Correction of base-line [Gd] offsets due to effective saturation pulse flip-angle variations in 3T liver DCE-MRI

A. B. Gill[1,2], A. N. Priest[2], R. T. Black[1], D. J. Bowden[2], M. J. Graves[2], and D. J. Lomas[2]
[1]Medical Physics, Addenbrooke's Hospital, Cambridge, United Kingdom, [2]Radiology, University of Cambridge, Cambridge, United Kingdom

Introduction

A method for acquiring human DCE-MRI data at 3T from the liver, aorta and portal vein has been previously described **[1]** and is summarised in Figure 1. Two slices with independent orientation are imaged in each heart-beat using a relatively B_1-insenstive saturation-recovery preparation implementation **[2]**. One slice is positioned sagittally through liver tissue, the other in an oblique plane providing a cross section through the portal vein and aorta. Different saturation-recovery times are used due to the differences in [Gd] in the vessels compared to the liver parenchyma. After a dual-input single compartment pharmacokinetic model was fitted to data collected in this way, results **[3]** showed reasonable agreement with the literature **[4]** though a number of issues remained. Firstly, there was a non-zero base-line offset on the calculated [Gd] uptake curves (see Figure 2a) and secondly, the delays associated with tissue arrival times (δ_a and δ_p) from the aorta and portal vein (and fitted as parameters in the model) were calculated to be unrealistically large. This work investigates applying a correction based on an apparent spatial variation in the effective saturation flip-angle for the aorta, portal vein and liver.

Theory

The following relationship holds for the magnetisation M_5 (see Figure 3) before the sagittal plane read-out, where M0 is the magnetisation recorded with a large saturation recovery time (i.e. at TS_1 = 10 seconds) and where perfect saturation flip-angles are assumed:- $M_5/M0 = (1-\exp(-TS_1/T_1))$. Using the Bloch equations, we can derive a more general expression when the saturation flip-angles are unknown by considering the evolution of magnetisation (M_1 to M_5, see Figure 3). We also assume a linear relationship $M = \lambda M_5 + \mu M0$ between the steady-state magnetisation in the GRE read-out, M, and the initial magnetisation, M_5, before the read-out. This relationship and the values of the linear coefficients λ and μ were determined by simulation of the evolution of magnetisation in a GRE sequence using the EPG (extended phase graph) method **[5,6]** and literature values of T_1 and T_2 for blood and liver tissue. This process yields Equation 1, where the symbols are defined in Figure 3. Note that time-stamps in the pulse sequence yield the time intervals τ_1 and τ_2 from which T_{eff2} and T_{D1} can be calculated, the read-out time being known from the TR. We further assume that the saturation flip-angles α_1 and α_2 are equal (= α) to re-arrange Equation 1 as a quadratic in A, the cosine of the flip-angle α (see Equation 2). When using the GRE sequence for DCE-MRI, the pre-contrast T_1 (T_{10}) is obtained from a separate Look-Locker based measurement **[7]**. T_{10} can be used, along with the pre-contrast signal, to derive all the coefficients in Equation 2 and hence solve for $\alpha = \cos^{-1}(A)$. The root closer to zero is chosen to give α nearer to 90°, and in the case of complex roots the real part is taken. With this knowledge of α, an inversion of Equation 1 can then be used to tabulate T_1 for any measured signal. Knowledge of $T_1(t)$ then enables calculation of the [Gd] time series using the following equation (where r is the relaxivity of the contrast agent used): $r.[Gd] = (1/T_1) - (1/T_{10})$. The process can be repeated for the first slice acquisition by exchanging the relevant timing parameters. The methods were implemented in Matlab (The Mathworks, Natick, MA).

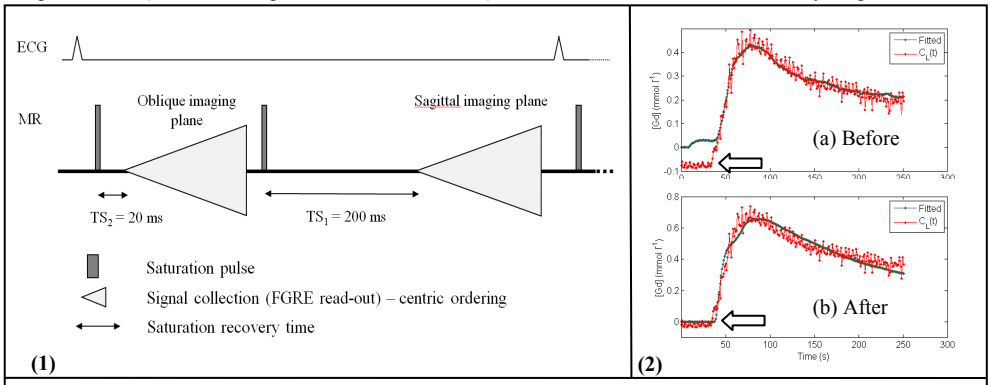

Fig 1: Dual Input-FGRE pulse sequence; Fig 2: fitted curve before and after flip-angle correction

Eq 1
$$\frac{M_5}{M0} = \frac{\left(\left(1-(1-\mu).e^{-T_{D1}/T_1}\right).e^{-T_{eff2}/T_1}.cos\alpha_2+\left(1-e^{-T_{eff2}/T_1}\right)\right).cos\alpha_1.e^{-TS_1/T_1}+\left(1-e^{-TS_1/T_1}\right)}{1-\lambda.e^{-T_{D1}/T_1}.e^{-T_{eff2}/T_1}.e^{-TS_1/T_1}.cos\alpha_1.cos\alpha_2}$$

$$\ldots and\ defining:-\ D = e^{-T_{D1}/T_1},\quad E = e^{-T_{eff2}/T_1},\quad F = e^{-TS_1/T_1},\quad A = cos\alpha,\quad M' = M_5/M0$$
$$P = (1-(1-\mu).D).E.F,\quad Q = (1-E).F,\quad R = 1-F,\quad L = \lambda.D.E.F\ \ldots yields:-$$

Eq 2
$$(P + LM').A^2 + Q.A + (R - M') = 0$$

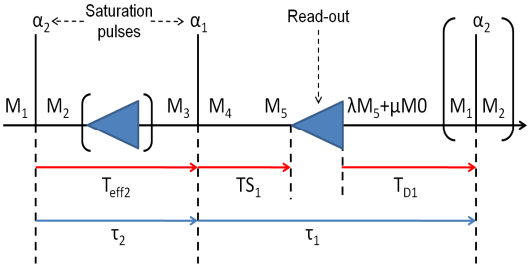

Figure 3: Evolution of magnetisation – definition of symbols

Methods and results

The method was applied to data from 7 volunteers who had been scanned as part of an ethically approved feasibility study **[3]** (preceding a study on patients with liver tumours). Of the 7 data-sets, 4 gave real roots and 3 complex roots. Analysis of all 7 data-sets gave a mean total perfusion of 63 ± 28 ml/min/100ml and a mean arterial fraction of 15 ± 12 %. The mean tissue arrival time delays, δ_a and δ_p, were measured as 3.9 ± 2.4 and 2.7 ± 2.3 s respectively. Interestingly, the mean flip-angle consistent with this analysis within the liver region of interest was 102 ± 13°, range [88.2, 120.6]), for the aorta 88.2 ± 0.9°, [87.0, 89.0] and for the portal vein, 87.9 ± 1.0°, [86.1, 88.9].

Conclusions

This flip-angle correction method has been used to correct base-line offsets in [Gd] (see Figure 2b), leading to improved kinetic modelling of liver DCE-MRI data. The results for total perfusion and arterial fraction are within the range reported by other groups **[4]**. The mean time delays of 3.9 ± 2.4 and 2.7 ± 2.3 s for δ_a and δ_p respectively show a significant reduction ($p < 0.01$) from values recorded without the correction (8.9 ± 3.2 and 8.3 ± 2.8 s, for δ_a and δ_p respectively) and are more realistic physiologically.

References

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