Quantification of Transversal Relaxation Time T2 using an Iterative Regularized Parallel Imaging Reconstruction

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Introduction

Nonlinear parallel imaging reconstruction using an iterative regularized Gauss Newton method (IRGN) has shown its potential in several applications [1]. This technique determines both the coil sensitivities and the image from undersampled multi-coil data. It enables high acceleration factors without pronounced local enhancement of noise. The numerical implementation of this sophisticated method requires data normalization steps which are usually performed individually for each slice and echo. In this study it was investigated if this type of reconstruction is applicable for quantitative imaging despite the complex reconstruction including image individual normalization. For that purpose high resolution multi-echo imaging with different acceleration factors was used for the quantification of the transverse relaxation time (T2).

Methods and Results

Three multi Spin-Echo (SE) datasets from a phantom and a healthy volunteer were acquired on a clinical 3T scanner with different acceleration factors (fully sampled, AF=2 and AF=4) using a 32CH tx/rx head coil and a 8Ch tx/rx knee coil. The phantom consisted of 6 samples with varying Gd-DTPA (Magnevist®) concentration ranging between 0.95 and 6.7 mM. Scanning parameters were TR=1800 ms, 10 echos, 150 mm FOV, 256x256 matrix, 10 slices, echo spacing=20/9.2 ms, slice thickness=5/2 mm for the phantom/in vivo respectively. To estimate the coil sensitivities 24 parallel imaging reference lines were used in the Cartesian k-space. Rawdata were exported from the scanner, and offline reconstructed using the IRGN method. Special care was taken to track all data normalization steps and to reverse their effect in the final step of image reconstruction. All T2 maps were computed using monoexponential linear least squares curve fitting on a pixel-by-pixel basis. The initial spin-echo was excluded from the fitting procedure to minimize artifacts in the T2 calculation due to non-ideal slice profile or B1-inhomogeneities [2]. Fig. 1 shows the images acquired without acceleration and with AF=2, 4 as well as the corresponding T2 maps. For the phantom study, circular ROIs were manually placed over each probe in the T2 maps of the central slice. For the in-vivo case, a small ROI was manually placed in a homogeneous region of the specific tissue in all slices of the scan with AF=1 and copied to the accelerated data. This procedure guarantees that identical ROI locations for all AF's were evaluated. Results of the different reconstruction methods, the T2 values of the phantoms and the mean T2 values of the different tissues averaged over ten slices, are shown in **Fig. 2**. Error bars represent the standard deviation (SD).

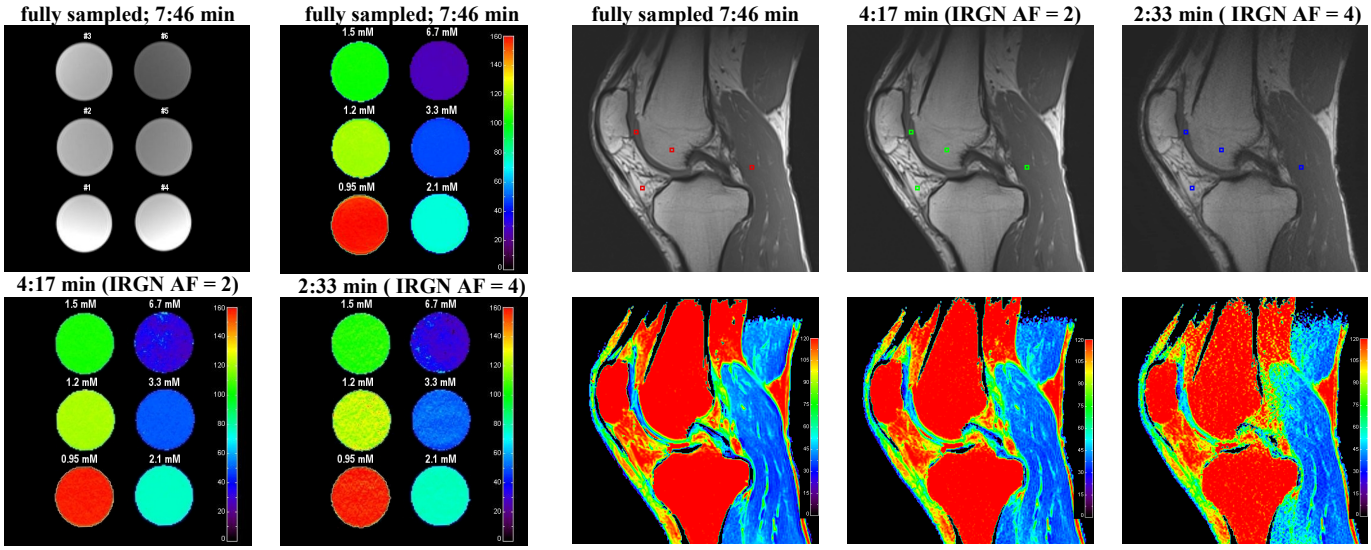

Fig. 1: Representative images of different reconstruction techniques for different acceleration factors and their corresponding T2 maps.

Discussion

Our experiments show that the image quality of all accelerated scans is visually comparable to the fully sampled data. No residual aliasing artifacts or local noise amplification were observed up to AF=4. At an acceleration factor of 4 the general noise enhancement introduces noisier T2 maps compared to the fully sampled data.Samples #3 and #6, situated nearby the center of the coil assembly, exhibit higher SD due to the inherent SNR characteristic of phased array coils [3] However, the comparison of the mean values show that T2 computed from the accelerated scans all lie in the interval mean ± SD of the fully sampled data, and the values are generally in agreement with literature values [4,5] for the in-vivo experiment. In this study we successfully demonstrated that nonlinear parallel imaging IRGN is applicable to quantitative MRI. To our best knowledge in condition of low SNR regime its homogenous noise distribution characteristic makes IRGN a valuable alternative to conventional parallel imaging for quantitative applications.

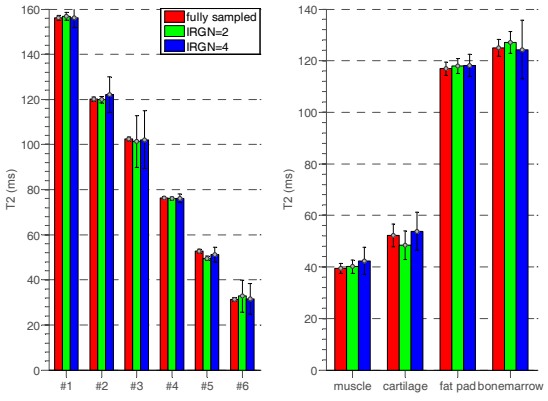

Fig. 2: Comparison of the T2 values from the different reconstruction methods and acceleration factors for the ex-/in-vivo experiments. T2 mean values and standard deviations are shown.

Acknowledgements

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References [1] Uecker et al., MRM 60:674-682 (2008), [2] Rubenstein et al., Radiol 201: 843-850 (1996), [3] de Zwart et al., MRM 51: 22-27 (2004), [4] Gold et al., AJR 183: 343-351, [5] Mosher et al., AJR 177: 665-669 (2001).