Exploring the complementarities of the MP2RAGE and the Sa2RAGE sequences - quantitative T_1 mapping

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Introduction

The MP2RAGE sequence has been recently introduced as a sequence that generates bias field free T_1-w images and jointly estimates T_1 maps (1,2). Despite the optimization of the sequence parameters (2) performed in order to reduce B_1^+ dependence of those images (which penalizes the maximum contrast obtainable), the resulting T_1-maps still suffer from some residual transmit field bias. Often, the temptation to increase the resolution (by increasing the number of low flip angle excitations per TR) and the need to keep the total acquisition time low (by reducing the TR of the MP2RAGE) increase the sensitivity of the MP2RAGE T_1 estimation to B_1^+ inhomogeneity. Recently, some attention has been drawn to the correlation between the observed cortical T_1 values and known distributions of myelination (3). For these correlations to be further evaluated at such high resolution and through such a large brain extent, it is imperative to obtain high resolution, robust and fully bias free T_1 values. In this work, we combine the MP2RAGE sequence with the Sa2RAGE sequence (4), to improve their individual estimate of the T_1 and B1 distributions.

Theory and Methods

Data from 2 subjects (28±4) were acquired in a 7T MR scanner (Siemens Medical Solutions, Erlangen, Germany) using an 8-channel head coil (Rapid Biomedical) and the following sequences:

a) MP2RAGE sequence: $MP2RAGE_{TR}/TI_1/TI_2$= 6/0.8/2.5s, either α_1/α_2=7/5 degrees (protocol A - high CNR) or α_1/α_2=4/5 degrees (protocol B - reduced B_1^+sensitivity). Matrix size and resolution were of 256x200x176 and 0.85mm isotropic, T_{acq}=10min;

b) Sa2RAGE sequence: $Sa2RAGE_{TR}/TD_1/TD_2$ = 2.4/0.058/1.8s, α_1/α_2= 4/11 degrees, matrix size and resolution were of 128x120x64 and 2x2x2.5mm^3 resolution, $iPat_{PE1}$=2 in the and 6/8 partial Fourier sampling were used in the phase encoding direction. T_{acq}=2.30 min;

The Sa2RAGE image and MP2RAGE image were co-registered using FLIRT (www.fmrib.ox.ac.uk/fsl) so that a pixel by pixel relationship could be used.

Lookup tables containing the T_1 values associated to certain MP2RAGE signal and B_1^+ value (see Figure 1a and 1b for the MP2RAGE protocol A and B) and the B_1 values associated to certain Sa2RAGE signal and T_1 value (see Figure 1c referring to the Sa2RAGE protocol) were computed. A two dimensional interpolation was iteratively performed for each pixel using the two lookup tables.

After two iterations, the variations in both B_1^+ and T_1 were found to be under 10^{-3}.

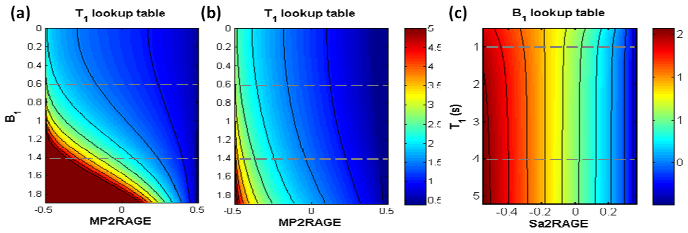

Figure 1 Lookup tables used to compute: (a) the T1 maps for the MP2RAGE sequence with $MP2RAGE_{TR}/TI_1/TI_2$ = 6/0.8/2.5s, **α_1/α_2=7/5**, (b) the T1 maps for the MP2RAGE sequence with $MP2RAGE_{TR}/TI_1/TI_2$ = 6/0.8/2.5s, **α_1/α_2=4/5**,(c) the B1 maps for the Sa2RAGE sequence with $Sa2RAGE_{TR}/TD_1/TD_2$ =2.4/0.058/1.8s, **α_1/α_2=4/11**. Grey dashed lines define the typical range of B_1 and T_1 observed in the human brain at 7T.

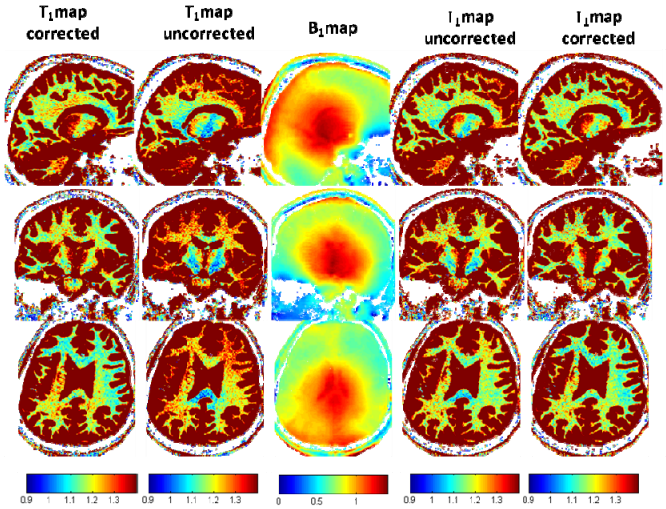

Figure 2 Sagittal, coronal and transversal slices of: (c) a corrected B_1^+ map; (b,d) uncorrected T1 map and (a,e) corrected T1 maps calculated using protocol A (a,b) and protocol B (c,d); the colorbars regarding each column are shown at the bottom of each column. The T1 maps are shown in color-scale (and in a short range from 0.9 to 1.4s) in order to emphasize the sensitivity of the T_1 maps to the B_1 in-homogeneity.

Results

Figure 2 shows T_1 maps of the human brain obtained with two sequences known to be sensitive to a different extent to transmit field inhomogeneity before and after correction. As expected, Protocol A has a larger sensitivity to B1 field in-homogeneities than Protocol B. The latter also shows some inhomogeneities that are increased in respect to those described in [2] due to the reduced TR and increased number of slices. It is possible to see that after the joint estimation of B_1 and T_1, the T_1 distributions in the human white matter decreased, notably reducing the artifacts due to the central brightening (where the relaxation rate was being overestimated), increasing the similarity between the two measurements and starting to reveal some underlying white matter structure.

Future and conclusions

While this proof of concept focused on the white matter variations of the T_1-map estimation for demonstration purposes, it is naturally valid for grey matter studies such as those performed in references [3,5]. The correction of the MP2RAGE T_1 maps could allow for either reduction of their acquisition time (decreasing TR) or increase of their contrast too noise ratio thanks to the possibility of using the protocol with increased contrast-to-noise ratio.

References

[1] Van de Moortele PF et al. Neuroimage 2009 ; [2] Marques JP et al Neuroimage, 2010 ; [3] Weiss M. et al Annual Meeting HBM 2010 #733; [4] Eggenschwiler F. et al MRM, 2011; ; [5] Glasser M.F. et al J. of Neuroscience, 2011;