T_1 Mapping – Should We Agree to Disagree?

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Summary

- Our simulations predict a systematic bias between three T_1 mapping methods due to inaccurate B_1 mapping and/or spoiling.
- These same trends were previously observed in vivo[1] for the same protocols.
- As these effects can be site/scanner specific, *we strongly suggest comparing T_1 maps to a gold standard IR map for each subject*, to account for any sequence dependent T_1 bias.

Introduction

- It was recently reported[1] that three commonly used methods[2-4] for quantitative T_1 produce similar T_1 values in phantoms, but exhibit significant disagreement in vivo (Fig. 1).
- Reported T_1 values in white matter are also inconsistent between methods and sites (Table 1).
- This work reports simulations demonstrating that inaccuracies in B_1 mapping and incomplete spoiling could explain some of the T_1 variations trend observed in vivo.

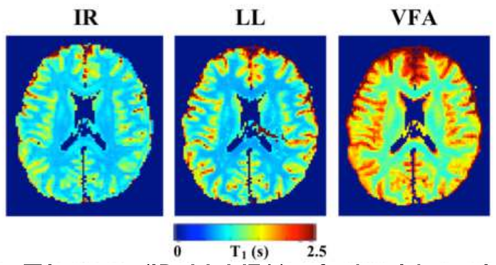

Figure 1. Single Slice T1 maps (IR, LL, VFA) of a healthy volunteer in a single session. The mode T_1 value in white matter was 825.5 ms (IR), 734.9 ms (LL) and 1037.0 ms (VFA).

	Ref [4]	Ref [5]	Ref [6]	Ref [7]	Ref [8]	Ref [9]	Ref [10]
IR	1000-1100	1084 (45)	690-810		943 (57)	800-940	
LL					964 (116)		755 (10)
VFA	1000-1100			1084 (79)		900-1020	

Table 1. Overview of reported T_1 values in healthy white matter at 3 T.

Simulations

- Bloch simulations were implemented using Matlab and were based on 100 spin isochromats, with T_1 matched to in vivo IR measurements[1] (825.5 ms).
- The pulse sequence parameters (LL, IR, VFA) were identical to those used in vivo[2] (see abstract for details).
- Data was fitted using an estimated 0.89 flip angle correction (estimated from whole brain AFI[11]).
- Simulation investigating inaccurate flip angle correction on T_1
  - Fractional error in measured B_1 varied between 0.9 and 1.1.
- Simulation investigating imperfect gradient spoiling on T_1
  - Spins dephased 80-100% of a 2π dispersion (incoherent state).

Results

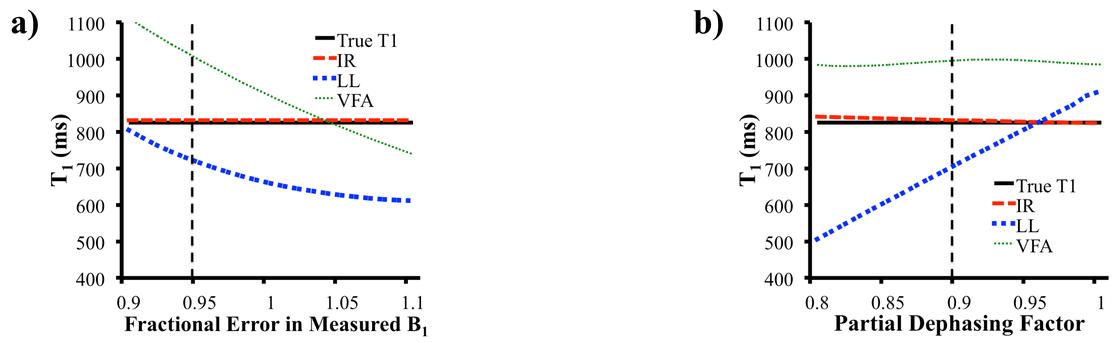

Figure 2. Shown in Fig. 2 a) is the simulated relationship between fitted T_1 and fractional error in measured B_1 for IR, LL and VFA using a partial dephasing factor of 0.9. Shown in Fig. 2 b) is the relationship between fitted T_1 and partial dephasing factor for IR, LL and VFA for a fractional error in measured B_1 of 0.95. The vertical line in both figures indicates the values for which the simulation parameters for Fig. 2 a) and b) are identical.

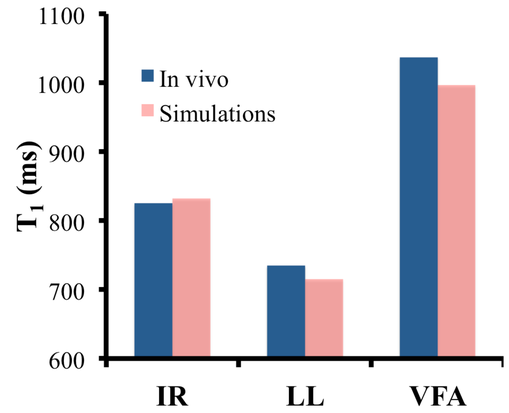

Figure 3. Comparison between the mode white matter T_1 measured in 10 healthy subjects[1], and simulations with similar parameters. The simulation values correspond to parameters represented by the vertical dashed line in Figs. 2 a) and b).

Discussion

The bar graph in Fig. 3 shows that the simulations follow a similar T_1 trend compared to the in vivo white matter T_1. Overall, these simulations suggests that for a typical set of protocols LL mostly underestimates T_1, and VFA overestimates it. For all the simulated parameters, T_1 measured with IR is very stable and only slightly deviates from the true T_1. Error in B_1 mapping has been shown[12] to be sensitive to factors such as RF pulse shape, slice-select gradients and B_0 inhomogeneities. Incomplete or variable dephasing could result from factors like diffusion anisotropy in white matter tracts[13], which could explain the agreement between T_1 methods in phantoms but not in vivo[1]. Our simulations did not account for magnetization transfer effects, which have also been shown to cause T_1 map inaccuracies in VFA[14]. Including magnetization transfer in VFA leads to an increase in fitted T_1 values, hence worsening the predicted disagreement between VFA and IR.

This work highlights the importance of accurate B_1 mapping, robust spoiling methods, and proper calibration with the IR gold standard.

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