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Automated patient-specific optimization of three-dimensional double inversion recovery magnetic resonance imaging

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Abstract

Purpose—To automatically optimize three-dimensional double inversion recovery (3D-DIR) MRI of the brain on a patient-by-patient basis.

Methods—DIR is a powerful MRI technique that allows simultaneous suppression of white matter (WM) and the cerebrospinal fluid (CSF) in brain imaging. Unfortunately, the tissue suppression is not always consistent across patients. We propose patient-specific optimization of WM suppression for improved gray matter (GM)-WM contrast. Relaxation times were measured in the same scan session and, through real time processing, used for calculating DIR inversion times for maximum tissue contrast. Signal evolution during the variable-flip-angle turbo-spin-echo readout was calculated using the extended phase graph algorithm. Patient-specific optimization was examined in five healthy volunteers, two of them scanned twice for reproducibility, and two multiple sclerosis patients. The contrast ratios, GM signal-to-noise ratio (SNR), and image histogram were used to assess the performance of this patient-specific approach.

Results—Automated optimization of 3D-DIR was successfully completed in all experiments with processing time of ~1 min. GM-WM contrast ratio tripled with the optimized DIR sequence with only 19% decrease in GM-CSF contrast, and 30% SNR penalty.

Conclusion—Patient-specific optimization is feasible and significantly improves GM-WM contrast on 3D-DIR with a moderate decrease in the GM SNR.

Keywords

patient-specific optimization; personalized imaging; relaxation time; image analysis; extended phase graph; multiple sclerosis

INTRODUCTION

Double inversion recovery (DIR) is a powerful MRI technique that allows simultaneous suppression of two tissues based on their T1 relaxation times. DIR can be used to selectively image the gray matter (GM) by suppressing the brain white matter (WM) and cerebrospinal

fluid (CSF) (1,2). Suppression of the confounding signals from WM and CSF improves the conspicuity of cortical lesions in multiple sclerosis (3–7). With the development of three-dimensional (3D) DIR, high-resolution imaging of GM is possible for improving the detection of small cortical lesions (8).

Due to the natural inter-subject variability in tissue relaxation times, good signal suppression on DIR images cannot be guaranteed across subjects, even if the imaging protocol is optimized on a group level. Patient-specific optimization is needed to obtain the desired image contrast in every exam. Customizing the scan for each patient requires knowledge of the tissue relaxation times and the ability to quickly modify the scan parameters based on this knowledge.

In addition to the relaxation times, contrast optimization also requires knowledge of the course of signal evolution. Single-slab 3D turbo spin-echo (TSE) sequences have become clinically feasible with the use of variable refocusing angles (9–11). Signal evolution in these sequences exhibits substantially slower decay, allowing a longer acquisition window (12). Unfortunately, signal evolution with a variable refocusing angle technique does not generally have a closed form solution and published formulae for the DIR signal (e.g. (13)) cannot be used. More elaborate techniques such as the extended phase graph (EPG) algorithm (14,15) are required to accurately calculate signal evolution.

We hypothesize that patient-specific customization of inversion times in 3D DIR MRI will result in improved WM suppression that translates into superior GM-WM tissue contrast. Scan parameter customization is based on relaxation time measurements performed in the same subject in a single imaging session and using an EPG-based signal evolution. This personalized imaging paradigm is enabled by a framework that integrates acquisition and analysis recently proposed for fast quantitative MR neuroimaging (16). In the rest of this paper we present details of the different elements of this personalized MRI approach for DIR optimization, and compare the results of this approach with conventional 3D DIR.

METHODS

DIR signal

The DIR pulse sequence used in this study is schematically shown in Fig. 1. Two 180° inversion pulses preceding data acquisition by periods TI_1 and TI_2 are applied to null the desired ranges of T1. The read-out sequence consists of a 90° excitation pulse followed by a train of refocusing pulses with a variable flip angle scheme. A recovery period (T_p) allows the magnetization to partially recover in preparation for the sequence to be repeated in the next TR interval. Calculation of the MRI signal evolution in the DIR experiment is performed using rotation matrices for radio-frequency (RF) pulse inversion and excitation, and using exponential relaxation during the inversion and the signal recovery periods (TI_1 , TI_2 , and T_p ; Fig. 1). Signal evolution during the long TSE readout can be described with the EPG algorithm using the following set of equations describing the excitation and evolution of the different coherence states (14,15),

$$\begin{pmatrix} F_n \\ F_n^* \\ Z_n \end{pmatrix}^+ = \begin{pmatrix} \cos^2 \alpha / 2 & e^{2i\varphi} \sin^2 \alpha / 2 & -ie^{i\varphi} \sin \alpha \\ e^{-2i\varphi} \sin^2 \alpha / 2 & \cos^2 \alpha / 2 & ie^{-i\varphi} \sin \alpha \\ -(i/2)e^{-i\varphi} \sin \alpha & (i/2)e^{i\varphi} \sin \alpha & \cos \alpha \end{pmatrix} \begin{pmatrix} F_n \\ F_n^* \\ Z_n \end{pmatrix} \quad [1]$$

and,

$$F_n^+ \rightarrow F_{n+1} = E_2 F_n^+ \quad Z_n^+ \rightarrow Z_n = E_1 Z_n^+ \quad (n \neq 0) \quad Z_0^+ \rightarrow Z_0 = E_1 Z_0^+ + (1 - E_1) M_0 \quad [2]$$

F and Z denote the transverse and longitudinal configurations, respectively, $^+$ denotes the signal immediately after excitation with an RF pulse with flip angle α and phase φ , n is the order of the pulse in the echo train ($n=1,2,\dots$), $E_{1,2} = \exp(-\tau/T_{1,2})$, τ is the echo-spacing, and the arrow designates the evolution of states between RF pulses. At the end of the echo train, the longitudinal magnetization is obtained from Z_0 . The MRI signal at the echo time is calculated from F_0 , and is used in subsequent optimization of DIR.

DIR contrast optimization

When the relaxation times and the proton densities (PD) of different tissues are known, the scan parameters can be adjusted to achieve the desired level of tissue contrast using the above signal evolution description. In this work, the inversion times TI_1 and TI_2 are chosen to suppress signals from WM and CSF, while at the same time maximizing the signal from GM. This is achieved by minimizing the following expression:

$$\Psi = (S_{WM} + S_{CSF}) / S_{GM} \quad [3]$$

where S denotes the MR signal at the effective echo time as obtained from F_0 —the fully coherent state in the EPG algorithm.

To investigate the effect of this customized optimization, the DIR signal was simulated for GM, WM, and CSF using a range of T_1 , T_2 , and PD values for each of the three tissues. Simulated signals were generated for a standard 3D DIR protocol with scan parameters recommended by the vendor (details in the Imaging protocol section). Proton density was assumed to be 0.93 for WM, and 1.0 for GM and CSF. The range of the simulated relaxation times was ($T_{1\min}$ – $T_{1\max}$, $T_{2\min}$ – $T_{2\max}$ in msec): WM (750–900, 85–100), GM (1200–1700, 100–125), CSF (3000–5000, 1500–2500). All the T_1/T_2 combinations for a single tissue were tested while fixing the other two tissues at their nominal mid-range values. The tissue signal was next simulated with the inversion times adjusted to maximize the expression in Eq. 3. The tissue contrast ratio between GM and WM (CR_{GM-WM}) and between GM and CSF (CR_{GM-CSF}) were calculated using the following expression: $CR_{1-2} = (S_1 - S_2) / S_2$.

Integrated image analysis framework

In the proposed approach, processing of MRI images is integrated within the MRI protocol. To prevent a conflict with the scanner workflow, data processing was performed on a dedicated system described elsewhere (16). The integrated acquisition-processing system for DIR optimization is schematically illustrated in Fig. 2, where processing of the relaxation data and optimization of the DIR parameters were performed concurrent with MRI data

acquisition to minimize the overall delay. A fast computing workstation (3.2-GHz 8-core Intel Core i7, 12 GB of memory) was connected to the scanner console through an internet communication protocol on a local network (1 Gbps). Custom software modules created an environment with a seamless interface to the scanner database. The setup allowed (i) automated extraction of images from the patient database into a compact image format, (ii) transfer of data to the post-processing workstation, (iii) remote launching of image analysis applications, and (iv) importing the processed images, data, and the optimized scan parameters back into the patient database on the scanner. Finally the operator manually entered the optimized parameters on the scanner console.

Imaging protocol

This study was approved by our Institutional Review Board. The study included five healthy subjects (age 24–32; F/M=3/2) and two relapsing-remitting MS patients (age 24 and 45 yrs; F/M= 1/1, EDSS 1.0/2.5, disease duration 3.5/5.0 yrs). All volunteers gave written informed consent. Two of the five healthy volunteers were scanned at two different days (separated by 3 and 6 days between the first and second sessions, respectively) to examine the test-retest reliability of the methods. The MRI exam included a high-resolution 3D magnetization-prepared rapid gradient-echo (MPRAGE) T1-weighted MRI for structural imaging. All experiments were performed on a Philips 3.0T Achieva system using a 32-channel SENSE-compatible head coil.

T2 relaxation mapping was performed using a multi-slice fat-saturated dual-echo TSE sequence that is part of our clinical brain protocol. The scan parameters of this dual echo TSE were: TR/TE₁/TE₂ = 6800/8.2/90 msec, FOV = 256×256 mm², slice thickness = 3 mm, matrix size = 256×256, number of slices=22, and total scan time of 3:24 min. To rapidly map T1 distribution, the protocol employed an additional scan of a single axial-oblique slice above the corpus callosum, using the steady-state Look-Locker method (17–19). The T1 mapping protocol was acquired with the following scan parameters: FOV = 256×256 mm², slice thickness = 3.1 mm, matrix size = 172×170, TR/TE=6.4/3.1, flip angle = 7°, number of images=67, shot interval = 6 sec, and a total acquisition time of 55 sec. Measurement of the relaxation times of CSF is complicated by its flow and the very long relaxation times, which requires long-TR 3D pulse sequences. To keep the scan time short, CSF relaxation times were assumed to be T1/T2=4300/2000 msec in all subjects (20,21). These were combined with the measured relaxation times (T1 and T2) of WM and GM to calculate the optimized DIR parameters. The average relative spin density of WM and GM were estimated from a mono-exponential fit of the dual-echo data, while that of CSF was obtained from the short-echo image.

After relaxation time measurements, 3D DIR images were obtained with the following scan parameters recommended by the scanner vendor: TR/TE = 5500/280 msec (equivalent TE = 121 msec), and first/second inversion times (TI₁/TI₂) = 2400/485 msec. Other scan parameters were FOV = 256×256×180 mm³, voxel size = 1×1×1 mm³, and SENSE factor of 2.5×2.5. The TSE readout used an echo train length (ETL) of 173, echo-spacing = 2.9 ms, and a variable refocusing angle scheme of the following form (180°, 140.9°, 76°, 52.9°, 42.7°, 40°, 40°, 40°, ...). The total DIR scan time was 6:14 min. Next, the 3D DIR

acquisition was repeated using the TI_1 and TI_2 parameters obtained from the scan optimization step, with all other parameters held constant.

Online image analysis and sequence optimization

Figure 2 shows the image analysis steps performed in each study. First, the dual-echo data from the TSE scans were automatically transferred to the remote workstation for generating the T2 maps immediately after completing the data acquisition. The second-echo (T2-weighted) image was skull-stripped using a brain extraction method for fat-saturated T2-weighted images (22). The T2 maps were next generated from a line fit of the logarithm of the two signals. The T2 map was segmented into WM, GM, and CSF using a custom two-step two-tissue segmentation, wherein CSF was segmented from the skull stripped brain in the first step, then WM/GM segmentation was performed on the brain with CSF masked. The two-tissue segmentations were performed using Atropos (23). Tissue-averaged T2 values were calculated and temporarily saved on the workstation until the T1 data was available. Once the Look-Locker acquisition was completed, the data were immediately transferred to the workstation where it was skull-stripped using BET (24) and pixel-wise least-squares T1 fitting was performed using the Levenberg Marquardt algorithm (25,26). Segmentation into WM, GM, and CSF was performed as described above, and the T1 tissue averages were computed. The calculated tissue T1 and T2 values were used as input and the DIR optimization process was invoked. The resulting optimized scan parameters (TI_1 and TI_2) were imported back into the scanner console to optimize the DIR protocol. The T1 and T2 maps and tissue segmentation were also imported into the patient database.

Data analysis and performance assessment

Both the DIR and optimized DIR (OPT-DIR) images were first registered to the structural MPAGE T1W image using the rigid-body registration (27) in SPM8 (<http://www.fil.ion.ucl.ac.uk/spm>). Ten regions of interest (ROI) were pre-defined on the MPAGE image to sample the GM signal in different lobes of the brain and deep GM. Another set of ten ROIs were placed in the neighboring WM tissue for contrast measurement (Fig. 4). An additional ROI sampled the ventricular CSF, and the mean signal in all ROIs was recorded. ROIs were approximately placed in the same region in all subjects. Computation of contrast-to-noise ratio is complicated by the difficulty of estimating the regional noise power in images generated by parallel imaging techniques as image reconstruction from the multi-element coils produces spatially-varying noise level (28). Therefore contrast ratios were estimated for assessing image quality. The contrast ratio between GM and the corresponding WM (CR_{GM-WM}) was calculated. CR_{GM-CSF} was also calculated to quantify the degree of CSF suppression.

To investigate the effect of optimizing WM suppression on the signal-to-noise ratio (SNR) of GM, the mean GM signal in different ROIs was divided by a global image noise estimate. We used a noise estimator based on the thresholded brain image, assuming no background is present (29). Two noise estimates from the DIR and optimized DIR images were averaged to decrease the uncertainty.

A paired t-test was used to compare the contrast ratio and GM SNR between the reference and optimized DIR images. All image analysis and post-processing were performed with in-house developed software written using the interactive data language (IDL, Exelis Visual Information Solutions, Boulder, CO), Matlab (The Mathworks, Natick, MA), and C programming languages. Processing times for the online calculation of the T1 and T2 maps and the optimization of the DIR sequence were recorded.

RESULTS

Figure 3 shows the simulated WM, GM, and CSF signals in the DIR experiments using the vendor and optimized protocols. Excellent suppression of WM and CSF was consistently achieved in all cases if the relaxation times are known, with negligible variations over a wide range of the relaxation parameters. On the other hand, substantial WM signal is left over with the vendor protocol.

Representative images from the brain of a healthy volunteer acquired with the standard and patient-optimized DIR protocols are shown in Fig. 4. Corresponding images in this figure (and in Fig. 5,6,8) are scaled to the same level and displayed with identical windowing. Better suppression of WM is evident at all levels in the brain on images obtained with the optimized DIR protocol. Figure 5 shows the performance of both protocols in the five healthy volunteers, where the patient-specific protocol again shows superior GM-WM contrast. Consistent performance is also noted on the MS studies as shown in Fig. 6. Fig 6 also shows axial, coronal, and sagittal reformats demonstrating the improved spatial resolution obtained with the volumetric DIR acquisition. A histogram of the resulting images in all subjects is shown in Fig. 7 (mean $\pm$ SEM, shaded area). Better GM-WM contrast is evident in the well separated peaks. The improved WM suppression is reflected in the spiked and left-shifted WM peak, corresponding to a larger proportion of signal-suppressed voxels. The range (min,max) of T1 and T2 of WM, in msec, measured in all subjects was (779,879) and (89,101), respectively, while those of GM were (1311,1600) and (106,121). The resulting ranges for TI₁ and TI₂ were (2632,2719) and (640,692), respectively.

Table 1 shows the contrast ratios CR_{GM-WM} and CR_{GM-CSF} in different brain regions averaged over all subjects. The optimized DIR protocol shows 1.1–4.7 times higher CR_{GM-WM} than DIR in different brain regions, with 3-fold average improvement over all subjects and brain regions ($P < 0.001$). CR_{GM-CSF} is decreased with the optimized DIR protocol by 19% on average as compared to DIR ($P < 0.001$), possibly due to differences in the assumptions about the relaxation times of CSF. Unfortunately, optimizing WM suppression came with a 30% penalty in the SNR of GM ($P < 0.001$). This is as expected since signal nulling moves to higher T1 values, compared to the vendor DIR protocol (Fig. 3), becoming closer to the T1 of GM.

Fig. 8 shows the OPT-DIR images for one volunteer scanned on two different days, illustrating the consistent improvement in contrast. Test-retest results in the two volunteers are shown in Table 2. The measured average T1 and T2 values of WM were reproducible ($< 2.5\%$ for T1 and $< 1\%$ for T2) between the two scans, resulting in small variation in the

optimized inversion times ($TI_1 = 17$ msec and $TI_2 = 10$ msec). The brain averaged contrast ratio CR_{GM-WM} showed similar improvement over the two scans (Table 2).

The average time for calculating the T1 map from the Look-Locker data was 6 sec, and 47 ± 2 sec for the T2 map. DIR optimization took 59 ± 2 sec. Thus, the delay from the completion of the T1 mapping acquisition to the completion of DIR optimization was ~ 65 sec. The processing time for the generation of the whole brain T2 map is not a limitation as it was performed during the acquisition of the Look-Locker data. The longer processing time for generating the brain T2 map compared to the single slice T1 map shows the need for performing the T2 acquisition first, as done in this study, to minimize processing delays. Overall, the processing time is clinically acceptable.

DISCUSSION

Despite the continuous developments in MRI, spatial resolution remains a limitation in applications that require high resolution, for example to reliably image the brain cortex (30), coronary arteries (31), or cortical lesions in MS (32). Recent studies showed the difficulty in detecting and measuring the extent of small cortical, mixed, and white matter lesions in MS with commonly acquired 3-mm slices with 2D DIR (8,32,33). High-resolution phase-sensitive inversion recovery (PSIR) acquisitions may alone (33), or combined with 2D DIR (5) provides an alternative. However, unlike DIR, lesions on PSIR appear with a negative contrast, which is more difficult to visualize. With the high resolution attainable with 3D DIR, better lesion detection is possible (8,34). TSE techniques with refocusing control allow the acquisition of single-slab 3D DIR in a clinically acceptable time.

Despite the power of DIR in detecting cortical lesions in multiple sclerosis (4,5,7,8,35,36), lesion scoring using DIR data sets from different centers showed a high inter-rater variability (35). Including cortical lesions as detected on DIR sequences in multi-center clinical trials as a potential outcome measure needs sequence optimization. The subject-specific customization of DIR sequences proposed in this work may be crucial for the optimization of cortical lesions on DIR images.

In this work we addressed the problem of optimizing GM-WM contrast in the 3D DIR sequence with a variable refocusing scheme. Refocusing modulation can achieve an extended length of the echo train by significantly slowing T2-related signal decay compared to conventional TSE sequences (9,10,12). The long sampling period allows the acquisition of k-space data in a reasonable scan time. Using the extended phase graph method, we were able to calculate the optimized scan parameters for 3D DIR on a patient-by-patient basis. The optimized DIR images showed a 3-fold average gain in GM-WM contrast as compared to the fixed vendor protocol, although this needs to be verified in a large cohort of patients who show larger variation in relaxation times as a result of pathology. This will be evaluated in further studies. Importantly, the improvement in contrast comes with no penalty in scan time, albeit with some loss in SNR. In addition, the protocol did not require any user input, avoiding subjectivity in the optimization process. Intervention by the user was required only to apply the optimized scan parameters. Future implementations of this approach will automate this step.

Improved conspicuity of the MS WM lesions was noted with the patient-specific DIR protocol (Fig. 6), but quantification was not pursued because of the small sample size. No cortical lesions were seen on these two scanned patients. However, based on the steep GM signal curve of the patient-specific DIR protocol in Fig. 3, and the expected increased relaxation times in GM lesions, we expect some improvement in the contrast of cortical lesions, as compared to the flat GM signal curve with the standard DIR protocol (Fig.3). Further studies with a large number of patients are needed to test this hypothesis. Improvement in the visualization of WM and/or cortical lesions could boost the sensitivity of lesion detection and lead to more accurate measurement of the lesion load. Another advantage of the improved WM suppression with the proposed approach is better delineation of GM/WM boundaries, which helps in differentiating various types of lesions (e.g. pure cortical vs. mixed GM-WM or pure WM lesions).

These results highlight the potential of patient-customized imaging wherein feedback from the patient data via integrated fast image analysis is used to guide subsequent image acquisitions. Such a dynamic and patient-specific protocol adapts to the natural inter-subject variability in tissue properties, and has a wide scope of potential applications in MR imaging and spectroscopy. The optimized 3D DIR, with substantial and consistent improvement in tissue contrast, demonstrates the power of this patient-adaptive imaging approach.

From the simulation results shown in Fig. 3, the WM signal appears to be suppressed for $T1_{WM} < 600$ msec in the vendor DIR protocol. This $T1_{WM}$ value is smaller than that reported in the literature or measured in this study. This may explain the observed sub-optimal suppression of WM with the vendor's protocol, although this comes with a higher GM signal. With the proposed approach, the individualized optimization successfully suppressed WM without any assumptions on the relaxation times. In this regard, even if the conventional DIR protocol is optimized for relaxation times that more closely match a specific group of subjects, the protocol may be sub-optimal if the pathology significantly alters the relaxation times. On the other hand the proposed approach is expected to adapt to variations in relaxation times with the patient-specific scan optimization.

Being the major contrast-controlling parameters in DIR, the two inversion times TI_1 and TI_2 were chosen as the adjustable variables. This choice resulted in a significant gain in contrast, but SNR was reduced by approximately one third. A tradeoff between this loss in SNR and the gain in contrast should be considered by the user. An alternative approach may seek to balance the optimization of tissue contrast and the SNR level in the objective function. Another choice may target a certain level of tissue contrast that would be consistent across patients rather than maximizing the contrast ratio. In addition, user defined limits may also be imposed to constrain the scan parameters to a certain range that would be expected by the radiologist. Extension of the present work for the joint optimization of all scan parameters (including TR, TE, flip angles, ETL, and echo spacing) may help minimize, or even reverse the loss in SNR.

A limitation of this work was the lack of measurement of the relaxation times of CSF, which resulted in some loss in CSF suppression performance. Measurement of CSF relaxation is complicated by the long relaxation times of CSF in addition to its flow and pulsation

(37,38). Optimizing the experiments for CSF measurement would have required longer TR/TE and possibly also 3D acquisitions, which would considerably lengthen the scan time. As the speed was a priority in this approach, we opted to using known population averages for CSF. Indeed, minimizing the total scan time was the motivation behind re-using the dual-echo TSE protocol for T2 mapping because it is commonly included in clinical brain protocols. Speed was also the motivation for using the steady-state Look-Locker sequence for T1 mapping. Nonetheless, the second T1-null point in DIR has a broader extension, and small variations in the relaxation of CSF are not expected to change the image contrast significantly. This may not however be the case if CSF relaxation is substantially affected by the pathology, and a practical method for CSF relaxation measurement remains to be developed.

It is important to note that the improved image contrast obtained with the proposed approach is not equivalent to better diagnostic accuracy. Whether the changes in tissue contrast would result in an improved accuracy of the detection of WM or cortical lesions and better definition of their spatial extent will be addressed in a future validation study.

In conclusion, we have developed a framework for patient-specific optimization of the 3D DIR sequence to maximize tissue contrast, and explicitly addressed optimization of turbo spin-echo sequences with variable refocusing. The proposed approach is fast, requires minimal user intervention, and appears to produce consistent results across subjects. We anticipate that the extension of this personalized MRI approach to other imaging and spectroscopic protocols will bring substantial improvement in image quality and diagnostic capability.

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Figure 1.

Schematic pulse sequence diagram of DIR. TR: repetition time; TE: effective echo time; TI_1 : first inversion time; TI_2 : second inversion time; τ : echo spacing; T_{RO} : read-out period; T_p : preparation (or recovery) time. For clarity, the gradient waveforms are omitted.

Figure 2.
Layout of the automated patient-specific DIR optimization pipeline.

Figure 3.

Results of simulations showing the signal from WM (left panel), GM (middle panel), and CSF (right panel) when using the fixed vendor-recommended scan parameters (labelled DIR) vs. the patient-customized protocol (OPT-DIR). The signal is calculated for different combinations of T_1 (msec; horizontal axes) and T_2 (individual curves in each subplot) for WM (top row), GM (middle row), and CSF (bottom row). Twenty T_2 values are simulated spanning the range of 85–100 msec for WM, 100–125 msec for GM, and 1500–2500 msec for CSF. Note the nulling of WM and CSF signal (left and middle panels) with patient-specific optimization.

Figure 4.

Slices at different levels in the brain of a healthy volunteer acquired with DIR (top row) and optimized DIR (bottom row) protocols. Note the improved WM suppression with optimized DIR. The locations of the selected ROIs are outlined in yellow circles.

Figure 5. Representative slices from the brains of five healthy volunteers acquired with DIR (top row) and optimized DIR (bottom row). Note the consistent suppression of WM across all five subjects.

Figure 6. Sagittal, axial, and coronal reformatted images from 3D DIR MRI of the brain of an MS patient acquired with DIR (top row) and optimized DIR (bottom row) protocols. Note the improved WM suppression with optimized DIR.

Figure 7.

Image histogram from all experiments (mean $\pm$ standard error in the mean; shading) using the standard (grey lines) and patient-specific (black lines) 3D DIR protocols. Note the improved suppression of WM (left peak) and the improved contrast between of GM (right peak) and WM using the patient-specific protocol.

Figure 8. Optimized DIR images from one healthy volunteer scanned at two different days. Note the consistent WM suppression between Day 1 (top) and Day 2 (bottom).

Table 1

GM-WM contrast ratio (CR_{GM-WM}), GM-CSF contrast ratio (CR_{GM-CSF}), and GM SNR (SNR_{GM}) in different brain regions for DIR and optimized DIR protocols as measured in seven subjects (five health controls and two MS patients).

	CR_{GM-WM}		CR_{GM-CSF}		SNR_{GM}	
	DIR	OPT- DIR	DIR	OPT- DIR	DIR	OPT- DIR
Cingulate gyrus	1.7±0.8	5.9±4.3	7.4±2.3	6.5±2.0	21.8±3.5	16.8±2.6
Caudate nucleus	1.7±0.9	2.9±1.5	6.2±2.9	4.8±2.4	18.6±6.4	12.3±3.6
Frontal lobe	1.7±0.6	4.0±2.7	5.6±1.2	4.6±1.5	17.4±2.1	12.6±2.3
Insular cortex	1.0±0.7	3.1±1.6	6.8±2.4	5.7±2.4	20.3±4.1	14.5±2.9
Occipital lobe	1.0±0.6	3.7±2.4	6.4±2.3	5.3±2.2	19.3±3.2	13.6±2.2
Parietal lobe	1.5±0.6	7.0±2.8	7.5±2.2	6.1±2.1	22.0±2.6	16.0±3.4
Parieto-occipital sulcus	1.3±0.6	5.3±1.6	7.8±2.7	6.7±2.7	22.9±5.1	16.7±3.8
Posterior Fossa	0.9±0.3	4.1±1.6	6.8±1.6	5.0±2.7	20.7±2.4	13.5±1.4
Putamen	1.5±0.9	1.7±1.4	5.7±2.0	3.4±1.7	17.4±3.7	9.5±2.2
Temporal lobe	1.4±0.7	4.4±2.8	7.6±1.8	6.7±1.8	22.7±3.0	17.2±1.5
All	1.4±0.3	4.2±1.4	6.8±0.8	5.5±1.0	20.3±2.0	14.3±2.3

Table 2

Test-retest analysis of two healthy volunteers showing the measured relaxation times, calculated optimized inversion times, and average GM-WM contrast ratio for DIR and optimized DIR protocols.

Test		T1 _{WM} , msec	T2 _{WM} , msec	T1 ₁ , msec	T1 ₂ , msec	CR _{GM/WM}	
						DIR	OPT-DIR
Volunteer 01	run 1	798	91	2649	650	2.3	4.7
	run 2	779	91	2632	640	1.7	6.1
Volunteer 02	run 1	855	97	2698	680	1.4	4.4
	run 2	871	97	2713	688	1.4	4.4