Optimized Method of Slopes (MoS) Produces Robust and Efficient 3D B1-corrected T1 Maps

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Introduction

A common method used for T_1 mapping is the variable flip angle, VFA [1] method or DESPOT1[2], which relies on the acquisition of 3D SPGR signal at different nominal flip angles, α_{nom}, and short TR (<10ms). This method is not expected to yield accurate results at high fields (≥3T) without a flip angle correction to account for B_1 inhomogeneities. However, the choice of flip angle correction method has been shown to introduce inaccuracies in the T_1 result [3]. In fact, the accuracy of the VFA method is known to be sensitive to the choice of α_{nom} used to sample the signal [1,2,4] as well as a large noise bias [4]. Much of the inaccuracy of the VFA method can be attributed to the transformation of the signal equation into a linear form. The Method of Slopes (MoS) [5] has been proposed to mitigate the shortcomings of the VFA method: it relies on a universal sampling scheme (choice of α_{nom} is T_1 independent for a large range of T_1 values) and solves the full 3D SPGR signal equation for B_1 and T_1 simultaneously, without introducing the noise bias.

The main weakness of the MoS, as originally proposed [5], is that it requires a longer TR than the VFA method and thus results in longer scan times. In this work, we show that the scan time efficiency for MoS can be increased by separating it into 3 steps and optimally trading off TR for resolution at the various steps. The result, eMoS, is a simultaneous, consistent and accurate 3D B_1 and T_1 mapping method, which can be achieved in the same amount of time as the VFA method with a B_1 correction. Furthermore, it is shown that eMoS is robust, thus lending itself to parallel imaging techniques, such as ASSET, with large gains in scan time.

Theory

The SPGR signal intensity, SI, can be written as a function of α_{nom}, TR and T_1: $SI = S_0 \sin(C_\alpha \cdot \alpha_{nom})(1-E_1)/(1-\cos(C_\alpha \cdot \alpha_{nom})E_1)$ where S_0 is the equilibrium signal, C_α is the flip angle calibration factor and $E_1 = exp(-TR/T_1)$. SI is thus a function of three unknowns: S_0, C_α and T_1. The MoS uses data, sampled at α_{nom} =(1˚, 40˚, 130˚,150˚), to uniquely determine the three unknowns as follows: (i) α_{nom} =(130˚,150˚) are used to extrapolate to the signal null, $SI(\alpha_{null})=0$, which determines C_α: $C_\alpha = 180^\circ / \alpha_{null}$, via a 2-point C_α-correction scheme [5,6] (ii) α_{nom} =1˚ is used to determine S_0 and, with the data from the previous step, an initial T_1 estimate whilst (iii) α_{nom} =40˚, has high SNR and is thus used in the final non-linear least squares fitting procedure to uniquely determine T_1. Step (i) requires TR=40ms because the extrapolation is shown to be challenging for TR/ T_1< 1/50 due to low signal and a less steep slope at these values [5]. Noting that the B_1 map is expected to vary slowly, a coarse resolution can be used for sampling α_{nom} =(130˚,150˚). However, because the ratio of slopes at high and low α_{nom} is used for initial T_1 estimates and all data points are used in the final fit, data sampled at α_{nom} =(1˚,40˚) must be acquired with the same TR as that used for sampling α_{nom} =(130˚,150˚). This long TR requirement, for α_{nom}=(1˚,40˚), results in long scan times for high resolution T_1 mapping.

In this work, several modifications are made to steps (ii) & (iii) of the MoS, to maintain accuracy while reducing scan time. First, data is sampled at α_{nom} =3˚ instead of α_{nom} =1˚ to gain a 3-fold increase in signal-to-noise, SNR, while maintaining T_1-independence of the signal: i.e. $SI(C_\alpha \cdot \alpha_{nom}) \sim S_0 C_\alpha \cdot \alpha_{nom}$ holds for α_{nom} =3˚. Second, data at α_{nom} =3˚ is used to uniquely determine S_0 once C_α is known from (i). Third, the choice of α_{nom} for high SNR data, α_{SNR} , is chosen so that both SNR and T_1 contrast are maximized , given a short TR. Calculating $\partial SI/\partial T_1$, it can be shown that maximal T_1-dependence occurs in the range α_{SNR} =10˚-20˚, close to the Ernst angle, for TR=10ms-20ms and a relevant range of T_1 values. Finally, an initial estimate of T_1=1000ms is used, with the previously determined S_0 and C_α values, to fit the three data points: SI at α_{nom} =(3˚, α_{SNR} , α_{null}), to the full nonlinear SI equation, yielding T_1.

Methods

The brains of three volunteers of varying ages: 29, 42 and 55 years, were scanned with several 3D whole volume sagittal acquisitions on a 3T scanner (MR750, GE Healthcare). First, two SPGR volumes, with α_{nom}=(130˚,150˚) were used for C_α determination. Scan time was optimized by using: TR=40ms, 4mm slice thickness, 24cm FOV, in-plane resolution 64×64, for a total scan time, t_{B1} ~4min, for step (i) [5]. Data for steps (ii) and (iii), with in-plane resolution of 256×256, were then acquired in a scan time, t_{T1}, with 3 different sequences to test the robustness of the results while minimizing t_{T1} (see table). For comparison, the VFA method was also performed with this data, with a flip angle correction given by C_α in step (i).

Sequence	TR(ms)	α_{nom}	t_{T1}	Total scan time: t_{B1} + t_{T1}
SPGR	16	(3˚,20˚)	13min	17min
FSPGR	10.9	(3˚,14˚)	8min	12min
FSPGR w/ASSET factor 2	10.9	(3˚,14˚)	4min	8min

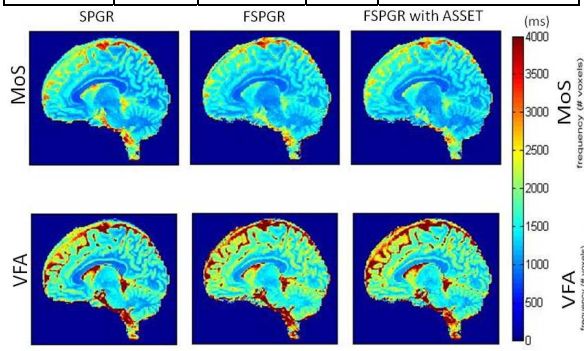

Fig.1

Results

Fig.1 shows resulting T_1 maps for a central slice. Fig.2 shows samples of central slice histograms computed for each subject. These figures show that the MoS results are more robust, accurate and precise for a larger range of T_1 values, i.e. the result is less dependent on scan type, gives expected grey and white matter values (distinguishable and narrower peaks in Fig.2), as well as realistic CSF T_1 values of 2000-3000ms. The inaccuracy of the VFA method is seen by the inconsistent results when α_{SNR} and TR were varied (less histogram overlap), as well as overestimated T_1 values in CSF and midbrain. Also, the noise bias in VFA results in greater differences between the FSPGR results, with and without ASSET.

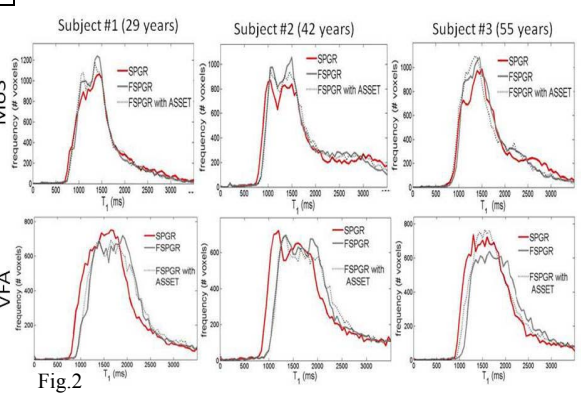

Fig.2

Conclusion

This work shows that the eMoS can produce accurate, T_1 maps in the same scan time as the VFA method. The eMoS T_1 results are more robust, less dependent on scanning parameters, and accurate over a larger range of T_1 values than the VFA results . This robustness can be exploited to further reduce the scan time via parallel imaging. The reduced flip angles proposed in this work may allow for a more accurate 2D calibration such as that presented at ISMRM in 2011 [6]. Future work involves comparison of brain T_1 results with an IR-based sequence to better assess the accuracy and precision of the proposed eMoS.

References [1] Wang et al., MRM 5, 1987 [2] Deoni et al., MRM 49, 2003 [3] Tardif et al., ISMRM 2745, 2011 [4] Cheng & Wright, MRM 55, 2006 [5] Chavez & Stanisz, NMR in Biomed (*accepted*), 2011 [6] Chavez & Stanisz, ISMRM 2744, 2011