Optimizing gray-matter white-matter contrast on three-dimensional double inversion recovery MRI using patient-specific inversion times

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TARGET AUDIENCE: Scientists and clinicians studying cortical function and pathology.

PURPOSE: To develop a patient-specific single-slab 3D double inversion recovery (DIR) imaging protocol.

BACKGROUND: Double inversion recovery is used to selectively image gray matter (GM) in the brain by suppressing white matter (WM) and cerebrospinal fluid (CSF) based on differences in their longitudinal relaxation times (T1) [1]. High-resolution three-dimensional (3D) DIR imaging is commonly used for visualizing cortical lesions in multiple sclerosis (MS). DIR protocols are usually optimized based on the expected T1 range in a representative group of subjects. The scan parameters of the sequence are then fixed and used for all subjects. Neglecting the natural and disease-related variations in the relaxation times between subjects render the DIR protocol sub-optimal for individual subjects, except when the patient relaxation properties match those used in the protocol. This results in variations in the degree of tissue suppression and contrast level across subjects. Moreover, single-slab 3D DIR sequences employ long echo trains using variable refocusing flip angles in turbo-spin-echo (TSE) [2]. This approach is efficient, but it introduces transverse relaxation time (T2) weighting, complicating the signal evolution pathway, and precluding the use of simple analytical expressions of conventional TSE DIR signal [3] for determining the inversion times. In order to account for the subject-specific mixed T1/T2 contrast, the DIR signal and inversion times have to be calculated based on the extended phase graph (EPG) algorithm [4].

METHODS: In the proposed protocol, DIR acquisition parameters were customized for each subject based on the T1 and T2 times measured with a fast relaxation scout during the same scan session. The EPG-modeled signal was then used to numerically optimize the DIR inversion times. Sequence optimization was carried out using a scanner-integrated pseudo-real-time image processing pipeline. To test this approach, five healthy volunteers were enrolled in an IRB-approved study and scanned with a 32-ch SENSE compatible head coil on a 3.0T Philips Achieva system. T1 mapping was performed using the steady-state Look-Locker sequence [5] in a single axial–oblique slice above the corpus callosum using: TR/TE=6.4/3.1, flip angle = 7°, number of images=67, and shot interval = 6 sec. T2 mapping was performed using a multi-slice dual-echo TSE protocol ($TR/TE_1/TE_2$ = 6800/8.2/90 ms). The acquired images were transferred to a separate workstation (3.2-GHz 8-core Intel Core i7, 12 GB of memory) to perform relaxation time calculations and brain tissue segmentation. Average T1 and T2 values were computed for WM and GM, and subsequently used for optimizing the two inversion times of DIR to minimize the following expression: $(S_{WM}+S_{CSF})/S_{GM}$, where *S* denotes the DIR signal at the effective echo time, and assuming CSF T1/T2=4.3/2 sec. The optimal inversion times were imported back to the scanner and applied for the DIR acquisition. For comparison, vendor-recommended parameters were used to acquire DIR in all subjects using: TR/TE = 5500/280 msec, first/second inversion times (TI1/TI2) = 2400/485 msec, FOV = 256×256×180 mm^3, voxel size = 1×1×1 mm^3, SENSE factor = 2.5x2.5, echo train length = 173, echo-spacing = 2.9 ms, and a variable refocusing angle scheme (180°, 141°, 76°, 53°, 43°, 40°, 40°,..). All scan parameters except for the inversion times were identical in both DIR protocols. The brain protocol also included a structural 3D T1-weighted (MPRAGE) acquisition. Nineteen regions-of-interest were placed on MPRAGE images throughout the brain to sample GM, WM, and CSF. GM-WM and GM-CSF contrast ratios, and GM signal-to-noise ratio (SNR_{GM}) were compared between the fixed and patient-specific DIR protocols using paired t-testing.

Fig. 1: A slice from the brains of 5 healthy volunteers acquired with DIR (top) and optimized DIR (bottom). Corresponding images are scaled to the same level and displayed with identical window settings.

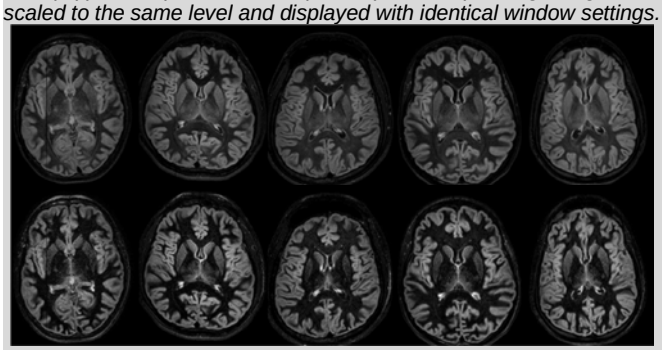
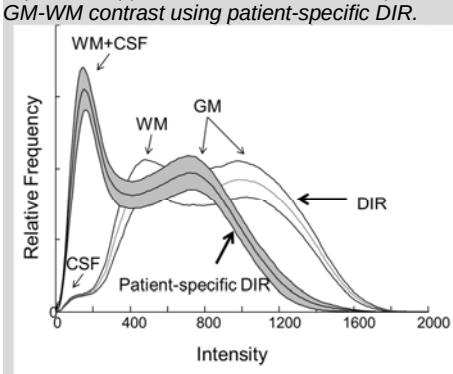


Fig. 2. Image histogram from all experiments (mean±SEM) for DIR (bright shading) and patient-specific DIR (dark shading). Note the improved suppression of WM and the improved GM-WM contrast using patient-specific DIR.



RESULTS: Automated optimization of DIR was successfully completed in all experiments with ~1 min processing time. Fig. 1 demonstrates improved WM suppression and superior tissue contrast obtained with patient-specific DIR. GM-WM contrast ratio was approximately doubled with the patient-specific DIR protocol (3.8±1.5) compared to the fixed DIR protocol (2.0±1.6; P<0.001). GM-CSF contrast was slightly decreased by ~18% (5.5±1.1 vs. 6.7±0.8, P<0.001), probably due to inaccurate assumptions on CSF relaxation times. SNR_{GM} of patient-specific DIR was reduced by ~30% (14.4±2.7 vs. 20.6±2.1, P<0.001) reflecting that a DIR null point is now closer to GM. The image histogram (Fig. 2) illustrates the better WM suppression and the improved GM-WM contrast obtained with the patient-specific DIR protocol.

CONCLUSION: Patient-specific DIR improves GM-WM contrast, and could be a valuable aid in improving the detection and classification of WM and cortical pathology in MS [6,7] and other neurological diseases.

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