

Normal Brain Metabolic Distributions and Age-Dependent Changes

A. A. Maudsley¹, C. Domenig¹, A. Darkazanli¹, V. Govindaraju¹, Y. Gu², L. Hall², and C. Studholme³

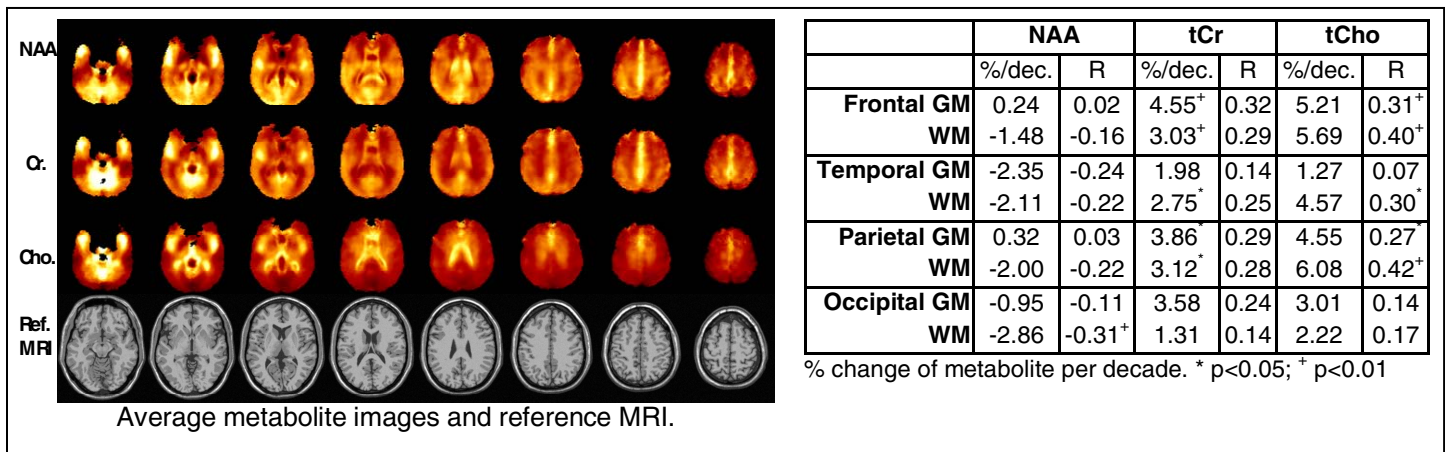
¹Radiology, University of Miami, Miami, FL, United States, ²Computer Science and Engineering, University of South Florida, Tampa, FL, United States, ³Radiology, University of California San Francisco, San Francisco, CA, United States

INTRODUCTION:

Detected signal intensities obtained by MRS in the brain vary according to location and a number of subject and acquisition variables. Therefore, the evaluation of metabolic alterations in individual subjects requires acquisition of comparison data for the same set of conditions. One of the aims of the MIDAS project¹ is to map metabolite distributions in normal subjects, thereby providing a comprehensive comparison database for use in MRS studies of disease and injury. Results from this analysis are presented.

METHODS:

MRSI data was obtained using volumetric EPSI at 3 T, with TE=70 ms, final voxel volume of 0.6 ml, and selection of a 14 cm slab covering the cerebrum. Data were acquired for 106 normal subjects, aged 19 to 59, of which 30% did not meet the required quality criteria. Reconstruction of the metabolite images using the MIDAS package¹ included spatial and signal intensity normalization of the metabolite images along with formation of images of the grey-matter, white-matter, and CSF content of each SI voxel, obtained by segmentation of coregistered T1- and T2-weighted MRIs.



The normal subject group was then analyzed using the PRANA program to obtain: a) images of the mean and standard deviation for each metabolite, and metabolite ratios, from selected age ranges; b) tissue-regression analysis by lobar region, as identified from a coregistered brain atlas based on the MNI BrainWeb MRI²; and c) voxel-based regression of metabolite values as a function of subject age.

RESULTS AND CONCLUSIONS:

The normal-subject tissue distributions are shown in the Figure for the fitted N-AcetylAspartate, creatine, and choline resonances, obtained using data from 35 subjects aged 19 to 30 (18 Male, 17 Female). Processing included exclusion of voxels with fitted metabolite results of linewidth greater than 10 Hz; exclusion of voxels with value exceeding 3 times the standard deviation of the data; correction for CSF signal loss if less than 40% CSF volume contribution; and calculation at a voxel only if more than 5 valid values were available. The results demonstrate differences between metabolite content from grey- and white-matter regions as well as variation within these regions.

Analysis of average metabolite values and alterations with age showed no variation between male and female subjects. Analysis of age-dependent changes in grey- and white-matter, obtained by tissue regression over lobar regions defined in the spatially-normalized reference atlas, is shown in the table, where the value is given as the % change, relative to the metabolite image for age 20, over each decade of age. A trend towards decreased white-matter NAA was observed, while the most significant age-dependent changes were observed for creatine and choline in both tissue types. Visual analysis of images generated directly from the voxel-based analysis of age-dependent changes of CSF-corrected metabolite values show no evidence of more localized changes.

In conclusion, the use of intensity and spatial normalization for MRSI provides a powerful approach for analysis of metabolite variations across subject groups.

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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). 2) D.L. Collins et al. Design and construction of a realistic digital brain phantom. *IEEE Trans. Med. Imag.* 1998; 17: 463-468.