Optimization method of MRI scan parameters of a double inversion recovery sequence using a T1 map and a developed analysis algorithm

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Aims and objectives

Gray matter (GM) imaging is important in the investigation of many neurological diseases, including schizophrenia, multiple sclerosis, stroke, Alzheimer’s disease, tuberous sclerosis, and epilepsy, all of which are associated with changes in the cortical GM [1-7]. Therefore, the ability to identify cortical abnormalities is of great importance [7]. However, it is difficult to capture the neocortical GM [7]. The neocortex is a very thin, highly convoluted structure that folds back upon itself in an unpredictable manner [7]. To delineate the neocortex, one must obtain high-resolution, thin-slice data. However, voxel size reduction during magnetic resonance (MR) acquisition also reduces the signal-to-noise ratio (SNR); therefore, a compromise must be determined [7].

A further complication is the partial volume (PV) effect, whereby a single pixel may contain variable amounts of GM, cerebrospinal fluid (CSF), and white matter (WM) [7]. By reducing the voxel size, one can also reduce the PV effect. The double inversion recovery (DIR) sequence [8] has also been implemented to overcome this complication. Previous studies [9, 10] have successfully implemented double inversion recovery (DIR) as a 2D multislice sequence [7].

The DIR sequence extends the commonly used fluid-attenuated inversion recovery (FLAIR) sequence for CSF suppression by adding a second 180° radiofrequency (RF) pulse, allowing the simultaneous suppression of signals from two different tissues with different T1 relaxation times [7, 8]. A WM-attenuated inversion recovery (WAIR) image with an enhanced GM region was obtained with the DIR sequence while suppressing the WM and CSF regions. A GM-attenuated inversion recovery (GAIR) image with an enhanced WM region was obtained with the DIR sequence while suppressing the GM and CSF regions. To suppress two different tissues, it is necessary to optimize the typical DIR sequence scanning parameters. The typical parameters include two different inversion times: a long inversion time (TI-1\textsuperscript{st}), which is the duration between the two inversion pulses, and a short TI (TI-2\textsuperscript{nd}), which is the duration between the second inversion and excitation pulses.

It is difficult to optimize the typical parameters for individual DIR MR imaging (MRI). Therefore, nearly all reported studies have used the parameters in previous reports or experimentally determined through phantom studies. Using the methodology published by Redpath and Smith [8], one can determine the typical parameters using initial information, which includes the repetition time (TR), echo time (TE), and T1 value of each suppressed tissue.
The purpose of this study is to investigate the method for optimizing the DIR sequence scan parameters using a T1 map sequence and developed analysis algorithm.
Methods and materials

#Participants and materials

The study population comprised 8 volunteers with no abnormalities (8 men; aged 22-39 years; average, 27.2 years). The volunteers underwent T1 mapping and DIR MRI using a 1.5-T MRI scanner (Ingenia 1.5T; Philips Medical Systems, Best, The Netherlands). This study was approved by our Institutional Review Board, and volunteers provided their written informed consent for participation.

#Optimized method for DIR images such as WAIR and GAIR images

Our method for optimizing the DIR sequence scan parameters comprised the following steps: 1) measurement of GM and WM T1 values on the T1 map obtained from the mixed sequence, 2) calculation of the optimized DIR sequence scan parameters using the developed analysis algorithm, and 3) scanning using the optimized DIR sequence parameters.

(1) Measurement of T1 values

We obtained T1 and T2 maps of the individual volunteers using a mixed sequence. This mixed sequence comprised the RLSQ algorithm [11]. The mixed sequence simultaneously obtains T1 and T2 maps within a few minutes during an examination. The WM and GM T1 values were obtained from regions of interest of WM and GM that were drawn on the T1 map (Fig. 1). The T1 value of the CSF region was manually defined as 4,250 ms [12] because it was difficult to measure the T1 values of the CSF region, which is similar to water, wherein the T1 value is very long.

(2) Calculation of optimized scan parameters of the DIR sequence

TI-1 and TI-2 were calculated using parameter-optimized software. The software could calculate the optimized TI-1 and TI-2 values from the initial parameters (TR, TE, and T1 values in two different suppressing tissues; Fig. 2).

(3) Scanning using optimized DIR sequence parameters

The optimized DIR sequence parameters were calculated from the initial parameters (TR, TE, and other imaging parameters) and T1 values of the suppressing tissues from the T1 map, which was obtained from the mixed sequence. The optimized DIR images, such as
WAIR and GAIR, were obtained from the DIR sequence using the optimized individual parameters.

# Evaluation

To estimate this optimization method, we obtained DIR images using the scan parameters reported in previous studies [10, 13-15]. The scan parameters used for the optimization and in previous reports are shown in Table 1.

Table 1. Scan parameters of the DIR sequence. "Optimized" values were calculated using the optimized method. "Previous" values are the values used in previous reports.

<table>
<thead>
<tr>
<th>Setting</th>
<th>TR [ms]</th>
<th>Optimized</th>
<th>Previous [10,13-14]</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>TI1st [ms]</td>
<td>TI2nd [ms]</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>TI1st [ms]</td>
<td>TI2nd [ms]</td>
<td></td>
</tr>
<tr>
<td>3D, 1.5T</td>
<td>6500</td>
<td>2358</td>
<td>370</td>
<td>[13] Radiology, 2006;241:873-879</td>
</tr>
</tbody>
</table>

Contrasts (C-GM) between the GM and suppressed region were measured using WAIR images using the optimized and previous scan parameters. C-GM was calculated using the following formula:

\[
C\text{-GM} = \frac{\{SI(GM) \# [SI(WM) + SI(CSF)]\}}{[SI(GM) + SI(WM) + SI(CSF)]},
\]

where SI(GM), SI(WM), and SI(CSF) are the respective signal intensities of the GM, WM, and CSF regions.
Further, contrasts (C-WM) between the WM and CSF were measured on WAIR images. C-WM was calculated using the following formula:

\[
C-WM = \frac{|SI(WM) - SI(CSF)|}{SI(WM) + SI(GM)}
\]

These regions were the suppressing regions. Therefore, in the DIR images with good suppression, the C-WM was lower than that in DIR images without sufficient suppression.

#Statistical analysis

Statistical analysis was performed with commercial software (Prism 5; GraphPad Software, Inc., San Diego, CA, USA). The contrasts (C-GM and C-WM) between the optimized and previous methods were compared with the Wilcoxon rank-sum test.
Fig. 1: Measurement of T1 values of white matter and gray matter on the T1 map.

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**Fig. 2:** DIR parameter optimized software

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Results

#DIR images obtained with optimized method

Fig. 3 shows the DIR images obtained with the optimized parameters and previous report parameters. Using the optimized DIR sequence scan parameter method, the WM and CSF regions were uniformly suppressed and GM was described in all different scan conditions. In contrast, the two suppressed tissues were not correctly suppressed when the scan parameters from previous studies were used.

#Results of the statistical analysis

Fig. 4 shows the C-GM results using the optimized and previous report parameters under different TR conditions. At a TR of 9,805 ms, C-GM was significantly higher with the optimized parameters than with the previous parameters (P < 0.01).

Fig. 5 shows C-WM results using the optimized and previous report parameters under different TR conditions. Under all conditions, the contrast between WM and CSF was significantly lower with the optimized parameters than with the previous parameters (P < 0.01). This result indicates that it is possible to correctly suppress the MRI signals of two different tissues when using the optimized parameters.

In this study, we described a method for optimizing DIR sequence MRI scan parameters that incorporated a T1 map and a developed analysis algorithm. Using our method, it was possible to optimize the scanning parameters for individual participants during MRI. Normally, it is difficult to briefly measure the T1 values of each region. However, it is possible to obtain T1 values of these regions using the mixed sequence. The mixed sequence provides T1 and T2 maps for the output images within a few minutes during an examination. Many previous reports have described T1 values [12, 16-18]; however, the range of these reported values is wide. Further, the T1 values markedly differed between female and male subjects [17]. Therefore, it is necessary to individually optimize the scanning parameter for suppressing the two different tissues in DIR MRI. From the known T1 values of the different suppressed tissues, the optimized TI-1\textsuperscript{st} and TI-2\textsuperscript{nd} could be simultaneously calculated using the developed analysis algorithm.

DIR has been most extensively used to study cortical GM lesions, and the accrual of GM lesions has been shown to correlate with disability in patients with established MS [19-22]; the presence of these lesions may also improve the specificity of current MS MRI diagnostic criteria [19, 22-24]. A recent combined histopathological and MRI study reported that 90% of cortical MS lesions observed via high-resolution 3D DIR
were histopathologically confirmed [25]. Therefore, to correctly diagnose GM lesions, it is necessary to obtain high-resolution WAIR images with correct suppression of the GM and CSF region. Our optimized method provided correctly suppressed DIR images in both standard 2D DIR as well as high-resolution 3D DIR MRI examinations.
Images for this section:

**Fig. 3:** Results of DIR images using the optimized or previous parameters.

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Fig. 4: Results of contrast (C-GM) in different TR.

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Fig. 5: Results of contrast (C-WM) in different TR.

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Conclusion

It is possible to correctly obtain suppressed DIR images using the optimized method of MRI scan parameters based on the mixed sequence and a developed analysis algorithm. This finding may lead to considerable consequences for future imaging studies that involve degenerative diseases.
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