Comparison of Analysis of Brain Relaxation Times in Standard Space with Analysis in Individuals' Real Space

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Introduction

One commonly used approach for image analysis is to register all images to a standard space. This approach has the major benefit that target regions on the standard space brain need only be defined once and can then be applied to any other dataset. However, we hypothesize that this approach introduces partial volume effects (PVE) as a result of re-sampling and spatial smoothing inherent in the registration processes, and that these PVE will bias analysis of quantitative parameters such as T_1 or T_2. We have previously proposed an alternative method[1] whereby the target ROIs are still defined in standard space, but are then transformed into real space where quantitative analysis is performed. We hypothesize that this approach should suffer from less PVE than performing analysis in a standardised space. In what follows we present and compare the performances of two algorithms based on the conventional standard-space approach and our alternative real-space approach.

Methods

Modelling: In both algorithms presented below we used our previously developed[1] standard brain regions template (STDT). STDT was developed from standard template of Brodmann's areas and MNI T_1w high resolution image (STDB), both images are supplied with MRIcro[2]. STDT comprises of the entire brain divided into 16 regions, these are 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. The first step in both algorithms described below is to extract the brain from the surrounding tissues in all the datasets to be analysed[3].

Algorithm 1 – Real Space Method (RSM): 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 image under analysis (QIMG, e.g. T_1 or T_2).

Algorithm 2 - Standard Space Method (SSM): The quantitative image (QIMG) is registered to STDB using a four stage registration[4]. Firstly the individuals' high-resolution anatomical scan (ANA) is registered to STDB and the transformation matrix TRM_A is computed. Next, the quantitative image to be analysed (QIMG) is registered to ANA and the transformation matrix TRM_B is computed. TRM_A is multiplied by TRM_B to derive TRM_C which is applied to QIMG to obtain QIMG_reg_STDB. Then ANA is registered to STDB to yield ANA_reg_STDB which is then classified into white matter, grey matter and CSF. Using STDT as a template each of the 3 tissue classes is then sub-divided into 16 regions to automatically generate 48 specific ROIs covering the whole brain in standard space. Finally, ROIs are applied to QIMG_reg_STDB.

MR Protocol: The two algorithms were tested on data acquired using 3.0T whole body 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. Scans acquired in each subject 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, and, (c) 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 times were calculated on a pixel by pixel basis to yield 3D isotropic relaxation maps. Both algorithms were then used to automatically determine the regional grey and white matter T_1 histograms.

Results and Discussions

The figure illustrates the location of one automatic ROI (right frontal lobe) together with the accompanying histograms obtained from WM and GM within the ROI using the 2 methods. In this region, the histograms show approximately Gaussian distributions with PVE manifesting as sidelobes and contributing about 42% (SSM) and 22% (RSM) of the total T_1WM area. These data show that SSM introduced more PVE errors than the RSM. This finding was supported by the regional mean relaxation times which showed that the T_1 WM values in the standard space method were all greater than those in the real-space method – illustrative data in table.

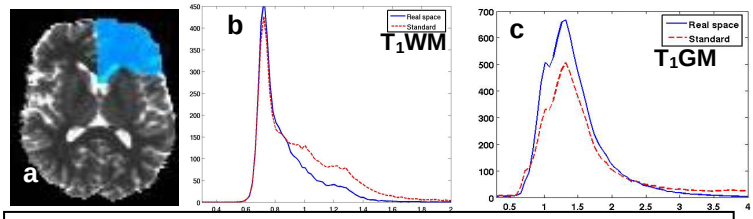

Fig1: (a) Quantitative T_1 image overlaid with Right Frontal Inferior lobe ROI, (b) and (c) quantitative histograms of white matter and grey matter T_1 in the overlaid region using both real space (blue) and standard space (red) methods.

	T1 White Matter ROI (s)	
Region	**Real Space Method**	**Standard Space Method**
Superior Frontal	866±143	1002±369
Temporal	879±234	965±320
Occipital	869±191	924±344
Parietal	880±212	995±382
Cerebellum	1036±315	1126±404

Conclusions

We have shown that regional analysis of MRI brain data in standard space introduces partial volume effects as a result of re-sampling and smoothing using in the registration processes and that these partial volume effects bias analysis of quantitative parameters such as T_1 or T_2. Therefore we propose analysis in the subject's real space whereby the target ROIs are defined in standard space, but are then transformed into real space where quantitative analysis is performed.

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