# T1-nonlinearity corrections for fast Transmit-Array $B_1^+$-mapping of the human brain in the small-tip-angle regime

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**Introduction:** Currently, $B_1^+$-mapping is particularly difficult due to the combination of time and conservative specific absorption rate (SAR) constraints applicable to parallel transmission studies involving human subjects. Measuring relative $B_1^+$-maps in the low-tip-angle regime provides a low SAR solution that can be upgraded to provide quantitative flip-angle (FA) maps using a single high angle measurement [1,2]. Inherently, this spoiled-gradient-echo-based method requires relatively long TR (0.2-1.0s) to remain in the domain where the signal intensity is linearly dependent for a large range of FA's. Considering 3D tailored excitation pulses, such TR values extend the total duration of the $B_1^+$-mapping and pulse validation procedure beyond the maximum scan time appropriate for a single human subject. Still, fast $B_1^+$-mapping is desired to validate non-selective tailored RF-pulses such as $k_T$-points [3]. To tackle the aforementioned problems, an optimized version of this method for the quantification of non-selective excitation pulses is presented.

**Theory:** Considering the T1 values corresponding to the main tissues in the human brain, gray and white matter (T1<2s [4]), the signal intensity difference is approximately 5% or less if FA < 6° and TR≥50ms at 7T. In this domain, the signal attenuation due to T1 in the spoiled Fast Low Angle SHot (FLASH) image can then be corrected, to first order, for a known FA distribution $\alpha$, by assuming an average T1. The ratio of signal intensities between the FA linear regime and the true spoiled FLASH sequence can readily be derived from the signal equation $S(\alpha,TR,T1,TE,T2)$ [5] as:

$$RS(\alpha,TR,T1)=\frac{\lim\limits_{TR\to\infty} S(\alpha,TR,T1,TE,T2)}{S(\alpha,TR,T1,TE,T2)}=\frac{1-\cos(\alpha)e^{-TRT1}}{1-e^{-TRT1}} \quad (1)$$

Eq. 1 may then be applied to correct the signal intensity in the reference image ($FLASH_{ref}$) in the relative $B_1^+$-mapping method [1,2], thus allowing the apparent FA-maps ($\theta_n$) to be found from:

$$\theta_n=\frac{c\left|FLASH_n\right|\left|AFI_{ref}\right|}{\left|FLASH_{ref}\right|RS(c\left|AFI_{ref}\right|TR,T1)} \quad (2)$$

where $AFI_{ref}$ is a quantitative FA measurement corresponding to $FLASH_{ref}$ and $c$ is the scaling factor between ithe $AFI_i$ & $FLASH_i$ excitation pulses pulses. These $\theta_n$ underestimate the actual FA's due to the so-far uncorrected T1 relaxation effects in $FLASH_n$, as shown in (Fig. 1). In principle this could be corrected by solving for $\alpha$ in $\theta=\alpha RS(\alpha,TR,T1)$. Unfortunately, algebraic solutions of sufficient accuracy are non-trivial. However, a simple solution is provided by inserting $\theta_n$ back into Eq.1 to estimate the signal intensity correction in $FLASH_n$. Re-evaluating Eq. 2 with the corrected $FLASH_n$ now provides an improved estimation of $\theta_n$. This procedure can then be iterated to provide the corrected FA-maps.

**Methods:** Experimental verification was performed on a Siemens 7T Magnetom scanner (Erlangen, Germany), equipped with an 8-channel transceiver-array. First a set of 8 relative B1-maps [1,2] was obtained from low FA (average: 3°, max: 6°) FLASH images (sequence parameters: TR=50ms, TE=1ms, 5-mm isotropic resolution with a 48x48x36 matrix). In order to increase the overall accuracy, the proposed method was implemented in the framework of the matrix-based $B_1^+$-mapping method [6]. Furthermore, quantitative high FA-maps were obtained for two approximately orthogonal Tx-array phase combinations. To this end, the AFI sequence [7] was used with the following sequence parameters: TR1/TR2 = 40/200ms, TE=1ms, same acquisition matrix as for the FLASH sequence. FA-maps measured in a phantom (T1≈2s) using both a full set of 8 AFI measurements and the proposed method are compared. In-addition, a set of FA-maps obtained in a human volunteer was used to design non-selective excitation pulses targeting a uniform excitation profile throughout the brain [3]. Informed consent was obtained from all subjects in accordance with guidelines of our institutional review board.

**Results:** The measured difference between the full set of AFI measurements and the proposed method without T1 correction is shown in FIG. 2**a**. Significant improvements are obtained using the corrected method as shown in FIG. 2**b**. Although, the overall correlation between the full set of AFI measurements and uncorrected method was already near 99%, inclusion of the correction method substantially reduced local excursions. When applied to validate non-selective tailored excitation pulses [3], considerable differences in performance were observed (FIG. 3, **a**-**c**). In particular, for a homogeneous target excitation profile (5°) an offset in the average FA between the corrected and uncorrected FA is found (FIG. 3, **b** & **c**). Perhaps of greater importance is the difference in FA uniformity (uncorrected: 6.5%, corrected: 7.8%).

**Discussion:** The method introduced in this work allows fast non-selective B1-mapping and pulse validation. The trade-off for the gain in time is a small reduction in accuracy compared to the full AFI method. Nonetheless, the appreciable reduction in acquisition time allows in-vivo quantification of non-selective transmit-SENSE pulses with sufficient accuracy, provided that T1 affects are corrected to first order. Hybrid solutions where slice-selective relative mapping is performed in combination with one or more non-selective reference images could also be used to quantify the non-selective pulses. However, this requires additional measurements. Furthermore, slice selective relative $B_1^+$-mapping could require a higher-resolution or dummy repetitions to reach the steady state, in turn effecting the overall measurement time. Even though two AFI measurements were used to obtain adequate accuracy throughout the volume of interest; a speed-up factor of more than 2 was achieved for the proposed $B_1^+$-mapping procedure. Furthermore, compared to the AFI (TR=240ms) or long-TR relative $B_1^+$-mapping method (TR=200ms), validation of non-selective excitation pulses is accelerated by a factor 4.

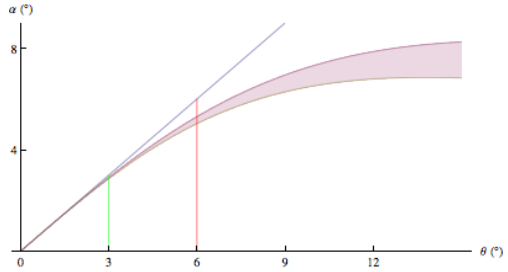


Fig 1: Deviation of signal intensity from linearity when TR=50ms. True FA $\alpha$ versus apparent FA $\theta$. Significant divergence from linearity starts at 3° (green line). The highlighted area represents the variation in signal intensity due to T1 contrast between white and grey matter. Below 6° (red line), the T1-variation is sufficiently small to allow correction based on an average T1.

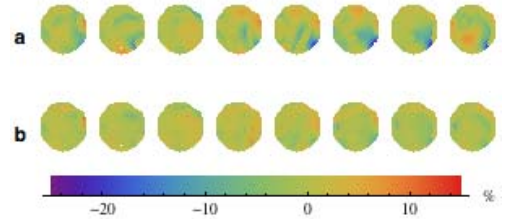


Fig 2: Difference in FA between the full set of AFI measurements and the un-corrected (**a**) and corrected (**b**) short-TR relative B1-mapping method. Different excitation modes corresponding to $FLASH_n$ are shown from left to right for a central slice in the phantom.

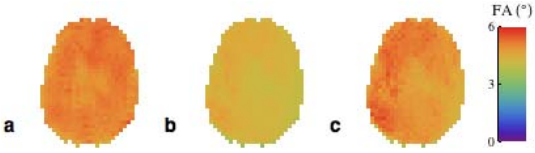


Fig 3: Validation of non-selective excitation pulse design in the human brain. Simulated excitation pulse (**a**), uncorrected measurement (**b**), corrected measurement (**c**).

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