Simultaneous 3D B1 and T1 mapping using the new Method of Slopes (MoS)

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Introduction

Current practical T1 mapping MR techniques (eg. VFA and DESPOT1) use the steady-state signal at various flip angles[1,2]. A pixel-wise linearization of the signal as a function of flip angle allows for T1 estimation, given that the true flip angle is known. At higher field strengths (≥3T) B1 inhomogeneities cause spatial variability in the true flip angle, thus a flip angle calibration (Cα) map (commonly called B1 map) is required to ensure T1 mapping accuracy. Usually, T1 mapping techniques require separate acquisitions for B1 mapping. Due to time constraints, B1 mapping is usually implemented in 2D while quantitative accuracy requires 3D acquisitions for T1 quantification. Slice profile inconsistencies thus compromise the accuracy of the T1 mapping methods.

In this work, a new approach is proposed to determine B1 and T1 maps simultaneously. It relies on the acquisition of a few 3D SPGR scans at different nominal flip angles (FAs) and relatively short TR. The quasi-linear relationship between signal intensity and FA for large and small FAs is exploited to uniquely determine the FA calibration and T1 values at each pixel. The B1 mapping technique, much like that proposed by Dowell & Tofts [3], has already been presented [4] but an improved, more efficient implementation is now possible.

Theory

For an SPGR scan, the signal intensity (SI) can be written as a function of true FA, αtrue, TR and T1:

\[ SI = M_0 \sin(\alpha_{true}) \left(1 - \frac{E_1}{1 - \cos(\alpha_{true})}E_1\right) \tag{1} \]

where \( E_1 = \exp(-TR/T1) \). Writing \( \alpha_{true} \) in terms of the nominal FA: \( \alpha_{true} = C_{α}\cdot\alpha_{nom} \), Eq.[1] can be rewritten as an expression for SI as a function of three unknowns: \( C_{α}, M_0 \) and \( T_1 \). Unfortunately, the parameters are coupled and it is therefore challenging to uniquely determine these from arbitrary subset of of SPGR data. Exploring the properties of the SI vs \( α_{nom} \) curve and its derivative can help guide the data sampling. The derivative of Eq.[1] respect to \( α_{nom} \) gives:

\[ SI' = \frac{\partial SI}{\partial \alpha_{nom}} = \frac{M_0 C_{α}(1 - E_1)}{(1 - \cos(C_{α}\alpha_{nom}))^2} \cdot (\cos(C_{α}\alpha_{nom}) - E_1) \tag{2} \]

Computing this derivative for \( \alpha_{nom} = 0° \) reveals that it is independent of \( E_1 \) at the origin: \( SI' = SI'(\alpha_{nom} = \alpha_{true} = 0) = M_0 C_{α}. \) Furthermore, it can be approximated by a straight line (Fig.1). For values of TR/\( T_1 > 1/50 \), SI can also be approximated by a straight line (with significantly negative slope for TR/\( T_1 > 1/50 \)) as the signal null is reached [3,4]. Using Eq.[1] to compute the slope gives:

\[ SI'_{null} = \frac{SI'(\alpha_{nom} = 180°)}{(-M_0 C_{α}(1 - E_1) + E_1)} \]

The method of slopes (MoS) proposed here uses the ratio of the slopes given by Eq.[2] at both ends: \( \frac{SI'_{null}}{SI'_{0}} = (-\frac{1 - E_1}{1 + E_1}) \) which yields: \( E_1 = -\frac{1 - SI'}{SI'}(SI'_{null})^{-1} \)

Methods

MoS consists of 3 steps: (1) three high flip angles are used to extrapolate to the signal null and determine \( C_{α} \). For the \( T_1 \) values of physiological interest (\( T_1 > 1/50 \)), it was found that a coarse resolution (FOV=20cm, 6x64, 28 slices, slice thickness=5mm) with TR=30ms yields sufficient pixel-wise SNR for extrapolation to the signal null with nominal FAs (120°, 140°, 160°). The slope of the straight line fit is also determined: \( SI'_{null} \). (2) a single data point for the lowest possible nominal FA (1°) is used to estimate the slope of the curve at the origin (3) the ratio of slopes is calculated and \( E_1 \) (and \( T_1 \)) extracted according to Eq.[3]. The \( T_1 \) estimation can be performed at a higher resolution by sampling the 3D-SPGR signal at FAs (1°, 120°) at a higher resolution (128×128, slice thickness=3mm) with a longer TR (TR=50ms) to compensate for SNR loss. Using the origin and null signal point (given by step (1)) the slopes at both ends can be determined and the \( T_1 \) extracted. Data were acquired using a 3D-SPGR sequence on a 3T scanner (MR750, GE Healthcare). The method was tested on phantoms of various sizes, locations and \( T_1 \) values in quadrature and 8-channel headcoils (total scan time <10min). In vivo, MoS was applied on the brains of two healthy volunteers. Slab profile imperfections were avoided by using a sagittal orientation full brain coverage and no slab select gradient as suggested by Dowell & Tofts [3]. \( T_1 \) maps obtained using MoS were then validated using values estimated from standard inversion recovery (SE-IR) measurements.

Results

MoS resulted in \( B1 \) maps with expected profile and flat \( T_1 \) maps for various homogeneous phantoms (Fig.2a). A range of \( T_1 \) values were compared with a SE-IR experiment (Fig.2b). Preliminary brain data (Fig.2c) at higher resolution (128×128, 3mm) shows the expected \( B1 \) trend and the \( T_1 \) values for gray and white matter fall within expected literature values [5]: (mean ± std in small ROIs) white matter=1196 ± 54ms, gray matter=1649±77ms.

Conclusion

A new, simple and readily available method for simultaneous 3D \( B1/T1 \) mapping has been presented. It requires sampling of the SPGR signal at FAs =\( (120°, 140°, 160°) \) to determine the \( B1 \) map and an additional sample at FA=1° for the \( T_1 \) map. Higher resolution for \( T_1 \) mapping requires the higher resolution acquisition of only two FAs (1°, 120°). Scan time efficiency is limited by the longest \( T1 \) value of interest such that TR/\( T_1 > 1/50 \).

References