Correction of Cerebral Metabolite Concentrations for Brain Tissue In Proton Spectroscopic Imaging

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Introduction

Segmenting different brain tissue of white matter (WM), gray matter (GM), cerebrospinal fluid (CSF) is very useful in various applications, especially for MRSI, in which probability maps of brain tissue are essential to quantify absolution concentration of metabolites [1]. Recently, fast spectroscopic techniques such as Proton Echo Planar Spectroscopy Imaging (PEPSI) have been repeated used to access metabolite information in different region because the properties of shorter acquisition time and better spatial resolution is very attractive in many applications [2]. Therefore it is desirable to have convenient process procedures for tissue type concentration correction on PEPSI. In this study, we investigate the possibility to do tissue type correction for metabolite concentrations on sagital view PEPSI using MRPAGE images and SPM. Two segmentation methods were enrolled. One is the widely used software SPM8 and another is Fuzzy C-Mean (FCM) based method [3]. We compare the performance of tissue segmentation and metabolite concentrations after correction between these two methods.

Material and Methods

Experiments were performed on a 3T system (Tim Trio, SIEMENS Medical Solutions, Erlangen, Germany). Five normal subjects were enrolled. Experiments were performed in following steps for each subject. 1.) Whole-brain MPRAGE,(slice thickness=1mm, TR=8.9msec, TE=2.27msec, Flip Angle= 7°, TI=1100msec, MAT =256*256, FOV =256*256) 2.) Sagital PEPSI slice collected in the left side of central line to cover cingulated gyrus (slice thickness=10mm, TR=2 sec., TE= 15 sec., MAT =32x32, FOV =256*256, NEX=8 for WS scan and NEX=1 for NWS scan). 3.) Five T1 weighted images collected by FLASH sequence (slice thickness=2mm, TR:250msec, TE:2.61msec, FA:70°, MAT:256*256, FOV:256*256) The spatial position of these 5 slices is located to match the position of PEPSI slice.

The whole analysis procedures can be separate in to following steps. 1) The spectroscopic analysis was done by LCModel [4]. Metabolites maps of NAA (N-Acetyl Aspartate), tCr (Creatine and Phosphocreatine) and Cho (Choline) were generated using water scaling. 2) Tissue segmentation was then carried out by SPM8 and self developed FCM based method on the MPRAGE images. Probability maps of GM, WM and CSF were generated. 3) We use image registration function provided by SPM8 to locate the five T1 images on the MPRAGE images. Since these five T1 images are in the same spatial position as PEPSI, the registration parameters can be then applied to the segmented results acquired in 2) to generate corresponding tissue probability maps for PEPSI, which is also carried out in SPM8 by re-slice function. 4) Metabolites maps generated in 1) can then be corrected according the tissue type using these tissue probability maps [1]. Comparison of segmentation methods was done by a regression analysis on the plot of corrected concentrations versus gray matter fraction (GM ratio/ (WM ratio + GM ratio)). Metabolites concentration in GM and WM can be extrapolated by the regression lines using pool data from five subjects or data from individual subject, as presented in ref [1].

Results

Method	Pooled data [NAA] (mM)		Individual subject data [NAA] ± SD (mM)		Inter-subject [NAA] CV	
	GM	WM	GM	WM	GM	WM
SPM	9.90	7.60	10.7 ± 0.88	6.5 ± 0.73	0.08	0.11
FCM	9.60	8.00	10.8 ± 0.98	7.3 ± 0.59	0.09	0.08

Table 1 List of Mean, Standard deviation (SD) and Coefficient of variance (CV) of NAA concentrations in GM and WM estimated by SPM and FCM.

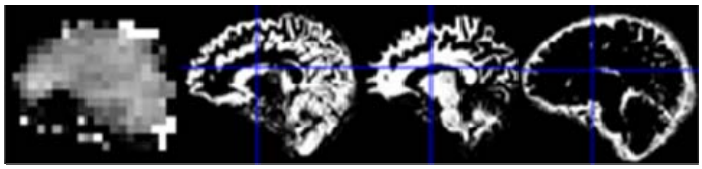

Figure 1 Corrected metabolite maps of NAA and corresponding tissue probability maps of GM, WM and CSF after re-slice by SPM8 (LEFT to RIGHT)

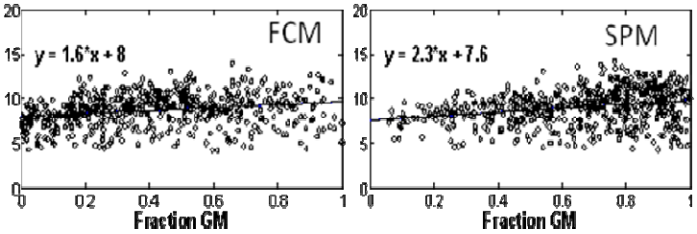

Figure 2 Regression analysis for pooled data [NAA] and fractional GM determined from FCM and SPM .

Figure 1 showed that segmentation results matched well with the metabolites maps after registration and re-slice by SPM. Figure 2 depicted the regression results of pooled data and summary of regression results were listed in Table 1. The difference of SPM and FMC estimated NAA concentrations in GM and WM were less than 0.4 mM. According to results reported in Ref [1], the inter-subject variability is low for both methods, which implies that segmentation on MPRAGE is quite reliable.

Discussion

In this preliminary study we have successfully integrated the MRSI process procedures with segmentation results carried out on MPRAGE images using SPM software. We also demonstrated that tissue type metabolite concentration correction can be done by the proposed procedures using both FCM based method and SPM itself. This is convenient in several ways. Firstly, 3D whole brain anatomic images are usually collected in the many experiments. Once the data is acquired, they can be applied to the following MRSI data collected at various slice orientation and different regions with only extra T1scans in corresponding slices. Secondly, segmentation on high resolution T1 image such MPRAGE is more reliable because of better tissue contrast and spatial information. By our results we also showed that SPM can be combined with self-developed segmentation method or other software. For further studies, we will enroll more subjects and carefully compares results of other metabolites and different slice orientation of PEPSI. We will also try to include other segmentation software such as FSL's FAST segmentation routine [5]. In conclusion, this proposed procedure can be potentially useful for studies when PEPSI are performed in multiple sessions and in different slice orientations.

Reference

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