Atlas-based analysis of brain MRSI data

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Introduction: Analysis of high-resolution, multi-slice or 3D magnetic resonance spectroscopic images (MRSI) of the brain using conventional tools is challenging due to the large number of spectra present. A commonly used approach is to average over voxels by defining regions of interest (ROI). However, identification of corresponding areas across subjects is not straightforward and, in addition of being time consuming, this approach may be biased by the inter-evaluator variations. We describe an approach to MRSI analysis based on atlas-based methods, where an automated 3D parcellation is applied in each individual, allowing to obtain an average spectrum, with high signal to noise ratio (SNR), for dozens of anatomically defined structures (ROIs) .

Methods: Experiments on 5 normal volunteers were performed on a 3T Achieva (Philips Healthcare Inc.) system equipped with a 32-channel head coil (InVivo). A 5-slice (13 mm thick) MRSI sequence was used to record images of choline (Cho), creatine (Cr), and N-acetyl aspartate (NAA), covering from the level of the 3rd ventricle to the vertex orientated parallel to the AC-PC line. High bandwidth RF pulses were used and an optimized dualband water and lipid suppression sequence. Scan parameters were TR/TE 3000/140 msec, FOV 240 x 240 mm, 32x32 matrix, voxel size 0.7 cm^3, scan time 14 minutes with a SENSE acceleration factor of 4. A non-water-suppressed MRSI scan and a high resolution 3D MP-RAGE scan were also recorded. Peak areas were automatically measured by integration, and for each slice, quantitative (mM) metabolic images were created by referencing to the brain water signal from the same voxel. As shown in Fig. 1, the MP-RAGE, co-registered with MRSI, was mapped to a single subject template[1] that was parceled into 73 3D ROIs, using large-deformation diffeomorphic metric mapping (LDDMM)[2]. Using the deformation fields from LDDMM and the linear matrix, the parcellation map was warped from our template to each subject original space. Each individual parcellation map was then eroded to account for sulcal or ventricular cerebrospinal fluid contamination and the cortex was segregate from white matter in peripheral ROIs, resulting in a final definition of 123 parcels per individual. The entire process was done using the software DiffeoMap and ROIEditor (www.mristudio.org). Cho, Cr and NAA concentrations, normalized by the water, were then automatically calculated from the defined parcels.

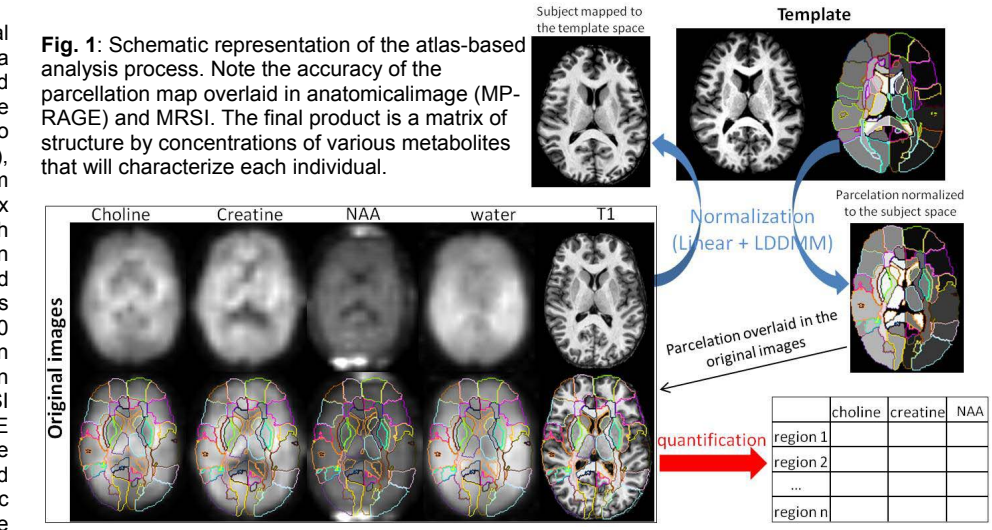

Fig. 1: Schematic representation of the atlas-based analysis process. Note the accuracy of the parcellation map overlaid in anatomicalimage (MP-RAGE) and MRSI. The final product is a matrix of structure by concentrations of various metabolites that will characterize each individual.

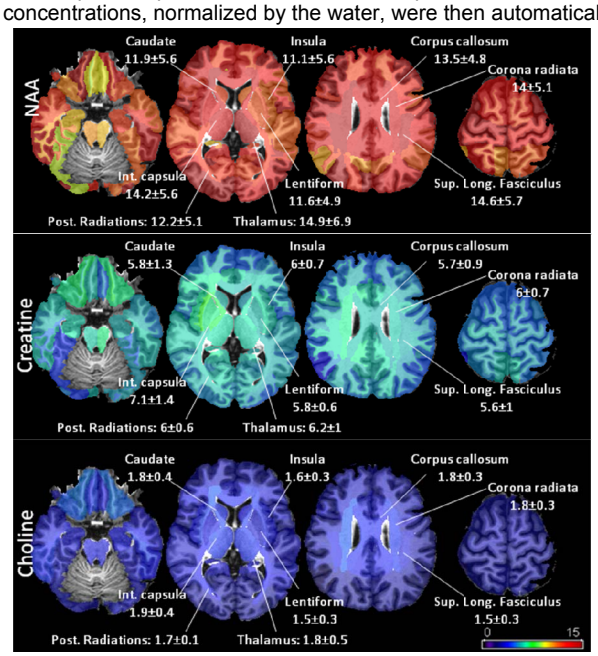

Fig. 2: Average of metabolic concentrations (±SD), per region. Colors represent concentrations in mM.

Results and Discussion: The average of metabolic concentrations, in mM, are represented in Fig. 2 and Table 1. These concentrations are in agreement to those previously described in gray and white matter. The average spectra from each parcel displayed substantial SNR improvement compared to spectra from individual voxels (typically >2 times higher SNR), as shown in Fig. 3.

Table 1	NAA	Cre	Cho
cortex	12.8±1.8	5.4±0.8	1.4±0.6
"peripheral" white matter	12.3±1.4	6±0.5	1.5±0.3
"deep" gray matter	13.2±1.7	6.3±0.6	1.7±0.2
Basal ganglia	12.8±1.4	6.1±0.5	1.7±0.1

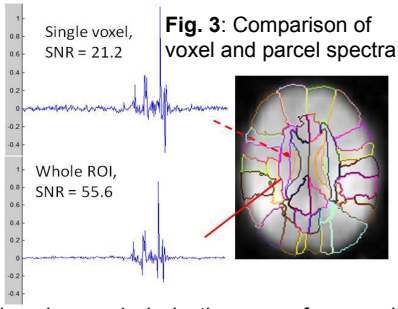

Fig. 3: Comparison of voxel and parcel spectra.

Using a highly reproducible method for automated 3D brain parcellation, we were able to average the spectra and quantify metabolites in multiple brain structures, therefore overcoming many of the limitations of the voxel-based analysis or of the manual techniques. Although the analysis of metabolites' signals in a common spatial reference was performed before[3], this study has several novelties, including the accurate algorithm used for normalization, the scheme of parcellation, and the possibility of integration of multimodality imaging analysis in the same framework. The definition of structure-specific normal concentrations is the first step for the future study of pathologies that affect the brain metabolism in a regional manner. Atlas-based methods may be suitable for patients vs. controls comparisons, or other applications such as longitudinal studies.

Conclusion: Automated, quantitative atlas-based analysis of MRSI data is feasible and yields results in good agreement with prior literature values obtained using manual analysis techniques. In the future, it may be used for automated comparison of patient and controls.

Bibliography: [1]Mori S, et al. *NeuroImage*, 40(2):570-582. [2]Miller MI, et al. 2005. *PNAS*, 102(27):9685-690. [3]Maudsley AA, et al. *NMR Biomed*. 2006;19:492-503. ***Acknowledges:*** NIH grants UL1 RR 025005 (AVF); P41RR15241, RO1AG20012, and RO1NS058299 (SM).