

Demonstrating the Influence of Magnetisation Transfer on Putative T_1 Relaxation Times: a Simulation Study

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Introduction

Quantitative MRI (qMRI) is gaining impact in the MRI community as a whole and recently clinical applications have also been made available by scanner manufacturers. In particular, the use of qMRI for the characterisation of either exogenous (for example USPIO, CEST PARACEST) or endogenous (T_1 , T_2 , T_2^* , phase, temperature) contrasts, has led to increased scrutiny of the different factors affecting quantification of data arising from sequences. One important factor is the presence of bound protons in different environments and the effect thereof on the free water pool via magnetisation transfer (MT) [1], [2]. Since free and bound protons are affected differently by RF pulses, for example, the correct description of the dynamics of each pool explicitly requires that the other is taken into account. Proper T_1 quantification therefore mandates consideration of MT effects, something has already been noted by several authors [3], [4], but this is difficult to quantify as there are many parameters that influence the final result. We present numerical simulations, based on an existing software package JEMRIS [5], that allow one to simulate MR sequences taking consideration of MT effects in order to study the effects on putative T_1 values.

Material and Methods

The well known and widely used modified Bloch equations for a two-pool model for chemical exchange, magnetisation transfer or spin diffusion were extended to n interacting pools. Each pool is characterised, on a per voxel basis, by the proton density, T_1 , T_2 and the centre frequency. The exchange properties of pool i to pool l are given by $k_{i,l}$. The modified Bloch equations for pool i of n pools may then be formulated as:

$$\dot{M}_{x/y}^i = - \left(\frac{1}{T_2^i} + \sum_{\substack{l=1 \\ l \neq i}}^n k_{i,l} \right) M_{x/y}^i \mp (\omega_i - \omega_{RF}) \cdot M_{y/x}^i \mp \omega_y \cdot M_z^i + \sum_{\substack{l=1 \\ l \neq i}}^n k_{l,i} \cdot M_{x/y}^l$$

$$\dot{M}_z^i = - \left(\frac{1}{T_1^i} + \sum_{\substack{l=1 \\ l \neq i}}^n k_{i,l} \right) M_z^i + \frac{1}{T_1^i} \cdot M_0^i - \omega_x \cdot M_x^i + \omega_y \cdot M_y^i + \sum_{\substack{l=1 \\ l \neq i}}^n k_{l,i} \cdot M_z^l$$

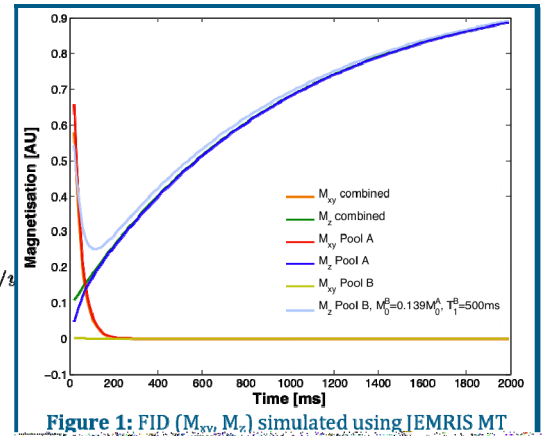


Figure 1: FID (M_{xy} , M_z) simulated using JEMRIS MT

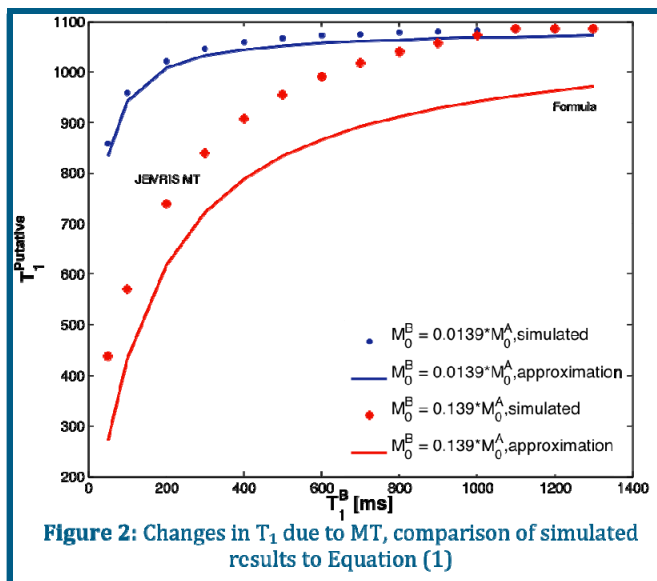


Figure 2: Changes in T_1 due to MT, comparison of simulated results to Equation (1)

A simple pulse-acquire sequence was simulated; this consisted of a 5-lobed sinc pulse of BW= 1KHz, flip angle=90°, apodization=0.5 and a read-out of 2000 points within 2000ms. For the investigation of T_1 effects an MT-type virtual sample [6] was created and characterised by: $T_1^A=1084$ ms, $T_2^A=40$ ms, T_1^B was varied from 50 to 1300ms, $T_2^B=0.14$ ms, $M_0^B=0.139M_0^A$, $\Delta\omega=\omega_A-\omega_B=0$ Hz, $k_{AB}=3.1$ Hz. M_z recovery was fitted to obtain T_1 using MATLAB (The MathWorks, Natick, USA). Figure 1 shows the effects of magnetisation transfer on the dynamics of the single pools, as well as the combined signal. Note that the T_2^B is so short that the decay is not visible in the figure. A widely used approximation ([1], derived in [7]) of the effect of MT on the observed relaxation rate of pool A for a two-pool model with $M_0^A \gg M_0^B$ is:

$$\frac{1}{T_1^{A,obs}} = \frac{1}{T_1^A} + \frac{M_0^B}{T_1^B + \frac{1}{k_{BA}}} \quad (1)$$

Figure 2 shows $T_1^{A,putative}$ for different values of T_1^B and compares the simulated results for two different pool sizes with the estimated value for $T_1^{A,obs}$ based on Equation (1). In Figure 2 $T_1^{A,putative}$ is the equivalent of $T_1^{A,obs}$, it is used as a surrogate thereof. Differences (ranging from 2% for very small pool B and similar T_1 values of pool A and B up to 40% for the larger pool B size and short T_1^B) between

the exact solution and the approximation can be seen even for parameter values where the approximation is expected to hold.

Discussion

The simulation software presented here can be employed to study the impact of MT on MR parameters, as shown here for influences on T_1 . Effects of single parameter changes on the signal obtained from a well-characterised sample can be studied, e.g. the effect of MT on T_1 for dedicated T_1 determination sequences such as TAPIR [8-10].

Furthermore, the simulation software can also be used to simulate complex MRI sequences and to design new sequences especially tailored for MT purposes. Within the same framework of JEMRIS-MT the parameter space can be investigated to determine the maximum sensitivity of a given sequence to MT effects, as well as seeking parameters for which the MT weighting is negligible.

References

- [1] Bloembergen et al. J. Chem. Phys 34, 842 (1961)
- [2] Berry et al., JMRI 9:441-446 (1999)
- [3] Ou et al., MRM 59:835-845 (2008)
- [4] Meara et al., MRM 58:825-829 (2007)
- [5] JEMRIS: Juelich Extensible MRI Simulator, www.jemris.org
- [6] Stanisz et al., MRM 54:507-512 (2005)
- [7] Luz et al. J. Chem. Phys 40, 2686 (1964)
- [8] Shah et al. US patent no 6803762 B2
- [9] Shah et al. NeuroImage 14:1175-1185 (2001)
- [10] Steinhoff et al., MRM 46:131-140 (2001)