Towards Standardization of Volumetric MRSI

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INTRODUCTION:

Although MR spectroscopic imaging offers considerable potential for detection of alterations in tissue metabolism, the use of these techniques for clinical studies remains limited. Reasons include variability of implementations across sites and instrument manufactures; restrictive implementations in terms of the spatial extent over which data is obtained; and relative complexity of the data analysis. To address these limitations a standardized volumetric 'whole brain' 1H MRSI acquisition has been implemented on instruments from three different manufacturers and combined with fully automated processing procedures.

METHODS:

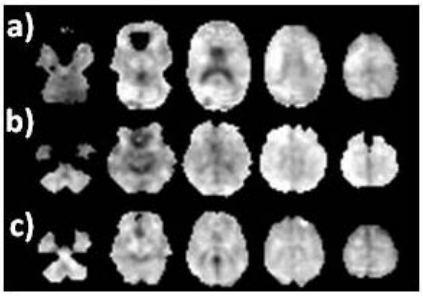
A spin-echo volumetric MRSI acquisition was developed on 3 Tesla MR instruments from GE, Philips, and Siemens. Pulse shapes, sequence timing, and gradient waveforms were identically implemented. The sequence used lipid inversion-nulling, CHESS water suppression, TE/TR/TI = 70/1710/198 ms, a 135 mm slab excitation, and echo-planar readout plus 2-dimensional phase encoding, for a final sampling resolution of 50x50x18 points. The sequence also included an interleaved water MRSI acquisition with identical spatial and spectral parameters. Standard manufacturer-provided B0 shimming methods and T1-weighted MRI sequences were used at all sites.

MRI and MRSI data was converted to a common format and automatically processed using the MIDAS package [3,4] to map N-acetylaspartate (NAA), creatine, and choline. Processing included lineshape and B0 correction; determination of grey-matter (GM), white-matter (WM) and CSF content at each MRSI voxel; signal normalization of individual metabolite images; and non-linear spatial registration to a reference image that was mapped to a brain atlas with lobar regions defined. Studies were performed for normal subjects, aged 22 to 30.

RESULTS AND CONCLUSIONS:

Sequences were identically implemented with the exception of removing sampling during the readout gradient ramp periods and a reduced sweep width, which was required due to sample-size limitations on one instrument. Lack of support for DICOM standard for raw data necessitated development of custom software to read data from GE and Philips and to define sequence parameters.

Metabolite images and spectral quality were comparable from all instruments, although signal to noise ratio varied due to differences in RF detection coils. Differences in EPSI readout echo drift and frequency drift were addressed by the data processing procedures. Figure 1 shows typical metabolite images for NAA.



NAA maps obtained on a) GE, b) Philips, and c) Siemens instruments.

This development indicates that volumetric MRSI acquisition can be implemented in a consistent and comparable manner across different instruments, and using standard setup procedures. The MRSI processing was done remotely from the scanner, but implemented in a fully automated manner following manual initiation of the data transfer. Key factors of this implementation include identical acquisition parameters and processing pipelines, and the use of signal normalization that enables direct comparison of individual metabolite values across instruments and subjects. Further developments will utilize a normative brain metabolite database for analysis of metabolite images from individual subjects for clinical studies.

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REFERENCES: 1) Maudsley, A.A., et al. NMR Biomed, 19:492, 2006. 2) Maudsley, A.A., et al. Magn. Reson. Med., 61:548, 2009.