CORRECTION OF RF INHOMOGENEITIES IN FLASH-BASED T1 MAPPING USING UNIFIED SEGMENTATION

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Introduction:
Quantitative T1 mapping based on 3D FLASH acquisitions with variable excitation flip angles (VFA) is fast and robust (1, 2). However, high accuracy can only be achieved when the local flip angle is known precisely (1). At higher static magnetic fields local flip angles may deviate considerably from the nominal flip angle due to inhomogeneities of the RF transmit/$B1^+$ field (3, 4). T1 maps can be corrected using maps of the local RF transmit field (1, 5), requiring the availability of precise and accurate whole-brain B1 mapping methods (3) and adding experimental time. Here we propose a method that corrects the bias in T1 maps due to RF inhomogeneities using post-processing only and does not require knowledge of local flip angles which must be provided by additional data. The method exploits the facts that 1) the local flip angle simply scales the local T1 value (1), 2) $B1^+$ distribution varies smoothly across the brain (3), and the assumption that 3) T1 values in gray/white matter and CSF are normally distributed and do not vary significantly across the brain. We compare the performance of the proposed model-based correction with the established correction based on measured RF transmit maps (1, 3).

Methods:
10 healthy adults (age 48±16 (mean±sd); m/f = 5/5) were examined on a 3T whole-body MRI system (Siemens Magnetom TIM Trio) operated with a 12-channel head receive and body transmit RF coil. Written informed consent was obtained as supervised by the local Ethics committee. Three whole-head 3D multi-echo FLASH datasets were acquired with predominantly T1-weighting (TR/α = 18.7 ms/20°), PDw (23.7 ms/6°) and MTw (not presented here) at 1 mm isotropic resolution (6). An additional RF transmit map was acquired using a 3D EPI acquisition of spin-echo and stimulated echoes with different flip angles (4) and B0 map based distortion correction, as described in (3).
Data processing and analysis were performed with SPM8 (Wellcome Trust Centre for Neuroimaging, http://www.fil.ion.ucl.ac.uk/spm) and custom-made scripts running under Matlab 7 (Mathworks, USA). Maps of the apparent T1 ($T1_{app}$) were estimated from the T1w and PDw data based on the rational approximation of the Ernst equation (1). Using a unified segmentation approach (7) the $T1_{app}$ maps (after masking based on PDw images) were simultaneously partitioned into 6 different tissue classes (gray matter, white matter, CSF, and 3 non-brain classes) using a Gaussian mixture model and the bias field (η) estimated. The bias field was modelled as a set of discrete cosine functions with free choice of smoothness (FWHM) and a regularization parameter (κ) to avoid over-fitting. $T1_{app}$ maps were multiplied with the bias field to minimize spatially smooth variations, resulting in T1 maps corrected using the proposed model-based approach ($T1_e = T1_{app}\,\eta$). To compare the model-based correction with the established measurement-based correction, RF maps (ψ_m = ratio of local flip angle over nominal flip angle) were estimated from the 3D EPI B1 mapping data and corrected for susceptibility-related distortion as described previously (3). T1 maps corrected using the established method were estimated as $T1_m = T1_{app}/\psi_m^2$ (1) plus additional (smaller) corrections for imperfect spoiling (5, 8). The performance of the model-based RF bias correction was compared to the established method based on the measured RF transmit map by calculating the median of $2*abs(T1_e-T1_m)/(T1_e+T1_m)$ across the whole brain. For relative comparison to the actual RF bias at 3T, also the median of $2*abs(T1_{app}-T1_m)/(T1_{app}+T1_m)$ was calculated. The performance was assessed for bias fields estimated using a range of regularization constants $\kappa = (10^{-4}, 10^{-3}, 10^{-2})$ and smoothness constants FWHM = (60, 90, 120 mm) and analyzed for significant differences using a 3x3 repeated measures ANOVA (SPSS) with significance threshold $p < 0.05$.

Results:
The choice of FWHM and κ influenced the effectiveness of the model-based RF bias correction significantly. The ANOVA revealed a significant main effect of FWHM ($p<0.001$) and a significant interaction of κ x FWHM ($p<0.001$). The main effect of κ did not reach significance ($p = 0.07$).
For the best parameter set ($\kappa = 10^{-2}$ and FWHM = 60 mm), the model-based RF bias correction significantly reduced the bias in the T1 maps from 14.4%±0.5% (mean±sem) to 6.5%±0.5% across the group (i.e., by more than 50%). The reduction in bias can be clearly seen in the center of the brain where T1 was overestimated without correction for RF transmit inhomogeneities (Fig. 1).

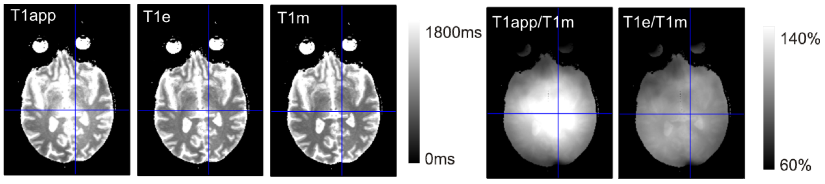

Fig. 1: Corrected and uncorrected T1 maps (left), ratio of uncorrected or model-based corrected T1 over B1 map corrected T1 (right).

κ \ FWHM (mm)	60	90	120
10^{-4}	10.9±1.3	10.1±1.4	9.9±1.3
10^{-3}	8.6±1.1	7.5±0.9	9.1±0.6
10^{-2}	6.5±0.5	11.1±0.4	13.1±0.4

Table 1: Group mean (±sem) of percent median deviation between $T1_e$ and $T1_m$.

Discussion:
We developed and optimized an approach for correcting RF inhomogeneities in dual-angle FLASH-based T1 mapping based on unified segmentation and bias correction (7). Cross-validation with the established correction method using measured RF transmit fields showed that the proposed model-based method reduces the bias by more than 50% compared to uncorrected T1 maps. Compared to a previous study (9) performing segmentation-based bias correction of T1 maps, our method allows the bias field to vary in 3 dimensions in contrast to 1 dimension only, more realistically modelling the known 3D RF field inhomogeneities (3, 4). The proposed approach is easy to implement, since the SPM software is publicly available and the 3D FLASH sequence is available on all scanners, unlike whole-brain RF transmit mapping sequences that are required for the standard correction approach and challenging to implement. Further, no additional scan time is necessary and the method is computationally efficient (< 10 mins processing time on state of the art personal computer). We are currently investigating the robustness of the approach in case of atypical brain anatomy often encountered in patient groups, e.g., large CSF filled spaces, hindering segmentation.

References:
1) Helms et al, 2008, MRM; 2) Deoni et al., 2005, MRM; 3) Lutti et al, under revision, MRM; 4) Jiru and Klose, 2006, MRM; 5) Lutti et al, 2009, HBM; 6) Helms et al, 2009, Neuroimage; 7) Ashburner and Friston, 2005, Neuroimage; 8) Preibisch and Deichmann, 2009, Neuroimage; 9) Chen et al, 2009, Int J Biomed Imaging.

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