Towards structure specific quantitative macromolecular content of mouse brain from Chemical Shift Imaging data at 11.7 T

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Introduction

The MR spectroscopic macromolecular signal usually considered as a nuisance contribution in the quantification of short echo time signals might reveal some interest as a spectroscopic biomarker by itself [1]. The present work aims at studying the specificity of the macromolecular patterns within the mouse brain structures. In this paper a whole MRS coupled to MRI protocol is proposed going from acquisitions of the macromolecules using spectroscopic imaging and of high resolution mouse brain images to automated mouse brain structure segmentation and dedicated MRS quantification procedure.

Material and Method

MR acquisitions: All experiments were performed on C57BL/6 mice (N=2) strain on a vertical 11.7T wide-bore system using a 25 mm micro probe (Bruker Biospin). A chemical shift imaging (CSI) sequence was designed to acquire the spatial distribution of the macromolecules. This sequence was based on an inversion recovery preparation preceding a k-space weighted spin-echo sequence (TR/TE = 2500/6.5 ms, 20x20x2 mm^3 FOV, 21x21 in-plane CSI matrix, 512 data-points, bandwidth of 8 kHz, Tacq = 40 min.) combined with diffusion-weighted spectroscopy to eliminate residual metabolite contributions as proposed for monovoxel acquisitions in [2]. Inversion recovery was performed using a secant hyperbolic RF pulse (4ms, 4.5kHz Band Width) with an inversion time of 700ms. Diffusion weighting was applied with a $\bar{\delta}/\Delta$= 1.5/4 ms and the equivalent gradient strength was set to 770 mT/m giving a b-value of 338 s/mm^2. Signal from the outer volume was suppressed by six bands of spatial saturation pulses interleaved in the water suppression pulses (VAPOR). Field homogeneity was adjusted using FASTMAP. T_2-weighted RARE images (TR/TE=5500/64ms, slice thickness 0.24 mm, RARE factor=8, field of view=20.5x20.5 mm, matrix=256x256) were also acquired. The parameters of the T_2-weighted images were optimized to enhance contrasts between the brain structures and enable the subsequent structure segmentation.

Image and Signal processing: The T_2-weighted images were segmented using an atlas-based segmentation method. The image of the first mouse was considered as the atlas and its brain structures were manually segmented. This segmentation was then mapped on the other mouse images after non-rigid registration [3]. The CSI data were interpolated to 64x64 matrix to address partial voluming. The estimated masks took into account the spatial function response of the weighted k-space CSI acquisition. The macromolecular spectra of interpolated spectroscopic voxel were decomposed into a mixture of Gaussian obtained by an adaptation of the Expectation Maximization (EM) algorithm to the MR spectrum fitting [4].

Results: Figure 1, the segmentation based on atlas registration is illustrated. Figure 2 are representing the cortex and hypothalamus & thalamus masks reduced to a 64x64 matrix with corresponding representative macromolecules fitted using the dedicated EM algorithm. Each nine group of resonances reported in [5] are decomposed into 1 to 3 gaussians. On these preliminary results, differences on the M1, M2, M6, M7, M8 groups are observed between the two highlighted structures.

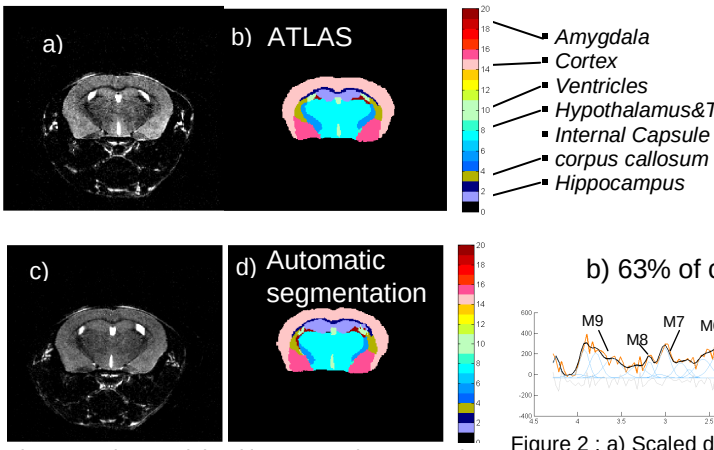

Figure 1 : a) T2 weighted image used to set up the b) atlas. c) T2 weighted image of a second brain mouse and the corresponding automatic brain structure segmentation d).

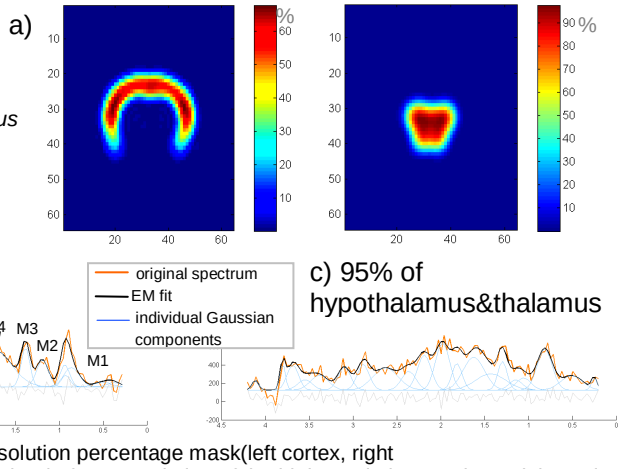

Figure 2 : a) Scaled down resolution percentage mask(left cortex, right thalamus&hypothalamus obtained after convolution of the high resolution masks and the Point Spread Function corresponding to the zero-filled 64x64 CSI-kspace weighted matrix. The original macromolecule spectra (orange) of a region containing b) 63% of cortex and c) 95% of hypothalamus&thalamus are fitted with the EM algorithm (black) as a mixture of Gaussian components (blue).

Conclusion: This novel method coupling MRS / MRI acquisition and dedicated post processing will enable quantitative and statistical exploration of the macromolecular contents to determine whether certain resonances of the macromolecular spectrum change with the brain structure or pathology.

Acknowledgements

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