

Accurate Estimation of Tissue Volumes by means of Quantitative MR on patients with Multiple Sclerosis

J. West^{1,2}, J. B. Warntjes^{2,3}, P. Lundberg^{1,2}, and A. M. Landtblom⁴

¹Department of Medicine and Health, Division of Radiation Physics, Linköping, Sweden, ²Center for Medical Imaging Science and Visualization, Linköping, Sweden, ³Department of Medicine and Health, Division of Clinical Physiology, Linköping, Sweden, ⁴Department of Clinical and Experimental Medicine, Division of Neurology, Linköping, Sweden

Introduction: Tissues in the human body are distinguishable based on their MR parameters, such as T1 relaxation, T2 relaxation and the proton density (PD). Recently a method to accurately quantify these parameters within a clinically feasible acquisition time was presented. It was also shown that brain tissues group into clusters in the Functional Relaxometric Classification (FRC) 3D parameter space formed by R1, R2 and PD ($R1 = 1/T1$, $R2 = 1/T2$) (Warntjes *et al.*, Magn Reson Med 2008;60:320-329). In voxels where two tissues are present both contribute to the MR signal and quantification yields a weighted average of these. In this work it is shown that the volume fraction of the tissues in these partial volume voxels can be determined based on the R1, R2 and PD measurements. When volume fractions have been determined it is straightforward to calculate tissue volumes for whole brain coverage this method was applied to a group of patients with Clinically Definite Multiple Sclerosis (CDMS) and it is shown that the absolute volume of MS lesions can be determined. This is very important input for quantitative patient follow-up monitoring the progress of the disease.

Method: The imaging method QRAPMASTER (*Quantification of Relaxation times and Proton density by Multi-echo Acquisition of Saturation recovery with TSE Read-out*) allows for the quantification of T1, T2 and PD. 21 healthy volunteers (16 male, 5 female, average age 29) were scanned using this imaging method to establish reference tissue clusters for white matter (WM), gray matter (GM) and cerebrospinal fluid (CSF). The relaxation behavior of partial volume voxels with different volume fractions of these tissues were then simulated, using an in-house Bloch simulator (MATLAB R2008a, MathWorks, 2008), in order to find a relation between observed R1-R2-PD and volume fraction. Removing all WM, GM and CSF from the complete brain, results in remaining tissue that can be considered pathological. Using this method brain tissue volumes were quantified in a group of MS patients. Resolution was 1 mm and a slice thickness 5 mm, 24 slices were acquired and scan time was 5:34 minutes. All scans were performed using a 1.5 T Achieva (Philips Healthcare, the Netherlands)

Results: The simulation of partial volumes is shown in Fig 1. Fig. 2 shows the quantified qMRI-maps for a single 5 mm slice of one patient brain (CDMS), containing plaque formation below the right ventricle. The result of the segmentation is shown in Fig 3.

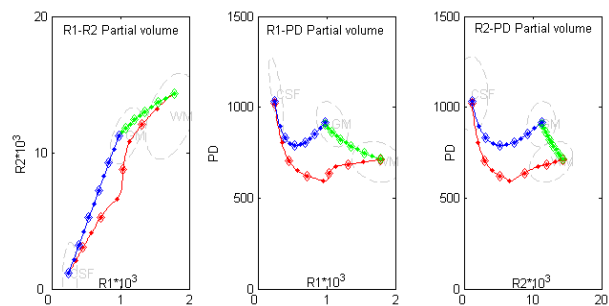


Fig 1. Simulated partial volume graphs with different volume fractions of WM, GM and CSF in R1-R2-PD space. The green lines show partial volume for GM->WM, blue lines shows CSF->GM and red lines show CSF->WM. Each diamond represents steps of 20% tissue and each dot represents steps of 10% tissue. The partial volumes in the R1-R2 plane correspond to volume fractions in a linear manner for straight lines between the tissues.

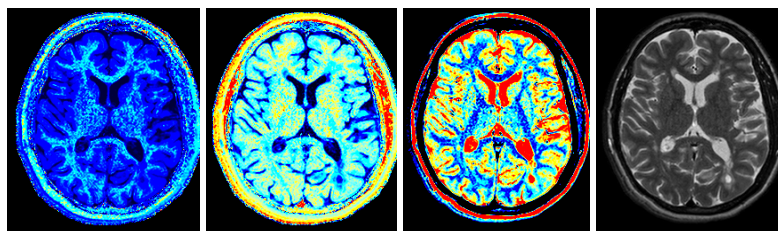


Fig 2. Patient brain: R1 map (scale 0-3 s^{-1}), R2 map (scale 0-2 s^{-1}), PD map scale (50-100% water). The last image shows a T2-weighted image as reference.

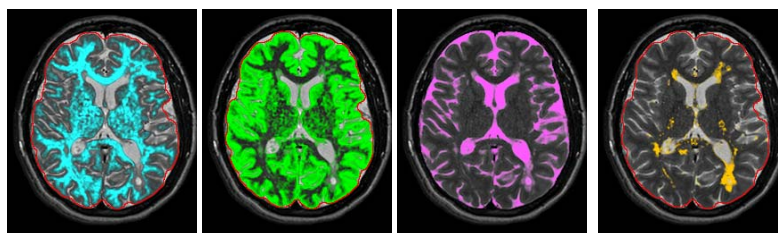


Fig 3. Segmentation overlay corresponding to WM (blue), GM (green), CSF (purple) and pathology (yellow). Notice the plaque formation in the lower right portion of the images. The calculated tissue volumes in this single slice were: WM 14.0 mL, GM 23.4 mL, CSF 8.2 mL and 0.9 mL pathological tissue.

Conclusion: R1-R2-PD values can be used to determine the volume fractions of WM, GM and CSF in the brain as well as identifying deviating tissues, i.e. pathologies. Volume estimation can be performed accurately on a sub-voxel basis, using the method described here and plaque volumes can be quantified. Using a quantitative approach for brain tissue volumes will greatly increase the ability to monitor disease progress in MS patients.