## Direct calculation of B1<sup>+</sup> and B1 from two point variable flip angle data for quantitative T1 and PD mapping

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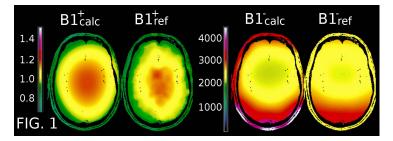
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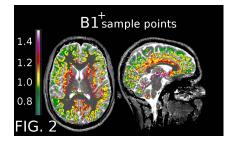
Introduction: Quantitative techniques for mapping T1 and the proton density (PD) are of increasing clinical interest as they provide information on basic physical properties of tissue. Several methods are based on the acquisition of standard spoiled gradient echo (GE) data with two excitation angles (i.e. the variable flip angle method, VFA [1]). However, this technique requires knowledge of the transmitted radio frequency (RF) field (B1<sup>+</sup>) and the receiver sensitivity profile (B1<sup>-</sup>) [1,2]. Several methods for B1<sup>+</sup> and B1<sup>-</sup> mapping have been proposed which, however, often require additional scans with sequences not routinely implemented on standard MRI systems [3]. A B1<sup>+</sup> mapping technique without further measurements is based on bias field correction [4]. However, although very accurate, this method depends on the correct choice of algorithms and parameters. The purpose of this work was to overcome these problems by developing a method for simultaneous B1<sup>+</sup> and B1<sup>-</sup> mapping directly from VFA data, which (i) does not require additional measurements, and (ii) is based on a simple and easy to implement postprocessing algorithm.

Theory: For TR << T1, TE << T2\*, and α << 1 (α: nominal flip angle), the signal S in spoiled GE data is given by the simplified Ernst equation:  $S = (B1^{\circ}) \cdot PD \cdot \alpha \cdot (B1^{\circ})/N$  (eq.1), with  $N = 1 + T1_{app} \cdot \alpha^{2}/(2 \cdot TR)$ , where  $T1_{app} = T1 \cdot (B1^{\circ})^{2}$  is the apparent T1 value obtained via VFA without B1<sup>+</sup> knowledge, assuming B1<sup>+</sup> = 1. Using Fatouros' approximation  $1/PD \approx K_1 + K_2/T1$  (eq.2) [5] with  $K_1 = 0.858$  and  $K_2 = 522$  ms [6], eq.1 yields:  $1/PD = K_1 + K_2 \cdot (B1^{\circ})^{2}/T1_{app} = (B1^{\circ}) \cdot (B1^{\circ}) \cdot \alpha/(S \cdot N)$  (eq.3). Replacing  $Y = K_1 \cdot (S \cdot N/\alpha)$  and  $X = -K_2/T1_{app} \cdot (S \cdot N/\alpha)$  in eq.3 yields:  $Y = (B1^{\circ}) \cdot (B1^{\circ}) + (B1^{\circ}) \cdot (B1^{\circ}) + (B1^{\circ}) \cdot (B1^{\circ}) \cdot (B1^{\circ}) + (B1^{\circ}) \cdot (B1^{\circ}) \cdot$ 

Materials and Methods: In 12 healthy subjects, spoiled GE imaging was performed using a FLASH-EPI hybrid readout technique with TR/TE/FA1/FA2=16.4ms/6.7ms/4°/24°], FoV=256x224x160 mm³, isotropic resolution 1 mm [6]. Reference B1<sup>+</sup> mapping was performed as described in [3]. Reference B1<sup>-</sup> maps were calculated via bias field correction [2]. The new algorithm for B1<sup>+</sup> and B1<sup>-</sup> calculation consisted of the following steps: 1. Sampling of X and Y within volumes V of size 3x3x3 voxels. Center voxels were located within a GM/WM mask (see below for a description of the calculation of this mask). 2. Linear fitting according to eq.4 and calculation of the correlation coefficient cc(X,Y). 3. For cc(X,Y)>0.7, derivation of B1<sup>+</sup> and B1<sup>-</sup> for the respective center voxel. B1<sup>+</sup> values >1.3 or <0.7 and B1<sup>-</sup> values >5000 or <1000 were considered outliers and excluded. 4. Second order (in case of B1<sup>-</sup> fourth order) 3D-polynomial fitting across sample points, yielding whole brain B1<sup>+</sup> and B1<sup>-</sup> maps. The initial GM/WM mask was derived via an initial run of this algorithm yielding an approximate B1<sup>+</sup> and thus an approximate T1 map. This map was thresholded according to 500ms<T1<2000ms. For reliable exclusion of CSF, the mask was further reduced in size by eroding all surface voxels.

Results: Calculated and reference B1<sup>+</sup> and B1<sup>-</sup> maps from axial slices through the thalamus are presented in Fig. 1. Figure 2 shows respective B1+sample points with cc>0.7, most of them being located at GM/WM borders. Absolute deviations of calculated B1<sup>+</sup> and B1<sup>-</sup> from reference values (i.e.  $|B1_{calc} - B1_{ref}|/B1_{ref}$  averaged across the whole brain) were similar for both fields and amounted to 3% only (all subject average).





<u>Discussion and Conclusion:</u> The presented technique produced accurate B1<sup>+</sup> and B1<sup>-</sup> maps in a sample of 12 subjects, as required for subsequent correction of T1 and PD maps. The method only employs the original VFA data acquired for T1 and PD mapping and is thus independent of any special MRI techniques for measuring B1<sup>+</sup> and B1<sup>-</sup> that may not be available on standard scanners. Thus, it holds promise to contribute to quantitative MRI applications in the clinical setting.

## **References:**

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