Correction of the T2* influence on the concentration estimation of T1-weigthed DCE-MRI data without measuring T2*

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Introduction

The use of contrast agents and T1-weighted MRI is a sensitive tool for the detection of tumors and for tumor therapy monitoring. Generally, quantitative pharmacokinetic parameters are analyzed from dynamic contrast enhanced (DCE)-MRI data which are transformed from a signal enhancement to a Gadolinium (Gd) concentration scale [1]. In this process, several simplifying assumptions are made which, if violated, result in errors in the modeled pharmacokinetic parameters by the process of error propagation [2]. For improvement, a combined T2* and T1 measurement technique has been developed [3]. This work aims to minimize the error of ignoring the influence of T2* relaxation in DCE-MRI based on spoiled T1-weighted gradient sequences without measuring T2*.

Methods

The theoretical enhancement of a DCE-MRI sequence is given by equation (1). There is an analytical solution for the concentration (2) if the impact of T2* shortening is neglected ($r_2^*=0$). However, there is a Gd-concentration dependent T2* shortening present also in T1-weighted sequences. Solving equation (1) by leaving T2* related terms on the right side, equation (3) is derived. Now, equation (2) can be used as a first approximation (iteration step n=0). Then a weighting factor E_{-2C} for the T2* process is calculated and placed in the right side of equation (3). The resulting concentration $C_n|_{n=1}$ is then used in an iterative manner again to calculated E_{-2C} and so on. If setting $r_2^*=0$ then equation (3) is identical to (2).

$$(1)\ Enhance = e^{-T_E \cdot r_2^* \cdot C} \cdot \frac{\sin\alpha \cdot (1-E_1)}{1-\cos\alpha \cdot E_1} \cdot \frac{1-\cos\alpha \cdot E_{10}}{\sin\alpha \cdot (1-E_{10})} - 1 \qquad (2)\ C_0 = \frac{1}{T_R \cdot r_1 \cdot T_1} \cdot \left[T_1 \cdot \log \frac{E_{-10} \cdot (\cos\alpha \cdot (Enhance+1) - 1) - \cos\alpha \cdot Enhance}{Enhance \cdot (E_{-10} - 1) + \cos\alpha - 1} - T_R \right]$$

$$with \quad E_1 = e^{-T_R \cdot (1/T_{10} + r_1 \cdot C)} \quad and \quad E_{10} = E_1\big|_{C=0} \qquad with \quad E_{-10} = e^{T_R / T_{10}}$$

$$(3)\ C_n = \frac{1}{T_R \cdot r_1 \cdot T_1} \cdot \left[T_1 \cdot \log \frac{\cos\alpha \cdot E_{-2C} \cdot (Enhance+1) \cdot (E_{-10}-1) - E_{-10} + \cos\alpha}{E_{-2C} \cdot (Enhance+1) \cdot (E_{-10}-1) - E_{-10} + \cos\alpha} - TR \right] \qquad with \quad E_{-2C} = e^{T_E \cdot r_2^* \cdot C_{n-1}}$$

To prove the effectiveness of equation (3) the relative error (C_n/C - 1)*100 was calculated. Hereby, the enhancement (1) for a given concentration C and T1 was calculated and then used to derive C_n (3). This was done for different T1 expressing different tissues and different concentrations. The highest concentration after a bolus is found in the first pass in the arteries. Therefore, an arterial input function (AIF) of a bolus Gd-DTPA (r_1=3.4/mMs, r_2=3.8/mMs, dose 0.1mmol/kg) with 2.5ml/s flow in a healthy volunteer was simulated and used for the comparison as the worst case. A "tissue-like" concentration of 1mM was considered in a further case.

Results

The simulation of the AIF has shown a maximum concentration of around 7mM. As seen in Figure 1, the relative error between the simulated and calculated concentration decreases logarithmically with the number of iteration steps and is smaller for larger T1. The proof of a logarithmic decrease can be easily derived by algebraic calculations. In tissue, the concentration will be underestimated without a correction (n=0) by around 5%, in blood it can be more than 20%. In the case of T1=200ms and C=7mM after 5 iteration steps the error will be smaller than 0.1%.

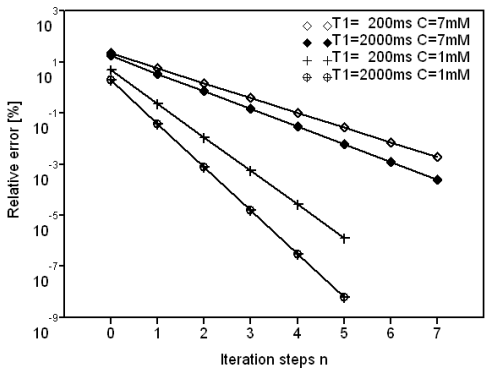

Figure 1. The decrease of the relative error on a logarithmic scale in dependence on concentration and T1 by increasing the number of iteration steps. With higher concentration and longer T1 times the error is higher and more iteration steps are needed to achieve a sufficient level.

Discussion

The equation (3) converges logarithmically over the entire regime of T1 times and concentrations (Figure 1). The situation of 7mM Gd-DTPA represents a realistic case that is achieved by GD-DTPA bolus in the first pass in blood. The corrections are limited to the ability of the T1-weighted sequence to be sensitive to high Gd-concentrations. In the examined concentration regime the enhancement must monotonically increase with the concentration. In tissue, the Gd-concentration is most likely lower than 1mM and thus the T2* effect is smaller. Here, an error of 1% might be accepted but for the determination of an AIF and the derived pharmacokinetic parameters is crucial.

Conclusion

With low effort it is possible to minimize the error caused by neglecting the T2* relaxation. Within several iteration steps a sufficient correction is achieved. Thus, the proposed method may help to provide a more accurate estimation of pharmacokinetics.

References

[1] Tofts and Kermode MRM (1991);17:357 [2] Tofts and Berkowitz JMRI (1993);B102:129 [3] De Bazelaire et al. Eur Radiol (2006);16:2083