Implementation of a 3D IR-trueFISP Tissue Relaxation Mapping Sequence

R. Newbould[1], M. T. Alley[1], R. Bammer[1]
[1]Dept. of Radiology, Stanford University, Stanford, CA, United States

Introduction

An inversion recovery prepared balanced SSFP sequence, known as IR-trueFISP, has recently been presented as a method to quantify tissue parameters from a single acquisition [1]. Analytical expressions for the signal recovery curve as a function of T_1, T_2, proton density (PD), and the flip angle α have been determined in previous work [1][2]. The IR-trueFISP sequence requires the sampling of the magnetization curve for each voxel in the volume of interest as it progresses from the initial inverted value towards its final, steady-state value. This method has now been adapted for rapid use in clinical studies of several tissue types. Further, once parameters have been mapped, the image contrast from several common imaging routines may be simulated.

Methods

A novel 3D CINE version of the IR-trueFISP sequence was implemented on a 1.5T GE EXCITE clinical MR scanner (GE Medical Systems, Waukesha, WI) with high strength 50mT/m gradients using receive-only 8-channel phased array coils (MRI Devices, Waukesha, WI). Each cardiac interval consists of an inversion pulse, followed by an $\alpha/2$ SSFP preparation pulse [2], which is followed by a train of SSFP α pulses. As the inversion time does not affect the SSFP TR, an adiabatic inversion pulse was implemented to give full inversion even in the presence of B_1 field inhomogeneity. The SSFP pulses, however, do greatly influence the TR, which influences the amount of off-resonance effects. The use of a 3-D slab aided the ability to reduce pulse length without sacrificing slice profile, however, the use of a short, standard RF pulse yielded unacceptable variation in magnetization, as shown in Figure 1. Even small variations in flip angle across the slices resulted in pronounced variations in the relaxation curve. For this reason, a short-time scale (600us) minimum phase profile-optimized SLR pulse was implemented.

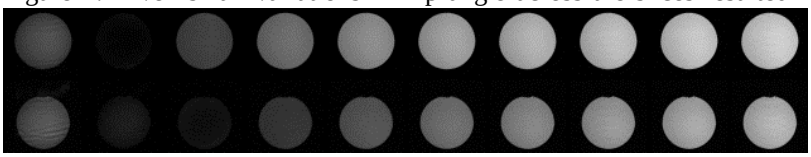

Figure 1. Magnetization magnitude of two slices from a 3D slab of a uniform phantom taken at 100ms intervals. A train of unoptimized 600us SSFP pulses was used; note the difference in value with time between the two.

Slice encoding in the 3D slab occurs after each readout period. Once a readout line in each slice has been acquired, the pattern is repeated. This readout set is repeated as quickly as possible until the magnetization has entered its steady-state value. A lack of fixed phase encodes influences only the time resolution of the sampling, rather than the number of locations sampled. This is allows an arbitrary resolution and number of slices in a fixed time period: additional slices only reduce the curve sampling. For a reasonable number of slices (up to 100), the curve is sampled enough to attain nominal fit values. This slice-sampling process is then repeated for the next phase encode in the next cardiac period. The entire data collection scheme is encapsulated in a respiratory compensating, cardiac-gated CINE sequence [3]. The relaxation mapping can thus occur in motion-free tissues in a straightforward manner, yet can also occur in areas with motion by simply enabling the gating control.

The relaxation curves were fit to a three-parameter expression [1] using a nonlinear least-squares fitting routine implemented in IDL (Research Systems Inc., Boulder, CO). Once parameter maps have been obtained, in-house software allows the construction of image contrast from standard imaging routines, such as PD-weighted, T_1-weighted, T_2-weighted, and FLAIR images.

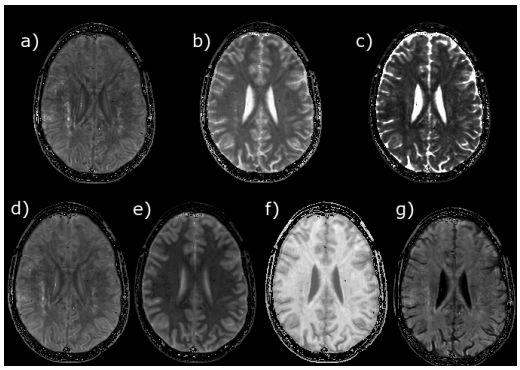

Figure 2. a) PD, b) T1, and c) T2 maps in the brain. From these images, d) PDw, e)T2w, f) T1w, and g)FLAIR images may be produced.

Discussion

The sequence is implemented as a slab-selective 3D SSFP sequence, using a novel CINE-based approach which varied sampling of the recovery curve, rather than scan timing parameters. The sampling of the relaxation curve at a number of points allows decreased SNR without reduced fidelity of the fitted tissue parameters. Furthermore, the relaxation curve is only scaled by off-resonant banding artifacts. That is, areas of characteristic banding were consistent through the time course. The relaxation curve was therefore only scaled by the passband value. This does not affect the estimated T1 and T2 values, though does scale the pseudo-PD. The resultant estimated tissue parameters have been noted to be extremely sensitive to the achieved SSFP flip angle. Attaining exact flip angles, with only small variation across the volume can be problematic. The angle achieved is a function of both the excitation slice profile as well as the B_1 field homogeneity. Furthermore, flatter slice profiles require longer excitation pulses, which can lengthen the T_R, enhancing off-resonance effects. The use of the body coil to transmit, and multi-channel phased-array coils for reception was noted to alleviate these problems.

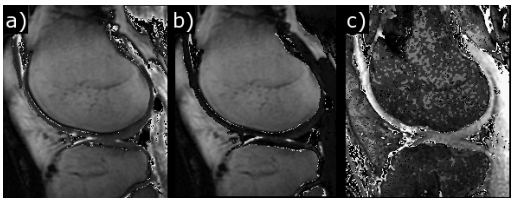

Figure 3. a) T1, b) T2, and c) PD maps of human knee cartilage.

Acknowledgments: This work was supported in part by the NIH (1R01EB002771), the Center of Advanced MR Technology at Stanford (P41RR09784), Lucas Foundation, and Oak Foundation.

References: Schmitt, et. al., MRM(51) 661-667, 2004. 2. K. Scheffler, MRM(49) 781-783, 2003. 3. M.T. Alley, et. al., JMRI(9) 751-755, 1999.