Simple Absolute Signal Scaling for Spectroscopic Data Acquired with Phased-Array Coils at 1.5T

T. Schirmer[1], S. Kohler[2], D. Gultekin[3], T. Raidy[3]

[1]Applied Science Lab Europe, GE Medical Systems, Hallbergmoos, Germany, [2]GE Medical Systems, Waukesha, Wisconsin, United States, [3]Radiation Oncology Department, Duke University Medical Center, Durham, North Carolina, United States

Abstract

Most of today's state of the art MR scanners are equipped with highly advanced multi-channel RF receive chains and appropriate phased-array coils. MR spectra, as well as images, acquired with such multi-element coils are usually a combination of the signals acquired with each individual element of the coil. The combined signal is based upon individual signals from coils with spatially varying B1 sensitivities. Thus, the resulting signal amplitude cannot be considered directly proportional to the metabolite concentration scaled by transmitter- and receiver-gains. We will demonstrate a simple method to rescale the signal to arbitrary units using an unsuppressed water signal acquired with the body coil as B1 insensitive reference.

Introduction

Quantitative analysis of single voxel spectra in arbitrary, institutional units has become a standard, which can be achieved with reasonable efforts [1]. Some of the methods rely on the direct proportionality of signal and metabolite concentrations scaled by the transmitter and receiver gains. This proportionality is true for RF signal trans-mission and reception with linear or quadrature volume resonators, but not for surface or phased-array coils with spatially varying B1 sensitivity (Fig.1).

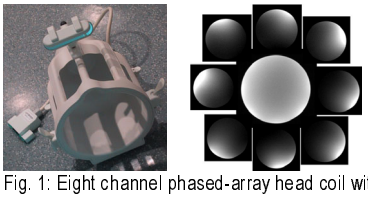

Fig. 1: Eight channel phased-array head coil with typical B1 pattern of the individual elements.

Phased-array coils allow combining the high SNR of a locally applied small surface coil with the extended field of view of a large volume resonator. Furthermore, phased-array coils are prerequisites for recently developed parallel imaging techniques [2], yielding both in increasing number of clinical applications with phased-array coils. As it is practically impossible to change during clinical exams between volume resonators and phased-array coils, spectroscopy data will be acquired with phased-array coils. This explains the demand for a method to rescale spectroscopic data acquired with these coils to absolute, arbitrary units, to preserve a quantitative approach for single voxel spectroscopy that had already become standard. This study will introduce a method to rescale single voxel spectra using the unsuppressed water signal acquired with the B1 insensitive body coil as a reference signal. The study will focus on 1.5T systems, where the effects of dielectric resonance are negligible and will not need to be taken into considerations.

Methods

All experiments were performed on a GE Signa Excite 1.5T (*General Electric Medical Systems, Milwaukee, WI, USA*), MRI scanner running under software revision 10.0 with an experimental setup as shown in Fig.2. The integrated body resonator was used for signal transmission and reception. Phantoms filled with copper sulfate were used to increase loading of the body coil. The actual data were acquired from the GE MRS HD Sphere, a 16 cm diameter spectroscopy phantom. Localized PRESS spectra were acquired at varying locations inside the MRS sphere with and without CHESS water suppression. TE was chosen to be 35 ms or 200 ms, TR=2s and voxel volume=8ml. As part of the GE product PROBE/SVQ, all spectra were automatically reconstructed with quantitative analysis providing semi-quantitative machine numbers in arbitrary units including a quantitative number for the water peak.

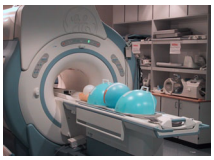

Fig.2: GE Signa Excite 1.5T whole body scanner with experimental setup.

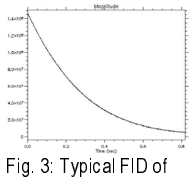

Fig. 3: Typical FID of unsuppressed water signal acquired with the body coil.

Additionally, all raw data were processed on a Sun Blade 2000 workstation (*Sun Microsystems Inc., Mountain View, CA, USA*), using a dedicated software package (*Spectroscopy Analysis General Electric* = SAGE) as well as the LCModel [3]. SAGE was used to estimate the signal intensity of the water peak based on the first point of the magnitude FID (Fig.3). No processing was applied to the data before automatic determination of the signal magnitude. The LCModel can also provide a value for the area under the unsuppressed water peak as described in [4], which is typically used for internal water referencing.

The results achieved from various locations in the phantom acquired in consecutive scans were also compared to the stability of the water signal in a CSI experiment. CSI data were acquired using TE=144ms, TR=1s, 24x24 matrix size and spatial resolution of 1 ml. First point of the magnitude spectra was used as an estimation of the water signal intensity.

Results

Table 1 shows the coefficient of variation (CV in %) for the water signal acquired with the body coil at six different locations in the phantom and quantified with the described methods. The CVs achieved using the first point of the magnitude FID (MoF) and the LCModel (LCM) are both at about 4% for the long and short echo times. The long echo time provides slightly better results, as the signal is less affected by eddy currents or other types of artifacts (Fig.4).

	MoF	p/SVQ CDA	p/SVQ FDA	LCM
TE=35ms	4,22	13,42	5,02	4,39
TE=200ms	3,94	18,78	4,35	4,13

Tab.1: CV [%] of the quantified water signal from different locations

The resulting numbers from standard PROBE/SVQ (p/SVQ CDA) are much worse, which is directly related to the method used in the quantitative analysis. As part of the analysis, all peaks are deapodized using the line width of the creatine peak (CDA=Creatine line width DeApodization). As the metabolite spectra acquired with the body coil are of poor quality, this approach will provide poor results. This also explains the higher CV at TE=200ms, were the line width of the creatine signal cannot be reliably determined. With SAGE, the standard PROBE/SVQ reconstruction can be executed with fixed deapodization (FDA) using a linewidth of 2Hz. This offline reconstruction (p/SVQ-FDA) yields results that come close to those achieved with MoF or LCM.

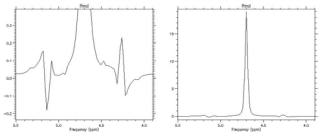

Fig.4: Unsuppressed water signal showing eddy current artifact.

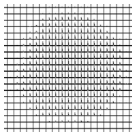

Fig. 5: CSI Acquisition of unsuppressed water

The CV of the water signal in a CSI experiment (Fig. 5), using only the inner 81 voxels for a statistical evaluation was found to be about 17%.

Discussion

Scaling metabolite data with the unsuppressed water signal acquired with the B1 insensitive body coil requires very reliable determination of the scaling factor. This study shows, that appropriate quantitative analyis can provide reliable values for the water signal. It is possible that the ~4% error demonstrated in the measurement will be compensated by the SNR gain of the metabolite signal achieved in regions of the phased-array coil. However, it is clear that using a CSI based acquisition to determine global scaling factors cannot be considered as an alternative due to the limited reliability of the data.

Reference

[1] Schirmer, T et al., NMR in Biomed, 13, 28-36 (2000)

[2] Barker, PB et al., Abstracts of the 44th ENC, p.78 (2003)

[3] Provencher S, Magn Reson Med, 30, 672-679 (1993)

[4] Provencher S, LCModel & LCMgui User's Manual July 2003; p.42, 117