B_1 Correction for Improved Bound Pool Fraction Maps

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Introduction: The bound pool fraction (f) is an indicator of myelin content in the brain, and cross-relaxation imaging is an efficient method of mapping the f parameter in vivo [1]. The first step in cross-relaxation imaging is obtaining an accurate T_1 map of the brain, but B_1 inhomogeneity makes this task difficult. Since correcting for B_1 inhomogeneity is essential for performing repeatable and reliable measurements of f across subjects [2], we incorporated B_1 correction in our T_1 mapping procedure [3]. We then observed the effect of this correction on the whole brain histograms of T_1 and f in three subjects.

Methods: We scanned three subjects with two different cross-relaxation procedures, using a GE Signa 1.5 T Excite system and an 8-channel head coil. The first procedure is a replication of the method proposed by Yarnykh and Yuan [1], where T_1 mapping is done using four variable flip-angle SPGR scans (TR = 20 ms, TE = 2.4 ms, α = 4°, 10°, 20°, 30°) and a linear fit that assumes no flip angle variation [4]. The T_1 mapping in the second procedure uses three variable flip-angle Fast SPGR scans (TR = 7 ms, TE = 1.5 ms, α = 4°, 10°, 18°) followed by an inversion prepared SPGR scan (TR = 7 ms, TE = 1.5 ms, TI = 450 ms.) The fit is done using a nonlinear fitting procedure that estimates the deviation from the desired flip angle [3]. Both T_1 mapping procedures were followed by magnetization transfer SPGR scans with variable offset frequency (TR = 32 ms, TE = 2.4 ms, α = 10°, Δ = 3, 6, 9, 12 kHz) which, combined with the T_1 maps, give the desired f maps [1]. The two procedures produced different whole brain histograms of f and T_1, and the differences were used to evaluate the two cross-relaxation techniques.

Results: Figure 1 shows the reconstructed T_1 and f maps for the same subject without (left) and with B_1 correction (right). The maps have similar contrast, but the whole brain histograms of the T_1 and f parameters in Fig. 2 show a significant difference. The white matter peaks for the uncorrected histograms differ across subjects by as much as 20% (subject 3 in Fig. 2a.) On the other hand, the procedure that corrects for B_1 inhomogeneity provides white matter peaks consistently centered around the same location (Fig. 2b). The B_1 correction procedure also provides T_1 values for white matter that are about 20% higher and closer to the values reported in [3] and [5]. Since the f value tends to decrease with higher T_1 values, the corrected bound pool fraction maps have lower average f values than the uncorrected ones. This can be seen from the different display scales used in Fig. 1, as well as the different peak locations of the histograms in Fig. 2.

Discussion: The f histograms are very sensitive to the T_1 parameter, and they tend to have larger variations across subjects compared to T_1 histograms [1, 7, 8]. It is important to know whether the variations in f are a result of different myelin content, or errors in T_1 measurement, so B_1 correction eliminates this dilemma by giving T_1 histograms that are consistent across subjects. As an additional benefit, the corrected T_1 maps can be obtained in about half the time compared to the uncorrected ones. This is because we substituted the SPGR sequences with Fast SPGR. The trade-off is a loss of SNR, but despite the SNR decrease the f maps (Fig. 1 bottom), and the f histograms (Fig. 2 bottom) look similar. The Fast SPGR scans can be averaged if more SNR is needed, all the while giving us a more reliable cross-relaxation procedure.

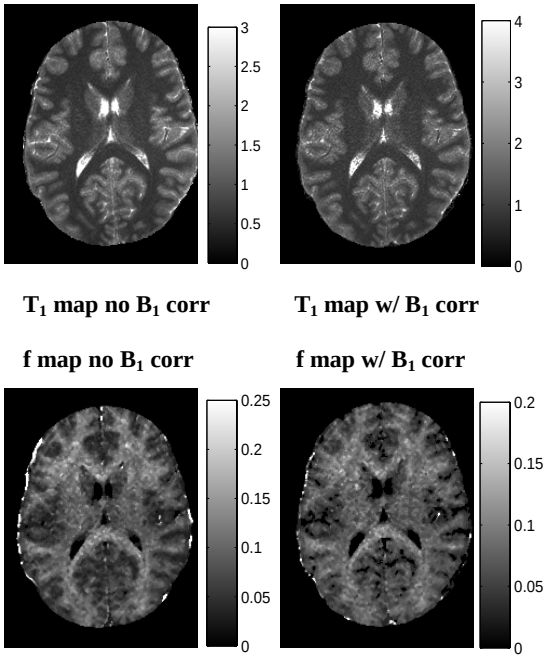

Figure 1: *T_1 maps (top) and f maps (bottom) without (left) and with B1 correction (right). Notice that the grayscale bars indicate higher T_1 and lower f values for the corrected maps.*

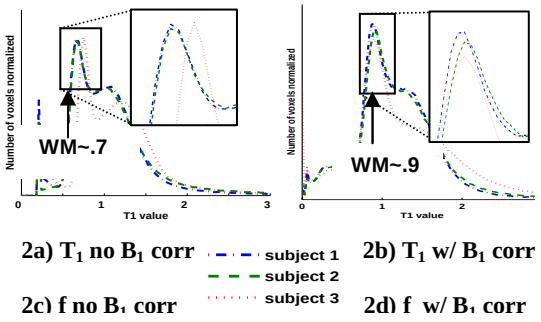

Figure 2: *(a) Uncorrected and (b) corrected T_1 histograms (no CSF) for three subjects; The zoomed part emphasizes the locations of the white matter peaks, showing that correction aligns the peaks. (c) Uncorrected and (d) corrected f histograms.*

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