A universal sampling scheme for the Method of Slopes (MoS) allows for rapid simultaneous B1 and T1 mapping in 2D

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Introduction

A novel method for simultaneous B_1 and T_1 mapping, the Method of Slopes (MoS) has already been proposed [1]. It relies on the acquisition of 3D SPGR signal 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 B_1 and T_1 values at each voxel. This method relies on an extrapolation of high flip angle signal to determine the signal null point [2]. Such an extrapolation is only accurate if the linear region of the SPGR signal *vs* FA is sampled. This linear region varies spatially as B_1 varies hence determination of a universally accurate sampling scheme becomes difficult. This work describes a method to correct for inaccuracies in the extrapolated signal null resulting from sampling away from the linear region of signal *vs* FA. Furthermore, it is shown that such a universal sampling scheme allows for the calibration of 2D SPGR signal relative to 3D SPGR signal at the given FAs. This is in contrast to methods such as DESPOT1 [3] which rely on acquisition of SPGR at FAs dependent on the expected T_1. This extends the MoS to 2D applications thus allowing for much faster single slice B_1 and T_1 measurements which could be used for dynamic studies or to overcome respiratory motion.

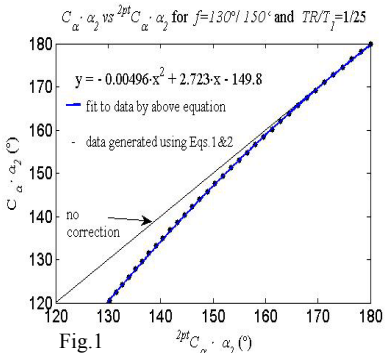

Fig.1

Theory For an SPGR scan, the signal intensity (*SI*) can be written as a function of true FA (α), *TR* and T_1:

$$SI = S_0 \sin(\alpha)\frac{1-E_1}{1-\cos(\alpha)E_1} \qquad \text{Eq.[1]}$$

where S_0 is the equilibrium signal and $E_1=exp(-TR/T_1)$. Writing α in terms of the nominal FA: $\alpha=C_\alpha \cdot \alpha_{nom}$, Eq.[1] can be rewritten as an expression for *SI* as a function of three unknowns: S_0, C_α and T_1. The MoS uses the ratio of the slopes of the curve at the origin (α=0˚) and signal null, $SI(\alpha_{null})=0$ to uniquely determine E_1 (and T_1) and C_α: C_α = 180˚/ α_{null}. Determination of α_{null} relies on accurate extrapolation to the signal null. This can be performed by sampling two data points SI_1 and SI_2, at nominal flip angles $\alpha_1<\alpha_2$. A 2-point extrapolation, resulting in ${}^{2pt}\alpha_{null}$, can be shown to underestimate α_{null} if α_1 and α_2 are sampled away from α_{null}, i.e. away from the linear region. The underestimation can be predicted however, since ${}^{2pt}\alpha_{null}$ can be written as a function of $f = \alpha_1/\alpha_2$ as follows:

$${}^{2pt}\alpha_{null}/\alpha_2 = (SI_1 - f \cdot SI_2)/(SI_1 - f \cdot SI_2) \qquad \text{Eq.[2]}$$

Methods Using Eq.[1] to write $SI_i=SI(C_\alpha \cdot \alpha_i)=SI(180˚/(\alpha_{null}/\alpha_i))$ for i=1,2, Eq.[2] can be written as an expression relating ${}^{2pt}\alpha_{null}$ and α_{null}. Although it cannot be solved analytically, curves can be generated whereby ${}^{2pt}\alpha_{null}/\alpha_2$ is determined as a function of f and several relevant values of E_1, and evaluated for α_{null}/α_2 in the range 1 - 1.5 because α_2 is chosen to be at most equal to the smallest expected α_{null} (to allow for extrapolation of magnitude signal). Fortunately, the curves are not strongly dependent on E_1 therefore an approximate E_1 (based on the *TR* and estimated/average T_1) is sufficient. Fig.1 shows an example of the quadratic relationship describing $C_\alpha \cdot \alpha_2 = 180˚/(\alpha_{null}/\alpha_2)$ as a function of ${}^{2pt}C_\alpha \cdot \alpha_2 = 180˚/({}^{2pt}\alpha_{null}/\alpha_2)$ for the given values of f, TR/T_1 (determined for brain: *TR*=40ms, T_1=1000ms).

Given that the sampling scheme for MoS consists of 2 FAs for both determination of α_{null} and the slope near α_{null}, another FA for determination of the slope near the origin and another high signal data point near the expected Ernst angle for stability, the scheme: FAs=(1˚, 40˚, 130˚,150˚) is used. This universal scheme has been tested on brain and works very well given 3D SPGR data but fails in 2D due to slice profile imperfections [4]. In this work, we demonstrate the feasibility of a 2D signal calibration, at the given FAs required for the MoS since the slice profiles should be independent of T_1 and only dependent on the RF pulse and slice-select gradients. The slice profile effect could be characterized for a given scanner at chosen FAs and then applied on future scans. The brains of three volunteers were scanned using the MoS sampling scheme with both 3D SPGR and 2D SPGR sagittal acquisitions on a 3T scanner (MR750, GE Healthcare) at FAs given above with the addition of a scan at FA=10˚ for normalization purposes. Scan parameters: FOV=24cm, 128x128, slice thickness=5mm,TE/TR=6ms/40ms were used. Full-brain 3D coverage was acquired in 3-4mins per data point (depending on head size) while the 2D single slice data points could be acquired in 5s allowing for signal averaging for the low SNR data points (up to 4 averages). Pixelwise signal was plotted: 3D vs 2D (Fig.2).

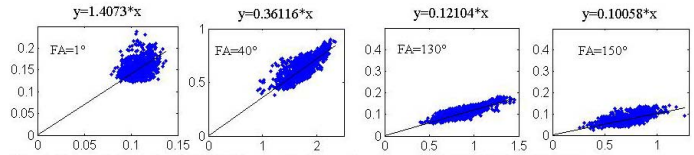

Fig.2 Plots of pixelwise 3D SPGR signal (y) as a function of 2D SPGR signal (x) (signal normalized to signal for FA=10°)

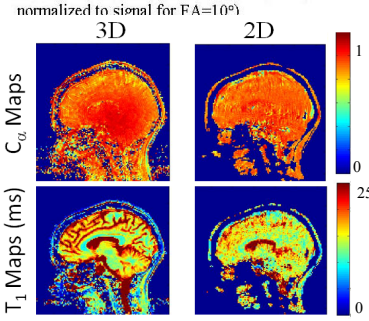

Fig.3

Subject	FA=1˚	FA=40˚	FA=130˚	FA=150˚
1	1.3789	0.3627	0.1215	0.0994
2	1.3581	0.3693	0.1268	0.1093
3	1.4073	0.3612	0.1210	0.1006

Results A strong correlation was found between the 3D and 2D SPGR signal. The 2D signal is scaled as expected with respect to the 3D signal due to the non-tophat slice profile at 2D [4]. The relationship between the 3D and 2D signal was found to be similar for all T_1 values of interest (gray/white matter) as expected and for all three volunteers scanned (Table). Hence, the relationship can be used to calibrate the 2D signal for future 2D SPGR brain scans, allowing for a 2D application of the MoS. The calibration was tested by correcting for 2D signal according to the average of the scaling factors shown in the above Table. The MoS was then applied on the scaled 2D data alone. Resulting 2D B_1 and T_1 maps (~25s scan time) were compared with those acquired in 3D (~12 min scan time) (Fig.3).

Conclusion This work shows that 2D SPGR signal can be calibrated with respect to 3D SPGR signal at a given FA despite inflow effects (Fig.2). Although this calibration is expected to depend on the B_1 map, it was found to vary little for the range of B_1 values expected in the brain. More investigation is needed to optimize the calibration but these preliminary results suggest that the MoS can be applied in 2D if a universal sampling scheme is used. This increases the temporal resolution drastically, allowing for dynamic studies and imaging of anatomical regions with respiratory motion.

References: [1] Chavez & Stanisz, *ISMRM* 240, 2010 [2] Dowell & Tofts, *MRM* 58, 2007 [3] Deoni , *JMRI* 26, 2007 [4] Parker et al., *MRM* 41, 2005