A New Protocol for T1 mapping of the Liver

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Abstract

Dynamic contrast-enhanced resonance imaging (DCE-MRI) is commonly used to access treatment response of hepatocellular carcinoma to anti-angiogenesis agents [1] and is recommended for surgery candidates [2] and for abnormality characterization [3]. In DCE-MRI, the concentration of Gd-DTPA which is tissue specific, can only be measured indirectly, through the relative signal enhancement and the T_1 value of the underlying tissue before injection of Gd-DTPA [4]. A more accurate estimation of T_{10} (T_1 prior to Gd-DTPA injection) would then facilitate improved tissue segmentation, based on the Gd-DTPA uptake curves of a pharmacokinetic model [4]. We present a new scanning protocol for signal acquisition in liver MR that optimizes the measurement of T_{10}, based on an extension of the method of [4] and [7] from the breast to liver. The novel protocol has been validated both on synthetic data and on clinical MRI scans and yields high quality T_{10} maps.

Introduction

The accurate of T_1 values has attracted considerable interest because it is closely associated with tissue segmentation [5]. Existing methods, which use a number of flip angles for T_{10} measurement from dynamic sequences, mostly lack a systematic analysis of the sources of error in T_{10} measurement. Equally, there does not appear to be a qualitative relationship between these sources of error and the resulting overall error in the estimated T_{10}. Recent methods by [6] are an improvement, in that they relate optimum flip angle acquisitions for T_{10} mapping to the signal to noise ratio. Similarly [4] is a combination of Monte Carlo simulations and probabilistic optimization to compute optimum flip angles that leads to the most accurate measurement of T_{10} up to date; however their method can be computationally infeasible in real time applications especially when the number of optimum flip angle increases. In this work, we use a hybrid model developed by [7], which was validated against the method of [4], and which combines a mathematical analysis of the sources of error and their impact in T_{10} measurement and Monte Carlo simulations. This model establishes quantitatively the relationship between the sources of error and the error in T_{10} and selects the scanning parameters to minimize this error.

Methods

The MR signal for FSPGR sequences is a function of the scanning parameters (TR, TE, flip angle) and the physiological parameters of interest [4]:

$$S = k*\sin(a)*[1-\exp(-TR/T_{10})]/[1-\cos(a)*\exp(-TR/T_{10})], \qquad \text{where } k = g*\rho*\exp(-TE/T_{20}^{*}).$$

S is the steady state MR signal, g is the scanner gain, ρ is the proton spin density, TE is the echo time, T_{20} is the transverse relaxation time before injection, TR the repetition time, T_{10} is the longitudinal relaxation time and α is the flip angle. Assuming unknown errors in the signal S and the parameter k denoted by ε_S and ε_k respectively, it is shown [7] that the error in T10, denoted by ε_{T10}, is given as:

$$([\varepsilon_S* (\exp(TR/T10)-\cos(a))- \varepsilon_k*\sin(a)*(\exp(TR/T10)-1)]*T_{10}^2)/(TR*(k*\sin(a)-S*\cos(a)) + O(\max(\varepsilon_S, \varepsilon_k)^2)$$

and is minimized when the flip angle satisfies the condition: $\exp(-TR/T_{10mean})*(\sigma_S*\cos(a)- \sigma_k*\sin(a))- (\sigma_S- \sigma_k*\sin(a))=0$, where ε_S follows a Normal distribution with standard deviation σ_S and ε_k follows a Normal distribution with standard deviation σ_k. The above condition will provide one optimum flip angle when the remaining parameters are given. A second flip angle is obtained by minimizing the cost function $\sigma_{T10}*\|T_{10mean}-\mathbb{T}_{10}\|$ as a function of flip angles via Monte Carlo simulations: T_{10mean} is the average value of T_{10} for the organ of interest, $\mathbb{T}_{10}$ is the mean value of T_{10} predicted by fitting of Monte Carlo simulations of FSPGR signals using different flip angles; σ_{T10} is the standard deviation of the predicted T_{10} values from these simulations. For TR/TE = 8.9/4.2msec and T_{10mean} = 586msec [8], the resulting low flip angles are 7° and 15°. The 3rd flip angle is chosen as 10°, known to optimize signal and contrast properties for enhancing tumours in post-contrast images [9]. This provides a new FSPGR sequence protocol for liver MR signal acquisition for optimum T_{10} mapping: TR/TE = 8.9/4.2msec, a=7°, 10°, 15°.

Results and Validation

We applied the obtained protocol to acquire liver MR images at the flip angles specified above and produced T_{10} maps of the liver as depicted in the figures below. We also validated the protocol against that of [4] for the same parameters. The proposed method is slightly more robust to noise for the average T_{10} for the liver than that of [4], but significantly more robust to noise for high T_{10} values which are typically characteristic of tumours (Figure 1).

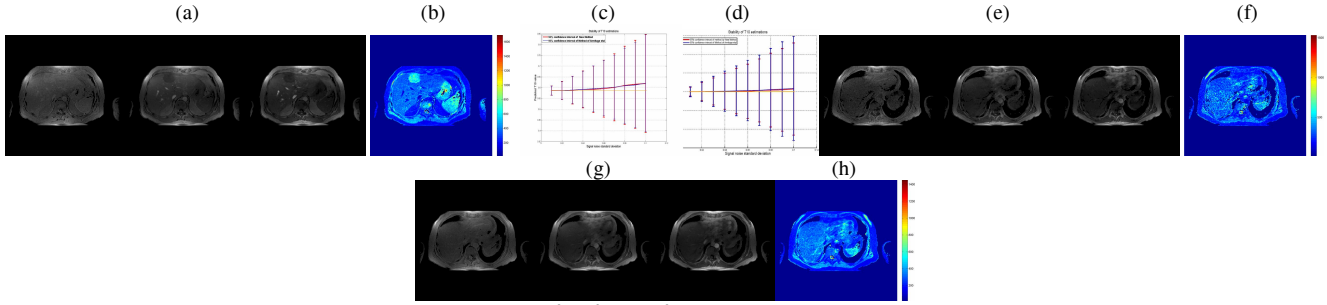

Figure 1: (a), (e) and (g) display three FSPGR signal acquisitions at 7°, 10° and 15° of different livers for TR/TE = 8.9/4.2msec and (b), (f) and (h) are the corresponding T_{10} maps. (c) displays the results of stability analysis of the used method versus that of [4] for the same parameter values, when the underlying T_{10} is the average for liver. The proposed protocol is only marginally more robust to noise but it is more feasible to establish computationally. (d) displays the results of stability analysis of the proposed method versus that of [4] for the same parameter values for an underlying value of T_{10}=1400msec, which is tumour characteristic. The proposed protocol is notably more robust to noise and more feasible to establish computationally and can therefore be used for tumour detection and improved T_{10} characterization of pathological tissues (characterized by long T_{10}).

Conclusions

The proposed protocol provides good quality T_{10} maps for the liver from FSPGR sequences. The increased accuracy of these maps provides improved tissue specific information to the radiologist for tissue segmentation, compared with the original data. The protocol has been validated on synthetic FSPGR data and is proved to be more robust to noise for increasing underlying T_{10} values than the method for optimum flip angle acquisitions of [4]. We propose to use the resulting T_{10} maps for the computation of contrast agent concentration in dynamic contrast enhanced studies for tissue segmentation and tumour characterization in liver MR.

References

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