B1+ and B0 Corrected High Resolution Whole Brain T1-mapping at High Field in a Clinically Acceptable Scan Time

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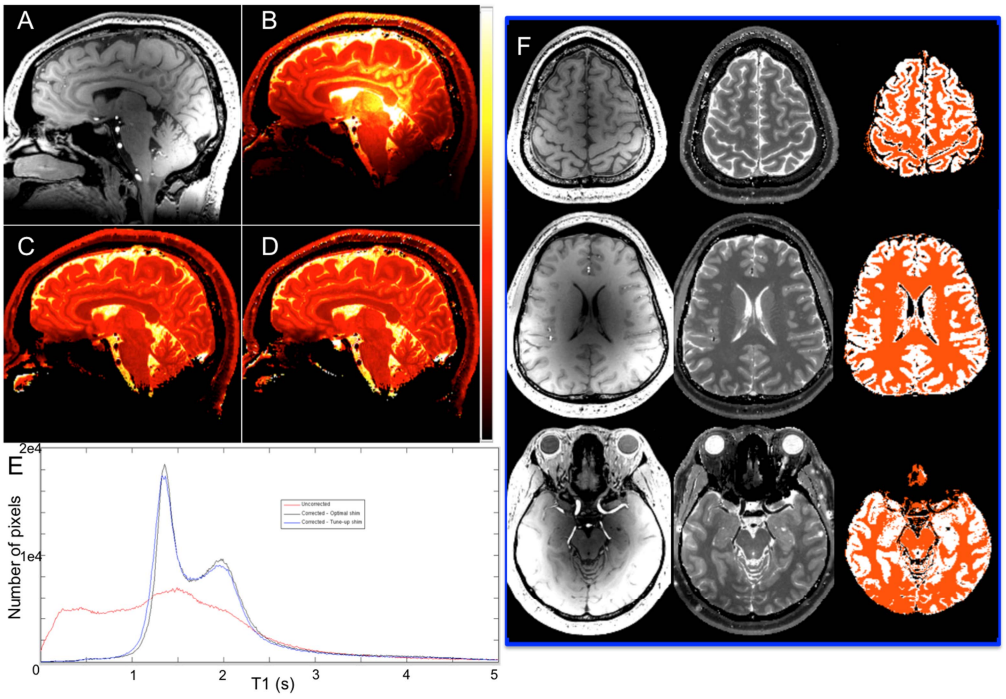
Target Audience: Researchers and clinicians interested in clinical quality human brain scans at high field strengths.

Purpose: Spatial variations in signal intensity, caused by transmit and receiver coil sensitivity profiles as well as B_0 inhomogeneity, cause severe non-uniformity in routine imaging at high field strengths, often rendering them unusable for group analysis or clinical diagnosis. Various post-hoc techniques such as non-parametric non-uniformity normalization (N3/N4) have been proposed to correct for such artifacts, however such methods do not measure and correct the individual bias-fields separately. Here we use a B_0 corrected Bloch-Siegert based B_1 mapping sequence[1] to obtain high resolution bias-free quantitative T_1-map from the human brain at 7T, and explore its use in brain tissue segmentation.

Methods: MRI was performed on a healthy volunteer (M, 40 y.o.) using a volume-transmit and 32-channel receive head coil (Nova Medical, USA) on the Siemens 7T MRI in two sessions (repeated once with optimal 3rd order shim and once with tune-up shim). Bloch-Siegert based B_1-mapping was performed using 3D GRE sequence (TR=130 ms, TE=9.18 and 11.22 ms, resolution of 4 mm isotropic, 6 min) prepped with a SAR optimized off-resonance pulse.[1] Two echoes were used to calculate a B_0 map for correcting any residual B_0 inhomogeneity effects on the B_1-maps. Multiple T_1-weighted images were acquired using 3D GRE sequence (TR/TE=7.8/2 ms, FA=2, 6, 13 deg, 1mm isotropic resolution, 6 min per FA). T_1-maps were reconstructed before and after correction of the FA with the B_1-map in Matlab.[2,3] Brain-extracted T_1-map (skull stripped in AFNI and thresholded between 0.5 and 2.5 s) from the two sessions was used as input to a rudimentary tissue segmentation algorithm based on k-means clustering in Matlab.



Results: Non-uniformity due to coil profiles can be appreciated in the T_1-weighted image (Fig A) and uncorrected T_1-map (B, range 0-5s). B_0 and B_1 corrected T_1-maps from the two sessions (C and D), on the other hand appear uniform and robust (voxelwise mean difference of 39 ± 0.5 ms). Fig E shows the histogram from uncorrected T_1- map (red) and distinct bi-modal distribution from corrected T_1-map in each imaging sessions (blue and black). Figure F shows T_1-weighted (left column), corrected T_1-map (middle column), and segmented gray (in white) and white matter (in orange) from three slices 3 cm apart in the brain. Centroids of the two tissue clusters in the segmentation algorithms were located at 1.4 and 2.0 s.

Discussion: Apart from the clinical utility of spatially uniform images at high field strength, the technique also offers increased SNR enabling sub-millimeter resolution or faster scans times, as well as increased CNR between tissue types allowing easy segmentation. Total scan time for each session was less than 30 minutes, but could be reduced to ~12 minutes by using just 2 flip angles and using parallel imaging. Segmentation results were excellent considering the rudimentary algorithm used herein, and could be improved by atlas-based techniques and including additional quantitative measures such as T_2 maps. In addition, the quantitative nature of the T_1-maps allow easy comparison of normal appearing regions in disease and healthy brains, such as normal appearing white matter in multiple sclerosis.

Conclusion: High-resolution T_1-mapping offers an opportunity to obtain bias-field corrected images of the human brain at high fields. Such quantitative images enable easy group analysis as well as cross-subject comparison in normal appearing regions. Further studies in healthy volunteers and patients with multiple sclerosis are underway.

References: [1]Duan et. al. NMR Biomed.(2013)26:1070; [2]Wang HZ et al. MRM (1987) 5:399; [3]Mintzopoulos and Inati Proc. ISMRM 14 (2006) 923.