Tissue-Dependent Analysis of Metabolic Alterations in the Brain by MR Spectroscopic Imaging

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INTRODUCTION:

Evaluation of metabolic alterations in the brain in individual subjects using ^{1}H MR Spectroscopic Imaging (MRSI) commonly requires a comparison against a reference, typically obtained from a group of normal subjects. Since metabolite concentrations are known to vary by tissue type, brain region, and subject age, these factors must be taken into account. Although such analyses can be done by manual selection of voxels from the subject and normal subject group, and accounting for tissue content in the selected voxels, this type of analysis is greatly facilitated by spatially registering all images, thereby enabling a direct comparisons between all image regions; however, alignment to the level of sulcal distributions and hence the relative contribution of grey- and white-matter content to each MRSI voxel, is impractical. To address this limitation, an analysis procedure has been implemented within the MIDAS (**M**etabolite **I**mage **D**ata **A**nalysis **S**ystem) MRSI processing package that first determines the tissue-specific metabolite distributions and then performs an analysis of the individual-subject data based on the fractional tissue content of each voxel.

METHODS:

MRSI data was obtained using a volumetric EPSI acquisition at 3 T for normal subjects and for two patient groups. Reconstruction of the metabolite images was carried out using the MIDAS package[1], and included spatial and signal intensity normalization. The normal subject group was then processed with a tissue regression procedure that used data for all subjects, obtained from a local region surrounding each voxel, to provide the metabolite value for each of the grey- and white-matter tissue types at each location over the whole brain. The standard deviation from this result was also calculated. The analysis of single-subject data then used the MRI-derived tissue segmentation results, converted to have the same spatial response function as the SI data, to calculate a simulated metabolite image based on the tissue-specific metabolite values in the reference image data. An image of the difference between the acquired and the simulated image for each metabolite was then created scaled by the number of standard deviations difference from the normal subject values, which is equivalent to generating a z-score image.

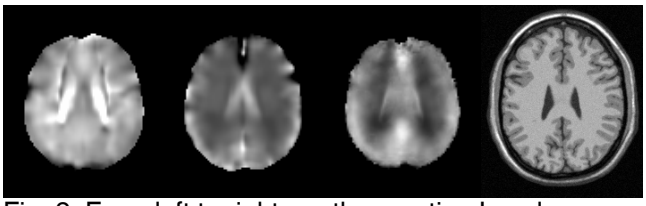

Fig. 2. From left to right are the creatine Local Regression Analysis images for grey- and white-matter, displayed at the same image scale; the creatine average value image; and the spatial-reference MNI at the same slice.

RESULTS AND CONCLUSION:

The results of the normal-subject local tissue regression analysis are shown in Figure 1 for Creatine (which exhibits the greatest grey-white image contrast), obtained using data from 35 subjects aged 19 to 30. For comparison, the image created by averaging over all creatine images from the subject group is also shown. All images are in normalized space. The tissue-specific metabolite images indicate only relatively small variation of the tissue-specific metabolite intensity in different brain regions and comparison with the average value image suggests that the regional metabolite image intensity variation largely reflects the underlying tissue distributions. In Figure 2 are shown example images using this analysis method for a subject with ALS, using the local tissue analysis of NAA. This indicates areas with significant (3 standard deviations) reduction of NAA levels in the white matter, in agreement with known pathology for this disease.

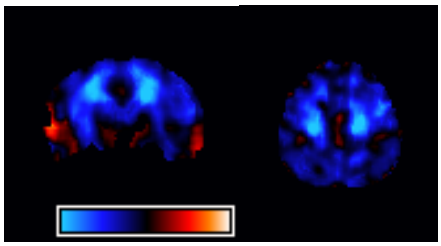

Fig. Coronal and axial sections of a NAA tissue-analysis map for an ALS subject. Color scale is for ±3 standard deviations in comparison to the normal subject data.

The proposed analysis method enables voxel-based comparison of metabolite distributions without the need for exact spatial registration of the subject data to the normal subject group.

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REFERENCES: 1) A.A. Maudsley, et al., Comprehensive processing, display and analysis for in vivo MR spectroscopic imaging, *NMR Biomed*, 19: 492-503 (2006).