

2D Multi-slice Quantitative Myelin Water Imaging at 3T

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INTRODUCTION: Myelin water fraction (MWF) can serve as a direct indicator of myelin integrity and provide quantitative measurements of myelin structure and component change due to white matter diseases such as multiple sclerosis (MS) and leukoencephalopathy (LE). MWF can be obtained from T2 or T2* component analysis [1, 2]. T2 spectrum can be derived from T2 decay signal data acquired using a multi-echo CPMG sequence, in which the acquisition time for a single slice is about 25 minutes [1]. In this study, we propose a multi-slice acquisition scheme with much higher efficiency and capturing the small contribution of the myelin-water signal.

METHOD: The first echo signal of Siemens original multi-slice 32-echo CPMG sequence is lower than the second echo signal due to refocusing RF imperfections [3]. The myelin-water signal in T2 spectrum analysis is dramatically underestimated due to this issue. Recently, simple modification to the similar pulse sequence was reported to diminish this issue by increasing slice thickness of refocusing RF three time larger than that of excitation RF for more accurate T2 measurement [4]. We took advantage of this technique for T2 spectrum analysis and proposed an efficient multi-slice acquisition scheme. Total ten brain axial slices from two scans were acquired using this modified sequence on a 3T Siemens Trio scanner using 12-channel head coil. The protocol for both scans was used as follows: FOV = 220×220 mm; slice thickness = 5 mm; 5 slices with 200% slice gap; TE_s = 10-N, (N = 1, 2, 3, ..., 32); TR = 3000 ms; receiver bandwidth = 300 Hz/pixel; GRAPPA reduction factor is 2 and the reference line is 24; the acquisition time for each scan was about 6 minutes. The second scan shifted 7.5 mm along slice direction relative to the first scan to form ten consecutive slices with 2.5 mm gap.

In this study, we acquired the data from the same volunteer using original and modified sequence for comparison. The decay curves resulting from the measured data could be described using the following equation [5]:

$$y_i = \sum_{j=1}^M e^{-TE_i/T_{2j}} s_j \Delta T_{2j} = \sum_{j=1}^M E_{ij} s_j^T, \quad i = 1, 2, \dots, N \quad (1)$$

where y_i is the signal intensity, $M = 96$ equally log-scale spaced T2 time points within the range of 15 ms to 2 sec, $N = 32$ is the number of echoes, s_j is the spectrum density of T2 distribution, and ΔT_2 is the T2 interval, and $s_j^T = s_j \Delta T_{2j}$. A weighted regularized nonnegative least squares (wrNLS) algorithm was used to minimize the residue norm and smooth the T2 distribution density curve. The wrNLS algorithm is as follows:

$$\min_s \{ \|Es^T - y\|_2 + \mu \|Ws^T\|_2 \}, \quad W_j = 1/\Delta T_{2j}, \quad s^T \geq 0 \quad (2)$$

where s^T , y , W and E are vectors or matrix corresponding to eq (1), and μ is equal to 1.2 for all the data. The T2 spectrum can be partitioned into four intervals: fast decaying components (the myelin sheath, T2=15 – 40 ms; Tissue water, 40 – 200 ms), and slow decaying components (tissue water with long T2, 200 – 800 ms; CSF, 800 – 2000 ms). The ratios of the integral of each interval to the overall integral correspond to MWF, tissue water fraction (TWF), long T2 tissue water fraction (LWF), and CSF fraction (CSF). After the weighted T2 spectrum s^T was computed, four fractions were calculated for each pixel to generate parametric maps.

RESULTS: Fig. 1 shows T2 signal decay curves of two data sets from original and new pulse sequences. The first point of Siemens original sequence is slightly lower than the second due to imperfect refocusing RF; and the first point of new sequence reduced this affect from refocusing RF. Fig. 2 shows parametric maps of the single slice acquired from the same volunteer using two different pulse sequences. Images in the first row were from the original sequence and images in the second row were from the new sequence. The numbers on the lower right corner of each map represent averaged fraction values from the same white-matter ROI shown on MWF map in the second row. MWF of the original sequence was about 3.2% much lower than that of the new sequence, which was 11.2% and consistent with the value 11.28% reported in other literature [1]. Correspondingly, the first TWF (96.5%) was much larger than the second (88.4%). Averaged values of LWF and CSF were very similar and less affected by the different sequences. Fig. 3 shows MWF maps of one-scan five slices of another volunteer. The percentage of MWF is shown in the color scale bar. Although SNR of T2 images used for Fig. 3 was almost twice lower than that for Fig. 2 due to the multi-slice crosstalk effect, the perceptual image quality of parametric maps was still sufficient and the MWF quantification was consistent with the result shown in the lower row of Fig.2.

CONCLUSION: We proposed an efficient 2D Multi-slice scheme of T2 spectrum analysis over most of the brain volume in less than 12 minutes. We also provided a weighted regularized nonnegative least squares algorithm for generating reliable LWF and CSF maps, which could display very important information for MS or LE patients. Further investigation on LE pediatric patients using this technique will be performed.

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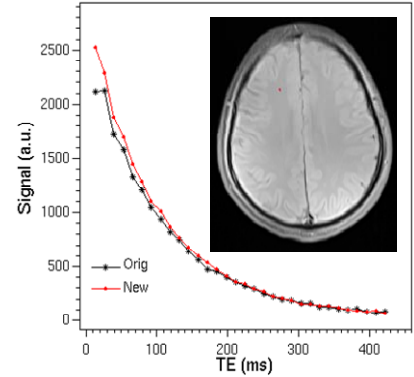


Fig. 1 Signal curves from original and new sequence. Small red ROI is shown on image.

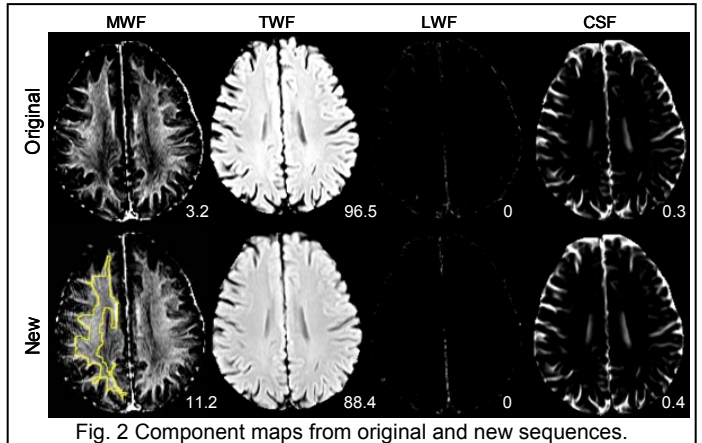


Fig. 2 Component maps from original and new sequences.

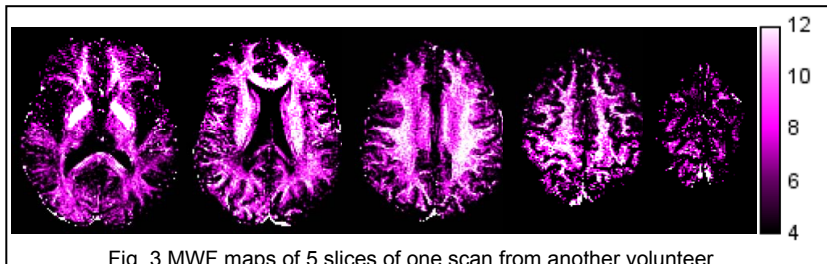


Fig. 3 MWF maps of 5 slices of one scan from another volunteer.