Fast Phase Based Registration for Robust Quantitative MRI

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INTRODUCTION: Quantitative magnetic resonance imaging has the major advantage that it handles absolute measurements of physical parameters. Quantitative MRI can for example be used to estimate the amount of different tissue types in the brain, but other applications are possible. Parameters such as relaxation rates R_1 and R_2 and proton density (PD) are independent of MR scanner settings and imperfections and hence are directly representative of the underlying tissue characteristics. Brain tissue quantification is an important aid for diagnosis of neurological diseases, such as multiple sclerosis (MS) and dementia. It is applied to estimate the volume of each tissue type, such as white tissue, grey tissue, myelin and cerebrospinal fluid (CSF). Tissue that deviates from normal values can be found automatically using computer aided diagnosis. In order for the quantification to have a clinical value, both the time in the MR scanner and the time for the data analysis have to be minimized. A challenge in MR quantification is to keep the scan time within clinically acceptable limits. The quantification method that we have used is based on the work by Warntjes et al. [1].

METHODS: The MR sequence used is a single multi-echo, multi-delay saturation recovery spin echo sequence, providing R_1, R_2, proton density (PD) and the B_1 field at high resolution (1 x 1 x 5 mm), in a scan time of 6 minutes, covering the whole brain. We collect 4 different volumes, with 6 echoes in each volume. Each volume has a resolution of 256 x 256 x 27 voxels.

In order for the tissue quantification to work properly, the collected volumes have to be perfectly aligned. The problem with the volumes is that they differ significantly in intensity, see Figure 1. We had to rescale the intensity values in order to show the four slices at the same time, the real intensity difference is thus even bigger. The most common approach to perform registration of volumes with different intensity, or from different modalities, is to find the translation and rotation parameters that maximize the mutual information between the volumes, as proposed by Viola et al. [2]. Our registration algorithm is instead based on optical flow, but instead of optical flow of the image intensity that is normally used, we use the local phase from quadrature filters. The advantages of using the local phase is that it is invariant to a change of intensity and that it varies more smoothly than the intensity itself. It thereby better suits the assumptions made in the optical flow algorithm. For details about phase based registration, see for example the work by Hemmendorff et al. [3]. Phase based registration is however quite computationally demanding, since one volume has to be convolved with a number of quadrature filters in each iteration. Therefore we have used the computational power of graphic cards to speedup the registration, similar work has been done by Muyan et al.[4]. Our GPU implementation is about 50 times faster than our CPU implementation.
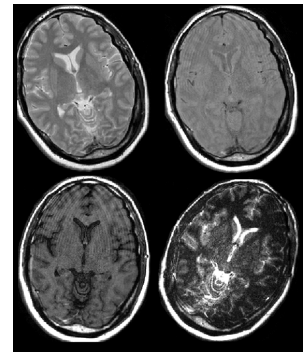
Fig 1. A slice of each of the four volumes that has to be registered to each other in order for the tissue quantification to work properly.

RESULTS: We collected two different datasets of the same subject, one where the subject tried to lie still during the whole scanning, and one where the subject was told to rotate the head between the volumes. As comparison to our registration algorithm we used the statistical parametric mapping (SPM) software, by Friston et al.[5], that is based on the mutual information approach. Volume 2, 3 and 4 were registered to the f irst volume. In order for SPM to manage the registration of volume 4, we had to apply a lowpass filter of size 7 mm (FWHM), otherwise the registration failed. The results of R_1 quantification and gray matter quantification, with and without registration, are given in Figure 2 and Figure 3.

DISCUSSION: We have presented a method for fast phase based registration of MR volumes that differ significantly in intensity and we have proved that our registration algorithm is more robust than SPM, since our method did not need any extra modification of volume 4. Our registration algorithm is also significantly faster since it performed the registration of the 3 volumes in 8 seconds, while SPM needed 2 minutes. Our algorithm makes the data analysis faster and in the future we would also like to speedup the tissue quantification itself.
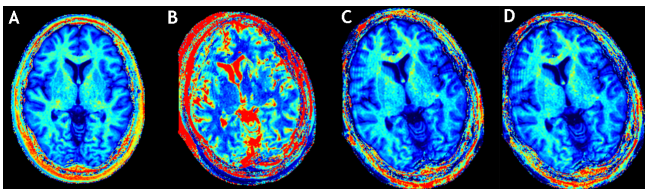

Fig. 2 Example of quantification of the relaxation rate R_1 on a healthy volounteer. **A:** Normal measurement without movement. **B:** Corrupted measurement where the subject rotated his head from left to right. **C:** Motion corrected image with our algorithm. **D:** Motion corrected image with SPM.

Fig. 3 Example of quantification of gray matter on a healthy volounteer. **A:** Normal measurement without movement. **B:** Corrupted measurement where the subject rotated his head from left to right. **C:** Motion corrected image with our algorithm. **D:** Motion corrected image with SPM.
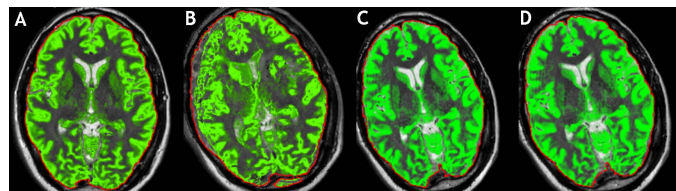
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