Metabolic Mapping of the Brain by Volumetric MR Spectroscopic Imaging

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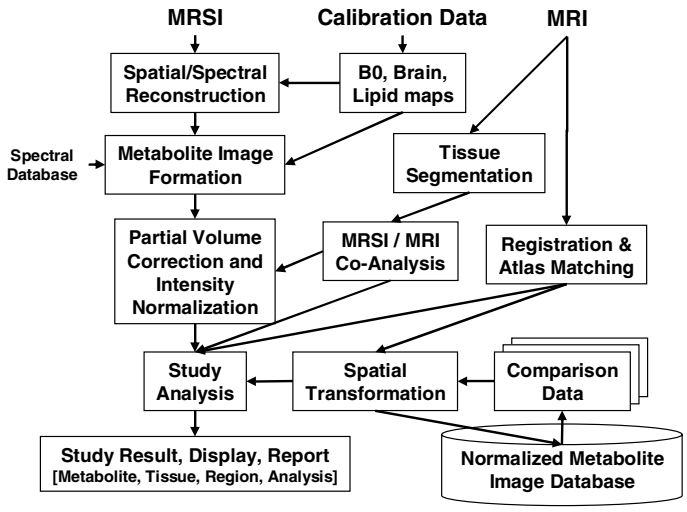
Analysis of MR spectroscopic data from the brain optimally requires comparisons with normal metabolite distributions, which are known to vary by tissue type, region, and demographic factors such as age. For MR Spectroscopic Imaging (MRSI) it is particularly beneficial if this information is available from the whole brain, facilitating statistical tests to detect both local and widespread metabolic changes. To this aim, an integrated set of processing tools has been developed (MIDAS) that provide fully-automated MRSI and MRI data, formation of a brain metabolite database, and comparisons between subject and database metabolite values.

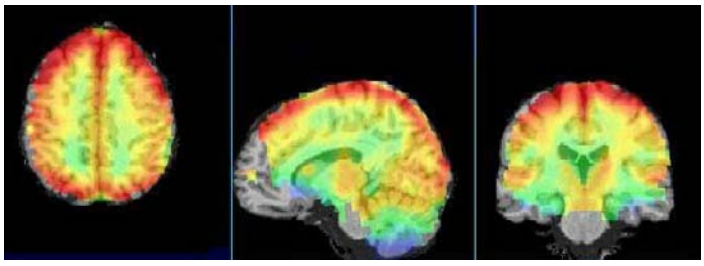
INTRODUCTION: The adoption of MR metabolic imaging for routine clinical applications has been constrained by the requirement for specialized data processing and analysis methods and by the need for extensive comparative data from normal subjects. Since normal MR-detected metabolite levels in the brain vary by tissue type, region, subject variables such as age, and acquisition parameters, the generation of comprehensive comparison data from normal subjects represents a major undertaking, ideally requiring that common acquisition and processing protocols be implemented at multiple sites. To address these considerations a suite of automated MRSI and MRI data processing, analysis, and visualization tools has been developed that is suited to processing ^{1}H MR Spectroscopic Imaging (MRSI) data for clinical research studies. Carried out under the MIDAS (**M**etabolite **I**mage **D**ata **A**nalysis **S**ystem) project, this effort also includes formation of a database of brain metabolite distributions in normal subjects that will contain comparison data to be used for evaluation of metabolic changes in individual subject data. A secondary aim of this project is to encourage the development of standardized MRSI acquisition and processing protocols and the MIDAS package will be made freely available to clinical research sites.

METHODS: The following figure illustrates that comprehensive reconstruction and analysis for MRSI data requires many inter-dependent processing steps, and incorporates reference and calibration data and information derived from spatially coregistered MRI of the subject, including tissue distribution functions, spatial transformation parameters, and brain region identification. The MIDAS package was developed to provide these functions in an integrated manner, including: i) automated MRSI processing and metabolite image formation; ii) Tissue segmentation; iii) spatial transformation and atlas matching; iv) Statistical analysis tools; and v) Image and spectral display. All processing functions can be run in a fully-automated manner. To manage the multiple data sets acquired and the complex processing sequence, a XML-based data management system was used. Additional features include open source software; support for Dicom and other image data formats from multiple manufacturers; and operation on multiple computer platforms.



Multiple 1H MRSI and MRI data of human brain have been obtained from normal subjects using a volumetric MRSI acquisition for TE=70 ms and lipid inversion-nulling, at 1.5 and 3 Tesla. Metabolite image results were normalized (to institutional units), spatially transformed to match a reference MRI dataset (BrainWeb, Montreal Neurological Institute), and averaged over all voxels.

RESULTS AND CONCLUSION: The following Figure shows the average NAA from 14 subjects, aged 27-48, obtained at 1.5T and displayed in the normalized MNI image space. The CSF-corrected metabolite concentration is displayed in color (highest concentration in red) and superimposed on the MNI data, shown in greyscale. All metabolites demonstrate considerable variation of concentrations throughout the brain. It is expected that comparisons between such average normal distributions and individual patient data will provide increased sensitivity to detection of disease and injury.



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