Influence of Magnetisation Transfer on established T1 mapping methods

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Introduction

T_1 mapping has proven to be useful for many purposes, e.g. in characterisation of different diseases or for quantitative water mapping [1,2]. Proper T_1 quantification mandates consideration of MT effects, as suggested e.g. by Ou [3]. However, consideration of MT introduces a large number of additional free parameters in T_1 fitting models. Thus, the stability of the fitting routine is decreased and high SNR is required in order to obtain robust fitting results. This limits the application of such methods to *in vitro*, phantom or post mortem studies. However, MT becomes important especially *in vivo*.
To account for MT, the Bloch Equations need to be extended. This is done by the Bloch McConnell Equations [4], which describe the dynamics of a system in the chemical exchange regime. There, the observed or putative T_1 relaxation time is given as:

$$\frac{1}{T_1^{putative}} = \frac{1}{2}\left(\frac{1}{T_1^A} + k_{AB} + \frac{1}{T_1^B} + \frac{k_{AB}M_0^A}{M_0^B} - \sqrt{\left(\frac{1}{T_1^A} + k_{AB} + \frac{1}{T_1^B} + \frac{k_{AB}M_0^A}{M_0^B}\right)^2 - 4\left(\frac{1}{T_1^A T_1^B} + \frac{k_{AB}}{T_1^B} + \frac{k_{AB}M_0^A}{M_0^B T_1^A}\right)}\right)$$

As a consequence, the standard fitting models and signal equations used for T_1 fitting fail and compromise the accuracy and precision of the obtained T_1 values. This study aims at quantifying changes in the accuracy of T_1 in presence of MT if the signal equations used for T_1 determination specifically neglect the MT effect.

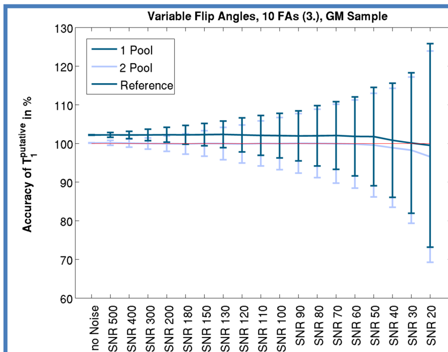

Figure 1: Accuracy (mean) and precision (error bars) of Method 3 for different Values of SNR.

Sample Parameter	White Matter (WM) No MT	White Matter (WM) Pool A	White Matter (WM) Pool B	Gray Matter (GM) No MT	Gray Matter (GM) Pool A	Gray Matter (GM) Pool B
M_0	1	0.861	0.139	1	0.95	0.005
T_1 / ms	1071	1084	1000	1748	1820	1000
T_2 / ms	69	69	0.01	99	99	0.0091
k_{AB} / Hz	-	3.197		-	2	
$T_1^{putative}$ / ms	1071			1748		

Table 1: Sample parameters used in the simulations.

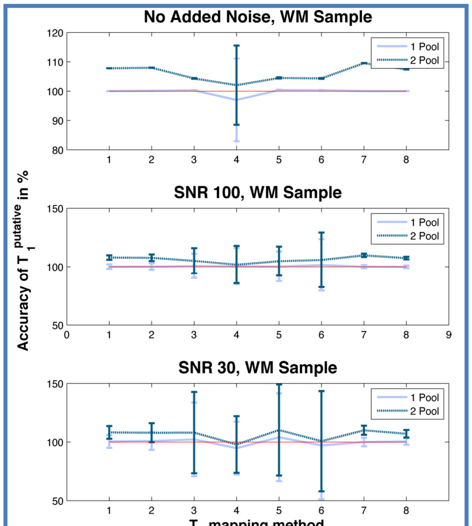

Figure 2: Accuracy (mean) and precision (error bars) of all simulated T_1 mapping methods of WM for different Values of SNR.

Material and Methods

Simulations of the following established T_1 mapping sequences were performed with JEMRIS MT [5]:

1. IR-FID, 41 inversion times (TIs) from 10 to 4010ms in steps of 100ms.
2. IR-Spin Echo, 21 TIs from 10 to 4010ms in steps of 200ms.
3. Spoiled Gradient Echo (SpGE), 10 flip angles (FAs), 10 to 100 degree, TR = 2500ms.
4. SpGE, 10 FAs from 10 to 100 degree, TR=2500ms, Ou's approximation of the Ernst Equation modified for MT (Equation 3 in [3]).
5. SpGE, 5 FA from 5 to 100 degree, TR = 2500ms.
6. SpGE, 40 and 100 degree FA, TR = 2500ms.
7. Look Locker with the TAPIR preparation module [6], 25 timepoints, TR=175ms, FA=40 degree, τ=4s
8. As 7., but with FA 15.

Two samples types were created (see Table 1), imitating white and grey matter [7]. Each sample was simulated as a one-pool sample, corresponding to "normal" imaging without MT, and as a two-pool sample, accounting for MT; both had the same $T_1^{putative}$. Gaussian noise was added to the simulated data prior to T_1 fitting, corresponding to different levels of SNR. T_1 maps were calculated neglecting possible effects on the signal equation due to MT. The $\text{accuracy}\,[\%] = 100 - \frac{\text{mean}\left(T_1^{sequence\_i}\right) - T_1^{putative}}{T_1^{putative}}100$ and $\text{precision} = \frac{\text{std}\left(T_1^{sequence\_i}\right)}{T_1^{putative}}100$ of the method were obtained for each sample consisting of 576 voxels.

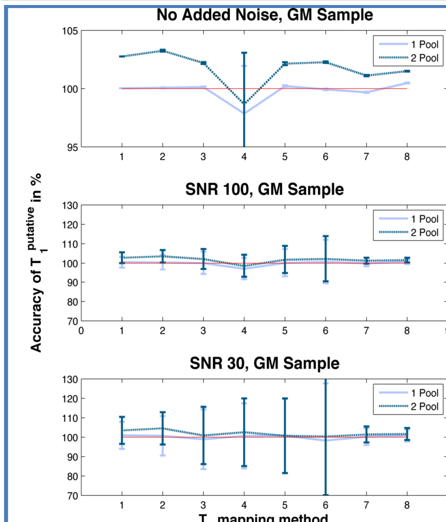

Figure 3: Accuracy (mean) and precision (error bars) of all simulated T_1 mapping methods of GM for different Values of SNR.

Results

Figure 1 exemplarily shows the precision and accuracy of the T_1 of GM for different SNR obtained through variation of the flip angles in SpGE (3). For all the discussed methods, the accuracy and precision of conventional T_1 quantification without added noise, SNR 100 and SNR 30 in WM and GM are displayed in Figures 2 and 3, respectively.

Conclusion/ Discussion

It was shown that all methods give accurate T_1 estimations, with an absolute error below 10% for both samples with or without MT. All methods but one perform more accurately without chemical exchange. Method 4 is the exception where the accuracy actually worsens without MT. This comes at no surprise, as its fitting model is only valid in presence of the effect. Even without added noise, the precision of method 4 is comparatively low; this can be attributed to the larger number of fitting parameters (4) and as a consequence the less stable fit. Furthermore, the Look Locker method exhibits high sensitivity to the right choice of the flip angles.
Adding noise (SNR≥20) to the simulated images decreases the precision while leaving the accuracy essentially unchanged. Consequently, the T_1 values of the two pool samples cannot be separated from the one-pool samples any more. One can conclude that the effect of MT is below the error of the method itself, if noise is present. The methods based on SpGE with different FAs are less prone to deviations due to MT, while the precision of the Look Locker based methods is higher, despite the fact that it is the approach with the shortest measurement time.

References

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