Metabolite Quantitation from MRSI Data Employing a Novel Tissue Segmentation Method

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Introduction

Quantitative analysis of MRSI data requires corrections for CSF voxel contributions. In addition, concentrations of some metabolites depend on gray (GM) and white matter (WM) voxel contributions, Therefore, tissue segmentation has been used in several studies to correct metabolite values for CSF voxel contributions and to obtain metabolite concentrations in pure GM and WM [1-5]. In this study, we present a novel method for tissue segmentation, which employs multi-compartment fitting of water components in voxels at the resolution of the MRSI measurement.

Methods

The method was tested in six measurements on five subjects.

Tissue segmentation: A modified Inversion Recovery Fast Spin-Echo (IR-FSE) sequence was used to acquire 32 images of one slice with different individual echo times (echo spacing: 11 or 17 ms). The sequence was repeated 5 times with different inversion times between 10 ms and 2010 ms, yielding 180 intensity values with different combinations of TE and TI for each pixel. For a subset of measurements, saturation bands were used and positioned similar to the MRSI measurement (see below). Images (FOV = 16 cm or 18 cm) were acquired with a 512×16 matrix, which was reduced afterwards to 32×16 and apodized, to match the MRSI resolution. Imaging time was ~5min. The data were fitted to obtain for each pixel M_0 values for three compartments and thus the contribution of GM and WM, and CSF. T_1 and T_2 values were fixed for GM and WM and constrained for CSF.

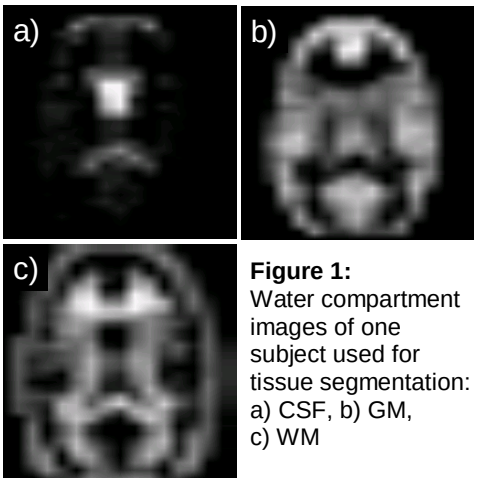

Figure 1: Water compartment images of one subject used for tissue segmentation: a) CSF, b) GM, c) WM

MRSI: Two MRSI sequences were used: 1.) A 2D-MRSI sequence with PRESS-volume pre-selection (TR/TE=1800/30ms, FOV=16cm, slice thickness 12 mm, Matrix: 32×16); 2.) A spin-echo CSI sequence with additional saturation bands to reduce contamination from subcutaneous lipid regions (TR/TE=1800/135ms, FOV=18cm, slice thickness 15 mm, Matrix: 32×16). Postprocessing included moderate apodization, water removal and spectral fitting using the FITT software-package (courtesy of A.A. Maudsley). Separate water phantom scans served as external quantitation standard based on the reciprocity principle. Metabolite values were quantitated and corrected for CSF contributions.

Results

Fig. 1 shows images of the three compartments (CSF, GM, WM) that were measured and used for metabolite correction and for regression analysis of metabolite concentrations depending on WM voxel contributions. Regression analysis between CSF-corrected metabolite concentrations and WM voxel contributions (see Fig. 2 for one subject) yielded for all six measurements significantly lower ($p<0.001$) Cr in WM than in GM, while only one significant correlation ($p<0.001$) was obtained for NAA and for Ch. Paired t-tests between metabolites in pure GM versus pure WM, showed significantly lower Cr in WM than in GM, while NAA and Ch were not significantly different (Fig. 3) CSF-corrected metabolite concentrations in pure WM and GM were: NAA: 9.8/10.9, Cr: 5.2/8.4, Ch: 1.8/1.8 mmol/kg wet wt. in GM/WM, respectively.

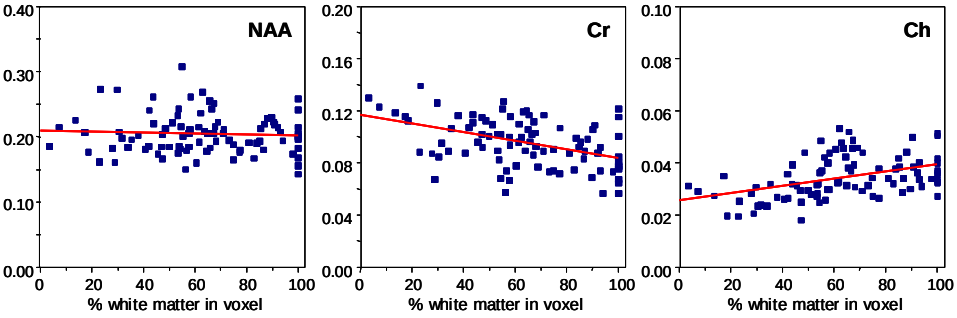

Figure 2: Regression analysis for one subject of NAA, Cr, Ch (in a.u.) depending on WM voxel contribution

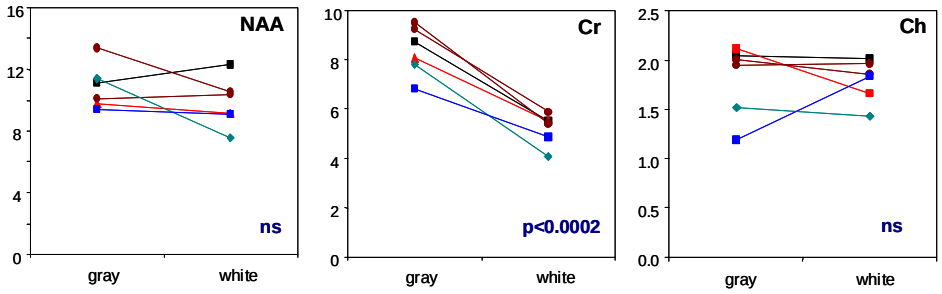

Figure 3: NAA, Cr, and Ch conc. (mmol/kg wet wt.) in pure GM and WM for all scans.

Discussion

The presented method for tissue segmentation differs in several aspects from other generally performed methods: 1) usually a pixel is assigned exclusively to one compartment, while here image pixels can consist of all three compartments (though at coarser resolution); 2) since the matrices for imaging and MRSI were identical, the correction for point spread function is inherent; 3) additional information is gained on water compartments, e.g. myelin water component. The method proved robust, metabolite values were similar to literature values.

References:

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Acknowledgment:

This work was supported by Swiss National Foundation (31-059082)