

Generating synthetic DIR images using multi-parameter maps: application to lesion detection in MS

Riddhi Rajgor¹, Nils Muhlert², Antoine Lutti³, Matteo Atzori^{4,5}, Nikolaus Weiskopf³, Claudia AM Wheeler-Kingshott², Xavier Golay¹, Alan J Thompson⁴, Olga Ciccarelli⁴, and David L Thomas¹

¹Department of Brain Repair and Rehabilitation, UCL Institute of Neurology, London, United Kingdom, ²NMR Research Unit, Department of Neuroinflammation, UCL Institute of Neurology, London, United Kingdom, ³Wellcome Trust Centre for Neuroimaging, UCL Institute of Neurology, London, United Kingdom, ⁴NMR Research Unit, Department of Brain Repair and Rehabilitation, UCL Institute of Neurology, London, United Kingdom, ⁵Department of Neurology, University of Padova, Padova, Italy

Introduction

Double inversion recovery (DIR) images are used in a range of applications to selectively suppress signal from specific tissues, and thereby improve image contrast (1). Brain DIR, when used with inversion times that suppress the signals from both white matter (WM) and cerebrospinal fluid (CSF), has been widely applied to patients with multiple sclerosis (MS) for the detection of grey matter (GM) lesions (2). It is thought that differences in tissue T_1 relaxation times are responsible for image contrast between lesions and normal tissue, but DIR image contrast is also affected by T_2 (due to non-negligible TE) and magnetisation transfer (MT), particularly in multi-slice 2D implementations. In order to improve image resolution, 3D acquisition schemes can be used. However, due to the long TI and TR required for optimal tissue suppression, the sequence is inherently inefficient and scan times tend to be long. On the other hand, recent developments in FLASH-based multi-parameter mapping sequences allow the generation of quantitative maps of T_1 , proton density (PD) and MT in an efficient manner (3, 4). The aim of this study was to generate synthetic DIR images from multi-parameter mapping data, to compare the quality of these synthetic images with acquired DIR images, and to use them to investigate the source of DIR lesion contrast in MS patients.

Methods

MR acquisition: Healthy controls and MS patients were scanned on a 3T Magnetom TIM Trio scanner (Siemens Healthcare, Erlangen, Germany). DIR images were acquired using a 3D FSE acquisition scheme with double inversion preparation (TI1=3000ms; TI2=510ms; TR=10s; 1.2mm in-plane resolution and 1.3mm partition thickness; turbo factor 191; TE=274ms; acquisition time 15 minutes. Multi-parameter mapping was performed using three 1mm isotropic spoiled 3D FLASH acquisitions: PD-weighted (TR=23.7ms, 8 echoes averaged with TE from 2.2ms to 19.7ms, flip angle 6°); T_1 -weighted (TR=18.7ms, 6 echoes averaged with TE from 2.2ms to 14.7ms, flip angle 6°, 4ms 220° Gaussian MT pulse applied 2kHz off-resonance during each TR). For correction of the T_1 maps, B_1 transmit field mapping was performed using a modified 3D actual flip angle imaging (AFI) method (5) with an alternative RF/gradient spoiling scheme (6).

Generation of synthetic DIR images: Synthetic images were generated using Matlab 7.10.0 (The Mathworks Inc.). The 3D FLASH images were used to create T_1 , PD and MT maps (4). These maps were then used as inputs for a Bloch equation simulation to calculate the signal behaviour during a double inversion recovery sequence on a pixel-by-pixel basis. The T_1 -w images were segmented using SPM8, and TI1 and TI2 for the synthetic DIR images were calculated based on the mean T_1 values of WM and CSF (*i.e.* to optimally null these signals). TR was chosen to be 10s to imitate the acquired DIR sequence. In addition to synthetic DIR images based purely on T_1 /PD-weighting, we also investigated the potential benefit for lesion visualisation of including MT-weighting by dividing the synthetic DIR images by the MT maps. The synthetic images were compared with the original acquired DIR images (after rigid registration) in terms of GM to WM intensity ratio (higher value indicating better WM suppression), GM to CSF intensity ratio (higher value indicating better CSF suppression), ratio of intensity difference between WM lesion and normal WM to that of WM lesion and, similarly, ratio of intensity difference between GM lesion and GM to that of GM lesion (higher values indicating better lesion visibility).

Results

An axial slice of both acquired DIR (acqDIR) and simulated DIR (simDIR) for an MS patient (best matched slice before registration) are shown in Fig 1. The periventricular WM lesions are clearly apparent in both images (yellow arrows show some examples). The signal from WM is better suppressed in the simDIR giving a higher contrast to noise ratio over the entire image. It was observed that in the simDIR images with only T_1 /PD-weighting, GM lesions were much more difficult to identify compared to the acqDIR images. Adding MT-weighting to the simDIR improved the visibility of GM lesions, but still not to the same level as acqDIR. Fig 2 shows a graphical comparison between the two images of the same patient after rigid registration: (a) shows that WM suppression is significantly better in the simDIR; (b) shows that simDIR's CSF suppression is close but not as good as in acqDIR; (c) shows that WM lesions are equally bright in both the images; (d) shows that GM lesions in simDIR are less hyperintense compared to acqDIR and are therefore more difficult to identify. Similar results were obtained for the healthy controls (for GM:WM and GM:CSF contrast; Fig 2(a) and (b)) and the other MS patients analysed.

Discussion

simDIR yields a better suppression of the signal from the WM compared with acqDIR, with consequent high SNR and good tissue contrast. A major advantage of simDIR is that TI1 and TI2 values are precisely chosen for each subject based on the T_1 maps (accounting for any inter-individual T_1 variation), compared to the fixed, pre-determined inversion times required for acqDIR. In addition, the use of multi-parameter mapping data to obtain simDIR, allowing elimination of the DIR scan, would reduce scanning time in clinical protocols. However, these results show that simDIR with simple T_1 /PD-weighting do not demonstrate GM lesions well, and that although the addition of MT-weighting increases lesion conspicuity, it is still inferior to acqDIR. It is therefore likely that the T_2 -weighting of the acqDIR 3D FSE acquisition contributes significantly to the overall acqDIR image contrast. Future work will investigate this by incorporating T_2 -weighting into the simDIR images.

References

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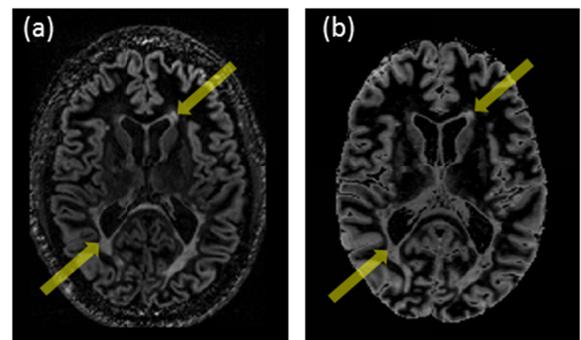


Figure 1: (a) Original acquired DIR; (b) Synthetic simulated DIR

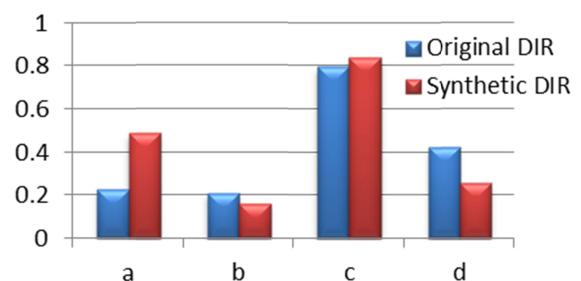


Figure 2: Intensity ratios: (a) normalized GM: WM; (b) normalized GM: CSF; (c) (WM Lesion-WM)/WM Lesion (typical values); (d) typical (GM Lesion-GM)/GM Lesion (typical values)