Automatic Brain Segmentation using Fractional Signal Modelling of a Multiple Flip-Angle Spoiled Gradient-Recalled Echo Acquisition

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Purpose: Automatic brain segmentation based on quantitative MRI has yielded significant interest in recent years [1,2]. Multi-component modelling of a multi-TI inversion recovery (IR) acquisition provides robust segmentation through the 'FRASIER' concept (developed by Shin et al. [1]), which has been applied to morphological imaging [1] and low-resolution perfusion MRI [3,4]. We suggest adapting multi-component quantitative MRI modelling to another common T1 mapping method, namely the spoiled gradient-recalled echo (SPGR) sequence with variable flip angle (VFA) acquisition [5]. The potential of the proposed segmentation method, dubbed 'SPGR-SEG', was previously demonstrated using simulations [6], and in this work we present the first in vivo results.

Methods: Assuming that each voxel contain up to three components, i.e., gray matter (GM), white matter (WM), and cerebrospinal fluid (CSF), each with a unique signal contribution (fractional signal) and a representative T1 value, the SPGR signal can be modelled as

$$S(\theta) = \sin(\theta) \sum_i f_{s,i} \frac{1 - \mathrm{e}^{-TR/T_{1,i}}}{1 - \cos(\theta)\, \mathrm{e}^{-TR/T_{1,i}}}$$

where θ is the flip angle (FA), TR is the repetition time, and $f_{s,i}$ and $T_{1,i}$ are the fractional signal and the longitudinal relaxation time of compartment $i = \{CSF, GM, WM\}$, respectively. Flip angle correction is important for T1 mapping with VFA, and was accomplished using the double angle method (DAM) [7].

Five healthy subjects (2F and 3M, 31±3.4 y) were scanned using a conventional 3D SPGR sequence. The study was performed in agreement with national and local ethics guidelines, and all volunteers gave written informed consent. The experiment was performed on a 3T MRI unit (MAGNETOM Skyra, Siemens Healthcare, Erlangen, Germany) using the following parameters: 52 slices, 3 mm slice thickness, 128×128 matrix, 1.72×1.72 mm^2 resolution, FA=2°/5°/10°/15°/20°/25°/30° , TR/TE=11/4.2 ms, at a total scan time of 4 min 40 s. For flip angle correction, two 2D SPGR sequences was performed: 52 slices, 3 mm slice thickness, 64×64 matrix, 3.44×3.44 mm^2 resolution, FA=45°/90°, TR/TE=10000/2 ms, at a total scan time of 12 min 4 s. For comparison purposes, data from a multi-TI IR experiment were also acquired using the following parameters: 52 slices, 3 mm slice thickness, 128×128 matrix, 1.72×1.72 mm^2 resolution, TR/TE=3750/11 ms, TI=50/250/500/750/1000/1500/2000/2500 ms, at a total scan time of 15 min 52 s.

Flip angle correction maps were calculated using the DAM [7], and T1 was estimated voxel-wise by nonlinear regression (i.e., conventional VFA T1 mapping [5]). T1 of GM and WM were estimated from the position of largest peaks in a whole brain T1 histogram. Due to the few voxels containing high fractions of CSF, the mean T1 in CSF was estimated from a manual ROI placed in the lateral ventricles. Segmentation was accomplished by linear least squares estimation of $f_{s,i}$ according to the proposed model. Fractional volumes were calculated by dividing fractional signals with assumed water contents of 100%, 89% and 73%, for CSF, GM and WM, respectively. Segmentation based on the IR data was performed as proposed by Shin et al. [1].

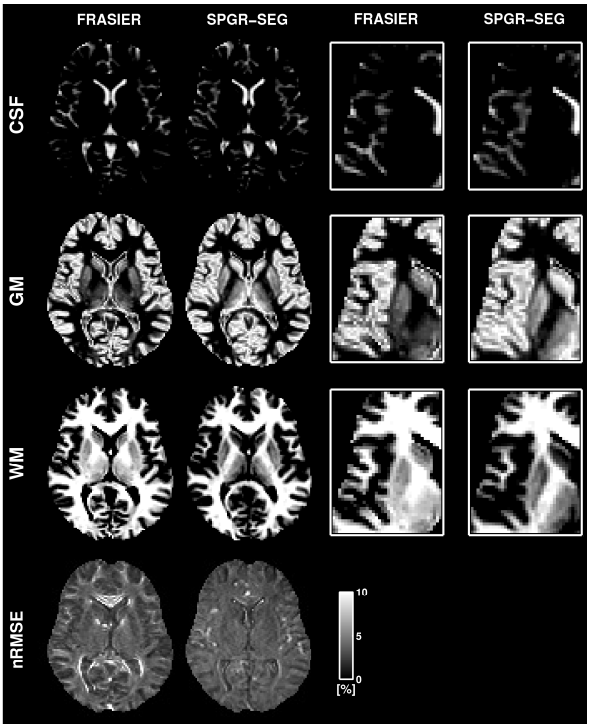

Figure 1. Segmentation of CSF, GM and WM using the reference method (FRASIER) and the proposed method (SPGR-SEG) in one slice of one subject. The two panels to the upper right display zoomed volume maps and the bottom row displays nRMSE of the respective model fit.

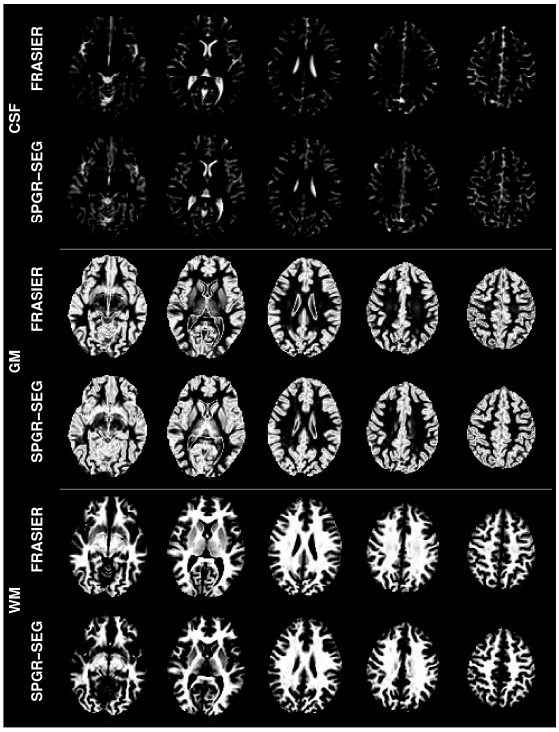

Figure 2. Comparison of segmentation results using FRASIER and SPGR-SEG in five slices of one subject.

Results: Figure 1 displays segmentation results using the reference method (FRASIER) and the proposed method (SPGR-SEG). A zoomed view of a part of the fractional volume maps is included to facilitate closer inspection of the quality of the segmented maps. Voxel-wise normalized root-mean-square error (nRMSE) of the respective model fit, corresponding to residual variance in percentage of the range of observable signal values, is also displayed. The mean nRMSE in all subjects was (mean±SE) 3.5±0.04 for FRASIER and 3.5±0.06 for SPGR-SEG. Figure 2 displays a comparison of segmentation results in five slices of one subject. Estimated SNR, defined as the maximum signal divided by the standard deviation in a background ROI (corrected for Rayleigh distribution), was (mean±SE) 376±35 for FRASIER and 582±32 for SPGR-SEG.

Discussion and Conclusion: The proposed method yielded robust and realistic segmentation results in all the investigated subjects. In general, the SPGR-SEG output agreed well with the segmentation maps produced by the reference method. However, it seemed as if deep gray matter structures were more clearly delineated in the GM map originating from SPGR-SEG (Fig. 1), and differences in segmented CSF are also noticeable between the two methods (Fig. 2). Observed segmentation differences are most likely associated with the modelling (i.e., how the methods handle mixed voxels), and with differences in T1 mapping, but could also be related to SNR (SPGR-SEG had a significantly higher SNR). Calculated nRMSE was equal for both methods which mean that no model explained its corresponding data better, overall. On the other hand, spatial differences in nRMSE can be clearly seen in Figure 1.

The segmentation quality of the proposed method was clearly comparable to the reference method, although differences between the methods do exist and need to be further investigated. SPGR-SEG is particularly suitable for applications in which SPGR-based T1-mapping is already included, e.g., dynamic contrast enhanced MRI (DCE-MRI), where implementation may be possible without additional scans. The data acquisition can be significantly reduced by using faster flip angle mapping methods and optimized protocols (the FRASIER acquisition time can be reduced by employing Look-Locker read-out [1]). Future work will focus on assessing the quantitative difference between the two methods and to design an acquisition protocol with a shorter, clinically more acceptable, scan time.

References: [1] Shin et al. NeuroImage 2010;52:1347–1354. [2] West et al. Eur Radiol 2012;22:998-1007. [3] Ahlgren et al. Proc. ESMRMB 2011, #554. [4] Petr et al. MRM 2012;doi:10.1002/mrm.24601. [5] Fram et al. MRI 1987;5:201-208. [6] Ahlgren et al. Proc. ESMRMB 2013, #618. [7] Insko et al. J Magn Reson A 1993;103:82-85.