Quantitative SENSE-MRSI of the Human Brain

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Introduction

Various techniques have previously been developed for the quantitative analysis of proton magnetic resonance spectroscopic imaging (MRSI) data from the human brain. This abstract describes the extension of one of these techniques (the phantom replacement method) for use with phased-array head coils and rapid (SENSE) spectroscopic imaging methods.

Materials and Methods

All scans were performed on a Philips Intera 3.0 Tesla system using a 6-channel phased-array receiver coil. RF pulses were transmitted using the body coil. A 3-slice, spin-echo circularly-encoded 2D-MRSI pulse sequence with "BOOZE" water/lipid suppression [1] and OVS, covering from the basal ganglia to the vertex, was collected (TR/TE 2000/144 msec, FOV 230x115 mm, matrix size 32x16, SENSE factor 2, scan time 12 minutes) [2]. Prior to MRSI, field homogeneity was optimized using high order shimming. After MRSI, additional rapid gradient echo MRI scans were recorded to calculate the coil sensitivity matrix **A(x,y)**. Multi-channel time-domain MRSI data (**b(t,x,y)**) was combined and un-folded using a SENSE algorithm, as described previously [3],

$$\mathbf{s}(t,x,y) = \mathbf{A}(x,y)^{-1}\mathbf{b}(t,x,y)$$

where **s(t,x,y**) is a combined, uniform spatial sensitivity MRSI data.

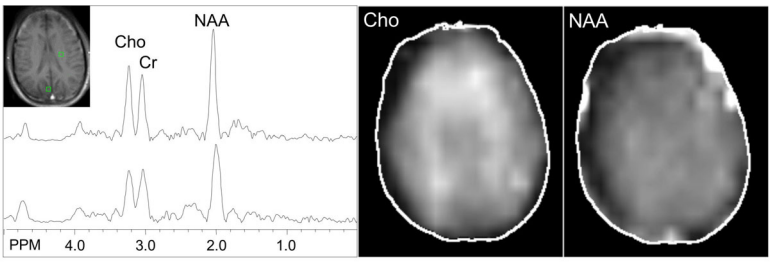
The protocol was tested in 5 normal adult subjects (age 34± 11 years, 4 male). Bilateral metabolite peak areas were measured in 6 representative white and gray matter regions. The identical protocol and reconstruction methods were also applied to a 4L sample containing 65 mM N-acetyl aspartate (NAA). *In vivo* metabolite concentrations [M] (where M = Choline (Cho), Creatine (Cr) or NAA) were calculated using the following expression

$$[M] = [NAA] * S_M/S_{NAA} * (LF_i/LF_{NAA}) * f(T_1, T_2)$$

where S is the peak area and LF_i and LF_{NAA} are the body coil transmitter load factors for the *in vivo* and phantom scans, respectively. $f(T_1,T_2)$ applies a correction factor to account for differences in relaxation times between the phantom and *in vivo* metabolites. *In vivo* relaxation times for normal human brain at 3T were taken from the literature [4-6].

Results

The figure shows a representative SENSE-MRSI dataset with 2 of the 6 selected voxel locations. Metabolite concentrations for all 6 brain regions analyzed (millimolar, mean ± st.dev.) are given in the Table.



Discussion

Metabolite concentrations are in reasonable agreement with those from prior MRSI and single-voxel studies [7,8]. MRSI with phased-array coils offers improved SNR compared to conventional volume head coils, and allows for shorter scan times using SENSE encoding. However, because of the spatially varying sensitivity (and loading) of the individual receiver coil elements, quantitation is more complex. Fortunately, collection of B_1 sensitivity maps and use of SENSE processing allows the reconstruction of uniform sensitivity metabolic images. Since the B_1 sensitivity maps are derived relative to the body coil, a global loading correction based on the body coil transmitter gain required for a 90˚ pulse can be applied. The phantom replacement technique has previously been demonstrated to be a reliable method for quantifying multi-slice MRSI data recorded with homogeneous, quadrature transmit-receive coils [7]. The procedure described here allows this method to be extended for use with any type of inhomogeneous coil array, either with conventional or SENSE-encoding.

Region	[Cho] Mean ± St.Dev.	[Cr] Mean ± St.Dev.	[NAA] Mean ± St.Dev.
Thalamus	2.48 ± 0.65	8.44 ± 1.44	11.71 ± 4.83
Corona Radiata	2.85 ± 0.73	9.72 ± 1.94	9.72 ± 1.94
Parietal Periventricular WM	2.83 ± 0.74	10.70 ± 1.68	13.69 ± 1.97
Mesial Occipital GM	2.39 ± 0.28	10.53 ± 2.01	12.06 ± 3.15
Centrum Semiovale	2.77 ± 0.41	11.03 ± 1.25	12.31 ± 1.46
Posterior Cortical GM	2.54 ± 0.48	10.24 ± 1.19	8.05 ± 2.91

References:

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