Accelerated T1 and T2 Relaxometry in the Human Brain Using UNFOLD

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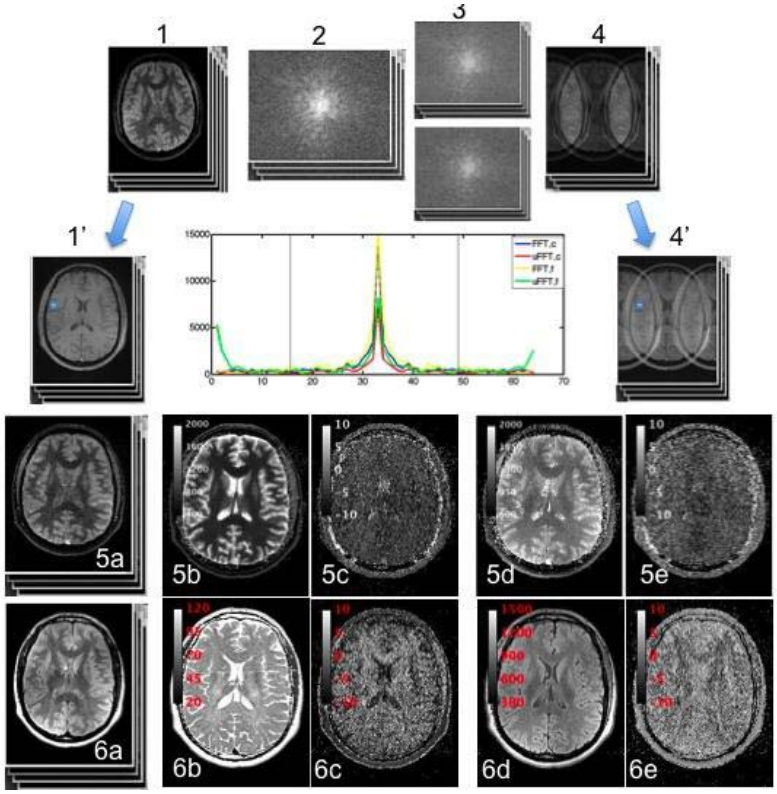
Introduction

Given that much of the diagnostic capability of MRI is related to changes in the longitudinal (T1) and transversal (T2) relaxation times induced by pathologies, mapping of relaxation times is relevant to potentially any disease. A step further into the microscopy of tissue, information about compartmentalisation of water can be gained from extensive sampling of the relaxation curves [1-4]. However, even fast relaxometric methods offering a high time resolution (e.g. Look-Locker-type T1, CPMG-type T2 measurements) usually require long measurement times. Already a decade ago the UNFOLD method was introduced for accelerating dynamic applications in which the temporal dimension of the *k-t* space was not densely filled [5]. Transferring information from the *k* to the *t* dimension allowed for a denser, smaller k–t space to be acquired, and resulted in significant reductions in the acquisition time of the temporal frames without loss in SNR. We present an application of the UNFOLD method to T1 and T2 relaxometry, which takes advantage of the high temporal resolution of two multi-point mapping methods and uses their extensive temporal information for reducing the acquisition time. One of the fastest multi-time-point multi-slice Look-Locker sequences developed to date, TAPIR [6-8], was used for T1 mapping and a conventional CPMG-type multi-slice multi-echo sequence for T2 mapping.



Materials and Methods

All measurements were performed on a 3T Tim-Trio Siemens scanner, with gradients of 40mT/m/axis. A body coil was used for RF transmit and a 12-channel phased-array coil for signal detection. Ten healthy volunteers (6 male, 4 female, mean age 35 years, from 23 to 48) were measured. The parameters of the TAPIR acquisition included: matrix size 256x200, resolution 0.8x0.8x2mm^3, 2 slices, TR=10ms, alpha=25deg, tau=2400ms, 64 equidistant time points from 10 to 1290ms. The parameters of the CPMG-type acquisition included: matrix size 256x200, resolution 0.8x0.8x2mm3, 2 slices, TR=2500ms, alpha=90/180deg, 32 equidistant echoes ranging from 6.8 to 217.6 ms. The full k-t space was acquired; resampling corresponding to an acceleration factor of two and reconstruction using UNFOLD was performed off-line as follows. For each time point the k-space (Fig. 2) was reconstructed starting from magnitude and phase DICOM images (shown as stack in Fig. 1) via 2D inverse Fourier transform. Every second line of each of the k-spaces was eliminated such that k-spaces corresponding to odd time points had all even k-space lines zeroed and k-spaces corresponding to even time points had all odd lines zeroed (Fig. 3). The total measurement time for such an UNFOLD-accelerated acquisition with k-spaces undersampled by a factor of two would therefore be reduced to half of its original value. Image data were reconstructed for each time point from the undersampled k-spaces by two-dimensional Fourier transform (Fig. 4). The stack of images corresponding to the 64 (TAPIR) or 32 (CPMG) time points for each slice was Fourier transformed in the time dimension (Fig. 4') resulting in a frequency spectrum for each voxel (central plot). The central half only of each spectrum (as included between vertical lines in the central plot) was kept and the rest of the spectrum set to zero. An inverse Fourier transform was performed in the time dimension and a stack of UNFOLDed images (Fig. 5a for TAPIR, 6a for T2) corresponding to the time points was obtained. The stack was fitted with a single component model corresponding to either the TAPIR signal equation [6-8] or the single-exponential T2 decay. The first and last image of the series still show artefacts due to the truncation in the time spectrum and were not included in the fit. The maps obtained from UNFOLDed data are compared to the ones obtained from the original, fully-sampled stack of images with all the measured time points included in the fit. The maps and the relative errors in percent are shown in Figs 5b-e for T1 and 6b-e for T2.

Results and Discussion

Undersampling of the k-space by a factor of 2 (Fig. 3) leads to severe ghosting in the corresponding Fourier transformed images (Fig. 4). The N/2 ghost in the undersampled series has half of the original intensity. However, the folded-in component has a different time behaviour than the original one (central plot, components at the Nyquist frequency) and can thus be eliminated by truncating the frequency spectrum. T1 and T2 maps corresponding to the undersampled data reconstructed by the UNFOLD method are shown in Fig. 5b (T1) and 6b (T2); the scale is given in ms. Figs. 5c and 6c present the distribution of relative errors in percent for the T1 and T2 maps. Similar information is shown in Figs. 5d-e and 6d-e for the M0 maps (signal intensity at zero echo- or inversion time). The mean value of the percentage error over the brain is below 3% and is not only due to the region where the ghost was present. There is a slight change in the values of the relaxation times in the ghost-free regions, showing the effect of the truncation of the Fourier spectrum on the time behaviour of the signal. However, for the parameters chosen here, this influence is minimal (below 2%). The crucial requirements for a successful UNFOLD reconstruction of multi-time-points relaxometric data are high enough band width of the sampling of the time curve, such that the original and folded component are well separated in the Fourier spectrum, and high number of time points, such that the effect of the truncation of the Fourier spectrum on the time behaviour of the reconstructed signal is not very large. It is striking from the images and maps that the reconstruction of undersampled data leads to no loss in SNR. This is due to the fact that by eliminating half of the Fourier spectrum, also the noise associated with these points is filtered out. The effective time resolution is halved and the missing points are recovered by zero-filling interpolation. However, for a large enough number of time points, no adverse effect is visible in the maps. In conclusion, UNFOLD reconstruction of relaxometric data with high temporal resolution is feasible. A moderate acceleration factor of two leads to no visible artefacts in the brain region and to a very tolerable change in the mapping accuracy of less than 5%. While we have addressed here separately acquired T1 and T2 data, it is conceivable to apply the UNFOLD method to correlated 2D T1/T2 information, reducing the acquisition time by at least a factor of four. This would open a whole new dimension of information about water compartmentalization in the living brain.

References: [1] MacKay A (1994) MRM 31, 767; [2] English MRM 22 (1991); [3] Travis and Does (2005) MRM 54, 743; [5] Madore B et al.(1999) MRM 42, 813; [6] Shah NJ et al. (2001) NeuroImage 14, 1175; [7] Steinhoff S et al.(2001) MRM 46, 131; [8] Zaitsev M et al.(2003) MRM 49, 1121.