Multi-Parametric Approach to Automatic Regional Analysis of Quantitative Relaxation Times in the Brain

B. S. Aribisala[1], and A. M. Blamire[1]

[1]Newcastle Magnetic Resonance Centre, Newcastle University, Newcastle upon Tyne, Tyne and Wear, United Kingdom

Introduction

A significant step in the analysis of quantitative imaging data (e.g. relaxation time mapping) is accurate definition of regions of interest within a single tissue type. Such analysis is often done using interactive definition of regions of interest on each of the quantitative images to be analysed (e.g. T_1 or T_2). This approach is sensitive to image resolution which introduces partial volume effects which can bias the analysis. Here we propose a fully automatic and multi-parametric approach whereby the complementary information in multiple quantitative images are considered in order to classify each quantitative image into its tissue classes. We report here the case of T_1 and T_2. The proposed analysis is divided into 2 stages. In the first stage we define the regions of interest for each of T_1 and T_2 using our previously proposed method[1]. These regions are re-defined in the second stage by combining T_1 and T_2 using a clustering algorithm.

Methods

Modelling: In the algorithm presented below we used our previously developed[1] real space analysis but using a standard brain regions template (STDT) developed from the template of Brodmann's areas and the MNI T_1w high resolution image (STDB), (supplied with MRIcro[2]). STDT comprises the entire brain divided into 16 regions (pairs of right and left inferior frontal lobe, superior frontal lobe, temporal lobe, temporal-occipital lobe, occipital lobe, temporal-parietal lobe, parietal lobe and the cerebellum) which are the target regions of interest to be automatically analysed.

Algorithm: For each dataset to be analysed, the brain region is extracted from the surrounding tissues using a standard algorithm [3]. The subject's high resolution anatomical scan (ANA) (e.g. T_1w) is re-sampled to the native resolution of the quantitative data to be analysed, yielding ANA_RE. For each subject STDT is then transformed to the individual subject's (real) space using a two stage registration[4]. Firstly STDB is registered to the ANA_RE and the transformation matrix TRM computed. TRM is then applied to STDT to obtain STDT_reg_ANA_RE. Next, ANA_RE is segmented into white matter, grey matter and CSF masks[5]. Using STDT_reg_ANA_RE as a template each of the 3 tissue classes is then sub-divided into the 16 spatial regions. This process automatically generates a set of 48 specific regions covering the whole brain in real space. Finally, these ROIs can be applied to the quantitative images under analysis (QIMG), but the accuracy of analysis is based on the initial tissue classification of ANA.

Multi-Parametric Analysis: In order to remove the PVE in each region data from multiple imaging channels is next combined. In this study spatially aligned quantitative T_1 and T_2 data were used. T_1 and T_2 relaxation times were normalised to unit variance and zero means and T_2 time was plotted against T_1 time on a regional basis. A clustering algorithm based on k-means using a Euclidean distance based measure was then applied to divide the entire points into 3 classes and the major cluster retained for final analysis of relaxation times.

MR Protocol: The method was tested on data acquired using a 3.0T whole body system (Philips Achieva, Best, NL) using an 8-channel SENSE head coil. Eleven normal adults (mean age 41yrs) with no clinical evidence of neurological diseases were scanned. Available data were (a) high resolution T_1w anatomical scan (TR=8.1ms, TE=4.6ms, 1mm isotropic), (b) a fast quantitative T_1 measurement using a custom IR-EPI sequence (TR=15s, TE=24ms, TIR=0.25-2.5s(12steps), matrix 128x128, 72 slices, resolution=2mm isotropic), (c) quantitative T_2 measurement using a multi-spin echo sequence (TR=3s, 8 echoes dTE=20ms, matrix as T_1 measurement) and, (d) Low resolution fieldmap using a dual echo 3D GRE (TR=27ms, TE=2.6,6.1ms) which was applied to all EPI data to correct for spatial distortion.

Analysis: Quantitative T_1 and T_2 times were calculated on a pixel by pixel basis to yield 3D isotropic relaxation maps. The algorithm was then used to automatically determine the regional grey and white matter T_1 and T_2 histograms.

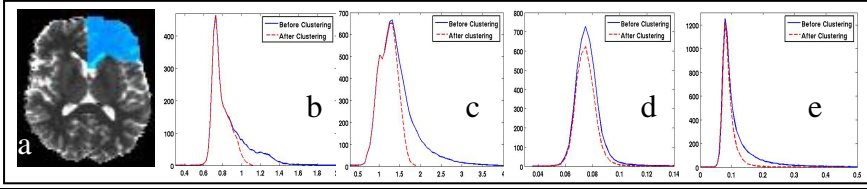

Fig1: (a) Quantitative T_1 image overlaid with Right Frontal Inferior lobe ROI, (b), (c), (d) and (e) are the quantitative histograms of white matter T1, grey matter T1, white matter T2 and grey matter T2 respectively in the overlaid region for before and after clustering.

	Before Clustering (quant. values in ms)				**After Clustering**(quantitative values in ms)			
Region	T_1WM	T_2WM	T_1GM	T_2GM	T_1WM	T_2WM	T_1GM	T_2GM
Superior Frontal	866± 143	86± 10	1400± 700	115± 122	809± 67	84± 5	1159± 261	90± 23
Temporal	879± 234	81± 36	1345± 431	101± 65	798± 89	78± 11	1210± 235	89± 19
Occipital	869± 191	83± 17	1236± 383	94± 44	793± 72	82± 7	1041± 176	81± 11
Parietal	880± 212	84± 17	1375± 507	108± 84	807± 80	83± 9	1171± 219	87± 19
Cerebellum	1036± 315	91± 44	1405± 420	107± 67	904± 115	85± 14	1286± 187	94± 20

References :[1] Aribisala et. al., ISMRM 2008,3043, [2] Rorden et. al. Behaviour Neurology, 200;12(4):191-200, [3] Jenkinson et. al., *NeuroImage*, 17(2):825-841, 2002. [4] Jenkinson et. al., *Eleventh Annual Meeting of the Organization for Human Brain Mapping*, 2005. [5] Zhang et. al.; *IEEE Trans. on Medical Imaging*, 20(1):45-57, 2001.

Results and Discussions

Figure 1 illustrates the location of one automatic ROI (right frontal lobe) together with the accompanying histograms obtained from WM and GM within the ROI before and after 2D clustering. The histograms show approximately Gaussian distributions with PVE manifesting as sidelobes and contributing about 22% (T_1WM), 4%(T_1GM), 3%(T_2WM), and 4%(T_2GM) of the total area before clustering. After clustering these values reduced to 4% (T_1WM), ~0%(T_1GM), 1%(T_2WM) and ~0%(T_2GM) of the total area. These data show that multi-parametric method substantially reduced PVE errors. This finding was supported by the regional mean relaxation times which showed that the all the mean values are reduced after clustering (table).

Conclusions

We have shown that a fully automatic multi-parametric algorithm significantly improves quantitative analysis of brain imaging data.

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