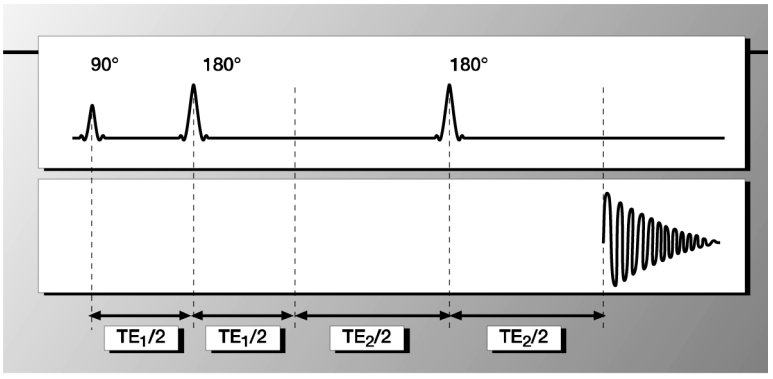
Sequences

SVS techniques as well as CSI techniques currently use sequences that are based on spin echoes (**SE**) or stimulated echoes (**STEAM**).

Spin echo sequence

With a spin echo sequence (**SE**), a slice-selective 90° pulse is followed by two slice-selective 180° pulses.

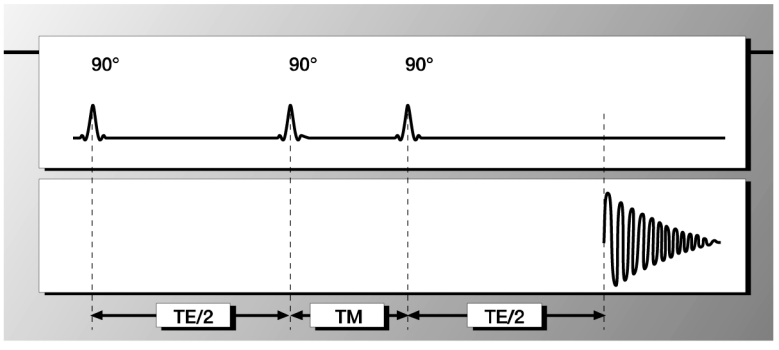
After excitation by a 90° pulse, magnetization will remain in the x-y plane up to data acquisition.



STEAM sequence

A stimulated echo is generated using the **STEAM** sequence (Stimulated Echo Acquisition Method).

Three slice-selective 90° pulses are used. The first pulse flips the magnetization into the xy plane. The second pulse flips part of the magnetization back into the Z direction. The remaining transverse magnetization decays during the medium time interval TM and therefore does not contribute to the signal (signal loss as compared to the SE method). The third pulse flips the magnetization back into the xy plane. After a defined time TE/2, the stimulated echo signal is measured.



During the time interval TM, the longitudinal magnetization is subject to T_1 relaxation. This means TM has to be short compared to the T_1 constants of the metabolites of interest to keep signal loss due to T_1 effects as low as possible.

Comparison of SE and STEAM sequences

SE

Advantages of **SE** sequences over **STEAM** sequences:

- ❏ The signal-to-noise ratio is improved by a factor of 2.
- ❏ The SE sequence is less sensitive to diffusion.

STEAM

Advantages of **STEAM** sequences over **SE** sequences:

- ❏ You can measure with shorter echo times.
- ❏ The STEAM sequence places lower demands on the RF system when generating RF pulses.
- ❏ Signal modulations are lower via J coupling than with SE sequences.

Suppressing the water signal

Water *in-vivo* has a 10 000 times higher concentration than the metabolites of interest. For this reason, it is necessary to suppress the water signal. The method most frequently used in clinical MR spectroscopy is selective excitation and dephasing of the water signal prior to the actual spectroscopy experiment (CHESS water suppression; CHESS = Chemical Shift Selective Suppression).

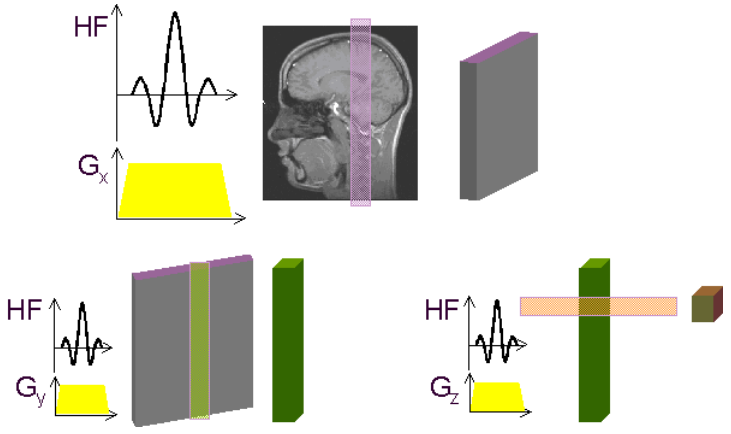
The amplitude of the water suppression pulse has to be adjusted correctly.

→ Page B.9–3, *Water suppression adjustment*
→ Page B.11–20, *Manual water suppression*

Single Voxel Spectroscopy (SVS)

For localization three mutually orthogonal slices are stimulated sequentially.

The VOI is the result of the intersection of the three slices. Only the spins in this voxel are measured.



The voxel edge length for SVS measurements ranges from 5 mm to 40 mm for the SE technique and from 10 mm to 40 mm for the STEAM technique.

The measurement time is based on the repetition time and the number of acquisitions: 256 acquisitions with a repetition time TR of 1.5 s would result in a measurement time of 6.4 min.

The measurement result is a single spectrum.

Echo times for SVS measurements

With echo times of approx. 135 ms and longer, ^{1}H MRS spectroscopy detects singlet signals of creatine, NAA, and choline in the healthy brain.

Shorter echo times permit display of additional metabolites such as myo-inositol and glutamine/glutamate. However, the broadened lines of macromolecules are also visible. It is therefore more difficult to interpret the spectrum with short echo times.

The detection of lactate is very important in clinical spectroscopy. In the healthy brain, lactate concentrations are near the limit of detectability, whereas in pathological ^{1}H spectra, lactate occurs frequently.

Depending on the echo time selected, the doublet signal of lactate at 1.33 ppm appears in phase or out-of-phase with the other singlet signals, or is eliminated altogether. Extremes occur if the echo time is an integer multiple of the reciprocal value of the coupling constant of 7.3 Hz. In addition, the lactate signal behavior depends on the detection method *(Ernst and Hennig, Magn. Reson. Med., 21, pp.82-96, 1991*).

With short echo times (TE < 50 ms), the lactate signal from the spin echo and the STEAM technique (with TM = 10 ms) is detected as an in-phase signal. With a medium echo time of TE = 135 ms, the signal appears inverted with the spin-echo technique, whereas in the STEAM technique (with TM = 10 ms) the signal is in-phase. With a long echo time of TE = 270 ms, both the spin-echo and the STEAM techniques exhibit an in-phase signal again.

Chemical Shift Imaging (CSI)

Using a readout gradient, imaging sequences obtain information about one spatial direction during signal acquisition. CSI sequences, on the other hand, scan the spectrum during signal acquisition.

Spatial directions are encoded in CSI sequences via phase-encoding gradients prior to read-out. These are varied as the experiment is repeated (phase-encoding tables). For a 2D-CSI measurement, two phase-encoding tables are required, for 3D-CSI measurement, three phase-encoding tables are required.

For evaluation of the CSI data, Fourier Transformations are performed over the spatial axes in addition to the Fourier Transformation for calculating the spectrum. The result of a CSI measurement is a spectral matrix.

Spectroscopy proton examinations using the CSI technique require installation of the “2D Spectroscopy CSI” and “Higher Order Shim Channels” options on your MR system. Additionally, for prostate examinations and 3D CSI examinations, the “3D Spectroscopy CSI” license is required.

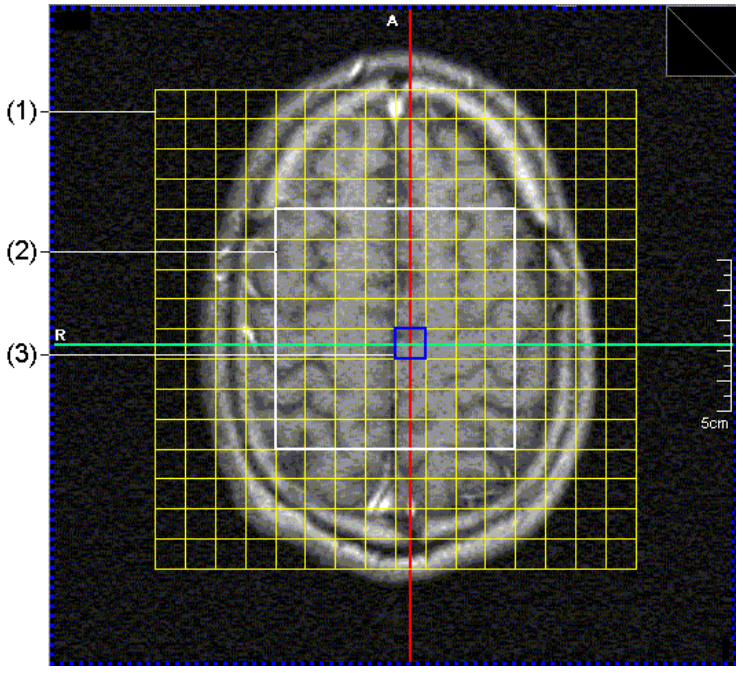
Hybrid CSI technique

By including phase-encoding tables in a SVS sequence, you are able to implement a hybrid CSI technique. This method allows you to additionally select a voxel during a CSI measurement.

The Hybrid CSI method also allows you to select the FoV such that the objects to be imaged protrude beyond the FoV. The aliasing artifacts expected along the phase-encoding directions are avoided by selecting the appropriate VOI.

The VOI is selected within the FoV. The spectra will be measured in this VOI which should contain as *little* fat as possible.

➪ In contrast to the SVS technique (in which the VOI consists of only one voxel), the VOI of the Hybrid CSI technique contains several voxels.



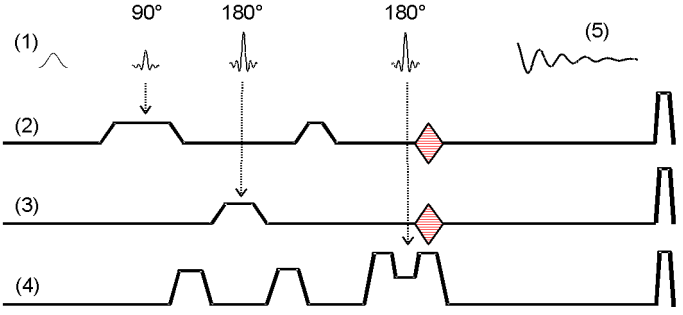
(1) FoV (16 phase-encoding steps)
(2) VOI (8 × 8 voxels)
(3) Selected voxel

Hybrid CSI sequences

2D as well as 3D sequences (**SE** or **STEAM**) are available for Hybrid CSI measurements.

STEAM sequences result in weaker signals than **SE** sequences. However, the chemical shift artifact is noticeably smaller.

The sample diagram below shows the pulse scheme of a hybrid, 2D spin-echo CSI sequence:



(1) Pulse for water suppression
(2) Phase-encoding gradient
(3) Phase-encoding gradient
(4) Slice-selection gradient
(5) Measurement signal

Measurement parameters and measurement time

When setting the parameters for a hybrid CSI measurement, it is important to closely observe the interdependencies between the parameters as well as their effect on the measurement time:

❏ A satisfactory signal-to-noise ratio requires sufficiently large voxels or a sufficient number of averages. When defining the CSI voxel sizes, rely on your experience with SVS techniques.

Example: For a 15 × 15 × 15 mm^3 large voxel, a measurement time of 6 minutes is required to detect the main metabolites. When measuring a voxel 3.4 times smaller with the dimensions 10×10×10 mm^3, it takes 11 times the measurement time (i.e., more than one hour) to achieve the same SNR.

❏ The minimum number of phase-encoding steps is 8, the maximum number is 32. The minimum FoV size is 80 x 80 mm^2 for csi_st and 55 x 55 mm^2 for csi_se. This enables voxels sizes smaller than 5 x 5 x 5 mm^3 to be realized.

However, an acceptable signal-to-noise ratio cannot be achieved within an acceptable measurement time for such small voxels, at least for brain applications.

❏ If the object to be displayed protrudes over the FoV of the CSI slice along one direction, select a VOI that is by that much smaller than the FoV to prevent aliasing artifacts.

Localization using phase-encoding

In this section, the localization procedure using phase-encoding steps used with the CSI technique is explained and examined quantitatively.

Unlike localization with slice-selective pulses used with the SVS technique, the localization results with phase-encoding depend on the intensity distribution to be measured:

- **Ideal case: Continuous intensity distribution**
  If the intensity distribution is continuous enough across the field of view (FoV) to be represented by a sum of Fourier terms, then the phase-encoding is perfect.
- **Real case: Intensity jumps**
  Intensity discontinuities lead to systematic errors in the image. Image errors of this kind are known as Gibbs ringing. During CSI measurements, these errors may be more predominant due to low resolution and deserve special attention.

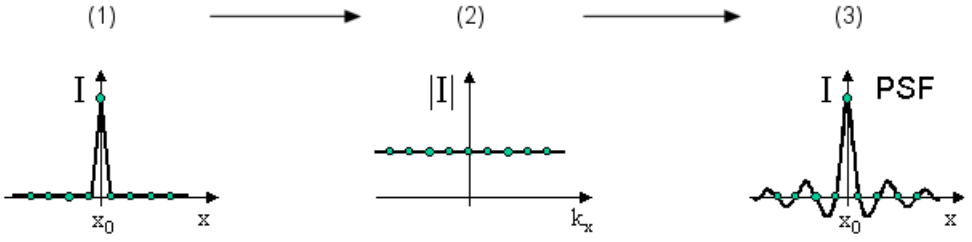
Point Spread Function (PSF)

To evaluate localization via phase-encoding, you have to consider a “worst case” image function, i.e., a single point intensity distribution (delta function).

If this image function is acquired using phase-encoding, all sampled points have the same absolute value of intensity.

The reconstructed image is generated from the measurement data via Fourier Transformation. In case of a delta image function, the reconstruction results are known as point spread function $S(x,x_0)$ (**P**oint**S**pread**F**unction, **PSF**).

⇨ The point spread function indicates how an intensity peak at position x_0 affects another position x in the reconstructed image.

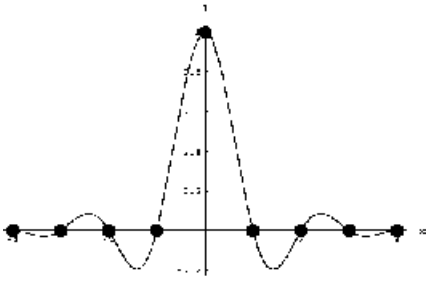


(1) Point intensity distribution (delta function)
(2) Measured values in k space after phase-encoding
(3) Reconstruction result after Fourier Transformation (point spread function)

Example: x_0= 0

The PSF of a delta image function with 9 sample points and an intensity peak at x_0= 0 is represented as a continuous line in the figure.

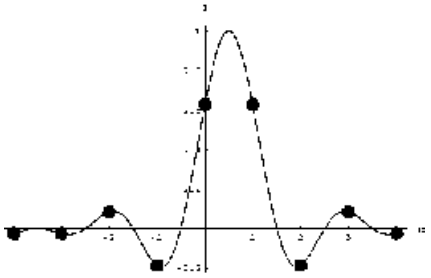
When interpreting results, keep in mind that after evaluating phase-encoding measurement data, the PSF is only known at points corresponding to the voxel positions. The progression of the PSF *between* the defining points is irrelevant for the case under consideration.



It can be seen that even a point-shaped intensity distribution is reconstructed exactly when x_0=0, because the PSF goes straight to zero at all other points.

Example: x_0= 0.5

The figure shows the PSF of a delta image function with an intensity peak when x_0= 0.5. The intensity peak is offset by half a voxel.



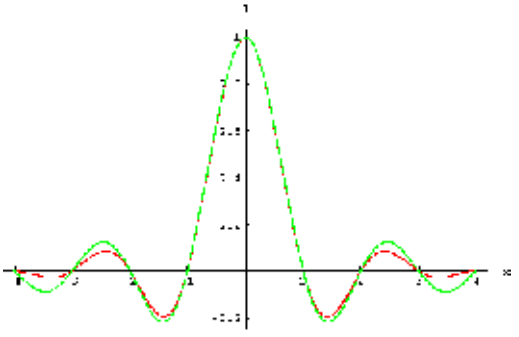
In the adjacent voxels the PSF is not equal to zero. This results in a noticeable contamination that decreases only slowly as the distance to the intensity peak increases.

The following assumptions can be made:

- ❏ Intensity discontinuities in the center of the voxel cause fewer localization errors than intensity discontinuities at the edge of the voxel. You may be able to take this phenomenon into account when positioning the CSI measurement matrix.
- ❏ The mean PSF progression (the “integral”) in the outer range is calculated as a measure of the mean contamination for any voxel position. For a single phase-encoding experiment, the progression of the PSF between the voxel positions is irrelevant.

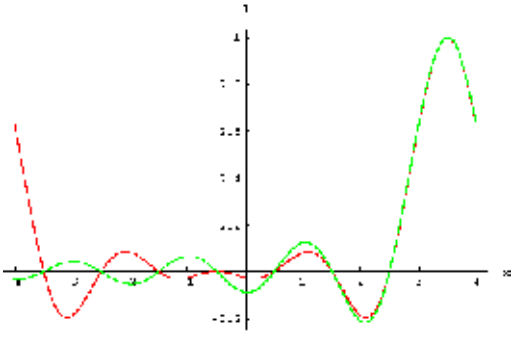
Effects of spatial resolution

The figure shows the PSFs of a delta function with 8 phase-encoding steps (red curve) and 32 phase-encoding steps (green curve). Both functions are plotted against the x axis in voxels.



If the intensity peak is in the center of the FoV ($x_0 = 0$), the probability of localization errors (cross-talk) decreases more slowly with a higher resolution and increasing distance than with a lower resolution.

If the intensity peak is at the edge of the FoV ($x_0 = 3.5$), the cyclic nature of the PSF is clearly visible.



With 8 phase-encoding steps and a FoV of -4 to 4, a voxel at the right-hand image margin will strongly contaminate the voxel of the same row at the left-hand image margin (red curve).

With 32 phase-encoding steps, a FoV of -16 to 16 is implemented. The intensity peak (x_0= 3.5) is still almost in the center of this FoV and no foldover or intensity aliasing occurs at this point.

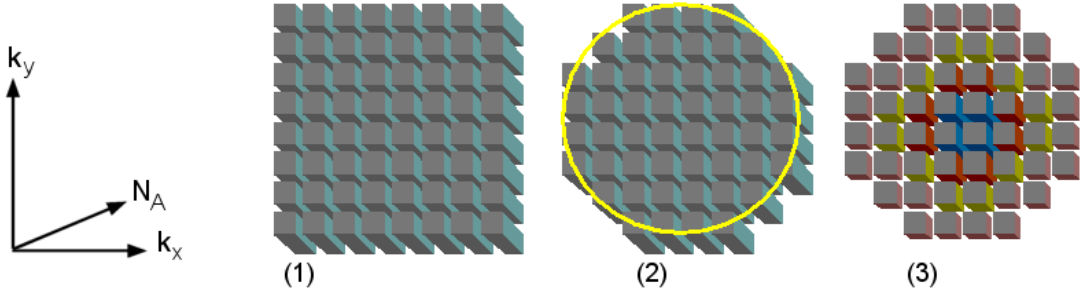
The following assumptions can be made:

- ❏ The edge voxels of a CSI experiment are not suitable for evaluation.
- ❏ The component of edge voxels may be limited by restricting the minimum permissible resolution. For this reason, the minimum resolution of the CSI protocols is 8 phase-encoding steps.

Phase-encoding schemes and localization

In addition to conventional *complete* sampling of the k space, it is also possible to limit sampling within the *elliptical* boundary of the k space.

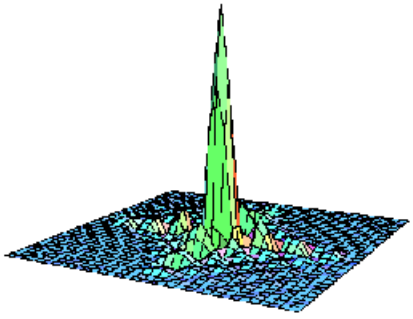
The purpose of reduced sampling and the extended method for *weighted* averaging is to maximize the signal-to-noise ratio obtained per measurement time.
→ Page A.2–21



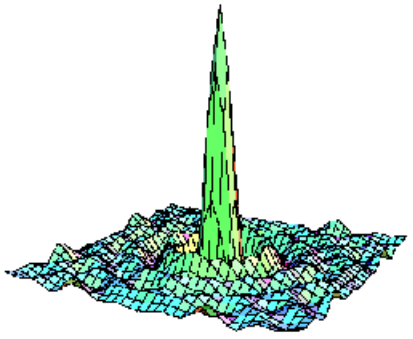
(1) Full sampling of the k space
(2) Elliptically reduced sampling
(3) Weighted sampling

This section focuses on how the sampling scheme affects localization. For this purpose, it is sufficient to analyze averaging (N_A=1). If N_A=1, “elliptical” and “weighted” sampling schemes are identical.

In the figures below, the PSFs are shown with full and elliptical k-space sampling. The FoV is 16×16 and the number of phase-encoding steps in both spatial directions is also 16.



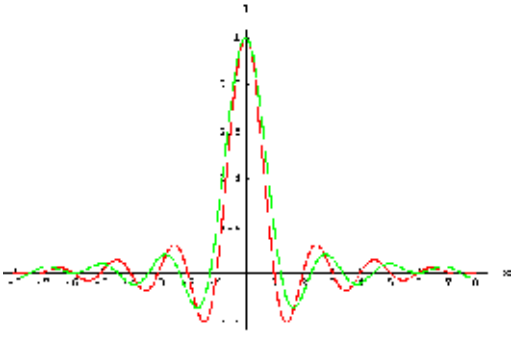
Full k space sampling



Elliptical k space sampling

The figures show that for full sampling, contamination is limited to the main axes; in the case of elliptically reduced sampling, contamination is more evenly distributed.

For a more precise comparison of the 2D-PSFs with different sampling schemes, the intersections along one of the main axes are shown in the diagram below.



- Red curve: Complete sampling
- Green curve: elliptical sampling

With reduced sampling, contamination is lower along at least one of the main axes. However, this advantage of elliptical sampling over complete sampling is obtained at the price of a slightly spreading main peak.

The following variables are used to quantify higher-dimensional PSFs (e.g. 2D-PSF):

- Line width Λ
  The range of the PSF where the intensity exceeds 50% of the maximum value is considered a square (or a cube for 3D-PSFs). The associated edge length is the line width.

- Contamination ratio K
  This is the ratio between the intensity contributions of the range outside the line width and the intensity contributions of the range inside the line width.

Please remember that localization using PSFs is based on a "worst case" scenario.

For physiological image functions typical of *in vivo* applications, contamination is considerably lower. K should therefore be considered a contamination hazard.

Depending on the resolution and phase-encoding method used, the following values for Λ and K are obtained for 2D-PSFs:

Resolution	Phase-encoding	Λ	K
8 × 8	Full	1.08	2.01
8 × 8	Elliptical	1.29	2.78
16 × 16	Full	1.09	3.06
16 × 16	Elliptical	1.27	4.79
32 × 32	Full	1.09	4.33
32 × 32	Elliptical	1.26	7.49

The table shows that elliptically reduced sampling unfortunately increases both the line width and the contamination.

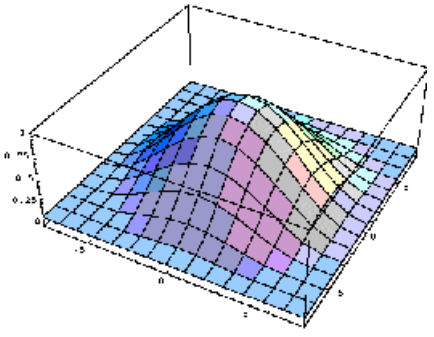
➪ You may reduce the values for contamination by applying a suitable filtering function.
→ Page A.2–18, *Phase-encoding and Hamming filter*

Phase-encoding and Hamming filter

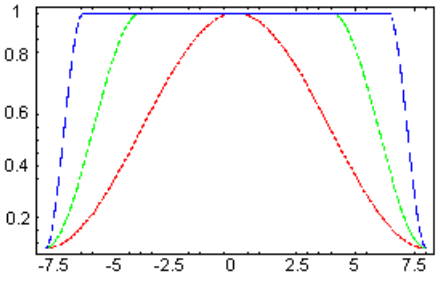
The possibility of contamination with Fourier Transformation is unreasonably high if no additional post-processing steps are performed.

One remedy is to filter the measurement data. The measurement data are multiplied by a suitable apodization function prior to Fourier Transformation. This causes the measurement data at the edge of the measurement volume to decay gradually and symmetrically.

One suitable function is the Hamming function of the distance from the center of the k space. This function guarantees that no measurement data are lost due to apodization, because the function does not drop to zero at the edge of the FoV but rather to 0.08.



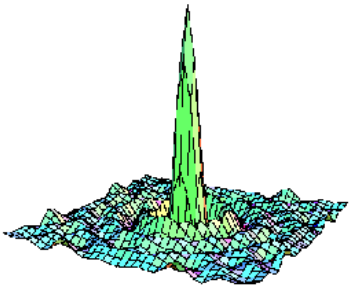
Hamming function along the phase-encoding directions



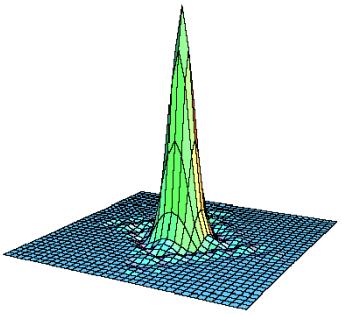
Sections of the Hamming function at the following filter widths:
w = 100 % red curve
w = 50 % green curve
w = 20 % blue curve

The filter width of the Hamming function specifies which part of the external k space apodization is applied. This parameter may be freely selected.

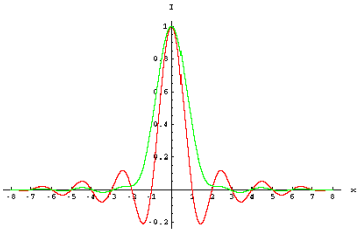
After elliptical k space sampling without filtration as well as with Hamming filtration, the PSFs' are compared in the following figures.



Without filter



With Hamming filter, w = 100%



Section along one of the main axes
red: without filter
green: with Hamming filter

The Hamming filter significantly reduces contamination. However, using a Hamming filter does result in a spread of the main maximum. Each voxel is actually wider than the nominally calculated voxel displayed in the measurement matrix.

During complete sampling or elliptical k space sampling, comparable results are obtained when applying the Hamming filter to measurement data. The k values and Λ values differ in their second decimal place only.

Since filtration of measurement data is used for most applications, the advantage of elliptical sampling (gain in measurement time) can be utilized without the concomitant disadvantage (contamination).

The following table shows the effect of apodization with respect to the risk of contamination and the line spread. Especially at low resolutions, you should select a filter bandwidth greater than 50 % to effectively reduce contamination. In these cases, the effective voxel size is approximately 1.5 times the nominal voxel size.

Resolution	Phase-encoding/filter	Filter width w in [%]	Λ	K
8 × 8	Full		1.08	2.01
8 × 8	Elliptical / Hamming	20	1.34	2.30
8 × 8	Elliptical / Hamming	50	1.49	1.51
8 × 8	Elliptical / Hamming	100	1.57	1.08
16 × 16	Full		1.09	3.06
16 × 16	Elliptical / Hamming	20	1.34	3.13
16 × 16	Elliptical / Hamming	50	1.49	1.64
16 × 16	Elliptical / Hamming	100	1.57	1.18
32 × 32	Full		1.09	4.33
32 × 32	Elliptical / Hamming	20	1.34	3.54
32 × 32	Elliptical / Hamming	50	1.49	1.74
32 × 32	Elliptical / Hamming	100	1.58	1.33

Signal-to-noise ratio with phase-encoding

The following table shows the effects of resolution and phase-encoding scheme on the signal-to-noise ratio (SNR).

Resolution	Phase-encoding	SNR	Measurement duration	SNR/√T
8 × 8	Full	1	6' 30 (100%)	1.0
8 × 8	Elliptical	1	3' 00 (46%)	1.5
8 × 8	Weighted	1	1' 24 (22%)	2.1
16 × 16	Full	1	25' 42 (100%)	1.0
16 × 16	Elliptical	1	15' 00 (58%)	1.3
16 × 16	Weighted	1	7' 12 (28%)	1.9
32 × 32	Full	1	102' (100%)	1.0
32 × 32	Elliptical	1	70' (69%)	1.2
32 × 32	Weighted	1	32' (31%)	1.8

Given the conditions stated previously as well as a repetition time of TR= 1.5 s and four accumulations, the signal-to-noise ratio of phantom spectra was determined experimentally after applying the Hamming CSI filter (filter width: 100%). At full sampling, the signal-to-noise ratio was set to 1 for each resolution.

The experiments showed that SNR is not significantly affected by different phase-encoding schemes. The measurement time saved has no negative effect on the SNR and is thus a true gain. The last column in the table indicates the effective SNR divided by the square root of the measurement time. This would be the SNR obtained if the same measurement time were to be applied to all experiments.

As a reminder, the CSI filter both increases the effective voxel size and prevents contamination. For this reason, the CSI filter is activated during standard CSI examinations. Under these circumstances, you should activate one of the phase-encoding schemes appropriate for the filter, either **elliptical** or – if the measurement time is sufficient – **weighted**. This will result in improved SNR without negative effects, as e.g. decreased resolution.

Chemical shift artifact in Hybrid CSI

With slice selection, the exact slice position depends on the resonance frequency of the excited spin ensemble. Therefore, the area in which fat is excited is shifted with respect to the area in which water is excited. This phenomenon is known as *chemical shift artifact*. The spatial shift of the selection is varied with the voxel size for a specified frequency offset. The shift for a CSI VOI with an edge length of 100 mm is therefore 10 times for a single voxel with an edge length of 10 mm. The offset also depends on the selection pulse.

Delta frequency

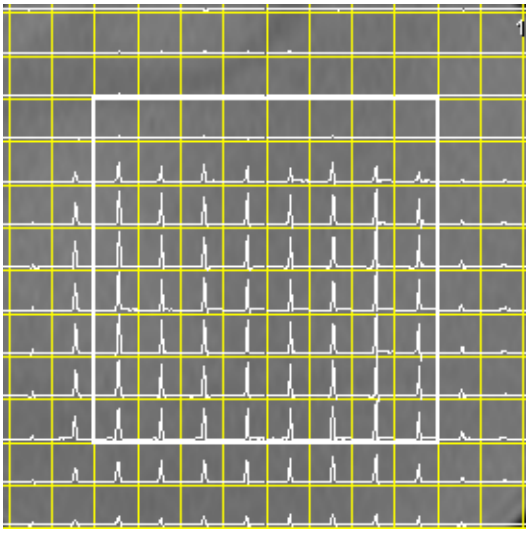
You can use the **Delta Frequency** parameter to specify the reference signal used for slice positioning. The spatial selection of voxels and CSI VOIs is precise for the specified frequency; the position offset increases linearly with the frequency offset. The delta frequency is specified in ppm independent of the magnetic field strength.

For example, you have detected the system frequency at 4.7 ppm in an *in-vivo* ^{1}H spectroscopy examination, and you set the frequency shift to -2.7 ppm. The result will be a highly accurate display of VOIs in the graphic slice positioning for the NAA signal at 2.0 ppm. If you want to use the VOI to suppress fat signals, it may be helpful to set an even higher frequency shift to minimize the shift for the frequency range of fat signals.

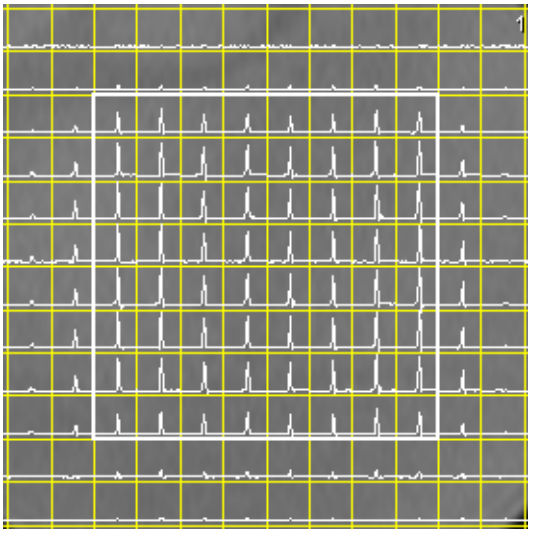
The following conclusions can be drawn regarding the use of hybrid CSI sequences:

- ❏ In CSI measurements it is to be expected that signals located outside the set selection frequency may be attenuated in the voxels near the edges of the VOI.
- ❏ The shift artifact does not affect fully excited inside voxels. The voxels are localized via phase-encoding, which has no shift artifact.

The two figures below show spectral maps of the acetate signals from Hybrid CSI measurements with a homogenous phantom. They show the effect of a frequency shift correction on the VOI selection.



Without frequency shift correction for the acetate signal



With frequency shift correction for the acetate signal (frequency shift: -2.9 ppm)

Outer Volume Suppression (OVS) – CSI

Chemical shift artifacts are more common at higher field strengths.
→ Page A.1–27, *Chemical shift artifact*

To compensate for this effect, the spin echo CSI sequence was enhanced to include Outer Volume Suppression (OVS). This allows you to suppress unwanted signals using regional saturation pulses.

The main areas of application include prostate spectroscopy and improved neuro-spectroscopic examinations in the marginal areas of the brain.

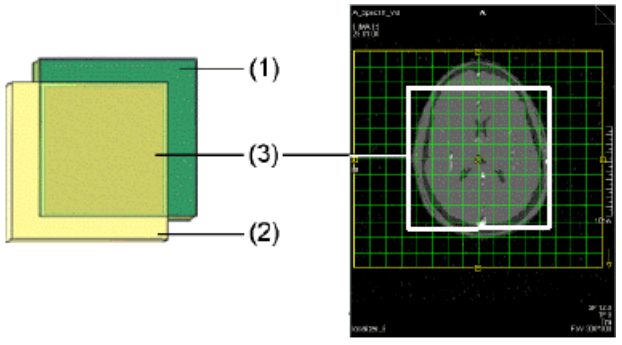
Your system offers the following two functionalities for OVS:

- ❏ **Fully excited VOI** option
- ❏ Adding freely positionable saturation regions

Fully excited VOI option

The **Fully excited VoI** option lets you achieve homogeneous excitation of all metabolites of interest in the selected volume while simultaneously suppressing interference signals from regions outside the VOI.

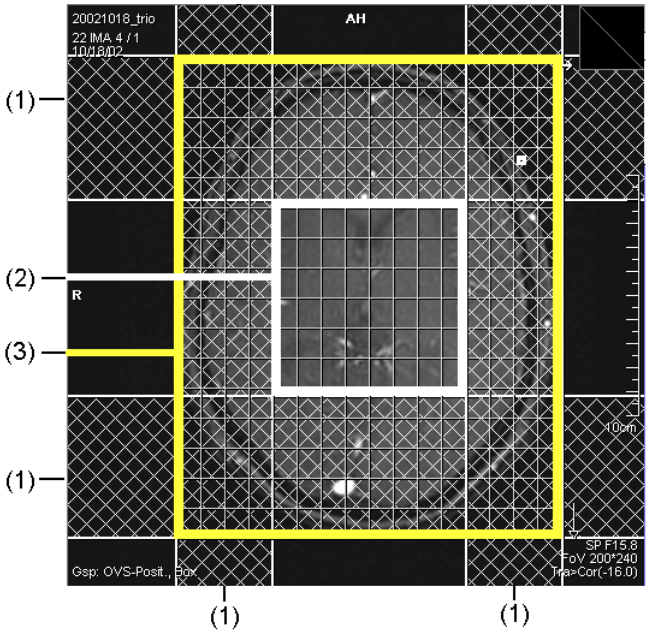
A full excitation of the displayed VOI is achieved since this region is the intersecting area of the excited volumes of the metabolites of interest. The excited volume for a specific metabolite (or a specific frequency) is larger than the selected VOI.



(1) VOI for excited water
(2) VOI for fat protons
(3) VOI of the measurement (intersecting area of the VOIs from (1) and (2); corresponds to the VOI drawn in the reference images)

The RF pulses used to excite the VOI are transmitted using a fixed median delta frequency.

Signals from the excited region that are outside the visible VOI are suppressed by four automatically positioned regional saturation pulses.



(1) Automatically positioned saturation regions
(2) Selected VOI
(3) Excited volume (across the entire frequency spectrum of interest)

➪ These automatically positioned saturation regions are *not* displayed for graphic slice positioning.

Freely positionable saturation regions

You may insert up to eight freely positionable saturation regions to further restrict the VOI.

The freely positionable saturation regions are designed to provide good *in-vivo* fat suppression.

Saturation regions – SVS

In SVS measurements with a spin-echo sequence, you can add up to eight freely positionable saturation regions to delineate the VOI. Signals from the minimally excited regions outside the visible VOI can be suppressed using these regional saturation pulses.

Spectral signal suppression

Selected spectral signals can be suppressed by implementing MEGA pulses in the spin echo sequences (M. Mescher et al. Journal of Magnetic Resonance **123**, 226-229 (1996)). The effect of these pulses is a frequency-selective dephasing of the transverse magnetization.

These pulses can be used to suppress two frequency bands simultaneously. This allows for spectral fat, water, or fat/water suppression.

Techniques with ^{31}P MRS

For ^{31}P MRS measurements, the signal can be improved using Nuclear Overhauser Enhancement (NOE).

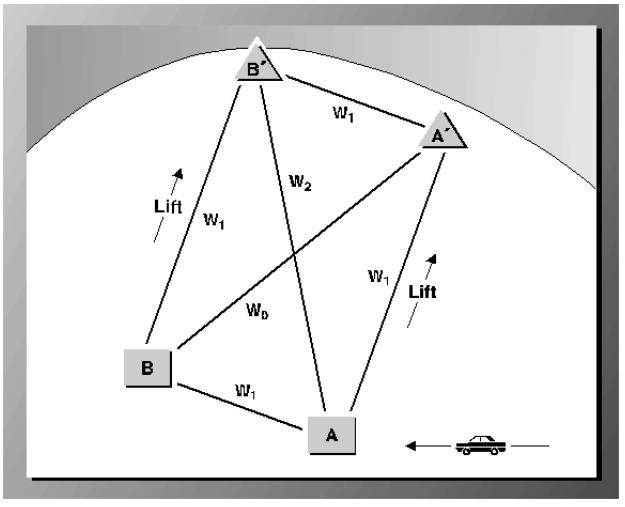
By using decoupling pulses, the ^{31}P spectrum can be simplified while enhancing the ^{31}P main signal.

Nuclear Overhauser Effect (NOE)

The Nuclear Overhauser Effect describes a phenomenon, in which the irradiation of one resonance (peak) causes population changes of energy levels resulting in signal intensity changes of another resonance.

Example of NOE

The following example provides a greatly simplified illustration of this effect. Imagine two ski resorts A and B, each with a ski lift leading to mountain stations A' and B' respectively. Both ski lifts are of equal length. Since village B is somewhat higher than village A, mountain station B' is higher than A' by the same amount.



W_1= Longitudinal relaxations for A and B
W_0 or W_2 = Cross relaxations

We now want to determine the relative popularity of each of the ski resorts based on the number of skiers in each village. Since village A is the first village off the access road, it has a slight advantage. A can be reached with less energy and is therefore the lower energy state. We can also observe this relationship between A' and B', provided that the capacity of both lifts is equal. In addition, we are also assuming that this relationship is not influenced by the normal "ski activity" (longitudinal relaxation).

The objective should now be more intense usage of the descent between B and A or between B' and A'. This is particularly attractive when the corresponding slopes are empty because there are fewer skiers in B and many in A, or fewer in B' and many in A'. In our analogy, we now ensure that the lifts between B and B' (and between A and A') are used intensively (saturation!) so that the number of people going up in the lifts is the same as the number of skiers going down the slopes. This saturation (somehow) makes it possible and attractive for skiers to ski from B' down to A ("cross relaxation or double quanta transition") but not from A' to B. This reduces the number of skiers in B' and increases the number of skiers in A. As a result, our objective has been met: the numerical difference of skiers increases between B and A as well as between B' and A'.

Physical Review

From a physics point of view, it is possible to influence one type of nucleus (e.g. A = ^{1}H) in an "AX" spin system that can be perturbed while a second type of nucleus (e.g. X = ^{31}P) is observed. In an NOE experiment, the populations of the AX spin system are modified via saturation of the ^{1}H resonances. As a result, the energy levels of the system no longer correspond to the Boltzmann distribution. The system then reacts to compensate. A new equilibrium is established in which the observed nucleus has a stronger spin polarization (population difference between both of the possible states). The NOE is a manifestation of the attempt by the entire system to remain in thermal equilibrium.

The NOE effects occur through dipolar relaxation of neighboring nuclei that are out of equilibrium. This dipolar relaxation is triggered via modulations of the B_0 field at the nuclear location. These are defined by the motion of the molecule. If they possess the appropriate frequency, these changing magnetic fields may result in changes to the spin status of the nuclei. The probability for these transitions is a function of the reorientation time of the molecule, the distance between both dipolar coupled nuclei, the Larmor frequency, and the g factors of the affected nuclei. As a result, the effectiveness of the NOE depends on these variables. It has been determined that the NOE is positive for small molecules in non-viscous solutions, because so-called double-quantum transitions are significant for relaxation. For macromolecules, or with highly viscous solutions, the so-called zero-quantum transitions are dominant and NOE is negative.

Quantitatively, the signal change via saturation in the NOE experiment is due to the NOE factor:

$$\text{NOE factor}_{max} = 1 + \gamma_{observed} / (2\,\gamma_{saturated}) = 1 + \eta$$

with η: Nuclear Overhauser enhancement (signal gain)

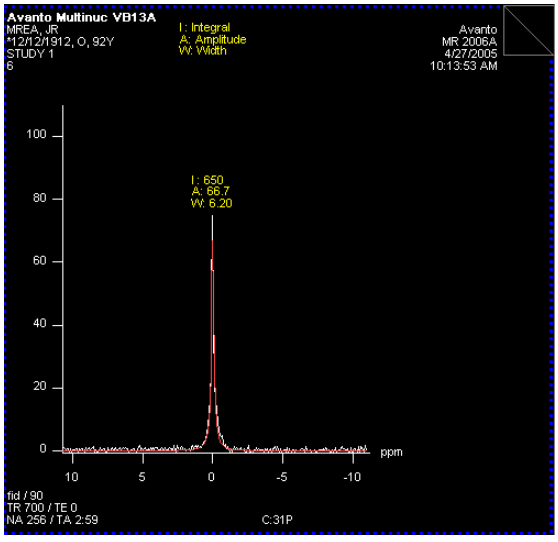
In the homonuclear case (i.e. when the saturated and the observed nucleus are of the same type), an enhancement factor of 1.5 can be obtained (50% more signal).

A factor of 2.235 can theoretically be achieved in the case of a ^{31}P experiment with saturation of the protons. In practice, however, the typical values for the NOE factor are in the range of 1.4 to 1.8.

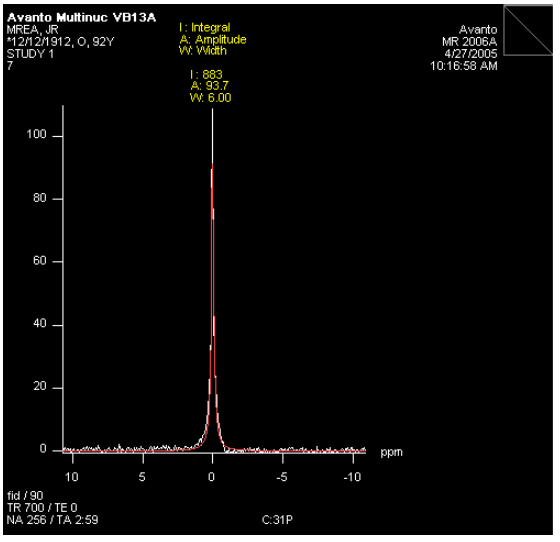
Since NOE is based on dipolar relaxation, the effect is only established with a time constant of T_1.

Signal Enhancement via NOE

The following spectra of a ^{31}P phantom measurement illustrate the enhancement effect of the ^{1}H saturation on the ^{31}P signal intensity: The signal enhancement is 0.73.



Spectrum of a ^{31}P phantom measurement without ^{1}H saturation



Spectrum of a ^{31}P phantom measurement with ^{1}H saturation

Decoupling

By sending ^{1}H decoupling pulses during the acquisition of the ^{31}P signal, the coupling between ^{31}P and ^{1}H nuclei is reduced. This results in a collapse of the multiplet lines into one single ^{31}P signal peak which then has an increased signal intensity.

Decoupling schemes

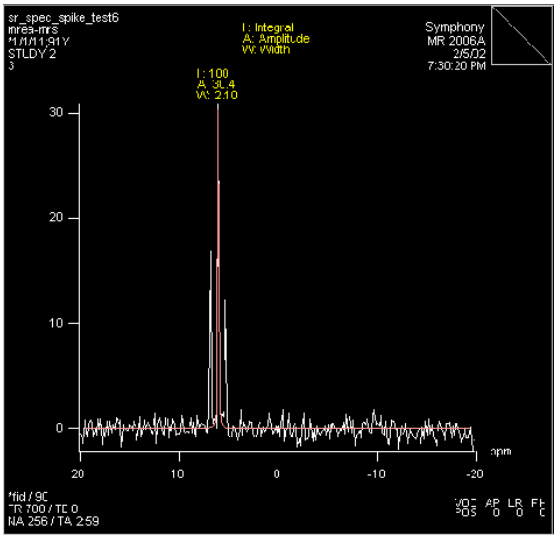
The following decoupling modes are available:

❑ **CW** decoupling
A decoupling pulse is continuously transmitted during data acquisition. The decoupling has a narrow bandwidth in the frequency domain. The decoupling frequency should be accurately set for optimal decoupling.

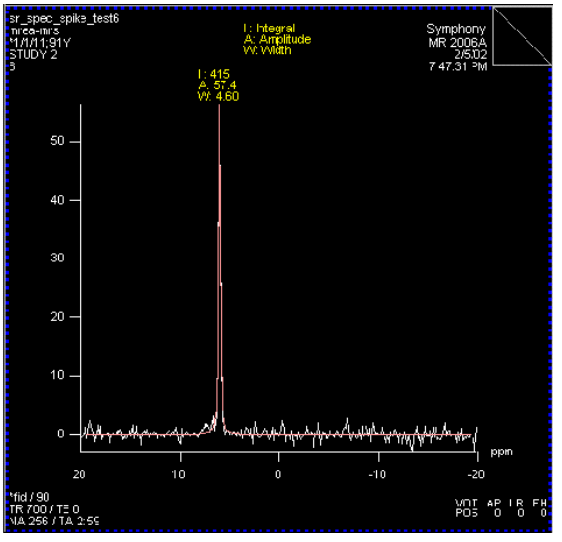
❑ **WALTZ-4** decoupling
A series of short decoupling pulses is transmitted during data acquisition. The decoupling has a broad bandwidth in the frequency domain and does not depend to the same degree on the setting of the decoupling frequency.

Signal enhancement via decoupling

The following spectra of a ^{31}P phantom measurement illustrate the effect of ^{1}H decoupling on the ^{31}P signal. In a measurement with ^{1}H Waltz4 decoupling, the ^{31}P triplet signal of a methylene diphosphoric acid solution appears as a singlet signal. The amplitude of the main signal is increased by a factor of 1.89 as compared to a measurement without ^{1}H decoupling.



^{31}P triplet signal of a methylene diphosphoric acid trisodium salt solution without ^{1}H decoupling



^{31}P triplet signal of a methylene diphosphoric acid trisodium salt solution with ^{1}H Waltz 4 decoupling

CHAPTER A.3

Applications

Spectroscopy protocols based on the SVS technique are used for different clinical applications than CSI protocols.

The various clinical applications are described in greater detail on the following pages.

SVS technique applications

^{1}H SVS measurement of the head

The SVS technique is used in ^{1}H MRS of the brain to examine focal pathologies (e.g. tumors).

In order to optimally distinguish between pathological and healthy structures, you have to acquire a reference spectrum from a healthy part of the brain in addition to the spectrum of the examination volume.

The SVS method allows to focus the shimming on the volume of the single spectrum which shall be measured.

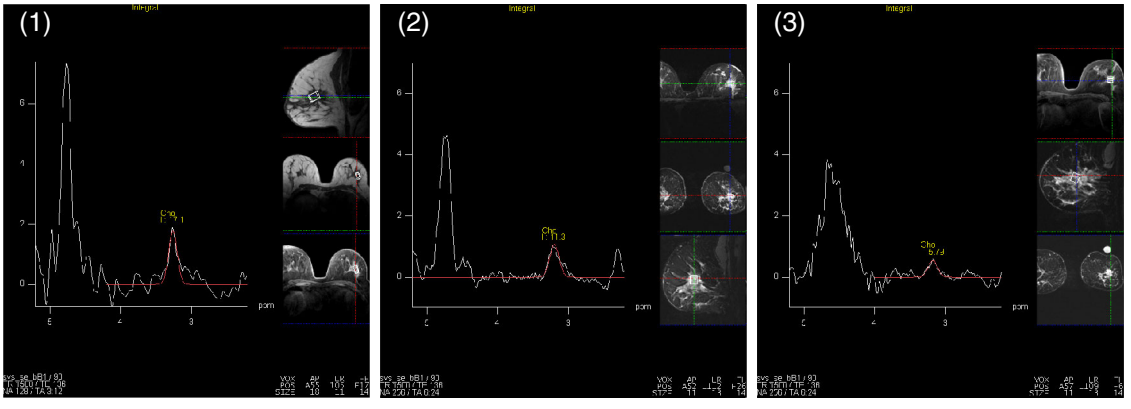
^{1}H SVS measurement of the breast (syngo GRACE)

syngo GRACE utilizes the ^{1}H MRS SVS technique on the breast. In addition to dynamic MRI, it is used as a tool helping in the differentiation of malignant from benign tumors. Moreover, ^{1}H MRS of the breast is used primarily for therapy monitoring, as well as for improved identification of possible vital residual findings after chemotherapy and preoperative intervention.

In ^{1}H MRS, the metabolite status in tumor tissue can be acquired via the (total) choline-signal (tCho). The choline concentration in healthy breast tissue is usually low. However, first studies of young healthy volunteers have shown an increased choline concentration. Therefore, clinical investigations have to produce evidence by quantifying the choline concentration. An increased choline signal in the spectrum usually correlates with a positive biopsy result.

Example

The following examples show tumor spectra of breast cancer before, and during chemotherapy. Biopsy correlates with high choline signal in the spectrum.



(1) Before chemotherapy
(2) Second cycle of chemotherapy
(3) Fourth cycle of chemotherapy

CSI technique applications

You can examine a larger image area with the CSI method than with SVS.

The CSI technique is used in the examination of multi-focal pathologies (e.g. multiple sclerosis) or when you are unable to precisely isolate the VOI (e.g. when determining the epileptical focus).

In addition, the CSI technique allows you to examine the metabolite distribution in the VOI.

The CSI technique is used in ^{1}H MRS of the brain or prostate as well as ^{31}P MRS of muscle, heart, liver.

^{1}H Hybrid CSI measurement of the brain

^{1}H MRS of the brain enables you to detect, e.g., changes in concentration of specific metabolites caused by strokes or tumors. This includes metabolites such as N-actylasparte (NAA), creatine (Cr) and choline (Cho). The detection and spatial distribution of lactate also plays an important role.

Unfortunately, the lactate signal is frequently covered by the fat signal which is a thousand times more intensive. The protons in subcutaneous fat are present in high concentration and have the same chemical shift as the protons of lactate. The problem is particularly acute in experiments with short echo times due to the short T2 relaxation times of fat signals.

The hybrid CSI method allows you to examine the spatial distribution of lactate without interference by the intensive signals of the subcutaneous fat.

Recommendation

Examine a series of healthy volunteers as part of a clinical spectroscopy program and compare the consistency of the results using the metabolite ratios. You can compare the results with the data from a Siemens multi-center pilot study listed below.

Metabolites	Relative ratio
NAA/Cho	2.73 ± 0.59
NAA/Cr	2.20 ± 0.41
Cho/Cr	0.82 ± 0.16

These values are based on 156 spectra of an 8 mm^3 volume of the occipital lobes of healthy volunteers.

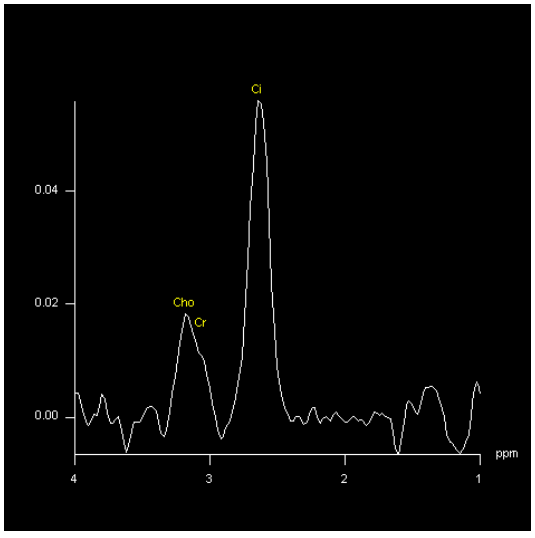
^{1}H Hybrid CSI measurement of the prostate

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

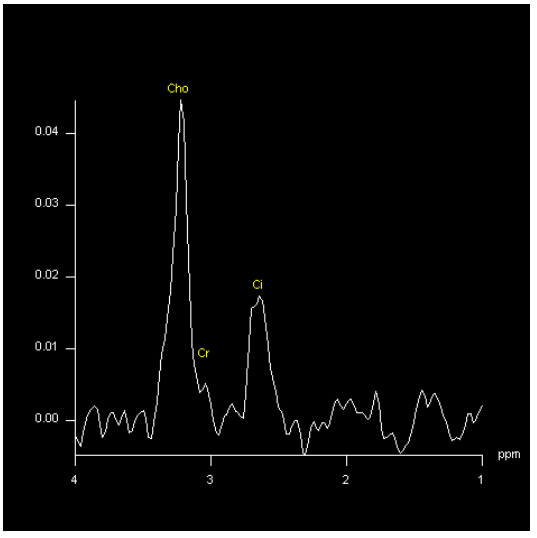
Citrate is an important metabolic product of the tricarboxolic acid cycle (Krebs cycle) in the mitochondria of living cells. Intracellular citrate concentrations are very low. However, citrate can be detected as secretion of the healthy prostate.

The spectrum of healthy prostate tissue shows a strong citrate signal, which is typically significantly higher than the choline signal.

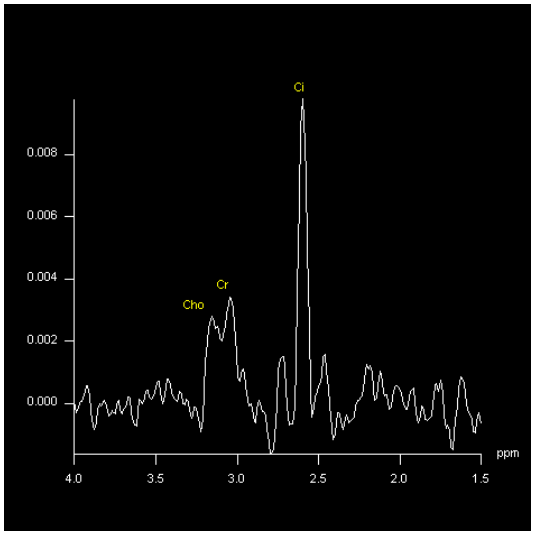
However, the citrate/choline signal ratio in the prostate is subject to regional differences. The highest ratios were found in the peripheral zone; in the area of the ureter, however, the ratio may be reversed even in the healthy prostate. High choline and low citrate signals were found in cancerous prostate tissue. However, the spatial inhomogeneity has to be considered for the evaluation. In addition, research is currently being conducted on, e.g., the effects of prostatitis on the signal ratio.



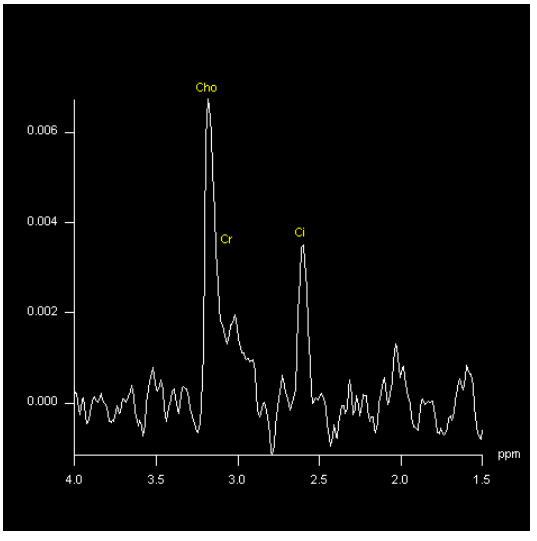
1.5 Tesla: Spectrum of healthy prostate tissue



1.5 Tesla: Spectrum for tissue of a prostate carcinoma



3 Tesla: Spectrum of healthy prostate tissue



3 Tesla: Spectrum for tissue of a prostate carcinoma

3D spin echo hybrid CSI sequence

The measurement protocols for the ^{1}H MRS examination of the prostate are based on a 3D spin echo hybrid CSI sequence.

This 3D sequence allows you to perform a full prostate examination in one step.

If combined with Outer Volume Spectroscopy and spectral signal suppression, interference from fat signals can be effectively reduced
→ Page A.2–24, *Outer Volume Suppression (OVS) – CSI*
→ Page A.2–27, *Spectral signal suppression*.

The shape of the strong coupling citrate signal changes depending on the magnetic field. Therefore, the timing of the RF pulses has to be optimized to determine the citrate signal:

- ❏ 1.5 T: TE = 120 ms
- ❏ 3 T: TE = 145 ms (plus a special timing
  → Page B.3–6, *Setting the sequence timing*)

^{31}P CSI measurement of muscle, heart, liver

^{31}P MRS acquires the most important energy carriers of the cell such as ATP, creatine phosphate and inorganic phosphate.
→ Page A.1–23, *The Most Important Signals of ^{31}P MRS*

Based on the relative concentrations of these phosphorous metabolites, information can be collected regarding the energy state of the cell.

The most important examination regions for ^{31}P MRS include the muscles, the heart, and the liver. Various pathologies of these regions result in typical abnormalities as compared to healthy patients.

These abnormalities affect:

- ❏ the absolute concentrations of specific phosphorous metabolites
- ❏ the pH value
- ❏ the speed of recovery from stress

! Physiologically triggered measurement via ECG signal is required for 31P MRS of the heart.
→ Page B.3–12, *Physiologically-controlled measurements*

CSI FID sequence

A CSI sequence with minimal echo time is required to minimize T_2 weighting. An additional volume selection (VOI) is not necessary for suppressing interference signals.

To meet these requirements, the ^{31}P MRS protocols are based on a CSI FID sequence that acquires data directly following localization via slice selection and phase encoding.

2D as well as 3D CSI FID sequences are available.



Due to the absence of a volume selection, a sufficiently large FoV should be selected for the CSI FID sequence to prevent aliasing artifacts.

This applies to each spatial direction, because in the CSI FID sequence each spatial direction is resolved via phase encoding.

^{1}H saturation

The ^{31}P signal may be enhanced via saturation of the ^{1}H spins (Nuclear Overhauser Effect, NOE).
→ Page A.2–28, *Nuclear Overhauser Effect (NOE)*

For this reason, in ^{31}P measurements ^{1}H saturation pulses are transmitted during the examination prior to the excitation pulses.

^{1}H decoupling

When transmitting ^{1}H decoupling pulses during ^{31}P data acquisition, spin-spin coupling between the ^{31}P and the ^{1}H nuclei can be reduced. This results in simplified spectra and increased signal intensities for certain ^{31}P signals.
→ Page A.2–31, *Decoupling*

PART B

Spectroscopy Measurements

B.1 *Licenses*

B.2 *Procedure for Spectroscopy Measurements*

B.3 *Preparing the Measurement*

^{1}H MRS measurements of the brain B.3–2

^{1}H MRS measurements of the breast B.3–4

^{1}H MRS examination of the prostate B.3–5

Suppressing fat signals B.3–5

Specialities for 3 T B.3–6

^{31}P MRS measurements of muscles, heart, liver B.3–7

Selecting the coil B.3–7

Positioning the patient, positioning the coil and determining the magnet isocenter B.3–8

B.4 *Preparing the Measurement Program*

B.5 *Reference Images*

Scan at Center B.5–2

Region in the isocenter B.5–3

Region outside the isocenter B.5–4

Measuring reference images B.5–4

Loading reference images B.5–7

Editing the display of reference images B.5–8

Selecting the nearest reference images B.5–8

B.6 *Graphic Display of Measurement Objects*

VOI display B.6–2

Display of a CSI slice B.6–4

Display of a CSI slab B.6–6

B.7 *Adapting the Parameters for an SVS Measurement*

Adapting the VOI B.7–1
Adapting the VOI graphically B.7–3
Adapting the VOI numerically B.7–5
Saving the reference image and VOI graphic B.7–9
Setting saturation regions B.7–9
Adjusting protocol parameters B.7–10
Setting contrast parameters B.7–10
Setting parameters for resolution B.7–15
Setting sequence parameters B.7–16

B.8 *Adapting the Parameters for a CSI Measurement*

Adjusting the CSI slice (2D CSI) B.8–1
Setting the display of the CSI matrix B.8–2
Showing the projection of the CSI slice B.8–4
Using the position and orientation from a reference image B.8–4
Adapting the CSI slice graphically B.8–5
Adapting the CSI slice numerically B.8–6
Saving the reference image and CSI slice graphic B.8–10
Adapting the CSI slab (3D CSI) B.8–11
Adapting the CSI slab graphically B.8–12
Adapting the CSI slab numerically B.8–13
Setting saturation regions B.8–16
Adjusting protocol parameters B.8–18
Setting contrast parameters B.8–18
Setting parameters for resolution B.8–25
Setting sequence parameters B.8–30
Setting parameters for ^{31}P MRS measurements B.8–33

B.9 *Configuring Adjustments*

Checking the adjustment settings B.9–1
Shim mode B.9–2
Water suppression adjustment B.9–3
Setting the adjust volume B.9–4

B.10 *Measuring*

Starting the measurement B.10–2
Monitoring the raw signal B.10–3
Modifying subsequent measurement protocols B.10–4

B.11 *Interactive Adjustment*

Automatic adjustment with interactive control B.11–2
Manual adjustment B.11–3
^{1}H frequency adjustment B.11–4
Multinuclear frequency adjustment B.11–7
Transmitter adjustment B.11–9
Multinuclear transmitter adjustment B.11–13
3D Shim B.11–14
Interactive shim B.11–17
Manual water suppression B.11–20

B.12 *Performing Quality Assurance*

Quality assurance for ^{1}H MRS B.12–1
Positioning the phantom and coil B.12–1
Registering the quality measurement B.12–2
Selecting a QA measurement program B.12–3
Localizer measurement B.12–3
Checking the shim quality B.12–4
Performing a localized QA measurement B.12–6
Checking the results B.12–8

Quality assurance for ^{31}P MRS B.12–9
Positioning the phantom and coil B.12–9
Registering the quality measurement and selecting a QA measurement program B.12–10
Localizer measurement B.12–11
Checking the shim quality B.12–11
Performing the ^{31}P MRS QA measurement B.12–12
Checking the results B.12–13

B.13 *Measurement Protocols*

Protocols for in-vivo application B.13–2
head_1H and pediatric_head_1H B.13–2
breast_1H B.13–4
prostate_1H B.13–5
head 31P (only Trio/Verio system) B.13–5
heart_31P (only 1.5 T) B.13–5
liver_31P (only 1.5 T) B.13–6
muscle_31P (only 1.5 T) B.13–7
x_nuc_library B.13–7
Protocols for quality assurance B.13–8
qa_1H B.13–8
qa_31P B.13–8
3D CSI protocols B.13–8

CHAPTER B.1

Licenses

The following licenses for MR spectroscopy measurements and evaluation are available for your system:

MAGNETOM	License						
	^{1}H SVS	^{1}H SVS *syngo* GRACE	2D ^{1}H CSI	3D ^{1}H CSI	Multinuclear Support	Multinuclear Spectroscopy	Spectroscopy Evaluation
Aera	●	●	●	●			●
Avanto	●	●	●	●			●
Skyra	●	●	●	●	●	●	●
Verio	●	●	●	●			●

! Spectroscopy proton examinations using the CSI technique require installation of the “2D Spectroscopy CSI” and “Higher Order Shim Channels” options on your MR system. Additionally, for prostate examinations and 3D CSI examinations, the “3D Spectroscopy CSI” license is required.

- The “syngo GRACE” license contains protocols for breast spectroscopy to detect choline and an internal or external reference signal. Frequency-corrected accumulation is applied to minimize artifacts caused by respiration. For quantification of tCholine, the evaluation protocols include automatic normalization of the breast signal to the reference signal.
- The “Multinuclear Support” license prepares the MR system with additional hardware and software for imaging and spectroscopy with the nuclei ^{3}He, ^{7}Li, ^{13}C, ^{19}F, ^{23}Na, ^{31}P, and ^{129}Xe. Additionally, ^{17}O for 3 Tesla systems. There is also an FID sequence available that can be used with all nuclei. Coils with preamplifiers and transmitter duplexers as well as optimized pulse sequences for the individual nuclei are not included.

- The “Multinuclear-Spectroscopy” license contains a spatial resolution spectroscopy sequence as well as basic spectroscopy measurement and evaluation protocols for nuclei ^{7}Li, ^{13}C, ^{19}F, and ^{31}P. In addition, the license includes ^{31}P protocols for special applications on muscles - (1.5 T), head (3 T), heart, and liver (1.5 T).

CHAPTER B.2

Procedure for Spectroscopy Measurements

In terms of process, a spectroscopy measurement corresponds to a measurement for imaging.
Refer to → ***syngo*** **MR** Operator Manual

	PROCESS	DETAILS
1	**Registering the patient**	→ *syngo* Operator Manual
2	**Positioning the patient and coil**	→ Chapter B.3
3	**Selecting the measurement protocols**	→ Chapter B.4
4	**Measuring reference images (optional)**	→ Chapter B.5
5	**Positioning the measurement volume**	→ Page B.7–1, → Page B.8–1, → Page B.8–11
6	**Setting saturation regions (optional)**	→ Page B.8–16
7	**Adapting the measurement parameters**	→ Page B.7–10, → Page B.8–18
8	**Configuring Adjustments** Automatic adjustment or: Automatic adjustment with interactive control or: Interactive adjustment	 → Chapter B.9 → Page B.11–2 → Page B.11–3
9	**Starting the measurement**	→ Chapter B.10
10	**Saving measurement data**	occurs automatically

➪ While the measurement is in progress, you can monitor the raw signal using the **Inline Display** or edit incomplete measurement protocols in the measurement queue.

CHAPTER B.3

Preparing the Measurement

Your system supports the following applications:

- ❏ ^{1}H MRS measurements of the brain
- ❏ ^{1}H MRS measurements of the breast
- ❏ ^{1}H MRS Examination of the prostate
- ❏ ^{31}P MRS measurements of muscles, head, heart, liver

Preliminary steps

In principle, you prepare for a spectroscopy measurement the same way you prepare for an imaging measurement:

- ✧ Select a coil, position and secure the patient in the orientation required on the patient table.
- ✧ Connect the coil required for the measurement.
- ✧ Define the magnet isocenter using the laser light localizer and move the patient into the isocenter.

➪ The region to be examined should be optimally positioned in the magnet isocenter as well as the coil center because large “off center” positions will make the examination more difficult.

! A detailed description of these preliminary steps is included in your *System Manual*. The measurement preparations described in this chapter are valid only in combination with the *System Manual* and the corresponding safety information.

^{1}H MRS measurements of the brain

For ^{1}H MRS examination of the brain, use the TxRx_Head coils or Head Matrix. In addition, this type of examination is also supported by the CP Head Array.

TxRx_Head

As a transceiver coil, the TxRx_Head is optimally suited for ^{1}H MRS examinations of the brain.

The TxRx_Head coil allows the application of the RF pulses with the highest B1 field, thereby minimizing the chemical shift artifact of the localization to a minimum.

Head Matrix

As compared to TxRx_Head, the Head Matrix uses the whole-body coil for excitation resulting in an increase of the chemical shift artifact.

However, there is the possibility of improving the **signal-to-noise ratio (SNR)** by combining the signals of the individual coil elements in phase (weighted with the signal intensity). Data sets combined in this way may be used for both SVS as well as CSI measurements.

➪ A residual water signal may be preferable for computing combined data sets (reduced water suppression option)

We recommend combining data sets in conjunction with the selection of the normalization filter to create a normalized, combined data set. A normalized, combined data set has the **homogeneity**, which is detected by the whole body coil. As a result, the signals of CSI data from various voxels can be compared better.

- If a normalization filter is not selected, a quadratically-weighted signal combination of the coil elements is performed, where the inhomogeneous receiver characteristic of the matrix coil is reflected in a variation of the integrals such that the integrals for the various voxels can no longer be compared.

We recommend the **CP mode** as the coil mode. If 4 coil elements are selected, in this mode you can apply the protocol settings with maximum resolution (32) from the 1-channel situation. While you may select up to 16 coil elements, maximum spectral resolution (vector size), CSI resolution (Final Matrix Size) and the number of measurements will be limited.

- You can freely combine the individual coil elements of the Head Matrix. We recommend that you only select the coil elements located at the volume of interest. In this way you avoid that coil elements detect overfolding artifact signals that may affect spectral quality.
- It is not required to select individual coil elements in the spectroscopy protocols. Coil selection is automatically transferred from the imaging and localizer protocols when the **Queue > Auto Coil select** option is switched on.
- For details with respect to coil positioning and patient positioning in the magnet isocenter, refer to your *System Manual*.

^{1}H MRS measurements of the breast

For ^{1}H MRS examination of the breast use either the Siemens Breast Matrix coil, the 16ch AI Breast Coil, or the 2/4/8-Channel Sentinelle Breast Coil (Sentinelle Vanguard for Siemens) in 8-channel configuration.

➪ A detailed description of these coils is included in your *System Manual*.

! Please ensure careful positioning and fixation of the breast. A short localizer measurement after the breast examination is recommended to check for any patient movement because this can move the tumor out of your voxel position.

➪ For the 1H MRS breast measurement, it is recommended to only select the coil element required.

External reference

A reference solution is present in the coil housing of each of the three breast coils given above for quantifying the choline signal. The choline signal is automatically normalized with an additional measurement of the reference sample signal.

➪ Use the “localizer_ref” protocol stored in the Siemens protocol tree for localizing the external reference solution. Perform a fast SVS measurement without water suppression by using the protocol “svs_se_breast_ref” (the voxel must be placed completely within the reference sample).

Internal reference

An additional possibility for quantifying the choline signal consists of an “internal” reference measurement, that is, in the potential tumor as such. For this purpose, you can perform a fast, non-water suppressed measurement in the potential tumor of identical voxel position and size.

➪ Use the “svs_se_breast_int_ref” protocol stored in the Siemens protocol tree for internal reference measurement.

! The internal reference method is not considered clinically sound for controlling the course of therapies. The behavior of internal water in the tumor during, e.g., chemotherapy is largely unknown.

^{1}H MRS examination of the prostate

For ^{1}H MRS examinations of the prostate the usage of the endorectal coil provides the highest SNR. At 3 T the Spine Matrix and Body Matrix coils can be used without the endorectal coil when the spatial resolution is reduced.

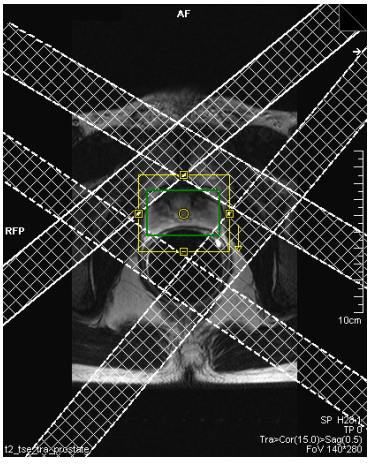
➪ A detailed description of these coils is included in your *System Manual*.

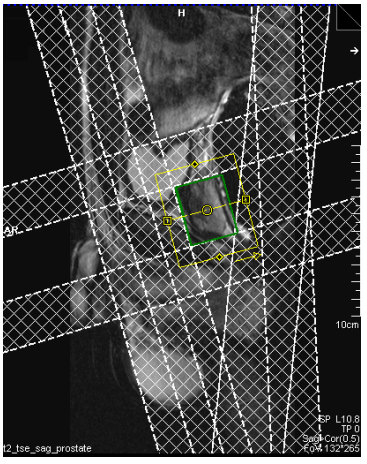
Suppressing fat signals

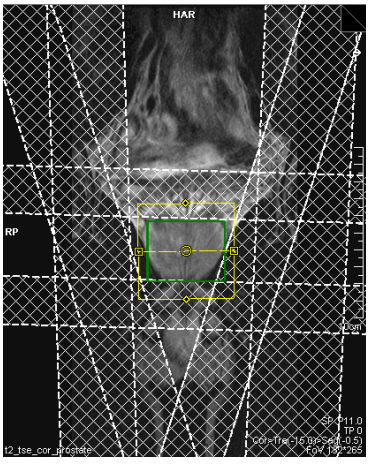
In combination with the “Outer Volume Suppression” and the spectral signal suppression, you are able to effectively suppress interfering fat signals.

It is important that you carefully position the regional saturation pulses for suppressing unwanted signals in the vicinity of the prostate, especially the fat signal.

The following images show the positioning of free saturation regions using the example of a ^{1}H hybrid CSI measurement of the prostate.







Specialities for 3 T

Setting the sequence timing

In the **Contrast/Common** parameter card:

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. It is therefore recommended to manually optimize the magnetic field homogeneity with the interactive shim after completion of the automatic adjustments.
→ Page B.11–17, *Interactive shim*

^{31}P MRS measurements of muscles, heart, liver

Selecting the coil

For ^{31}P MRS measurements of muscles, heart, liver, use the Heart/Liver coil (only for 1.5 T).

The Heart/Liver coil is doubly resonant, i.e., it is resonant for both ^{1}H and ^{31}P frequencies (63.6 MHz or 25.7 MHz; at 1.5 T) and can be toggled between the two resonance frequencies.

The Heart/Liver coil is used for both acquiring ^{31}P spectra as well as anatomical reference images. In addition, the coil is used for frequency adjustment and for shimming based on the ^{1}H signal.

Components of the heart-liver coil

The Heart/Liver spectroscopy coil comprises the following components:

- ❏ Coil cushion
- ❏ Transmitter (for ^{1}H and ^{31}P) and receiver coil (for ^{1}H) with linear polarization (LP)
- ❏ ^{31}P receiver coil with circular polarization (CP)
- ❏ Adapter

Coil cushion

The coil cushion is shaped to fit the patient table. The two coils are located inside the coil cushion.

Transceiver coil

The transceiver coil has the following functions:

- ❏ Excitation and signal reception of the ^{1}H nuclei at 63.6 MHz (at 1.5 T)
- ❏ Shimming based on the ^{1}H water signal
- ❏ Excitation of the ^{31}P nuclei at 25.7 MHz (at 1.5 T)

^{31}P receiver coil

The ^{31}P receiver coil with integrated preamplifier receives the signal of the ^{31}P nuclei at 25.7 MHz (at 1.5 T) with good SNR.

Adapter

The adapter is used to connect the coils to the coil sockets on the patient table. In addition, the adapter housing contains the Tx/Rx switch that allows the transmitter coil to receive signals. A support cushion may be mounted on the adapter housing so that the adapter may be used as a head support for the patient.

➪ The Heart/Liver coil is described in detail in the *System Manual*.

Positioning the patient, positioning the coil and determining the magnet isocenter

!

Do *not* connect another local coil while the Heart/Liver coil is connected.

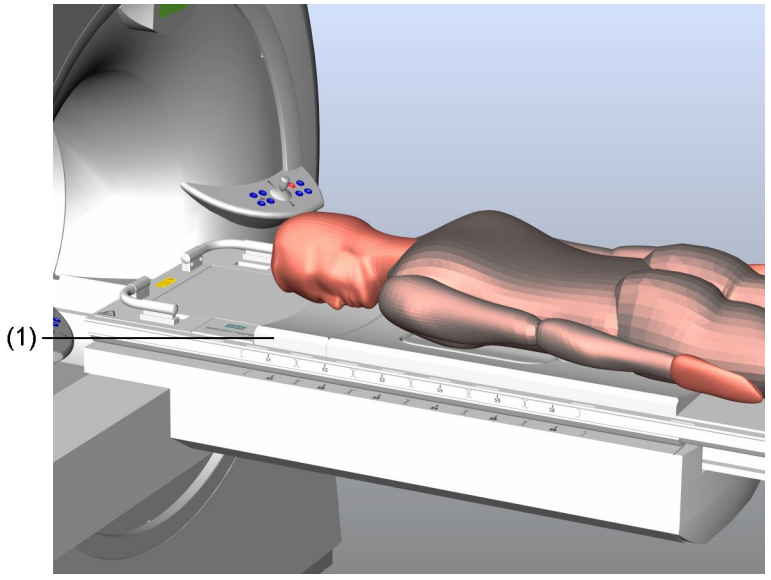
!

The Heart/Liver coil may undesiredly touch the patient's head, especially when examining small children.

If this is the case, use cushions for patient positioning to ensure a distance of at least 2 cm between the patient's head and the Heart/Liver coil.

Measurements in the prone position

- ✧ Remove all Array coils from the patient table.
- ✧ Position the adapter of the Heart/Liver coil at the head end of the patient table.
- ✧ Connect the adapter to coil sockets 1 and 4 on the patient table.
- ✧ Position the adapter cushion on the adapter.
- ✧ Position the coil cushion for the Heart/Liver coil on the patient table so that the recess for the preamplifier is facing away from the magnet.
- ✧ Position the Heart/Liver coil in the coil cushion with the center marking facing down.
- ✧ Connect the Heart/Liver coil to the adapter.
- ✧ Route the coil cable along the side of the patient table and secure it to the table using the cable clamps.
- ✧ Position the patient in the prone position on the coil cushion with the head toward the magnet.
- ✧ Position the patient so that the region to be examined is located in the center of the coil (point of maximum coil sensitivity).
- ✧ Position the patient on the Heart/Liver coil in the prone position. This position suppresses respiratory artifacts better than the supine position.

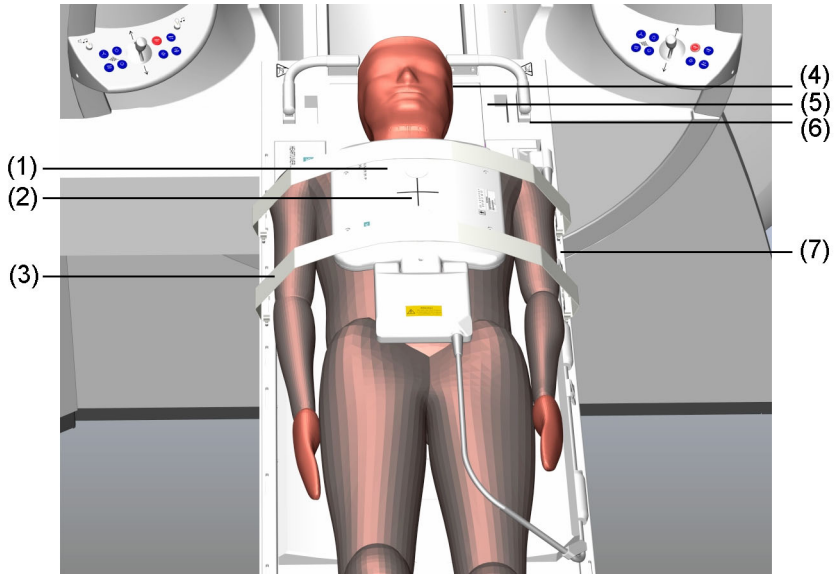


(1) Coil cushion

Measurements in the supine position

- ✧ Remove all Array coils from the patient table.
- ✧ Position the adapter of the Heart/Liver coil at the head end of the patient table.
- ✧ Connect the adapter to coil sockets 1 and 4 on the patient table.
- ✧ Position the back head support on the adapter.
- ✧ Position and secure the patient in the supine position on the patient table with the head toward the magnet.
- ✧ Position the Heart/Liver coil with the center mark facing up on the patient so that the cable outlet is facing away from the magnet.
- ✧ Position the Heart/Liver coil so that the region to be examined is located in the center of the coil (point of maximum coil sensitivity).

- ✧ Secure the Heart/Liver coil using the straps.
- ✧ Connect the coil to the adapter.
- ✧ Route the coil cable along the side of the patient table and secure it to the table using the cable clamps.
- ✧ Position the patient in supine position. Ensure that the Heart/Liver coil is centered over the organ to be examined (if necessary, have the patient move slightly to his side to position both the coil and the organ as close to the magnet isocenter as possible).



(1) Heart/Liver coil
(2) Center marking
(3) Straps
(4) Back-of-the-head support
(5) Adapter
(6) Coil socket
(7) Patient table

Physiologically-controlled measurements

Physiological movements in the body of the patient, such as heartbeat or respiration, may cause motion artifacts, adversely affecting the results of your ^{31}P MRS measurement of muscle, heart, liver. You can prevent such motion artifacts by synchronizing the measurement times with physiological signals (ECG signal, pulse, respiration).
Refer to → ***syngo*** **MR** Operator Manual

If you want to use physiological triggering for a ^{31}P MRS measurement, you have to position special sensors on the patient as part of the measurement preparation.
Refer to the System Manual

These sensors acquire the signals used for physiological triggering.

➪ You can monitor the acquired signals in the examination room via the PMU display at the magnet aperture.

! Physiological triggering is a requirement for ^{31}P MRS cardiac measurements.

The ECG signal is used to trigger the system.

Determining the center of the measurement field

After positioning the patient and coil, you determine the magnet isocenter using the laser light localizer.

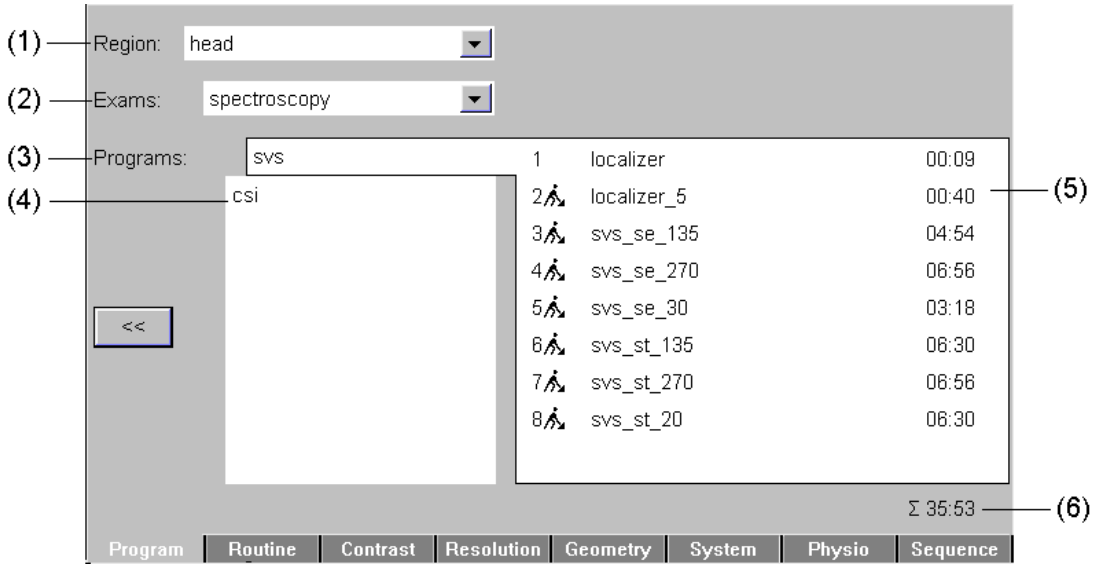
✧ For the ^{31}P MRS examination of the heart, position the laser light localizer on the center mark of the heart/liver coil.

CHAPTER B.4

Preparing the Measurement Program

Once you have registered the patient, the **Program** parameter card is displayed in foreground on the **Exam** task card.

The spectroscopy examination entered during patient registration is now displayed.



(1) Examination region
(2) Available examinations for the selected region
(3) Selected measurement program
(4) Available measurement programs for the selected examination
(5) Protocols with measurement times
(6) Sum of measurement times

The spectroscopy measurement programs contain all protocols available for MR spectroscopy. Unlike the standard measurement programs for MR imaging corresponding to an examination procedures, they are only used as “protocol containers”.

How to compile a “real” spectroscopy measurement program:

✧ Select the suitable protocols from the **Program** parameter card.

✧ Transfer the selected programs to the program control.

✧ Compile the program instructions into a suitable measurement sequence.

You can then edit, stop, or restart the spectroscopy program just like a normal measurement program.
→ ***syngo* MR** Operator Manual

!

You may combine spectroscopy protocols with imaging protocols and store them as measurement programs in the customer area of the **Exam Explorer**.

Selecting the measurement protocols

✧ Select the protocols to be used from the spectroscopy measurement program.

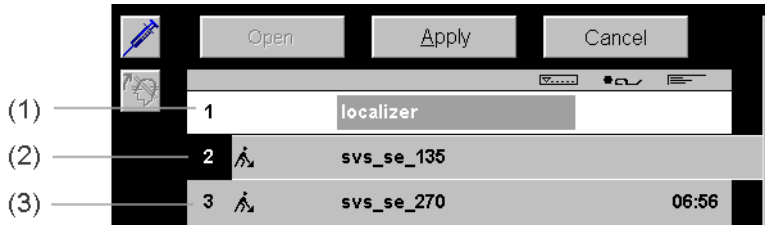
➪ Pressing the **Ctrl** or **Shift** key on your keyboard allows you to select multiple protocols.

Transferring measurement protocols



✧ Click the **<<** button on the **Program** parameter card.
- Or -
Select **Queue** > **Append**.

The selected protocols are transferred to the program control.



(1) Protocol in process for an overview measurement
(2) Open spectroscopy measurement protocol
(3) Spectroscopy measurement protocol in the job queue

➪ You can also drag the selected protocols with the mouse to the program control.

Changing the sequence of measurement protocols

After you have transferred the protocols for your measurement to the program control, adapt the sequence of the measurement protocols. However, you can modify only the lower section of the queue which has not been processed yet.

✧ Select the protocol in the job queue that you want to move and drag it with the mouse to the desired position.

CHAPTER B.5

Reference Images

After transferring the protocols to the program control, you measure a localizer to obtain reference images for positioning the measurement object (VOI/CSI slice/CSI slab). The reference images have to be measured at the same table position and exist as ND images.
→ Page B.5–2, *Scan at Center*

! How to guarantee the correct spatial allocation of spectra to reference images:

- ❏ Make sure that the patient's position does not change during or between the acquisition of reference images and spectra.
- ❏ Instruct the patient not to move if at all possible during the entire examination as well as during measurement pauses.
- ❏ Please note that reference images are usually acquired at the beginning of the examination and spectra at the end of the examination.

If reconstructed reference images of the selected region exist, you may use these reference images for positioning and load them into the image area of the **Exam** task card. When loading with an open spectroscopy protocol, the table moves to the position of the reference images. DIS2D images are converted automatically to ND images.

⇨ An MRI always precedes a ^{1}H MRS measurement. When planning ^{1}H MRS, always use reference images in 3 spatial orientations. Optimally, use subtraction images in 3 planes for precise tumor coverage.

Scan at Center

In this software version, during imaging you can plan isocentric measurements in distortion-corrected reference images (DIS2D/DIS3D) for various measurement regions. This results in MR images being created at various patient table positions.

To plan spectroscopy and for post-processing however, non-distortion corrected images (NDIS) in the three main orientations are required. The spectroscopy measurements have to be performed at the same table position as the NDIS images used for planning.

scan@center-Localizer

To ensure an optimized acquisition in the isocenter for spectroscopy, the spectroscopy protocols contain an additional *scan@center* localizer. As a result, NDIS images are generated in the isocenter for a prescribed measurement region. The images are used for optimum planning and post-processing in spectroscopy.

Planning in existing reference images

When performing spectroscopy after a routine imaging examination, the existing images are generally used to plan the measurement:

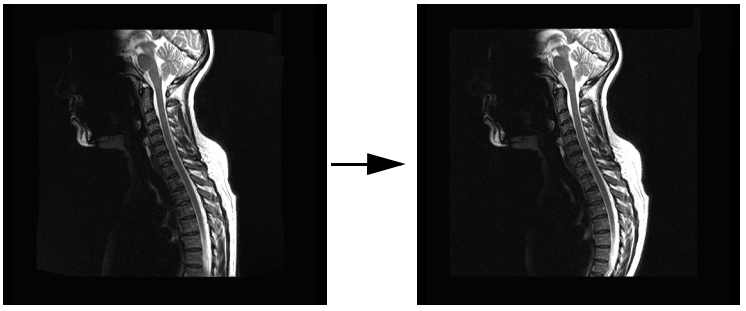
- **Region in the isocenter**
  In the images, the region to be examined using spectroscopy is in the cranial-caudal direction near the isocenter.
- **Region outside the isocenter**
  In the images, the region to be examined using spectroscopy is in cranial-caudal direction further outside (> 5 cm) the isocenter.

Region in the isocenter

Centrally localized images of the examination region exist. The distortion-corrected images have to be converted to NDIS images:

✧ Select a reference image with high contrast in the GSP.

✧ Select **Evaluation > Inverse Distortion 2D Correction**.



All images of the series are converted to NDIS images. DIS2D/ DIS3D images and images from other table positions are unloaded. A new series with the appendix “Sx_ND” (Sx= xth newly converted series) is created.
→ ***syngo* MR** Operator Manual

✧ Select **Scroll > Find Localizer** to find reference images of other orientations.

➪ The master layout serves as an orientation tool.
→ ***syngo* MR** Operator Manual

Or

✧ Acquire the missing planning images with the **localizer_5** protocol.

Region outside the isocenter

Centrally localized images of the examination region do not exist. New NDIS images have to be acquired in the isocenter:

✧ Position the slices in the existing reference images.

✧ Start the **localizer_5@center** protocol.

The table moves to the optimum position in the isocenter. 5 NDIS images are acquired in each of the 3 main orientations. They are used as planning and reference images for the spectroscopy examination.

Measuring reference images

The following protocols for localizer measurements are available in the spectroscopy measurement programs:

❏ **localizer**

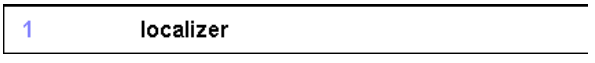
❏ **localizer_5** for precise localization of the measurement region

❏ **localizer_@center**, **localizer_5@center** for optimized acquisition in the isocenter

❏ **localizer_ref** for localizing the reference solution as part of a breast measurement with external reference

❏ **localizer_in-plane_CSI** and **loc_in-plane_CSI@center** for planning a CSI examination

The protocol currently being measured is highlighted in white in the program control.



The progress of the measurements is displayed on the status bar.

After the measurement, the program reconstructs the reference images. After the image reconstruction is complete, the protocol is highlighted in grey in the queue and the series icon for the image data is displayed to the right:



The reference images measured are automatically loaded in the image area of the **Exam** task card.

! If you measure a second localizer using a different table position, these reference images are *not* automatically loaded into the image area.

localizer



The protocol measures three orthogonal slices.

The protocol starts automatically once you load it into the program control.

localizer@center



The protocol measures three orthogonal slices in the isocenter.

The protocol is provided for regions in cranial-caudal direction away from (> 5 cm) the isocenter. The table then moves to the optimum position for the examination region.

Measuring “localizer_5”





The protocol measures 5 slices along each main direction.

✧ Position the slices.

✧ Click **Apply**.

The **localizer_5** measurement is started.

➪ For examination regions further outside the isocenter, the protocol **localizer_5@center** may be used in the same manner.

localizer_ref



The protocol measures three orthogonal slices to localize the reference solution for Choline quantification.

Measuring “localizer_in-plane_CSI”



The protocol measures a reference image that matches the position, tilt, and orientation of the CSI slice to be measured.



✧ Click **Apply**.

The **localizer_in-plane_CSI** measurement is started.

➪ For examination regions further outside the isocenter, the protocol **loc_in-plane_CSI@center** may be used in the same manner.

You can then apply the geometry parameters of the protocol to a CSI protocol.
→ Page B.10–5, *Copying measurement parameters*

Loading reference images

Images from an examination that have already been reconstructed may be used as reference images if they come from the same table position. For example, images acquired with a specific weighting, or that clearly show the structures of interest, are suitable.

If the reference images come from the current examination and have not been distortion corrected (ND), you can load them directly from the **Program Control**. Otherwise, generate an ND image series from suitable distortion-corrected images.
→ ***syngo* MR** Operator Manual

!

The reference images of the localizer normally show the region to be examined in the three main orientations (sagittal, transverse, and coronal).

However, the orientation of reference images loaded manually depends on the orientation of the measured slices of the protocol and may deviate from the main orientations.

Loading from the program control



✧ Double-click the series icon of the corresponding localizer.

- Or -
Select the processed localizer protocol from the job list and select **Load Series** from the pop-up menu.

Loading from the patient browser

✧ Double-click the reference image series in the **Patient Browser**.
- Or -
Drag the reference image series with the mouse to the image area of the **Exam** task card.

Editing the display of reference images

Before planning the region to be examined, you should first optimize the display of reference images. Reference images can be windowed, zoomed, or moved within the image segment. You can show position lines to indicate the position of the other reference images.

✧ Change the contrast and brightness of the reference images.

✧ Change the size and position of the reference images.

✧ Show reference image position lines.

➪ For detailed information, please refer to
→ ***syngo* MR** Operator Manual

Selecting the nearest reference images

After measuring and loading reference images into the image segments, you are going to search the image stacks for the reference image that best visualizes the structure to be examined.

The measurement volume of the current protocol (VOI for SVS measurement or CSI slice for 2D CSI measurement) will typically be located in front of or behind the plane of the selected reference image. This can be identified by the dashed lines in the measurement volume graphic.
→ Chapter B.6, *Graphic Display of Measurement Objects*

For the measurement, however, the measurement volume should be positioned in the plane of the selected reference image. The **Nearest** function lets you automatically move the center of the measurement volume into the plane of the reference image. The reference images with planes nearest to the position of the measurement volume are displayed in the other two reference image segments.

Selecting a reference image

✧ Scroll through the image stacks until you find a suitable reference image.

➪ For detailed information on scrolling with the dog ears, icons, or menu commands, refer to
→ ***syngo* MR** Operator Manual

Aligning a CSI slice in parallel

For a 2D CSI measurement, it is sensible to align the CSI slice parallel to the reference image plane prior to using the **Nearest** function.

✧ Select **Tools > Copy Image Position**.

The position and orientation of the selected reference image is applied to the CSI slice.

Selecting the nearest images

✧ Select **Scroll > Nearest**.

The center of the measurement volume is moved into the plane of the selected reference image. The direction of movement is perpendicular to the plane of the reference image.

The measurement volume graphic in the active reference image segment is no longer displayed as dashed lines, but rather as solid lines.

The reference images with planes nearest to the position of the measurement volume are displayed in the other two reference image segments.

CHAPTER B.6

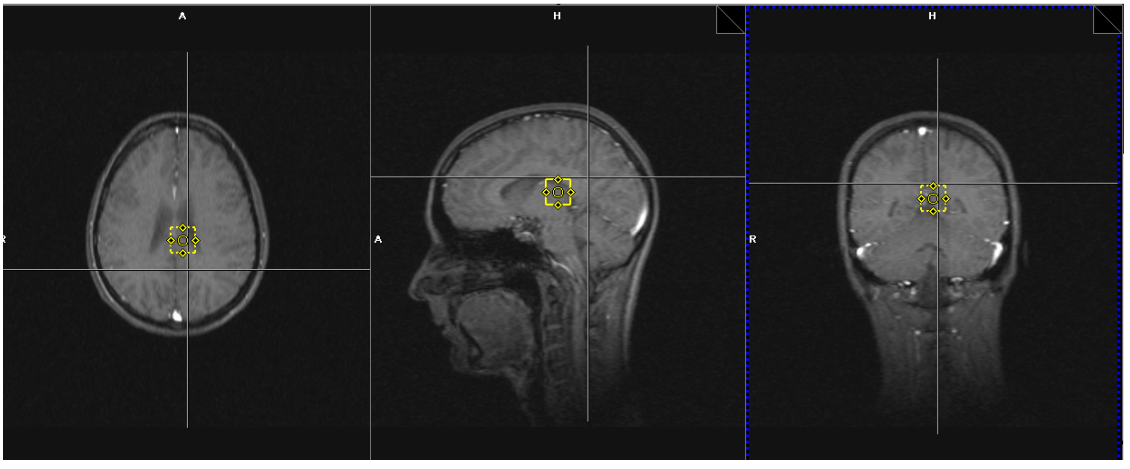
Graphic Display of Measurement Objects

The graphic displayed in the reference images depends on the measurement object of the current protocol:

Measurement	Reference image
SVS measurement	Graphic for the **VOI** defined in the protocol
2D CSI measurement	Graphic for the **CSI slice** defined in the protocol
3D CSI measurement	Graphic for the **CSI slab** defined in the protocol

VOI display

The VOI is displayed in reference images as a square with yellow contour lines.



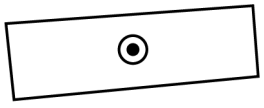
Transverse view Sagittal view Coronal view

- If the VOI *intersects* the reference image, it is displayed as solid lines.
- If the VOI is located *fully behind* or *in front of* the reference image (i.e., the VOI does not intersect the reference image), it is displayed as dashed lines.

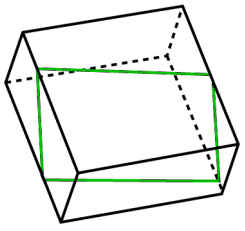
The dashed lines indicate a warning: You are alerted to the fact that the region displayed in the image is *not* located inside the VOI.

In contrast to the projection of slice groups, the hidden corners of a volume element are indicated by dashed lines.

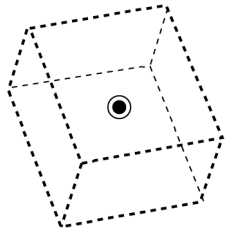
Examples



Volume element intersects the reference image *vertically*.



Volume element intersects the reference image *obliquely*.
The intersecting plane is displayed with green lines.

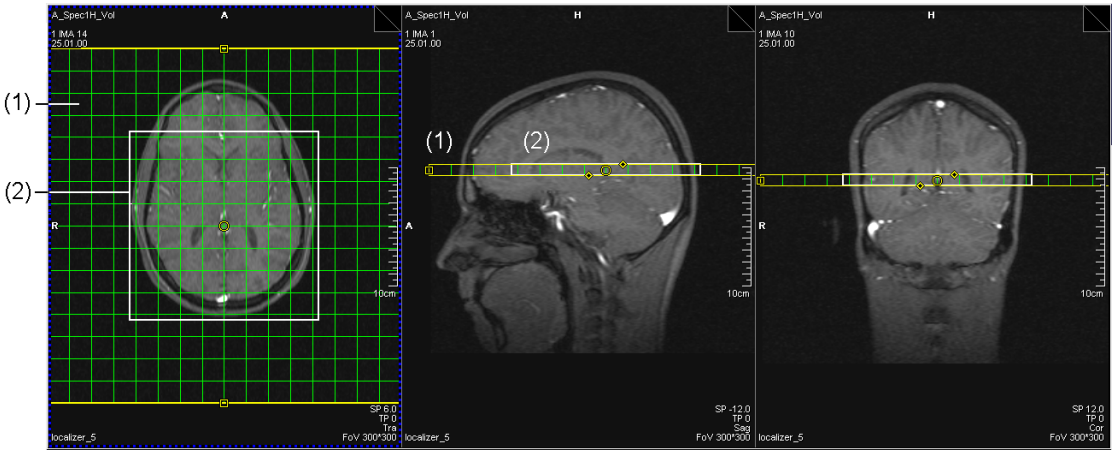


The volume element is located *in front of* or *behind* the reference image.

Display of a CSI slice

The display of the CSI slice is defined by its spatial position with regard to the reference image. Therefore, the display of graphic objects is an indicator of their position.

For hybrid CSI sequences, e.g. **csi_se**, the excited volume (VOI) is displayed together with the actual CSI slice. It is located in the center of the CSI slice and matches the CSI slice with respect to position, orientation, and thickness. The extent of the VOI, however, is always less than that of the CSI slice to prevent overfolding or cross-talk of signals. Consequently, the VOI should be adapted to the patient's anatomy.

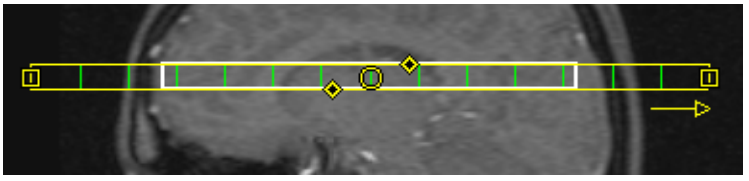


(1) CSI slice
(2) VOI

Guidelines for CSI slice display:

❏ The display guidelines are basically the same as for slices and slabs.
→ ***syngo* MR** Operator Manual

❏ If the CSI slice intersects the reference image, it is indicated by solid lines:



❏ If the CSI slice is located completely behind or in front of the reference image (i.e., the VOI does not intersect the reference image), it is indicated by dashed lines:



❏ CSI slices can be displayed in box or package mode only. Line mode is not supported.

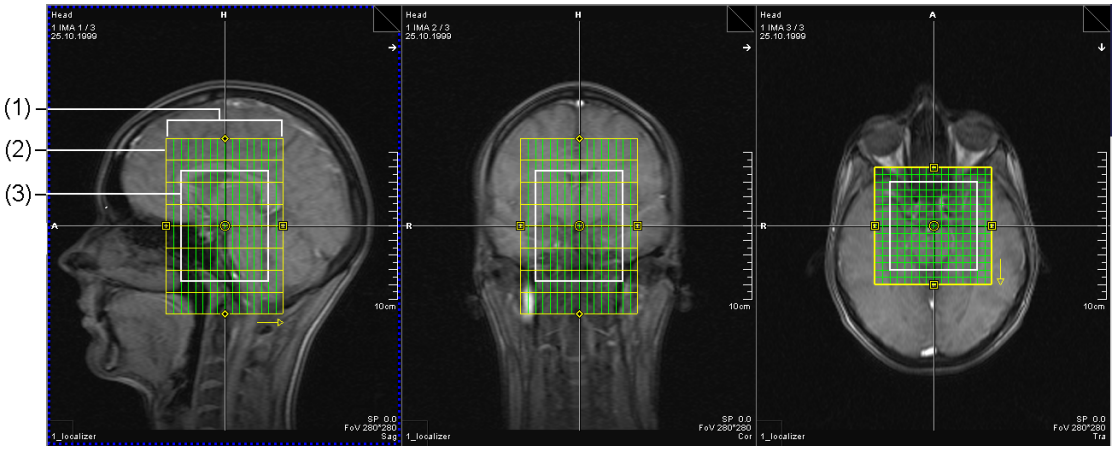


❏ The arrow displaying the phase-encoding direction is irrelevant for planning a CSI measurement. The reason for this is that phase-encoding is used in all directions for spatial encoding of CSI measurements.

Display of a CSI slab

For 3D CSI measurements, an additional phase-encoding is applied to the spins in the slice-selection direction. This allows you to measure an entire volume range.

For graphic slice positioning, these volume ranges are defined as CSI-slabs. These CSI-slabs consist of individual CSI slices that adjoin without a gap or overlap.



(1) CSI slab
(2) Individual CSI slice
(3) VOI

CHAPTER B.7

Adapting the Parameters for an SVS Measurement

You start by adapting the position, orientation, and size of the measurement volume (VOI) to the patient's anatomy.

You can then check all other protocol parameters and make adjustments as necessary.

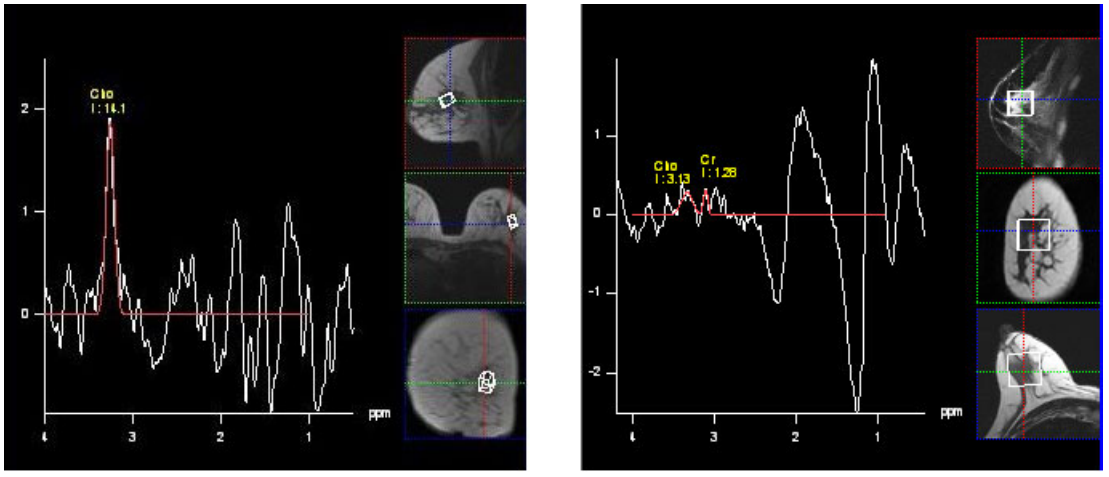
Parameters modified for the open protocol can be copied and applied to other measurement protocols.
→ Page B.10–5, *Copying measurement parameters*

Adapting the VOI

Properly setting the position and size of the VOI has a significant impact on the quality of the resulting spectrum and on its suitability for subsequent evaluation.

Example

When adjusting the VOI for ^{1}H MRS at the breast, a suitably small VOI has to be selected and fully positioned within the potential tumor to obtain a meaningful evaluation. If there is fat tissue within the voxel, the fat signal may be so high that it hides the choline signal.



(1) VOI suitably small and placed correctly, clear choline signal
(2) VOI too large, choline is suppressed by strong lipid signals

Procedure

You can adapt the VOI

❏ *graphically* with the mouse
❏ *numerically* on the **Routine** or on the **Geometry-Common** parameter cards.

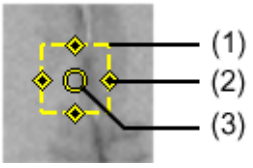
You can save a reference image with the modified VOI graphic for documentation purposes.

➪ If the VOI does not intersect the reference images, you can search for reference images nearest to the position of the VOI.
→ Page B.5–8, *Selecting the nearest reference images*

Adapting the VOI graphically

The VOI in each segment can be moved, rotated, and resized using the mouse. The display of the VOI in other segments is adapted accordingly.

Handles are displayed on the contours lines and on the center point of the selected VOI to allow for graphical editing:



(1) Contour line
(2) Handles for resizing
(3) Center handle for moving

During graphical adjustments, a tool tip indicating position, extent, orientation, or rotation of the VOI is displayed in the reference image and updated dynamically.

After graphical adjustment, the corresponding values in the input fields of the **Routine** and **Geometry - Common** parameter cards are updated automatically.

Moving the VOI



✧ Click the center point with the mouse and move the VOI to the required position.

➪ When moving the VOI with the **Shift** key pressed, the current position of the VOI is displayed.

Resizing the VOI



✧ Click a handle with the mouse and adjust the VOI to the required size.

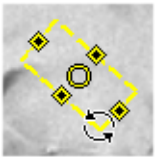
The VOI is enlarged or reduced symmetrically without changing the center.

➪ If you drag the mouse while pressing the **Alt** key, the VOI is enlarged or reduced in one direction only. In this case, the center is shifted accordingly.

! Once the VOI has been resized to its maximum or minimum dimensions, the contour line becomes thicker.

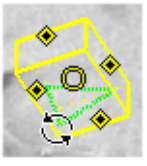
Rotating/tilting the VOI

How to rotate the volume element about that axis that runs through the center *perpendicular* to the reference image:



✧ Click the contour line with the mouse and rotate the VOI in the required direction.

How to tilt the volume element about that axis that runs through the center *parallel* to the reference image:

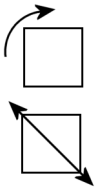


✧ Click the contour line with the mouse while pressing the **Alt** key and tilt the VOI in the required direction.

➪ The point of intersection with the reference image is displayed in green.

How to rotate and tilt the volume element freely in space:

✧ Click the contour line with the mouse while pressing the **Ctrl** key and rotate or tilt the VOI in the required direction.



Rotate the volume element with a tangential movement.

Tilt the volume element with a radial movement.

! For free rotation, please note the limitation regarding the preferred transverse orientation.
→ Page B.7–7, *Setting the orientation of the VOI*.

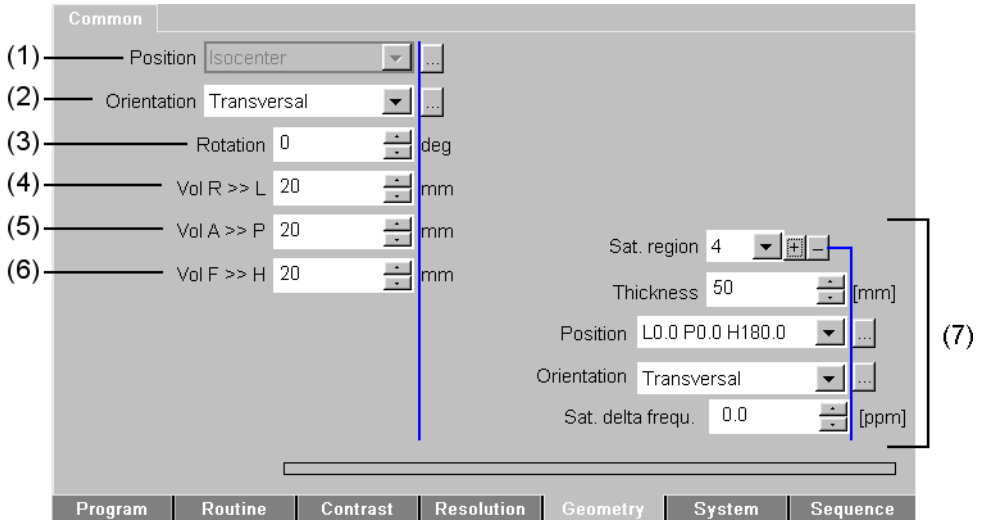
Adapting the VOI numerically

In addition to graphical adjustment, you can set the geometric parameters of the VOI (position, orientation, angle of rotation, size) numerically. Perform numerical adjustments the **Routine** or **Geometry - Common** parameter cards.

Once you press the **Enter** key after a numerical adjustment or switch to a different operating element, the VOI graphic updates.

Displaying the parameter card

✧ Click the **Geometry - Common** (or **Routine**) parameter card.



(1) Position of the VOI (center)
(2) Orientation of the VOI
(3) Angle of rotation
(4) Extent from right to left (R-L direction)
(5) Extent from anterior to posterior (A-P direction)
(6) Extent from feet to head (F-H direction)
(7) Saturation region parameters

Setting the position of the VOI

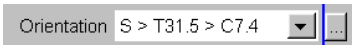


✧ Click the **...** button next to the **Position** field.

The **Position** dialog window opens.

✧ Establish the exact position of the VOI in the **Position** dialog window.
→ ***syngo* MR** Operator Manual

Setting the orientation of the VOI



✧ Select a basic orientation (**Sagittal**, **Coronal**, or **Transverse**) from the **Orientation** selection list.

➪ The orientation parameter consists of a *basic orientation* (e.g., **S** for sagittal) and two rotation values (optional) indicating a *direction of rotation* and an *angle of rotation* (e.g. **T31.5**: transverse direction of rotation with an angle of 31.5 degrees; **C7.4**: coronal direction of rotation with an angle of 7.4 degrees).

✧ Click the **...** button next to the selection list.

The **Orientation** dialog window opens.

✧ Establish the exact orientation of the VOI in the **Orientation** dialog window.
→ ***syngo* MR** Operator Manual

!

For spectroscopy measurements of the head, always select the basic **Transverse** orientation.

Since you can freely select the extent of the VOI, this does not constitute a real limitation. The basic **Transverse** orientation effects a temporal sequence for slice selection proven to be the preferred method for spectroscopy applications of the head (*T. Ernst, L. Chang; Magn. Reson. Med., 36; 462-468; 1996*).

Setting the angle of rotation of the VOI



Rotation determines the angle about which the VOI is rotated in the slice plane defined by the orientation:

✧ Enter the angle (between -44° and +44°) in the **Rotation** field.

Setting the size of the VOI

Use the **VOI** parameters to define the extent of the volume element in the three spatial directions.

Expansion	Direction
Vol R >> L	Extent of the VOI in the R-L direction in millimeters [mm]
Vol A >> P	Extent of the VOI in the A-P direction in millimeters [mm]
Vol F >> H	Extent of the VOI in the F-H direction in millimeters [mm]

✧ Enter the size values (in mm) in the corresponding fields.

Saving the reference image and VOI graphic

After completing graphical and numerical adjustments, you can document the VOI definition by saving a reference image including VOI graphic.

✧ Select the reference image.

✧ Select **Patient > Save As**.

The **Save As** dialog window opens.

In the **Save As** dialog window, you set whether the reference image is added to the measured reference series or stored in a new series, and start the Save process.
→ ***syngo* MR** Operator Manual

Setting saturation regions

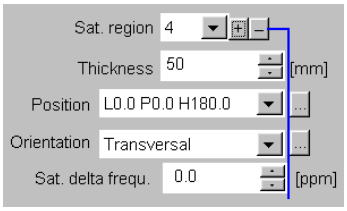
In SVS measurements with a spin-echo sequence, you can add up to eight freely positionable saturation regions to delineate the VOI. Signals from the minimally excited regions outside the visible VOI can be suppressed using these regional saturation pulses.

Displaying the parameter card

✧ Open the **Geometry - Common** parameter card.
→ Page B.7–6

Adding saturation regions

The saturation regions are numbered and may be positioned as required.



✧ If necessary, you can add up to eight saturation regions and adjust their thickness, position, and orientation.
→ ***syngo* MR** Operator Manual

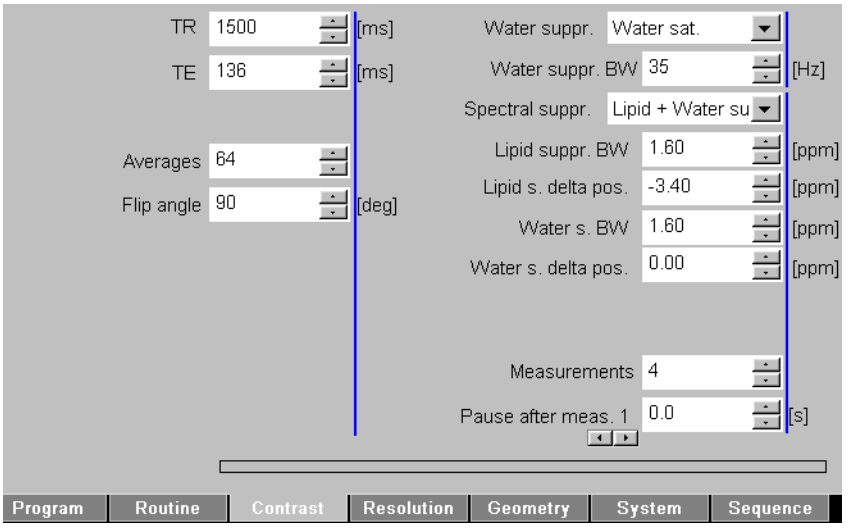
✧ In the field **Sat. delta frequ.**, enter the value of the frequency shift in the saturation pulse (e.g., -3.4 ppm for lipids).

Adjusting protocol parameters

After adjusting the VOI to the patient's anatomy, you can check and edit the other protocol parameters.

Setting contrast parameters

✧ Click the **Contrast** parameter card.



✧ Change the parameters desired in the corresponding fields.

The following briefly describes the individual parameters.

TR

The **Repetition Time** (TR) is the time that elapses between two excitations in sequence. Changing the repetition time affects image contrast:

❏ Short repetition times produce good T1 contrast for spin-echo sequences.

❏ Long repetition times produce good T2 contrast for spin-echo sequences.

TE

The **Echo Time** (TE) is especially important e.g. for lactate measurements. Phase reversal of the lactate peak during a spin-echo measurement (at 135 ms) is another indicator for determining lactate.

TM

With the **TM** parameter (specific time interval, for STEAM sequences only), you set the time interval between the 2nd and 3rd RF pulse for protocols based on STEAM sequences.
→ Page A.2–2, *STEAM sequence*

During this time, the measured magnetization is oriented in the longitudinal direction and therefore only subject to T1 relaxation. This means that the duration of the TM interval does not contribute to echo time TE.

➪ The T1 weighting can be enhanced by extending the TM interval.

Averages

Through the number of averagings, you establish how often the results of repeated measurements are averaged in order to improve signal-to-noise ratio.

➪ Please note that the greater the number of measurements, the longer the measurement time.

Flip angle

The flip angle of the spin rotational axis in degrees [°] indicates the extent to which the longitudinal magnetization is moved out of the z-direction of the magnetic field by the RF pulse. With a 90° excitation pulse, for example, the longitudinal magnetization is rotated by 90° out of the z-direction. The flip angle directly affects image contrast.

For spin echo sequences, you can enhance the T1 contrast by reducing the flip angle.

Water suppression

To reduce the high-intensity water signal, it should be suppressed already during data acquisition.

Option	Description
Water sat.	During the measurement, a water suppression pulse is transmitted to fully suppress the water signal.
Weak water suppr.	The water signal is reduced but not fully suppressed. This allows you to include the water line in various post-processing functions.
None	No water suppression is applied during the measurement. The water suppression module is completely deactivated.
Only RF off	This option can be used to measure a reference raw data set if you want to perform eddy current compensation during a spectroscopy evaluation. → Page C.8–21, *Adjusting eddy current compensation*

! To measure a reference raw data set for eddy current compensation, the protocol is measured twice: for the first measurement, water suppression is activated (**Water sat.** or **Weak water suppr.** options) to acquire the spectroscopy raw data. For the second measurement, the **Only RF off** option is selected to acquire the reference raw data.

! Activating or deactivating water suppression does *not* affect the configuration of the water suppression adjustment.
→ Page B.9–2, *Shim mode*

Water suppr. Bandwidth

Use this parameter to set the bandwidth of the high-frequency pulse for water suppression. A value of 35 Hz is highly suitable for a magnetic field strength of 1.5 T. A higher value should be set at 3 T.

⇨ Due to the higher bandwidth, the water signal is suppressed more effectively. However, the effect on adjacent signals (e.g., creatine, (CH_2)) increases as well.

Spectral signal suppression

Selected spectral signals can be suppressed using MEGA RF pulses within the localizing part of the sequence. The following options are available:

Spectral signal suppression	Description
Lipid suppr.	Suppression of fat signals
Water suppr.	Suppression of water signals
Lipid + Water suppr.	Suppression of fats and water signals
None	No spectral suppression

Fat suppression pulse

If you have selected *Lipid suppression* or *Lipid + Water suppression* for spectral signal suppression, you can set the bandwidth of the fat suppression pulse used in the **Lipid suppr. BW** input field.

⇨ If *Lipid + water suppression* is selected, the bandwidths of the two suppression pulses are coupled. The value for **Lipid suppr. BW** input field also applies as the bandwidth for the water suppression pulse, and is automatically entered in the **Water suppr. BW** input field

Spectral shift

If you have selected *Lipid suppression* or *Lipid + Water suppression* for spectral signal suppression in the field **Lipid s. delta pos.**, you can set the spectral shift of the fat suppression pulse to be used.

Water suppression pulse

If you have selected *Water suppression* or *Lipid + Water suppression* for spectral signal suppression, you can set the bandwidth of the water suppression pulse used in the **Water suppr. BW** input field.

- If *Lipid + water suppression* is selected, the bandwidths of the two suppression pulses are coupled. The value for **Water suppr. BW** also applies as the bandwidth for the water suppression pulse, and is automatically entered in the **Lipid suppr. BW** input field

Spectral shift

If you have selected *Water suppression* or *Lipid + Water suppression* for spectral signal suppression in the field **Water s. delta pos.**, you can set the spectral shift of the water suppression pulse to be used.

Measurements

For dynamic or spectroscopy measurements with time resolution, you can define how many times a measurement should be performed.

Pause after meas.

This parameter allows you to set the delay times between the individual measurements of a dynamic spectroscopic examination.

- If you allow the mouse pointer to rest on the field name, a brief text regarding the pause time is displayed.
- If you hold the mouse pointer over an input field of the spin box, a tool tip will appear that shows the starting and ending time of the first 10 scans.

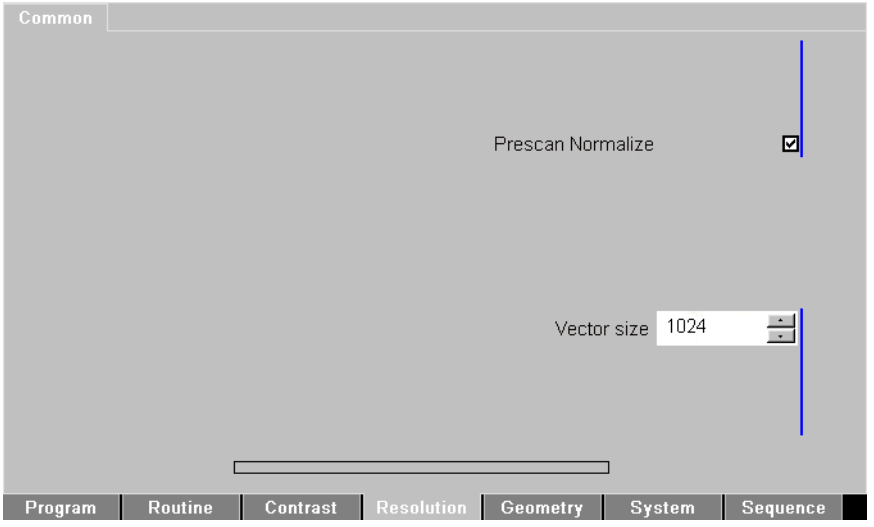
!

Up to 64 individual pauses may be entered. However, in most cases you will only enter one pause time for all measurements or set the pause time to zero.

If you increase the number of measurements to 66, you can set only one pause automatically.

Setting parameters for resolution

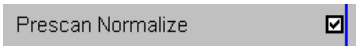
✧ Click the **Resolution - Common** parameter card.



Prescan Normalization filter

This filter has to be switched on when using surface and matrix coils. As a result, inhomogeneities produced by the receiver profile of the coil element are normalized. The Prescan normalization filter is selected/deselected as default in the respective protocols.

➪ **Prescan Normalization** should be selected when using the Endorectal coil in conjunction with a Spine or Body Matrix element.



✧ Select the **Prescan Normalize** checkbox to activate this filter.

Modifying the vector size

With the **Vector size** parameter, you set the number of measurement points for sampling the spectral dimension (data points), and therefore the resolution.

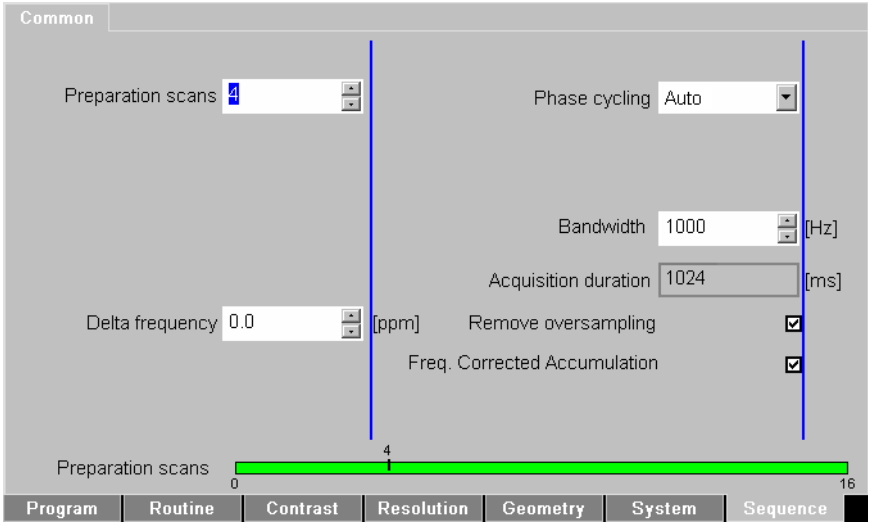
The following settings are available:
- ❏ 512
- ❏ 1024 (default)
- ❏ 2048



✧ Enter the value for the vector size in the field.

Setting sequence parameters

✧ Click the **Sequence-Common** parameter card.



✧ Change the parameters desired in the corresponding fields.

The following briefly describes the individual parameters.

Preparation scans

With this parameter you set the number of preparation measurements. The result is an equilibrium magnetization for the following MR experiment.

➪ Data acquisition is deactivated during preparation scans.

Delta frequency

With this parameter you indicate a frequency shift based on the system frequency. This lets you determine the spectral component for which you want to obtain precise slice selection.
→ Page A.2–22, *Delta frequency*

Phase cycling

You select a phase cycle to eliminate the signal interference. The following options are available:

Option	Description
None:	no phase cycle (not recommended)
Auto	selects the phase cycle of the longest cycle that fits into the number of acquisitions
2 steps	single phase cycle
8 steps	eliminates all signal interference of the slice-selective pulses (J. Hennig; J. Magn. Reson. 71; 212-228; 1987)
EXOR cycle	4 steps (G. Bodenhausen et al.; J. Magn. Reson. 27; 511-514; 1977)
16 EXOR cycle	16 steps, eliminates all signal interference of the slice-selective pulses

Bandwidth

With this parameter you determine the current ADC bandwidth during data acquisition. The bandwidth may be varied between 1 and 2 kHz. The typical ^{1}H MRS signals are completely resolved at magnetic field strengths of 1 T and 1.5 T using a bandwidth of 1 kHz and 2 kHz at a magnetic field strength of 3 T.

Acquisition duration

The parameter indicates the current read-out time. The read-out time is the product of the number of measurement points (vector size) and the inverted bandwidth. The read-out time is read-only and cannot be modified.

Remove oversampling

This checkbox is activated by default. The oversampling data are removed during automatic evaluation of spectroscopy raw data. This produces a ringing effect in the time signals which does not adversely affect the frequency data.

➪ If you do not want to evaluate measured spectroscopy data with SIEMENS software, it is advisable to not remove the oversampling data.

Frequency Corrected Accumulation

The ^{1}H MRS SVS sequence contains internal frequency correction to minimize the artifacts caused by respiration.

When this function is switched on, the frequency of each individual acquisition is adjusted to the frequency of the first (reference) acquisition. The corrected scan is then accumulated. This correction algorithm is switched on in breast spectroscopy protocols and is automatically applied during measurements.



✧ Select the **Freq. Corrected Accumulation** checkbox to activate this function.

➪ When this parameter is activated, the **Water suppression** parameter is set to **Weak water suppr.** automatically. Spectral water suppression should not be activated.

CHAPTER B.8

Adapting the Parameters for a CSI Measurement

Start by adjusting the position, orientation, and size of the measurement object (CSI slice for 2D CSI measurements or CSI slab for 3D CSI measurements) to the patient's anatomy.

- In case of CSI measurements using a spin echo sequence, you can also position saturation regions, minimize the chemical shift artifact using the **Fully excited VOI** option, or select spectral saturation.

After adjusting the measurement object, you continue by checking and if necessary adjusting the other protocol parameters.

- Parameters modified for the open protocol can be copied and applied to other measurement protocols.
  → Page B.10–5, *Copying measurement parameters*

Adjusting the CSI slice (2D CSI)

You can adjust the display of the CSI slice by showing or hiding the CSI matrix or by showing the projection on the reference image in case of double-oblique CSI slices.

Next, you can adjust the CSI slice parameters. You either work with the mouse in the reference image (graphical adaptation) or on the parameter cards **Routine** or **Geometry-Common** (numerical adaptation).

You can save a reference image with the modified CSI slice graphic for documentation purposes.

Hybrid CSI slices

When you move, rotate, or modify the slice thickness of a hybrid CSI slice, the VOI is changed accordingly.

Oblique CSI slices

In addition to orthogonal slices, you may perform measurements using oblique or double-oblique CSI slices. To post-process these CSI data, at least one reference image has to have the same position and orientation as the oblique or double-oblique slice. For this reason, you should use the slice parameters from the reference image of a suitable localizer (**Localizer_in-plane_CSI**) when positioning oblique CSI slices.

You can subsequently adapt the position in the defined plane ("in-plane") and the extent of the CSI slice to the anatomy of the patient.

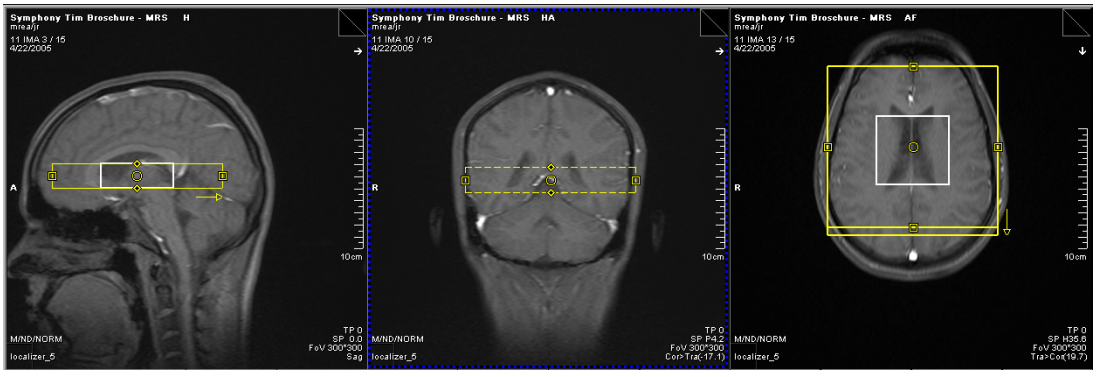
Setting the display of the CSI matrix

You can select whether to display the CSI slice graphic without a matrix, with the measurement matrix, or with the image matrix available after reconstruction.

Hiding the matrix

✧ Select **View > CSI Matrix > No Matrix**.

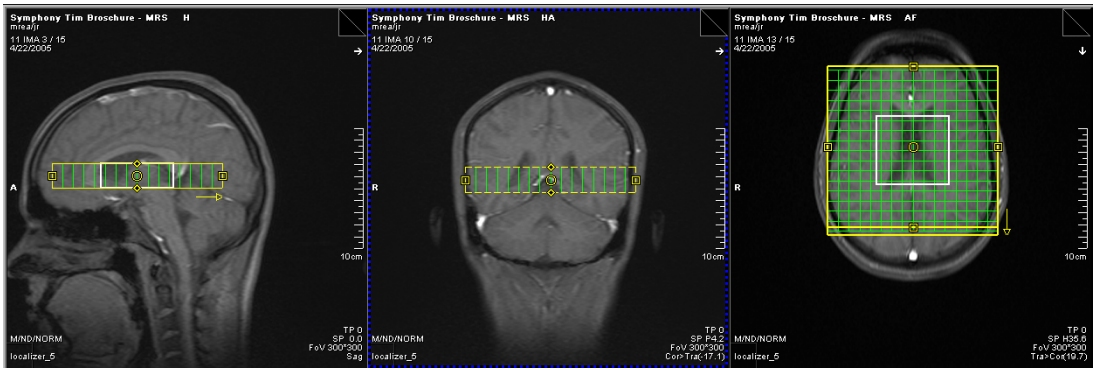
The CSI slice graphic is displayed without a matrix.



Measurement matrix

✧ Select **View > CSI Matrix > Scan Matrix**.

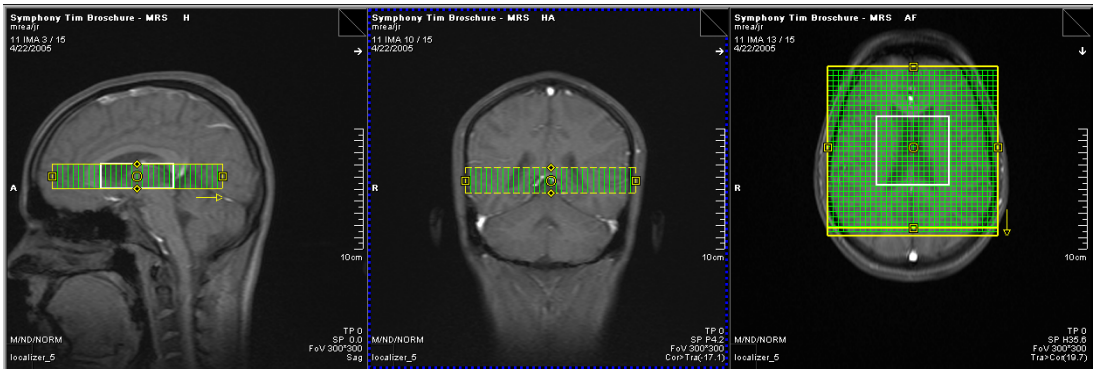
The CSI slice graphic is displayed with the scan matrix.



Showing the interpolated matrix

✧ Select **View > CSI Matrix > Interpolated Matrix**.

The CSI slice graphic is displayed with the interpolated image matrix.

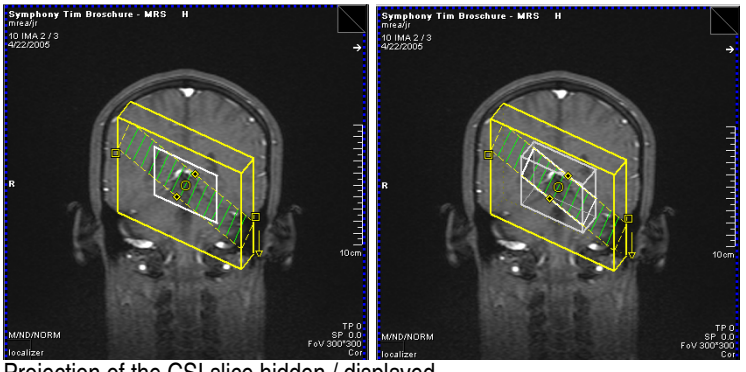


Showing the projection of the CSI slice

For CSI slices that are double-oblique with regard to the reference image, you may display the projection of the CSI slice onto the reference image.

✧ Select **View > Graphics > Projection On**.

The projection of the CSI slice is displayed.



Projection of the CSI slice hidden / displayed

Using the position and orientation from a reference image

When positioning oblique CSI slices, you should use the slice parameters from a reference image of the corresponding localizer (**Localizer_in-plane_CSI**).

✧ Load the reference image to be used for positioning the CSI slice into an image segment.
→ ***syngo* MR** Operator Manual

✧ Select **Image Tools > Copy Image Position**.

✧ If the CSI protocol is open, select **Image Tools > Paste Image Position**.

The position and orientation of the reference image is applied to the CSI slice.

- You can still change the position of the CSI slice in the predefined plane (“in-plane”). Do not make further changes to the orientation or the position perpendicular to the plane.
- Similar to SVS measurements, the preferred slice orientation for CSI measurements is transverse.
  → Page B.7–7, *Setting the orientation of the VOI*
  → Page B.8–8, *Orientation of the CSI slice*

Adapting the CSI slice graphically

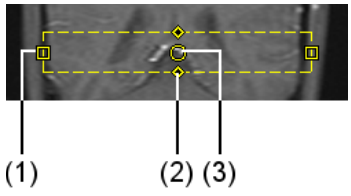
You have applied the orientation and position from a reference image to the CSI slice.

The procedure for adapting the position and extent of the CSI slice to be measured precisely to the anatomy of the patient is similar to the procedure for slice positioning in MR imaging.
→ ***syngo* MR** Operator Manual

In addition, you can rotate the CSI slice in the slice plane.

- The orientation of the CSI slice should not be modified during subsequent adjustments.

Use the handles for graphical editing such as changing the FoV, as well as the Pivot and Extent handles:



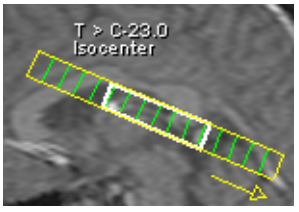
(1) Handle for resizing the FoV
(2) Extent handle for modifying the CSI slice thickness
(3) Pivot handle for moving the slice

Tool tip during adjustment

During graphical adjustments, a tool tip indicating position, extent, orientation, or rotation of the CSI slice is displayed in the reference image and updated dynamically. After graphical adjustment, the corresponding values in the input fields of the **Routine** and **Geometry - Common** parameter cards are updated automatically.

Rotating the CSI slice

The CSI slice is rotated in-plane about the center point of the CSI slice. The rotational axis is now perpendicular to the reference image.



✧ Click the contour line with the mouse and rotate the CSI slice in the required direction

➪ The farther away you are from the center point when you click on the contour line, the more precisely you can rotate the slice.

Adapting the CSI slice numerically

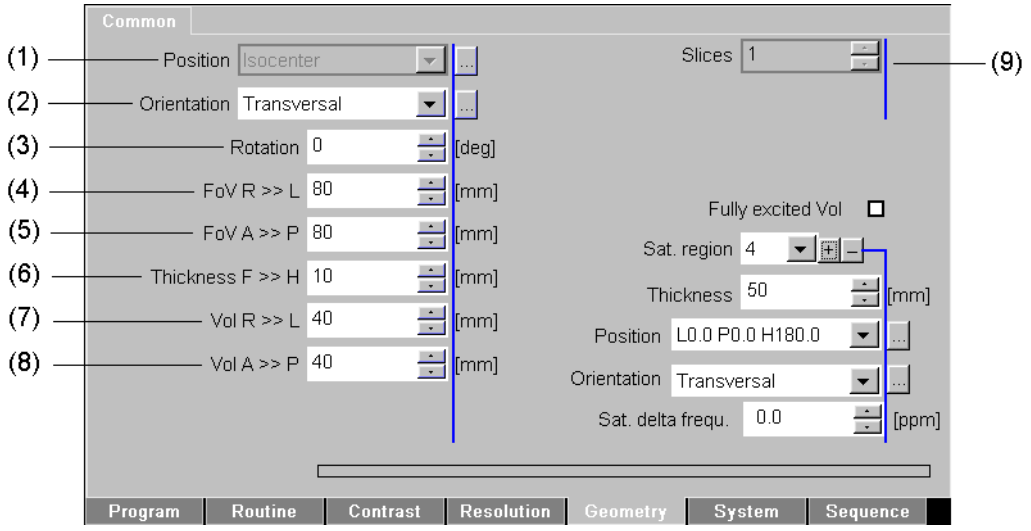
In addition to graphical adjustment, you can set the geometric parameters of the CSI slice (position, orientation, angle of rotation, FoV, thickness, size) numerically. Perform numerical adjustments the **Routine** or **Geometry - Common** parameter cards.

➪ The size of the VOI within a hybrid CSI slice can *only* be changed numerically.

Once you press the **Enter** key after a numerical adjustment or switch to a different operating element, the CSI slice graphic updates.

Displaying the parameter card

✧ Open the **Geometry - Common** (or **Routine**) parameter card.



(1) Common position of the CSI slice and VOI
(2) Common orientation of the CSI slice and VOI
(3) Common “in-plane” angle of rotation
(4) Extent of the CSI slice in the R-L direction
(5) Extent of the CSI slice in the A-P direction
(6) Extent of the CSI slice in the F-H direction (thickness of the CSI slice)
(7) Extent of the VOI in the R-L direction
(8) Extent of the VOI in the A-P direction
(9) Number of slices (multislice CSI sequences only)

Position of the CSI slice



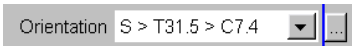
How to set the position of the CSI slice

✧ Click the **...** button next to the **Position** field.

The **Position** dialog window opens.

✧ Establish the exact position of the CSI slice in the **Position** dialog window.
→ ***syngo* MR** Operator Manual

Orientation of the CSI slice



How to set the orientation of the CSI slice

✧ Select a basic orientation (**Sagittal**, **Coronal**, or **Transverse**) from the **Orientation** selection list.

➪ The orientation parameter consists of a *basic orientation* (e.g., **S** for sagittal) and two rotation values (optional) indicating a *direction of rotation* and an *angle of rotation* (e.g. **T31.5**: transverse direction of rotation with an angle of 31.5 degrees; **C7.4**: coronal direction of rotation with an angle of 7.4 degrees).

✧ Click the **...** button next to the selection list.

The **Orientation** dialog window opens.

✧ Establish the exact orientation of the CSI slice in the **Orientation** dialog window.
→ ***syngo* MR** Operator Manual

!

For spectroscopy measurements of the head, always select the basic **Transverse** orientation.

Since you can freely select the extent of the VOI, this does not constitute a real limitation. The basic **Transverse** orientation effects a temporal sequence for slice selection proven to be the preferred method for spectroscopy applications of the head (*T. Ernst, L. Chang; Magn. Reson. Med., 36; 462-468; 1996*).

Rotational angle of the CSI slice

How to set the angle about which the VOI is rotated in the slice plane defined by the orientation:



✧ Enter the angle (between -44° and +44°) in the **Rotation** field.

FoV of the CSI slice

The **FoV** parameters can be used to resize the CSI slice without affecting the VOI.

✧ Enter the following values in the corresponding fields.

Expansion	Direction
FoV R >> L	Extent of the CSI slice in the R-L direction in millimeters [mm]
FoV A >> P	Extent of the CSI slice in the A-P direction in millimeters [mm]

➪ If you want to set the CSI Voxel precisely on individual pathological image areas, determine the position of the voxel through the settings on the **Resolution - Common** parameter card.
→ Page B.8–25, *Setting parameters for resolution*

CSI slice thickness

The **Thickness** parameter is used to define the extent of the CSI slice in the slice-selection direction.



✧ Enter the thickness of the CSI slice in the **Thickness F >> H** field.

➪ For 2D hybrid CSI protocols, the thickness of the CSI slice also defines the extent of the VOI in the slice selection direction.

Size of the VOI

The **VoI** parameters can be used to resize the VOI without affecting the CSI slice.

➪ Please note that the VOI should be smaller than the FoV of the CSI slice by a factor of at least 0.75. Otherwise, convolution artifacts cannot be ruled out.
→ Page A.2–9, *Measurement parameters and measurement time*

✧ Enter the following values in the corresponding fields.

Expansion	Direction
VOI R >> L	Extent of the VOI in the R-L direction in millimeters [mm]
VOI A >> P	Extent of the VOI in the A-P direction in millimeters [mm]

Saving the reference image and CSI slice graphic

After completing graphical and numerical adjustments, you are able to document the CSI slice definition by saving a reference image including the CSI slice graphic.

✧ Select the reference image.

✧ Select **Patient > Save As**.

The **Save As** dialog window opens.

In the **Save As** dialog window, you set whether the reference image is added to the measured reference series or stored in a new series, and start the Save process.
→ ***syngo* MR** Operator Manual

Adapting the CSI slab (3D CSI)

You can adjust the display of the CSI slab by showing or hiding the CSI matrix or by showing the projection on the reference image in case of a double-oblique CSI slab. The procedure is the same as for CSI slices.
→ Page B.8–2, *Setting the display of the CSI matrix*
→ Page B.8–4, *Showing the projection of the CSI slice*

Next, you can adjust the CSI slice parameters. You either work with the mouse in the reference image (graphical adaptation) or on the parameter cards **Routine** or **Geometry-Common** (numerical adaptation).

You can save a reference image with the modified CSI slice graphic for documentation purposes.

Oblique CSI slabs

Similar to positioning oblique CSI slices, the slice parameters from the reference image of a suitable localizer (**Localizer_in-plane_CSI**) should be used when positioning oblique CSI slabs.
→ Page B.8–4, *Using the position and orientation from a reference image*

Adapting the CSI slab graphically

You have applied the orientation and position from a reference image to the CSI slab.

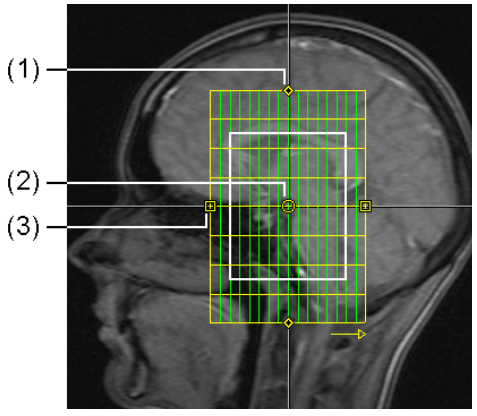
The procedure for adapting the position and extent of the CSI slab precisely to the anatomy of the patient is similar to the procedure for graphical slice positioning in MR imaging.
→ ***syngo* MR** Operator Manual

In addition, you can rotate the CSI slab in the slice plane.

➪ The orientation of the CSI slab should not be modified during subsequent adjustments.

Handles

The CSI-slab can be edited graphically using the handles.

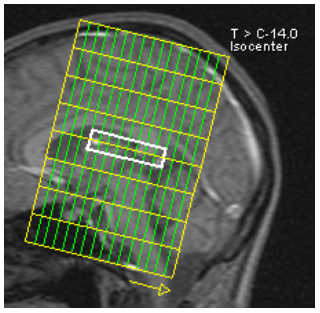


(1) Handle for resizing the FoV in the F-H direction
(2) Pivot handle for moving the CSI slab
(3) Handle for resizing the FoV in the A-P direction

Tool tip during adjustment

During graphical adjustments, a tool tip indicating position, extent, orientation, or rotation of the CSI slice is displayed in the reference image and updated dynamically. After graphical adjustment, the corresponding values in the input fields of the **Routine** and **Geometry Common** parameter cards are updated automatically.

Rotating the CSI slab



The CSI slab is rotated in-plane about the center point of the CSI slab. The rotational axis is now perpendicular to the reference image. The procedure is the same as rotating a CSI slice.
→ Page B.8–6, *Rotating the CSI slice*

Adapting the CSI slab numerically

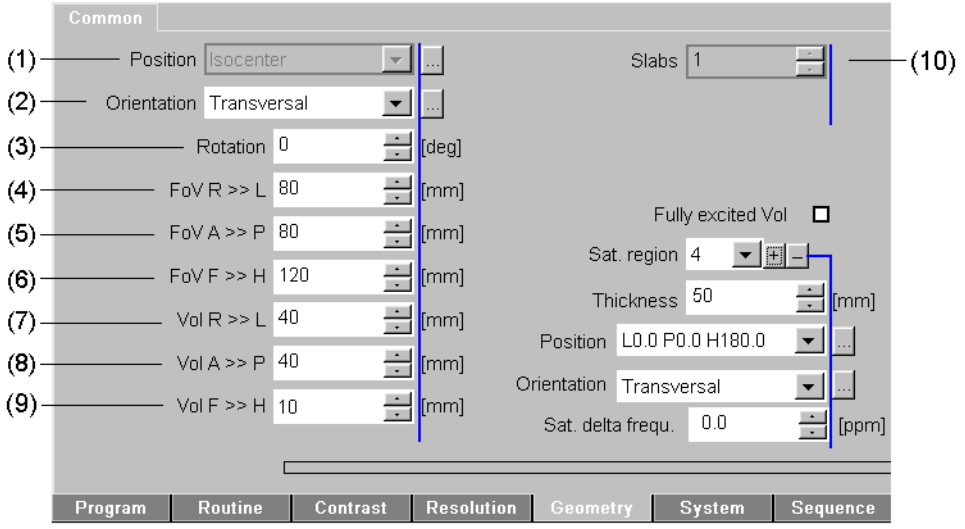
In addition to graphical adjustment, you can adjust the parameters of the CSI slab numerically.

Once you press the **Enter** key after a numerical adjustment or switch to a different operating element, the CSI slab graphic updates.

The procedure is the same as numerically setting the geometric parameters of a CSI slice.
→ Page B.8–6, *Adapting the CSI slice numerically*

Displaying the parameter card

✧ Open the **Geometry - Common** (or **Routine**) parameter card.



(1) Common position of the CSI slab and VOI
(2) Common orientation of the CSI slab and VOI
(3) Common “in-plane” angle of rotation
(4) Extent of the CSI slab in the R-L direction
(5) Extent of the CSI slab in the A-P direction
(6) Extent of the CSI slab in the F-H direction
(7) Extent of the VOI in the R-L direction
(8) Extent of the VOI in the A-P direction
(9) Extent of the VOI in the F-H direction
(10) Number of slabs (multislice CSI sequences only)

When setting the following parameters, the procedure is the same as setting the parameters of a CSI slice:

❏ Position → Page B.8–8
❏ Orientation→ Page B.8–8
❏ Angle of rotation (Rotation) → Page B.8–9

FoV of the CSI slab

The **FoV** parameters can be used to resize the CSI slab without affecting the VOI.

✧ Enter the following values in the corresponding fields.

Expansion	Direction
FoV R >> L	Extent of the CSI slab in the R-L direction in millimeters [mm]
FoV A >> P	Extent of the CSI slab in the A-P direction in millimeters [mm]
FoV F >> H	Extent of the CSI slab in the F-H direction in millimeters [mm]

➪ If you want to set the CSI Voxel precisely on individual pathological image areas, determine the position of the voxel through the settings on the **Resolution - Common** parameter card.
→ Page B.8–25, *Setting parameters for resolution*

Resizing the VOI

The **VoI** parameters can be used to resize the VOI without affecting the CSI slab.

➪ Please note that the VOI should be smaller than the FoV of the CSI slab by a factor of at least 0.75. Otherwise, convolution artifacts cannot be ruled out.
→ Page A.2–9, *Measurement parameters and measurement time*

✧ Enter the following values in the corresponding fields.

Expansion	Direction
VoI R >> L	Extent of the VOI in the R-L direction in millimeters [mm]
VoI A >> P	Extent of the VOI in the A-P direction in millimeters [mm]
VoI F >> H	Extent of the VOI in the F-H direction in millimeters [mm]

Setting saturation regions

In case of CSI measurements using a spin echo sequence, you can minimize the chemical shift artifact using “Outer Volume Suppression” (OVS).
→ Page A.2–24, *Outer Volume Suppression (OVS) – CSI*

The **Fully excited Vol** option results in a volume with full excitation of all metabolites. Signals from the excited region that are outside the visible VOI are suppressed by four automatically positioned regional saturation pulses.

Additionally, you may insert up to eight freely positionable saturation regions to further restrict the VOI.

Displaying the parameter card

✧ Open the **Geometry - Common** parameter card.
→ Page B.8–14

Select “Fully excited VOI”



✧ Select the **Fully excited VOI** checkbox.

The actual excited volume is enlarged compared to the displayed VOI. This allows you to acquire all metabolites with maximum intensity within the displayed VOI.

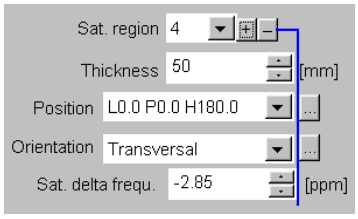
Additionally, four saturation regions are positioned at the edges of the VOI to suppress the signals from the areas outside the VOI.

➪ The automatically positioned saturation regions are *not* displayed in the image area.

➪ The FoV may have to be enlarged to prevent aliasing artifacts. The recommended minimum size for the FoV is displayed when you let the mouse pointer rest on the **VOI** field.

The **Delta frequency** parameter on the **Sequence - Common** parameter card is set at a fixed value of -2.85 ppm.

Adding saturation regions

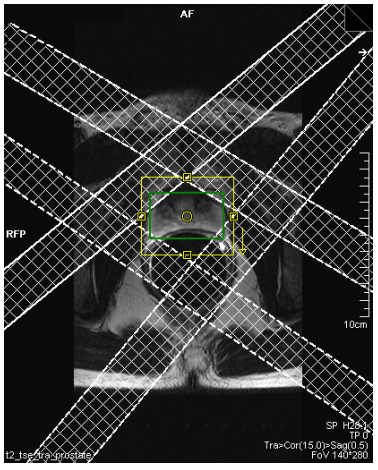


The freely positionable saturation regions are designed to provide good *in-vivo* fat suppression.

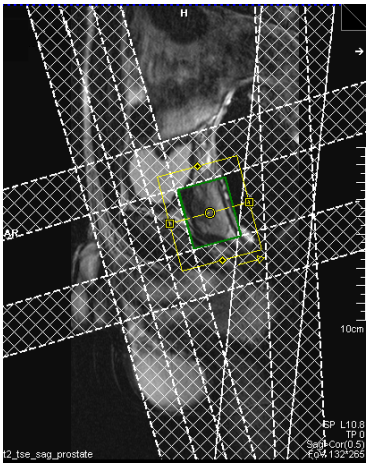
✧ If necessary, you can add and freely position up to eight saturation regions and adjust their thickness, position, and orientation.
→ ***syngo* MR** Operator Manual

✧ In the field **Sat. delta frequ.**, enter the value of the frequency shift in the saturation pulse.

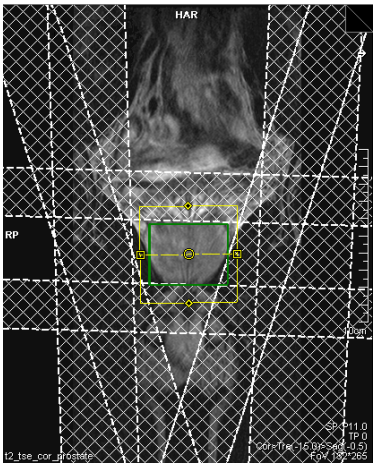
Example: The following images show the positioning of free saturation regions using the example of a ^{1}H hybrid CSI measurement of the prostate.



Transverse view



Sagittal view



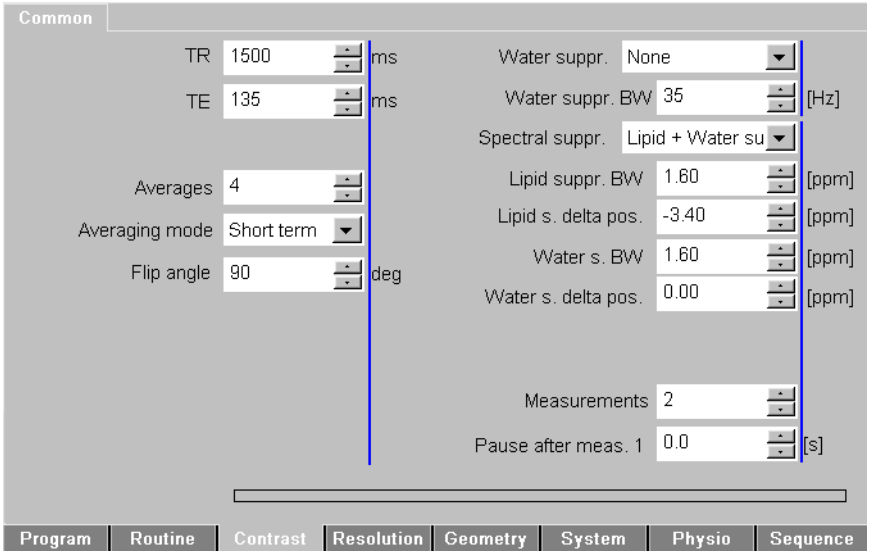
Coronal view

Adjusting protocol parameters

After adjusting the CSI slice or CSI-slab and the VOI to the patient's anatomy, you can check and edit the other protocol parameters.

Setting contrast parameters

✧ Open the **Contrast** parameter card.



✧ Change the parameters desired in the corresponding fields.

The following briefly describes the individual parameters.

TR

The **Repetition Time** (TR) is the time that elapses between two excitations in sequence. Changing the repetition time affects image contrast:

- ❏ Short repetition times produce good T1 contrast for spin-echo sequences.
- ❏ Long repetition times produce good T2 contrast for spin-echo sequences.

TE

The **Echo Time** (TE) is especially important e.g. for lactate measurements. Phase reversal of the lactate peak during a spin-echo measurement (at 135 ms) is another indicator for determining lactate.

TM

With the **TM** parameter (specific time interval, for STEAM sequences only), you set the time interval between the 2nd and 3rd RF pulse for protocols based on STEAM sequences.
→ Page A.2–2, *STEAM sequence*

During this time, the measured magnetization is oriented in the longitudinal direction and therefore only subject to T1 relaxation. This means that the duration of the TM interval does not contribute to echo time TE.

➪ The T1 weighting can be enhanced by extending the TM interval.

Averages

Through the number of averagings, you can establish how often the results of repeated measurements are averaged in order to improve signal-to-noise ratio.

➪ Please note that the greater the number of measurements, the longer the measurement time.

Averaging mode

This parameter determines the method for averaging measurements when several averages are performed.

- ❏ **Short term**
  measures all averages for a point in the data matrix consecutively, and goes to the next point in the data matrix afterwards.
- ❏ **Long term**
  measures all points of the data matrix prior to data acquisition of the next averaging.
  This leads to a better suppression of motion artifacts in most cases.

⇨ CSI measurements can be terminated in **Long term** mode without complete loss of data if, at least one average has already been acquired. The Long term mode is recommended, if the possibility of motion artifacts exists.
Terminating of a CSI measurement leads to a reduced signal-to-noise ratio. In addition it may lead to inhomogeneous noise with respect to different voxels.
The **Inline Display** provides information regarding the averaging that was just performed.
→ Page B.10–4

Flip angle

The flip angle of the spin rotational axis in degrees [°] indicates the extent to which the longitudinal magnetization is moved out of the z-direction of the magnetic field by the RF pulse. With a 90° excitation pulse, for example, the longitudinal magnetization is rotated by 90° out of the z-direction. The flip angle directly affects image contrast.

For spin echo sequences, you can enhance the T1 contrast by reducing the flip angle.

Water suppression

To reduce the high-intensity water signal, it should be suppressed already during data acquisition.
→ Page A.2–3, *Suppressing the water signal*

Water suppression	Description
Water sat.	During the measurement, a water suppression pulse is transmitted to fully suppress the water signal.
Weak water suppr.	The water signal is reduced but not fully suppressed. This allows you to include the water line in various post-processing functions.
None	No water suppression is applied during the measurement. The water suppression module is completely deactivated.
Only RF off	This option can be used to measure a reference raw data set if you want to perform eddy current compensation during a spectroscopy evaluation. → Page C.8–21, *Adjusting eddy current compensation*

! To measure a reference raw data set for eddy current compensation, the protocol is measured twice: for the first measurement, water suppression is activated (**Water sat.** or **Weak water suppr.** options) to acquire the spectroscopy raw data. For the second measurement, the **Only RF off** option is selected to acquire the reference raw data.

! **In addition, please note:** If the first measurement is performed using spectral signal suppression instead of the CHESS water suppression described here, you *cannot* measure a reference raw data set.

! Activating or deactivating water suppression does *not* affect the configuration of the water suppression adjustment.
→ Page B.9–3, *Water suppression adjustment*

Water suppression bandwidth

Use this parameter to set the bandwidth of the high-frequency pulse for water suppression. A value of 35 Hz is highly suitable for a magnetic field strength of 1.5 T. A higher value should be set at 3 T.

➪ Due to the higher bandwidth, the water signal is suppressed more effectively. However, the effect on adjacent signals (e.g., creatine, (CH_2)) increases as well.

Spectral signal suppression

Selected spectral signals can be suppressed using MEGA RF pulses within the localizing part of the sequence. The following options are available:

Spectral signal suppression	Description
Lipid suppr.	Suppression of fat signals
Water suppr.	Suppression of water signals
Lipid + Water suppr.	Suppression of fats and water signals
None	No spectral suppression

Fat suppression pulse

If you have selected *Lipid suppression* or *Lipid + Water suppression* for spectral signal suppression, you can set the bandwidth of the fat suppression pulse used in the **Lipid suppr. BW** input field.

➪ If *Lipid + water suppression* is selected, the bandwidths of the two suppression pulses are coupled. The value for **Lipid suppr. BW** input field also applies as the bandwidth for the water suppression pulse, and is automatically entered in the **Water suppr. BW** input field

Spectral shift

If you have selected *Lipid suppression* or *Lipid + Water suppression* for spectral signal suppression in the field **Lipid s. delta pos.**, you can set the spectral shift of the fat suppression pulse to be used.

Water suppression pulse

If you have selected *Water suppression* or *Lipid + Water suppression* for spectral signal suppression, you can set the bandwidth of the water suppression pulse used in the **Water suppr. BW** input field.

⇨ If *Lipid + water suppression* is selected, the bandwidths of the two suppression pulses are coupled. The value for **Water suppr. BW** also applies as the bandwidth for the water suppression pulse, and is automatically entered in the **Lipid suppr. BW** input field

Spectral shift

If you have selected *Water suppression* or *Lipid + Water suppression* for spectral signal suppression in the field **Water s. delta pos.**, you can set the spectral shift of the water suppression pulse to be used.

Measurements

For dynamic or spectroscopy measurements with time resolution, you can define how many times a measurement should be performed.

Pause after meas.

Use parameter **Pause after Meas.** to establish delay times between the individual measurements of a temporal resolution or dynamic spectroscopy examination.

- If you allow the mouse pointer to rest on the field name, a brief text regarding the pause time is displayed.
- If you hold the mouse pointer over an input field of the spin box, a tool tip will appear that shows the starting and ending time of the first 10 scans.

!

Up to 64 individual pauses may be entered. However, in most cases you will only enter one pause time for all measurements or set the pause time to zero.

If you increase the number of measurements to 66, you can set only one pause automatically.

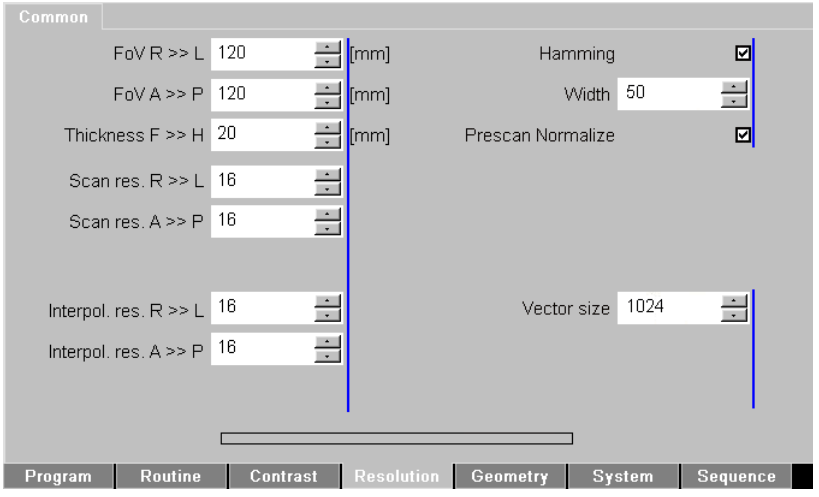
Setting parameters for resolution

✧ Open the **Resolution-Common** parameter card.

Special parameters are adapted or added for 3D CSI protocols. For this reason, the parameter cards for 3D CSI protocols and 2D CSI protocols differ little from one another.

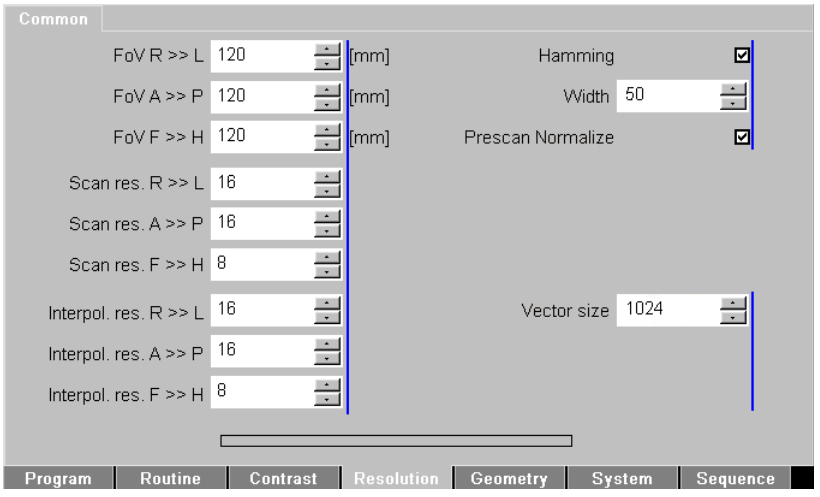
Example 1

Content of the **Resolution-Common** parameter card for a 2D CSI protocol with a transverse CSI slice:



Example 2

Content of the **Resolution-Common** parameter card for a 3D CSI protocol with a transverse CSI slab:



Set the parameters

✧ Change the parameters desired in the corresponding fields.

The following briefly describes the individual parameters.

FoV

The FoV parameters are used to adjust the size of a CSI slice or CSI slab. You normally set these parameters during graphical or numerical adaptation of the CSI slice or CSI slab. However, you can review and if necessary change the parameters on the **Resolution-Common** parameter card.

→ Page B.8–9, *FoV of the CSI slice*
→ Page B.8–15, *FoV of the CSI slab*

Thickness

With this parameter, you define the extent of the CSI slice in the slice-selection direction. Normally, this parameter has already been set. However, you can review and if necessary change it on the **Resolution - Common** parameter card.
→ Page B.8–9, *CSI slice thickness*

Measurement (Scan) resolution

With the Scan res. parameters you define the number of phase-encoding steps in the two spatial directions of a CSI slice or in the three spatial directions of a CSI slab.

- Contrary to MR imaging, the resolution may be a value other than a power of 2. This allows a more flexible setting of the total measurement duration.

Scan resolution	Description
Scan res. R >> L	Number of phase encoding steps in the R-L direction
Scan res. A >> P	Number of phase encoding steps in the A-P direction
Scan res. F >> H	For 3D CSI only: Number of phase encoding steps in the F-H direction

- The maximum number of phase-encoding steps in the first two spatial directions is 32.
- for 3D CSI only: The maximum number of phase-encoding steps along the third spatial direction is 16.
- The maximum size of a reconstructed data set is 128 MB. This is equivalent to a 3D CSI data set of e.g. 32*32*16*1024 complex measurement points.

Interpolation resolution

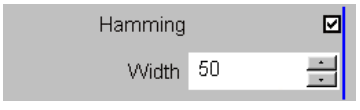
With the parameters for interpolation resolution you define the number of reconstructed spectra in the two spatial directions of a CSI slice or in the three spatial directions of a CSI slab.

Scan resolution	Description
Interpol. Res. R>>L	Number of spectra in the R-L direction
Interpol. Res. A>>P	Number of spectra in the A-P direction
Interpol. Res. F>>H	For 3D CSI only: Number of spectra in the F-H direction

- Interpolation resolution can be set to 8, 16, or 32.
- The number of reconstructed spectra must be greater than or equal to the number of phase-encoding steps.
- If the number of reconstructed spectra is greater than the number of phase-encoding steps, the displayed spectra are interpolated from the measured spectra.
- The maximum size of a reconstructed data set is 128 MB.

Hamming filter

The Hamming filter should be used for CSI measurements to prevent voxel bleeding.



- ✧ Select the **Hamming** checkbox to activate the **Hamming filter**.
- ✧ Set the filter width regarding the raw data matrix in the **Width** spin box.
  → Page A.2–18, *Phase-encoding and Hamming filter*

Prescan Normalization filter

This filter has to be switched on when using surface and matrix coils (exception: prostate protocols which use only the endorectal coil). As a result, inhomogeneities produced by the receiver profile of the coil element are normalized. The Prescan normalization filter is selected/deselected as default in the respective protocols.

➪ **Prescan Normalization** should be selected when using the Endorectal coil in conjunction with a Spine or Body Matrix element.



✧ Select the **Prescan Normalize** checkbox to activate this filter.

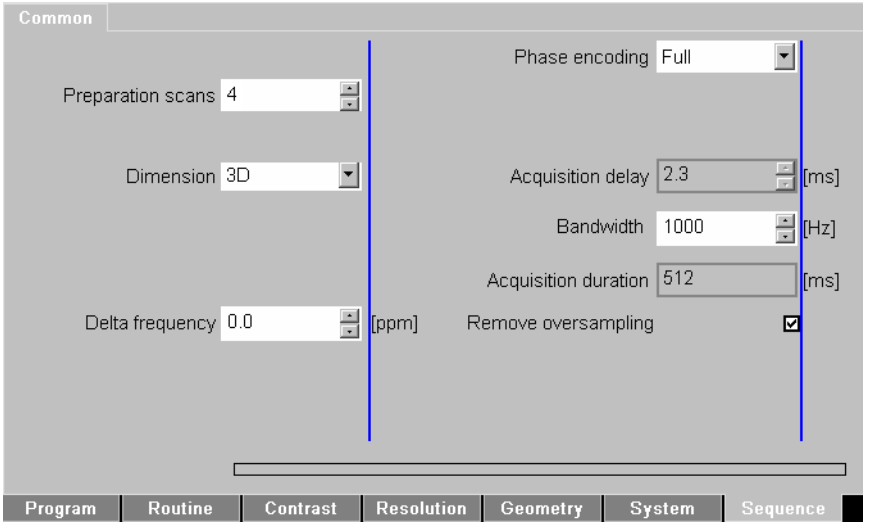
Vector size

With the **Vector size** parameter, you set the number of measurement points for sampling the spectral dimension (data points), and therefore the resolution.

The following settings are available:
❏ 512
❏ 1024 (default)
❏ 2048

Setting sequence parameters

✧ Open the **Sequence-Common** parameter card.



✧ Change the parameters desired in the corresponding fields.

Acquisition delay



For ^{31}P MRS protocols, the **Acquisition delay** defines the delay before starting data acquisition. The delay time (in milliseconds [ms]) refers to the center of the excitation pulse.

The following briefly describes the individual parameters.

Acquisition duration

This parameter shows the readout time which is the product of the number of measurement points (vector size) and the inverted bandwidth. The read-out time is read-only and cannot be modified.

Preparation scans

With this parameter you set the number of preparation measurements. The result is an equilibrium magnetization for the following MR experiment.

⇨ Data acquisition is disabled during preparation runs.

Dimension

With this parameter, you establish via the selection list whether a 2D or 3D CSI measurement will be performed with the measurement protocol.

⇨ When you switch from 2D to 3D, the entries on various parameter cards change: CSI slab parameters are shown instead of CSI slice parameters.

Delta frequency

With this parameter you indicate a frequency shift based on the system frequency. This lets you determine the spectral component for which you want to obtain precise slice selection.
→ Page A.2–22, *Delta frequency*

⇨ If you select the **Fully excited VOI** option on the **Geometry Common** parameter card, the **Delta frequency** parameter is set to a fixed value and cannot be changed.

Phase encoding

For CSI measurements, you can select between different phase-encoding procedures (sampling procedures):

Phase-encoding procedure	Description
Complete	The entire k space defined by the number of phase-encoding steps is measured.
Elliptical	Only the points located on or within the k-space ellipse are measured. This reduces the measurement time by almost one quarter without a significant loss in spatial resolution.
Weighted	Is identical to **Elliptical** with *one* averaging (NA=1). If *multiple* averaging steps are performed (NA>1), the central points of the k space are measured NA times and the points on the elliptical boundary at least once. For the intermediate points, the measurement frequency is determined by their radial distance from the center of the k-space.

➪ The **Weighted** option lets you realize the Hamming filter (**Resolution Common** parameter card) during the measurement, resulting in an improved signal-to-noise ratio per measurement time.

Bandwidth

The **Bandwidth** parameter defines the current ADC bandwidth during data acquisition. The bandwidth may be varied between 1 and 2 kHz. The typical ^{1}H MRS signals are completely resolved at magnetic field strengths of 1 T and 1.5 T using a bandwidth of 1 kHz and 2 kHz at a magnetic field strength of 3 T.

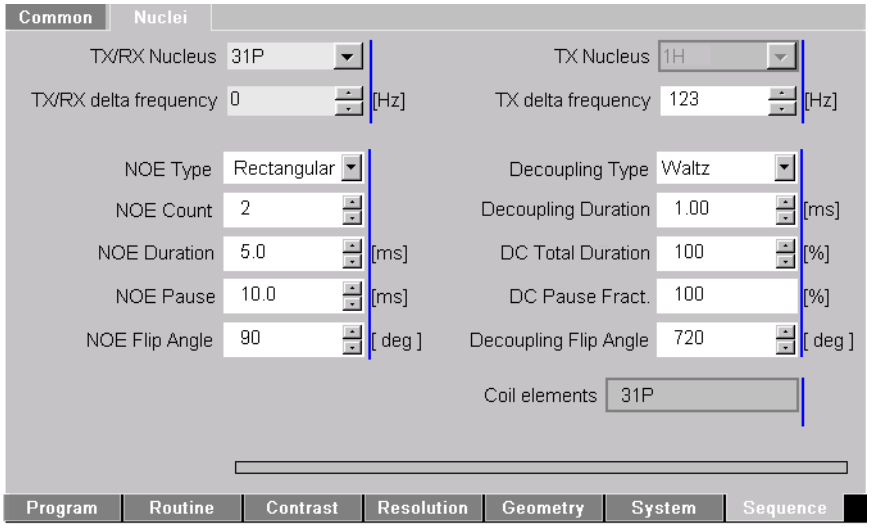
Remove oversampling

This checkbox is activated by default. The oversampling data are removed during automatic evaluation of spectroscopy raw data. This produces a ringing effect in the time signals which does not adversely affect the frequency data.

➪ If you do not want to evaluate measured spectroscopy data with SIEMENS software, it is advisable to not remove the oversampling data.

Setting parameters for ^{31}P MRS measurements

✧ Open the **Sequence-Nuclei** parameter card.



✧ Change the parameters desired in the corresponding fields.

The following briefly describes the individual parameters.

TX/RX nucleus

With this parameter, you set the primary nucleus for your measurement. For a ^{31}P MRS measurement, you select the ^{31}P nucleus accordingly.

TX/RX delta frequency

With this parameter, you set the frequency shift for receiving the signal from the primary nucleus. The frequency shift refers to the adjustment frequency for the primary nucleus.

TX nucleus

With this parameter, you set the ^{1}H nucleus as the secondary nucleus for your ^{31}P MRS measurement. During data acquisition, ^{1}H saturation pulses may then be sent to enhance the ^{31}P signal.

TX/RX delta frequency

With this parameter, you set the frequency shift for sending the saturation pulse for the secondary nucleus. The frequency shift refers to the adjustment frequency for the secondary nucleus.

NOE type

With this parameter, you define the pulse type for the ^{1}H saturation pulses.

⇨ This software version supports the **Rectangular** pulse type only.

NOE count

With this parameter you set the number of ^{1}H saturation pulses that are transmitted prior to excitation of the ^{31}P signal.

NOE duration

With this parameter you set the duration of a ^{1}H saturation pulse.

NOE pause

With this parameter you define the time interval between two ^{1}H saturation pulses.

NOE flip angle

With this parameter you set the flip angle of the ^{1}H saturation pulse. The flip angle is spatially dependent on the Heart/Liver coil. The setting should be seen as a pulse-enhancing factor and not as a calibrated flip angle.

The setting directly affects the voltage of the ^{1}H saturation pulses which can be set using the **System Transmitter/ Receiver** parameter card.

⇨ The purpose of ^{1}H saturation pulses is to achieve saturation. Therefore, you should try to maximize pulse amplification. The SAR monitor ensures that the stress level for the patient remains within limits.

Decoupling type With this parameter you set the mode for the ^{1}H decoupling.

Decoupling type	Description
CW	A decoupling pulse is continuously transmitted during data acquisition. The decoupling has a narrow bandwidth in the frequency domain. The decoupling frequency should be accurately set for optimal decoupling.
WALTZ 4	A series of short decoupling pulses is transmitted during data acquisition. The decoupling has a broad bandwidth in the frequency domain and does not depend to the same degree on the setting of the decoupling frequency.

Decoupling duration With this parameter you define the duration of a ^{1}H decoupling pulse for ^{31}P MRS measurements using Waltz 4 decoupling.

➪ The **Decoupling duration** parameter can be edited only for the **Waltz 4** decoupling mode.

DC total duration With this parameter you set the proportion of decoupling duration relative to readout duration in [%].

➪ Ideally, the decoupling duration should correspond to the readout duration (100%). Values < 100% reduce the decoupling phase to a corresponding time interval at the beginning of the decoupling window. This is useful in preventing a TR increase as a result of the SAR limit.

DC pause fraction With this parameter you define the time interval between ^{1}H decoupling pulses (in [%] of **decoupling duration**) for ^{31}P MRS measurements using Waltz 4 decoupling.

➪ The **DC pause fract.** parameter can be edited only for the **Waltz 4** decoupling mode.

Decoupling Flip angle

With this parameter you define the flip angle of the ^{1}H decoupling pulse for a ^{31}P MRS measurement.

- ❏ With Waltz 4 decoupling, the flip angle refers to the center 180° pulse. It should therefore be 180°.
- ❏ With CW decoupling, the flip angle is specified over an interval of 10 ms.

The flip angle is spatially dependent on the Heart/Liver coil. The setting should be seen as a pulse-enhancing factor and not as a calibrated flip angle. The setting directly affects the voltage of the ^{1}H saturation pulses which can be controlled using the **System Transmitter/Receiver** parameter card.

CHAPTER B.9

Configuring Adjustments

You may check and modify the settings of the individual adjustment steps prior to starting the measurement and the automatic adjustment. You may also determine size, position and orientation of the adjustment volume.

➪ The default settings of the adjustment configuration are optimized for most applications.

! For detailed information about adjustment steps, please refer to the → ***syngo* MR** Operator Manual.

Checking the adjustment settings

Use the **System-Adjustments** and **System-Transmitter/Receiver** parameter cards to check the adjustment parameters.

The following adjustment steps are checked:

❏ Shim mode

❏ Water suppression adjustment

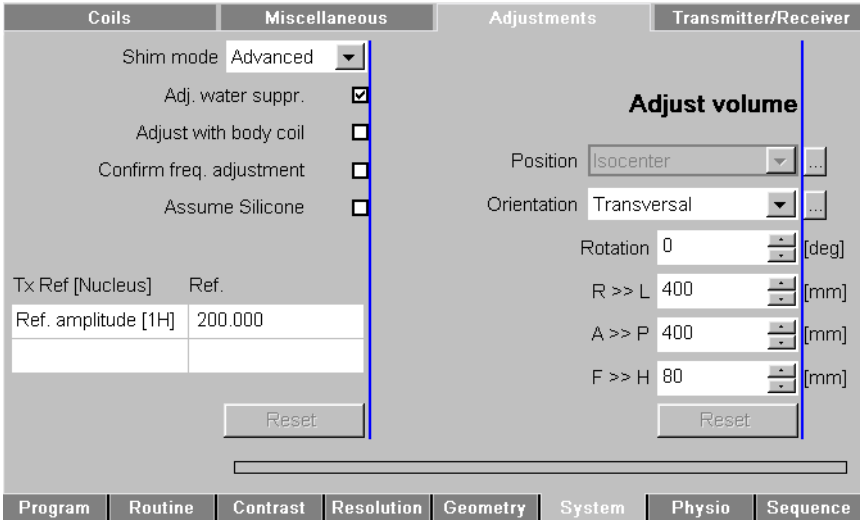
Shim mode

For maximum spectral resolution, the homogeneity of the magnetic field is optimized over the VOI of a spectroscopic examination. An automatic, volume-selective shimming method (3D shim) is available for this purpose.

➪ For spectroscopy measurements, shimming should be performed in **Advanced** mode.

➪ Using double measurements with gradient inversion and one iteration step, you can achieve greater homogeneity than in **Standard** mode. However, the measurement time increases approximately fourfold.

✧ Open the **System-Adjustments** parameter card.



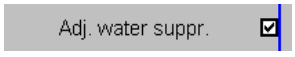
✧ Check the settings in the **Shim mode** selection list.

Water suppression adjustment

A special pulse train is used for ^{1}H MRS measurements to suppress the water signal. The **Adj. water suppr.** option is selected for this purpose.

➪ For ^{31}P MRS measurements, water suppression adjustment is not necessary.

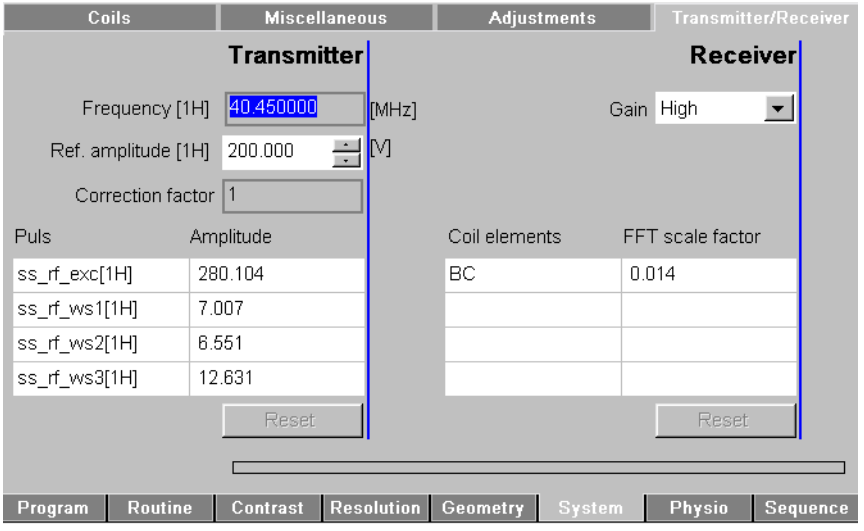
The correction factor calculated for the calibration of the water suppression pulses is displayed on the **System-Transmitter/Receiver** parameter card.



✧ On the **System-Adjustments** parameter card, click the **Adj. water suppr.** checkbox to calibrate the amplitude of the suppression pulse.

Checking the correction factor

✧ Open the **System-Transmitter/Receiver** parameter card.



You can read the frequency and correction factor in the corresponding fields. You can change the remaining automatic adjustment parameters as needed.
→ ***syngo* MR** Operator Manual

Setting the adjust volume

At its default setting, the adjust volume and VOI are identical. This is the correct setting for most applications.

For special applications, you may also set the adjust volume independently of the VOI.

Display the adjust volume



✧ To display the adjust volume, select **View > Adjust Volume On**.
- Or -
Click this button in the **Position Toolbar**.

The adjust volume is indicated by a green rectangle above the VOI graphic.

Setting the adjust volume

The adjust volume may be edited graphically or numerically as described for the VOI.
→ Page B.7–3, *Adapting the VOI graphically*
→ Page B.7–5, *Adapting the VOI numerically*

➪ The parameters for numerical editing of the adjust volume are available on the **System Adjustments** parameter card.

➪ Modified adjust volume parameters can be identified by a preceding exclamation mark on the **System Adjustments** parameter card.

➪ By clicking the **Reset** button, you can restore the automatically calculated adjust volume at any time. The exclamation points are hidden again.

CHAPTER B.10

Measuring

Start the measurement after checking and, if necessary, modifying the measurement parameters and adjustment settings.

While the measurement is in progress, you can monitor the measured raw signal using **Inline Display** or change the parameters of the subsequent measurement protocols.

After the measurement is completed, the spectroscopy data (measurement data, measurement parameters, patient data) are automatically stored in the patient database.

In case the **Save uncombined** function is activated in the **System - Miscellaneous** parameter card, a series with the uncombined images of the individual elements is created in addition to the combined original images.
→ ***syngo*** **MR** Operator Manual

!

To perform the measurement, you need to have full user access rights.

Detailed information regarding all security settings in *syngo* are included in the *syngo* Security Package brochure.

Starting the measurement



✧ Click **Apply** in the program control.

The edited protocol is loaded and executed in the measurement system. Any additional adjustments necessary are performed automatically prior to the actual measurement.

➪ The measurement of a protocol can be stopped, e.g. to correct protocol parameters or to restart the measurement.
→ ***syngo* MR** Operator Manual

! A sequence cannot be stopped and later resumed.

➪ You can repeat the measurement of protocols already processed.
→ ***syngo* MR** Operator Manual

! The adjustment results of a protocol measured previously are applied automatically only if the following parameters remain the same for both protocols: the *table position*, the *coil elements* used, the *adjustment configuration* (e.g., shim mode), and the *adjust volume*.

Monitoring the raw signal

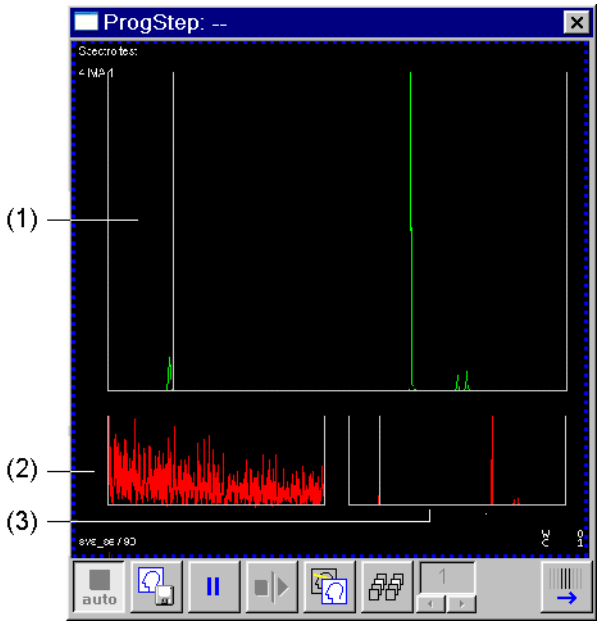
SVS and FID measurements

During the measurement, you can view the raw signal of SVS and FID measurements via the **Inline Display**. This allows you to monitor the measurement and intervene, if necessary.



✧ Select **View > Inline Display**.
- Or -
Click this button on the tool bar of the **Exam** task card.

The raw data measured are displayed in three different ways:



(1) Current accumulated magnitude spectrum
(2) Magnitude time signal of the current acquisition
(3) Magnitude spectrum of the current acquisition

Detailed information:
→ ***syngo* MR** Operator Manual

CSI measurements

For CSI measurements in the **Long term** averaging mode, the **Inline Display** shows the current averaging performed by the measurement.



➪ As soon as the first averaging is completed, a CSI measurement can be terminated without complete loss of data.
→ Page B.8–20

Modifying subsequent measurement protocols

While a measurement is in progress, you can use the wait time to complete additional protocols. In this way, you reduce the overall measurement time.

Procedure

❏ Opening a protocol
❏ Setting or copying measurement object and protocol parameters from a measured protocol
❏ Accepting parameter settings

Opening a protocol

✧ Select the protocol you want to edit from the section of the queue not yet processed.



✧ Click **Open** in the program control.

The parameter settings for the open protocol are displayed on the parameter cards. The graphic of the measurement object defined in the protocol (VOI, CSI slice, hybrid CSI slice, CSI slab) is displayed in the reference images.

Setting the measurement object and protocol parameters

You start by adapting the position, orientation, and size of the measurement object (VOI, CSI slice, or CSI slab) to the patient's anatomy. You can then check all other protocol parameters and make adjustments as necessary.

✧ Adjust the measurement object.
→ Page B.7–1, *Adapting the VOI*
→ Page B.8–1, *Adjusting the CSI slice (2D CSI)*
→ Page B.8–11, *Adapting the CSI slab (3D CSI)*

✧ Check and change the remaining protocol parameters as needed.
→ Page B.7–10, *Adjusting protocol parameters*
→ Page B.8–18, *Adjusting protocol parameters*

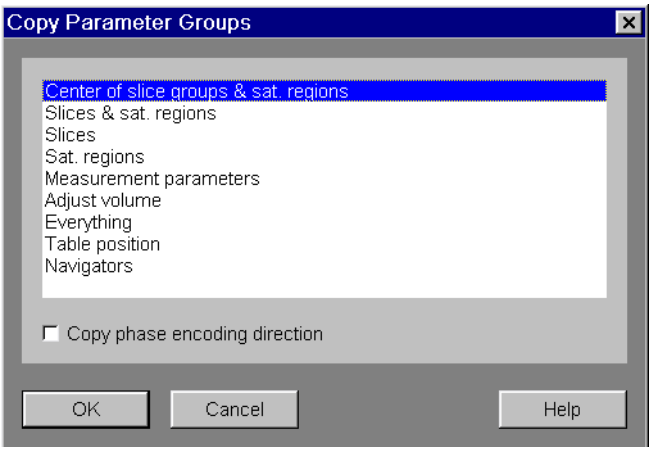
Copying measurement parameters

You can copy the entire geometric definition from a measured protocol to the protocol currently opened.

✧ Select the desired protocol in the completed section of the queue.

✧ Select **Queue > Copy Parameter...**.
- Or -
Select **Copy Parameter** from the pop-up menu.

The **Copy Parameter Groups** dialog window is displayed.



✧ Select the **Measurement parameters** parameter group.

✧ Click **OK**.

The definition of the VOI or CSI slice (or CSI slab) is copied to the open protocol. The repetition time TR, the echo time TE and the averagings are *not* transferred.
→ ***syngo* MR** Operator Manual

➪ For measurements with identical VOI definition, the adjustment results remain valid.

Example: You have performed a measurement with TE = 135 ms and would like to perform an additional measurement with TE = 30 ms at the same position. Open the **svs_se_30** measurement protocol and copy the measurement parameters from the previous measurement.

Accepting parameter settings

After adjusting or copying the measurement parameters, you accept the settings.



✧ Click **Apply** in the program control.

The measurement protocol is closed and its status is set to Complete. When it reaches its turn in the queue, it is automatically loaded into the measurement system and processed.

CHAPTER B.11

Interactive Adjustment

Successful spectroscopy measurements require accurately adjusted measurement parameters.

The following adjustment modes are available for selection:

Adjustment modes

- **Automatic adjustment**
  Adjustment is performed automatically immediately after the start of the measurement. This mode is recommended for most applications.
- **Automatic adjustment with interactive control**
  Adjustment is started manually prior to the actual measurement. After the adjustment, you check the results of adjustment and modify them manually, if necessary. Start the measurement after performing these steps.
  → Page B.11–2, *Automatic adjustment with interactive control*
- **Manual adjustment**
  Experienced users can perform the entire adjustment manually. You can change the parameters of individual adjustments and perform each adjustment step by step until you are satisfied with the results.
  → Page B.11–3, *Manual adjustment*

! All adjustments apply to the ^{1}H signal with the exception of the multinuclear frequency and transmitter adjustment. This is the case even if a ^{31}P MRS measurement protocol is currently open.

Automatic adjustment with interactive control

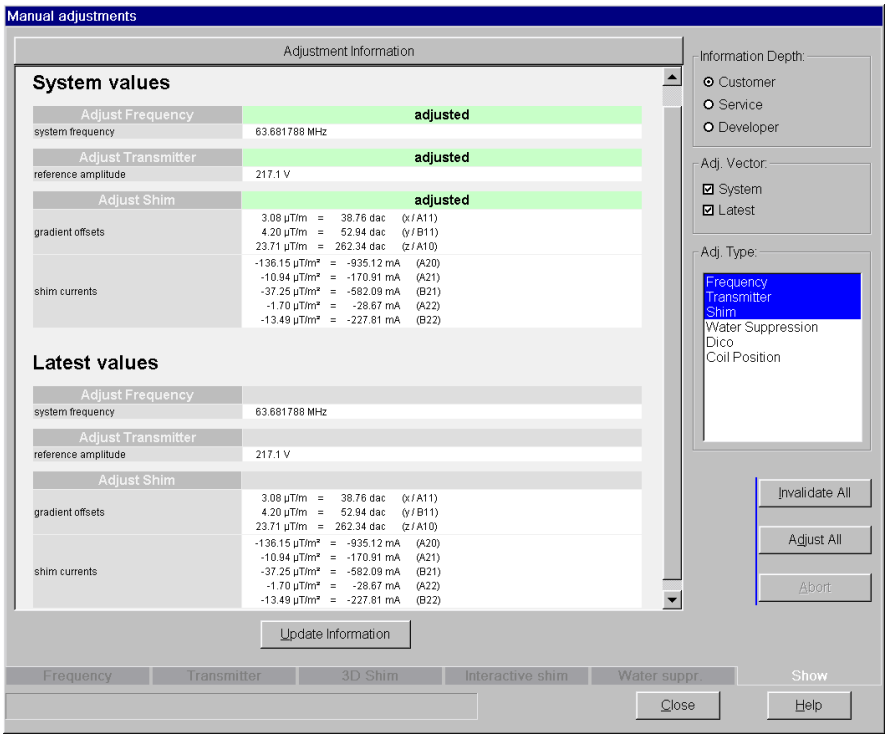
With some applications it is advisable to check the results of protocol adjustments prior to the measurement. If required, you may then manually adjust the system. For this purpose, you manually start the protocol adjustments.

Starting adjustments manually

✧ Select **Options > Adjustments**.

The **Manual Adjustments** dialog window is opened.

✧ Open the **Show** subtask card.



Adjust All

✧ Click **Adjust All** to manually start the protocol adjustments.

Only the protocol adjustments are performed.

Checking results

After you have performed protocol adjustments, you can check the adjustment results obtained. For this purpose, you may use the interactive adjustment options available in the **Manual Adjustments** dialog window already open.
→ Page B.11–3, *Manual adjustment*

⇨ The quality of shimming and water suppression is especially important for spectroscopy examinations. Interactive shimming is used to check and, if necessary, improve the shim quality.

Manual adjustment

During manual adjustment, you define the sequence of the adjustment steps yourself.

The following is a suitable sequence of adjustment steps:

❏ Frequency adjustment
❏ Shimming
❏ Repeated frequency adjustment
❏ Water suppression adjustment (for ^{1}H MRS)

⇨ Additional tuning and transmitter adjustments prior to the spectroscopy measurement are not necessary as long as at least one image has been measured using the current patient position and coil configuration.

The following describes the parameter settings and the results output for the various adjustment procedures.

⇨ Further information as well as a detailed description of the measurement sequence is included in:
→ ***syngo* MR** Operator Manual.

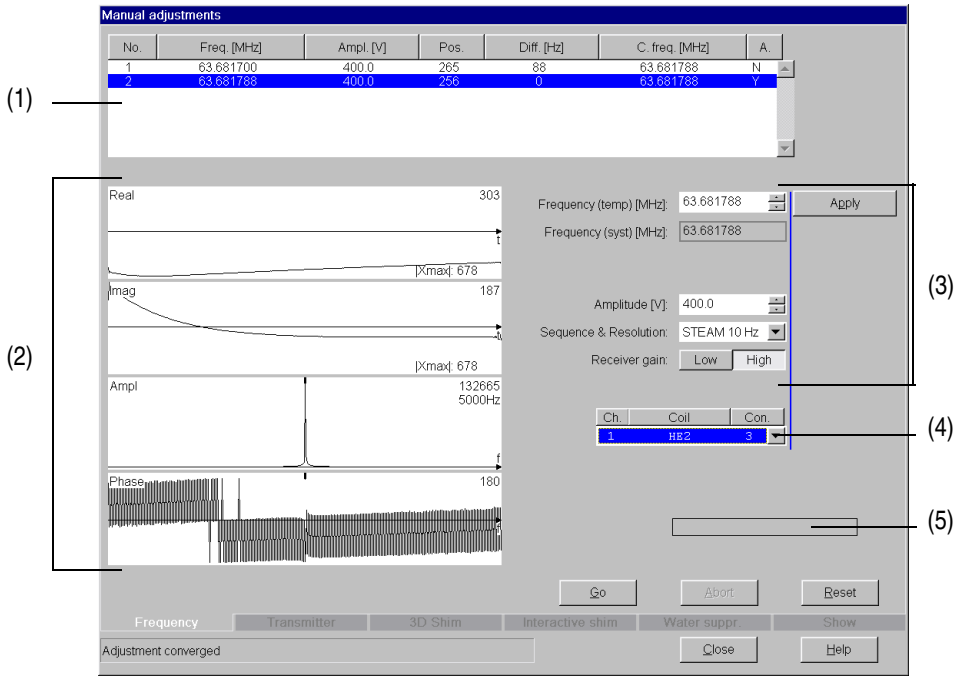
^{1}H frequency adjustment

In this manner, you determine the exact proton resonance frequency.

➪ For a detailed description of this procedure, refer to:
→ ***syngo* MR** Operator Manual

Frequency subtask card

Set the adjustment parameters on the **Frequency** subtask card in the **Manual adjustment** dialog window.



(1) Numeric results
(2) Graphical results display
(3) Adjustment parameters
(4) Coil measurement signal for graphical display
(5) Range display

Settings The following parameters can be set or displayed:

Parameters	Description
Frequency (temp) [MHz]	Enters the (temporary) transmit frequency for the pending adjustment measurement. The frequency can be reselected for each iteration.
Frequency (Syst) [MHz]	Displays the system frequency currently being used for examinations *On '**?**' means that the final value of the adjustment parameters is not yet known. When starting the next measurement, the system will perform at least one measurement to determine the unknown parameter(s).*
Amplitude [V]	Enters the transmit amplitude for the pending adjustment measurement
Sequence & Resolution	**FID 400 Hz**: Broadband, not volume selective **FID 10 Hz**: Narrow band, not volume selective **STEAM 10 Hz**: Narrow band, volume selective
Receive gain	**Low**: for strong receive signal **High**: for weak receive signal
Range display	Checks whether the frequency or amplitude entered is in the acceptable range

Results

The results of the adjustment measurement are displayed graphically in both the time and the frequency domain. The table with the numerical results contains the following entries:

Parameters	Description
No.	Running number of the adjustment measurement
Freq. [MHz]	Transmit frequency in MHz
Ampl. [V]	Transmit amplitude of the adjustment measurement
Pos.	Position of the highest amplitude peak in the frequency domain
Diff. [Hz]	Difference between the transmit frequency and the calculated (better) frequency
C.Freq. [MHz]	Calculated (better) frequency (Calculated Frequency)
A.	Adjustment successful (**Y**es/**N**o)

Multinuclear frequency adjustment

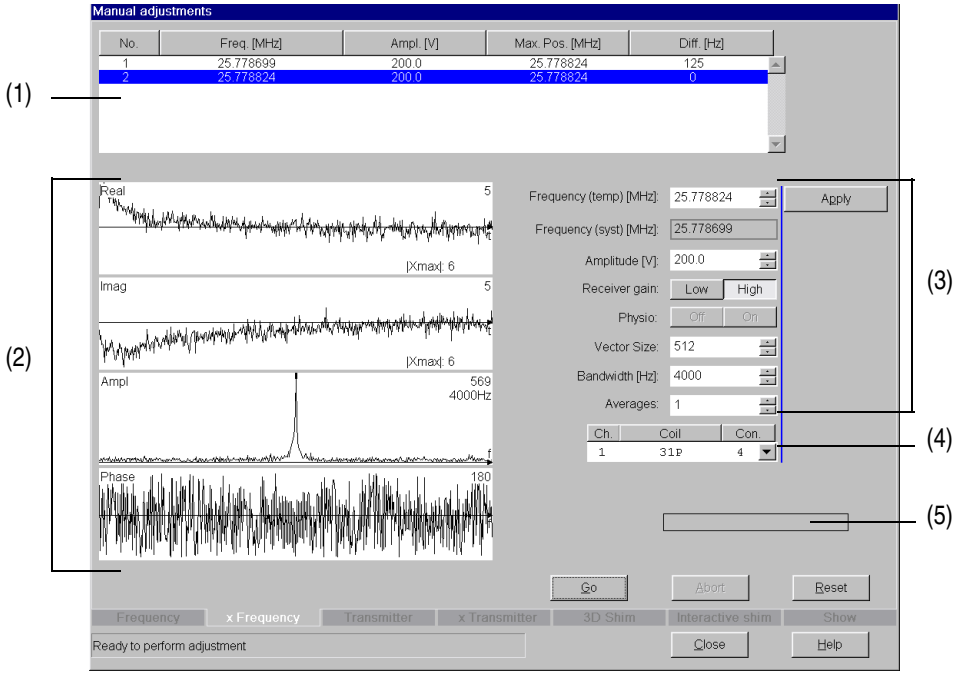
You determine the exact resonance frequency for the nucleus determined by the protocol.

➪ For a detailed description of this procedure, refer to the → ***syngo* MR** Operator Manual.

X-frequency subtask card

Set the adjustment parameters on the **X-Frequency** subtask card in the **Manual adjustment** dialog window.

➪ This card is shown only if you have a multinuclear license and have connected the X-nucleus transmit-receive coil.



(1) Numeric results
(2) Graphical results display
(3) Adjustment parameters
(4) Coil measurement signal for graphical display
(5) Range display

Settings The following parameters can be set or displayed:

Parameters	Description
Frequency (temp) [MHz]	Enters the (temporary) transmit frequency for the pending adjustment measurement. The frequency can be reselected for each iteration.
Frequency (Syst) [MHz]	Displays the system frequency currently being used for examinations *On '**?**' means that the final value of the adjustment parameters is not yet known. When starting the next measurement, the system will perform at least one measurement to determine the unknown parameter(s).*
Amplitude [V]	Enters the transmit amplitude for the pending adjustment measurement
Receive gain	**Low**: for strong receive signal **High**: for weak receive signal
Physio	Select / deselect the transfer of physiological measurement parameters from the **Physio** parameter card of the measurement protocol.
Vector size	Number of measurement points to be acquired
Bandwidth [Hz]	Width of the frequency range that will be used for the measurement, with the set transmit frequency as the center point
Averages	The resonance frequency is determined after adding up the individual measurements (to reduce noise).
Range display	Checks whether the frequency or amplitude entered is in the acceptable range

Results

The results of the adjustment measurement are displayed graphically in both the time and the frequency domain. The table with the numerical results contains the following entries:

Parameters	Description
No.	Running number of the adjustment measurement
Freq. [MHz]	Transmit frequency in MHz
Ampl. [V]	Transmit amplitude of the adjustment measurement
Max. Pos.	Position of the highest amplitude peak in the frequency domain
Diff. [Hz]	Difference between the transmit frequency and the calculated (better) frequency

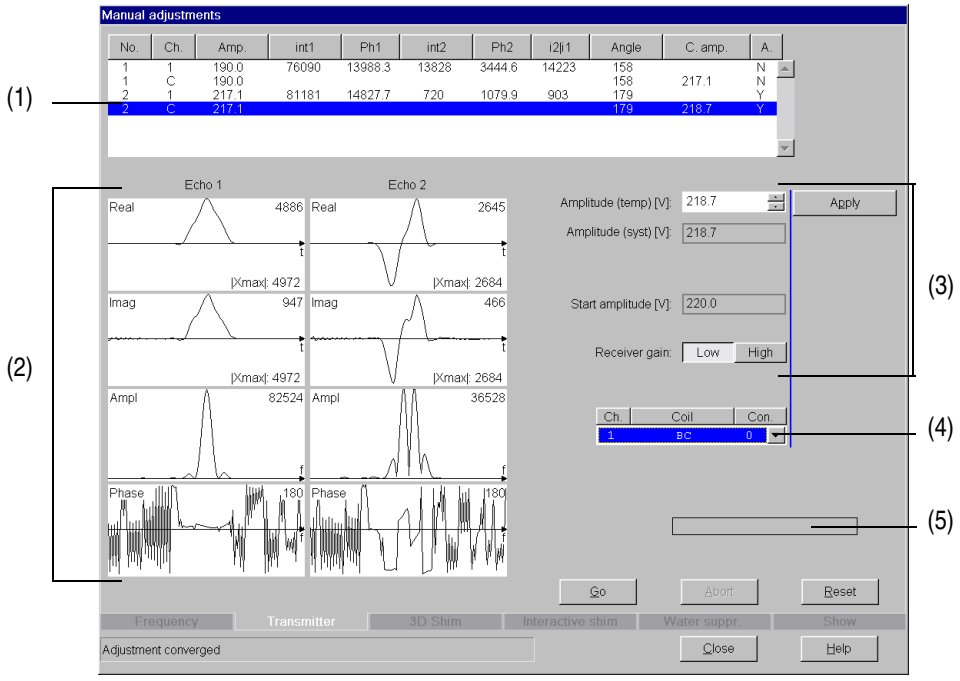
Transmitter adjustment

Transmitter adjustment is used for calibration of the transmitter. It does not refer to the adjustment volume, but rather to a range at the isocenter. 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.

⇨ For a detailed description of this procedure, refer to:
→ ***syngo* MR** Operator Manual

Transmitter subtask card

Set the adjustment parameters on the **Transmitter** subtask card in the **Manual adjustment** dialog window.



(1) Numeric results
(2) Graphical results display for normal (Echo1) and stimulated echo (Echo2)
(3) Adjustment parameters
(4) Coil measurement signal for graphical display
(5) Range display

Settings

The following parameters can be set or displayed:

Parameters	Description
Amplitude (temp) [V]	Enters the (temporary) reference amplitude for the pending adjustment measurement.
Amplitude (Syst) [V]	*Displays the system reference amplitude currently being used for examinations* *On '**?**' means that the final value of the adjustment parameters is not yet known. When starting the next measurement, the system will perform at least one measurement to determine the unknown parameter(s).*
Start Amplitude [V]	Displays the amplitude value for the first iteration (specific parameter of the transmit coil)
Receive gain	**Low**: for strong receive signal **High**: for weak receive signal
Range display	Checks whether the amplitude entered is in the acceptable range

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 table with the numerical results contains the following entries:

Parameters	Description
No.	Running number of the adjustment measurement
Ch.	Receive channel used to determine results
Amp.	Transmit amplitude of the adjustment measurement
int1	Integral of the first echo
Ph1	Phase of the first echo
int2	Integral 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.	Adjustment successful (**Y**es/**N**o)

Multinuclear transmitter adjustment

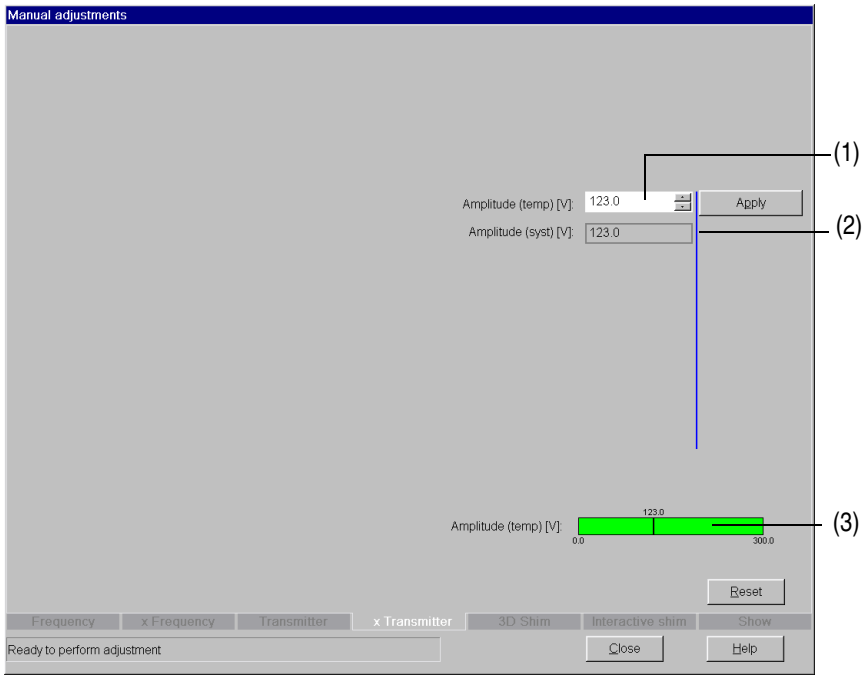
Since the signal strength is minimal, transmit adjustment measurements are not possible during multinuclear measurements. However, you can define a reference amplitude and apply it as the new system reference amplitude.

➪ For a detailed description of this procedure, refer to:
→ ***syngo* MR** Operator Manual

X-transmitter subtask card

Set the reference amplitude on the **X-transmitter** subtask card in the **Manual adjustment** dialog window.

➪ This card is shown only if you have a multinuclear license and have connected the X-nucleus transmit-receive coil.



(1) Temporary reference amplitude
(2) System reference amplitude
(3) Range display

Settings The following parameters can be set or displayed:

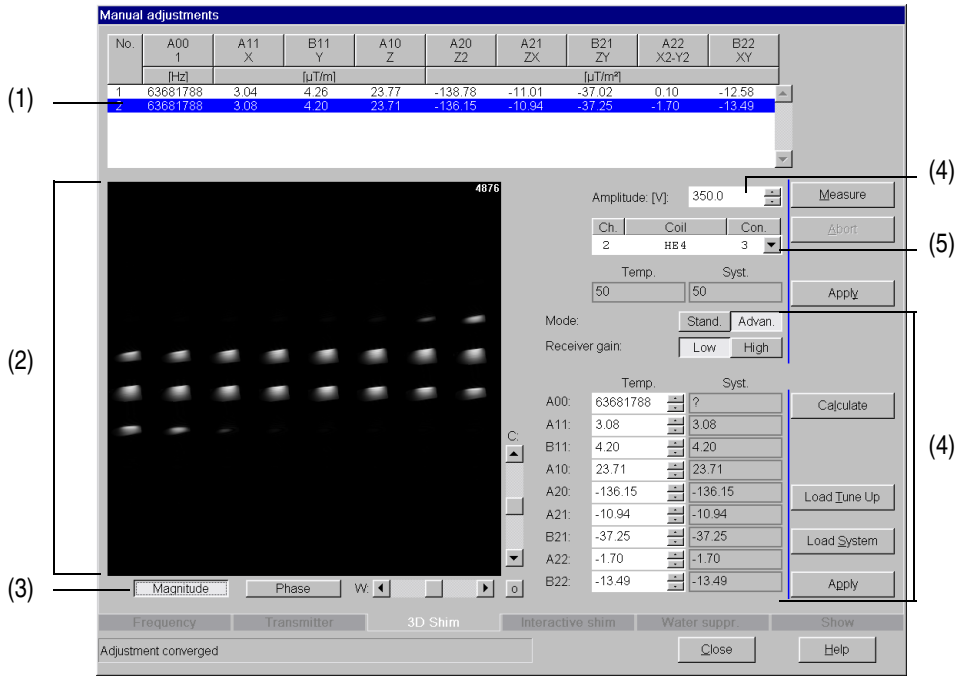
Parameters	Description
Amplitude (temp) [V]	Enters the (temporary) reference amplitude for the nucleus used
Amplitude (Syst) [V]	Displays the system reference amplitude currently being used for examinations *On '**?**' means that the final value of the adjustment parameters is not yet known. When starting the next measurement, the system will perform at least one measurement to determine the unknown parameter(s).*
Range display	Checks whether the amplitude entered is in the acceptable range

3D Shim

During 3D shim, a 3D data set is acquired using the default shim parameters and a field map is generated. Optimized shim parameters can be calculated using the field map and applied as the basis for the next iteration.

➪ For a detailed description of this procedure, refer to:
→ ***syngo* MR** Operator Manual

3D Shim subtask card Perform the shim on the **3D Shim** subtask card in the **Manual adjustment** dialog window.



(1) Numeric results
(2) Image area for displaying the field map
(3) Control elements for field map display
(4) Adjustment parameters
(5) Coil measurement signal for graphical display

Settings The following parameters can be set:

Parameters	Description
Amplitude [V]	Enters the transmit amplitude for the pending adjustment measurement.
Mode	Shim mode for the adjustment measurement. The standard or enhanced mode that is optimum for the protocol is set as default.
Receive gain	**Low**: for strong receive signal **High**: for weak receive signal

Parameters	Description
A00	**Temp.**: Transmitter frequency for the adjustment measurement **Syst.**: Current system parameters
A11, B11, A10	**Temp.**: Portion of the linear gradients for the adjustment measurement **Syst.**: Current system parameters
A21, B21, A22, B22	**Temp.**: Shim currents of the second order for the adjustment measurement **Syst.**: Current system parameters

➪ You can use the current system shim parameters or those from the last tune-up as the starting set for the shim. Click the **Load system** or **Load Tune Up** button.

Results

The field map is scaled accordingly and shown in the image area of the dialog window. After **Calculation** is performed, the new shim parameters are listed under **Temp.**:

Parameters	Description
A00	Transmitter frequency
A11, B11, A10	Linear gradients
A21, B21, A22, B22	Second order shim currents

➪ Click **Apply** to transfer the temporary results to the system for subsequent measurements.

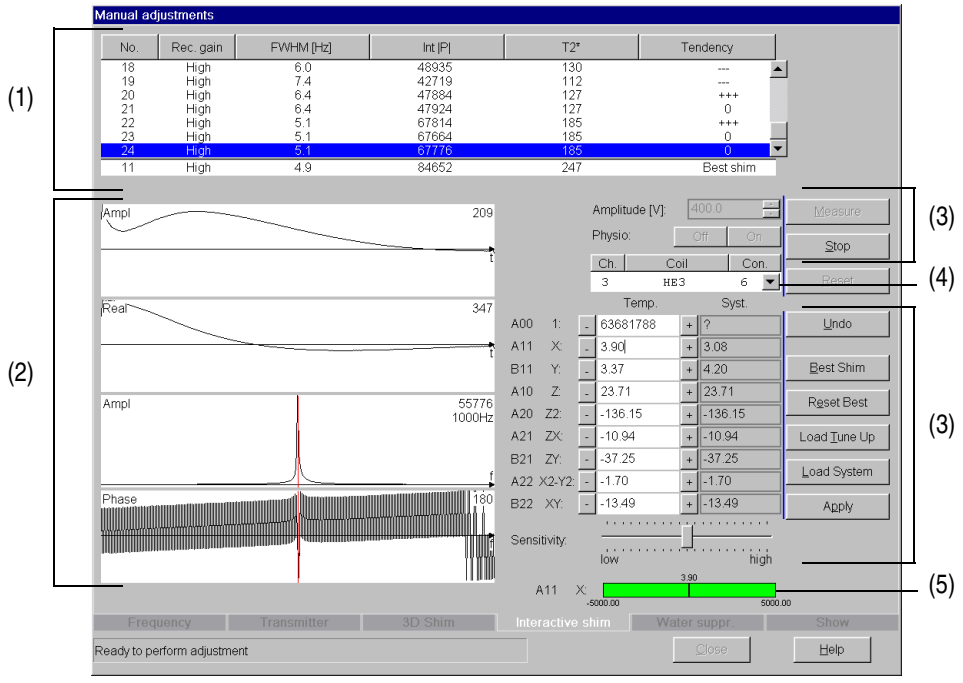
Interactive shim

During interactive shim, you can track the measurement of the MR signal in real time on screen and iteratively optimize the shim currents.

➪ For a detailed description of this procedure, refer to:
→ ***syngo* MR** Operator Manual

Interactive shim subtask card

Perform the shim on the **Interactive shim** subtask card in the **Manual adjustment** dialog window.



(1) Numerical results and best shim result
(2) Graphical results display
(3) Shim parameters
(4) Coil measurement signal for graphical display
(5) Range display

Settings The following parameters can be set:

Parameters	Description
Amplitude [V]	Enters the transmit amplitude for the pending adjustment measurement.
Physio	Select / deselect the transfer of physiological measurement parameters from the **Physio** parameter card of the measurement protocol.
A00	**Temp.**: Transmitter frequency for the adjustment measurement **Syst.**: Current system parameters
A11, B11, A10	**Temp.**: Portion of the linear gradients for the adjustment measurement **Syst.**: Current system parameters
A21, B21, A22, B22	**Temp.**: Shim currents of the second order for the adjustment measurement **Syst.**: Current system parameters
Sensitivity	Controller to set the sensitivity (increments) of the +/- keys for the numerical shim parameters
Range display	Checks whether the amplitude or shim parameter entered is in the acceptable range

➪ You can use the current system shim parameters or those from the last tune-up as the starting set for the shim. Click the **Load system** or **Load Tune Up** button.

Results

The following results are displayed graphically:

- ❏ Amplitude and real part of the measurement signal in the time domain
- ❏ Amplitude and phase of the measurement signal in the frequency domain

The table with the numerical results contains the following entries:

Parameters	Description
No.	Running number of the adjustment measurement
Rec. gain	Gain setting used
FWHM (Hz)	Width of the pulse received (frequency domain) at half the maximum amplitude (Full Width Half Maximum). During spectroscopy measurements, please note that the line width will decrease considerably in the post-processed real part spectrum.
Int |P|	Integral of the amplitude in the time domain
T2*	Transverse relaxation time (approximation)
Tendency	indicates whether the parameter changes result in shim improvement (+++) or degradation (---) or whether the status remains the same (o).

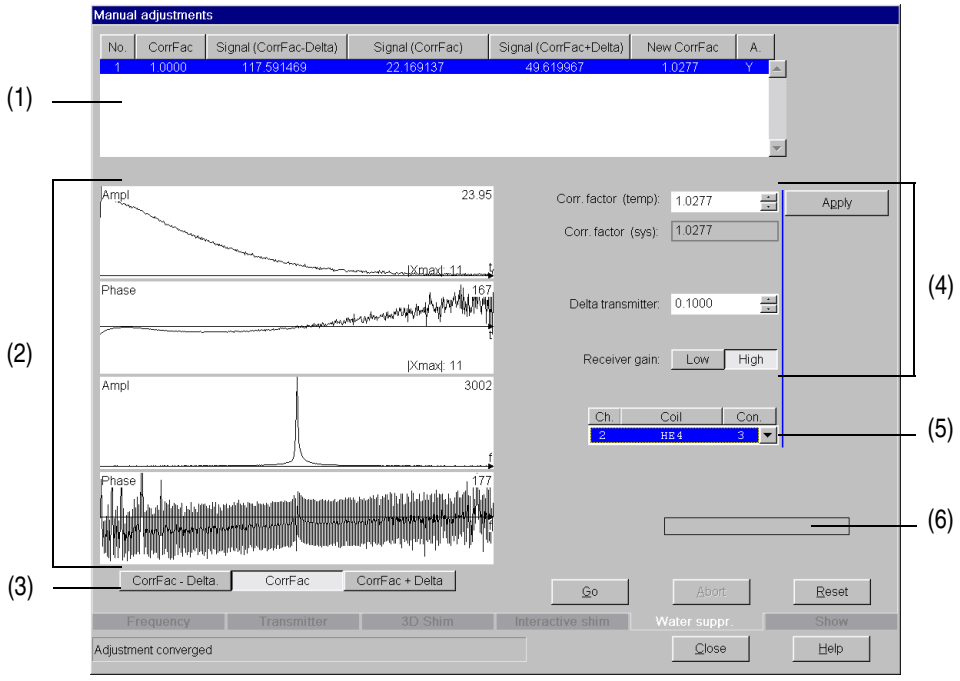
Manual water suppression

Use this adjustment to correct the transmitter amplitude for a special RF pulse to suppress the water signal.

➪ For a detailed description of this procedure, refer to:
→ ***syngo* MR** Operator Manual

Water suppr. subtask card

Perform the adjustment on the **Water suppr.** subtask card in the **Manual adjustment** dialog window.



(1) Numeric results
(2) Graphical results display
(3) Signal selection for graphical results display
(4) Adjustment parameters
(5) Coil measurement signal for graphical display
(6) Range display

Settings

The following parameters can be set:

Parameters	Description
Corr. factor (temp)	Enters the (temporary) correction factor for the transmitter amplitude.
Corr. factor (Syst)	Displays the correction factor currently being used for examinations *On '**?**' means that the final value of the adjustment parameters is not yet known. When starting the next measurement, the system will perform at least one measurement to determine the unknown parameter(s).*
Delta transmitter	Increment of the measurement range comprising 11 measurement points
Receive gain	**Low**: for strong receive signal **High**: for weak receive signal
Range display	to check whether the correction factor entered is in the acceptable range

Results

The amplitude and phase of the respective measurement signal are displayed graphically in the time and frequency domains. Use the signal selection buttons to view the measurement signals for the minimum that was found, as well as the measurement signals acquired to the left and right of the minimum (–/+ Delta).

The table with the numerical results contains the following entries:

Parameters	Description
No.	Running number of the adjustment measurement
CorrFac	(Start) correction factor of the adjustment measurement
CorrFac new	Optimum correction factor of the measurement range
Signal (CorrFac -Delta)	Signal strength for measurements using “CorrFac new” minus increment
Signal (CorrFac)	Signal strength for measurements using “CorrFac new”
Signal (CorrFac+Delta)	Signal strength for measurements using “CorrFac new” plus increment
A.	Adjustment successful (**Y**es/**N**o)

CHAPTER B.12

Performing Quality Assurance

Similar to standard examinations, you may perform quality assurance for spectroscopy to consistently ensure high-quality spectra.

Quality assurance may be performed by yourself or by Siemens Service as part of a Maintenance Agreement.

Quality assurance (QA) follows the same procedure as a routine examination. Instead of the spectroscopy program, you select a QA program. A phantom is positioned in the coil to simulate the patient.

Quality assurance for ^{1}H MRS

The following accessories are required for performing ^{1}H MRS quality assurance:

- ❏ Body loader
- ❏ Spherical phantom, filled with a 0.1 M solution of lithium acetate and sodium acetate.
- ❏ Head matrix, CP Head Array or head transmit/receive coil

Positioning the phantom and coil

The phantom and coil are positioned in the examination room.

- ✧ Position the head matrix, the CP Head Array or the head transmit/receive coil on the patient table and connect the coil. *Refer to the System Manual*
- ✧ Position the 1H spherical phantom with a pad in the center of the coil.
- ✧ When using the head matrix or the CP Head Array, position the body load phantom on the patient table.

✧ Align the laser light localizer with the marking on the coil to define the center of the measurement field.

✧ Move the patient table into the magnet.

The remaining preparations for the QA measurement are performed at the console in the control room.

Registering the quality measurement

Similar to standard examinations, you have to start the QA measurement by entering mandatory information in the **Patient Registration** dialog window.

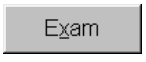
✧ Open the **Patient Registration** dialog window.
→ ***syngo* MR** Operator Manual

✧ Enter the mandatory information in the **Name**, **PatientID**, **Birth Date**, **Weight**, and **Sex** fields.

➪ You can enter “unknown” or “phantom” for sex.

✧ Select a QA measurement program in the **Study** selection list.

✧ Select the **Head first - Supine** option from the **Patient Position** list.

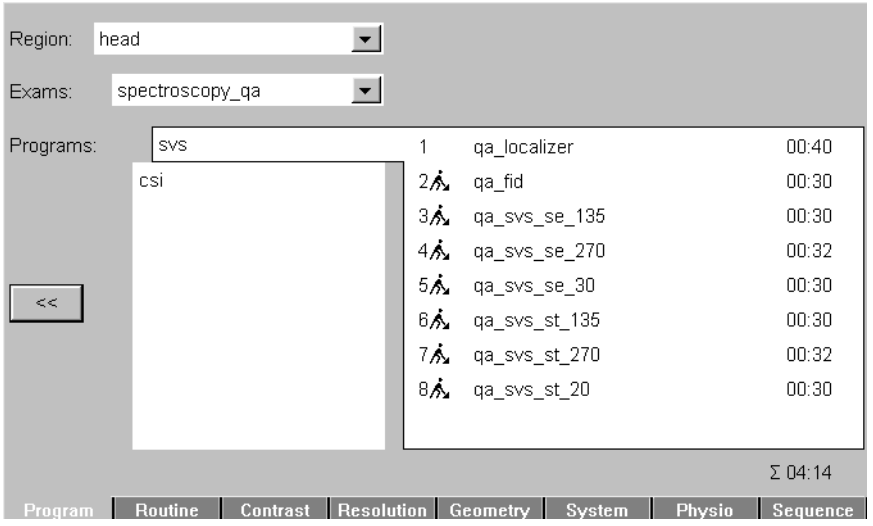


✧ Click **Exam**.

The **Exam** task card is displayed. The **Program** parameter card is opened in the parameter card stack.

Selecting a QA measurement program

The content area of the **Program** parameter card lists the individual steps of the QA measurement program selected during registration.



➪ You may now select the correct QA measurement program if it was selected incorrectly during registration.

✧ Click the **<<** button to transfer the selected QA measurement program to the program control.

Localizer measurement

After transferring the QA measurement program to the program control, the scout measurement (localizer) is started automatically.

The reference images measured are displayed in the image area of the **Exam** task card.

Checking the shim quality

Before you can start the QA measurement, you have to optimize the homogeneity of the magnetic field across the entire volume of the phantom. The spatially non-selective FID sequence is used to check the homogeneity.

Measuring the FID sequence

✧ Open the **qa_fid** protocol with a double-click.

The parameter settings of the protocol are displayed on the individual parameter cards.

✧ Open the **System > Adjustments** subtask card.

✧ Select the **Advanced** entry from the **Shim mode** list to set the shim automatically.

➪ You can perform a manual shim to achieve even better results.
→ Page B.11–17, *Interactive shim*

➪ Since you are viewing the water signal, water suppression and the corresponding adjustment are deactivated.

Once the required settings have been made, start the measurement.



✧ Click **Apply** in the program control.

The raw data measured are stored in the database under the quality patient.

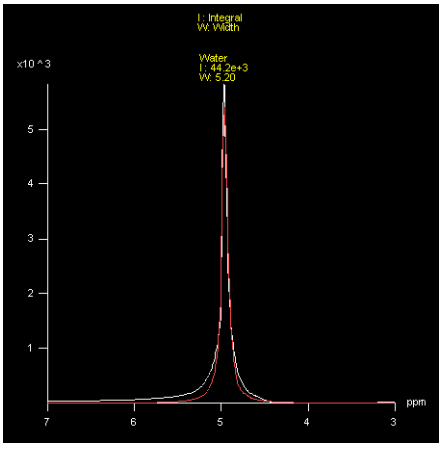
Evaluating FID raw data

Load the FID raw data measured into the **Spectroscopy** task card for evaluation. After the evaluation, you can check the quality of the shim.

✧ Select the FID raw data in the **Patient Browser**.

✧ Select **Applications > Spectroscopy**.
- Or -
Double-click the raw data.

The **Spectroscopy** task card is displayed and the FID data are evaluated automatically. The results are displayed as an FID spectrum.



Determining the full width at half maximum

The full width at half maximum (FWHM) of the water peak helps you evaluate the shim quality. Display the peak information:

✧ Select **Signal > Peak Information**.

The **Display parameters** dialog window with the **Peak Info** subtask card opens.



✧ Click on **Width**.

➪ The calculated full width at half maximum is displayed next to the water peak. The value for a good shim should be below 15 Hz at 1.5 T or below 30 Hz at 3 T.

➪ If no peak information is displayed, check if a curve fit is entered in the post-processing protocol.

Performing a localized QA measurement

After measuring the localizer and the FID sequence, you perform the QA measurement for localized SVS protocols or hybrid CSI protocols.

Measuring the localized QA SVS protocol

✧ Open a localized QA SVS protocol,e.g. **qa_svs_se_30**.

✧ Check the VOI settings on the **System-Adjustments** parameter card.

Make the following settings:

❏ Sag = 20 mm, Cor = 20 mm, Tra = 20 mm

❏ The VOI should be located in the center of the spherical phantom.



✧ Click **Apply**.

The settings are applied and the measurement is started automatically.

The measurement results are stored in the database as a spectroscopy raw data set.

✧ Load the raw data into the **Spectroscopy** task card for evaluation.

→ Page C.2–2, *Loading raw data*

Measuring the localized QA hybrid CSI protocol

✧ Open a localized QA CSI protocol,e.g. **qa_csi_se_30**.

✧ Check the VOI settings on the **System-Adjustments** parameter card.

Make the following settings:

❏ Sag = 80 mm, Cor = 80 mm, Tra = 15 mm
❏ The VOI should be located in the center of the spherical phantom.



✧ Click **Apply**.

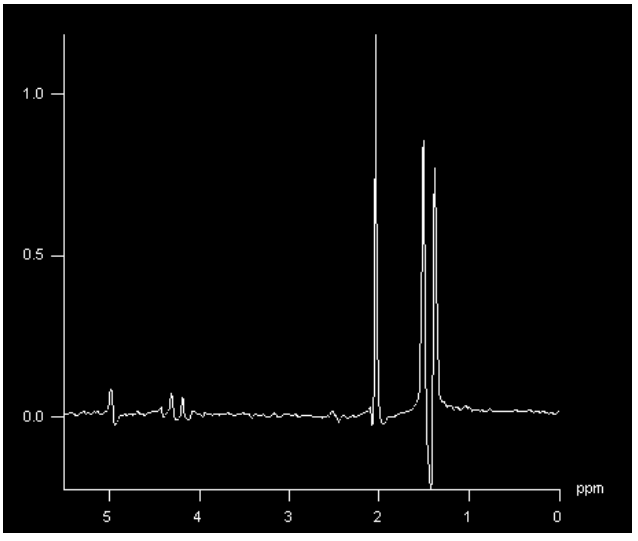
The settings are applied and the measurement is started automatically.

The measurement results are stored in the database as a spectroscopy raw data set.

✧ Load the raw data into the **Spectroscopy** task card for evaluation.
→ Page C.2–2, *Loading raw data*

Checking the results

The results of a successful ^{1}H MRS QA measurement are shown in the figure below. The example shows the spectrum of a raw data set measured using the **qa_svs_se_30** QA protocol.



❏ The spectrum has a clean baseline.

❏ The acetate peak and the lactate doublet of the phantom fluid are clearly delimited and narrow.

➪ With STEAM measurements, the lactate and acetate signals are always in phase (using TM = 10 ms). With spin echo measurements, the lactate and acetate signals have an inverted phase if TE = 135 ms and are in phase if TE = 270 ms.

Quality assurance for ^{31}P MRS

The following accessories are required for performing ^{31}P MRS quality assurance at 1.5 T:

- ❏ Body loader
- ❏ Phosphate bottle phantom, filled with a 0.05 M phosphate buffer solution (pH 7.2)
- ❏ Heart/Liver coil
- ❏ Coil cushion

Positioning the phantom and coil

The phantom and coil are positioned in the examination room.

✧ Position the Heart/Liver coil on the patient table and connect the coil.
→ Page B.3–9

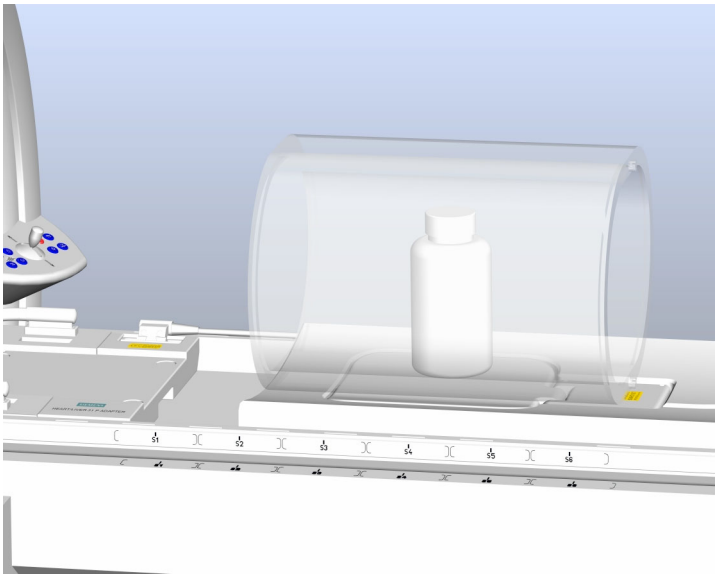
✧ Position the body load phantom *exactly* in the *center* of the Heart/Liver coil.

!

Do not place additional cushions etc. beside the support cushion between the coil and the body load phantom. Otherwise, the body load phantom may touch the inside wall of the MR system when you move the patient table into the magnet opening.

✧ Position the phosphate bottle phantom in the center of the body load phantom.

✧ Determine the center of the measurement field using the laser light localizer and move the patient table into the magnet isocenter *slowly and closely monitored*.



The remaining preparations for the QA measurement are performed at the console in the control room.

Registering the quality measurement and selecting a QA measurement program

Proceed according to a ^{1}H MRS quality measurement. As the examination, select a QA measurement program for the ^{31}P MRS.

→ Page B.12–2, *Registering the quality measurement*
→ Page B.12–3, *Selecting a QA measurement program*

Localizer measurement

After transferring the QA measurement program to the program control, the scout measurement (localizer) is started automatically.

The reference images measured are displayed in the image area of the **Exam** task card.

Checking the shim quality

The homogeneity of the magnetic field is checked using the same spatially non-selective FID sequence as for the ^{1}H MRS quality measurement.

Measuring the FID sequence and evaluating the FID raw data is largely similar to the procedure for ^{1}H MRS quality measurements as well.
→ Page B.12–4, *Checking the shim quality*

However, contrary to ^{1}H MRS quality measurements, the adjust volume is limited to the phantom due to the small dimensions of the ^{31}P phantom.

Performing the ^{31}P MRS QA measurement

There is no difference between a ^{31}P MRS QA measurement and a regular ^{31}P MRS measurement.

✧ Open a ^{31}P MRS QA protocol, e.g., **qa_fid_31P**.

A system message indicates that an adapted adjustment volume has been set instead of the standard adjustment volume.
→ Page B.12–11



✧ Click the **Manual** button to confirm the modified adjust volume and close the message window.

✧ To display the adjust volume, select **View > Adjust Volume On**.

✧ Modify the adjust volume according to the position of the phantom.



✧ Click **Apply** in the program control.

The settings are applied and the measurement is started automatically.

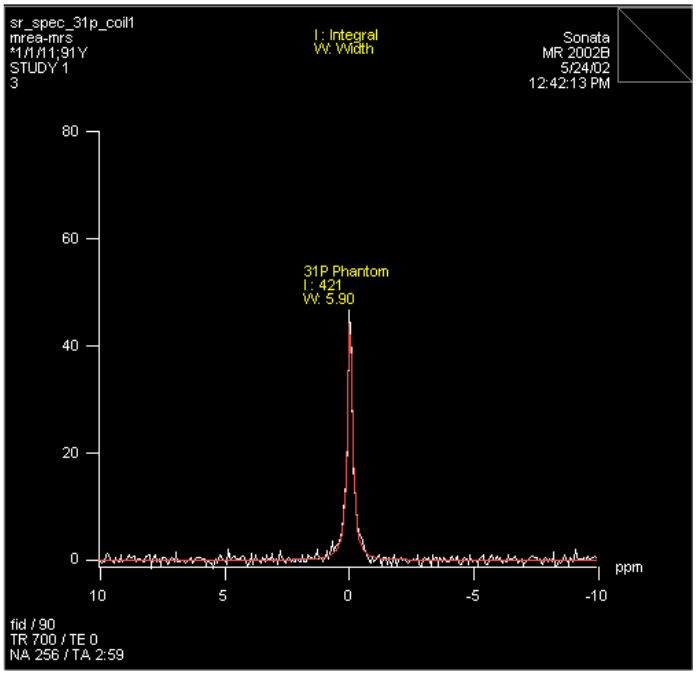
The measurement results are stored in the database as a spectroscopy raw data set.

✧ Load the raw data into the **Spectroscopy** task card for evaluation.
→ Page C.2–2, *Loading raw data*

✧ Ensure that the raw data are evaluated using the **qa_fid_31P** post-processing protocol.

Checking the results

The results of a successful ^{31}P MRS QA measurement are shown in the figure below. The example shows the spectrum of a raw data set measured using the **qa_fid_31P** QA protocol and evaluated using the **qa_fid_31P** post-processing protocol.

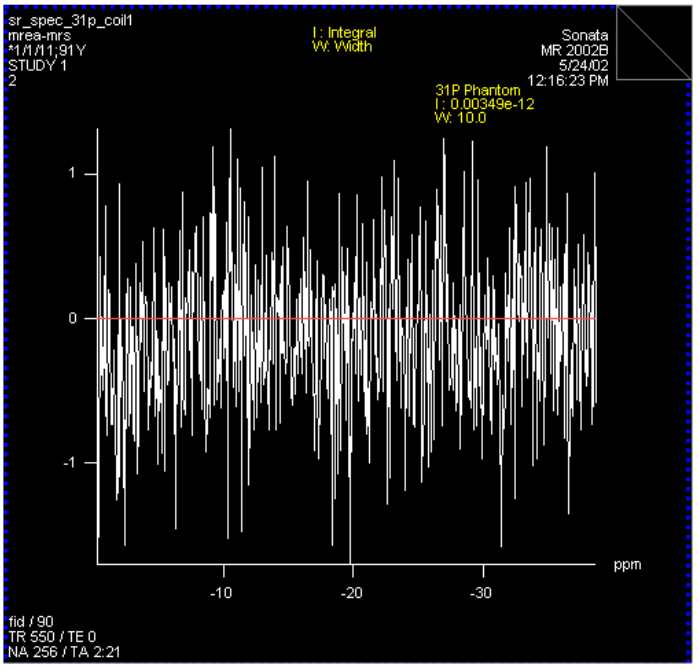


Ensure that the individual ^{31}P signal is adjusted. A critical variable may be the signal position which does not always correspond to the values preset in the protocol.

Check the following values for the adjusted signal:

- ❏ The line width of the signal should not exceed 20 Hz.
- ❏ The integral-to-noise ratio should be 300 or higher. The integral value is shown in the peak fit; e.g., an integral value of 421 is provided in the figure above.

To obtain an estimate of the standard distribution, display a signal-free area of the real part of the spectrum, making full use of the y-axis.
→ Page C.4–2, *Adjusting the signal display*



A number of viewers estimated a standard deviation of approx. 0.6.

To calculate the standard deviation quantitatively, follow these steps:

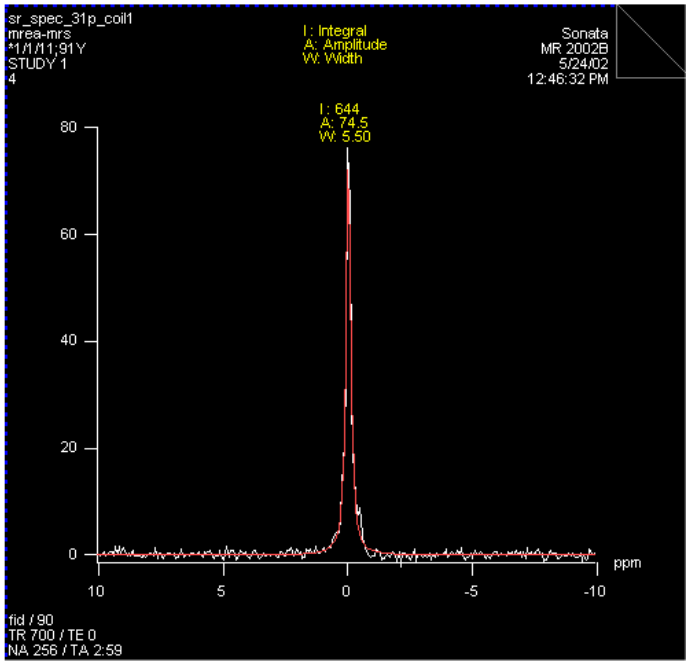
✧ Limit the calculation interval for the phantom peak to a signal-free area of the phantom spectrum, or select the entire area of a noise spectrum acquired using the **qa_fid_31P_noise** protocol.

✧ Fit the phantom peak to the noise.

The deviation of the adjusted signal to the noise is displayed in the fit dialog as **Fit error**.

The average deviation per point corresponds to the standard deviation of the noise. Therefore, you have to divide the fit error by the number of points in the evaluation area. The number of points across the entire evaluation area is equal to the vector size, if Zero-Filling is not selected. In the example above, a noise level of 0.33 is produced. Often, the visual estimate of noise exceeds the actual noise level.

The **qa_fid_31P_noe** protocol allows you to detect signal enhancement in the phantom signal via NOE saturation. The acquisition parameters of the subsequent spectrum correspond to those displayed above, with the exception of additional NOE pulses used.



The signal amplitude should increase by a factor of 1.4.

A suitable substance to show the decoupling effect is Methylenediphosphonic acid; Sigma Chemical, St. Louis, USA, product # M-1886.

Please observe the safety warnings and regulations when preparing and handling a phantom. You may dissolve 1 g of the substance in 50 ml of water in a small bottle. To facilitate shimming, you may insert it into a larger bottle with water. Without decoupling, the substance displays a ^{31}P triplet signal. Proton decoupling enables you to collapse the signal into a singlet signal.

CHAPTER B.13

Measurement Protocols

Siemens provides optimized measurement protocols for spectroscopy examinations. You will find them in the protocol directory under **spectroscopy** and the corresponding examination directories (**head_1H**, **breast_1H**, **prostate_1H**, **head_31P**, **heart_31P**, **liver_31P**, and **muscle_31P**).

The measurement protocols use sequences for Single Voxel Spectroscopy (SVS) as well as ^{1}H and ^{31}P MR spectroscopy.

The spectroscopy protocols for phantom measurements (in the **qa_1H** and **qa_31P** folders) marked with the "**qa**_" prefix (**q**uality **a**ssurance) differ from the protocols for *in vivo* measurements only by the smaller number of acquisitions. The different measurement protocol names result in the selection of different, specially adapted post-processing protocols.

You can optimize and save the protocols for your applications. We recommend starting from the Siemens protocols.
→ Page C.11–1, *Managing Post-processing Protocols*

!

Spectroscopy proton examinations using the CSI technique require installation of the "2D Spectroscopy CSI" and "Higher Order Shim Channels" options on your MR system. Additionally, for prostate examinations and 3D CSI examinations, the "3D Spectroscopy CSI" license is required.

Use of the ^{31}P CSI protocols also requires the installation of the "Multinuclear Support" and "Multinuclear Spectroscopy" options.

Protocols for in-vivo application

In the following you will find brief descriptions of the measurement protocols in the individual examination directories for the 1.5 and 3 T systems.

➪ The ^{1}H measurement protocols for 3 T have e.g. different **Averages** and **TR** measurement parameters than the 1.5 T measurement protocols.

head_1H and pediatric_head_1H

localizer

Localizer protocols are used to acquire reference images for positioning the spectroscopy VOIs and CSI slices.

The localizers listed under **pediatric_head_1H** are adjusted to the smaller dimensions of the head of a child

The **_5** suffix specifies the acquisition of 3 orthogonal slice stacks with 5 slices each.

The **@center** extension means that Iso-Center Mode is active in this protocol.

The **Localizer_in_plane_CSI** protocol is used to plan double-oblique CSI slices.

The protocols described in the following are subdivided into individual programs such as SVS and CSI. Since the introduction of **Tim technology**, the spectroscopy protocols are also differentiated according to the coil used. For this reason, two protocol trees identical except for a few coil-specific parameter adjustments (coil selection and normalization filter) are filed with the appendices _matrix and/or _TxRx.

svs_se

The **svs_se** designation specifies protocols used for Single Voxel Spectroscopy with a spin echo localization method.

The **_135**, **_270**, and **_30** suffixes specify the selected echo times. An echo time of 135 ms allows you to visualize the main metabolites with inverted lactate peak. A short echo time (30 ms) allows you to acquire signals of strong coupling spin systems and signals with short T2 relaxation times. A long echo time (270 ms) causes the lipid signal to gradually fade out. As a result, this protocol is suitable for lactate quantification.

_pediatric identified protocols suitable for faster acquisitions.

svs_st

The **svs_st** designation specifies protocols used for Single Voxel Spectroscopy with a STEAM localization method.

The **_135**, **_270**, and **_20** suffixes specify the selected echo times. A short echo time (20 ms) allows you to acquire signals of strong coupling spin systems and signals with short T2 relaxation times. A long echo time (270 ms) causes the lipid signal to gradually fade out. As a result, this protocol is suitable for lactate quantification.

csi_se

The **csi_se** measurement protocols trigger a highly localized Chemical Shift Imaging sequence with spin echo volume excitation.

The **_135**, **_270**, and **_30** suffixes specify the selected echo times. An echo time of 135 ms allows you to visualize the main metabolites with inverted lactate peak. A short echo time (30 ms) allows you to acquire signals of strong coupling spin systems and signals with short T2 relaxation times. A long echo time causes the lipid signal to gradually fade out. As a result, this protocol is suitable for lactate quantification.

The **_3D** suffix specifies CSI protocols with 3D spatial encoding.

_pediatric identified protocols suitable for faster acquisitions.

csi_st

The **csi_st** measurement protocols trigger a highly localized Chemical Shift Imaging sequence with STEAM volume excitation.

The **_135**, **_270**, and **_20** suffixes specify the selected echo times. A short echo time (20 ms) allows you to acquire signals of strong coupling spin systems and signals with short T2 relaxation times. A long echo time causes the lipid signal to gradually fade out. As a result, this protocol is suitable for lactate quantification.

The **_3D** suffix specifies CSI protocols with 3D spatial encoding.

Pediatric spectroscopy protocols are also listed under the region **pediatric_head**.

breast_1H

localizer_ref

3 orthogonal images to localize the reference solution for choline quantification.

svs_se_breast

Single voxel spectroscopy with spin echo technique used for breast MRS. For choline detection in breast cancer the spectral lipid suppression, weak water suppression and frequency corrected accumulation technique is used.

svs_se_breast_ref

Optimized external reference scan (reference solution inside the breast coil) to quantify the choline-signal in breast cancer, mainly in follow-up studies during chemotherapy. The “normalization” with respect to the reference signal is automatically applied during postprocessing.

svs_se_breast_ref_int

Internal reference scan (internal water signal inside the lesion) to quantify the choline-signal in breast cancer.

prostate_1H

localizer

t2_tse sequences with slice selection in three main orientations (**_tra** for transverse, **_cor** for coronal, and **_sag** for sagittal) can be used to acquire reference images.

csi3d_se_prostate

Highly localized 3D spectroscopy of the prostate using a **csi_se** sequence to visualize citrate and choline.

Water and fat suppression is achieved using the selected spectral signal suppression (**Spectral suppr.** parameter).

Outer Volume Suppression is done by up to eight freely selectable regional saturation regions predefined in the protocol.

head 31P (only Trio/Verio system)

fid: localizer

Localizer protocols are used to acquire reference images for positioning the spectroscopy VoIs and CSI slices.

fid: head_fid

Basic non-localized spectroscopy to examine the energy state. NOE enhancement or proton decoupling can be switched on with $^{31}P/^{1}H$ double resonant coils.

csi_fid: localizer

Localizer protocols are used to acquire reference images for positioning the spectroscopy VoIs and CSI slices.

csi_fid: head_csi_fid

Basic localized spectroscopy of the head to examine the energy metabolism using the csi_fid sequence. NOE enhancement or proton decoupling can be switched on with $^{31}P/^{1}H$ double resonant coils.

heart_31P (only 1.5 T)

tfl_loc_

By default, reference images are acquired using TurboFlash sequences (**tfl_**).

The **_multi**, **_2-chamber**, **_4-chamber**, and **_short-axis** suffixes specify the acquisition of reference images of a 2 or 4 chamber view and the short cardiac axis.

heart_csi

Highly localized spectroscopy of the myocardium to examine the energy metabolism using an ECG-triggered **csi_fid** sequence.

The **_noe** suffix specifies the addition of ^{1}H saturation pulses to utilize the Nuclear Overhauser Effect.

The **heart_csi** measurement protocol is provided for systems with a magnetic field strength of 1.5T.

liver_31P (only 1.5 T)

localizer

Acquisition of 5 transverse and 5 coronal reference images using a **tfl** sequence.

The **_multi** suffix specifies the acquisition of 5 transverse, 5 coronal, and 2 sagittal reference images.

liver_csi

Highly localized spectroscopy of the liver to examine the energy metabolism using a **csi_fid** sequence.

The **_noe** suffix specifies the addition of ^{1}H saturation pulses to utilize the Nuclear Overhauser Effect.

The **liver_csi** measurement protocol is provided for systems with a magnetic field strength of 1.5T.

muscle_31P (only 1.5 T)

localizer

Acquisition of reference images using a **tfl** sequence.

The **_tra** suffix specifies the acquisition of 3 transverse planning images for the **_sag+cor** protocol.

The **_sag+cor** suffix specifies the acquisition of 6 sagittal and 6 coronal reference images.

muscle_fid

Non-localized spectroscopy to examine the energy state of the muscle.

The **_noe** suffix specifies the addition of ^{1}H saturation pulses to utilize the Nuclear Overhauser Effect.

The **muscle_fid** measurement protocol is provided for systems with a magnetic field strength of 1.5T.

muscle_csi_fid

Highly localized spectroscopy of the muscle (e.g., peroneal muscle) to examine the energy state.

The **_noe** suffix specifies the addition of ^{1}H saturation pulses to utilize the Nuclear Overhauser Effect.

The **muscle_csi_fid** measurement protocol is provided for systems with a magnetic field strength of 1.5T.

x_nuc_library

Comprises several basic protocols for x-nuclei based on the corresponding fid sequences of nuclei ^{7}Li, ^{13}C, and ^{19}F, and ^{31}P.

Protocols for quality assurance

Quality assurance protocols are identified by the prefix **qa_** (directories **qa_1H** and **qa_31P**).
→ Chapter B.12, *Performing Quality Assurance*

qa_1H

The ^{1}H **qa_svs** and ^{1}H **qa_fid** protocols are provided for magnetic field strengths of 1.5T and 3T.

qa_31P

The ^{31}P **qa** protocols are provided for systems with a magnetic field strength of 1.5T and 3T.

3D CSI protocols

The 2D CSI protocols can be easily adapted to 3D CSI protocols if the “3D CSI Spectroscopy” license is installed. To create a 3D CSI protocol, select the **Sequence-Common** parameter card and switch the **Dimension** parameter from **2D** to **3D**.

Please note the increased scan time due to the higher number of phase-encoding steps. You may reduce the measurement time by, e.g., reducing the phase-encoding steps or the number of averages. In addition, the weighted acquisition mode is particularly suited to 3D CSI.

PART C

Spectroscopy Evaluation

C.1 *Spectroscopy Task Card*

Task card layout C.1–2
Control Area C.1–3
Image area for result display C.1–3
Image area for reference image display C.1–7
Setting the display mode C.1–10

C.2 *Loading Raw Data and Reference Images*

Opening the empty Spectroscopy task card C.2–2
Loading raw data C.2–2
Determining the evaluation protocol automatically C.2–3
Loading raw data from the program control C.2–5
Loading raw data from the Patient Browser C.2–5
Loading additional raw data sets C.2–6
Loading other reference images C.2–7
Displaying a different data set C.2–8
Closing a data set C.2–9

C.3 *Editing the Display of Reference Images*

Browsing the reference images C.3–1
Displaying the reference image in the large image segment C.3–2
Automatically selecting reference images C.3–3
Activating automatic selection mode C.3–4
Searching for the nearest reference images C.3–4
Zooming and panning the reference image C.3–4
Fitting the reference image to the segment size C.3–5

Windowing the reference image C.3–5
Assigning automatic window values C.3–5
Showing/hiding graphic tools and image text C.3–6

C.4 *Editing the Display of the Spectrum*

Displaying coordinates C.4–2
Adjusting the signal display C.4–2
Selecting the display type C.4–4
Defining the X axis C.4–4
Defining the Y axis C.4–5
Setting the origin C.4–5
Showing/hiding spectrum text C.4–6
Showing/hiding miniature reference images C.4–6
Showing peak information C.4–7
Selecting peak information C.4–9
Showing/hiding the fit error C.4–9
Showing/hiding the curve fit C.4–10
Annotating the spectrum C.4–10
Undoing entries C.4–11

C.5 *Evaluating Data Using a Different Protocol*

Selecting a post-processing protocol C.5–2
Copying the post-processing protocol C.5–3

C.6 *Displaying Evaluation Results in Table Format*

Configuring the result table C.6–2
Displaying the result table C.6–2
Defining the reference metabolite C.6–3
Displaying and selecting metabolites with hidden peak information C.6–4
Combining metabolites C.6–5
Applying the settings C.6–6
Showing/hiding miniature reference images C.6–6
Showing/hiding image text C.6–6
Saving the result table as a text file C.6–7

C.7 *Evaluating CSI Data*

Selecting the CSI slice (for 3D CSI data only) C.7–3
Displaying individual spectra C.7–6
Creating a spectral map C.7–6
Generating metabolite images C.7–13
Spectral map/metabolite image C.7–21
Editing the display C.7–21
Displaying a metabolite movie C.7–24
Calculating the sum spectrum C.7–26
Modifying Fourier Transformation C.7–29

C.8 *Evaluating Data Interactively*

Arranging post-processing steps C.8–2

Adapting post-processing steps C.8–5

- Opening the dialog window C.8–5
- Adjusting a post-processing step (general) C.8–6
- Adjusting filtering C.8–8
- Adjusting zero-filling C.8–13
- Adjusting water suppression correction (^{1}H MRS only) C.8–15
- Adjusting the FID shift C.8–19
- Adjusting eddy current compensation C.8–21
- Fourier Transformation C.8–24
- Adjusting baseline correction C.8–26
- Adjusting phase correction C.8–32
  - Performing phase correction manually C.8–34
  - Automatic phase correction C.8–37
- Adjusting the frequency shift correction C.8–40
  - Moving the peak to its theoretical peak position .. C.8–42
  - Entering the frequency shift value C.8–43
- Normalizing to reference C.8–43
- Adjusting curve fitting C.8–46
  - Performing curve fitting manually C.8–47
  - Automatic curve fitting C.8–54

Opening the original protocol version C.8–56

C.9 *Editing Peaks and Peak Lists*

Editing peaks C.9–2
Displaying the Peak Editor C.9–2
Adjusting the graphic display C.9–4
Changing the peak settings C.9–8
Applying the settings C.9–13
Adding a peak template to the peak list C.9–14
Creating peak templates C.9–16
Managing the customer list C.9–19

C.10 *Saving and Documenting Results*

Saving results and reference images C.10–1
Loading stored images in the Viewer C.10–4
Filming and printing results and reference images C.10–5

C.11 *Managing Post-processing Protocols*

The Protocol Browser C.11–2
Changing the display of the browser window C.11–3
Setting the display of the protocol list C.11–3
Modifying a post-processing protocol C.11–4
Opening the post-processing protocol C.11–5
Modifying properties C.11–6
Saving the post-processing protocol C.11–8
Creating a new post-processing protocol C.11–9
Creating a new protocol directory C.11–11
Deleting customer protocols C.11–13
Exporting/importing customer protocols C.11–15
Exporting protocols C.11–15
Importing protocols C.11–17

C.12 *Exporting Raw Data*

Exporting Raw Data in DICOM format C.12–1

Exporting Raw Data in ASCII Format C.12–2

Performing the export C.12–2

Content of the ASCII file C.12–4

C.13 *Ending a Spectroscopy Evaluation*

C.14 *Post-processing Protocols for ^{1}H MRS*

Short echo times C.14–1

CHAPTER C.1

Spectroscopy Task Card

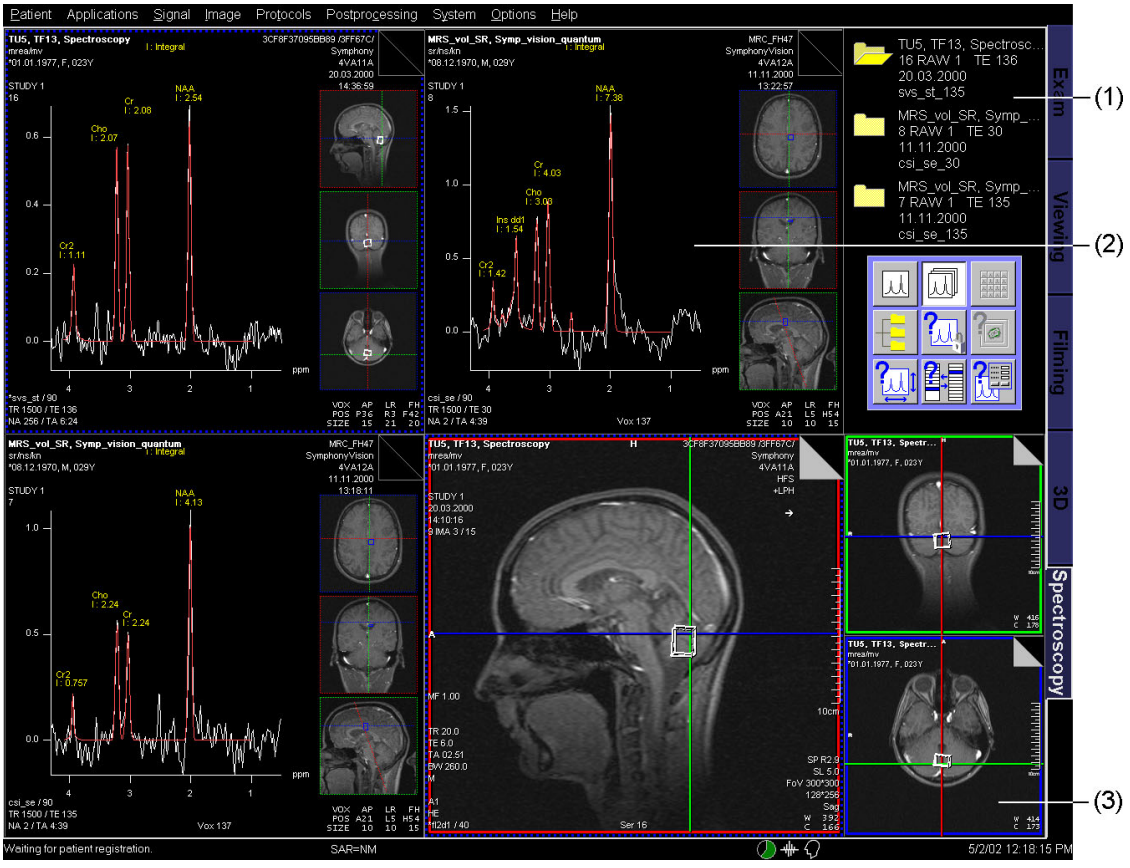
The set of raw data generated by the spectroscopy measurement is stored in the database under the name of the patient.

The following evaluation types are available:

Evaluation	Description
Automatic	Based on the specific properties of the measurement protocol used (system type, nucleus type, protocol name, sequence name, TE time, TM time) the raw data is automatically assigned a suitable post-processing protocol when loaded into the Spectroscopy Task Card. Said post-processing protocol comprises individual evaluation steps automatically applied to the raw data in sequence to calculate a spectrum. → Page C.2–3, *Determining the evaluation protocol automatically*
Interactive	You can also interactively evaluate the raw data by applying the individual post-processing functions to the data in sequence.
CSI data	In case of CSI data, you can simultaneously evaluate all the voxels of the defined area of the CSI matrix, e.g. to generate a *Sum Spectrum*, *Spectral Map*, or *Metabolite Image*.

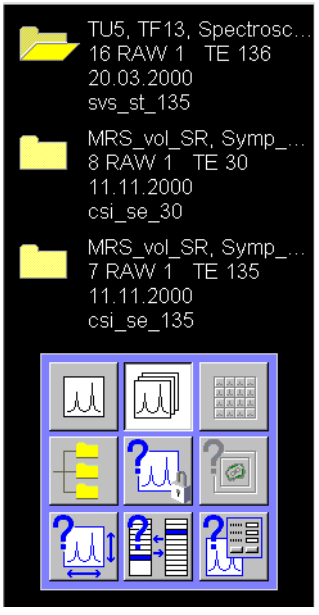
Load the raw data into the **Spectroscopy** task card for evaluation.

Task card layout



(1) Control Area
(2) Image area for result display
(3) Image area for reference image display

Control Area



The control area contains three Patient Folders, each of which can contain a patient data set. This means you can simultaneously work with up to three data sets in the **Spectroscopy** task card.

Information about the loaded raw data are displayed next to the patient folders.

A subtask card with buttons for quick access to important functions is located below the patient folders.

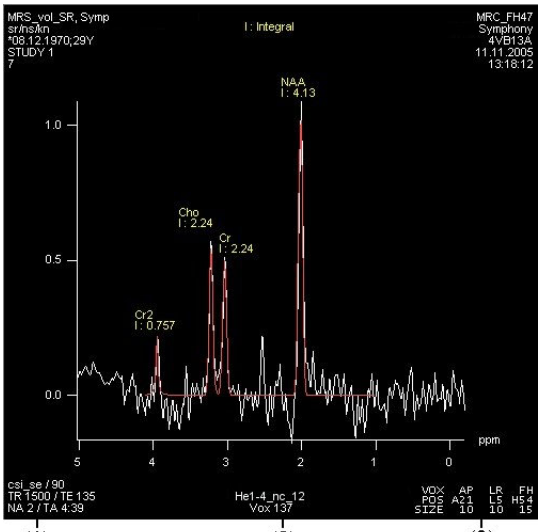
Image area for result display

The results of the automatic evaluation or the current evaluation function (spectrum, result table, sum spectrum, spectral map, or metabolite image) are displayed in the active segment (identified by a dashed blue border) of the image area for result display. Important text information with respect to the result are displayed along the outer margin of the segment.

Image text

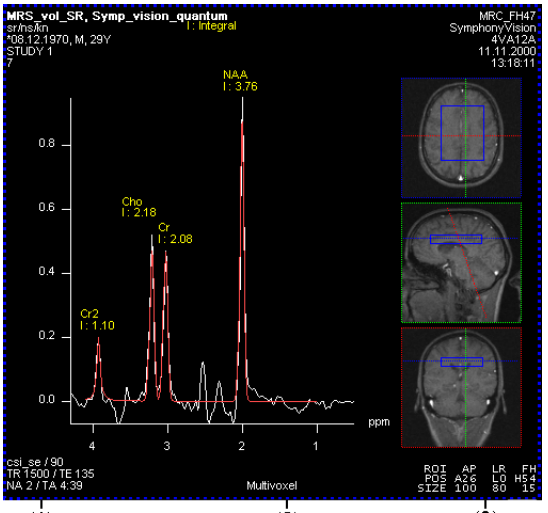
The image text (spectral text) displayed in the lower section of the image varies according to the result type.

Image Text for Individual Spectra and Results Tables:



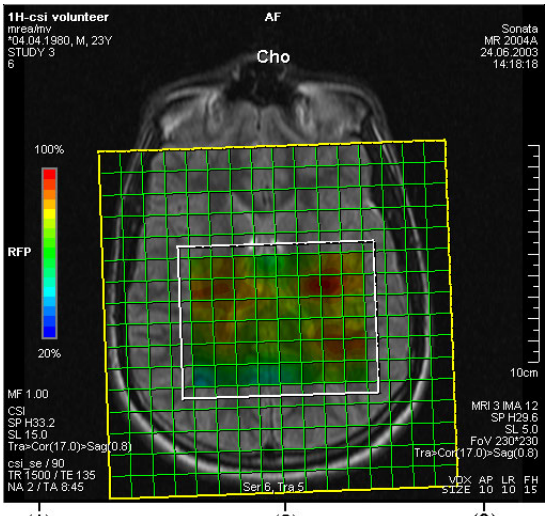
Lower left (1)	**Lower center (2)**	**Lower right (3)**
– Sequence name/Flip angle, e.g., **csi_se / 90** – Repetition time (**TR**) / Echo time (**TE**) – Number of measurements (**NA**)/ Duration of measurement (**TA**)	1. line: Coil: – Abbreviation for coil name; e.g., **He** for Head Matrix – List of elements used, e.g., **1-6** or **1,3-5** – Combination algorithm **u**: uncombined **c**: combined **nu**: normalized, uncombined **nc**: normalized, combined – Number of contributing channels, e.g., **12** 2. line: For CSI data: Number of displays Voxels (e.g., **Vox 137**) The line remains blank for SVS data.	For CSI data: Position (**POS**) and size (**SIZE**) of the selected voxel For SVS data: Position and size of the VOI

Image text for Sum Spectrum



Lower left (1)	Lower center (2)	Lower right (3)
– Sequence name/Flip angle, e.g., **csi_se / 90** – Repetition time (**TR**) / Echo time (**TE**) – Number of measurements (**NA**)/ Duration of measurement (**TA**)	1. line: refer to individual spectra 2. line: **Multivoxel** to indicate many voxels	– Rectangular ROI: Position (**POS**) and size (**SIZE**) of the ROI – Other ROIs: blank

Image Text for spectral maps and metabolite images



Lower left (1)	Lower center (2)	Lower right (3)
– Image magnification factor, e.g., **MF 1.00** Reference to CSI slice parameters – Header **CSI** – CSI slice position (**SP**) – CSI slice thickness (**SL**) – Orientation of the CSI slice – Sequence name/Flip angle, e.g., **csi_se / 90** – Repetition time **(TR)**/ Echo time (**TE**) – Number of measurements (**NA**)/ Duration of measurement (**TA**)	1. line: refer to individual spectra 2. line: Series number from which the raw data originated e.g., **Ser 6** For CSI data in addition: Selected primary direction and number of the selected plane e.g., **Tra 5** If a different segment containing a spectrum or results table is selected, the number of the corresponding voxel is also specified.	Note regarding the reference image underneath – Header **MRI** with series and image number of the corresponding reference image (format **n IMA m**) – Slice position (**SP**) – Slice thickness (**SL**) – Field of View (**FoV**) and – Orientation of reference image – Size (**SIZE**) of a Voxel

Image area for reference image display

In general, three reference images are loaded when loading a raw data set into the **Spectroscopy** task card. The reference images used for graphical positioning of the measurement object (VOI/CSI slice/3D-CSI slab) serve as the origin.

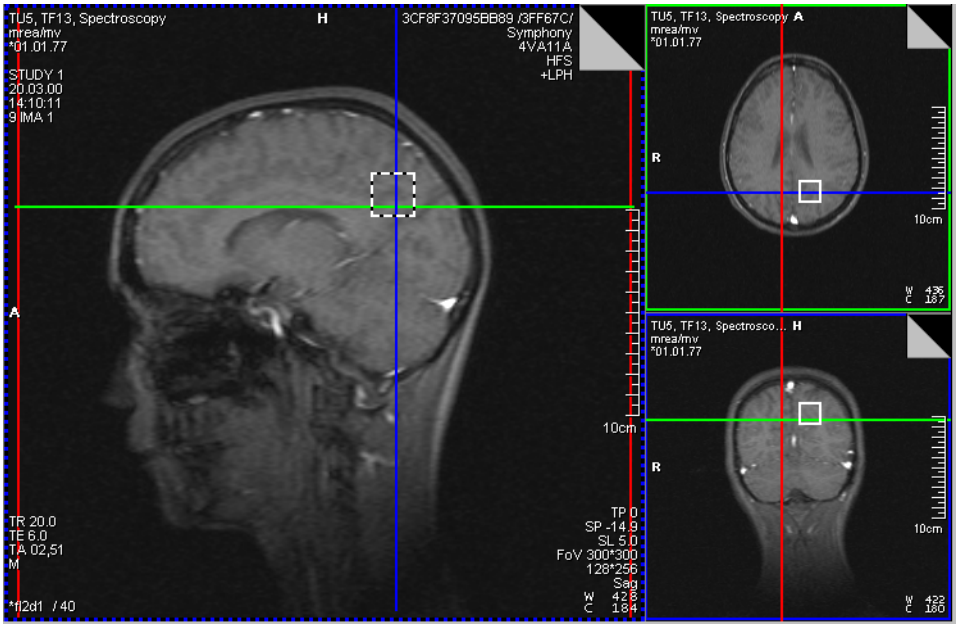
⇨ Which images are actually output depends on whether automatic selection mode is activated or not. If deactivated, the output images themselves are loaded. If activated, the output images are used to search for suitable reference images.
→ Page C.3–4, *Activating automatic selection mode*

The reference images (transverse, sagittal, and coronal) are displayed in the lower right section of the task card.

One of the reference images is displayed in the large reference image segment, the other two in the small reference image segments. The lines show the edges at which the reference images intersect. The line colors match the colored boundaries of the corresponding reference images.

Image display for the SVS technique

If you have loaded an SVS raw data set, the VOI used for the examination is identified by a white border in the reference image.



➪ If the VOI border is dashed, the VOI is outside the reference image plane. The following message window is displayed:

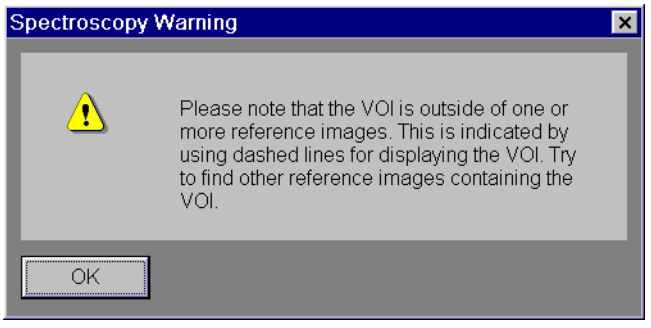
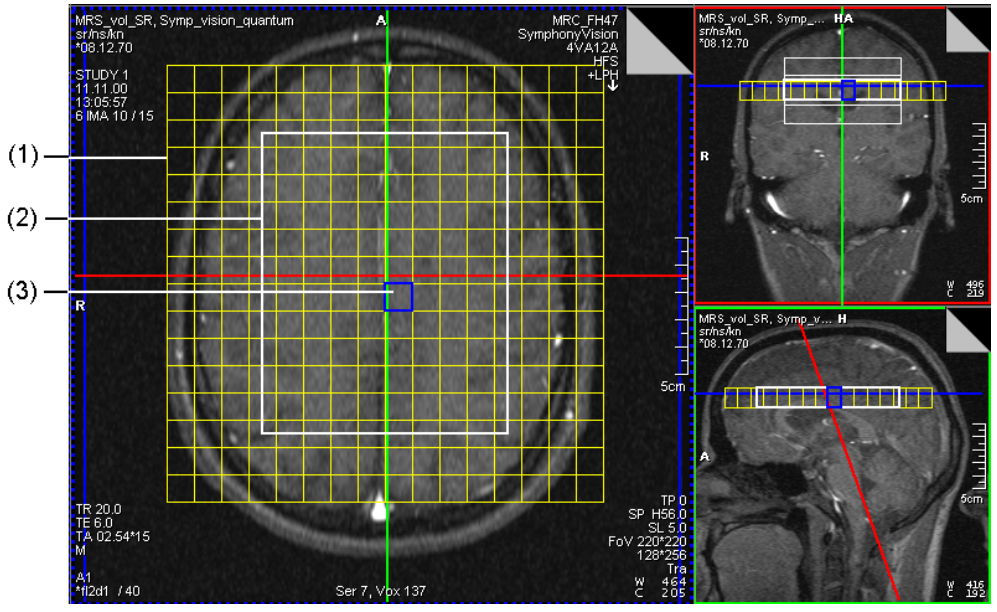


Image display for the CSI technique

When loading 2D CSI raw data, the reference image parallel to the CSI slice is displayed in the large segment. In case of 3D CSI raw data, the reference image parallel to the last selected main orientation is displayed in the large segment.

The CSI matrix is displayed as a yellow grid and the VOI (if available) as a white rectangle. The voxel to be evaluated is highlighted by a blue border.



(1) CSI slice
(2) VOI within the CSI slice
(3) Voxel to be evaluated

➪ If the CSI slice display is dashed, the slice is outside the reference image plane.

The number of the selected voxel is shown at the center of the footer both in the reference images and in the displayed spectrum. It uniquely assigns a spectrum to the highlighted voxel position in the reference images.

For 3D CSI data, the footer also shows the main orientation and the number of the selected slice (e.g., Sag 9).

Setting the display mode

Two display modes are available for presenting the evaluation results:

- ❏ **Single Dataset Mode**
- ❏ **Multiple Dataset Mode**

Single Dataset Mode

All segments of the image area are used to display the results of a data set.

➪ This mode is useful for evaluating CSI data; it allows you to display the spectra of different voxels side by side.

✧ Select **Signal > Single Dataset Mode**.
- Or -
Click the button in the control area.



Multiple Dataset Mode

The evaluation results of up to three data sets can be displayed in parallel on the **Spectroscopy** task card.

Multiple Dataset Mode is the default setting when you start the **Spectroscopy** task card.

✧ Select **Signal > Multiple Dataset Mode**.
- Or -
Click the button in the control area.





➪ If you display multiple spectra for a data set in **Single Dataset Mode** and switch to **Multiple Dataset Mode**, the spectra are retained and stacked in the respective segment. Use the dog-ears to scroll to the desired spectrum.

CHAPTER C.2

Loading Raw Data and Reference Images

The first step of a spectroscopy evaluation involves loading the raw data of a spectroscopy measurement.

Data can be loaded in one of two ways:

- ❏ Open the empty **Spectroscopy** task card and load the raw data set
- ❏ Load the raw data set (the **Spectroscopy** task card is opened automatically)

⇨ When the raw data is loaded, the corresponding reference images are loaded as well.
→ Page C.1–7, *Image area for reference image display*

After the raw data are loaded, they are *automatically* evaluated using a suitable post-processing protocol.
→ Page C.2–3, *Determining the evaluation protocol automatically*

The resulting spectrum is displayed in the image area of the **Spectroscopy** task card together with the corresponding reference images.

! Spectroscopy evaluation requires that the user has full access rights to the patient data to be evaluated.

Refer to the *syngo* Security Package brochure for detailed information regarding user administration.

Opening the empty Spectroscopy task card

You can open the empty **Spectroscopy** task card (without the raw data set) from the other task cards.

✧ Select **Applications > Spectroscopy**.

The **Spectroscopy** task card is displayed empty.

Loading raw data

To evaluate spectroscopy raw data immediately following the measurement, you have to load it directly from the program control into the **Spectroscopy** task card.

In all other cases, load the raw data from the **Patient Browser** to the **Spectroscopy** task card.

When loaded, the raw data is automatically assigned to an evaluation protocol, which will be used to calculate a spectrum.
→ Page C.2–3, *Determining the evaluation protocol automatically*

In the case of CSI data, the calculation is performed only for a single voxel in the center of the CSI slab.

➪ Loading CSI raw data measured with the NUMARIS/3 predecessor software requires a special procedure. These data have to be Fourier Transformed before being loaded.

Determining the evaluation protocol automatically

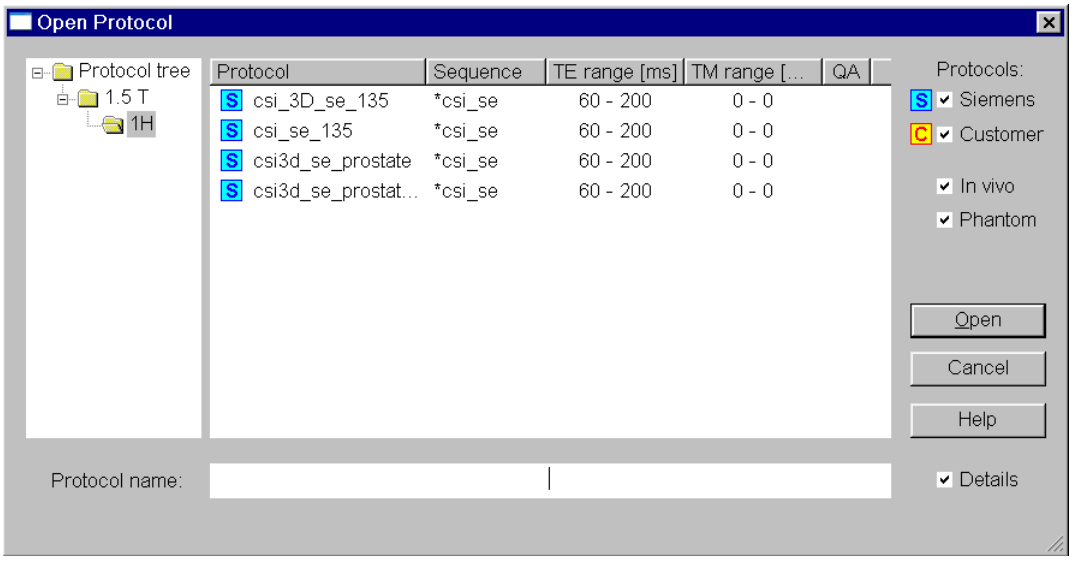
To find a suitable evaluation protocol, the following measurement parameters stored with the raw data are compared with the properties of the evaluation protocols:

Measurement parameters	Property
Magnetic field strength (rounded to 0.5 T)	Type of system
Nucleus name	Type of nucleus
Name of sequence	Sequence
Echo time	Has to be in the TE range
Mixing time	Has to be in the TM range
1. Protocol name beginning with “qa_” 2. In all other cases:	1. Purpose = Phantom 2. Purpose = In vivo

If several suitable evaluation protocols are determined, the system checks whether one of these protocols has the same name as the measurement protocol.

❏ **If so**, this protocol is used for automatic evaluation.

❏ **If not**, a list of the suitable protocols is displayed.



If a suitable protocol is not found, the program reads the *standard* protocol from the **General** folder and temporarily assigns it the name of the measurement protocol. A corresponding message is displayed in the status bar.

The following options are available if you do not want to use the standard protocol:

❏ Manually select a different protocol.
→ Page C.5–2

❏ Define a customer protocol for the raw data.
→ Page C.11–7

Loading raw data from the program control

Spectroscopy raw data are identified by a special symbol in the program control.



✧ Double-click on the raw data icon of the processed **Spectroscopy** measurement protocol.
- Or -
Select the protocol in the processed section of the queue and select **Load Series** from the context menu.

The raw data are loaded into the **Spectroscopy** task card.

➪ If closed, the **Spectroscopy** task card is opened automatically.

Loading raw data from the Patient Browser



Spectroscopy raw data are identified by this symbol in the **Patient Browser**.

✧ Select the spectroscopy raw data set for evaluation in the content area of the **Patient Browser**.

✧ Select **Applications > Spectroscopy**.

The raw data are loaded into the **Spectroscopy** task card.

➪ If closed, the **Spectroscopy** task card is opened automatically.

➪ If the **Spectroscopy** task card is already open and in foreground, the raw data set can also be loaded by *double-clicking* or using *Drag & Drop*.
→ Page C.2–7, *Loading the raw data set*

Loading additional raw data sets

You can load up to three different raw data sets into the **Spectroscopy** task card for evaluation.

➪ The storage space for raw data sets cannot exceed 128 MB. This is equivalent to a 3D CSI raw data set with 32*32*16*1024 data points.

Opening an empty patient folder



✧ Click an empty patient folder in the control area.
- Or -
Place the input focus on an empty spectral segment in the image area (only in **Multiple Dataset Mode**).



The patient folder is opened.

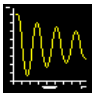
! If you open a full folder instead of an empty patient folder, the old data set is unloaded from the **Spectroscopy** task card and replaced with the new one.

Displaying the Patient Browser



✧ Select **Patient > Patient Browser**.
- Or -
Click the button in the control area of the task card.

Selecting a raw data set



✧ Select the **Spectroscopy** raw data set for evaluation in the content area of the **Patient Browser**.

Loading the raw data set

✧ Double-click the raw data set.
- Or -
Drag the raw data set into the active spectral segment (input focus) with the mouse.

The raw data are loaded into the open patient folder.

Loading other reference images

You can also load other reference images, e.g., that more clearly show specific anatomical features, in the **Spectroscopy** task card.

These new reference images have to meet the following criteria:

❏ They belong to the same series block as the spectroscopy data to be evaluated.

❏ They were acquired at the same table and patient positions.

❏ They have not been remapped for distortion correction.
→ ***syngo* MR** Operator Manual

Selecting a reference image



✧ In the content area of the **Patient Browser**, select the reference image you want to load or use as a starting point.

Loading the reference image

✧ Double-click the reference image.
- Or -
Drag the reference image to the reference image segment with the mouse.

If automatic selection mode is switched off, the reference image is loaded directly.

➪ However, if auto selection mode is active, the selected reference image only serves as the starting point to search for a suitable reference image. If necessary, a more suitable image from the same series is loaded.
→ Page C.3–4, *Activating automatic selection mode*

➪ A corresponding message is displayed if the reference image does not contain the measured VOI.

! A message window is displayed if the selected reference image does not belong to the same series block (e.g. if the patient table was moved in a non-defined fashion). You may continue working with this reference image **at your own risk** after confirming the message.

Displaying a different data set

The image area for reference image display contains only the reference images for the selected data set. You can work in this data set. If you want to work with one of the other loaded data sets, you have to switch to this data set first.

✧ Click the patient folder containing the desired data set in the control area.
- Or -
In the image area, click the segment with the spectrum you want to edit (only in **Multiple Dataset Mode**).



The patient folder is opened.

The input focus in the image area for result display moves to the respective spectral segment (only in **Multiple Dataset Mode**).

The reference images in the image area for reference image display are replaced with the reference images of the current data set.

Closing a data set

Close the current data set after the evaluation is complete if you want to evaluate additional data sets.

✧ Select the data set or a corresponding result.

✧ Select **Patient > Close Dataset**.

The data set is unloaded from the patient folder.

You can load a new data set into the empty patient folder for evaluation.
→ Page C.2–2, *Loading raw data*

CHAPTER C.3

Editing the Display of Reference Images

You can browse the stack of reference images to locate a suitable reference image for spectroscopy evaluation. Reference images in the small image segments can also be displayed in the large image segment.

You can also search for suitable reference images automatically using automatic selection mode.
→ Page C.3–4, *Activating automatic selection mode*

The functionality for windowing, zooming, panning, or fitting reference images to the segment size is similar to the **Viewing** task card. In addition, you can show or hide image text and special graphic tools.

Browsing the reference images

If the loaded reference image series contains several reference images, these reference images are stacked on top of each other. You can locate a suitable reference image by browsing the image stacks.

Scrolling from image to image

✧ Scroll from image to image using the dog-ears or icons.
→ ***syngo* MR** Operator Manual

➪ In the case of 3D CSI with active automatic selection mode, the CSI slice closest to the new reference image is selected automatically when scrolling through reference images that are parallel to the main orientation set.
→ Page C.7–4, *Activating or deactivating automatic selection mode*

Scrolling from series to series

✧ Scroll from series to series using the corresponding icons.
→ ***syngo*** **MR** Operator Manual

➪ When automatic selection mode is deactivated, the first valid image of the new series is displayed.
When automatic selection mode is activated, the first valid image of the new series is used as the starting point to search for a suitable reference image.

Displaying the reference image in the large image segment

The large image segment provides a clearer view of anatomical details.

✧ To display a small reference image in the large image segment, double-click the small image segment.

The previously large reference image is now displayed in the small segment.

Automatically selecting reference images

You can also search for suitable reference images automatically using the **Auto Selection Mode** option. Up to three reference images are used as the starting point.

The effect of automatic selection depends on the results that are displayed or to be displayed in the current spectral segment.

Spectra and result tables

Based on the prescribed images, the system searches in the series for parallel reference images that have the shortest distance to the VOI or voxel to which the spectrum or table belongs.

Spectral maps and metabolite images

For all prescribed images that are parallel to the CSI slice, a search is made in the series for parallel reference images at the shortest distance to the CSI slice.

Automatic selection mode is activated by default

Updating the results display

The results display in the current segment updates automatically when the following actions are performed:

- ❏ Activate automatic selection mode
  → Page C.3–4
- ❏ One-time search for adjacent reference images
  → Page C.3–4
- ❏ Loading a reference image from another series
- ❏ Scrolling from one series to another
- ❏ Scrolling through reference images of a series in the case of 3D-CSI
- ❏ Selecting another CSI slice in the case of 3D-CSI

Activating automatic selection mode

✧ Select **Image > Auto Selection Mode**.

➪ You deactivate automatic selection in the same manner.

➪ A checkmark next to **Auto Selection Mode** indicates that it is selected.

After automatic selection mode is activated, the reference images currently displayed are used as the starting point, and the search for reference images is performed as described above.

Searching for the nearest reference images

You can search individually for adjacent reference images as follows:

✧ Select **Image > Select Nearest**.

The displayed reference images are used as the start point to search for reference images as described above. In this case, however, automatic selection mode is not switched on.

Zooming and panning the reference image

To optimally display a reference image, you can change its size and pan within the segment.

Detailed instructions may be found in the description of the **Viewing** task card in the → ***syngo* MR** Operator Manual.

➪ In contrast to **Viewing**, the **Spectroscopy** task card does not contain buttons for the zoom functions.

Fitting the reference image to the segment size

If you resize or pan a reference image, you can fit it to the size of the segment.

✧ Place the input focus on the reference image.

✧ Select **Image > Fit to segment**.
- Or -
Select **Fit To Segment** from the pop-up menu.

Windowing the reference image

You can change the window values (brightness and contrast) of a reference image individually or assign automatic window values.

For details on windowing, refer to the
→ ***syngo* MR** Operator Manual

Assigning automatic window values

Automatic window values can be applied to the selected image only or to all reference images at once.

Windowing an individual reference image automatically

✧ Select **Image > Auto Windowing**.
- Or -
Double-click a reference image using the *center* mouse button.

Automatic windowing of all reference images

✧ Select a reference image.

✧ Select **Image > Display Parameters**.
- Or -
Select **Display Parameters** from the pop-up menu.

The **Display Parameters** dialog window opens.
→ Page C.3–7, *Defining the scope*



✧ On the **Images** subtask card under **Apply to:**, select the **All shown images** option.



✧ Click **Auto Windowing**.

Showing/hiding graphic tools and image text

You can show or hide graphic tools and image text in the reference images.

The display parameters are selected in the **Display Parameters** dialog window on the **Images** subtask card. The new settings are automatically applied by the system. The reference image is updated after each change.

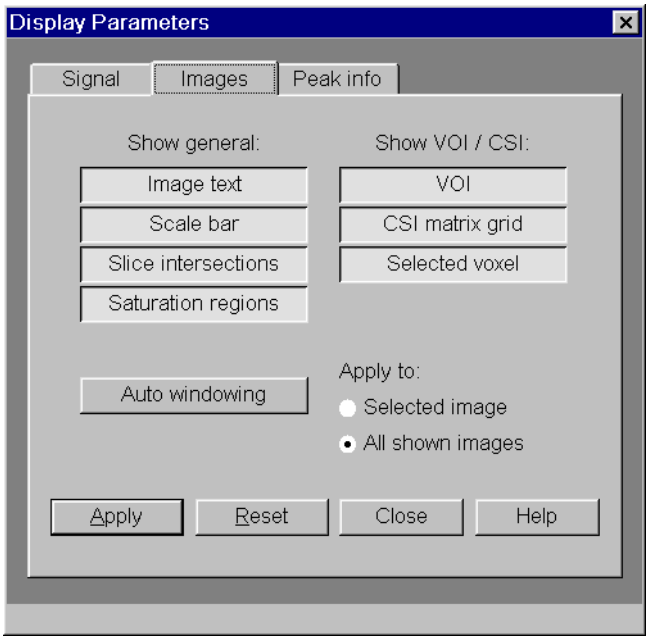
Procedure:
❏ Selecting a reference image for editing
❏ Displaying the **Display Parameters** dialog window
❏ Defining the scope
❏ Selecting graphic tools and image text

Opening the dialog window

✧ Select a reference image.

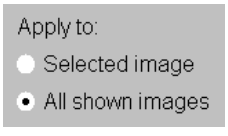
✧ Select **Image > Display Parameters**.
- Or -
Select **Display Parameters** from the pop-up menu.

The **Display Parameters** dialog window is displayed with the **Images** subtask card.



Defining the scope

You can apply the set display parameters for all displayed reference images or only the selected reference image.



✧ Under **Apply to:** select the desired option.

Selecting graphic tools and image text

Make the selections using the following buttons in the upper section of the dialog window:

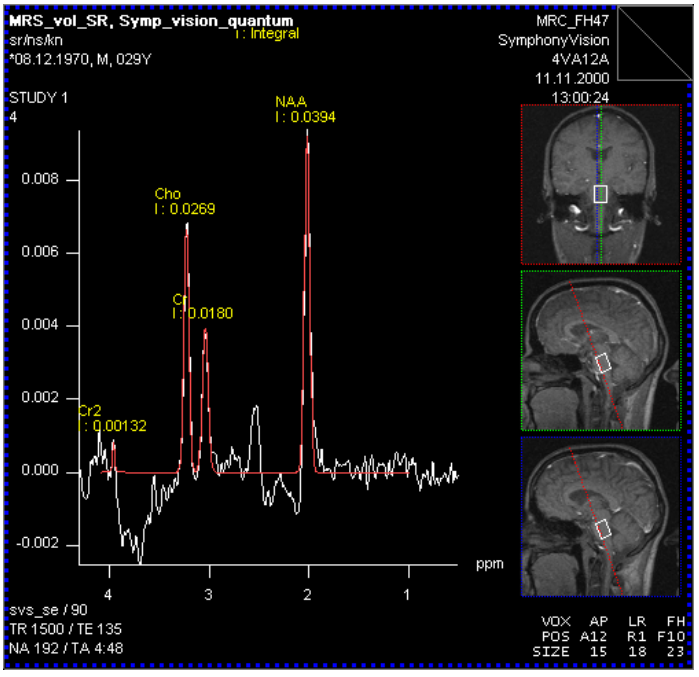
Button	Description
Image text	The image text is shown/hidden.
Scale bar	The scale bar is shown/hidden.
Slice intersections	The slice intersections are shown/hidden.
Saturation regions	The saturation regions (if available) are shown/hidden.
VOI	The VOI (if available) is shown/hidden.
CSI matrix grid	The CSI matrix grid (if available) is shown/hidden.
Selected voxel	The selected voxel of the CSI matrix (if available) is highlighted in color (blue) or hidden.

✧ Click the buttons to activate or deactivate the individual graphics tools.

CHAPTER C.4

Editing the Display of the Spectrum

Following the evaluation of the raw data using a post-processing protocol, a spectrum is displayed in the active segment.



!

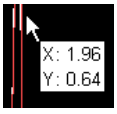
Depending on the post-processing protocol used, either the real part of the spectrum in the frequency domain (protocol with Fourier Transform) or the complex data in the time domain (protocol without Fourier Transform) are displayed by default.

Displaying coordinates

You can assess positions within the spectrum based on the scaling of the X axis (chemical shift) and y axis (peak amplitude). In addition, you can display the exact coordinates for each point within the spectrum.

✧ Click the desired position in the spectrum with the mouse.

The coordinates are displayed in the center of the status bar.



➪ The coordinates are indicated below the mouse pointer while you keep the *left* mouse button pressed.

Adjusting the signal display

Use the **Display Parameters** dialog window on the **Signal** subtask card to establish how the signal should be displayed.

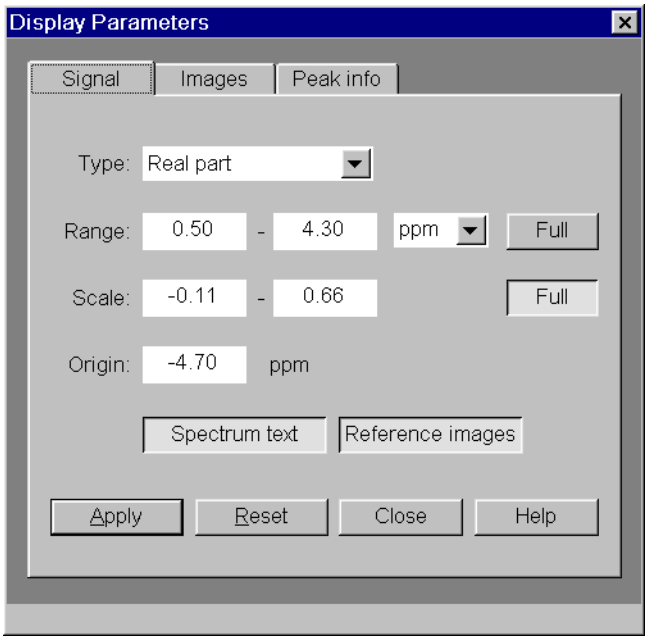
Opening the dialog window

✧ Select the spectral segment.

✧ Select **Signal > Display Parameters**.
- Or -
Click this button in the control area.



The **Display Parameters** dialog window opens with the **Signal** subtask card.



The following display parameters can be set:

- ❏ Display type
- ❏ Unit of X axis
- ❏ Display range of X axis
- ❏ Display range of Y axis
- ❏ Origin

New parameters are automatically applied by the system. After you update values in the input fields, the spectrum is updated once you press the **Enter** key or switch to a different operating element.

Selecting the display type

The following display types are available for the spectra:

Display type	Description
Complex	Complex data (default setting in the time domain)
Real part	Real part of the spectrum (absorption signal; default setting in the frequency domain)
Imaginary part	Imaginary part of the spectrum (dispersion signal)
Magnitude	Magnitude data
Phase	Phase data



✧ Select the desired display type from the **Type** selection list.

The spectral display is updated.

Defining the X axis

Select unit

For a display in the frequency domain, you can select “parts per million” [ppm] or Hertz [Hz] as the unit for the X axis (frequency shift).



✧ Select the unit for the frequency shift (**ppm** or **Hz**) in the selection list under **Range**.

Limiting the display range

The display range of the X axis (chemical shift) can be limited to the area of interest.

✧ Define the display range of the X axis using the two fields in **Range**.
- Or -
Click in the spectrum to define the starting point and drag the mouse pointer *horizontally* to the desired end point while pressing and holding the *left* mouse button.

Displaying the entire value range

How to set the display of the X-axis to include the complete value range:



✧ Click the **Full** button in the **Range** line.

Defining the Y axis

Limiting the display range

You may limit the display range of the Y axis (peak amplitude), e.g. to magnify peaks with less intensity.



✧ Define the lower and upper value of the display range of the Y axis using the two input fields in **Scale**.
- Or -
Click in the spectrum to define the starting point and drag the mouse pointer to the desired end point (*vertically*) while pressing and holding the *left* mouse button.

Displaying the entire value range

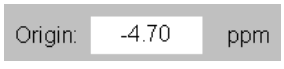
How to set the display of the Y-axis to include the complete value range:



✧ Click the **Full** button in the **Scale** line.

Setting the origin

The ppm scale is based on a reference signal defining the origin (0 ppm). You can set this origin by defining e.g. the water signal as a reference.



✧ Enter a value in the **Origin** field.

➪ For water this value is -4.7 ppm.

Showing/hiding spectrum text

The image text displayed (spectrum text) provides valuable information regarding patient, measurement, and spectrum.

✧ Select the spectral segment.

✧ Click the **Signal** subtask card in the **Display Parameters** dialog window.
→ Page C.4–2, *Opening the dialog window*



✧ Click to activate (deactivate) the **Spectrum text** button.

The spectrum text is displayed (hidden).

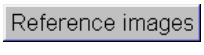
Showing/hiding miniature reference images

Miniatures of the images from the three reference image segments are displayed along the right edge of the spectral segment. Both the selected voxel and the slice lines of the reference image planes are displayed to provide anatomical orientation. The zoom factor and window values are taken from the corresponding images in the reference image segments.

How to show or hide miniature reference images:

✧ Select the spectral segment.

✧ Click the **Signal** subtask card in the **Display Parameters** dialog window.
→ Page C.4–2, *Opening the dialog window*



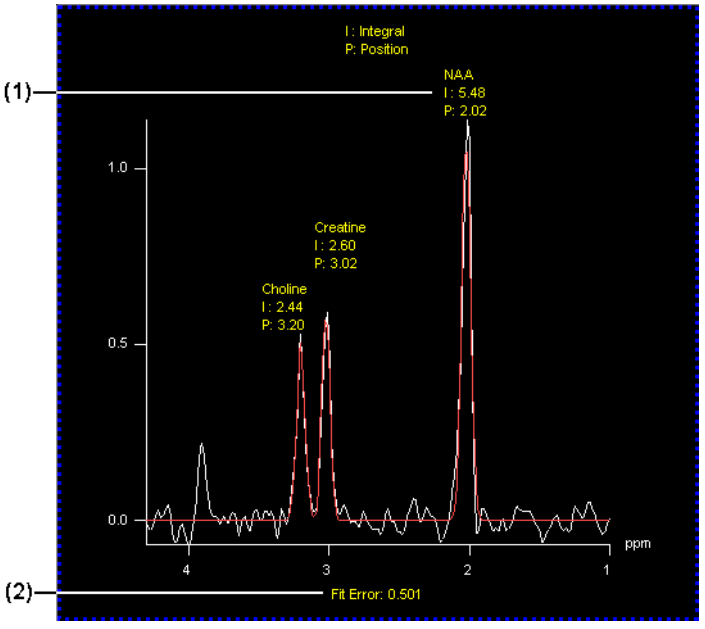
✧ Click to activate (deactivate) the **Reference images** button.

The miniature reference images are displayed (or hidden).

Showing peak information

If curve fitting was performed during evaluation, you can display information regarding the peaks of the theoretical spectrum (red curve). The so-called peak information is displayed as image text above each peak. You can hide it if you only want to display the measured spectrum including the peak information.

In addition, you can display a fit error.



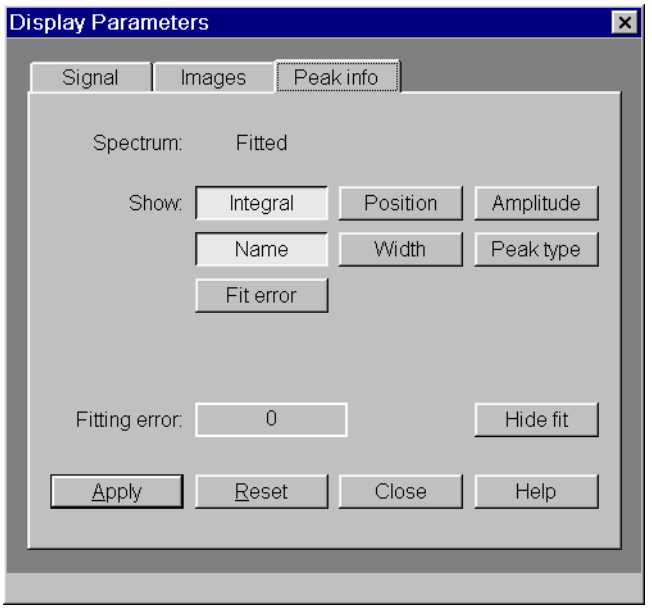
(1) Peak information
(2) Fit error

Opening the dialog window

✧ Select the spectral segment.

✧ Select **Signal > Peak Information**.
- Or -
Select **Peak Information** from the context menu.

The **Display Parameters** dialog window is opened with the **Peak Info** subtask card.



You perform the following processing steps:

❏ Selecting peak information
❏ Showing/hiding the fit error (optional)
❏ Showing/hiding the curve fit (optional)

The settings are automatically applied by the system. The display of the spectrum is updated following each change.

Selecting peak information

Up to three categories of peak information can be displayed simultaneously. Select each item using the buttons in the **Show** field.

Button	Function
Integral	Show/hide peak integrals
Position	Show/hide peak positions
Amplitude	Show/hide peak amplitude
Name	Show/hide peak name
Width	Show/hide peak full width at half maximum
Peak type	Show / hide peak types (Gaussian, J-Coupling, or Lorentzian)

➪ The amplitudes shown (A) are the amplitudes of the individual fit signals. They are not the amplitudes of the entire fit.

✧ Click the buttons to activate or deactivate the peak information desired.

! If three categories of peak information are already displayed, you have to deselect one of the categories to select another one.

Showing/hiding the fit error





The fit error is always displayed on the **Peak Info** subtask card.

How to show or hide the fit error in the spectrum:

✧ Click to activate or deactivate the **Fit error** button.

When you activate the button, the fit error is displayed below the spectrum.

Showing/hiding the curve fit

How to show or hide the red curve of the theoretical spectrum (curve fit):



✧ Click to activate or deactivate the **Hide fit** button.

Annotating the spectrum

You can add annotations to a spectrum, move the annotations within a segment, or delete it if necessary. Annotations are saved when you save the spectrum.

Adding a comment

✧ Select the spectrum you want to annotate.

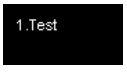
✧ Select **Signal > Annotate Spectrum**.
- Or -
Select **Annotate Spectrum** from the context menu.



✧ Click the mouse at the position of the spectrum where the annotation should appear.

A light gray input field is displayed.

✧ Enter the annotation in the field.



✧ Press the **Enter** key to complete the entry.

Moving comments

How to move a comment to a different position in the spectrum:

✧ Click the comment.



The comment is now marked.

✧ Move the annotation to the desired position in the spectrum with the mouse.

➪ When editing comments, ensure that you do not accidentally modify the display area of the spectrum.

Deleting a comment

✧ Click the comment to mark it.

✧ Press **Del.**

The comment is deleted from the spectrum.

Undoing entries

You can reset the changes made on the **Signal, Images** and **Peak Info** subtask cards.

Resetting the last change

✧ Select **Signal > Reset**.

The last change made on the **Signal** subtask card is reset.

All changes

✧ Click **Reset**.

All changes made in the current subtask card since the **Display Parameters** dialog window was selected are reset.

CHAPTER C.5

Evaluating Data Using a Different Protocol

The raw data used for automatic evaluation of a spectrum can be evaluated using different post-processing protocols. When evaluating multiple spectra of a raw data set, you can use different post-processing protocols for the individual spectra. In addition, you may copy the current post-processing protocol and apply it to the raw data of other spectral segments.

A comprehensive presentation regarding protocol management and editing may be found in chapter
→ Chapter C.11, *Managing Post-processing Protocols*

Refer to this chapter for an overview of the various editing options.

Keep Common option

The **Keep common** option means that all spectra of a raw data set are evaluated using the same post-processing protocol. It is activated by default.

If the option is activated, all changes to the post-processing protocol of the current spectrum affect all other spectra of the raw data set. However, the graphic is only updated in the current segment.

Deselect the **Keep common** option to evaluate the individual spectra of a raw data set using different post-processing protocols.

✧ Deselect **Protocols > Keep Common**.

Changes to the post-processing protocol affect only the current spectrum.

Selecting a post-processing protocol

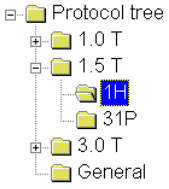
The **Open Protocol** dialog window lets you access all the post-processing protocols stored in your database.

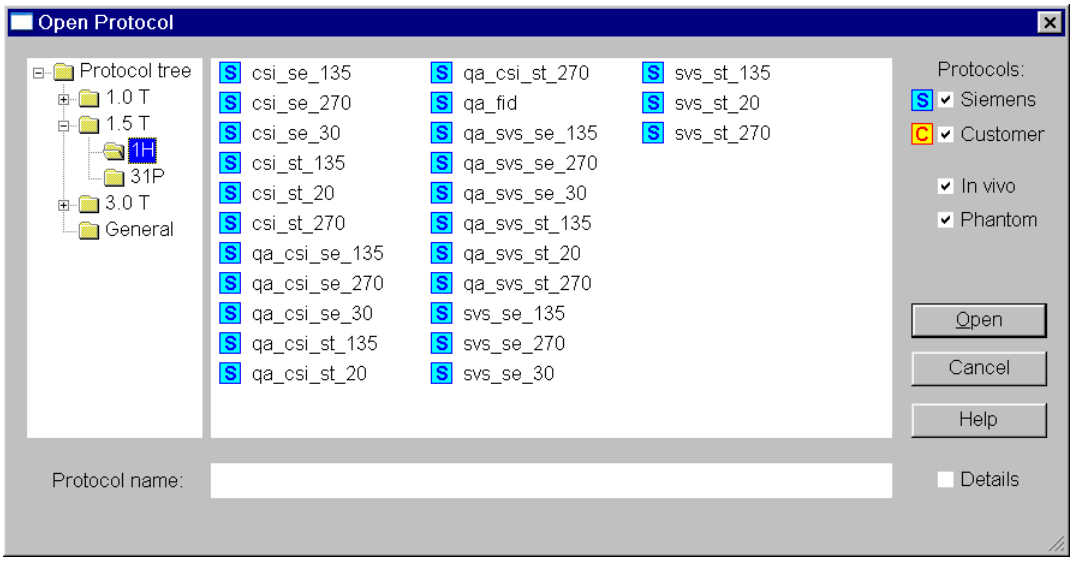
✧ Select **Protocols > Open**.

The **Open Protocol** dialog window opens.

✧ Open the protocol directory containing the desired post-processing protocol.

The content area lists the post-processing protocols available in the selected directory.







✧ Select the post-processing protocol in the list.

✧ Click **Open**.
- Or -
Double-click the desired protocol.

The opened post-processing protocol is applied to the current raw data. The spectrum in the active segment is replaced with the newly calculated spectrum.

➪ If you are unable to find a suitable post-processing protocol for your evaluation needs, you can create your own.
→ Page C.11–9, *Creating a new post-processing protocol*

Copying the post-processing protocol

You can apply the current post-processing protocol to other raw data using the **Copy** and **Paste** functions.

Within a dataset, the copy function should only be used when the **Keep Common** option is deactivated. Otherwise, the same post-processing protocol will be used for all spectra.

Additionally, the **Copy to All** function is available for CSI data sets. This allows you to apply the current post-processing protocol to the other two spectral segments of the data set in one step.

➪ When you copy a post-processing protocol, all parameter changes to the spectral display are applied as well.

Applying the protocol to a spectral segment

✧ Select **Protocols > Copy**.

✧ Select the spectral segment where you want to copy the protocol.

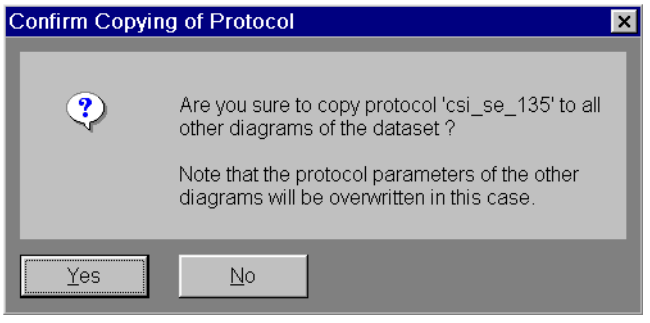
✧ Select **Protocols > Paste**.

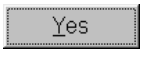
The raw data in the active spectral segment are evaluated using the copied post-processing protocol.

Applying the protocol to all spectral segments

✧ Select **Protocols > Copy to All**.

The following security question is displayed:





✧ Confirm the copy job with **Yes**.

The raw data in the other two spectral segments of the data set are evaluated using the copied post-processing protocol.

CHAPTER C.6

Displaying Evaluation Results in Table Format

After you have successfully evaluated the raw data, you can view the results in a table (in addition to the spectral display). It contains the following data:

Data	Description
Metabolite	Short name of the chemical compound
Position/ppm	Chemical shift in ppm
Integral	Peak area
Ratio	Integral ratios based on the value of a user-defined reference metabolite

In addition to the data mentioned above, you can add combinations of two or more metabolites to the result table. In this case, the result table shows the sum of the individual integrals selected.

The result table is usually displayed in the **Spectroscopy** task card. As an alternative, the result table can be saved as a text file.

Configuring the result table

Proceed as follows:

- ❏ Displaying the **Result Table Of Current Spectrum** dialog window
- ❏ Defining the reference metabolite
- ❏ Showing and selecting metabolites with hidden peak information (optional)
- ❏ Combining metabolites (optional)
- ❏ Applying the settings
- ❏ Showing/hiding miniature reference images
- ❏ Showing/hiding image text

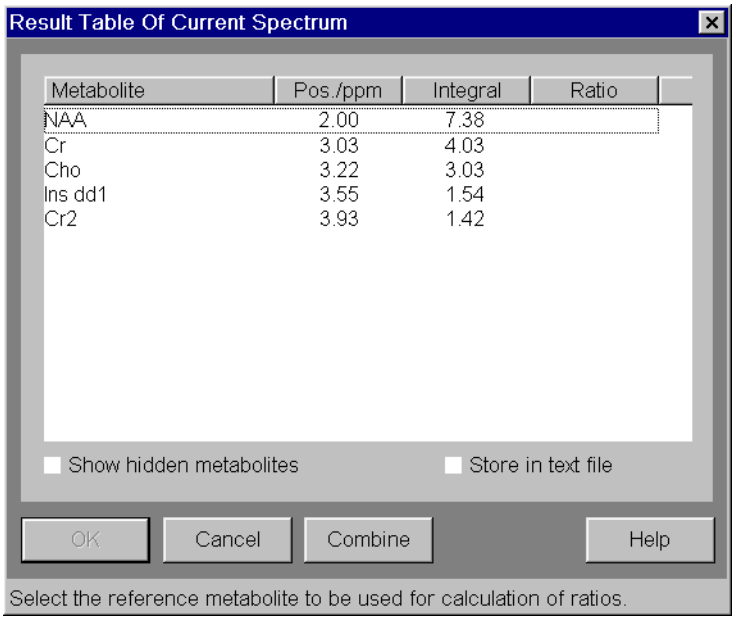
Displaying the result table

✧ Select an empty spectral segment.

✧ Select **Signal > Result Table**.
- Or -
Select **Result Table** from the pop-up menu.

The **Result Table Of Current Spectrum** dialog window opens.

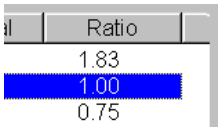
! For a CSI case opened in the **Single Dataset Mode**, the results for the table are provided by the spectrum last displayed.



Defining the reference metabolite

You start by defining one of the metabolites as the reference metabolite. Its peak area is used as a reference for calculating the integral ratios.

✧ Select the reference metabolite from the list.



The calculated integral ratios are displayed in the **Ratio** column. The default value for the reference metabolite is 1.00.

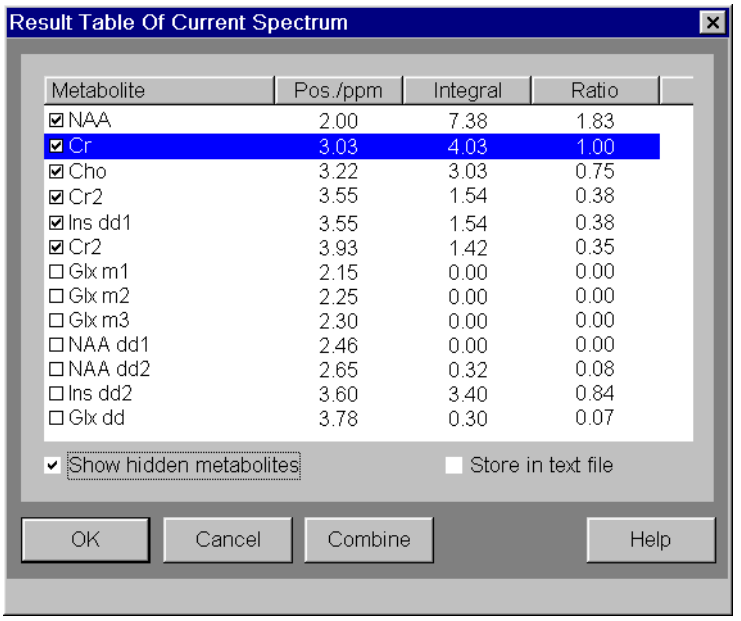
Displaying and selecting metabolites with hidden peak information

The list only displays metabolites with visible peak information. You may also display the other metabolites used for curve fitting in the list and select them for output in the result table.



✧ Activate the **Show hidden metabolites** checkbox.

The list now includes the metabolites with hidden peak information.



➪ A deactivated checkbox indicates metabolites with hidden peak information.

➪ The result table can contain a maximum of 20 metabolites.

✧ Click the checkboxes of the metabolites to be displayed in the result table.

Combining metabolites

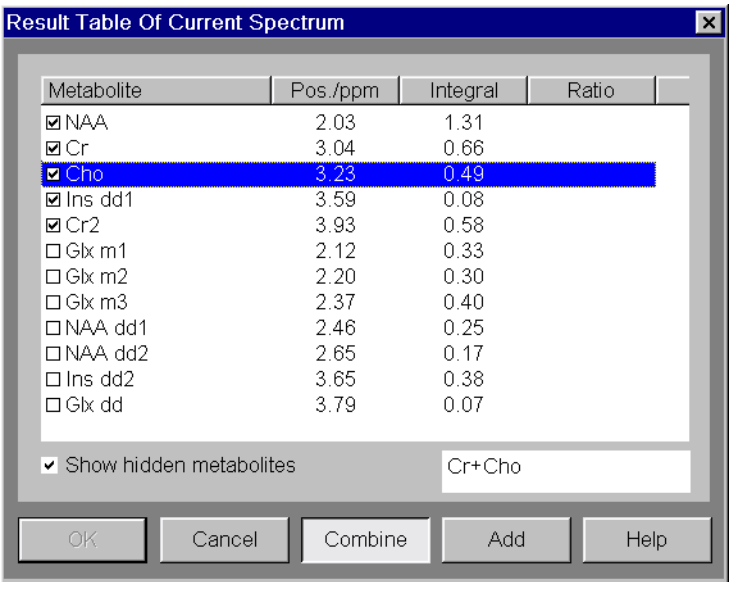
You can add sum integrals (as combinations of metabolites) to the result table.



✧ Click **Combine**.

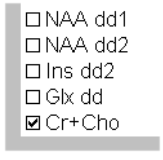
An input field for combining the metabolites is displayed at the lower right of the dialog window.

✧ Click in sequence the metabolites to be combined.
- Or -
Enter the metabolites to be combined in the input field on the lower right and link them with a plus sign.





✧ Click **Add**.



The sum integral of the selected metabolites is added to the result table.

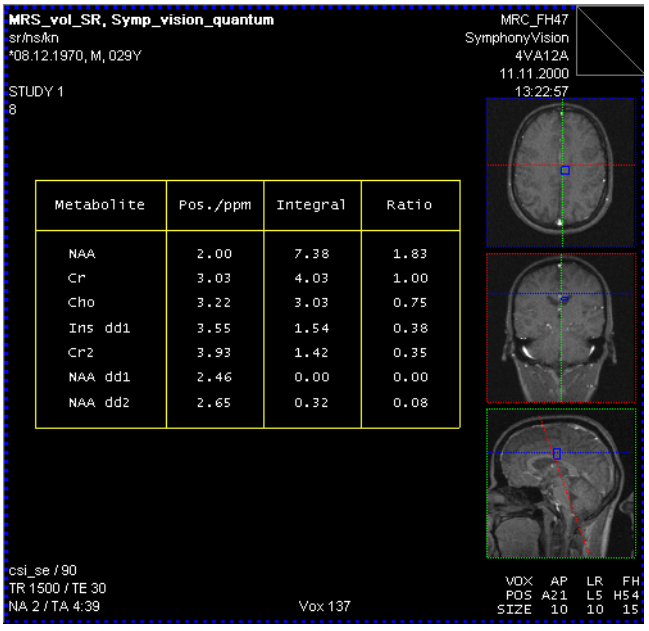
➪ You can cancel the entry by deselecting the **Combine** button.

Applying the settings

Apply the required settings once they have all been made.

✧ Click **OK**.

The result table is displayed in the active spectral segment.



Showing/hiding miniature reference images

You can also hide/show miniature reference images in the result table.

→ Page C.4–6, *Showing/hiding miniature reference images*

Showing/hiding image text

result tables are labeled with the same image text as the spectra. You are able to hide/show the image text.

→ Page C.4–6, *Showing/hiding spectrum text*

Saving the result table as a text file

✧ Open the **Result Table Of Current Spectrum** dialog box.
→ Page C.6–2

✧ Define the reference metabolite.
→ Page C.6–3

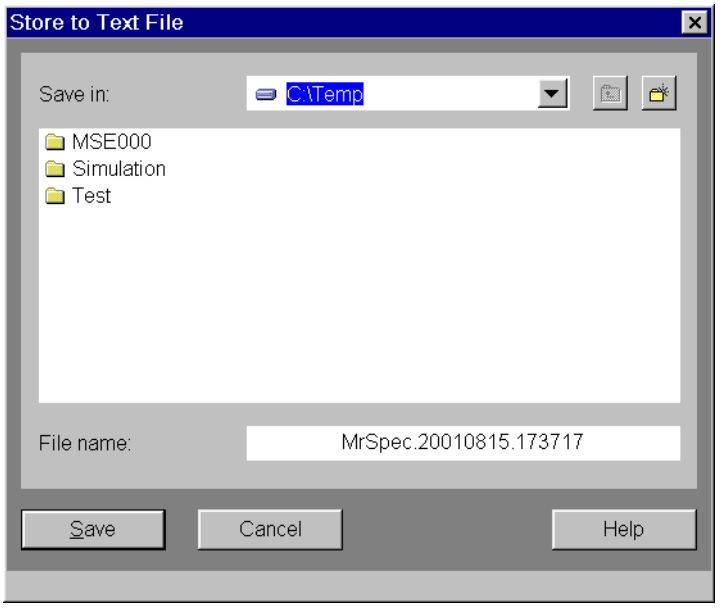
✧ If necessary, you can show the metabolites with hidden peak information and select additional metabolites for display in the result table.
→ Page C.6–4



✧ Activate the **Store to text file** checkbox.

✧ Click on **OK**.

The **Store to text file** dialog window opens.



✧ From the **Save in** list, select the target directory or create a new folder.

✧ Enter a unique name for the text file in the **File name** field or accept the name suggested by the system.

➪ The name suggested by the system consists of the current date and time.

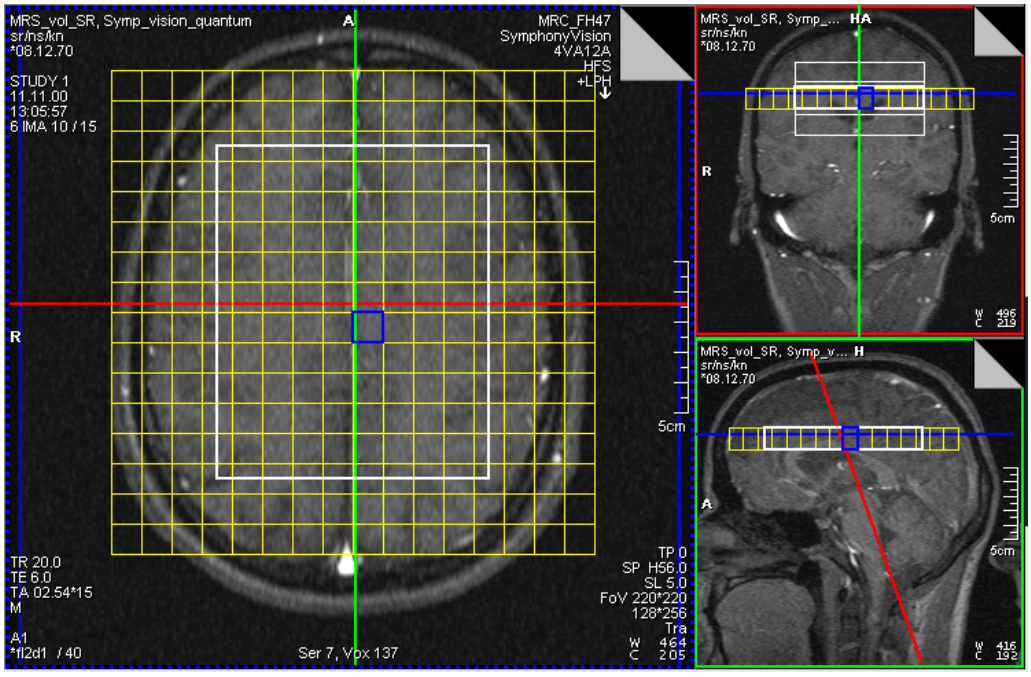


✧ Click **Save**.

The result table is saved as a text file (“.txt” file extension) in the open target directory.

CHAPTER
C.7 Evaluating CSI Data

When working with CSI data sets, a predefined voxel in the center of the CSI grid is evaluated automatically. This voxel is marked by a blue border.



➪ Please note that only *one* CSI slice is displayed and evaluated for 3D CSI raw data. This slice is selected prior to the evaluation.

Evaluations

CSI data can be evaluated as follows:

Evaluation	Description
Displaying individual spectra	A single voxel is evaluated and displayed as a spectrum.
Create a spectral map	All calculated (individual) spectra are drawn into the corresponding voxels to provide an overview.
Generating metabolite images	The voxel-dependent intensities of one metabolite or the ratios of two metabolites are displayed.
Calculating the sum spectrum	Individual spectra are added and displayed as a sum spectrum.
Performing spatial Fourier Transformation	The Fourier Transformation can be repeated after changing individual parameters.

➪ For CSI data, you can also keep the voxel-specific parameter settings for repeat evaluations.

General procedure

You can evaluate CSI data automatically and then correct individual spectra. Alternatively, you can display the spectra of individual voxels, correct them if necessary, and then evaluate the remaining spectra automatically.

Recommended settings

The following basic settings are recommended when evaluating CSI data:

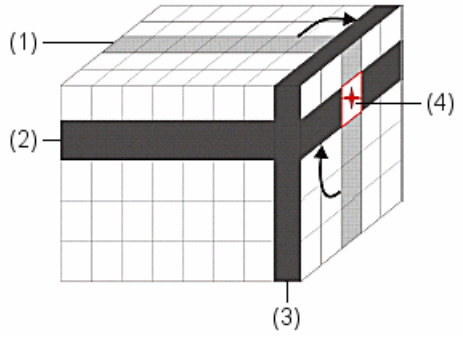
❏ **Single Dataset Mode** (→ Page C.1–10)
❏ **Keep Common** option(→ Page C.5–1)

➪ In addition, you should select the automatic options as well as the **Keep voxel specific** option for the phase correction, curve fitting, and frequency shift correction post-processing steps.
→ Page C.8–5, *Adapting post-processing steps*

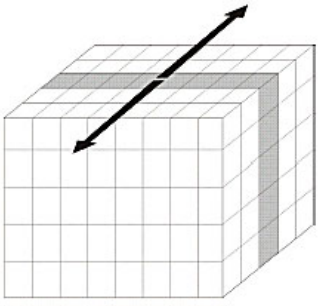
Selecting the CSI slice (for 3D CSI data only)

Any slice of the measured CSI volume can be selected for evaluation. You can change the main orientation of the CSI slice (transverse, sagittal, or coronal).

The current voxel remains selected after you change the main orientation.



(1) Current CSI slice in the original main orientation (e.g., sagittal)
(2) CSI slice after changing the main orientation (e.g., from sagittal to transverse)
(3) CSI slice after changing the main orientation (e.g., from sagittal to coronal)
(4) Selected voxel

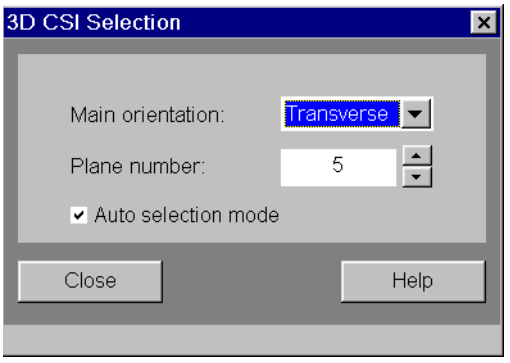


Browse the CSI volume in the current main orientation to select the CSI slice for evaluation. The column and row position of the selected voxel remains the same and is applied to the current slice.

➪ With the automatic selection mode, you can link the selection of the 3D CSI grid plane to the selection of a reference image.
→ Page C.7–4, *Activating or deactivating automatic selection mode*

Opening the dialog window

✧ Select **Postprocessing > 3D CSI Selection**.
- Or -
Select **3D CSI Selection** in the pop-up menu of the reference image segment.



Set the main orientation

✧ Select a different main orientation for the CSI slice in the **Main orientation** selection list (if applicable).

Selecting a CSI slice

✧ Browse the 3D volume for the desired CSI slice using the arrow buttons of the **Plane number** input field.
- Or -
Enter the number of the desired CSI slice in the **Plane number** field.

Activating or deactivating automatic selection mode

Automatic selection mode works as follows:
❏ When selecting a CSI slice, the most suitable reference image in terms of orientation and position is selected.
❏ When scrolling through reference images, the most suitable CSI slice is selected.

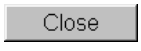


✧ Select or deselect the **Auto Selection Mode** checkbox.

Calculation results

- ❏ The CSI slice is automatically updated in the reference images after each change in the main orientation or slice number.
- ❏ In addition, the spectrum (or result table) in the active segment is recalculated if the slice number is changed.
- ❏ In automatic selection mode, the CSI slice and reference image are aligned with one another.
- ❏ If *only* the main orientation of the CSI slice changes, the selected voxel (including the spectrum/result table) in the active segment remains unchanged.
- ❏ If the active spectral segment contains a spectral map or metabolite image and the *only* change in the current CSI slice is the slice position, the spectral map or metabolite image is automatically recalculated using the new data. This allows you to “roam” the CSI volume using the spectral map or metabolite image.
- ❏ However, when you change the main orientation of the CSI slice, the **Spectral Map** or **Metabolite Image** dialog window is opened. You can define a new calculation region and recalculate the spectral map or metabolite image.

Closing the dialog window



✧ Click **Close** once you find the CSI slice desired.

Displaying individual spectra

You can calculate a spectrum for each voxel of the current CSI slice.

✧ Place the input focus on the spectral segment selected for display.

✧ Click the desired voxel in the matrix grid.

The blue border moves to the new position in the matrix grid. The position of the selected voxel is adjusted accordingly in the other two reference images. The calculated spectrum is displayed in the active spectral segment.

➪ If the active spectral segment already contains a spectrum, it is replaced with the newly calculated spectrum.

Creating a spectral map

You create a spectral map to obtain an overview of the calculated spectra of a defined region in the current CSI slice.

The individual spectra of the defined region are drawn into the corresponding voxels of the CSI slice graphic as miniatures. The CSI slice graphic is overlaid on the selected reference image.

You can display an individual spectrum from the spectral map in one of the other two spectral segments in regular size.

To continue working in the spectral map, switch back from the spectrum to the spectral map.

Proceed as follows:

- ❏ Selecting a reference image
- ❏ Determining the result segment
- ❏ Open the **Spectral Map** dialog window
- ❏ Set the calculation range (system or user defined)
- ❏ Setting calculation options
- ❏ Starting the calculations

Selecting a reference image

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

✧ Browse the reference image series and select a suitable reference image.
→ Page C.3–1, *Browsing the reference images*

! If *no* suitable reference image is selected, the operation is aborted after selecting the **Spectral Map** menu command and a message is displayed.

Determining the result segment

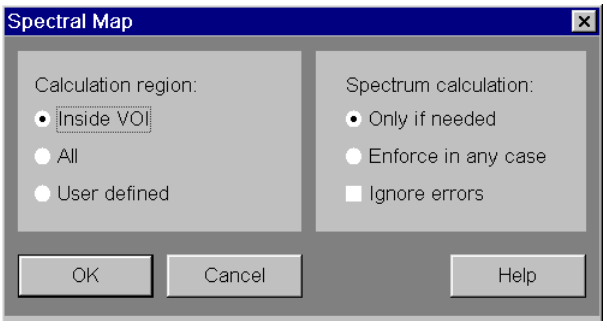
✧ Select the spectral segment that will be used for displaying the spectral map.

Opening the dialog window



✧ Select **Post-processing > Spectral Map**.
- Or -
✧ Click the button in the control area.

The **Spectral Map** dialog window is displayed.

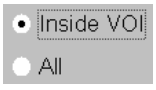


Setting the system-defined calculation region

The calculation region defines the voxels of the current CSI slice to be evaluated using the current post-processing protocol.

You can simply select a system-defined calculation region. Two options are available under **Calculation region**:

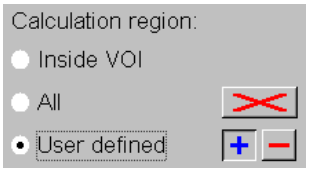
Option	Effect
Inside VOI	Only voxels within the VOI of the current CSI slice are included in the evaluation.
All	All voxels of the current CSI slice are included in the evaluation.



✧ Select the desired option.

Setting the calculation range manually

In addition to system-defined calculation regions, you can set a user-defined calculation region.



✧ Select the **User defined** option under **Calculation region**.

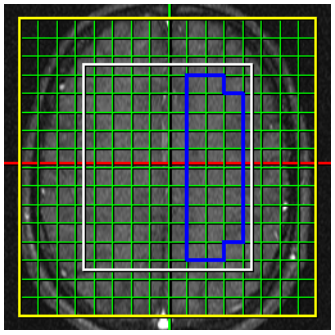
Additional buttons are displayed next to the option field.



✧ Click this button.

The Expand Calculation Region mode is activated.

✧ Position the mouse pointer on the reference image.



✧ Press and hold the **Ctrl** key while drawing a polygon curve with the mouse. Ensure that it contains all voxels that should be included in the calculation region.

The outline of the selected voxels is drawn into the reference images in blue.

✧ If necessary, draw additional polygon curves to include more voxels of the current CSI slice in the calculation region.



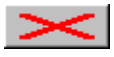
✧ Click this button.

The Reduce Calculation Region mode is activated.

✧ Position the mouse pointer on the reference image.

✧ Press and hold the **Ctrl** key while drawing a polygon curve with the mouse. Ensure that it contains all voxels that should be removed from the calculation region previously defined.

The outline of the selected voxels is drawn in red into the reference images. After releasing the mouse button, the selected area is removed from the previously defined overall calculation region.



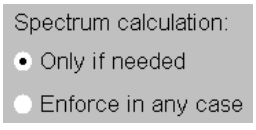
➪ If you wish to redefine the calculation region, you can delete the previously defined overall calculation region using this button.

➪ **TIP:** The defined calculation region can be applied to other evaluation functions within the current data set. For this purpose, simply select a different spectral segment (only in **Single Dataset Mode**) and perform the desired evaluation. The calculation region from the old spectral segment is applied. The calculation region in the old spectral segment is reset to the values applicable prior to opening the dialog window.

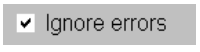
Setting calculation options

The following options for evaluating the voxels within the calculation region are available under **Spectrum calculation**.

Option	Description
Only if needed	The evaluation includes only those voxels within the calculation region for which no data or clearly inconsistent data are available. A clear inconsistency would be e.g. the use of a different protocol.
Enforce in any case	The evaluation includes all voxels within the calculation region even if consistent data are already available for some of them. If the **Keep voxel specific** option is selected, the voxel-specific settings are retained. If the option is not selected, the voxel-specific settings are lost.
Ignore errors	If this option is activated, the calculation does not terminate when errors occur. The system lists the errors in a protocol. After the calculations are completed, a message window informs you about the number of errors and refers you to the log for further information. If this option is deactivated, the calculation stops when errors occur. You can then decide whether you want to continue or stop the calculations.



✧ Select the desired option under **Spectral Calculation**.

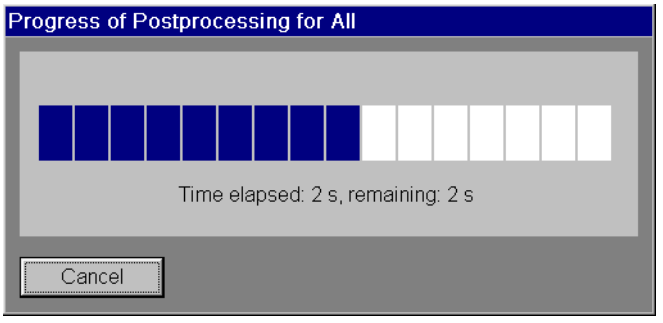


✧ Select or deselect the **Ignore error** checkbox.

Starting the calculations

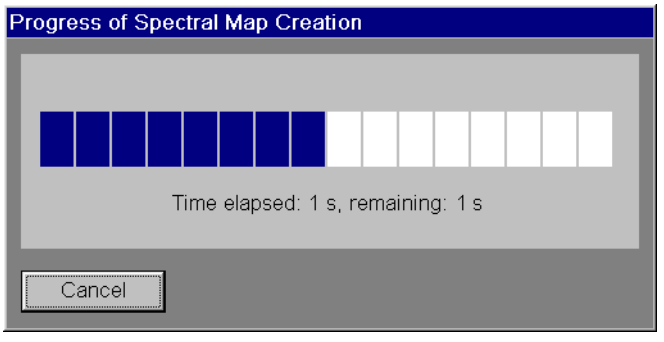
✧ Click **OK**.

The calculations start and the **Progress of Postprocessing for All** information window is displayed. You can track the progress of the calculations in this window.

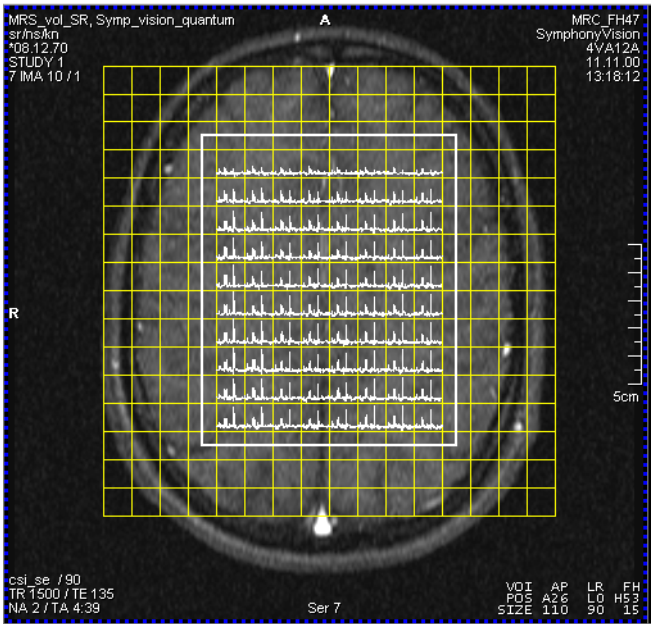


This information window closes automatically once all voxels in the calculation area have been evaluated.

The **Progress of Spectral Map Creation** information window opens. You can track the progress of spectral map creation in this window.



Once the process is complete, the information window automatically closes and the spectral map is displayed in the active spectral segment.



! While the evaluation of all voxels of the calculation region and the creation of the spectral map are in progress, you cannot perform other actions in the **Spectroscopy** task card.

Enlarging the spectrum of a voxel

✧ Place the input focus on the spectral segment selected for display.

✧ Click the voxel with the spectrum to be enlarged in the spectral map.

The spectrum is enlarged to segment size in the active spectral segment. The respective voxel in the spectral map is highlighted in color.

! A single spectrum from the spectral map can only be displayed in one of the other spectral segments in **Single Dataset Mode**.

Switching from spectrum to spectral map

✧ Click the spectral map in an area *outside* the matrix grid.
- Or -
Use the arrow keys on your keyboard to navigate to the spectral segment with the spectral map.
- Or -
Click the center mouse button on the spectral map.

Generating metabolite images

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

In addition, you can visualize the sum intensities of two or more metabolites or the sum intensity ratios.

The intensities or intensity ratios within the defined region are translated into gray or color shades and drawn into the corresponding voxels of the CSI slice graphic. Alternatively (or additionally), the intensities or intensity ratios can be displayed in the voxels as numeric values. The CSI slice graphic is overlaid on the selected reference image by default. The overlay transparency can be set.
→ Page C.7–24, *Setting the transparency*

Similar to spectral maps, you can display the spectrum of a voxel within the defined region in one of the other two spectral segments when working with metabolite images.

To continue working in the metabolite image, return from the spectrum to the metabolite image.

Proceed as follows:

- ❏ Selecting a reference image
- ❏ Determining the result segment
- ❏ Open the **Metabolite image** dialog window
- ❏ Set the calculation range (system or user defined)
- ❏ Setting calculation options
- ❏ Selecting a metabolite
- ❏ Displaying intensity ratios of two metabolites (optional)
- ❏ Deactivating reference image overlay (optional)
- ❏ Setting the intensity range
- ❏ Selecting grayscale or color scale
- ❏ Interpolating gray or color values
- ❏ Showing intensities or intensity ratios (optional)
- ❏ Starting the calculations

Selecting a reference image

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

✧ Browse the reference image series and select a suitable reference image.
→ Page C.3–1, *Browsing the reference images*

!

If no suitable reference image is selected, the operation is aborted after selecting the **Metabolite Image** menu command and a message is displayed.

Determining the result segment

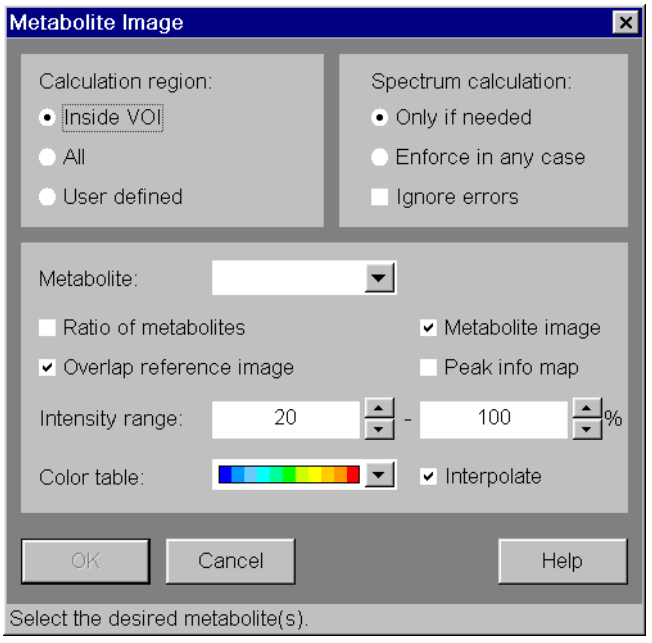
✧ Select the spectral segment that will be used for displaying the metabolite image.

Displaying the dialog window



✧ Select **Postprocessing > Metabolite Image**.
- Or -
Click the button in the control area.

The **Metabolite Image** dialog window is displayed.



Setting the calculation range

Use the calculation region to define the voxels of the current CSI slice to be evaluated with the current post-processing protocol and for which you want to calculate the pixel values for the metabolite image.

You can set either a system-defined or a user-defined calculation region.

✧ Select a system-defined calculation region.
→ Page C.7–8

Or

✧ Set a user-defined calculation region.
→ Page C.7–8

Setting calculation options

Special options for evaluating the voxels within the calculation region are available under **Spectrum calculation**.

✧ Select calculation options as required.
→ Page C.7–10

Selecting a metabolite

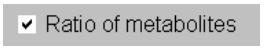


✧ Select the metabolite from the **Metabolite** selection list for which you want to display the voxel-dependent intensities in the metabolite image.

✧ To display sum intensities, enter the desired metabolites manually and connect them with a plus sign.

Intensity ratios of two metabolites

Instead of the intensities of a single metabolite, you can also display the voxel-dependent intensity ratios of two metabolites or the sum intensity ratio in the metabolite image.



✧ Select the **Ratio of metabolites** checkbox.

Two selection lists are displayed in the **Metabolite** line.



✧ Select the two metabolites from the selection lists.

✧ To display the sum intensity ratio, enter the desired metabolites manually and connect them with a plus sign.

! When selecting the two metabolites, note the order of the selection lists: The slash between the two lists corresponds to the slash in the formula for calculating the intensity ratios.

Deactivating reference image overlay

The **Overlap reference image** option is selected by default. This means that the CSI slice graphic in the metabolite image is overlaid on the selected reference image. If you want to generate a metabolite image with a black background, switch off the option:



✧ Deselect the **Overlap reference image** checkbox.

Setting the intensity range

Under **Intensity range**, define the upper and lower limit for the display of the metabolite pixels. The values are listed as a percentage of the maximum metabolite intensity.

For voxels with metabolite intensities beyond this range, the pixels of the reference image are displayed instead of the metabolite pixels.



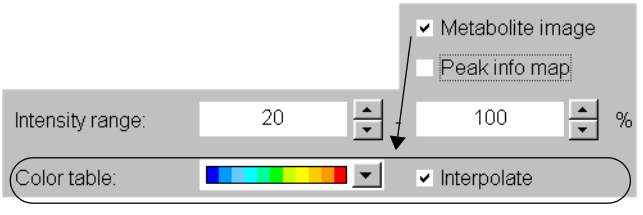
✧ Enter the start and end values of the intensity range in the corresponding fields.

Selecting grayscale or color scale

You can display the voxel-dependent intensities or intensity ratios in a metabolite image as gray/color shades.

✧ Deselect the **Metabolite image** checkbox.

The **Color table** selection list and the **Interpolate** option are displayed in the dialog window:



✧ Select the grayscale or one of the linear color scales from the **Color table** selection list.

Interpolating gray or color shades

The **Interpolate** option is selected by default. The gray or color shades between the individual voxels are calculated using interpolation. As a result, continuous color gradations are generated in the metabolite image. The metabolite image also can be displayed without interpolation.



✧ Select or deselect the **Interpolate** checkbox.

Displaying the intensity values

The metabolite intensities or intensity ratios can be displayed in the metabolite image as numerical values. This results in a **Peak info map**.



✧ Click the **Peak info map** checkbox.

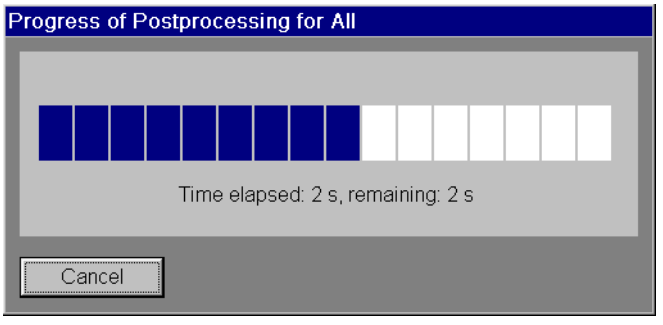
➪ The **Metabolite image** and **Peak info map** options may both be selected at the same time. In this case, the numerical values of the metabolite intensities or intensity ratios are displayed in the image on top of the gray/color shades. If the **Peak info map** option is activated and the **Metabolite image** option is deactivated, only the numerical values are shown on the reference image.

Starting the calculations

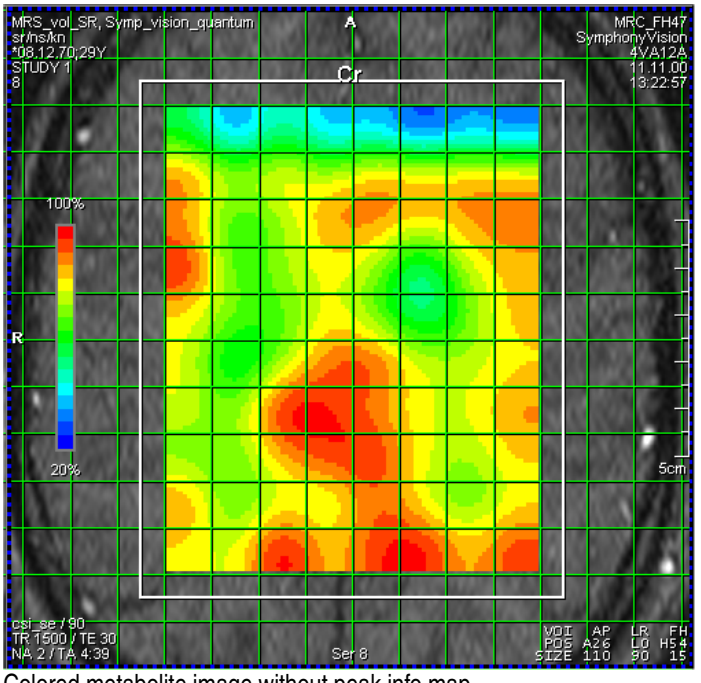
After setting the display options for the metabolite image, start the calculations.

✧ Click **OK**.

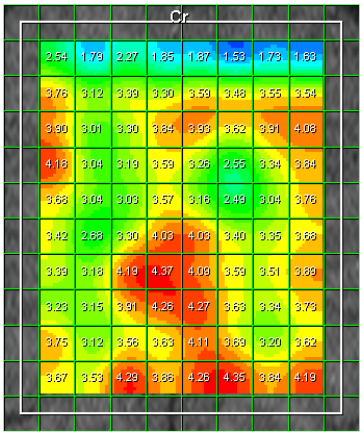
The **Progress of Postprocessing for All** information window is displayed.



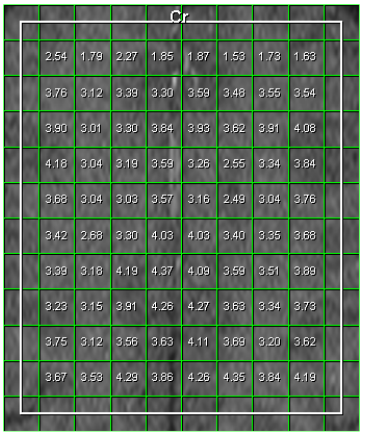
After the calculations are completed, the information window is automatically closed and the metabolite image is displayed in the active spectral segment.



Colored metabolite image without peak info map



Colored metabolite image with peak info map (section)



Reference image with peak info map (section)

! While the evaluation of all voxels of the calculation region is in progress, you cannot perform other actions in the **Spectroscopy** task card.

Enlarging the spectrum of a voxel

✧ Select the spectral segment that will be used for the display.

✧ Click the voxel with the selected spectrum in the metabolite image.

The spectrum is enlarged to segment size in the active spectral segment. The respective voxel in the metabolite image is highlighted in color.

! Displaying an individual spectrum of the metabolite image in one of the other spectral segments is only possible in **Single Dataset Mode**.

Switching from spectrum to metabolite image

✧ Click the metabolite image in an area *outside* the matrix grid.
- Or -
Use the arrow keys on your keyboard to navigate to the spectral segment with the metabolite image.
- Or -
Click the center mouse button on the spectral map.

Spectral map/metabolite image

Editing the display

Just like reference images, spectral maps and metabolite images can be zoomed, panned, or fitted to the segment size.
→ Page C.3–4, *Zooming and panning the reference image*
→ Page C.3–5, *Fitting the reference image to the segment size*

You can window the background reference image of a spectral map or metabolite image. This will normally not change the overlaid CSI slice graphic. Grayscale metabolite images without reference image background are treated differently. The grayscales within the voxels of the CSI slice graphic for these metabolite images change when applying windowing. The background remains black.
→ Page C.3–5, *Windowing the reference image*

Certain display options (**Auto windowing** and **Fit to segment**) are also available on the **CSI** subtask card in the **Display Parameters** dialog window. You have to use the **CSI** subtask card to set graphic tools and image text or the transparency for metabolite images with reference image background.

The new settings on the **CSI** subtask card are automatically applied by the system. After you update values in the input fields, the spectrum is updated once you press the **Enter** key or switch to a different operating element.

Proceed as follows:

- ❏ Open the **CSI** subtask card
- ❏ Assigning automatic window values (optional)
- ❏ Fitting the image size to the segment size (optional)
- ❏ Showing/hiding graphic tools and image text
- ❏ Setting transparency (only for metabolite images with a reference image background)

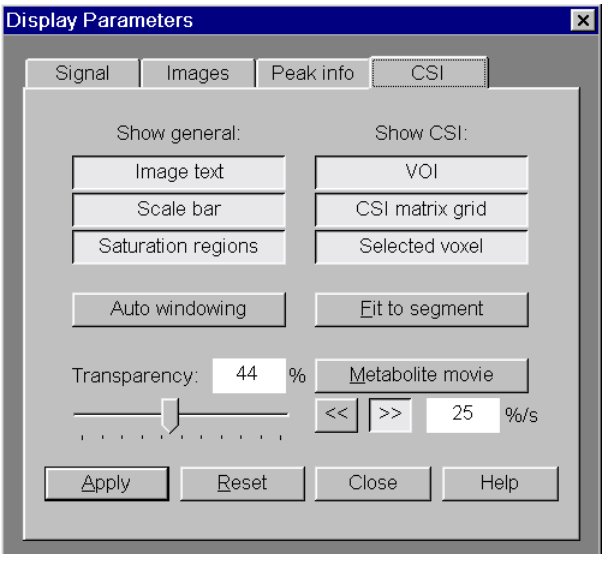
! You can reset the changes made on the **CSI** subtask card. Click the **Reset** button. This restores the settings applicable prior to opening the **Display Parameters** dialog window.

Displaying the subtask card

✧ Place the input focus on the spectral map/metabolite image you want to edit.

✧ Select **Signal > CSI Parameters**.
- Or -
Select **CSI Parameters** from the context menu.

The **CSI** subtask card opens the **Display Parameters** dialog window.



Automatic windowing



✧ Click **Auto Windowing**.
- Or -
Double-click the spectral map/metabolite image using the *center* mouse button.

Fit image to segment

You can fit the size of the selected spectral map or metabolite image to the size of the segment.

✧ Select **Signal > Fit to segment**.
- Or -
Click **Fit to segment**.



Showing/hiding graphic tools and image text

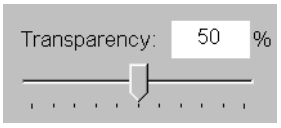
You can show or hide various graphic tools and image text in the selected spectral map/metabolite image.

Button	Description
Image text	The image text is shown/hidden.
Scale bar	The scale bar is shown/hidden.
Saturation regions	The saturation regions (if available) are shown/hidden.
VOI	The VOI is shown/hidden.
CSI matrix grid	The CSI matrix grid is shown/hidden.
Selected voxel	The selected voxel is highlighted in color (blue) or hidden.

✧ Click the buttons to activate or deactivate the graphics tools:

Setting the transparency

You can set the transparency of the overlaid CSI slice graphic for metabolite images with reference image background. 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 can be seen.



✧ Enter the value in the **Transparency** input field.
- Or -
Move the slider to the left to decrease transparency, or to the right to increase transparency.

The display is updated immediately.

Displaying a metabolite movie

When you have overlaid metabolite images in the spectral segment, you can display a movie; in this case, the transparency of the metabolite image can be changed step by step. The transparency can be raised to a maximum 100% and lowered to a minimum 0%.

Setting parameters for metabolite film

✧ Open the **Display Parameter** dialog window with the **CSI** subtask card.
→ Page C.7–22, *Displaying the subtask card*



✧ Click the button for the initial direction of the metabolite image.



✧ In the input field enter the percent per second the transparency in the film should change.

Starting the metabolite movie

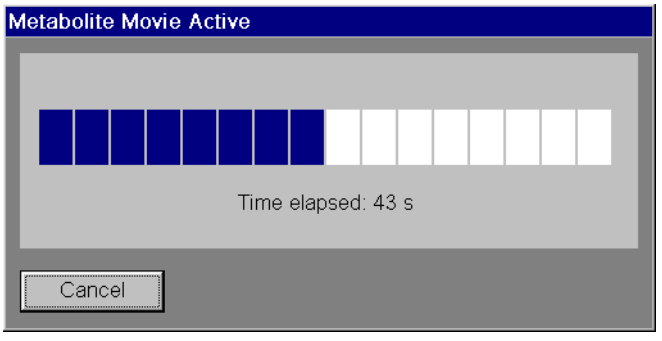


✧ Click **Metabolite Movie** in the **CSI** subtask card of the **Display Parameters** dialog window.

Or, if you have not opened the dialog window:

✧ Select **Post-processing > Start Metabolite Movie** in the task card menu.

The **Metabolite Movie Active** dialog window is displayed; it shows the change in movie transparency:



✧ Click **Close** to cancel the metabolite movie.

Calculating the sum spectrum

You can define a region of the current CSI slice. The individual spectra of all voxels contained are calculated and added up. This results in a sum spectrum which is displayed similar to an individual spectrum.

You edit a sum spectrum in the same manner as a single spectrum.
→ Chapter C.4, *Editing the Display of the Spectrum*

Proceed as follows:

- ❏ Selecting a reference image
- ❏ Determining the result segment
- ❏ Displaying the **Add Spectra** dialog window
- ❏ Setting the calculation range
- ❏ Setting calculation options
- ❏ Starting the calculations

Selecting a reference image

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

✧ Browse the reference image series and select a suitable reference image.
→ Page C.3–1, *Browsing the reference images*



If *no* suitable reference image is selected, the operation is aborted after selecting the **Add Spectra** menu command and a message is displayed.

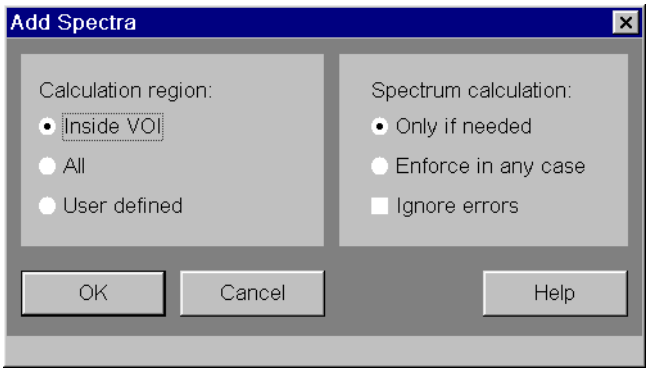
Determining the result segment

✧ Place the input focus on the spectral segment selected for displaying the sum spectrum.

Opening the dialog window

✧ Select **Postprocessing > Add Spectra**.

The **Add Spectra** dialog window is displayed.



Setting the calculation range

The calculation region defines the voxels of the current CSI slice evaluated for the calculation of the sum spectrum using the current post-processing protocol.

✧ Set a user-defined calculation region.
→ Page C.7–8

Setting calculation options

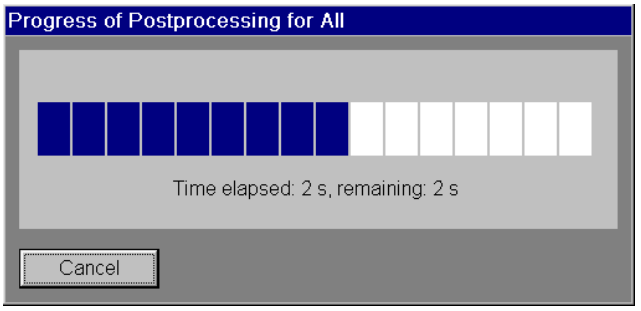
Special options for the evaluation are available under **Spectrum calculation**.

✧ Select calculation options as required.
→ Page C.7–10

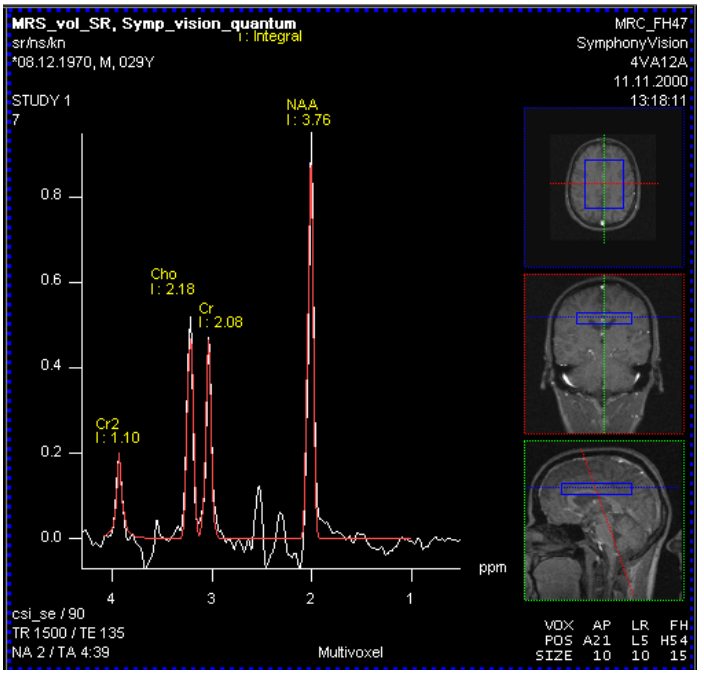
Starting the calculations

✧ Click **OK**.

The calculations start and the **Progress of Postprocessing for All** information window is displayed.



After the calculations are completed, the information window is automatically closed and the sum spectrum is displayed in the active spectral segment.



! While the evaluation of all voxels of the calculation region is in progress, you cannot perform other actions in the **Spectroscopy** task card.

Modifying Fourier Transformation

When post-processing CSI raw data, you can modify specific parameters for spatial Fourier Transformation (CSI-FT):

❏ You can change the interpolation resolution to achieve a higher spatial resolution.

❏ You can change the width of the Hamming filter to achieve optimal signal smoothing.

❏ You can shift the CSI grid to better match it to the patient's anatomy.

The original raw data in the k space are restored using CSI-FT inversion. Next, the modified parameter settings are applied to the raw data. The procedure is completed by performing a spatial CSI-FT.

To prevent confusion with the evaluation results of the old data set, the newly calculated data set is automatically saved as a new series and displayed in the **Spectroscopy** task card as the current data set. The old data set including evaluation results is automatically unloaded.

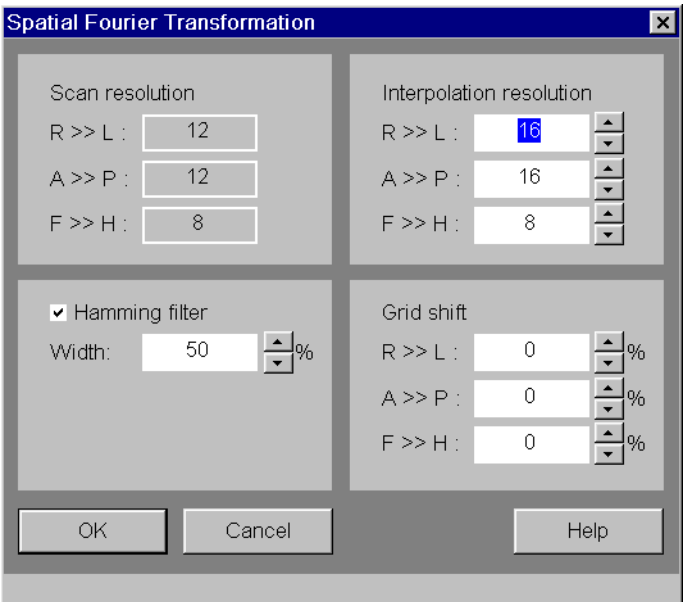
Proceed as follows:

❏ Open the **Spatial Fourier Transformation** dialog window
❏ Changing the interpolation resolution
❏ Activating/deactivating the Hamming filter
❏ Changing the width of the Hamming filter
❏ Shifting the CSI grid
❏ Starting the calculations

Opening the dialog window

✧ Select **Postprocessing > Modify CSI-FT**.

The **Spatial Fourier Transformation** dialog window opens.

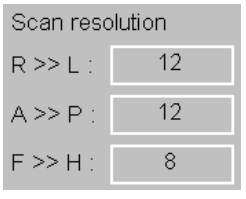


The **Scan resolution** fields indicate the scan resolution of the current data set:

❏ For 2D CSI data sets, the number of phase-encoding steps in the two spatial directions of the CSI slice is displayed.

❏ For 3D CSI data sets, the number of phase-encoding steps in the three spatial directions of the CSI slab is displayed.

Example:



Measurement resolution of a CSI slab with transverse basic orientation

Changing the interpolation resolution

The fields under **Interpolation resolution** are used to define the number of reconstructed time signals in the two (three) spatial directions of a CSI slice (CSI slab). The following rules apply:

- ❏ Interpolation resolution can be set to 8, 16, or 32.
- ❏ The number of reconstructed time signals must be greater than or equal to the number of phase-encoding steps (scan resolution).
- ❏ If the number of reconstructed time signals is greater than the number of phase-encoding steps, the displayed spectra are interpolated from the measured spectra.
- ❏ The maximum size of a reconstructed data set is 128 MB.

Example: Changing the interpolation resolution of a CSI slab with transverse basic orientation



✧ Enter the interpolation resolution in the R-L direction (from right to left) in the **R >> L** field.



✧ Enter the interpolation resolution in the A-P direction (from anterior to posterior) in the **A >> P** field.



✧ Enter the interpolation resolution in the F-H direction (from feet to head) in the **F >> H** field.

Activating/deactivating the Hamming filter

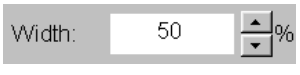
Use of the Hamming filter is recommended for CSI measurements because it results in signal smoothing. However, the Hamming filter may also be deactivated.



✧ Select or deselect the **Hamming filter** checkbox.

Changing the width of the Hamming filter

Activating the Hamming filter displays the **Width** field. The current filter width is displayed as a percentage with regard to the raw data matrix. You can change this value.



✧ Enter the new filter width in the **width** field.

Shifting the CSI grid

The **Grid shift** fields allow you to set a CSI grid shift for each main orientation. The shift is indicated as a percentage of the voxel expansion (based on the measurement resolution, not the interpolation resolution). The shift of the CSI grid in each direction cannot exceed one voxel size.

Example: CSI slice or CSI slab with transverse basic orientation

Expansion	Direction
R >> L	Shift of the CSI grid in R-L direction, in percent
A >> P	Shift of the CSI grid in A-P direction, in percent
F >> H	Shift of the CSI grid in F-H direction, in percent (for CSI-3D only)

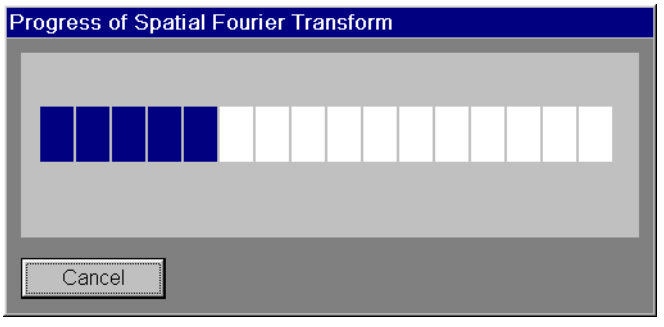
➪ By pressing the **Ctrl** key, you can drag the CSI grid into the reference image with the mouse.

In addition, the original CSI grid changes color in shift mode.

Starting the calculations

✧ Click **OK**.

The calculations start and the **Progress of Spatial Fourier Transform** information window is displayed.



The information window is automatically closed following the CSI-FT. The newly calculated data set is automatically saved as a new series and displayed in the **Spectroscopy** task card as in the current data set. The old data set including evaluation results is automatically unloaded.

! While the calculations are in progress, you *cannot* perform other actions in the **Spectroscopy** task card.

CHAPTER C.8

Evaluating Data Interactively

In addition to automatic evaluation using a standard post-processing protocol, you can evaluate spectroscopy raw data interactively:

- ❏ You can change the number and sequence of post-processing steps of the current post-processing protocol.
- ❏ You can modify the individual parameters for each post-processing step and individually apply them to the raw data. This allows you to monitor how the individual post-processing steps affect the spectrum.

⇨ If you change a post-processing protocol during interactive evaluation, you can save it as a new customer protocol.
→ Page C.11–8, *Saving the post-processing protocol*

Arranging post-processing steps

In most cases, you will use the existing post-processing steps of the current protocol and only adjust the parameters of the individual post-processing steps when performing interactive evaluation. However, you may also change the number and order of post-processing steps by adding/deleting or rearranging them.

Proceed as follows:

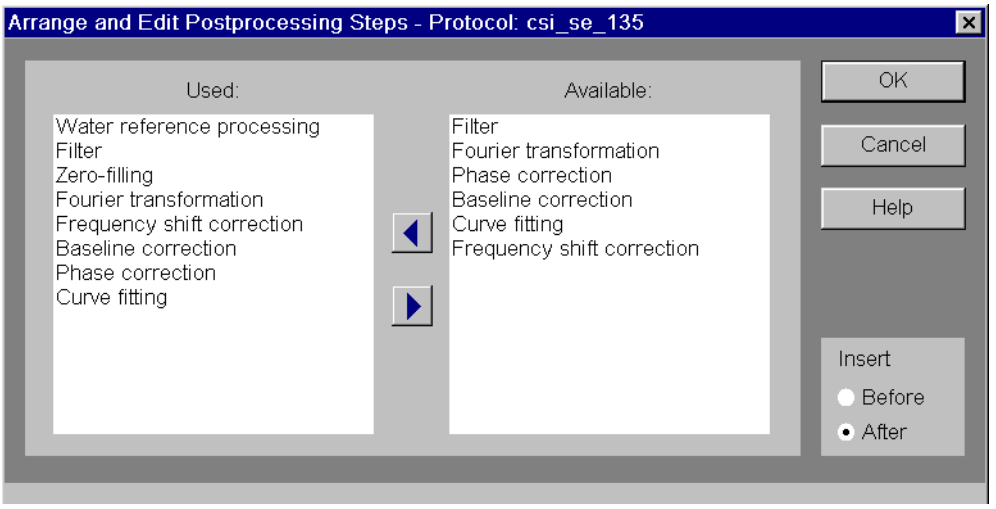
- ❏ Open the **Arrange and Edit Post-processing Steps** dialog window
- ❏ Adding post-processing steps (optional)
- ❏ Removing post-processing steps (optional)
- ❏ Changing the sequence of post-processing steps (optional)
- ❏ Applying the changes

Opening the dialog window



✧ Select **Protocols > Edit** or **Postprocessing > Arrange Steps**.
- Or -
Click this button.

The **Arrange and Edit Postprocessing Steps** dialog window opens.



The respective content in the **Available** list depends on the post-processing step currently selected in the **Used** list because certain features can only be used in the time domain (*pre*-Fourier Transform) or in the frequency domain (*post*-Fourier Transform).

Adding post-processing steps

Post-processing steps can be copied from the **Available** list to specific positions in the **Used** list.

✧ Drag the post-processing step with the mouse from the **Available** list to the position desired in the **Used** list.

Or

✧ Select the post-processing step in the **Used** list before or after which you want to add the new post-processing step.

✧ Under **Insert**, select the option **before** or **after**.

✧ Select the new post-processing step from the **Available** list.



✧ Click this button.

The new post-processing step is transferred to the selected position in the **Used** list.

Removing post-processing steps

✧ Use the mouse to drag the post-processing step out of the **Used** list until the mouse pointer takes the shape of a trash can. Then release the mouse button.

Or

✧ Select the post-processing step in the **Used** list.



✧ Click this button.

The post-processing step is removed from the **Used** list.

➪ The Fourier Transformation can be deleted only when at the end of the list.

Modifying the sequence

How to change the position of a post-processing step in the list.

✧ Drag the post-processing step to the desired position with the mouse.

➪ The sequence of post-processing steps is subject to certain restrictions. Entries may be moved within their domain only.

Applying the changes

✧ Click **OK**.

The **Arrange and Edit Postprocessing Steps** dialog window is closed.

➪ You can accept the changes and simultaneously start the adjustment of post-processing steps by double-clicking an entry in the **Used** list. The **Interactive Postprocessing** dialog window opens automatically. The number and sequence of post-processing steps in the list is updated.

Adapting post-processing steps

During interactive evaluation, you adjust the parameter settings of the existing post-processing steps (functions).

The following post-processing steps can be included in a protocol:

- ❏ Eddy current compensation
- ❏ FID shifting
- ❏ Water reference processing
- ❏ Filter
- ❏ Zero-filling
- ❏ Fourier Transformation
- ❏ Baseline correction
- ❏ Frequency shift correction
- ❏ Phase correction
- ❏ Normalization to reference
- ❏ Curve fitting

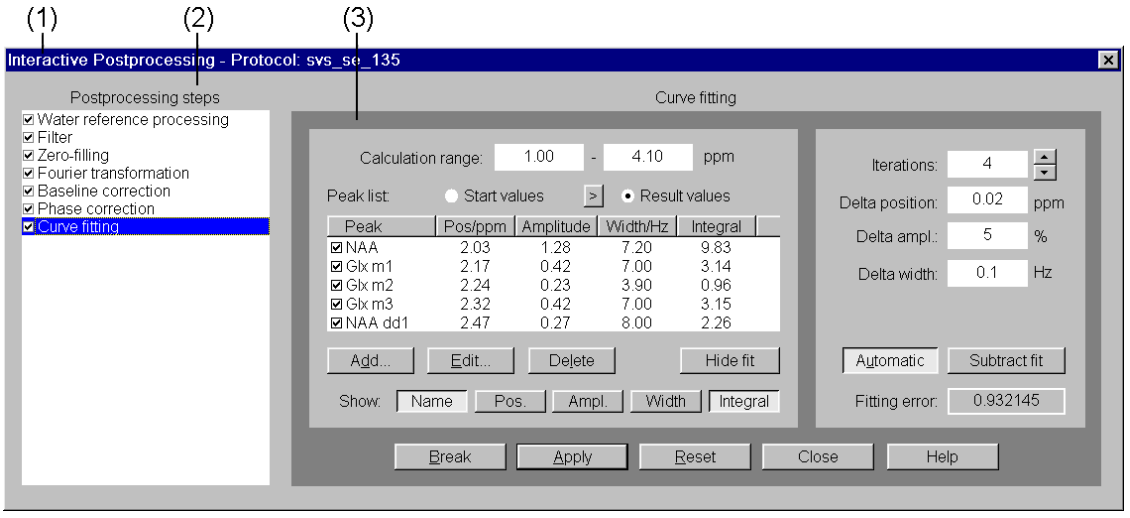
Opening the dialog window

You edit the post-processing steps in the **Interactive postprocessing** dialog window.

✧ Select **Postprocessing > Interactive**.
- Or -
Click the button in the control area.



The **Interactive Postprocessing** dialog window opens.



(1) Title bar indicating the protocol name
(2) List of post-processing steps
(3) Parameter area

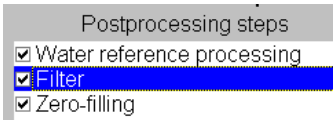
The post-processing steps of the current protocol are shown in the list of post-processing steps. When you open the Interactive Post-processing dialog window for the first time, the steps displayed belong to the post-processing protocol allocated to the measurement protocol of the raw data.

Adjusting a post-processing step (general)

The procedure for adjusting post-processing steps always follows the same process: You select the post-processing step and adjust the parameters. The new settings are automatically applied and the spectrum is updated. For each post-processing step, you can check if your changes improve the spectral display. If not, you can undo the changes.

Deactivate the post-processing steps, which should not be performed, in the list.

Selecting a post-processing step



✧ Select the post-processing step you want to change in the list.

Setting and applying functional parameters

You can set parameters for all post-processing functions (except Fourier Transformation) to customize the evaluation.

✧ Set the parameters for the selected post-processing function.

The new settings are automatically applied by the system. After you change parameter values in the input fields, the spectrum is updated once you press the **Enter** key, switch to a different operating element, or click **Apply**.

! Please note that selecting improper evaluation parameters may cause artifacts in the spectrum.

Verifying parameter changes



After setting the parameters for a post-processing step, check whether the settings result in an improved spectrum.

✧ Click **Break**.

The evaluation of the raw data stops after the selected post-processing step. The spectral display is updated and you can check the effect of the changes to the post-processing step. The evaluation remains stopped until you switch off the button.

! If the **Break** button is not activated, all post-processing functions are applied to the raw data. The updated spectrum is therefore the result of running all post-processing steps.

Undoing changes

If the new settings do not result in an improvement, you can undo all changes you have made in the selected post-processing step.



✧ Click **Reset**.

Deactivating a post-processing step

You can deactivate a post-processing step for an evaluation without having to change the protocol.

✧ Deselect the checkbox of the corresponding function in the list of post-processing steps.

Adjusting filtering

Four filters are available for improving the quality of the spectrum.

If the time signal measured has not decayed completely by the end of the acquisition window, this discontinuity causes spurious, secondary peaks (“Gibbs ringing”).

In this case, you can force the signal to decay more rapidly using the exponential, Gaussian, or Hanning filters. This suppresses Gibbs ringing. The steeper the forced signal decay, i.e. the shorter the full width at half maximum of the filters, the better the suppression. However, shorter filter half widths cause broadening of the spectral lines (full width at half maximum) and therefore a degradation of the spectral resolution.

The individual filters differ moderately in their suppression of Gibbs ringing and their primary peak broadening (*see also R. Ernst, G. Bodenhausen, A. Wokaun, “Principles of Nuclear Magnetic Resonance in One and Two Dimensions,” Oxford, 1987*).

➪ Normally, the use of filter functions is useful in the time domain only.

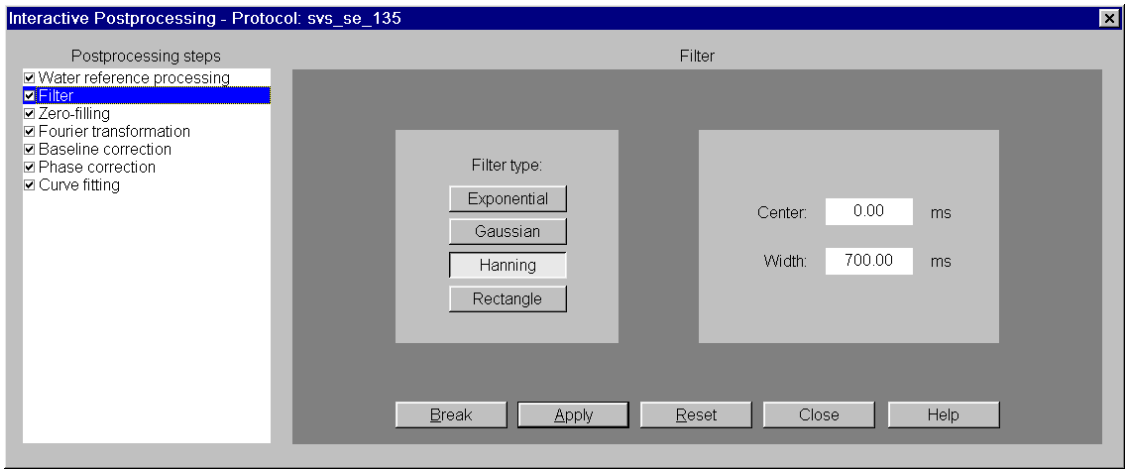
Proceed as follows:

❏ Selecting and activating the **Filter** post-processing step
❏ Selecting a filter
❏ Setting the position of the filter center
❏ Setting the half width of the filter
❏ Checking the curve of the filter function

Selecting a post-processing step

✧ Select the **Filter** checkbox in the list of post-processing steps.

The **Filter** post-processing step is activated and selected for editing. Entries specific to filtering are displayed in the parameter area of the dialog window.



Selecting a filter

The following filters are available for improving the quality of the spectrum:

❏ Exponential filter
❏ Gaussian filter
❏ Hanning filter
❏ Rectangular filter

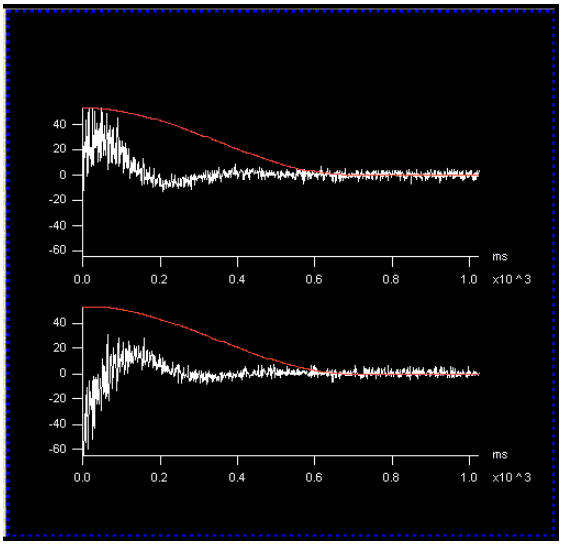
After selecting a filter, the signal is multiplied by the corresponding filter function.

Filter type / button	Calculation
Exponential	The signal is multiplied by an exponential function.
Gaussian	The signal is multiplied by a Gaussian function.
Hanning	The signal is multiplied by a Hanning function.
Rectangle	The signal is multiplied by a rectangular function. All values inside the filter width are multiplied by one and all values outside by zero.

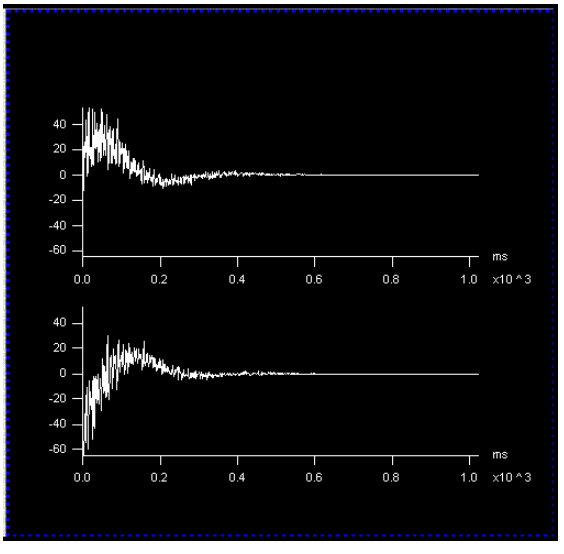
✧ Click the button for the filter function(s) desired.

Examples for using a filter function:

The images below show how a raw data set is displayed in the time domain, with the Hanning filter both deactivated and activated.



Complex signal in the time domain (unfiltered)



Filtered signal (Hanning)

Setting the position of the filter center

The position of the filter center can be set for each filter function.



✧ Enter a value for the position of the filter center in the **Center** field.

➪ In the time domain (before Fourier Transform), you enter the values in [**ms**]; in the frequency domain, in [**ppm**].

Or

✧ Click in the **Center** field.

✧ Click the mouse on the correct position in the time signal display (time domain) or in the spectrum (frequency domain).

The numeric value of the graphically defined position is copied to the **Center** field.

➪ The center is normally set to zero in the time domain.

Setting the half width of the filter

The half width of the filter can be set for each filter function.



✧ Enter the half width of the filter in the **Width** field.

Or

✧ Click in the **Width** field.

✧ Drag a line from the desired origin to the end point with the mouse.

The distance between the starting and end point is the new half width and copied to the **Width** field.

Checking the curve of the filter function

If you disable the **Filter** post-processing step, the corresponding filter function is shown as a red curve in the time signal display or spectrum.



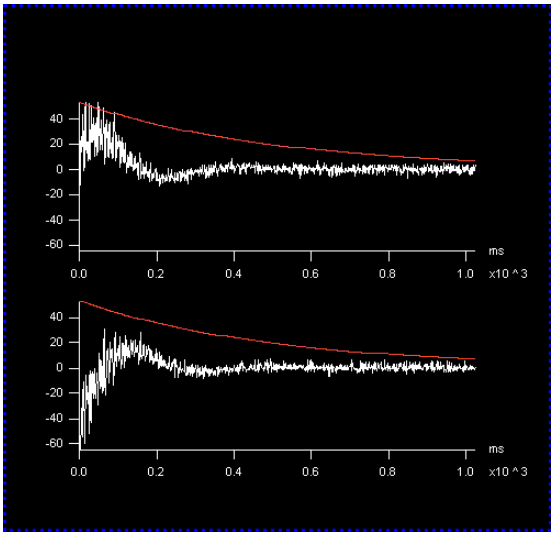
✧ Click **Break**.



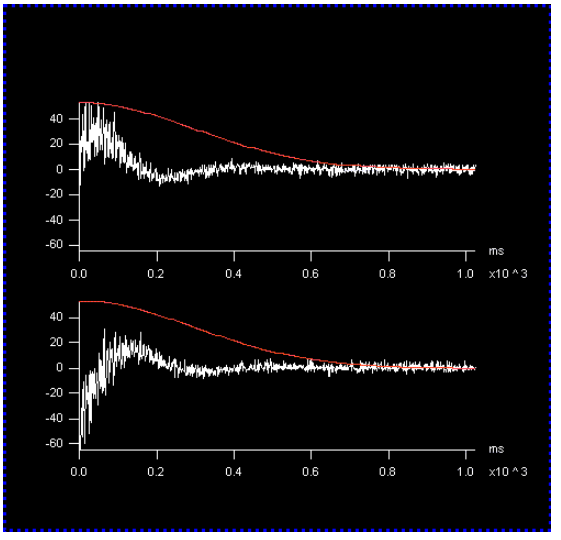
✧ Deselect the **Filter** checkbox.

The time signal/spectral display is updated. In addition to the unfiltered signal, the selected filter function is indicated by a red curve.

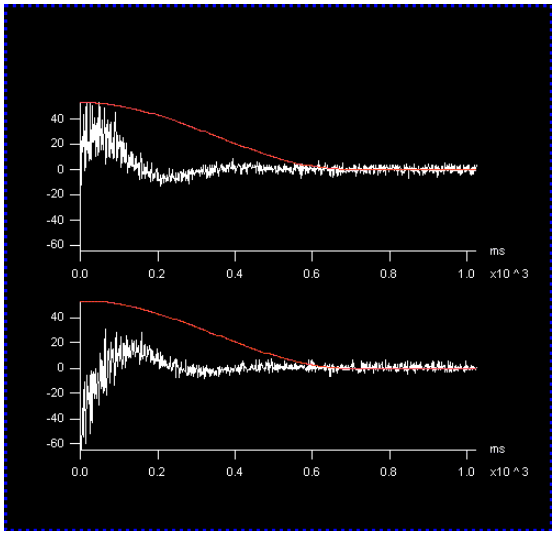
By changing the filter parameters (filter center, half width), you can adapt the filter function to the signal as shown in the following figures:



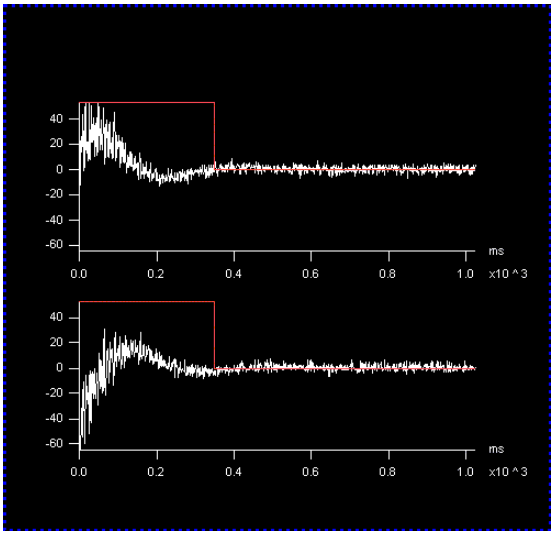
Exponential filter function in the time domain



Gaussian filter function in the time domain



Hanning filter function in the time domain



Rectangular filter function in the time domain

Adjusting zero-filling

Zero filling is used to improve the spectral resolution after Fourier Transform. In this case, zeros are appended to the end of the raw data vector.

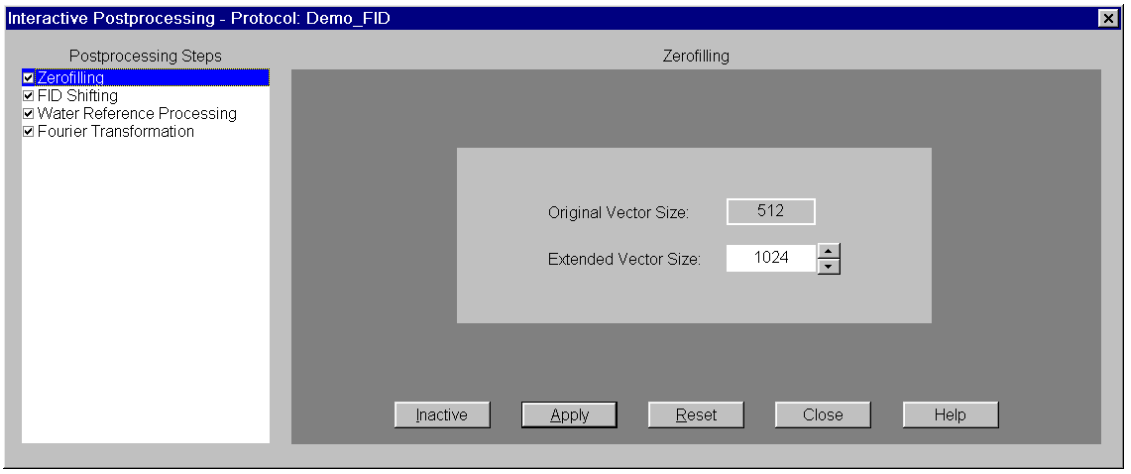
To enable Fourier Transform after zero-filling, the length of the raw data vector must be equal to a power of two, e.g. 1024.

➪ Zero filling is supported in the time domain only (before Fourier Transform).

Selecting a post-processing step

✧ Click the **Zero-Filling** checkbox in the list of post-processing steps.

The **Zero-Filling** post-processing step is activated and selected for editing. Entries specific to zero-filling are displayed in the parameter area of the dialog window.



Setting the vector length

The original vector length is displayed for your information. You can increase the original vector length:

✧ Enter a value in the **Extended Vector Size:** field.

➪ The new vector length must be a power of two (e.g. 2048).

Example: You have a data set that consists of 512 data points (vector length) and has a bandwidth of 2000 Hz. The resolution per data point is approximately 4 Hz. Extending the data set to 1024 will result in a resolution of 2 Hz.

! The maximum vector size is limited to 16 KB. The maximum amount of memory allocated to all loaded data sets is 128 MB.

Adjusting water suppression correction (^{1}H MRS only)

The water signal is the signal in the spectrum with the highest intensity and is therefore always suppressed. For this purpose, water suppression is already optimized during the adjustment. If the water signal is not completely suppressed, the residual signal can be corrected.

➪ Water suppression can be corrected in the time domain only.

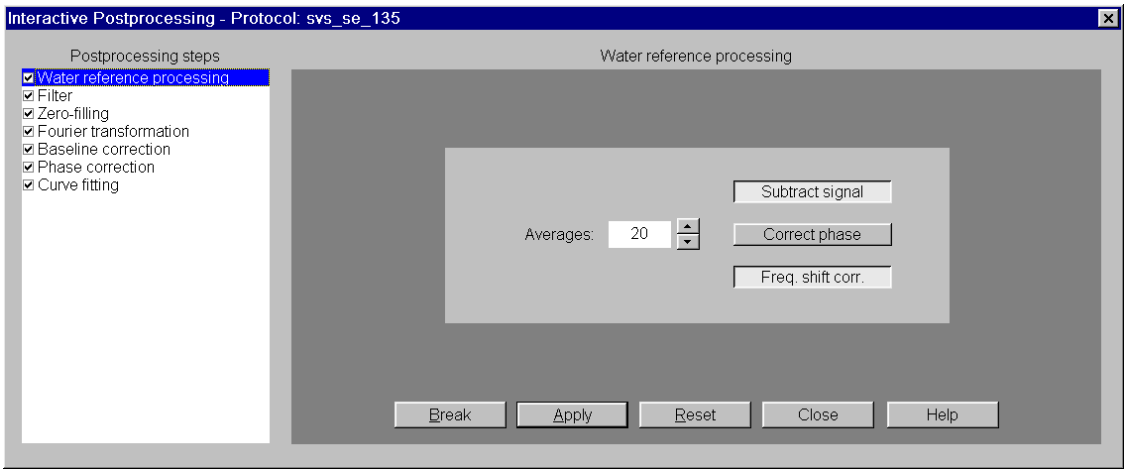
Proceed as follows:

❏ Selecting and activating the **Water reference processing** post-processing step
❏ Entering the number of points to be averaged
❏ Performing signal subtraction
❏ Performing phase correction
❏ Performing frequency shift correction
❏ Checking the curve of the water signal

Selecting a post-processing step

✧ Click the **Water reference processing** checkbox in the list of post-processing steps.

The **Water reference processing** post-processing step is activated and selected for editing. Parameters specific to water reference processing are displayed in the parameter area of the dialog window.



Entering the number of points to be averaged

The water signal is calculated in the time domain. A total of *n* adjacent points are averaged for the calculation.

✧ Enter the number of points in the **Averages** field.

Performing signal subtraction

Subtract signal

You can remove the residual water signal by subtracting it from the time signal.

✧ Click **Subtract signal**.

➪ Signal subtraction can be combined with phase correction or frequency shift correction.

Performing phase correction

Correct phase

The time signal can be corrected with the phase of the water signal. This includes a frequency shift of the time signal.

✧ Click **Correct phase**.

➪ Phase correction can be combined with signal subtraction.

➪ If phase correction is enabled, water reference processing automatically corrects the constant phase of the spectrum.

Performing frequency shift correction

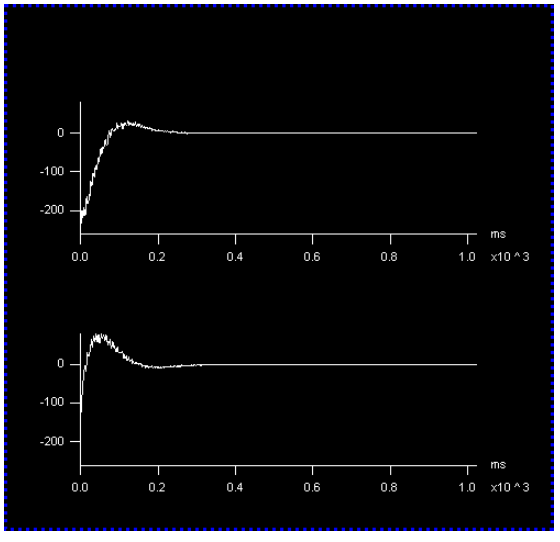
Freq. shift corr.

Instead of correction with the phase of the water signal, you can also perform a simple frequency shift correction.

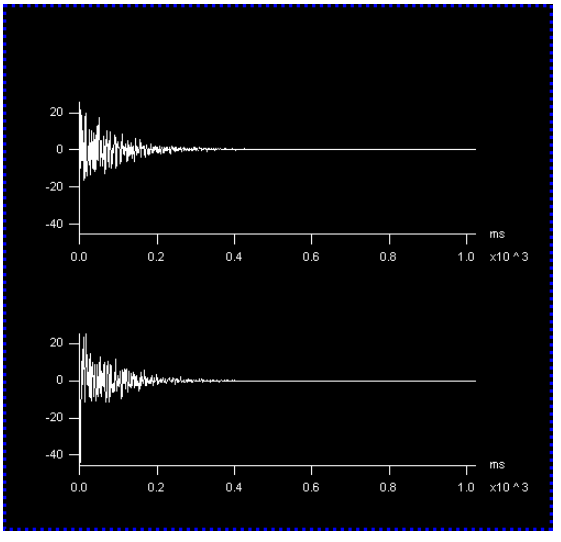
✧ Click **Freq. shift corr.**

➪ Frequency shift correction can be combined with signal subtraction.

Example: Time signal after water reference processing with signal subtraction and frequency shift correction



Time signal without correction



Time signal with signal subtraction and frequency shift correction

Checking the curve of the water signal

If you disable the **Water reference processing** post-processing step, you can check the curve of the calculated water signal.

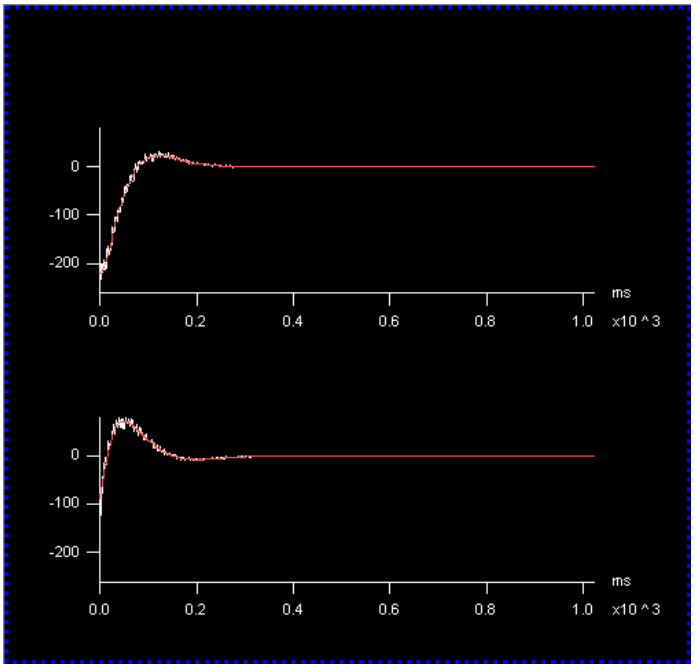


✧ Click **Break**.



✧ Deselect the **Water reference processing** checkbox.

The time signal display is updated. In addition to the time signal, the calculated water signal is indicated by a red curve.



Adjusting the FID shift

The first readout values may still contain signal overshoots of the RF pulse. FID shift allows you to shift the signal in the time domain by a predefined number of points to the left to remove these points. This function generally supports right-shifts as well. However, this does not eliminate signal overshoots.

➪ FID shifting is supported in the time domain only. Additionally, FID shifting makes a linear, frequency-dependent phase shift necessary.

! FID shifting is not necessary if the spectroscopy measurement protocols are based on Siemens SE or STEAM sequences.

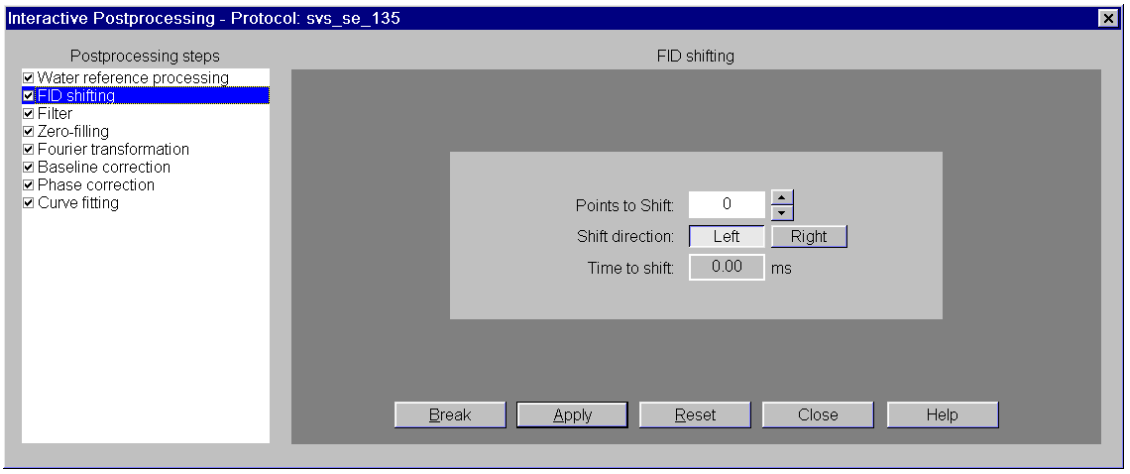
Proceed as follows:

❏ Selecting and activating the **FID shifting** post-processing step
❏ Setting the shift value
❏ Setting the shift direction

Selecting a post-processing step

✧ Click the **FID Shifting** checkbox in the list of post-processing steps.

The **FID shifting** post-processing step is activated and selected for editing. Parameters specific to FID shifting are displayed in the parameter area of the dialog window.



Setting the shift value

You can define by how many points the signal is shifted.



✧ Enter a value in the **Points to Shift** field.



The **Time to shift** field shows the shift value in [**ms**].

Setting the shift direction

You can select the direction for shifting the signal.



✧ Click **Left** to shift the signal to the left.

Or



✧ Click **Right** to shift the signal to the right.

Adjusting eddy current compensation

In case of protocols with short echo times, the raw data may be subject to phase shifts due to eddy currents induced by the measurement procedure. This applies to both SVS data and CSI data.

The effect of these eddy currents on the spectrum can be compensated by subtracting the phase of the water signal from the signal to be evaluated.

In this case, perform two measurements using the same protocol:

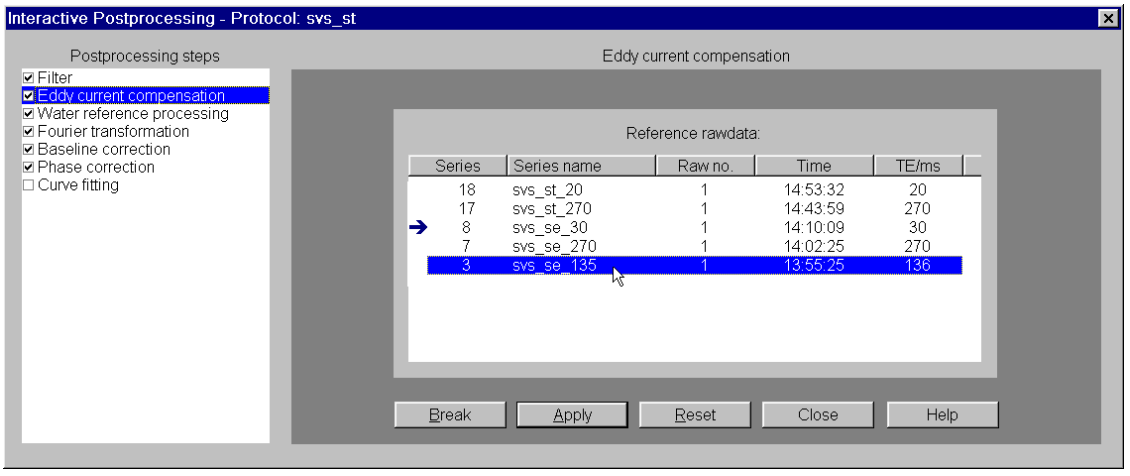
- ❏ one without water suppression to acquire the reference raw data (**Water suppr.** measurement parameter set to **Only RF off**)
- ❏ one with water suppression to acquire the spectroscopy raw data (**Water suppr.** measurement parameter set to **Water sat.** or **Weak water suppr.**)

⇨ Eddy current compensation is supported only in the time domain. It is usually the first post-processing step to be performed.

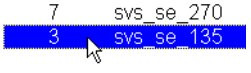
Selecting a post-processing step

✧ Click the **Eddy current compensation** checkbox in the list of post-processing steps.

The **Eddy current compensation** post-processing step is activated and selected for editing. The parameter area of the dialog window displays a list of suitable reference raw data sets. The arrow identifies the reference raw data set currently loaded.



Selecting a reference raw data set



✧ From the list, select the reference raw data set you want to load to perform the eddy current compensation.

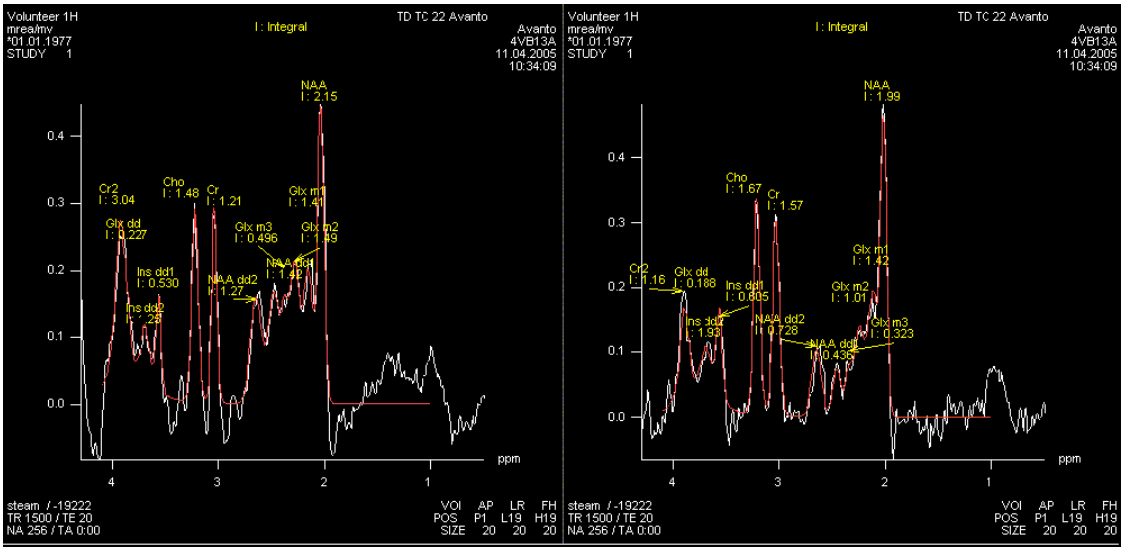
Starting Eddy current compensation



✧ Double-click the reference raw data set.
- Or -
Click **Apply**.

Eddy current compensation is performed after the reference raw data set is loaded.

The following figure shows how eddy current compensation affects the spectral display.



Without eddy current compensation

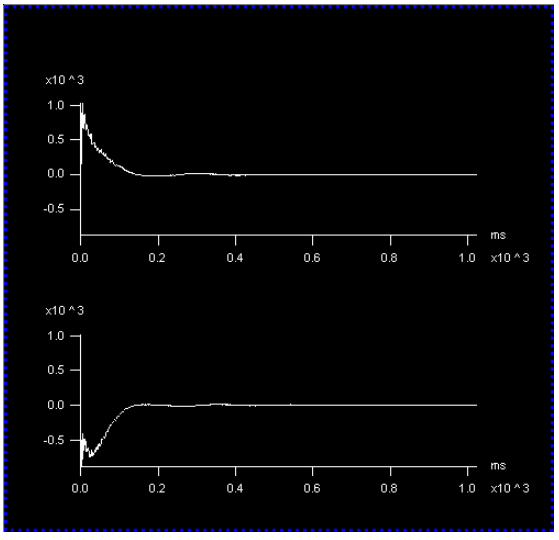
With eddy current compensation

➪ Eddy current compensation automatically corrects the constant phase of the spectrum.

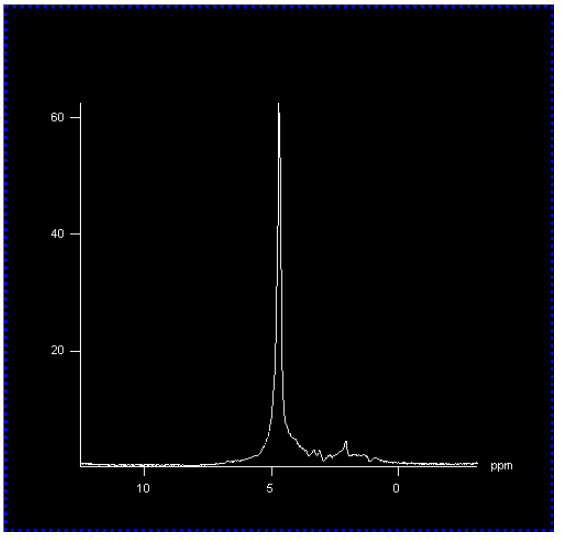
Fourier Transformation

Fourier Transformation (FT) is a mathematical algorithm used to translate the measurement signals from the time domain (the physically measured signal) into the frequency domain (displayed spectrum).

If you apply FT to the spectrum a second time, the data are retranslated from the frequency domain into the time domain.



Signal in the time domain before Fourier Transformation

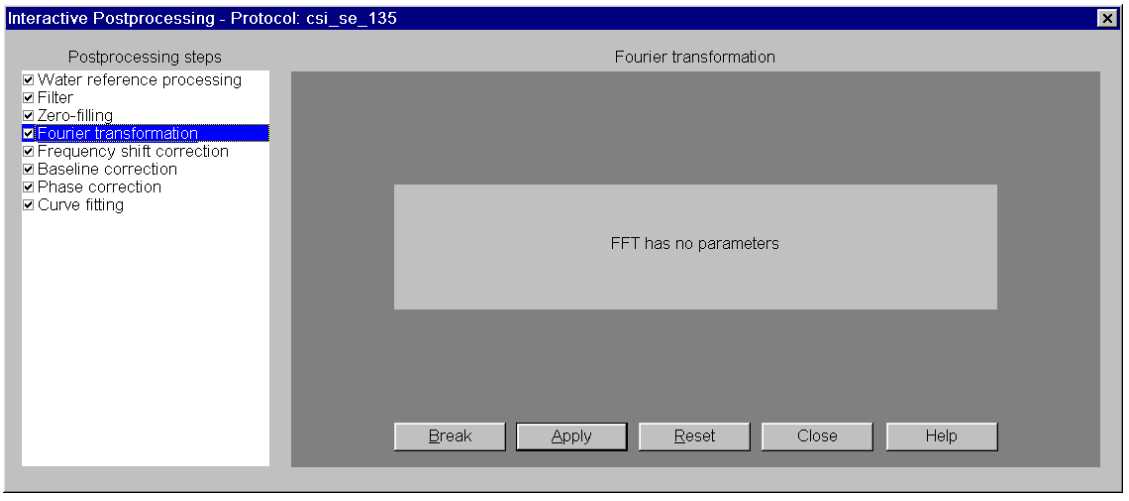


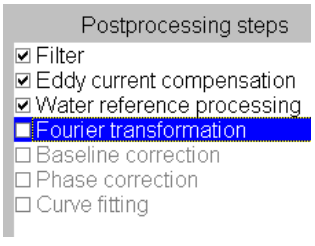
Signal in the frequency domain after Fourier Transformation (magnitude)

Selecting a post-processing step

✧ Click the **Fourier Transformation** checkbox in the list of post-processing steps.

The Fourier Transformation is performed and the signal display is updated. Fourier Transformation does not support parameter modifications. As a result, the parameter area of the dialog window is empty.



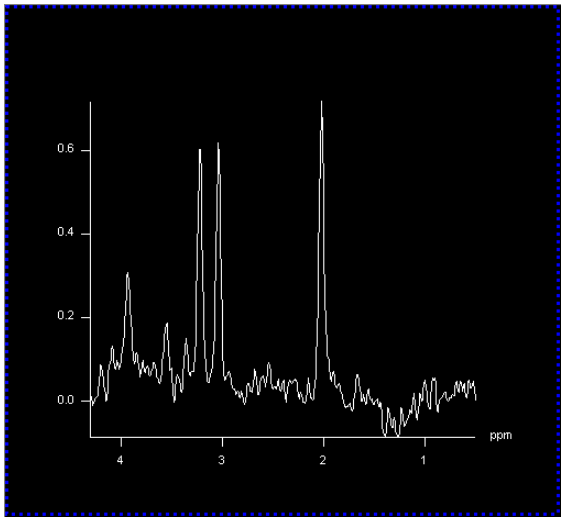


➪ If you deactivate Fourier Transformation, all subsequent post-processing steps are deactivated as well and can no longer be selected.

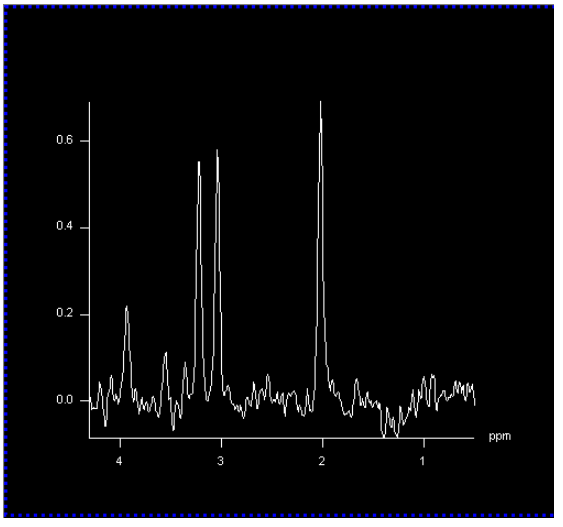
Adjusting baseline correction

Spectra may exhibit baseline distortion, due to incomplete suppression of the water signal. This can often be identified by a left-to-right slope of the baseline. The signals are to the side of the water signal.

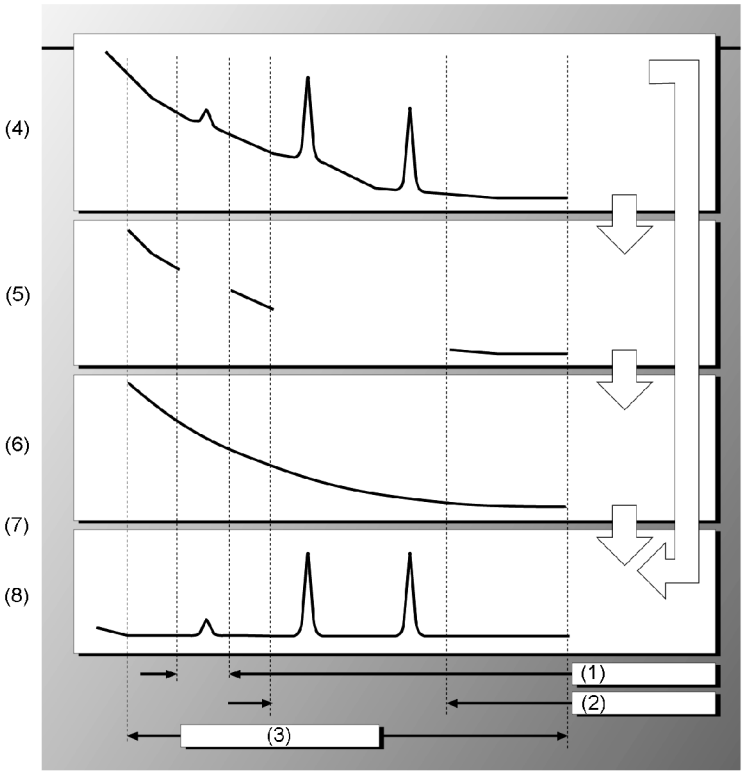
The baseline is corrected by fitting an nth order polynomial to the signal curve within the peak-free areas of the spectrum. The polynomial is subtracted from the spectral curve, resulting in a more horizontal baseline.



Spectrum without baseline correction



Spectrum with baseline correction



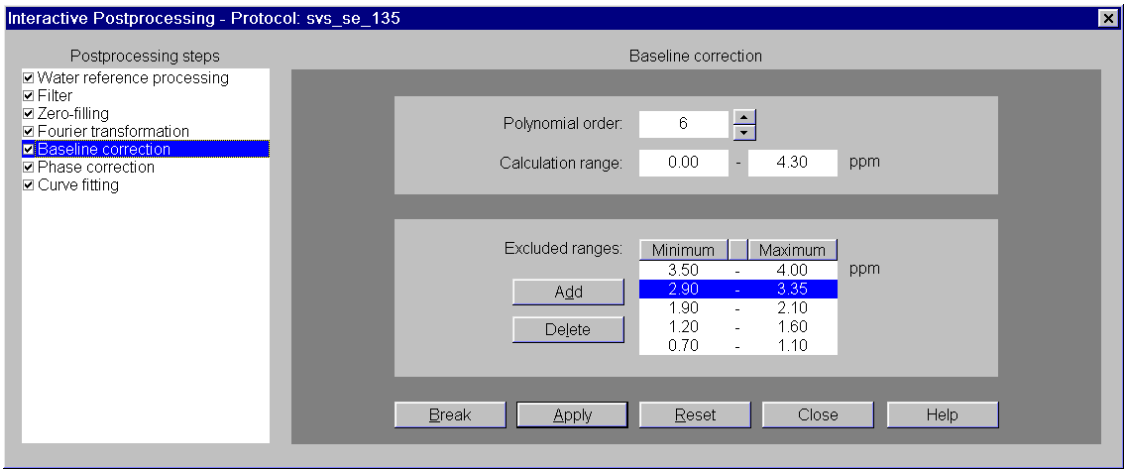
(1) Peak 1
(2) Peak 2
(3) Calculation region
(4) Signal
(5) Selected ranges
(6) Calculated baseline
(7) Subtraction
(8) Signal after baseline correction

➪ Baseline correction is supported in the frequency domain only.

Selecting a post-processing step

✧ Click the **Baseline correction** checkbox in the list of post-processing steps.

The **Baseline correction** post-processing step is activated and selected for editing. Parameters specific to baseline correction are displayed in the parameter area of the dialog window.



Setting the calculation range

You may apply baseline correction to a specific range of the spectrum only. Outside the calculation range, the baseline is corrected by subtracting a constant.

✧ Enter a minimum and maximum threshold for the calculation range in the **Calculation range** input fields.

Or

✧ Click in an input field of **Calculation range**.

✧ Drag a line from the desired origin to the end point with the mouse.

The graphically defined values are copied to the fields under **Calculation range**.

Setting the polynomial order

The spectral curve is approximated by polynomial fitting using nth order polynomials. The polynomial order refers to the highest power of the polynomial. A polynomial of the third order, for example, is $ax^3 + bx^2 + cx + d$.



✧ Enter the order of the polynomial in the **Polynomial order** input field.

Defining an excluded range

Spectral ranges containing peaks have to be excluded from baseline correction. Otherwise, the algorithm would try to suppress these peaks.

This is why you set “excluded ranges” for these regions.



✧ Click **Add** to define a new excluded range.



A new excluded range is added to the **Excluded ranges** list.

You now define the minimum and maximum threshold for the excluded range. These values can be defined both graphically or numerically.

Setting a new excluded range (graphically)

✧ Drag a line in the spectrum from the desired origin to the end point with the mouse.

The graphically defined values are copied to the **Excluded range** list.

Setting a new excluded range (numerically)

✧ Enter the minimum threshold for the excluded range in the left field (**Minimum** column).

✧ Enter the maximum threshold for the excluded range in the right field (**Maximum** column).

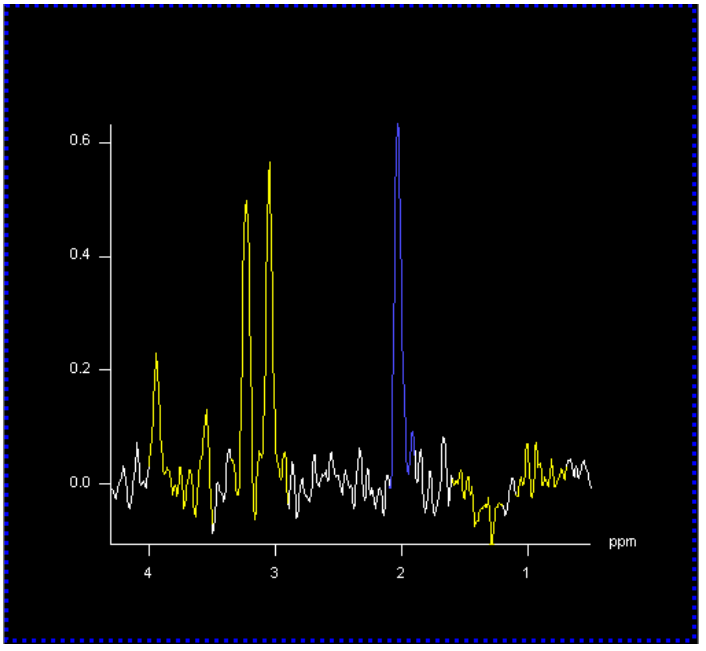
✧ Press the **Enter** key.

Showing the excluded range in the spectrum

Minimum		Maximum	
1.80	-	2.20	ppm
2.90	-	3.30	
3.80	-	4.10	

The selected exclusion range is colored blue in the spectrum for control purposes. All other excluded ranges are colored yellow.

✧ Select an entry from the **Excluded ranges** list.



Changing existing excluded ranges

The thresholds of existing excluded ranges can be edited both graphically or numerically.

✧ Select an entry from the **Excluded ranges** list.

✧ Reset the excluded range graphically or numerically.
→ Page C.8–29

➪ To set the selected excluded range numerically, click inside one of the two display fields. The display fields become editable.

Sorting excluded ranges

The entries in the **Excluded ranges** list can be sorted in ascending or descending order based on the minimum or maximum thresholds.



✧ To sort the excluded ranges in ascending order to the lower threshold value, click **Minimum**.

➪ Click **Minimum**, again to sort the excluded ranges in descending order to the lower threshold.

Or



✧ To sort the excluded ranges in ascending order to the upper threshold value, click **Maximum**.

➪ Click **Maximum**, again to sort the excluded ranges in descending order to the upper threshold.

Deleting excluded ranges

If you want to include a range for baseline correction, you can delete it from the list.

✧ Select an entry from the **Excluded ranges** list.



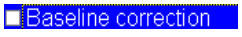
✧ Click **Delete**.
- Or -
Press **Del.**

Checking the baseline curve

If you disable the **Baseline correction** post-processing step, you can check the curve of the calculated baseline.

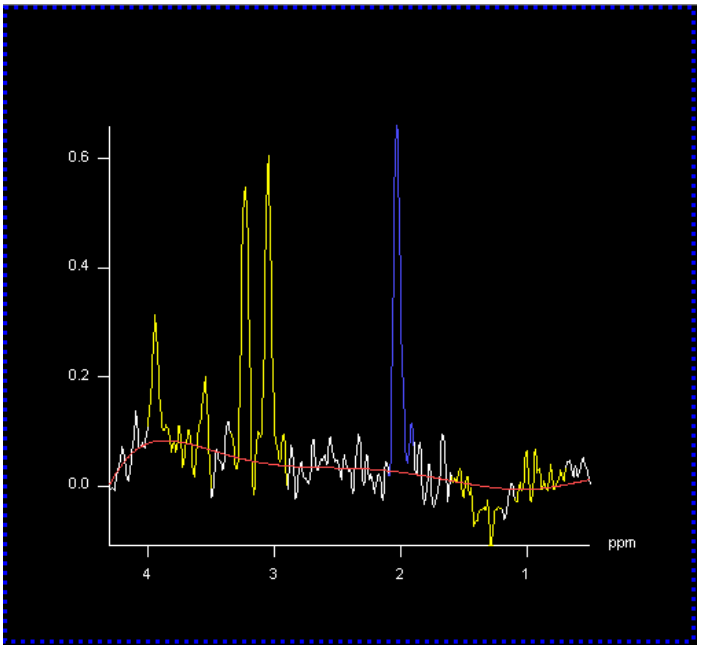


✧ Click **Break**.



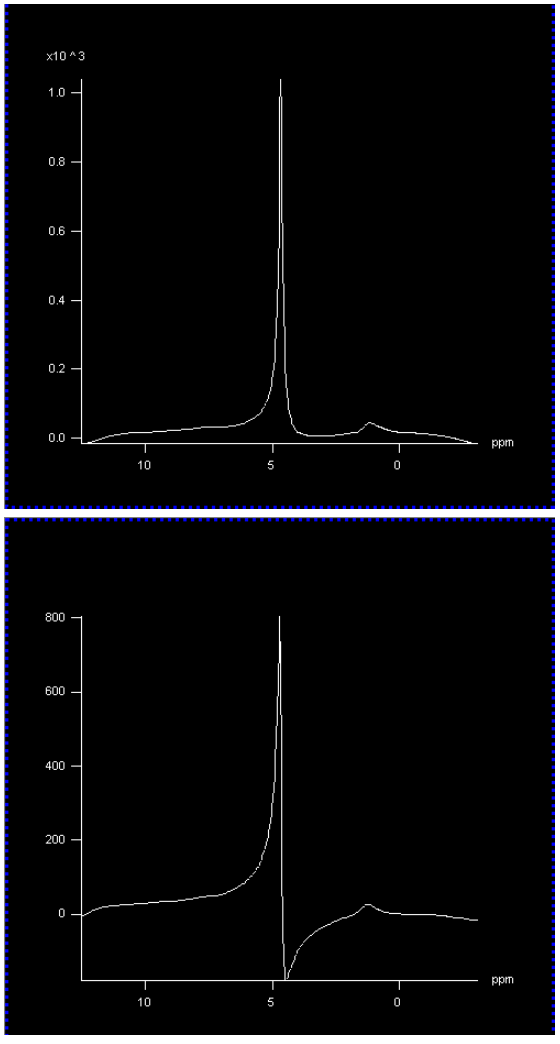
✧ Deselect the **Baseline correction** checkbox.

The spectral display is updated. In addition to the spectral curve, the calculated baseline is indicated by a red curve.



Adjusting phase correction

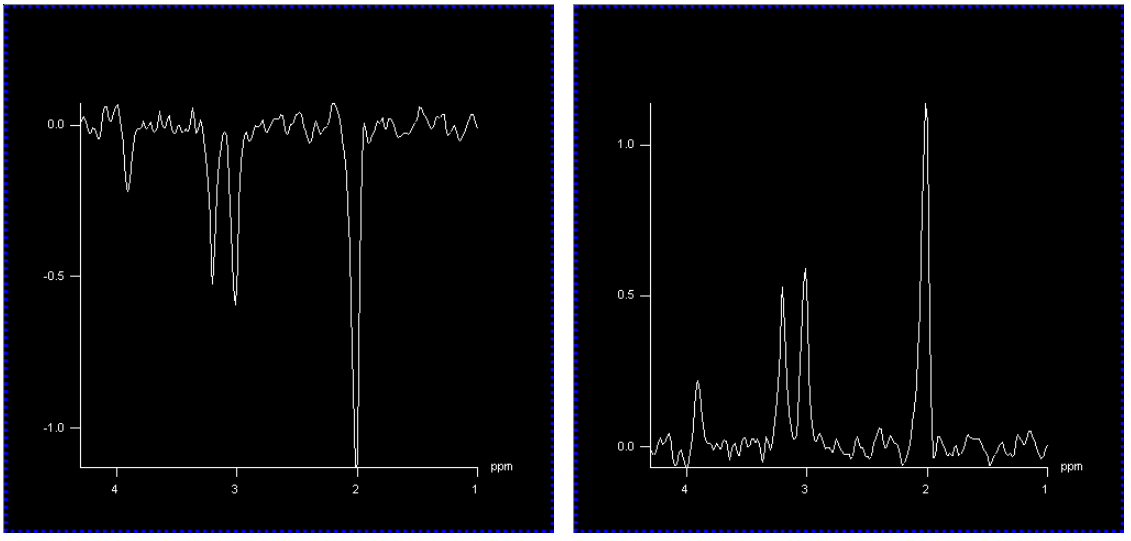
The complex spectrum consists of the real part (absorption signal) and the imaginary part (dispersion signal). These represent the frequency-dependent x and y projections of the transverse magnetization of the spins. If the phase is rotated, the real and imaginary parts may blend.



Absorption signal (real part) upper Heft
Dispersion signal (imaginary part) upper right
Phase-shifted absorption signal lower left

Phase correction allows you to adjust the phase so that the absorption signal is once again displayed in the real part and the dispersion signal in the imaginary part.

Example: The following figure shows a spectrum before and after phase correction.



Before phase correction (180° phase shift) After phase correction

- Phase correction can be performed both manually (interactively) and automatically.
- Phase correction is supported in the frequency domain only (after FT).

Performing phase correction manually

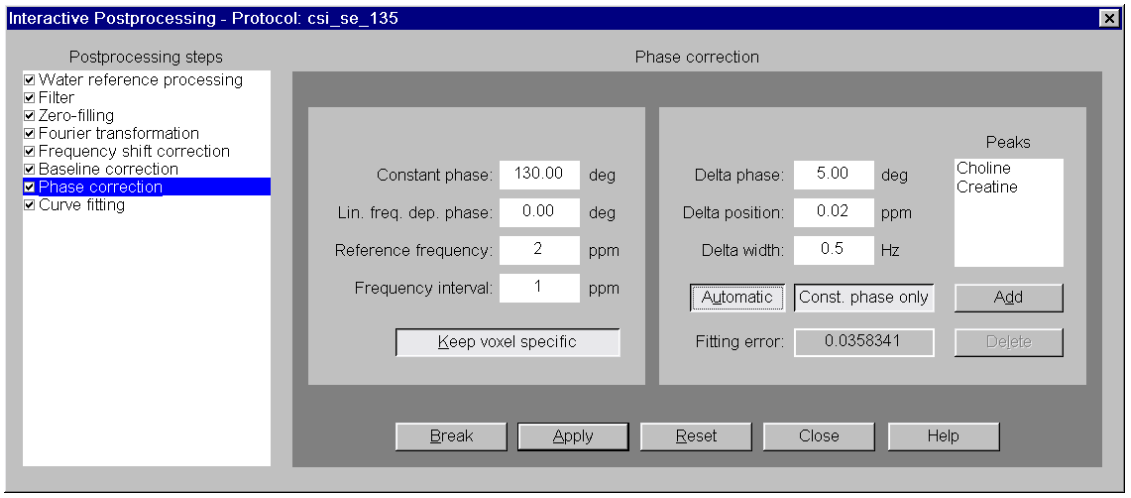
The phase of the signal consists of a constant phase and a frequency-dependent phase parameter. The phase parameter represents the change in phase within a defined frequency interval.

Phase parameters can be set numerically or graphically. The new settings are automatically applied and the spectrum is updated.

Selecting a post-processing step

✧ Click the **Phase correction** checkbox in the list of post-processing steps.

The **Phase correction** post-processing step is activated and selected for editing. Parameters specific to phase correction are displayed in the parameter area of the dialog window.



Keep voxel specific option

If the **Keep voxel specific** option (only for CSI data) is switched on, the following parameters / settings are saved voxel-specific, and are not lost during repeated evaluation:

- ❏ Constant phase
- ❏ Linear frequency-dependent phase
- ❏ Reference frequency
- ❏ Frequency interval
- ❏ **Automatic** on/off
- ❏ **Only const. Phase** on/off

➪ However, voxel-specific data is not saved when saving to the hard drive.



✧ Click **Keep voxel specific** on or off.

Setting phase parameters (numerically)



✧ Go to the **Constant phase** and enter the angle to be used to shift the constant phase.



✧ Enter the angle by which you want to shift the frequency-dependent phase component in the **Lin. freq. dep. phase** field.



✧ Enter the reference frequency for the frequency-dependent phase component in the **Reference frequency** field.

➪ The frequency-dependent phase has no effect at this point of the spectrum.



✧ Enter the frequency interval for the frequency-dependent phase component in the **Frequency interval** field.

➪ The display of the spectrum is updated following each change.

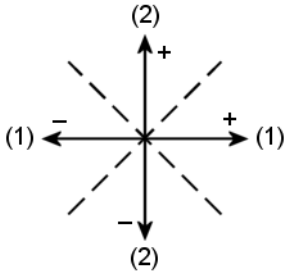
Setting phase parameters (using the mouse)

In place of numerically entering the two parameters **Constant phase** and **Lin. freq. dep. phase** for manual phase correction, you can also set them interactively using the mouse.

✧ Position the mouse pointer in the parameter area of the **Interactive Post-processing** dialog window and press the *center* mouse button.

The mouse pointer changes shape.





✧ Drag the mouse to the right or left to change the constant phase (1).

✧ Drag the mouse up or down to change the frequency-dependent phase components (2).

The spectral display is updated immediately.

➪ Only one phase parameter is changed at a time, even if you drag the mouse diagonally (45° boundary).

➪ Pressing and holding the *center* mouse button hides the peak information and the red curve of the theoretical spectrum in the active spectral segment. The selected voxel is hidden in the miniature reference images. Release the center mouse button to redisplay the information.

Automatic phase correction

Automatic phase correction can be applied to the constant phase only or to both phase parameters (including frequency-dependent component). For this purpose, the program uses the reference peaks in the **Peaks** list and determines the best fit in the spectrum. The algorithm used is the same as for **Curve fitting**.
→ Page C.8–46, *Adjusting curve fitting*

The program attempts to minimize the difference between the theoretical and measured spectrum by varying individual parameters. The phase of the measured spectrum is adapted to the theoretical spectrum.

Proceed as follows:

❏ Selecting and activating the **Phase correction** post-processing step
→ Page C.8–35

❏ Setting parameters for automatic phase correction

❏ Selecting reference peaks

❏ Starting automatic phase correction

Keep voxel specific option

When evaluating CSI data, you can retain the voxel-specific parameter settings.
→ Page C.8–35, *Keep voxel specific option*



✧ Click **Keep voxel specific** on or off.

Setting automatic phase correction



✧ Enter the value by which the phase should change with each iteration in the **Delta phase** field.



✧ Enter the value by which the peak position should change with each iteration in the **Delta position** field.



✧ Enter the value by which the full width at half maximum should change with each iteration in the **Delta width** field.



✧ To correct both constant and frequency-dependent phase parameters, deselect the **Const. phase only** button.

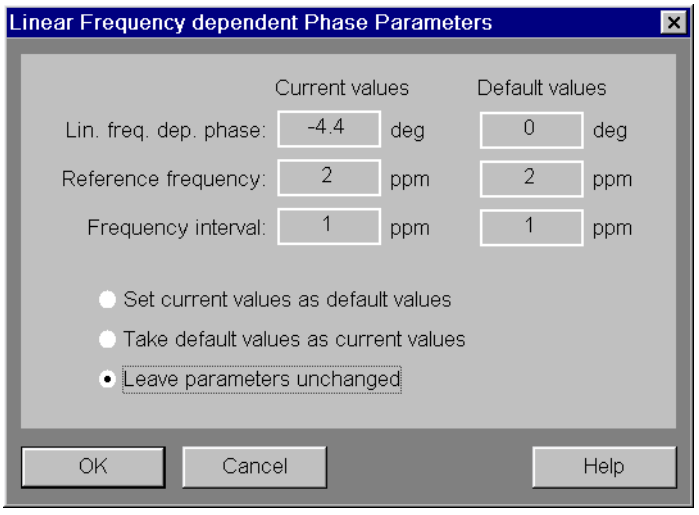
Or

✧ To correct only the constant phase parameters, select the **Const. phase only** button.

If you only correct the constant phase automatically, the system uses standard values to correct the frequency-dependent phase parameters. However, you can also set these values manually.

✧ Enter the individual values as needed in the corresponding input fields for the frequency-dependent phase parameters.

If the entered values differ from the standard values, the following dialog window is opened.



With the **Leave parameters unchanged** option, standard values and current values may remain different.

✧ If you want to set the current values as standard values or vice versa, select the corresponding option.

✧ Click **OK**.

The current frequency-dependent phase parameters are used.

Selecting reference peaks

One reference peak is sufficient to correct only the constant phase parameter. At least two reference peaks are necessary to correct the frequency-dependent phase parameters as well.

A new reference peak can be selected using the **Peak Editor**.



✧ Click **Add**.

The **Peak Editor** opens.

✧ Select a new peak in the **Peak Editor** and add it to the list.
→ Page C.9–16, *Adding a peak to the peak list*

All peaks included in the peak list are used for automatic phase correction.



➪ Peaks can be deleted from the peak list by clicking the **Delete** button or pressing the **Delete** key on your keyboard.

➪ You can also edit the characteristics of a reference peak using the **Peak Editor**.
→ Page C.9–2, *Editing peaks*

Starting automatic phase correction



✧ Click on **Auto**.

Automatic phase correction is performed. The spectrum is updated based on the corrected phase. The phase parameters used for the correction are displayed in the **Const. Phase only** and **Lin. freq. dep. phase** fields.



The fitting error is shown in the **Fitting error** field. It is equivalent to the sum of least squares.

Adjusting the frequency shift correction

This post-processing step is important for CSI data. It is best performed immediately after the Fourier Transform (and always prior to the baseline and phase correction, as well as curve fitting).

The frequency position of the individual voxels within the FoV must be corrected because of magnetic field fluctuations due to poor shimming.

You have two options to correct the frequency position:

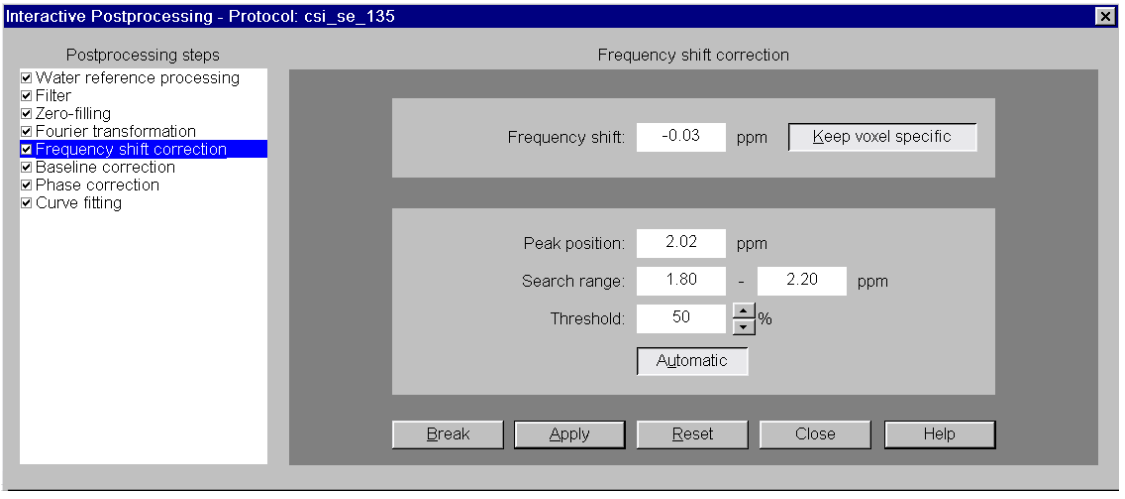
❏ Move a peak of the spectrum that can be clearly identified to its theoretical peak position.

❏ Enter a value for the frequency shift.

Selecting a post-processing step

✧ Click the **Frequency shift correction** checkbox in the list of post-processing steps.

The **Frequency shift correction** post-processing step is activated and selected for editing. Parameters specific to frequency shift correction are displayed in the parameter area of the dialog window.



Keep voxel specific option

If the **Keep voxel specific** option (only for CSI data) is switched on, the following frequency shift and automatic settings are saved voxel-specific, and are not lost during repeated evaluation:

➪ However, voxel-specific data is not saved when saving to the hard drive.



✧ Click **Keep voxel specific** on or off.

Moving the peak to its theoretical peak position

The objective of this algorithm is to find a peak within a prescribed frequency range, and then move the spectrum so that the peak is at a theoretical predefined position.

For this purpose, a search is made within the search region for the signal value with maximum magnitude amplitude, and its position determined. Weighted averaging is performed to enable precise determination of this position. The weighting includes all signal values in the search range whose magnitude exceeds a predefined threshold value. Finally, the entire spectrum is moved so that the peak that is found is in the position desired.



✧ Enter the theoretical position of the peak in the **Peak position** field.



✧ Use the two fields under **Search range** to set the frequency range for searching for the peak.



✧ In the **Threshold** field, enter the threshold values for the signals to be taken into account in the weighted averaging.

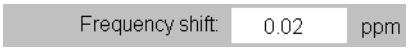
The threshold value is indicated as a percentage of the maximum magnitude amplitude in the search region.



✧ Click on **Auto**.

The search for the peak is started.

The frequency shift resulting from the peak search is entered in the **Frequency shift** field:



The entire spectrum is shifted by the amount indicated.

Entering the frequency shift value



✧ Enter a value in the **Frequency shift** input field.



✧ Click **Apply**.
- Or -
Press the **Enter** key.

The entire spectrum is shifted by the amount entered.

Normalizing to reference

Normalizing to a reference is required when quantifying the tCholine signal as part of breast spectroscopy (*syngo* GRACE option). The breast signal is normalized using an additionally measured reference data set.

The reference data are previously created using a fast SVS measurement without water suppression. Normally, an external reference probe is used. The probe is integrated into the coil housing of the breast coils. Respective breast coils:
→ Page B.3–4, *^{1}H MRS measurements of the breast*.

The result of the evaluation step is a normalized spectrum, and the integrals and amplitudes are identified by I* and A* respectively.

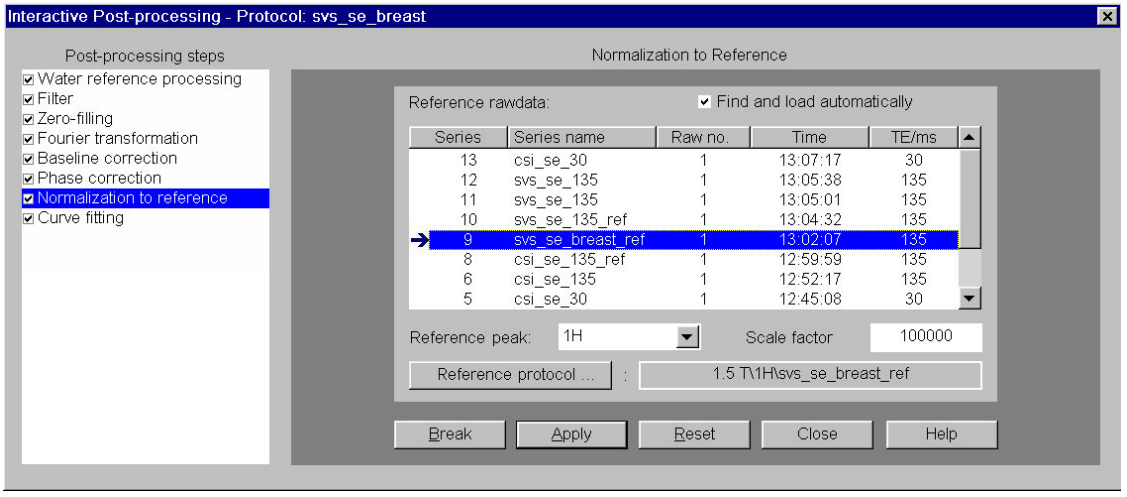
➪ Normalization is available in frequency domain only.

➪ The **Normalization to reference** post-processing step should be performed before **Curve fitting**.

Selecting a post-processing step

✧ Click the **Normalize to reference** checkbox in the list of post-processing steps.

The **Normalize to reference** post-processing step is activated and selected for editing.



➪ The parameters in the lower part of the dialog window are preset and, in general, need not to be altered: **Reference peak** (usually ^{1}H), **Scale factor** (predominance of the water signal with respect to the signals of the spectrum will be taken into account), and **Reference protocol** (post processing protocol for the reference data set).

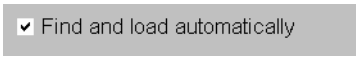
A list of reference raw data sets suitable for performing normalization is displayed in the parameter area of the dialog window. The arrow in the parameter area identifies the reference raw data set currently loaded.

There are several ways to select a different raw data set:

❏ Automatic reference selection
The system automatically searches for and loads a suitable reference data set (series with the name extension "_ref").

❏ Manual reference selection
All suitable reference data sets are displayed. You select the data set required from the list.

Automatic reference selection

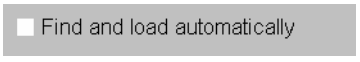


✧ Click the **Find and load automatically** control box.

Normalization is performed using the reference data set loaded automatically.

➪ If several suitable reference raw data sets are found, select the required data set from the list, as in manual reference data selection.

Manual reference selection



✧ Deselect the **Find and load automatically** control box.

✧ From the list, select the reference raw data set you want to load to perform the normalization.



✧ Click **Apply**.
- Or -
Double-click the reference raw data set.

Normalization is performed after the reference raw data set is loaded.

Adjusting curve fitting

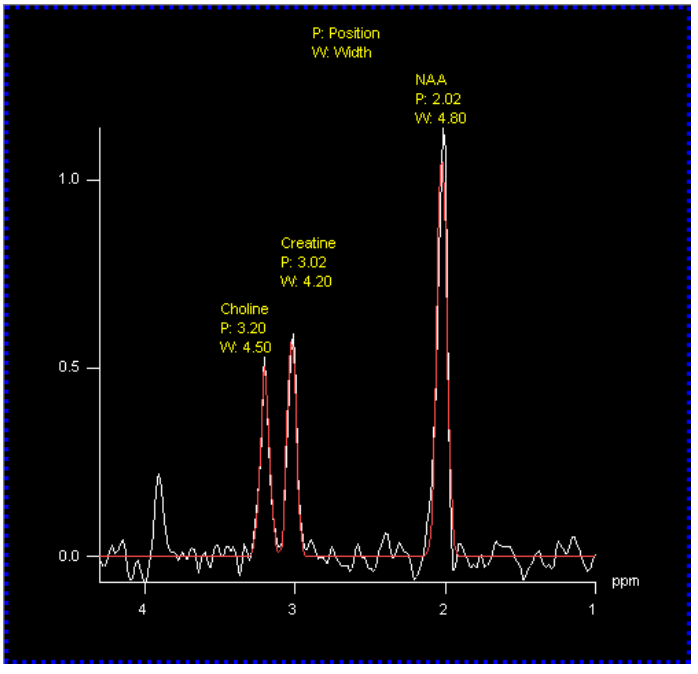
Spectra often contain a large number of peaks, making it difficult to assign metabolites to the individual peaks. Curve fitting allows you to adapt a theoretical spectrum to the experimental spectrum.

➪ Curve fitting is supported for the frequency domain only and should be the last step within the post-processing protocol.

You can choose between manual or automatic curve fitting.

➪ Curve fitting is based on empirical values. Assignment errors cannot be ruled out.

When the calculation is completed, the theoretical spectrum is displayed as a red curve and the selected peak information is displayed as yellow spectrum text.



Performing curve fitting manually

For manual curve fitting, you select the peaks of the metabolites you assume to be represented in the spectrum. The calculated theoretical spectrum is updated after each change.

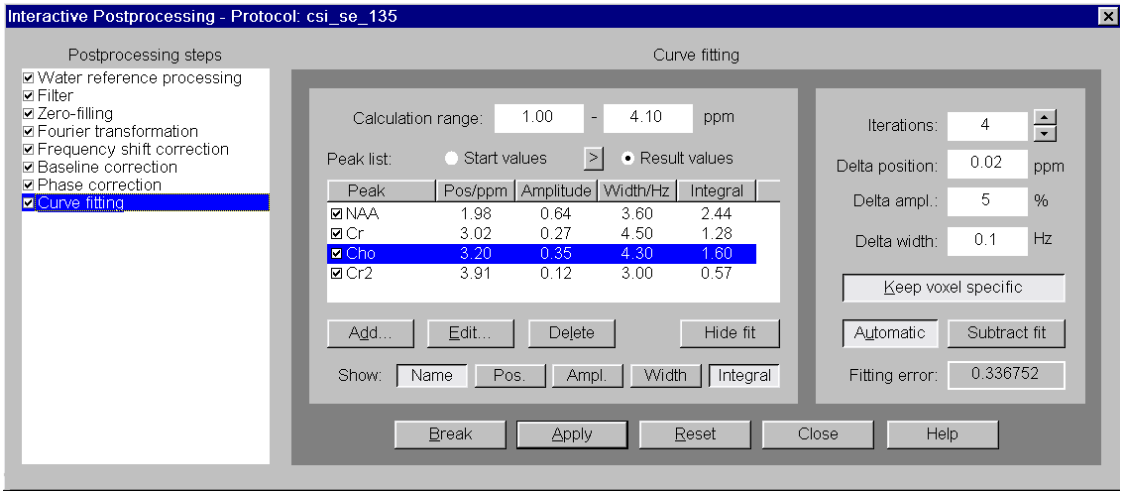
Proceed as follows:

- ❏ Selecting and activating the **Curve fitting** post-processing step
- ❏ Setting the calculation range
- ❏ Displaying start or result values in the peak list
- ❏ Using result values as start values (optional)
- ❏ Using start values as result values (optional)
- ❏ Adding new peaks to the peak list (optional)
- ❏ Removing peaks from the peak list (optional)
- ❏ Sorting entries in the peak list (optional)
- ❏ Editing peak parameters (optional)
- ❏ Showing peak information
- ❏ Hiding the peak information of individual peaks (optional)
- ❏ Hiding the fit curve (optional)
- ❏ Subtracting the theoretical spectrum from the measured spectrum (optional)

Selecting a post-processing step

✧ Click the **Curve fitting** checkbox in the list of post-processing steps.

The **Curve fitting** post-processing step is activated and selected for editing. Entries specific to curve fitting are displayed in the parameter area of the dialog window.

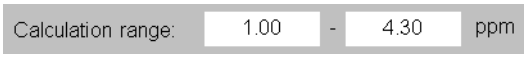


Keep voxel specific option

If the **Keep voxel specific** option (only for CSI data) is switched on, the peak list (name, position, amplitude, width, and integral of the individual peaks) and automatic settings are saved voxel-specific, and are not lost during repeated evaluation:
→ Page C.8–41, *Keep voxel specific option*

Setting the calculation range

You can select a range of the spectrum and apply curve fitting to this specific range.



✧ Enter a minimum and maximum threshold for the calculation range in the **Calculation range** input fields.

Or

✧ Click into one of the fields in the line **Calculation range**.

✧ Drag a line in the spectrum from the desired origin to the end point with the mouse.

Displaying start or result values in the peak list

The peak list displays the peaks selected for the current post-processing protocol including the most important parameters. During curve fitting, the parameters of these theoretical peaks are adapted to the measured spectrum. After curve fitting has been performed, the new parameter values (**Result values**) are displayed in the peak list. You can toggle between the result values and the **Start values** (values prior to curve fitting).



✧ To display the start values in the peak list, select the **Start values** option.

Or

✧ To display the result values in the peak list, select the **Result values** option.

Applying values

How to apply the current result values as start values when the **Start values** option is selected:



✧ Click this button between the option fields.

How to apply the current start values as result values when the **Result values** option is selected:



✧ Click this button between the option fields.

Adding new peaks to the peak list

If the spectrum contains peaks that are not fitted, you can add new peaks to the peak list.



✧ Click **Add...**.

The **Peak Editor** opens. Peaks can be selected or created and added to the peak list.
→ Chapter C.9, *Editing Peaks and Peak Lists*

Removing peaks from the peak list

Peaks no longer needed for curve fitting can be removed from the peak list.

✧ Select the entry in the peak list.

Delete

✧ Click **Delete**.
- Or -
Press the **Del** key.

The entry is deleted from the peak list.

Sorting peak lists

The peaks in the peak list can be sorted in ascending or descending order according to the values in each parameter column. The header of the peak list provides buttons for this purpose.

Button	Function
Peak	The peaks are sorted alphabetically by peak name in ascending order.
Pos/ppm	The peaks are sorted according to their position in the spectrum in ascending order.
Amplitude	The peaks are sorted according to their amplitude height in ascending order.
Width/Hz	The peaks are sorted according to their full width at half maximum in ascending order.
Integral	The peaks are sorted according to the magnitude of their integral in ascending order.

➪ Click the button for the sorting desired.

➪ If you click one of the buttons again, the peaks are sorted in descending order.

Editing peak parameters

Peak	Pos/ppm	Amplitude	Width/Hz	Integral
NAA	2.02	1.04	3.70	4.11
Cr	3.04	0.50	4.20	2.25
Cho	3.22	0.55	3.80	2.23
Cr2	3.95	0.23	1.90	0.67

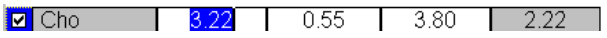
The **Pos/ppm**, **Amplitude**, and **Width/Hz** parameters can be edited directly in the peak list.
→ Page C.9–9, *Changing the thresholds for fitting*

Peak name and Integral cannot be changed in the peak list.

✧ Select the peak you want to edit.

✧ Click a parameter field of the selected peak.

The field becomes an input field:



✧ Use the **Tab** key to jump to the field where you want to change the value.

Field	Parameters
Pos/ppm	Peak position
Amplitude	Peak amplitude
Width/Hz	Peak full width at half maximum

✧ Enter the new parameter value.

✧ Make all changes for the selected peak in this manner.

✧ Press the **Enter** key to complete the editing for the peak.
- Or -
Select a different peak.

The new settings are applied.

! Open the **Peak Editor** to edit the other parameters of the selected peak as well. Click the **Edit** button or double-click the entry in the peak list.
→ Page C.9–2, *Editing peaks*

Showing peak information

Up to three different categories of peak information can be displayed simultaneously in the fitted spectrum. Use the buttons in the **Display** line to make your selections.

Button	Peak information
Name	Showing/hiding peak names
Pos.	Showing/hiding peak position
Ampl.	Showing/hiding peak amplitude
Width	Showing/hiding peak full width at half maximum
Integral	Showing/hiding peak integrals

➪ If three categories of peak information are already displayed, you have to deselect one of the categories to select another one.

➪ You can set additional peak information on the **Peak info** subtask card in the **Display Parameters** dialog window.
→ Page C.4–7, *Showing peak information*

Hiding the peak information of individual peaks

You can selectively hide the peak information of less relevant peaks for more clarity of the spectral display.

☐ Cr2

✧ Deselect the checkboxes of the peaks for which you do not want to display the peak information.

Hiding the fit curve

You can hide the red curve of the theoretical spectrum.

Hide fit

✧ Click **Hide fit**.

The fit curve is hidden.

The curve fit is still calculated. You can therefore display the peak information.

✧ To display the fit curve, click **Hide fit** again.

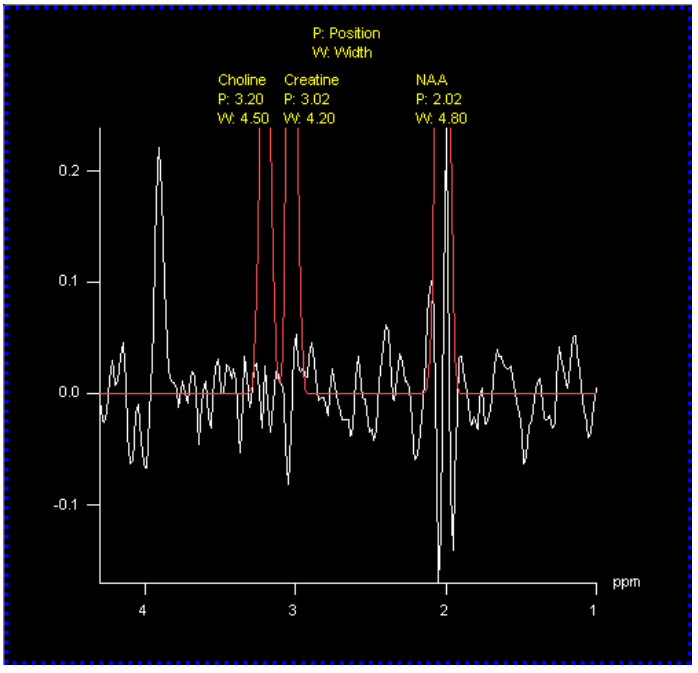
Subtracting the theoretical spectrum

You can subtract the theoretical spectrum from the measured spectrum to check how well they match. In case of a good match, only the background noise should be visible.



✧ Click **Subtract fit**.

The spectral display is updated.



✧ To display the spectrum without subtraction, deselect **Subtract fit**.

Automatic curve fitting

During automatic curve fitting, the theoretical spectrum is fitted to the measured spectrum through a series of iterations. The **Peak position**, **Amplitude**, and **Full width at half maximum** parameters are changed iteratively to optimize the **Fit error**.

Proceed as follows:

❏ Selecting and activating the **Curve fitting** post-processing step
→ Page C.8–47

❏ Setting the calculation range
→ Page C.8–48

❏ Setting parameters for automatic curve fitting

❏ Starting automatic curve fitting

❏ Showing peak information
→ Page C.8–52

❏ Hiding the peak information of individual peaks (optional)
→ Page C.8–52

❏ Hiding the fit curve (optional)
→ Page C.8–52

❏ Subtracting the theoretical spectrum from the measured spectrum (optional)
→ Page C.8–53

Keep voxel specific option

When evaluating CSI data you can retain the voxel-specific parameter settings.
→ Page C.8–48, *Keep voxel specific option*



✧ Click **Keep voxel specific** on or off.

Setting automatic curve fitting



✧ Enter the number of **iterations** (maximum 100) in the Iterations field.



✧ Enter the value by which the peak position should change with each iteration in the **Delta position** field.



✧ Enter the percentage by which the peak amplitudes should change with each iteration in the **Delta ampl.** field.



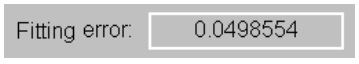
✧ Enter the value by which the full width at half maximum should change with each iteration in the **Delta width** field.

Starting automatic curve fitting



✧ Click on **Auto**.

Automatic curve fitting is performed. The spectrum is updated based on the curve fit. The new peak parameters are displayed in the peak list.

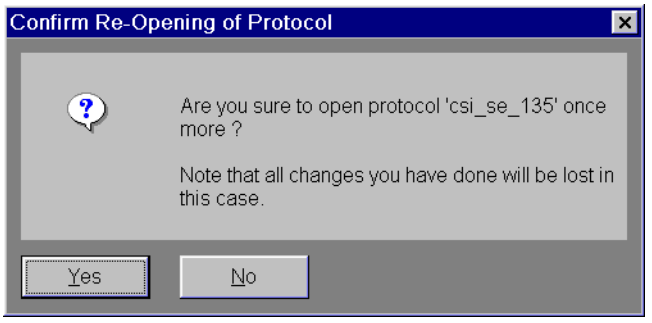


The fitting error is shown in the **Fitting error** field. It is equivalent to the sum of least squares.

Opening the original protocol version

If you have changed the current post-processing protocol during an interactive evaluation, but the results are not satisfactory, you can reapply the original saved version of the current post-processing protocol to the raw data in the active spectral segment. Any changes made to the current post-processing protocol (i.e., the spectrum) during interactive evaluation are lost.

✧ Select **Protocols > Re-Open**.



✧ Click **Yes**.

The spectrum in the active spectral segment is updated.

CHAPTER C.9

Editing Peaks and Peak Lists

Quite frequently, you will interpret spectra that contain a large number of peaks. You can edit these peaks using the **Peak Editor**, a specialized tool on the **Spectroscopy** task card. You can edit or generate the peaks of individual metabolites.

The **Peak Editor** provides a variety of peak templates which can be applied or used to create customized templates.

The system includes Siemens peak templates which can be selected from the Siemens list of peak templates. In addition to the Siemens list, you can save and select user-defined peak templates from a customer list.

Modified or newly created peaks are copied to the peak lists for **Curve fitting** and **Phase correction** as part of the interactive evaluation.

→ Page C.8–32, *Adjusting phase correction*
→ Page C.8–46, *Adjusting curve fitting*

Editing peaks

During interactive evaluation, you selected a peak in one of the two peak lists (phase correction or curve fitting) and want to view and edit the corresponding parameters.

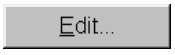
Proceed as follows:

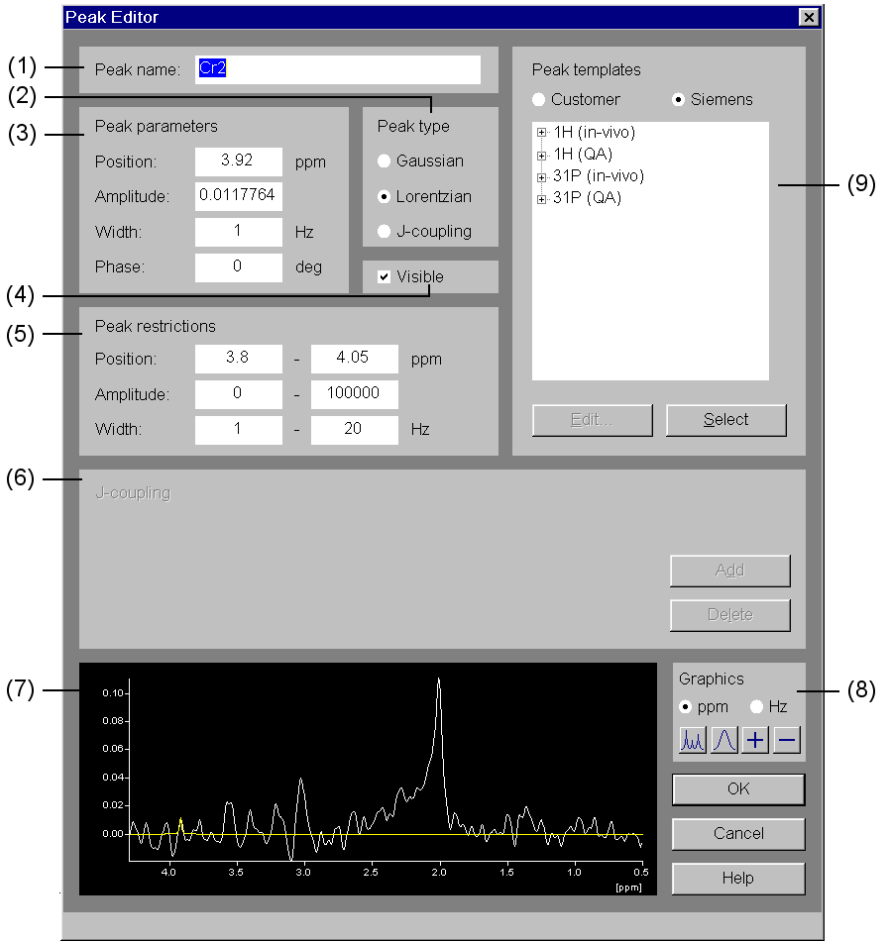
- ❏ Displaying the **Peak Editor**
- ❏ Adjusting the graphic display (optional)
- ❏ Changing the peak settings
- ❏ Applying the settings

Displaying the Peak Editor

Display the **Peak Editor** to edit the selected peak.

- ✧ Double-click the peak.
  - Or -
  Click **Edit** (for curve fit only).

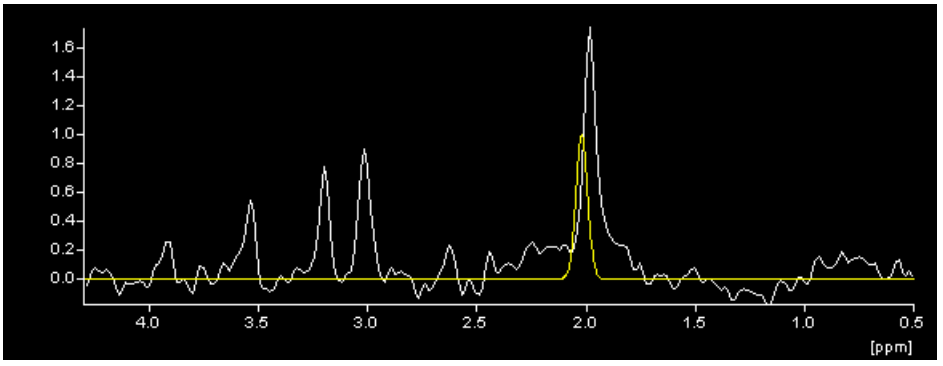




(1) Name of the peak
(2) Curve type of the peak
(3) Peak parameter
(4) Display/hide peak information
(5) Restrictions for the curve fit
(6) J-coupling parameters
(7) Graphic display for curve fitting
(8) Establishing the graphic display
(9) List of peak templates

Adjusting the graphic display

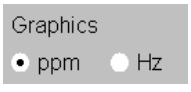
The selected peak (yellow curve) and measured signal curve (white curve) are displayed in the graphic window of the Peak Editor across the entire frequency range.



To optimize graphics display, you can:

❏ Change the frequency range unit
❏ Change the frequency and amplitude range displayed
❏ Hide the signal or peak curve

Changing the frequency range unit



You can display the frequency range in the unit “**p**arts **p**er **m**illion” or Hertz.

✧ Select an option under **Graphics**.

The graphic display is updated.

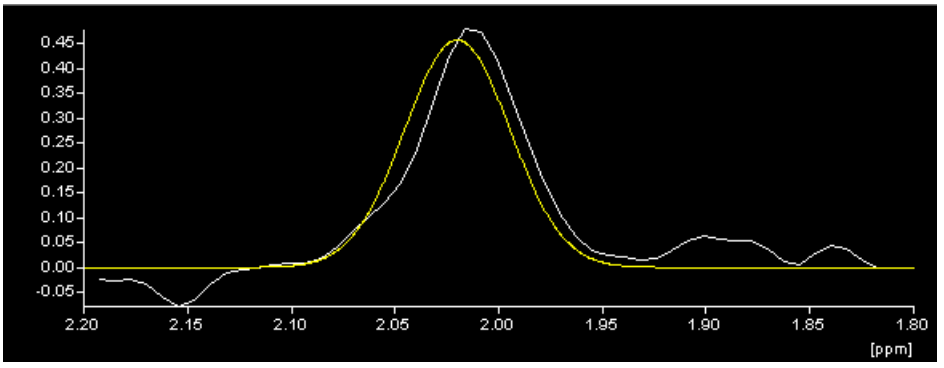
Limiting the frequency range to the peak



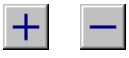
When editing the selected peak, it may be useful to limit the frequency range displayed to the selected peak.

✧ Click this button.

The graphic display is updated.



Expanding/reducing the frequency range



You can expand / reduce the displayed frequency range step-by-step.

✧ Click the **Plus** (**Minus**) button to reduce (expand) the frequency range displayed.

Displaying the complete frequency range



How to undo a limitation in the displayed frequency range:

✧ Click this button.

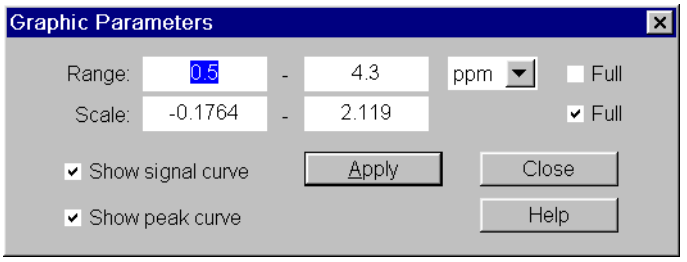
The entire frequency range of the signal curve is displayed.

Setting the frequency range numerically

You can also set the frequency range numerically, instead of with the buttons.

✧ *Right-click* inside the graphic window.

The **Graphic Parameters** dialog window opens.



✧ Select the unit for the frequency range (ppm or Hz) in the selection list of the line **Range**.

✧ Enter a minimum and maximum threshold for the frequency range in the **Range** input fields.

Or

✧ To display the entire frequency range, click the **Full** checkbox in the line **Range**.

The graphic window display is updated after you switch to a different input field or click the **Apply** button.

If both the peak and the signal curve are displayed while the **Full** option is selected, the scaling of the frequency range is determined by the maxima of the two curves.

Setting the amplitude range numerically

In the **Graphic parameters** dialog window, you can also numerically set the amplitude range to be displayed in the graphic.
→ Page C.9–6



✧ Enter a minimum and maximum threshold for the amplitude range in the **Scale** fields.

Or

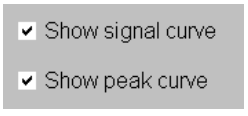
✧ To display the entire amplitude range, click the **Full** checkbox in the line **Scale**.

The graphic window display is updated after you switch to a different input field or click the **Apply** button.

If both the peak and the signal curve are displayed while the **Full** option is selected, the scaling of the amplitude range is determined by the maxima of the two curves.

Hiding the signal or peak curve

In the **Graphic Parameter** dialog window you can also establish whether the signal curve and peak curve should be displayed or hidden.
→ Page C.9–6



✧ To display (hide) the signal curve, activate (deactivate) **Show signal curve** check box.

✧ To display (hide) the peak curve, activate (deactivate) **Show peak curve** check box.

Changing the peak settings

The settings for the selected peak in the **Peak Editor** are grouped in logical sections.

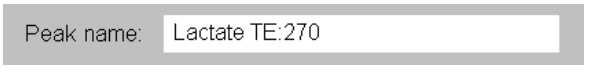
You can change the following peak settings.

- ❏ Name of the peak
- ❏ Peak parameter
- ❏ Thresholds for fitting
- ❏ Display of peak information
- ❏ Peak type

For peak type **J-Coupling** you can also:

- ❏ Edit the peaks of a multiplet
- ❏ Add a new component to a multiplet
- ❏ Delete a peak from a multiplet

Changing the peak name



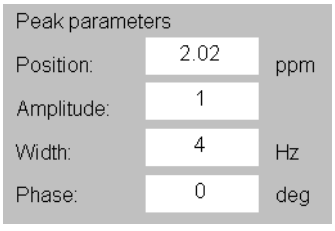
✧ Enter the new name for the peak in the **Peak name** field.

The name of the peak is overwritten while the parameter values are retained.

Changing peak parameters

A peak is defined by the following parameters:

Parameters	Description
Position	Chemical shift of the peak in [ppm]
Amplitude	Peak amplitude
Width	Full width at half maximum of the peak in [Hz]
Phase	Phase of the peak in degrees (arithmetic sign changes at 180°)



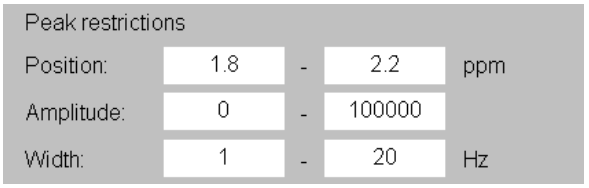
✧ If necessary, change the parameters by entering new values in the corresponding fields.

The graphic window display is updated after you leave the current input field.

Changing the thresholds for fitting

To fit the theoretical spectrum to the measured spectrum, you have to define thresholds for the **Position**, **Amplitude**, and **Width** peak parameters. Within these thresholds, the parameters may be changed during the course of the curve fit.

Parameters	Description
Position	Upper and lower threshold limits for the chemical shift of the peak in [ppm]
Amplitude	Upper and lower threshold limits for the amplitude
Width	Upper and lower threshold limits for the full width at half maximum of the peak, in [Hz]



✧ Enter the thresholds desired in the corresponding fields.

The graphic window display is updated after you leave the current input field.

Display/hide peak information

How to establish whether the peak information regarding the current peak should be displayed in the theoretical spectrum:

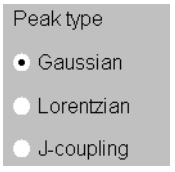


✧ Select or deselect the **Visible** checkbox.

Changing the peak type

The **Peak type** option lets you determine the shape of the peak. The following options are available:

Option	Description
Gaussian	The peak curve is displayed as a Gaussian curve.
Lorentzian	The peak curve is displayed as a Lorentzian curve.
J coupling	The peak curve is displayed as a multiplet (at least doublet).

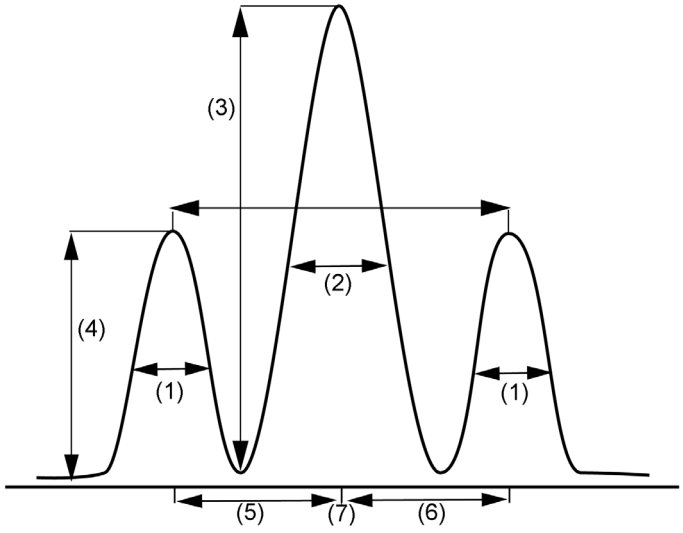


✧ Select the desired option.

➪ If you have selected the **J-coupling** peak type, you have to set the parameters for the individual components of the multiplet using the **J-coupling** input field.

Editing the peaks of a multiplet

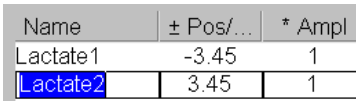
You edit a peak list entry defined as a multiplet (**J-coupling** option selected). In this case, the settings in the **Peak parameters** field apply to the complete multiplet. The parameters for the individual peaks are listed in the **J-coupling** field. The following figure illustrates certain parameters:



(1) Width factor of edge peak (factor 0.1)
(2) Width factor of center peak (factor 0.15)
(3) Amplitude of multiplet (factor 1)
(4) Amplitude factor of edge peak (factor 0.5)
(5) Delta position (plus)
(6) Delta position (minus)
(7) Position of the entire multiplet

You can change the following parameters for the individual peaks:

Parameters	Description
Name	Name of the peak
± Pos/Hz	Distance of the peak from the position of the entire multiplet
Ampl.	Amplitude factor based on the amplitude of the entire multiplet
Width	Width factor based on the width of the entire multiplet
± Phase	Delta phase based on the phase of the entire multiplet
Type	Curve type of the peak (Gaussian or Lorentz)



✧ Click the entry you want to edit.

The line is marked blue in the list.

✧ Click the entry again.

The entry is now selected and can be modified.

✧ Enter the required value.

➪ Press **Tab** on your keyboard to move to the next input field.

✧ Press the **Enter** key to complete the editing for the peak.
- Or -
Select a different peak.

The new settings are applied.

Adding a peak to a multiplet



If you want to create a new multiplet or expand an existing one, you can add a new peak. For example, a doublet now becomes a triplet.

✧ Click **Add** in the **J-coupling** input field.

A new entry is created. You can then set the individual parameters.
→ Page C.9–11, *Editing the peaks of a multiplet*

Deleting a peak from a multiplet



Peaks no longer needed can be deleted from the multiplet.

✧ Select the peak from the list in the **J-coupling** input field.

✧ Click **Delete**.
- Or -
Press the **Del** key.

Applying the settings

You can apply the changes after editing a peak.

✧ Click **OK**.

The new settings are applied and the **Peak Editor** is closed.

➪ Click **Cancel** to abort the peak modification at any time. The **Peak Editor** is closed without applying the changes.

Adding a peak template to the peak list

As part of the interactive evaluation, you are going to perform phase correction or curve fitting and would like to add a peak from the peak templates to the peak list.

➪ As an alternative to using a peak template, you can define a peak using the **Peak Editor** and add it to the peak list.

Displaying the peak editor



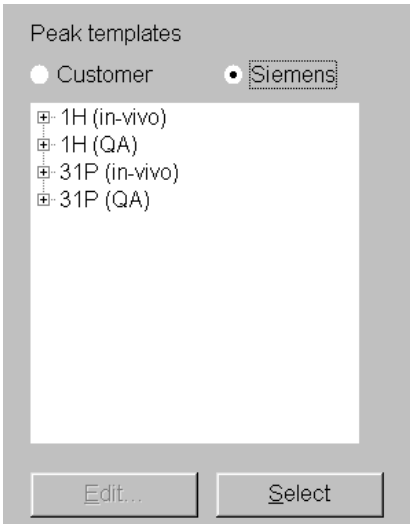
✧ In the **Interactive Postprocessing** dialog window, click **Add** (for phase correction) or **Add...** (for curve fitting).

The **Peak Editor** opens.
→ Page C.9–3

Selecting a peak template

In both the Siemens and the customer lists, the peak templates are arranged in corresponding directories according to nucleus (**1H** or **31P**) and purpose (**in vivo** or **QA**).

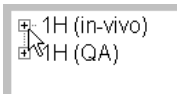
➪ During software installation, the same peak templates are created in the customer list as in the Siemens list.



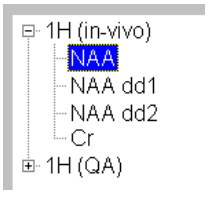
✧ Select the **Siemens** option to select a peak template from the Siemens list.

Or

✧ Select the **Customer** option to select a peak template from the customer list.



✧ Click the Plus sign to open the directory.



✧ Select a peak template in the directory.



✧ Click **Select**.
- Or -
Double-click on the peak template.

Adding a peak to the peak list

You have selected a peak template in the **Peak Editor** and have verified the peak settings. Next, you want to add the peak template to the peak list for phase correction or curve fitting.

✧ Click **OK**.

The peak is added to the peak list for phase correction (in alphabetical order) or added to the end of the peak list (for curve fitting).

Creating peak templates

For frequently used peaks not included with the peak templates provided by Siemens, you can create your own peak templates.

Proceed as follows:

❏ Open the **Edit customer peak templates** dialog window
❏ Creating a new directory (optional)
❏ Creating a new peak template
❏ Applying the settings

Opening the dialog window

✧ Open the **Peak Editor**.
→ Page C.9–2

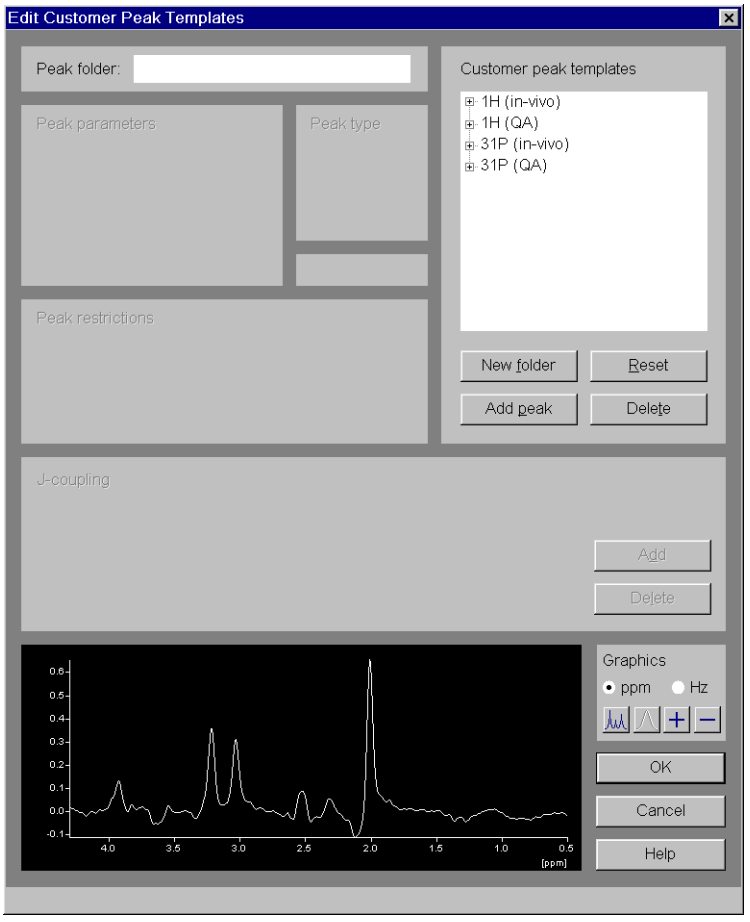


✧ Select the **Customer** option under **Peak templates** in the **Peak Editor.**



✧ Click **Edit**.

The **Peak Editor** becomes the **Edit customer peak templates** dialog window.



Creating a new directory

The directories and peak templates of the customer list are displayed in the **Customer peak templates** field.

How to create a new directory

✧ Mark the folder after which you want to create the new folder.



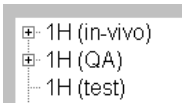
✧ Click **New folder**.

The new directory is named **<New folder X>** by default.



✧ Enter a name for the new directory in the **Peak folder** field.

The name is applied as soon as you exit the input field.



Creating a new peak template

New peak templates are created in one of the directories of the customer list.

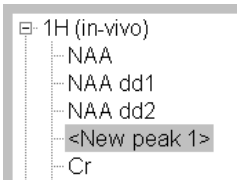
✧ Open the directory where you want to add a new peak template.

✧ Mark the peak template (or folder) after which the new peak template should be added.



✧ Click **Add peak**.

The new peak is named **<New peak X>** by default.





✧ Enter a name for the new peak template in the **Peak name** field.

The name is applied as soon as you exit the input field.

✧ Make the selections for the peak as required.
→ Page C.9–2, *Editing peaks*

➪ You can click the **Reset** button to reset the customer list to the point before you opened the **Edit Customer Peak Templates** dialog window.

Applying the settings

✧ Click **OK**.

The **Edit Customer Peak Templates** dialog window is closed.

➪ Click **Cancel** to abort the customer list modification at any time. Previous changes to the customer list are *discarded*.

Managing the customer list

Entries in the customer list (directories and peak templates) can be renamed, moved, copied, deleted, and sorted.

✧ How to show the **Edit Customer Peak Templates** dialog window.
→ Page C.9–16

Renaming a list entry

How to rename a directory or peak template

✧ Select the list entry that you want to rename.

✧ Overwrite the existing name in the **Peak Folder** or **Peak Name** field with the new name.

Moving a list entry

You can move selected peak templates or complete peak template directories in the customer list.

✧ Drag the object to the desired position in the customer list with the mouse.

Copying a list entry

You can copy selected peak templates or complete peak template directories into the customer list:

✧ Drag the object with the mouse while pressing the **Ctrl** key to the desired position in the customer list.

Deleting a list entry

You can delete selected peak templates or complete peak template directories in the customer list:

✧ Select the list entry that you want to delete.

✧ Click **Delete**.
- Or -
Press **Del.**

Sorting directories

How to alphabetically sort directories within the customer list:

✧ Select a directory in the customer list.

✧ Select **Sort** from the context menu.

Sorting peak templates

How to alphabetically sort peak templates within a directory of the customer list:

✧ Select a peak template in the desired directory.

✧ Select **Sort** from the context menu.

Applying the changes

After editing the customer list, you can apply your changes.

✧ Click **OK**.

The **Edit Customer Peak Templates** dialog window is closed.

➪ Click **Cancel** to abort the customer list modification at any time. Previous changes to the customer list are *discarded*.

CHAPTER C.10

Saving and Documenting Results

Following the evaluation, you can save the results (spectra, result tables, spectral map, metabolite images) as images in the database. Image text and miniature reference images (for spectra and result tables) are saved as well.

In addition or alternatively, you can save the corresponding reference images in regular size including graphic objects (VOI, CSI matrix grid).

For documentation purposes, you can send the results and reference images to a camera or printer. Prior to that, you may want to check the result and reference images using the **Viewing** task card.

Saving results and reference images

The selected data are stored in the database under the patient and series associated with the raw data.

The image type generated varies depending on the type of data to be saved. Explanation of image types:

- Image type **MR**
  Medical MRI image (with a fixed pixel format and possibly overlaid graphics)
- Image type **SC**
  Secondary **C**apture images are independent of modality. In contrast to MRI images, the pixel format does not have a fixed definition. The images do not have scale or orientation marks.

Data to be saved	Resulting image type
Reference image	MR
Spectrum	SC
Result table	SC
Spectral map	MR
Metabolite color image	SC
Metabolite grayscale image	MR
Sum spectrum	SC

Proceed as follows:

❏ Selecting the result or reference image
❏ Open the **Save data** dialog window
❏ Selecting a save option
❏ Confirming the save

Select the result

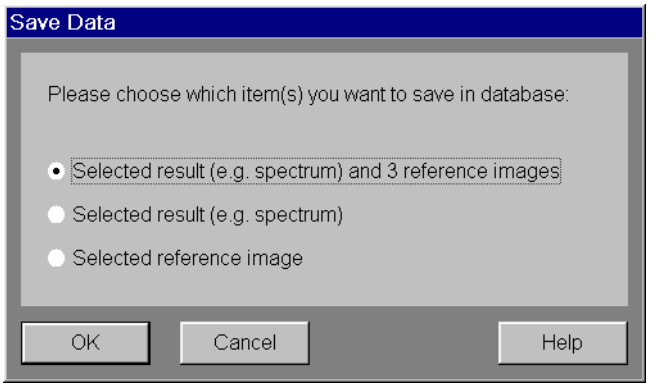
✧ Select the result or reference image to be saved in the **Spectroscopy** task card.

Opening the dialog window



✧ Select **Patient > Save Data**.
- Or -
Click the button in the control area.

The **Save Data** dialog window opens.



Select option

✧ Select the desired save option.

! If the current result has already been saved, the **Selected result (e.g. spectrum)** option is deactivated. In this case, if you select the **Selected result (e.g. spectrum) and 3 reference images** option, only the three reference images will be saved.

Confirming selection

✧ Click **OK**.

The selected data are saved as images in the database.

Loading stored images in the Viewer

After saving a result or reference image, you can view it in the **Viewing** task card.

Proceed as follows:
❏ Displaying the **Patient Browser**
❏ Selecting data
❏ Loading data into the **Viewing** task card

Displaying the Patient Browser

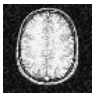
✧ Select **Patient > Browser**.

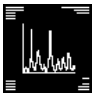
Selecting data

✧ Select a patient in the navigation area of the **Patient Browser**.

The content area of the **Patient Browser** displays the data saved for the selected patient.

Reference images and spectroscopy measurement results are indicated by the following symbols (if symbol display is activated):


(1)


(2)


(3)


(4)


(5)

(1) Reference image(s)
(2) Individual or sum spectrum
(3) Result table
(4) Spectral map
(5) Metabolite image

Loading data into the Viewing task card

✧ Select the result or reference images to be displayed in the **Viewing** task card.

➪ Pressing the **Ctrl** or **Shift** key on your keyboard allows you to select multiple data sets.

✧ Select **Patient > Load images to viewer**.
- Or -
Click this button.



The selected data is loaded into the **Viewing** task card.

Filming and printing results and reference images

Results and reference images may be sent to the virtual film sheet for documentation purposes.

Proceed as follows:

❏ Selecting the result or reference image
❏ Open the **Copy to film sheet** dialog window
❏ Selecting filming/printing options
❏ Confirming the copy to film sheet operation

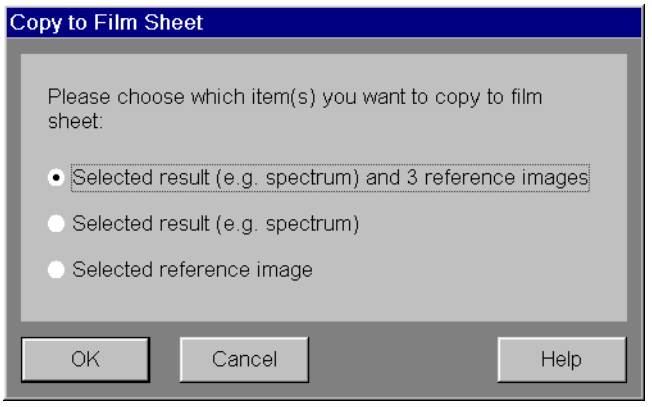
Select the result

✧ Select the result or reference image to be filmed or printed in the **Spectroscopy** task card.

Opening the dialog window

✧ Select **Patient > Copy to Film Sheet**.

The **Copy to Film Sheet** dialog window is displayed.



Selecting an option

✧ Select the desired filming/printing option.

Confirming selection

✧ Click **OK**.

The selected data are copied to the virtual film sheet.

Further steps

If the **Auto Expose** option is selected in the **Filming** task card, the selection is filmed or printed immediately.

If the **Auto Expose** option is *not* selected, you can switch to the **Filming** task card or start the film preview to send your selection to the camera or printer.

➪ Colored metabolite images can be filmed using a Kodonix film camera.

➪ A color printer can be used for hardcopy printouts.

CHAPTER C.11

Managing Post-processing Protocols

Your system includes a set of post-processing protocols developed by SIEMENS. The evaluation functions of these protocols have been optimized based on tests with volunteers.

The **Protocol Browser** is available for opening, saving, deleting, and exporting protocols stored in the database.

S

- **Siemens protocols** cannot be overwritten. Siemens protocols can be identified by a blue “S” in the list of post-processing protocols.

In addition, you can create your own post-processing protocols. These are usually based on existing post-processing protocols (including Siemens protocols) and adapted as necessary.

C

- These **Customer Protocols** can be modified, overwritten, or deleted as necessary. They can be identified by a yellow “C” in the list of post-processing protocols.

Directories

The directories displayed in the **Protocol Browser** are named by system type (e.g., **1.5 T**), their subdirectories by nucleus type (e.g., **1H**). You store the individual post-processing protocols in these directories.

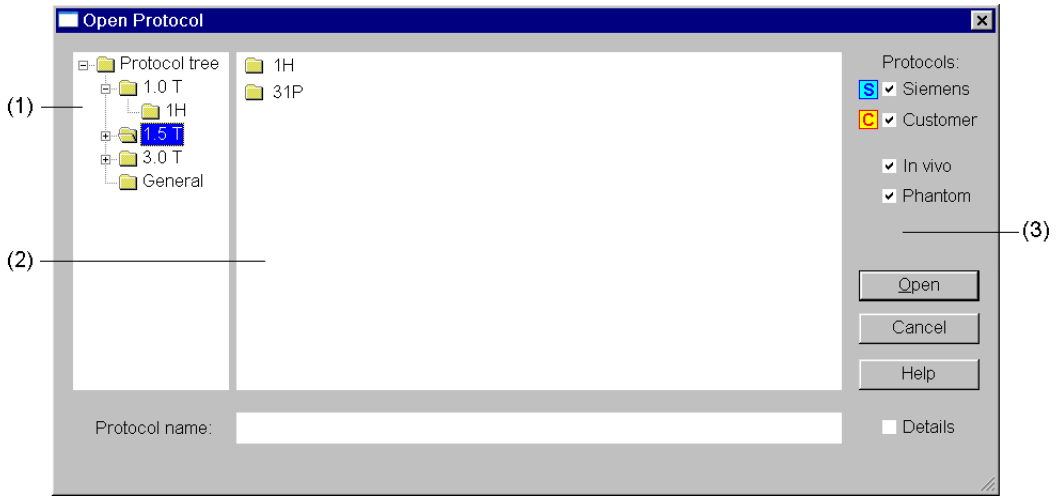
- Non-system or nuclear type-specific post-processing protocols are stored in the **General** directory.

The Protocol Browser

The **Protocol Browser** enables you to access protocols already stored in the database.

The **Protocol Browser** can be accessed via the respective dialog window for opening, saving, exporting, or deleting protocols.

Example: View of the **Protocol Browser** under **Open Protocol**.



(1) Navigation area
(2) Content area
(3) Control Area

Changing the display of the browser window

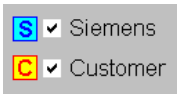
You can adjust the display of the browser window:

- ❏ Enlarge or reduce and move the browser window
- ❏ Move the dividing line between the navigation and content areas
- ❏ Vary the column width in the content area (detail display only)

➪ Use is similar to Windows Explorer.

Setting the display of the protocol list

You can show or hide protocol types and properties to adjust the amount of information displayed in the content area of the **Protocol Browser**.



✧ Deselect the **Siemens** or **Customer** checkbox.

The Siemens or customer protocols are hidden.

➪ You can only hide one of the protocol types at a time.



✧ Deselect the **In vivo** or **Phantom** checkbox.

The post-processing protocols for evaluating in-vivo measurement data or for quality assurance are hidden.

➪ You can only hide one of the protocol types at a time.

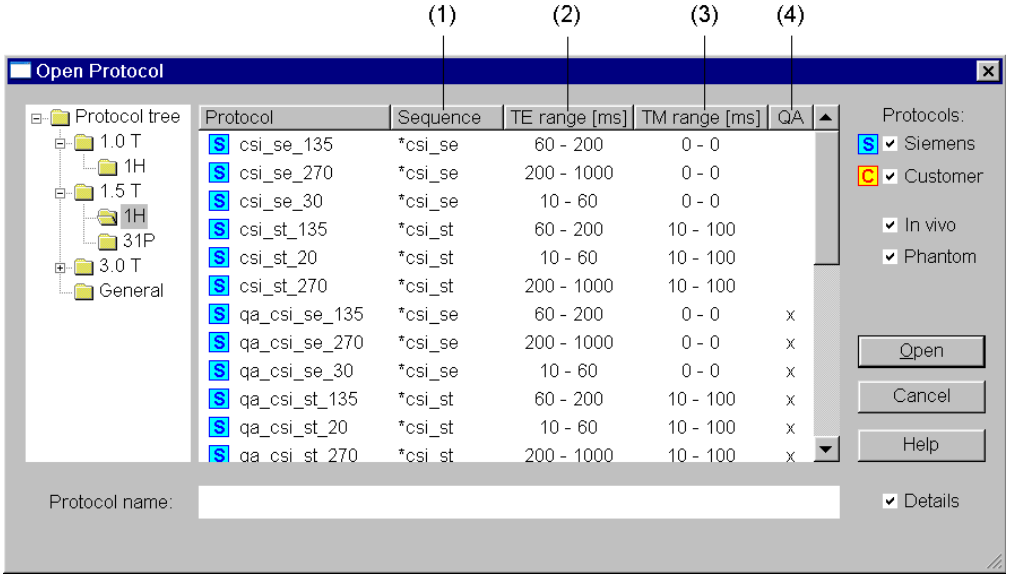


✧ Select or deselect the **Details** checkbox.

The properties of the post-processing protocols next to the protocol names are shown/hidden.

➪ The display settings for the protocol list remain in effect after the **Protocol Browser** is closed.

Example: Protocol list display in the **Open Protocol** dialog window when all protocol types and protocol properties are shown.



(1) Sequence suitable for the protocol
(2) TE range suitable for the protocol
(3) TM range suitable for the protocol
(4) Purpose of the protocol (x in the QA column identifies post-processing protocols used for quality assurance)

Modifying a post-processing protocol

You can use Siemens protocols as a template for creating your own protocols, and save them as new customer protocols. Customer protocols can be modified as desired.

Proceed as follows:

❏ Opening the post-processing protocol

❏ Changing the number and sequence of post-processing steps (optional, → Page C.8–2)

❏ Changing the parameters of post-processing steps (optional,→ Page C.8–5)

❏ Change the properties of the post-processing protocol (optional)

❏ Saving the post-processing protocol

Opening the post-processing protocol

To modify a post-processing protocol, you have to open it, that means use it on actual raw data.

✧ Select **Protocols > Open**.

The **Open Protocol** dialog window opens.

✧ Switch to the protocol directory containing the corresponding post-processing protocol.

✧ Select the protocol from the list.



✧ Click **Open**.
- Or -
Double-click the desired protocol.

The post-processing protocol is opened. The **Open Protocol** dialog window closes.

! If the selected spectral segment contains a spectrum, the corresponding raw data are re-evaluated using the current post-processing protocol. The spectral display is updated.

If a post-processing protocol has already been opened and modified in the current spectral segment, opening a new post-processing protocol will display a message window. Here, you decide how to proceed:

- ❏ Save changes (**Yes** button)
- ❏ Cancel changes (**No** button)
- ❏ Do *not* open a new post-processing protocol (**Cancel** button)

Modifying properties

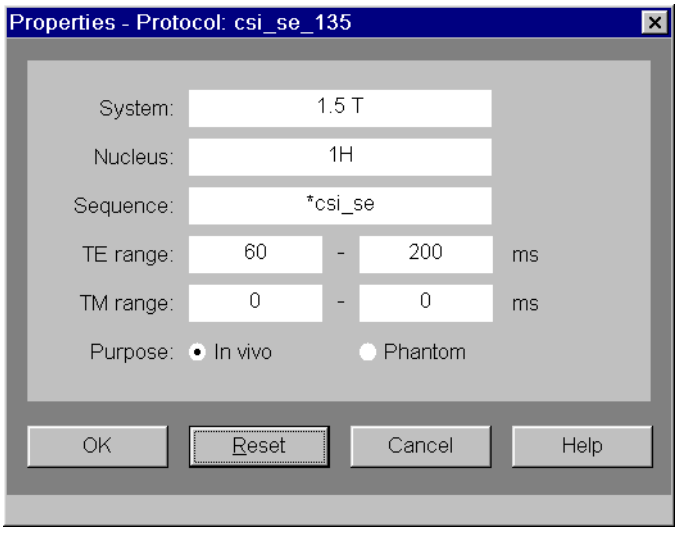
When loading raw data, the protocol properties are used to find the correct post-processing protocol.
→ Page C.2–2, *Loading raw data*

You can change the properties of the selected post-processing protocol in the **Properties** dialog window.

Opening the dialog window

✧ Select **Protocols > Properties**.

The **Properties** dialog window opens.



Property	Description
System	Magnetic field strength of the system (**1.0 T, 1.5 T**, or **3.0 T**)
Nucleus	Identified the nucleus type (**1H** or **31P**)
Sequence	Sequence name
TE range	Limits for echo time
TM range	Limits for mixing time
Purpose	**in vivo** for the evaluation of in-vivo measurement data, or **Phantom** for the evaluation of quality assurance measurement data

Defining properties

✧ Enter the properties in the input fields.

✧ Select the corresponding Purpose option.

Applying the changes

✧ Click **OK**.

➪ If you do not want to accept the changes, click the **Reset** button to restore the status prior to opening the dialog window. Click the **Cancel** button to close **Properties** dialog window without transferring the settings to the current post-processing protocol.

Example: Linking a measurement protocol with a new evaluation protocol

If you cannot find a suitable post-processing protocol when loading raw data, you can link a customer measurement protocol to a customer post-processing protocol. The following is the procedure in brief:

✧ Select **Protocols > Properties**.

The **Properties** dialog window is displayed. The displayed parameters were generated during creation of the temporary protocol.

✧ Record the properties of the temporary protocol, including the protocol name in the header of the dialog window.

✧ Click **Cancel** to close the Properties dialog window.

✧ Open the post-processing protocol you want to use to perform the evaluation.

✧ Select the **Properties** dialog window for this protocol.

✧ Enter the recorded property parameters in the dialog window input fields.

➪ Do not overwrite the parameters for TE and TM range if the recorded values are within the range of the displayed values.

✧ Click **OK** to close the dialog window.

✧ Save the post-processing protocol under a new name. Use the recorded protocol names.

Saving the post-processing protocol

Saving customer protocols

How to save changes in a customer protocol and thereby overwrite the old version:

✧ Select **Protocols > Save**.

The **Confirm Saving of Protocol** dialog window opens.

✧ Click **Yes** to confirm.

➪ Siemens protocols cannot be overwritten.

Saving as a new customer protocol

If you want to keep an edited customer protocol in its original edition, or have edited a (write-protected) Siemens protocol, save the modified data in a new customer protocol.

✧ Select **Protocols > Save As**.

The **Save Protocol** dialog window opens.

✧ Open the protocol directory where you want to store the new customer protocol.

Or

✧ Create a new protocol directory.
→ Page C.11–11



✧ Enter a name for the post-processing protocol in the **Protocol name** field.

➪ Choose a name that identifies the spectroscopy measurement protocol and describes the purpose of the protocol.



✧ Click **Save**.

Creating a new post-processing protocol

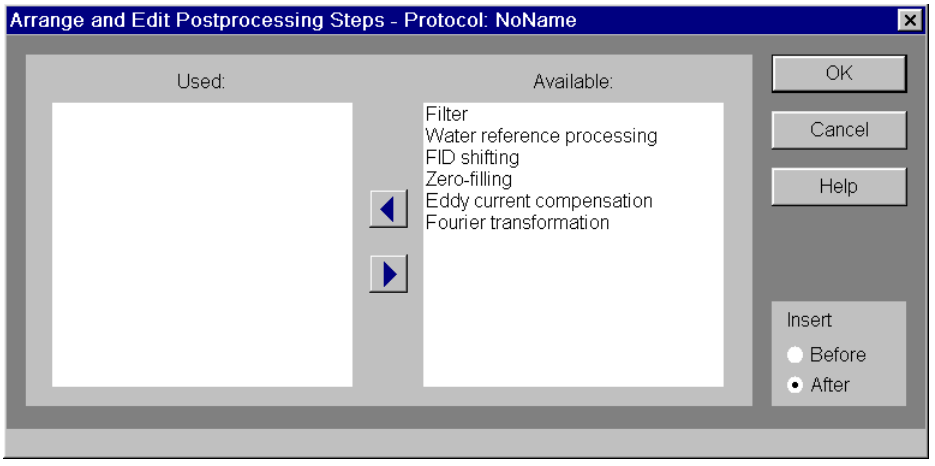
If you are unable to find a suitable post-processing protocol that you can adapt for your evaluation needs, you can create your own.

Opening an empty post-processing protocol

To create a new post-processing protocol, start by opening an empty protocol.

✧ Select **Protocols > New**.

The **Arrange and Edit Postprocessing Steps** dialog window opens.



! If the selected spectral segment contains a spectrum, the complex time signal is displayed after opening an empty post-processing protocol.

Editing the post-processing protocol

The procedure for adding and editing post-processing steps as well as setting the protocol properties is the same as for existing post-processing protocols.

✧ Add the post-processing steps for the new protocol in the desired order to the **Used** list.
→ Page C.8–2, *Arranging post-processing steps*

✧ Check and, if necessary, change the parameters of the post-processing steps.
→ Page C.8–5, *Adapting post-processing steps*

✧ Check and, if necessary, change the protocol properties.
→ Page C.11–6

Saving the post-processing protocol

A newly created post-processing protocol is added to the database as a new customer protocol.

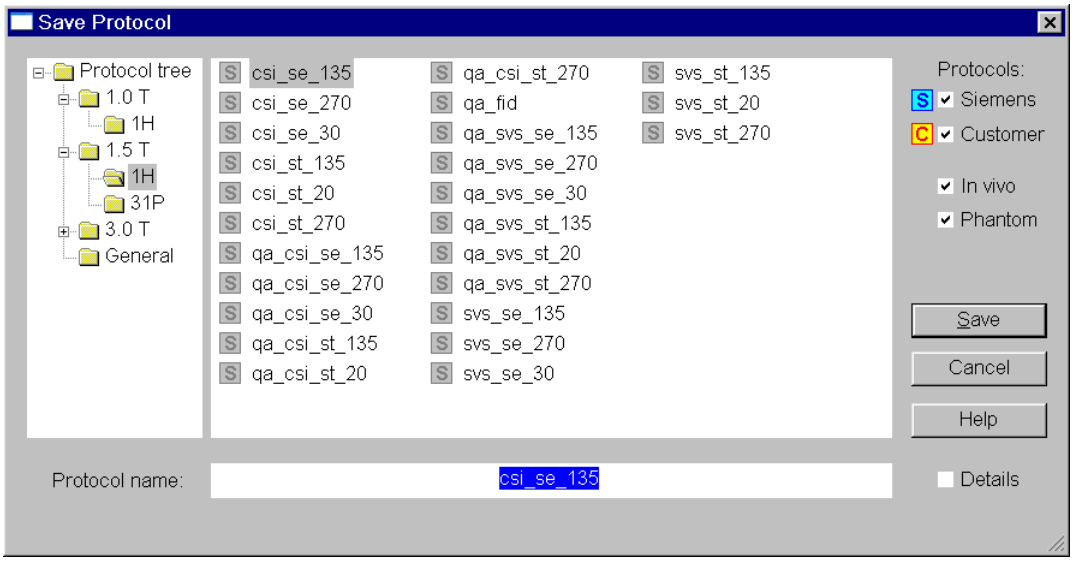
✧ Save the post-processing protocol as a new customer protocol.
→ Page C.11–8, *Saving the post-processing protocol*

Creating a new protocol directory

You can create new protocol directories within the directory structure.

✧ Select **Protocols > Save As**.

The **Save Protocol** dialog window opens.



Selecting the parent directory

New protocol directories can be created on the system type or nuclear type directory level. You have to select the parent directory first.

✧ Select the **Protocol tree** directory to create a new directory on the system type directory level.

Or

✧ Select a directory on the system type directory level to create a new directory on the type of nucleus directory level below.

Assigning a directory name



✧ Enter a name for the new protocol directory in the **Protocol name** field.

Adding the new protocol directory



✧ Click **Open**.

The new protocol directory is added to the directory structure.



The new protocol directory is initially created on a temporary basis. If you do not save a post-processing protocol in the new directory, it is removed from the directory structure.

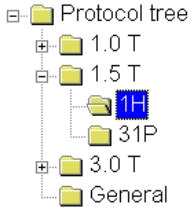
Deleting customer protocols

Customer protocols no longer needed can be deleted from the database.

✧ Select **Protocols > Delete**.

The **Delete Protocol(s)** dialog window opens.

Selecting protocols



✧ Open the protocol directory containing the post-processing protocols to be deleted.

The content area lists the customer protocols available in the selected directory.

! Siemens protocols cannot be deleted. For this reason, the list contains only customer protocols.

✧ Select the protocols from the list.

➪ Pressing the **Ctrl** or **Shift** key on your keyboard allows you to select multiple protocols.

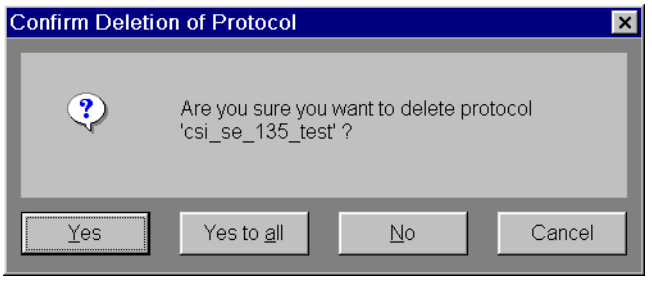
➪ Click the **Select all** button to select all customer protocols in the current directory. You can then use the **Deselect all** button to deselect all protocols.

Deleting protocols



✧ Click **Delete**.

The **Confirm Deletion of Protocol** dialog window opens.



Here, you decide how to proceed:

Button	Function
Yes	The protocol displayed in the dialog window is released for deletion.
Yes to all	All selected protocols are released for deletion.
No	The delete job for the protocol currently displayed in the dialog window is cancelled.
Cancel	The dialog window closes. None of the selected protocols are deleted, and confirmed delete jobs are not performed.

✧ Click the button for the desired function.

Exporting/importing customer protocols

The export function allows you to copy customer protocols to a removable storage device to share them with other users or use them on a different system.

The import function allows you to load customer protocols into the local database.

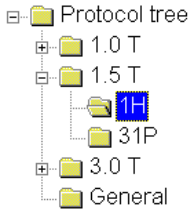
Exporting protocols

Customer protocols can be exported from the local database to a directory on your hard disk drive or to a removable media drive.

On the hard disk drive only special directories are available. These directories are the same as offered by the **File Browser**, e.g.
C:\MedCom\temp\CDR_OFF_LINE
C:\MedCom\user

✧ Select **Protocols > Export...**.

The **Export Protocol(s)** dialog window is displayed.



✧ Open the protocol directory containing the post-processing protocols to be exported.

The content area lists the customer protocols available in the selected directory.

✧ Select the protocols from the list.

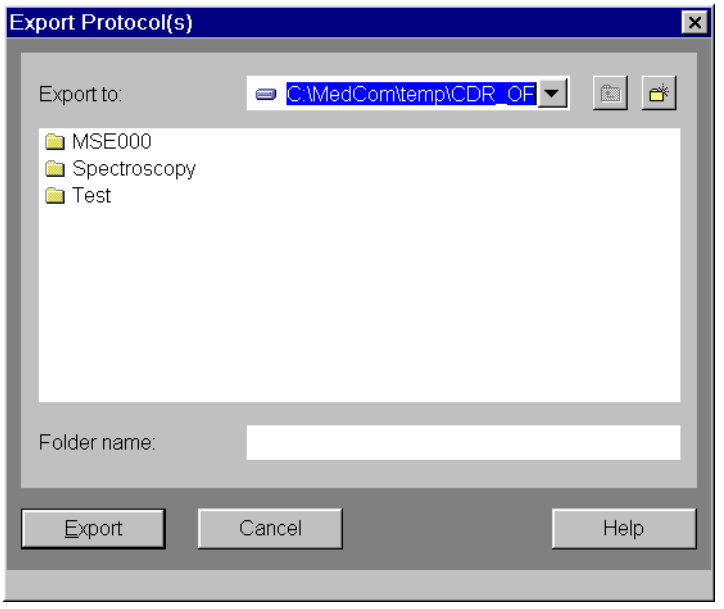
➪ Pressing the **Ctrl** or **Shift** key on your keyboard allows you to select multiple protocols.

➪ Click the **Select all** button to select all customer protocols in the current directory. You can then use the **Deselect all** button to deselect all protocols.



✧ Click **Export**.

A second **Export Protocol(s)** dialog window opens.



✧ Select the target directory from the **Export** selection list.



➪ Click this button to create a new subdirectory.



✧ Click **Export**.

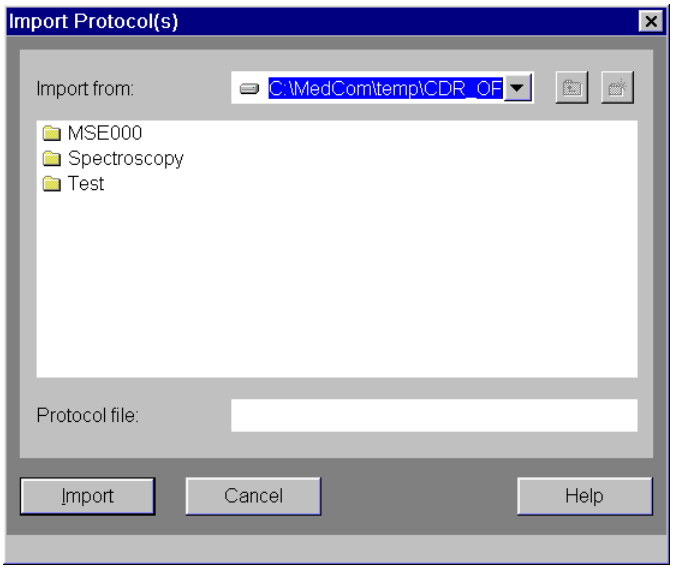
The protocols are copied to the selected directory and assigned a ".pro" file name extension.

Importing protocols

Customer protocols can be copied to the local database from a directory on your hard drive or another suitable drive.

✧ Select **Protocols > Import**.

The **Import Protocol(s)** dialog window opens.



✧ Select a directory on your hard disk drive or a removable media drive in the **Import from** selection list.

➪ On the hard disk drive only special directories are available (cf. → Page C.11–15, *Exporting protocols*).

✧ Double-click the subdirectory containing the customer protocols in the directory window.

✧ Select the protocols to be imported.

➪ Pressing the **Ctrl** or **Shift** key on your keyboard allows you to select multiple protocols.



✧ Click **Import**.

The protocols are copied to your local database.

CHAPTER
C.12 Exporting Raw Data

For evaluation with other programs, you can send the spectroscopy raw data to external computers.

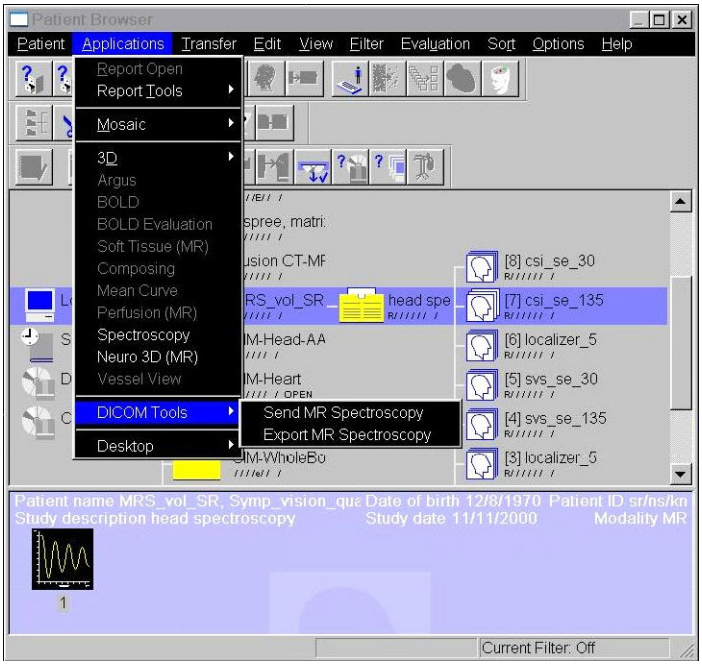
Several methods are available for the data transfer:

- ❏ Send or export raw data in DICOM format
- ❏ Export raw data to an ASCII file

Exporting Raw Data in DICOM format

Using the **DICOM Tools** function, you can send spectroscopy raw data in DICOM format to an address preconfigured on the system (DICOM node), or export them locally to a hard drive.

✧ Open the **Patient Browser**.



✧ Select the raw data from the content area.



➪ If **Icon View** is activated, the spectroscopy raw data can be identified in the **Patient Browser** by this symbol.

➪ You can export the spectroscopy raw data of a complete study or series by selecting the corresponding study or series.

✧ Select **Applications > DICOM Tools > Send MR Spectroscopy** to send the raw data.

Or

✧ Select **Applications > DICOM Tools > Export MR Spectroscopy** to export the raw data to the hard drive.

Preset target directory is:
C:\MedCom\temp\CDR_OFF_LINE\MrSpectroscopy.

Exporting Raw Data in ASCII Format

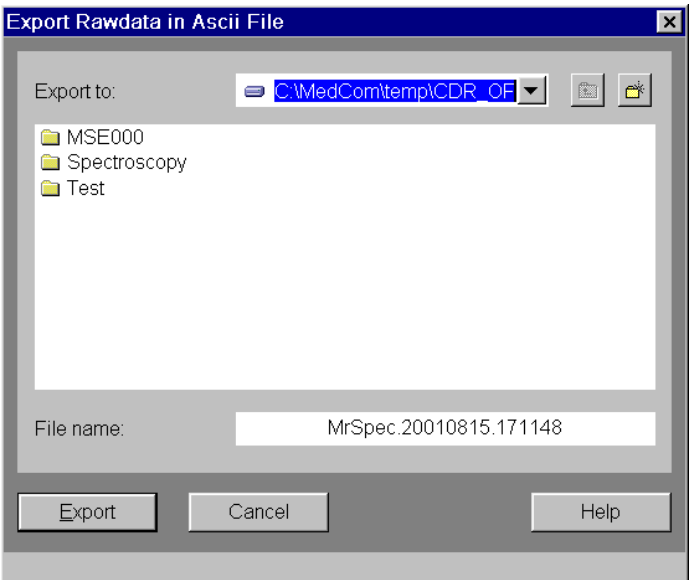
The **Export Rawdata in Ascii File** function allows you to export the current set of raw data as an ASCII file to a selectable target directory. You can also assign a name to the ASCII file.

Performing the export

✧ Select the desired data set from the **Spectroscopy** task card.

✧ Select **Options > Export raw data**.

The **Export Rawdata in Ascii File** dialog window is displayed.



➪ You can save the data to a directory of your hard disk drive or a removable media drive.
On the hard disk drive only special directories are available. These directories are the same as offered by the **File Browser**, e.g.
C:\MedCom\temp\CDR_OFF_LINE
C:\MedCom\user

✧ Select the target directory from the **Export** selection list.

➪ Only small sets of raw data, such as SVS raw data, can be exported to floppy disk.



➪ Click the button to create a new subdirectory.



✧ In the **File name** field, enter the file name desired or accept the name suggested by the system.

➪ The name suggested by the system consists of the current date and time.



✧ Click **Export**.

The raw data are exported. The exported ASCII file can be identified by the ".rda" file name extension.

Content of the ASCII file

The file created during export has a special header and data format.

Header format

The Header parameters are stored in a block of text lines between "**>>> Begin of header <<<**" and "**>>> End of header <<<**".

Every header parameter comprises a key word and corresponding value, separated by commas. There is no fixed order for the individual header parameters. Parameters can be uniquely identified only via their keywords.

The following is an example of saved header parameters:

>>> Begin of header <<<
PatientName: noname
PatientID: 12345
PatientSex: M
PatientBirthDate: 19760527
StudyDate: 20050222
StudyTime: 130106.703000
StudyDescription: prostate
PatientAge: 028Y
PatientWeight: 90.000000
SeriesDate: 20050222
SeriesTime: 133942.171000
SeriesDescription: csi3D_se_prostate
ProtocolName: csi3D_se_prostate
PatientPosition: FFS
SeriesNumber: 7
InstitutionName:
StationName: AKMRC25009
ModelName: Avanto
DeviceSerialNumber: 25009
SoftwareVersion[0]: syngo MR 2006A 4VB13A
InstanceDate: 20050222
InstanceTime: 133942.218000
InstanceNumber: 1
InstanceComments:
AcquisitionNumber: 1
SequenceName: csi_se
SequenceDescription: csi_se
TR: 700.000000
TE: 120.000000
TM: 0.000000
TI: 0.000000
DwellTime: 769
NumberOfEchoes: 1
NumberOfAverages: 6.000000
MRFrequency: 63.696549
Nucleus: 1H

MagneticFieldStrength: 1.494000
NumOfPhaseEncodingSteps: 12
FlipAngle: 90.000000
VectorSize: 512
CSIMatrixSize[0]: 16
CSIMatrixSize[1]: 16
CSIMatrixSize[2]: 16
CSIMatrixSizeOfScan[0]: 12
CSIMatrixSizeOfScan[1]: 12
CSIMatrixSizeOfScan[2]: 12
CSIGridShift[0]: 0
CSIGridShift[1]: 0
CSIGridShift[2]: 0
HammingFilter: On
HammingFilterWidth: 100
TransmitCoil: Body
TransmitRefAmplitude[1H]: 260.644000
SliceThickness: 5.000000
PositionVector[0]: -66.444089
PositionVector[1]: -67.878142
PositionVector[2]: -73.908750
RowVector[0]: 1.000000
RowVector[1]: 0.000002
RowVector[2]: 0.000146
ColumnVector[0]: 0.000000
ColumnVector[1]: 0.999945
ColumnVector[2]: -0.010471
VOIPositionSag: -26.449580
VOIPositionCor: -27.487618

VOIPositionTra: -36.823797
VOIThickness: 40.000000
VOIPhaseFOV: 35.000000
VOIReadoutFOV: 55.000000
VOINormalSag: -0.000146
VOINormalCor: 0.010471
VOINormalTra: 0.999945
VOIRotationInPlane: 0.000000
FoVHeight: 80.000000
FoVWidth: 80.000000
FoV3D: 80.000000
PercentOfRectFoV: 1.000000
NumberOfRows: 16
NumberOfColumns: 16
NumberOf3DParts: 16
PixelSpacingRow: 5.000000
PixelSpacingCol: 5.000000
PixelSpacing3D: 5.000000
WipMemoryInteger[0]:2
>>> End of header <<<

Parameters	Description
CSIMatrixSize[0] **CSIMatrixSize[1]** **CSIMatrixSize[2]**	Number of columns Number of rows 3D direction Definition of the interpolated CSI matrix size. Also corresponds to the parameters **NumberOfRows**, **NumberOfColumns**, and **NumberOf3DParts**
CSIMatrixSizeOfScan[0] **CSIMatrixSizeOfScan[1]** **CSIMatrixSizeOfScan[2]**	Definition of the matrix size used in the measurement
CSIGridShift[0] **CSIGridShift[1]** **CSIGridShift[2]**	Definition of the CSI matrix shift in % of voxel dimensions relative to the measurement matrix size

Parameters	Description
SliceThickness	Definition of slice thickness. Also corresponds to the parameter **PixelSpacing3D**
VOIPositionSag **VOIPositionCor** **VOIPositionTra**	Definition of the VOI center position
VOIThickness	Definition of VOI thickness in normal direction
VOIPhaseFOV	Definition of VOI size in phase encoding direction
VOIReadoutFOV	Definition of VOI size in readout direction
VOINormalSag **VOINormalCor** **VOINormalTra**	Definition of the VOI normal vector
VOIRotationInPlane	Definition of the VOI rotation in the slice perpendicular to the normal vector
NumberOfRows **NumberOfColumns** **NumberOf3DParts**	Definition of the interpolated CSI matrix size. Also corresponds to the parameters **CSIMatrixSize[0], CSIMatrixSize[1], CSIMatrixSize[2]**
PixelSpacing3D	Definition of slice thickness. Also corresponds to the parameter **SliceThickness**

➪ The VOI volumes for SVS and CSI measurements, as well as the size of an individual CSI voxel, may be calculated as follows:

VOI Volume **=** VOIThickness **x** VOIPhaseFoV **x** VOIReadoutFoV

Voxel Volume **=** PixelSpacingRow **x** PixelSpacingCol **x** PixelSpacing3D

Data format

The exported data are stored in binary format as complex double values (8 bytes each). They start immediately after the last line of text (“>>> End of header <<<”).

The exported data contains the complex time signals of all voxels. The dimensions of one of these data vectors are determined by the **VectorSize** parameter. It comprises 2x **VectorSize** double values, which are stored alternately as real part and imaginary part (real [1], imaginary [1], real [2], imaginary [2], ...).

The data vectors are in the sequence of the voxel numbering. To find the voxel number refer to:
→ Page C.1–9

CHAPTER C.13

Ending a Spectroscopy Evaluation

If you are finished working in the **Spectroscopy** task card or want to display a different task card, close the **Spectroscopy** task card.

✧ Select **Applications > Close Spectroscopy**.

! If the current post-processing protocol has been changed, but not yet saved, you will be prompted to save when you close the **Spectroscopy** task card. If you confirm, a copy of the modified post-processing protocol is saved. The original protocol is kept.

The copy is available for future evaluations. The name is a combination of the original name, the current date and time, the data set index, as well as the diagram index.

! When you close the **Spectroscopy** task card, unsaved spectra, result tables, spectral maps, and metabolite images are lost. However, you can easily reproduce the unsaved evaluation results by running the corresponding post-processing protocol for the raw data again.

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

Always check for unsaved data and save any data you want to keep before logging off.

CHAPTER C.14

Post-processing Protocols for ^{1}H MRS

The *in-vivo* Siemens post-processing protocols for ^{1}H MRS raw data are suitable for measurement data from healthy brain tissue. Therefore, they do *not* contain a lactate signal. The only differences are between the post-processing protocols for short echo times and those for medium and long echo times.

Short echo times

For measurements with short echo times, the quantification of coupling signals (especially Glx) is difficult.

For example, the Glx multiplets that form the left shoulder of the NAA signal at 2.02 ppm in healthy brain tissue have been entered in the post-processing protocol for precise quantification of the NAA signal and *not* for precise quantification of the Glx multiplet.

Especially in this spectral range, complete quantification of coupling signals requires that further metabolites be considered, such as GABA.

CSI measurements

Strong signals from subcutaneous fat in the range of 1.3 ppm to 0.7 ppm are to be expected in the outer regions of the brain during CSI measurements with short echo times.

Please note that, similar to water signals, the intensity of fat signals is several thousand times greater than the signal intensity of metabolites. However, contrary to water signals, fat signals *cannot* be suppressed by frequency-selective pulses, as this would also suppress the signals of many metabolites. Therefore, use the spatial selection mechanism of the CSI protocols to reduce interference from fat signals.

A

Absorption signal C.8–32
Acquisitions A.1–16
Adapter B.3–8
Adapting the measurement parameters
  For CSI measurement B.8–1, B.8–18
  For SVS measurement B.7–1, B.7–10
  VOI for SVS measurement B.7–1
Adenosine triphosphate (ATP) A.1–23
Adjusting the signal display C.4–2
Adjustment
  Adjusting water suppression B.9–3
  Adjustment modes B.11–1
  Automatic adjustment with control B.11–2
  Checking results B.11–3
  Manual adjustment B.11–3
Adjustment parameters
  Checking B.9–1
Adjustment volume
  For 31P MRS QA measurements B.12–11
  Setting B.9–4
Alanine (Ala) A.1–22
Aliasing artifacts A.2–6
Amplitude range
  Setting in the peak editor C.9–7
Apodization A.2–18
Automatic adjustment
  Checking adjustment parameters B.9–1
  Set the adjustment volume B.9–4
  Water suppression adjustment B.9–3
Averages
  Adjusting for interactive evaluation C.8–16
Averaging A.1–16

B

Baseline correction
  Adjusting for interactive evaluation C.8–26
  Checking the baseline C.8–31

C

Changing the size
  Adapting the VOI position graphically (SVS) B.7–4
  Adjusting the size of the VOI numerically (2D CSI) B.8–10
  Adjusting the size of the VOI numerically (3D CSI) B.8–15
  Enlarging the spectrum of a voxel C.7–12, C.7–20
  Fitting the metabolite image to the segment size C.7–23
  Fitting the reference image to the segment size C.3–5
  Fitting the spectral map to the segment size C.7–23
  Resizing the VOI numerically (SVS) B.7–8
  Zooming reference image C.3–4
Characteristic values of MRS signals A.1–19
Characteristics of a Peak A.1–8
Checking
  Baseline (Baseline correction) C.8–31
  Changed post-processing steps C.8–7
  Filter function C.8–12
  Water signal (water reference processing) C.8–18
Chemical shift
  At 3 T A.1–26
  Basics A.1–4, A.1–9
  Dependence on the magnetic field strength A.1–9
Chemical shift artifact A.1–27, A.2–22
Chemical shift imaging (CSI) A.2–6
CHESS water suppression A.2–3
Choline (Cho) A.1–20
Citrate A.1–22

Closing
Data set C.2–9
Task card C.13–1
Coil cushion B.3–7
Coils B.3–2, B.3–5, B.3–7
Combine
Metabolites for the result table C.6–5
Comments
Adding and governing comments in the spectrum C.4–10
Contamination A.2–15, A.2–16
Contrast parameters
Adapt (SVS) B.7–10
Adjusting (CSI) B.8–18
Control Area C.1–3
Copy
Geometry parameters B.10–5
Peak template or directory C.9–19
Postprocessing protocol C.5–3
Copying measurement parameters B.10–5
Correction factor for water suppression adjustment B.9–3
Coupling constant J A.1–12
Creatine (Cr) A.1–20
CSI data
Calculating the sum spectrum C.7–26
Create a Spectral map C.7–6
Evaluate (overview) C.7–1
Evaluating individual voxels C.7–6
Generating metabolite images C.7–13, C.7–14
Modifying Fourier Transformation C.7–29
Reference image display C.1–9
Setting a calculation range C.7–8
Setting calculation options C.7–10
CSI FID sequence A.3–7
CSI matrix grid
Display C.1–9
Shifting for Fourier Transformation C.7–32
Showing/hiding in reference image B.8–2
Showing/hiding in the reference image C.3–8
Showing/hiding on the metabolite image C.7–23
Showing/hiding on the spectral map C.7–23
CSI measurement
Activating/deactivating the Hamming filter B.7–15, B.8–28, B.8–29
Adapting contrast parameters B.8–18
Adapting the Parameters for a 31P measurement B.8–33
Adapting the resolution parameters B.8–25
Adapting the sequence-specific parameters B.8–30
Adjusting Measurement Parameters (Introduction) B.8–1
Setting saturation regions B.8–16
Short echo times C.14–1
CSI slab
Adapting graphically B.8–12
Adapting numerically B.8–13
Adjusting (overview) B.8–11
Display B.6–6
Handles B.8–12
Measuring oblique CSI slabs B.8–11
CSI slice
Adapting graphically B.8–5
Adapting numerically B.8–6
Adjusting (overview) B.8–1
Display B.6–4, C.1–9
Handles B.8–5
Selecting within a CSI 3D slab C.7–3
Showing the projection of the CSI slice B.8–4
Using the position and orientation from a reference image B.8–4

CSI technique
Applications A.3–3
Basics A.2–6
Localization A.2–10
Curve fit
Adjusting for interactive evaluation C.8–46
Automatic curve fitting C.8–54
Manual curve fitting C.8–47
Peak restrictions C.9–9
Showing/hiding in the spectrum C.4–10
Customer protocol C.11–1
CW decoupling A.2–31, B.8–35

D

Data set
Closing C.2–9
Switching C.2–8
Deactivating
Postprocessing step C.8–8
Decoupling
Basics A.2–31
Decoupling pulses A.3–8
Decoupling schemes A.2–31
Define reference metabolite (result table) C.6–3
Delta frequency A.2–22
Delta function A.2–10
Dispersion signal C.8–32
Display
Adjusting the signal display C.4–2
CSI slab B.6–6
CSI slice B.6–4
Reference images (CSI) C.1–9
Reference images (SVS) C.1–8
VOI Display in reference images B.6–2
Display modes for evaluation results C.1–10
Displaying coordinates C.4–2
Displays
CSI matrix grid B.8–2
Projection of the CSI slice B.8–4

E

Echo time
Echo times for SVS measurements A.2–5
Measurements with short echo times C.14–1
Eddy current compensation
Adjusting for interactive evaluation C.8–21
Effective voxel size A.2–20
Equilibrium magnetization B.7–17, B.8–31
Evaluation results
Display Modes C.1–10
Filming/printing C.10–5
Saving C.10–1
Evaluation types C.1–1
Examination techniques A.2–1
EXOR cycle B.7–17
Exponential filter C.8–9
Exporting
Postprocessing protocol C.11–15
Raw data C.12–1

F

Fat suppression A.2–27
FID sequence
For quality measurement B.12–4, B.12–11
FID shifting
Adjusting for interactive evaluation C.8–19
Field of view (FoV)
Adjusting the FoV of the CSI slab numerically B.8–15
Adjusting the FoV of the CSI slice numerically B.8–9
Fieldmap B.11–14
Filming C.10–5
Evaluation results C.10–5
Reference images C.10–5

Filter
Adjusting post-processing step C.8–8
Checking the filter function C.8–12
Selecting for post-processing C.8–9
Setting the half width C.8–11
Setting the position of the filter center C.8–11
Filter width (Hamming filter) B.7–15, B.8–28, B.8–29
Finding
Nearest reference images C.3–4
Fine splitting of the resonance lines A.1–11
Fit error
Fit error of a curve fitting C.8–55
Fit error of a phase correction C.8–40
Showing/hiding in the spectrum C.4–9
Format
Data format of exported raw data C.12–9
Header format of exported raw data C.12–4
Fourier Transformation
Basics A.1–4, A.1–7
For interactive evaluation C.8–24
Modifying C.7–29
Frequency adjustment B.11–4
Frequency range
Changing the unit (peak editor) C.9–4
Defining (peak editor) C.9–5
Frequency representation A.1–7
Frequency shift A.1–9, A.2–22
Frequency shift correction
Adjusting for interactive evaluation C.8–40
Effect A.2–23
Water reference processing C.8–17
Full Width at Half Maximum (FWHM) A.1–8
Full width at half maximum (FWHM)
FWHM of the water peak at 1H MRS QA B.12–5
Full width of peak at half maximum (FWHM) A.1–8

G

Gamma Amino Butyrate (GABA) A.1–22
Gaussian filter C.8–9
Glutamate (Glu) A.1–21
Glutamine (Gln) A.1–21
Gyromagnetic ratio A.1–3

H

Hamming filter
Activating/deactivating for Fourier Transformation C.7–31
Activating/deactivating (CSI) B.7–15, B.8–28, B.8–29
Basics A.2–18
Changing the filter width (CSI) B.7–15, B.8–28, B.8–29
Changing the width of the filter for Fourier Transformation C.7–31
Handles
CSI slice handles B.8–5
Handles for CSI slab B.8–12
VOI handles B.7–3
Hanning filter C.8–9
Heart/Liver coil B.3–7
Height of the peak A.1–8
Homogeneity of the magnetic field A.1–4, B.12–4, B.12–11
Hybrid CSI technique
Chemical shift artifact A.2–22
Introduction A.2–6
Sequences A.2–8

I

Image text
Overview C.1–3
Showing/hiding in the reference image C.3–6
Showing/hiding in the result table C.6–6
Showing/hiding in the spectrum C.4–6
Showing/hiding on the metabolite image C.7–23
Showing/hiding on the spectral map C.7–23
Image type
MR C.10–1
Secondary Capture (SC) C.10–1
Importing
Postprocessing protocol C.11–17
Inline Display B.10–3
Inorganic phosphate (Pi) A.1–24
Intensity distribution A.2–10
Interactive adjustment
Frequency adjustment B.11–4
Manual water suppression B.11–20
Multinuclear frequency adjustment B.11–7
Multinuclear transmitter adjustment B.11–13
Sequence of adjustment steps B.11–3
Shimming interactively B.11–17
Transmitter adjustment B.11–9
Interactive evaluation
Adjusting baseline correction C.8–26
Adjusting curve fitting C.8–46
Adjusting eddy current compensation C.8–21
Adjusting filtering C.8–8
Adjusting phase correction C.8–32
Adjusting the FID shift C.8–19
Adjusting the frequency shift correction C.8–40
Adjusting the water suppression correction C.8–15
Adjusting zero-filling C.8–13
Editing post-processing steps C.8–5
Fourier Transformation C.8–24
Managing post-processing protocols C.8–2
Overview C.8–1
Interpolation
Interpolating a metabolite image C.7–18
Interpolation (CSI measurement) B.7–15, B.8–28, B.8–29
Interpolation resolution C.7–31
Isocenter B.5–2
Isotope table A.1–6
Isotopic abundance A.1–6

J

J coupling
Coupling constant A.1–12
Coupling parameters of a multiplet C.9–11
Introduction A.1–11
Peak type C.9–10
Selecting the echo time A.1–13
Strong coupling A.1–12
Weak coupling A.1–12

K

k space sampling A.2–14, B.8–32

L

Lactate (Lac)
Distribution in the brain A.3–3
Influence of echo time on the signal A.2–5
Signals A.1–21
Larmor frequency A.1–3, A.1–6
Licenses B.1–1
Line intensities for weak coupling A.1–12
Line width A.2–16

Loading
Measurement protocols B.4–2
Other reference images C.2–7
Raw data C.2–2
Reference images B.5–7
Stored images into the Viewer C.10–4
Localization
Effect of the phase-encoding schemes A.2–14
Using phase encoding (introduction) A.2–10
Localizer B.5–4
Localizer measurement B.5–4

M

Magnetic field
Automatic B.9–2
Shimming interactively B.11–17
Shimming (basics) A.1–4
Magnetic field homogeneity B.12–4, B.12–11
Magnetic spin A.1–5
Managing
Comments C.4–10
Peak templates C.9–19
Postprocessing protocols C.11–1
Post-processing steps C.8–2
Manual adjustment B.11–3
Manual water suppression B.11–20
Manual 3D shim B.11–14
Measurement parameters
Acquisition delay B.8–30
ADC bandwidth B.7–17
Averages B.7–11, B.8–19
Averaging mode B.8–20
Bandwidth B.8–32
DC pause fraction B.8–35
DC total duration B.8–35
Decoupling duration B.8–35
Decoupling Flip angle B.8–36
Decoupling type B.8–35
Delta frequency B.7–17, B.8–31
Dimension B.8–31
Fat suppression BW B.7–13, B.8–22
Fat suppression delta position B.7–13, B.8–23
Filter B.7–15, B.8–28, B.8–29
Flip angle B.7–11, B.8–20
FoV B.8–26
Interpolation resolution B.8–28
Measurement duration B.7–18, B.8–30
Measurements B.7–14, B.8–23
NOE count B.8–34
NOE duration B.8–34
NOE flip angle B.8–34
NOE pause B.8–34
NOE type B.8–34
Pause after measurement B.7–14, B.8–24
Phase cycling B.7–17
Phase-encoding B.8–32
Preparation scans B.7–17, B.8–31
Remove oversampling B.8–32
Repetition time (TR) B.7–10, B.8–19
Scan resolution B.8–27
Spectral signal suppression B.7–13, B.8–22
TE (echo time) B.7–11, B.8–19
Thickness B.8–27
TM (time interval) B.7–11, B.8–19
TX delta frequency B.8–34
TX nucleus B.8–34
TX/RX delta frequency B.8–33
TX/RX nucleus B.8–33
Vector size B.7–16, B.8–29
Water suppression B.7–12, B.8–20
Water suppression BW B.7–14, B.8–23
Water suppression delta position B.7–14, B.8–23
Water suppr. Bandwidth B.7–13, B.8–22
Measurement programs B.4–1

Measurement protocols
For in-vivo application B.13–2
For quality assurance B.13–8
For 3D CSI measurements B.13–8
Introduction B.13–1
Loading B.4–2
Modifying the sequence B.4–3
Measurement time for 1H Hybrid CSI A.2–9
Measuring
Isocentered B.5–2
Monitoring the raw signal B.10–3
Performing the measurement B.10–1
Procedure of a Spectroscopy Measurement B.2–1
Reference images B.5–4
MEGA pulse A.2–27
Metabolite image
Creating C.7–13
Editing the display C.7–21
Filming/printing C.10–5
Saving C.10–1
Setting the properties for generating C.7–14
Metabolite ratios
Of the brain at 1H Hybrid CSI A.3–4
Miniature reference images
Showing/hiding in the result table C.6–6
Showing/hiding in the spectrum C.4–6
Modifying
Fourier Transformation (CSI-FT) C.7–29
Monitoring the raw signal B.10–3
MRS signal
Characteristic values A.1–19
Display A.1–7
Quantification A.1–15
Multi-line spectrum A.1–4
Multinuclear frequency adjustment B.11–7
Multinuclear transmitter adjustment
Overview B.11–13
Temporary reference amplitude B.11–14
Multiplet
Editing components C.9–11
Myo-inositol (Ins) A.1–21

N

N-Acetylaspartate (NAA) A.1–20
NOE saturation pulses A.3–8
NOE (basics) A.2–28
Nuclear magnetization A.1–2
Nuclear Overhauser Effect (NOE) A.2–28
Nuclear spin A.1–2

O

Orientation
Adapting the CSI slab orientation numerically B.8–14
Adapting the CSI slice orientation numerically B.8–8
Applying CSI slice orientation from reference image B.8–4
Changing the VOI orientation numerically (SVS) B.7–7
Outer Volume Suppression (OVS) A.2–24

P

Peak
Adding to the peak list C.9–14
Changing peak parameters C.9–9
Changing the peak name C.9–8
Changing the peak settings in the peak editor C.9–8
Characteristics of a peak A.1–8
Define thresholds for fitting C.9–9
Display/hide peak information C.9–10
Editing (overview) C.9–2
Selecting a type (Gauss, Lorentzian, J coupling) C.9–10
Peak amplitude A.1–8
Peak area A.1–15

Peak curve in the peak editor
Adjusting the graphic display C.9–4
Showing/hiding C.9–7
Peak editor
Adding a peak template to the peak list C.9–14
Adjusting the graphic display C.9–4
Changing the peak settings C.9–8
Creating a new peak template C.9–16
Creating a new peak template directory C.9–17
Editing a peak (overview) C.9–2
Introduction C.9–1
Managing the peak templates C.9–19
Peak info map (metabolite image) C.7–18
Peak information
Selectively hiding the peak information of peaks (curve fitting) C.8–52
Showing/hiding in the spectrum C.4–7
Showing/hiding (curve fit) C.8–52
Peak integral A.1–8, A.1–15
Peak integration A.1–14
Peak list (curve fitting)
Adding new peaks C.8–49
Displaying start or result values C.8–49
Editing peak parameters C.8–51
Remove peaks C.8–50
Sorting C.8–50
Peak templates (customer list)
Creating a new directory C.9–17
Creating a new peak template C.9–16
Managing the customer list C.9–19
Phase correction
Adjusting (interactive evaluation) C.8–32
Automatic C.8–37
Manual C.8–34
Selecting reference peaks C.8–39
Water reference processing C.8–17
Phase cycle B.7–17
Phase-encoding
Effects of spatial resolution A.2–13
Hamming filter A.2–18
Introduction A.2–10
Schemes A.2–14, B.8–32
Signal-to-noise ratio A.2–21
Phosphocreatine (PCr) A.1–20, A.1–23
Phosphodiester (PDE) A.1–24
Phosphomonoester (PME) A.1–23
Physiological triggering B.3–12
Point of origin of the spectral axis
Basics A.1–10
Setting C.4–5
Point Spread Function (PSF) A.2–10
Contamination ratio A.2–16
Line width A.2–16
Polynomial order (baseline correction) C.8–29
Position
Adapting the CSI slice position numerically B.8–8
Adapting the VOI position graphically (SVS) B.7–3
Adapting the VOI position numerically (SVS) B.7–7
Applying CSI slice position from reference image B.8–4
Changing the CSI slab position numerically B.8–14
Postprocessing protocol
Open C.5–2
Postprocessing protocols
Arranging steps C.8–2
Changing C.11–4
Copy C.5–3
Creating new C.11–9
Customer protocols C.11–1
Delete C.11–13
Editing steps C.8–5
Exporting C.11–15
For 1H MRS C.14–1
Importing C.11–17
Managing C.11–1
Opening the original protocol version C.8–56
Saving C.11–8
Siemens protocols C.11–1

Post-processing steps
Adding C.8–3
Adjusting filtering C.8–8
Arranging (overview) C.8–2
Changing the sequence in the protocol C.8–4
Deactivating C.8–8
Editing (overview) C.8–5
Remove C.8–4
Resetting parameter changes C.8–8
Verifying parameter changes C.8–7
Precession A.1–3
Preparing a Spectroscopy Measurement B.3–1
Printing C.10–5
Evaluation results C.10–5
Reference images C.10–5
Projection of the CSI slice B.8–4
Protocol adjustments B.11–2
Protocol Browser
Modifying display C.11–3
Overview C.11–2
Setting the display of the protocol list C.11–3
Protocol properties
Showing/hiding in the Protocol Browser C.11–3

Q

Quality assurance
Checking the shim quality B.12–4, B.12–11
For 1H MRS B.12–1
For 31P MRS B.12–9
Introduction B.12–1
Protocols for quality assurance B.13–8
Queue
Changing the sequence of measurement protocols B.4–3

R

Raw data
Automatic saving B.10–1, B.10–6
Data format of exported raw data C.12–9
DICOM format C.12–1
Evaluating interactively (overview) C.8–1
Evaluation with different postprocessing protocol (overview) C.5–1
Exporting C.12–1
Header format of exported raw data C.12–4
Loading C.2–2
Rectangular filter C.8–9
Reference amplitude B.11–14
Reference images
Adapt to segment size C.3–5
Automatically selecting C.3–3
Display for CSI data C.1–9
Display for SVS data C.1–8
Displaying in the large image segment C.3–2
Editing the display C.3–1
Filming/printing C.10–5
Introduction B.5–1
Loading B.5–7
Loading others C.2–7
Measuring B.5–4
Overlap (metabolite image) C.7–17
Reference image display in image area C.1–7
Save with VOI graphic B.7–9
Saving C.10–1
Saving with CSI slice graphic B.8–10
Scrolling C.3–1
Searching for the nearest reference images B.5–8, C.3–4
Showing/hiding graphic tools C.3–6
Showing/hiding image text C.3–6
Windowing C.3–5
Zoom/Pan C.3–4

Reference peaks (phase correction) C.8–39
Reference raw data
Eddy current compensation C.8–21
Reference signal A.1–9, A.1–10, C.4–5
Relative nuclear ratio A.1–14
Relative sensitivity A.1–6
Relaxation time A.1–3
Rename
Peak template or directory C.9–19
Repetition time TR A.1–17
Resolution
Effects on phase-encoding A.2–13
Signal-to-noise ratio A.2–21
Spectral Resolution A.1–13
Resolution parameters
Adapt (SVS) B.7–15
Adjusting (CSI) B.8–25
Resonance frequency A.1–3, A.1–8
Resonance lines A.1–11
Result display in image area C.1–3
Result table
Combining metabolites C.6–5
Defining the reference metabolite C.6–3
Filming/printing C.10–5
Generating a result table C.6–2
Overview C.6–1
Saving C.10–1
Saving as a text file C.6–7
Showing metabolites with hidden peak information C.6–4
Showing/hiding image text C.6–6
Showing/hiding miniature reference images C.6–6
RF exposure A.1–29
RF penetration A.1–29
RF power A.1–29
Ringing effect B.8–32
Rotating
Adapting the CSI slab rotation angle numerically B.8–14
Adapting the CSI slice rotation angle numerically B.8–9
Adapting VOI rotational angle numerically (SVS) B.7–8
Rotate VOI graphically (SVS) B.7–4
Rotating the CSI slice graphically B.8–6
Rotating the CSI-3D slab graphically B.8–13

S

Sampling of the k space
Sampling schemes A.2–14, B.8–32
Saturation regions
Automatically positioned saturation regions A.2–26
Freely positionable saturation regions A.2–26
Setting (CSI) B.8–16
Setting (SVS) B.7–9
Showing/hiding in the reference image C.3–8
Showing/hiding on the metabolite image C.7–23
Showing/hiding on the spectral map C.7–23
Saving
Evaluation results C.10–1
Postprocessing protocol C.11–8
Reference images C.10–1
Results and reference images C.10–1
Saving automatically
Raw data B.10–6
Scale bar
Showing/hiding in the reference image C.3–8
Showing/hiding on the metabolite image C.7–23
Showing/hiding on the spectral map C.7–23
Scan at Center B.5–2
Scrolling in the reference images C.3–1
Searching
Nearest reference images B.5–8

Select “Fully excited VOI” A.2–25
Selected voxel
Showing/hiding in reference image C.7–23
Showing/hiding in the reference image C.3–8
Showing/hiding on the metabolite image C.7–23
Selecting the color scale for a metabolite image C.7–17
Selecting the primary nucleus B.8–33
Selecting the secondary nucleus B.8–34
Sequences A.2–1
Sequence-specific parameters
Adapt (SVS) B.7–16
Adjusting (CSI) B.8–30, B.8–33
Setting the vector length (Zero-Filling) C.8–14
Setting the X axis of the spectrum C.4–4, C.4–5
Shim quality
Checking B.12–4, B.12–11
Full width at half maximum of the water peak B.12–5
Shimming
Basics A.1–4
Interactive B.11–17
Manual 3D shim B.11–14
Shim mode B.9–2
Shimming automatically B.9–2
Shimming interactively B.11–17
Show
Curve fit in the spectrum C.4–10
Fit curve (curve fitting) C.8–52
Fit error in the spectrum C.4–9
Graphic tools in reference images C.3–6
Graphic tools in the spectral map C.7–23
Graphic tools of the metabolite image C.7–23
Image text in reference images C.3–6
Image text in the result table C.6–6
Image text in the spectrum C.4–6
Image text on the metabolite image C.7–23
Image text on the spectral map C.7–23
Metabolites with hidden peak information C.6–4
Miniature reference images in the result table C.6–6
Peak information C.4–7, C.9–10
Protocol properties in the Protocol Browser C.11–3
Protocol types in the Protocol Browser C.11–3
Signal curve/peak curve in the peak editor C.9–7
Show matrix B.8–2
Showing/hiding fit curve C.8–52
Showing/hiding graphic tools
On the metabolite image C.7–23
On the spectral map C.7–23
Siemens protocol C.11–1
Signal curve in the peak editor
Adjusting the graphic display C.9–4
Showing/hiding C.9–7
Signal intensities A.1–15
Signal subtraction (water reference processing) C.8–16
Signal suppression
Spectral A.2–27
Signal-to-noise ratio (SNR)
At Phase-encoding A.2–21
At 3 T A.1–26
Increase through averaging A.1–16
Increase through greater volume A.1–18
Introduction A.1–16
Optimal repetition time A.1–17
Single Voxel Spectroscopy (SVS) A.2–4
Slice intersections
Showing/hiding in the reference image C.3–8
Sorting
Peak template directories C.9–20
Peak templates C.9–20
Peaks in the peak list C.8–50
Spectral map
Editing the display C.7–21
Enlarging the spectrum of a voxel C.7–12
Filming/printing C.10–5
Generating C.7–6
Saving C.10–1
Spectral Resolution
At 3 T A.1–26
Basics A.1–13

Spectral signal suppression A.2–27
Spectrum
Adding and governing comments C.4–10
Adjusting the signal display C.4–2
Basics A.1–4, A.1–7
Displaying coordinates C.4–2
Display/hide peak information C.4–7
Filming/printing C.10–5
Saving C.10–1
Setting the X axis C.4–4
Setting the y axis C.4–5
Showing/hiding image text C.4–6
Showing/hiding miniature reference images C.4–6
Showing/hiding the curve fit C.4–10
Showing/hiding the fit error C.4–9
Spin Echo (SE) Sequence A.2–1
Spin quantum number A.1–5
STEAM sequence A.2–2
Storing
Reference image with CSI slice graphic B.8–10
Reference image with VOI graphic B.7–9
Result table as a text file C.6–7
Saving raw data automatically B.10–1
Subtracting
Theoretical spectrum (curve fitting) C.8–53
Water signal (water reference processing) C.8–16
Sum spectrum
Calculating C.7–26
Filming/printing C.10–5
Saving C.10–1
Susceptibility effects A.1–13, A.1–27
SVS measurement
Adapting contrast parameters B.7–10
Adapting the resolution parameters B.7–15
Adapting the sequence-specific parameters B.7–16
Adapting the VOI graphically B.7–3
Adapting the VOI numerically B.7–5
Setting saturation regions B.7–9
SVS Technique
Echo times for SVS measurements A.2–5
Introduction A.2–4
Use A.3–1
Switching
Data set C.2–8

T

Task card
Closing C.13–1
Configuration C.1–2
Opening empty C.2–2
Taurine (Tau) A.1–21
Temporary reference amplitude B.11–14
Thickness
Adapting the CSI slice thickness numerically B.8–9
Time interval TM A.2–2
Time representation A.1–7
TM (time interval) A.2–2
Transmitter adjustment B.11–9
Transparency
Setting for the metabolite image C.7–24
Transverse magnetization A.1–3
T2 relaxation time at 3 T A.1–28

U

Use
CSI technique A.3–3
SVS Technique A.3–1
1H Hybrid CSI Measurement of the brain A.3–3
1H Hybrid CSI of the prostate A.3–4
31P CSI of heart, muscle, liver A.3–7

V

Viewing
Loading stored images in the Viewer C.10–4
Volume of Interest (VOI)
Adapting graphically (SVS) B.7–3
Adapting numerically (SVS) B.7–5
Adjusting (overview) B.7–1
Display for CSI data C.1–9
Display for SVS data C.1–8
Display in reference images B.6–2
Handles B.7–3
Showing/hiding in the reference image C.3–8
Showing/hiding on the metabolite image C.7–23
Showing/hiding on the spectral map C.7–23
Voxel size
Effective A.2–20
Nominal A.2–20

W

WALTZ 4 decoupling A.2–31, B.8–35
Water reference processing
Adjusting for interactive evaluation C.8–15
Checking the water signal C.8–18
Frequency shift correction C.8–17
Performing phase correction C.8–17
Setting the averages C.8–16
Subtracting the water signal C.8–16
Water suppression A.2–3, A.2–27, B.11–20
Water suppression adjustment B.9–3
Correction factor B.9–3
Windowing
Metabolite image automatically C.7–23
Reference image C.3–5
Spectral map automatically C.7–23

Z

Zero-filling
Adjusting for interactive evaluation C.8–13
Zooming
Reference image C.3–4

Numerics

1H decoupling
Basics A.2–31, A.3–8
Decoupling types B.8–35
1H Hybrid CSI
Measurement parameters and measurement time A.2–9
Metabolite ratios of the brain A.3–4
of the brain A.3–3
Of the prostate A.3–4
Sequences A.2–9
1H MRS
Postprocessing protocols C.14–1
Preliminary steps (brain) B.3–2
Preliminary steps (prostate) B.3–5
Quality assurance B.12–1
Signals A.1–20
1H saturation
Basics A.3–8
Defining pulse type B.8–34
2D CSI measurement
Adapting the CSI slice graphically B.8–5
Adapting the CSI slice numerically B.8–6
Adjusting the CSI Slice (Overview) B.8–1
Display of a CSI slice B.6–4
Showing the projection of the CSI slice B.8–4
2.3-Diphosphoglycerate (DPG) A.1–25
3 T spectroscopy
Effects during 3 T measurements A.1–29
Introduction A.1–26

3D CSI measurement
Adapting the CSI slab graphically B.8–12
Adapting the CSI slab numerically B.8–13
Adjusting the CSI Slab (Overview) B.8–11
Display of a CSI-3D slab B.6–6
Measuring oblique CSI slabs B.8–11
3D CSI protocols B.13–8
3D spin echo hybrid CSI sequence A.3–6
31P MRS
Measurements in the supine position B.3–10
Physiological triggering B.3–12
Preliminary steps (muscle, heart, liver) B.3–7
Quality assurance B.12–9
Signal enhancement via decoupling A.2–32
Signal enhancement via NOE A.2–31
Signals A.1–23
Techniques A.2–27
1H decoupling A.3–8
1H saturation A.3–8
31P CSI of heart, muscle, liver A.3–7
31P receiver coil B.3–8

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