Optimisation of the MP2RAGE sequence to thalamic nuclei and brain stem imaging

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Introduction The MP2RAGE sequence has been recently introduced as a mean to obtain bias field free T_1-weighted images at ultrahigh field [1,2]. In the original work, the sequence parameter optimization was developed to obtain the conventional range of contrast (covering the T1 range from WM to CSF). Although such a large range of T_1 range is desirable for normal segmentation applications, it is not ideal when looking at detailed visualization or segmentation of, for example, thalamic nuclei whose observation is essential in the neuro-surgical treatment of a wide range of neurological disorders (such as Parkinson's and neuropsychiatric disorders) [3]. In this work we evaluate the possibility of optimizing the sequence parameters to deliver optimum contrast on a shorter range of T_1 values.

Theory and Methods

The predicted MP2RAGE signal amplitudes for several tissues were numerically calculated after solving the Bloch Equations as in reference [1], with the following parameters being varied: $MP2RAGE_{TR}$, TI_1 and TI_2 (Fig. 1); Number of excitations per GRE module was set to 160 (full k-space coverage) or 120 (partial fourier k-space coverage); α_1 and α_2 (flip angles of the two GRE blocks); 5 T_1 values ranging from 1.1 (~WM) to 1.9s(~GM) (that should cover the different tissue T_1 values in the brain and thalamus area).

Contrast to noise by unit of time between two tissues was defined as: (S1-S2)/sqrt($\sigma_{S1}^2+\sigma_{S2}^2$)/sqrt(MP2RAGE TR) and the final contrast quality was evaluated as the sum of the 4 contrasts evaluated. The noise of the S, σ_S, was estimated by error propagations and all sequence parameters were chosen from simulations in order to optimise the CNR for the desired T_1 range.

Experiments were performed on a 7T MR scanner (Siemens Medical Solutions, Germany). MP2RAGE data from 2 subjects (34±4) were acquired using an 8-channel head coil (Rapid Biomedical) using the following sequences: a) $MP2RAGE_{TR}/TI_1/TI_2$=6/0.8/2.5s and α1/α2=4/5 degrees (Protocol A); b) optimized for the white to grey matter T1 range $MP2RAGE_{TR}/TI_1/TI_2$=6/0.7/1.6s and α1/α2=7/7 degrees (Protocol B). Both acquisitions were performed using $iPAT_{PE}$=2 and 6/8 k-space coverage on the slice encoding direction, acquisition time of 10 mins. The matrix size and resolution were varied between the different subjects and was either: 256x192x160 and 1mm isotropic or 256x200x176 and 0.85mm isotropic.

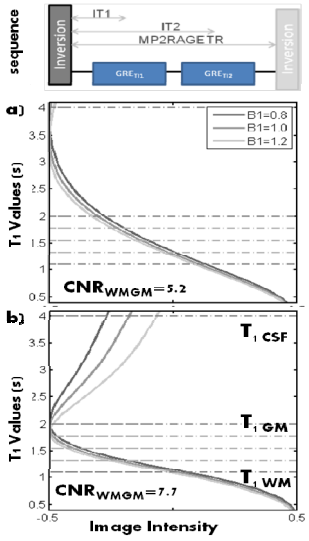

Figure 1 MP2RAGE sequence diagram. Within each GRE block the phase-encode steps in the third dimension (slab) are acquired Image intensity of the MP2RAGE as a function of T_1 for (a) the parameters that optimize contrast over all values of T1 present in the brain and (b) the parameters that optimize contrast for T1 values between those of WM and GM. The black and gray lines represent errors on the effective B_1^+ of 0 and ±20% respectively.

Results

Figure 1 shows the lookup tables of the MP2RAGE signal intensity as a function of the T1 values for the protocols with TR=6 secs optimized for full T_1 range contrast (Fig. 1a- Protocol A) or WM-GM contrast (Fig. 1b – Protocol B). The increased contrast between WM and GM is obtained by reducing the spacing between the two different inversion times. By using partial k-space sampling in the slice encoding direction it was possible to reduce the number of excitations per GRE block and the sensitivity of the resulting image to transmit B_1 field inhomogeneities (note that in Protocol A α1/α2=4/5 while Protocol B α1/α2=7/7); The computed CNR for range of T_1 values for which the optimization was performed increased by 51%, which when taking into account the reduced number of excitations due to partial Fourier sampling is of ~33%. The penalty paid is the ability to distinguish CSF which appears wrapped and overlaps the intensity of WM (see Fig.1b).

Figure 3 shows midbrain MP2RAGE and $MP2RAGE_{WMGM}$ images. It is possible to see an increased delineation of the thalamus and its medio dorsal, ventral lateral and pulvinar nuclei (red arrows) as well as increase contrast within the brain stem (yellow arrows). The two columns on the right side show the synthetic image created with the new sequence using the FLAWS concept [4], (note that in this acquisition both CSF and white matter were acquired close to their null point at the first and second inversion times respectively) or the unwrapped approach obtained by combining the knowledge between the ratio of both images [2] and the MP2RAGE intensity [1].

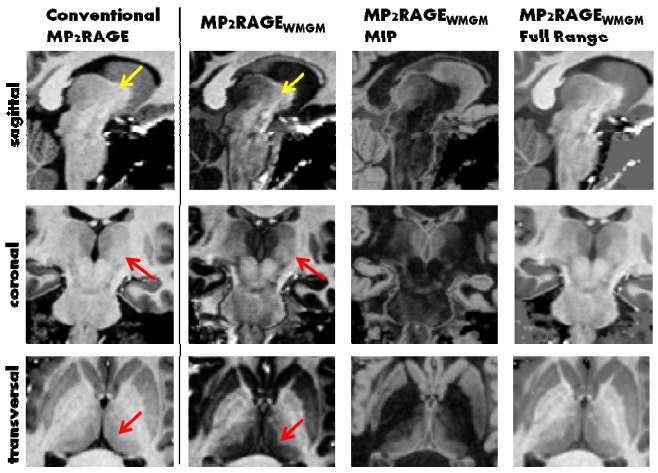

Figure 2 three perpendicular slices through the midbrain of: (1st column) conventional MP2RAGE; (2nd column) MP2RAGE optimized for WM GM contrast;. Subsequently this dataset was pos-processed in two alternative ways: (3rd column) MIP= $(\min(GRE_{TI1},GRE_{TI2})/(GRE_{TI1}+GRE_{TI2})$); and (4th column)Full range $MP2RAGE_{WMGM}$

Future and conclusions

We have shown that, by optimizing the contrast of the MP2RAGE sequence to a specific range of T1's, it is possible to gain access to clear anatomical delineation of thalamic nuclei and brain stem which could find important applications in the context of automatic segmentation or pre-surgical planning. **References** [1] Marques JP et al Neuroimage, 2010**,** [2]Van de Moortele PF et al. Neuroimage 2009**;** [3] Friehs G et al Neurosurg. Focus 23(6), 2007; [4] M. Tanner et al, JMRI, submitted