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

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Introduction

Current practical T_1 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 T_1 estimation, given that the true flip angle is known. At higher field strengths (≥3T) B_1 inhomogeneities cause spatial variability in the true flip angle, thus a flip angle calibration (C_α) map (commonly called B_1 map) is required to ensure T_1 mapping accuracy. Usually, T_1 mapping techniques require separate acquisitions for B_1 mapping. Due to time constraints, B_1 mapping is usually implemented in 2D while quantitative accuracy requires 3D acquisitions for T_1 quantification. Slice profile inconsistencies thus compromise the accuracy of the T_1 mapping methods.

In this work, a new approach is proposed to determine B_1 and T_1 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 T_1 values at each pixel. The B_1 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, α^{true} , TR and T_1 :

$$SI = M_0 \sin(\alpha^{true}) \frac{1-E_1}{1-\cos(\alpha^{true})E_1} \qquad \text{Eq.[1]}$$

where $E_1 = \exp(-TR/T_1)$. Writing α^{true} in terms of the nominal FA: $\alpha^{true} = C_\alpha \cdot \alpha^{nom}$, 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:

$$SI' = \frac{\partial SI}{\partial \alpha^{nom}} = \frac{M_0 C_\alpha (1-E_1)}{(1-\cos(C_\alpha \alpha^{nom})\cdot E_1)^2}(\cos(C_\alpha \alpha^{nom}) - E_1) \qquad \text{Eq.[2].}$$

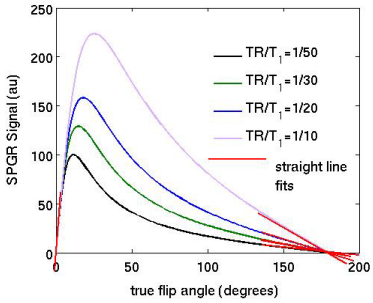

Fig.1: SPGR vs true flip angle

Computing this derivative for $\alpha^{nom} = 0°$ reveals that it is independent of E_1 at the origin: $SI'_0 = SI'(\alpha^{nom} = \alpha^{true} = 0) = M_0 C_\alpha$. 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: $SI'_{null} = SI'(\alpha^{true} = 180°) = -M_0 C_\alpha (1-E_1)(1+E_1)^{-1}$. The method of slopes (MoS) proposed here uses the ratio of the slopes given by Eq.[2] at both ends: origin ($\alpha^{true} = 0°$) and signal null ($\alpha^{true} = 180°$) to uniquely determine E_1 (and T_1):
$rSI' = SI'_{null} / SI'_0 = -(1-E_1)(1+E_1)^{-1}$ which yields: $E_1 = -(1-rSI')(rSI'-1)^{-1}$ Eq.[3].

Methods

MoS consists of 3 steps: (1) three high flip angles are used to extrapolate to the signal null and determine C_α [3,4]. For the T_1 values of physiological interest (T_1 :300-2200ms), it was found that a coarse resolution (FOV=20cm, 64x64, 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 (128x128, 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 B_1 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 (128x128, 3mm) shows the expected B_1 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 .

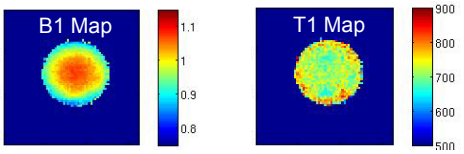

Fig.2a: phantom B_1 and T_1 maps in quadrature headcoil

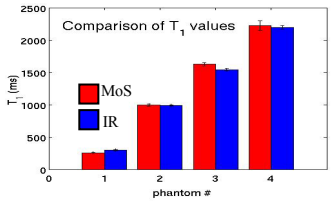

Fig.2b: phantom data in a central ROI

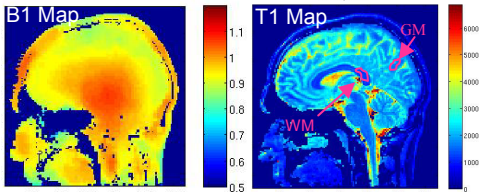

Fig.2c: in vivo brain data using 8-channel headcoil

Conclusion : A new, simple and readily available method for simultaneous 3D B_1 / T_1 mapping has been presented. It requires sampling of the SPGR signal at FAs =(120°,140°,160°) to determine the B_1 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 T_1 value of interest such that TR/ T_1 > 1/50.

References: [1] Stollberger & Wach, *MRM* 35, 1996 [2] Deoni et al., *MRM* 49, 2003 [3] Dowell & Tofts, *MRM* 58, 2007 [4] Chavez & Stanisz, *ISMRM* 3076, 2009 [5] Cheng & Wright, *MRM* 55, 2006.