

Rapid T1 Mapping by Variable Flip Angles: Analytic Expression for B1-error Influences and Optimization for Large T1 Range

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INTRODUCTION

Quantification of T_1 relaxation time is valuable in dynamic contrast-enhanced studies of cancer and for enhanced discrimination of other diseases, such as epilepsy and Parkinson's. To be clinically useful, the imaging time must be short to allow for time-resolved T_1 measurements over a large volume. The measurements must also be accurate over a large range of T_1 's. Previous work (1, 2) shows that the variable flip-angle (VFA) method achieves an accuracy similar to conventional inversion- and saturation-recovery techniques but with a significant reduction in imaging time. It is also shown that only two ideal angles are required. However, the precision is optimized only over a narrow range of T_1 values, and the sensitivity to errors in flip angle, although acknowledged (3), has not been examined in detail.

In this study, the influence of errors in flip angle is developed theoretically and verified with numerical simulations. The accuracy and efficiency of T_1 measurements over a wide range of T_1 values are investigated using Monte Carlo simulations for different combinations of flip angles and are verified in phantoms.

THEORY

The signal time course of a SPGR experiment is a function of T_1 , TR , flip angle α_i , and spin density M_0 , and is given by Eq.[1], where $E_1 = \exp(-TR/T_1)$. The graph of S_i versus α_i can be linearized according to Eq.[2], and T_1 can be extracted from the slope E_1 (1):

$$S_i = M_0 \sin \alpha_i (1 - E_1) / (1 - E_1 \cos \alpha_i) \quad [1] \quad (S_i / \sin \alpha_i) = E_1 (S_i / \tan \alpha_i) + M_0 (1 - E_1) \quad [2]$$

The error in T_1 (dT_1) due to errors in flip angle ($d\alpha_i$) can be derived by propagating $d\alpha_i$ through the ordinates and slope of Eq.[2] into T_1 . For small $d\alpha_i$, the error in T_1 is:

$$dT_1 = \frac{-T_1^2 e^{TR/T_1}}{TR \cdot N(X^2 - \bar{X}^2)} \sum_{i=1}^N d\alpha_i \left(\frac{1}{\tan \alpha_i} \right) \left\{ Y_i (X_i - \bar{X}) + X_i \left[1 + \tan^2 \alpha_i \right] \left(Y_i - \bar{Y} - 2e^{-TR/T_1} (X_i - \bar{X}) \right) \right\} \quad [3]$$

where N is the number of flip angles, $X_i = S_i / \tan \alpha_i$, $Y_i = S_i / \sin \alpha_i$, and \bar{X} and \bar{Y} represent the mean values.

METHODS

Simulations were performed by generating signal data for $T_1=200-3000$ ms using Eq.[1]. Pairs of angles optimized for single T_1 values (1) in this range were considered, as were combinations of three or more of these angles. Precision was assessed by corrupting the signal with Gaussian noise ($\mu=0, \sigma=0.002 M_0$), estimating T_1 from Eq.[2], and computing μ_{T_1} and σ_{T_1} from 65,000 independent trials. Different parameter settings were compared on the basis of efficiency by normalizing the precision (σ_{T_1}) by the square root of the imaging time ($N \times TR$). The impact of $d\alpha$ errors was simulated by using the nominal α to estimate T_1 from biased data.

Phantom experiments were performed on solutions in seven vials ($T_1=54$ to 1009 ms), imaged on a clinical 1.5-Tesla MRI system (Signa EXCITE TwinSpeed, GE). A 3D fast SPGR sequence was employed to acquire 12 slices in 43 sec ($TE/TR=5.4/14$ ms, $BW=15.6$ kHz, $FOV=20$ cm, $matrix=256 \times 192$, 3 mm slices, 1 average). T_1 was estimated by repeating the sequence for different flip angles and fitting Eq.[2], assuming accurate knowledge of flip angles.

RESULTS

Fig.1 shows simulation results for $T_1=200-3000$ ms in the absence of flip angle errors. Accurate measurements over the large T_1 range are possible using as few as two angles that are optimized for the specific TR (Fig.1a). The pair $\{3, 20^\circ\}$, optimized for $T_1=500$ ms and $TR=5$ ms, is shown to illustrate errors incurred when improper angles are used. Also, efficiencies are comparable when appropriate angles are used and are generally higher with fewer angles (Fig.1b). Agreement between T_1 measured in phantoms and the true values is shown in Fig.2 for the angle settings determined from simulations.

The influence of flip angle errors is shown in Fig.3. The error introduced in T_1 estimates is proportional to the true T_1 value. Even an error of 15%, not uncommon in many imaging coils such as the head coil, results in a 28% underestimate of T_1 . Also evident in Fig.3 is that the magnitude of error in T_1 cannot be reduced by choice of flip angles, since the relationship is independent of the number of angles or their values, as can be demonstrated from the analytic solution of Eq.[3].

CONCLUSIONS

Simulation and in vitro studies demonstrate that rapid, accurate 3D T_1 mapping over a wide T_1 range is feasible using the VFA method. The flip angles must be optimized for the TR and the T_1 range of interest, and, in general, efficiency is maximized when two angles are used. However, imprecise knowledge of the flip angle, due to B1 field non-uniformity, can introduce significant error in the T_1 estimate that cannot be reduced by changing the number of flip angles or their values. Measurement of subject-specific B1 variations is necessary to correct the measured T_1 through Eq.[3], especially at 3.0 T or higher. The time resolution of the study would not be affected if the B1 map is acquired prior to T_1 measurement.

REFERENCES

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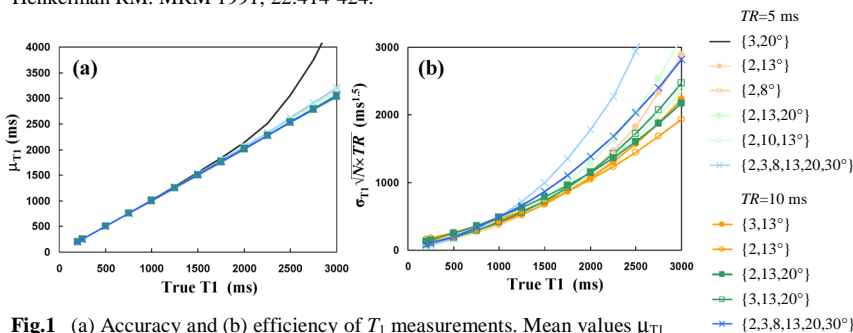


Fig.1 (a) Accuracy and (b) efficiency of T_1 measurements. Mean values μ_{T_1} and std.dev. σ_{T_1} normalized for imaging time are shown for select combinations of flip angles yielding accurate estimates over the range of interest. Values were obtained from 65,000 simulation runs.

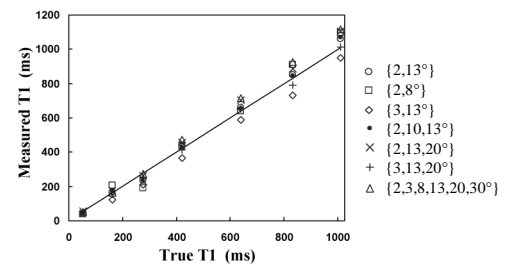


Fig.2 T_1 measured in phantoms versus true values.

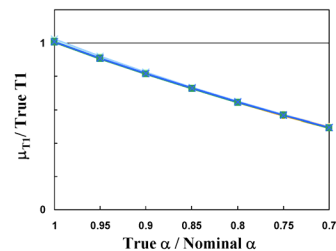


Fig.3 T_1 error due to error in flip angle α . The ratio of the measured versus the true T_1 under simulated noisy conditions was averaged for all $T_1=200-3000$ ms. Flip angle combinations shown are identical to those in Fig.1 (see legend).