On Automatic Regional Analysis of Quantitative Relaxation Times Mapping in the Brain

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Introduction

Quantitative assessment of MR images is an important step in the analysis of many types of scan data. Manual definition of regions of interest (ROI) is time consuming and may display user bias or poor reproducibility due to human error. Alternatively, automatic algorithms can be used. A significant step in many automatic methods is registration of the individual brain to a standard space (e.g. Talairach space) which normalises variation in brain size and shape and allows use of standardised ROIs. While this process is less subjective than manual ROI definition, image registration requires spatial smoothing and re-sampling and introduces partial volume effects, biasing analysis of quantitative parameters such as T_1 or T_2 and does not handle atrophy well. Here we propose an automatic division into ROIs and we use the inverse process whereby regions of interest in standard space are registered to the *individual*, thereby analyzing each brain in its own real space. This approach reduces partial volume errors while taking into account variations in brain shapes and sizes. Additionally quantitative data is analysed at the native matrix size allowing analysis of data with differing resolution. The proposed algorithm requires a high resolution anatomical image together with the image to be analyzed; both of which are commonly acquired.

Methods

Modelling: Starting from a single reference brain in standard space (STDB), a standard brain region template (STDT) was developed by dividing STDB into 16 regions based on lobes and hemisphere. These regions 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*.

Algorithm: For each dataset to be analysed, the brain region is extracted from the surrounding tissues using a standard algorithm [1]. The subjects' high-resolution anatomical scan is re-sampled to the native resolution of the image to be analysed (e.g. quantitative T1 or T2 maps), this produces ANA_RE. STDT is transformed into the subject's space using a 2 stage registration process. Firstly, STDB is registered to ANA_RE [2] and the transformation matrix TRM is computed. TRM is then applied to STDT to obtain STDT_REG_ANA_RE. Then ANA_RE is classified into white matter, grey matter and CSF [3]. To reduce partial volume effect only tissues that were at least 99% classified were accepted. Using STDT_REG_ANA_RE as a template, each of the 3 tissue classes are sub-divided into 16 regions generating a set of 48 specific ROIs (ANA_RE_48) covering the whole brain in real space. Finally, ROIs are applied to quantify the dataset to be analysed (see Figure 1a and 1b).

MR Protocol: The modelling and analysis were tested on data acquired on a 3.0T whole body Philips Achieva System (Best, NL) using an 8-channel SENSE head coil. Ten normal adults (mean age 44yrs, SD 15yrs) with no evidence of neurological diseases were scanned. Four scans were acquired in each subject (a) high resolution T_1weighted anatomical scan (TR=8.1ms, TE=4.6ms, matrix 150x240x240, resolution = 1mm isotropic), (b) a fast quantitative T_1 measurement using a custom IR-EPI sequence (TR=15s, TE=24ms, TIR=0.25 to 2.5s(12steps)) matrix 128x128, 72 slices, resolution=2mm isotropic, (c) a quantitative T_2 measurement (TR=4.7s, 8 spin echoes at 20ms spacing, EPI factor 5, matrix 128x128, 72 slices, resolution=2mm isotropic) and, (d) Low resolution B_o 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 grey and white matter relaxation times. Finally, a cost-based method [4] was used to compute each regional histogram.

Results

Table 1 summarises the values of T_1 and T_2 in all the regions studied. These show agreement with published data at 3T [5, 6]. Typical histograms in Figures 1c and 1d show approximately Gaussian distributions. These figures confirm that the analysis is largely free from partial volume errors. Inter-subject variation is higher in grey matter than white matter due to partial volume effects inherent in the *acquired* quantitative data (2mm resolution).

Table 1: Quantitative T_1 and T_2 (mean and standard deviation) values in 10 control subjects using the proposed analysis method

Region		T1 White Matter (ms)	T1 Grey Matter (ms)	T2 White Matter (ms)	T2 Grey Matter (ms)
Frontal Inferior	R	786 ± 132	1421 ± 264	75 ± 8	104 ± 45
	L	774 ± 113	1432 ± 275	75 ± 7	104 ± 47
Frontal Superior	R	839 ± 113	1553 ± 240	87 ± 8	141 ± 119
	L	822 ± 102	1516 ± 284	87 ± 7	147 ± 127
Temporal	R	826 ± 137	1391 ± 286	80 ± 14	100 ± 45
	L	798 ± 118	1357 ± 266	80 ± 12	102 ± 46
Temporal Occipital	R	788 ± 116	1408 ± 252	82 ± 8	98 ± 33
	L	749 ± 63	1388 ± 288	82 ± 8	97 ± 34
Occipital	R	803 ± 150	1243 ± 272	84 ± 7	90 ± 27
	L	771 ± 78	1263 ± 277	84 ± 7	90 ± 28
Temporal Parietal	R	837 ± 133	1458 ± 329	79 ± 12	99 ± 36
	L	830 ± 136	1384 ± 251	79 ± 12	95 ± 30
Parietal	R	840 ± 159	1454 ± 269	86 ± 12	115 ± 67
	L	828 ± 116	1472 ± 301	87 ± 11	120 ± 78
Cerebellum	R	949 ± 226	1393 ± 211	93 ± 44	104 ± 40
	L	946 ± 206	1390 ± 210	91 ± 35	104 ± 48

Conclusions

We have shown that regional analysis of MRI brain data in subject space can be performed using a simple automated algorithm which is time efficient, reproducible and largely free of partial volume effect.

References

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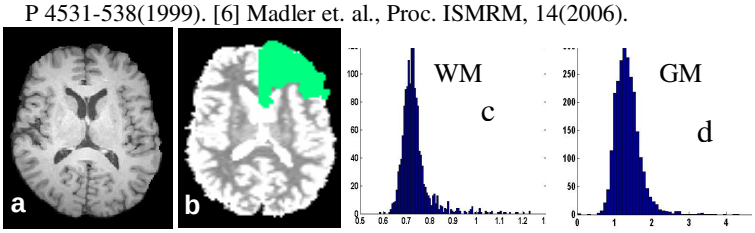

Fig1: (a) Anatomical image, (b) Quantitative T_1 image overlaid with Right Frontal Inferior lobe ROI, (c) and (d) are the histograms of the quantitative T_1(seconds) of white matter and grey matter in the Right Frontal Inferior lobe

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