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Published in:
Proceedings of the International Society for Magnetic Resonance in Medicine Annual Meeting 2015

2015

Document Version:
Publisher's PDF, also known as Version of record

Link to publication

Citation for published version (APA):
Helms, G. (2015). Correction for Residual Effects of B1+ Inhomogeniety on MT Saturation in FLASH-Based Multi-Parameter Mapping of the Brain. In *Proceedings of the International Society for Magnetic Resonance in Medicine Annual Meeting 2015* (Vol. 23, pp. 3360). Article 3360 (Proceedings of the ISMRM; Vol. 23). International Society for Magnetic Resonance in Medicine. https://index.mirasmart.com/ISMRM2015/PDFfiles/3360.pdf

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Correction for residual effects of B1+ inhomogeniety on MT saturation in FLASH-based multi-parameter mapping of the brain

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Target audience

MR physicists

Purpose

In magnetization transfer (MT) imaging, the evolution of the binary spin bath after the off-resonant saturation pulse can be described by simulataneous apparent T1 relaxation of both pools as in fast exchange and simultaneous equilibration of the partial saturation (1). From MT-w(eighted) FLASH, the MT-related partial saturation of the free water can be calculated using a PD-w and a T1-w reference signal (2). Such MT-sat(uration) maps are independent of the underlying T1 and largely compensated for flip angle inhomogeneities. For an established multi-parameter mapping (MPM) protocol at 3T (3), we discuss the source and correction of residual effects of flip angle inhomogeniety.

Theory

With increasing flip angle α_sat of the MT-pulse, the z-magnetization of bound macromolecular pool is destroyed, but the effected saturation becomes increasingly lower than α_sat^2 (as expected for small changes in Mz). Thus, the inherent B1+ correction of the MT-sat maps (by α_sat^2), results in a residual overestimation in regions of low B1+ and underestimation at high B1+ (Fig. 1A). For any given tissue and MPM protocol, an additional linear dependence of the MT-sat value δ on α_sat was assumed: $\delta(\alpha\_sat) = A\,[1–B\,\alpha\_sat]\,\alpha\_sat\text{\^{}}2$ (1) where A and B are heuristic constants that can be calibrated by varying α_sat. When α_sat is spatially modulated by the flip angle bias field f, the square contribution cancels by calculation and the residual bias term is corrected by: $\delta(\alpha\_sat) = \delta(f\,\alpha\_sat)\,[1–B\,\alpha\_sat] / [1– f\,B\,\alpha\_sat]$ (2)

Methods

In an established multi-parameter mapping (MPM) protocol (3) on a 3T MR system (Siemens TIM-Trio), the nominal flip angle of the MT-pulse (220°, 4ms Gaussian, 2kHz off-resonance) was varied between 280° and 120° in five healthy adults. The estimated MT-sat values from ROIs in splenium, caudate head and lateral ventricle were divided by α_sat^2 to show the linear relationship of eq. (1). Maps of A and B were derived by linear regression with pertinent bias fields (4) using FSL. Estimated MT-sat maps were corrected by eq. (2) with B α_sat = 0.4 and displayed as a color-overlay (Fig. 1).

Results

The linear relationship in (Fig 2) confirmed the residual bias model. Deviations were observed at α_sat < 120°. In the caudate head B was slightly smaller than in splenium (0.043±0.004 vs. 0.046 ±0.005), but the maximum of the gray matter (GM) mode of $\delta(\alpha\_sat)$ was consistent to splenium. Accordingly, maps of B did a single mode in brain tissue without differences between GM and WM (not shown). Thus, the averaged B across tissue and subjects can be used for a post hoc correction of MT-sat maps; with B α_sat = 0.4 in eq. (2). Of note, the model is not valid for cerebro-spinal fluids with MT-sat being close to zero.

Bias-corrected MT-sat maps were more symmetric (Fig 1) and show more consistent values in subcortical WM and brainstem and a better seperation of modes in the histograms.

Discussion

We presented a heuristic model for B1-heterogeneity of MT-sat maps rooted in the saturation dynamics of the MT-pulse. The model parameter B needs to be calibrated for the specific MT-pulse and protocol. The model can also be used to scale MT-sat maps to a different value of α_sat. WM and GM yielded very similar values, which is in line with reports of similar absorption lineshapes in qMT (5). This permits a simple post-hoc correction of MT-sat using B1+ mapping yielding a small, but considerable improvement of MT-sat maps.

References

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Figure 1: MT-sat map prior (left) and after (right) bias correction

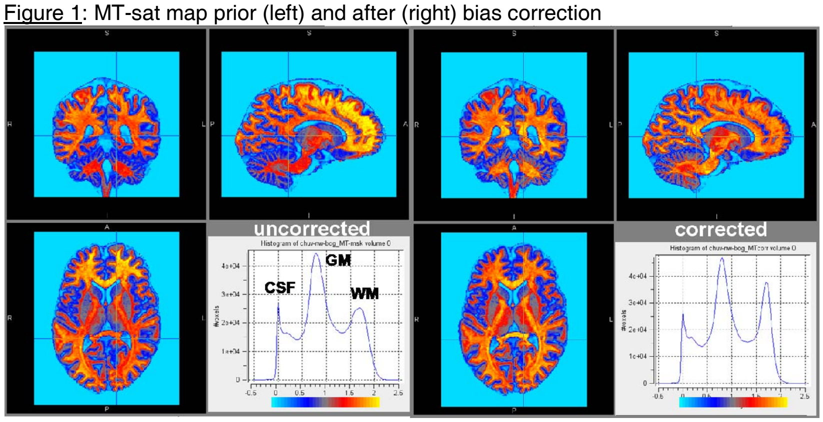

Figure 2: Plot of δ / α_sat^2 over α_sat (in rads)