Multiple Echo and Inversion Time MPRAGE with Inner Loop GRAPPA Acceleration and Prospective Motion Correction for Minimally Distorted Multispectral Brain Morphometry

Andre J. W. van der Kouwe[1], M. Dylan Tisdall[1], Himanshu Bhat[2], Bruce Fischl[1], and Jonathan R. Polimeni[1]
[1]*Radiology, Massachusetts General Hospital, Charlestown, MA, United States,* [2]*Siemens Healthcare USA, Charlestown, MA, United States*

Target audience: Clinicians and researchers interested in efficient high quality brain imaging, multispectral morphometry and tissue parameter mapping with a single modified MPRAGE acquisition.

Purpose: Distortions and blurring in MPRAGE affect morphometric measurements (e.g. cortical thickness) that are signatures of brain disease[1].

Remaining B_0-inhomogeneities after shimming result in accumulated phase errors across each readout and therefore erroneous spatial encoding (susceptibility distortions). In addition, T_2*-decay across the readout results in broadening of the point spread function (PSF). Replacing the single, low-bandwidth gradient echo readout with multiple shorter, high-bandwidth readouts results in reduced susceptibility distortion and a narrower PSF in the readout direction. SNR is recovered by combining the readouts in image reconstruction. T_2* may be estimated by fitting signal decay across the echoes.

T_1-recovery during partition (k-space "slice") encoding after each inversion (MP) pulse in 3D MPRAGE similarly results in a broadened PSF in this phase encoding direction. Partition encoding time can be reduced by GRAPPA acceleration in this inner phase encoding loop ("inner-loop GRAPPA", ILG), thus reducing distortion but also reducing SNR. Replacing each partition encoding block with multiple ILG-accelerated blocks experiencing different inversion times recovers SNR when the partitions are combined in image reconstruction. T_1 may then be estimated by fitting the signal predicted by Bloch simulation across inversion times[2].

Images may be blurred further by subject motion during the long high resolution acquisitions, which may require several minutes even with outer loop acceleration.

Methods: We implemented a generalized MPRAGE sequence[2] that allows ≤12 gradient echoes, ≤8 inversion times, ILG acceleration, and incorporates vNavs for real-time prospective motion correction and reacquisition of damaged TR intervals[3]. The excitation scheme is shown in Figure 1 alongside that of a standard MPRAGE protocol recommended for brain morphometry[4]. Motion-corrected volumes for each TE and TI are reconstructed immediately on the scanner using improved "IcePat" routines for GRAPPA acceleration.

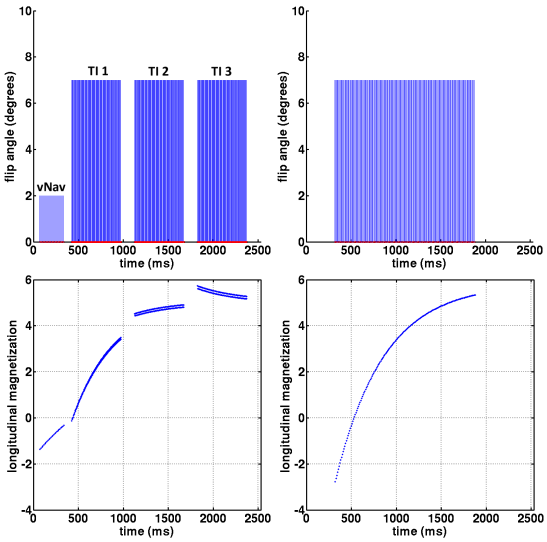

Figure 1: Single steady-state TR (between inversions) of (left) MEMPxRAGE-ILG and (right) conventional MPRAGE sequence. (Top) Excitation scheme (blue), ADC events (red). (Bottom) Signal evolution for white matter at 3 T, sampled at times of ADC reads.

The method was evaluated in two volunteers on a 3 T Skyra (Siemens Healthcare, Erlangen) with a 32-channel head coil. The protocol was selected to match the timing of the conventional 1×1×1 mm^3 3D MPRAGE (no acceleration), with optimal gray matter/white matter/CSF contrast for morphometry[4]. MEMPxRAGE parameters: 2 gradient echoes, 3 inversion times, TR 2.53 s, TE 1.69/3.55 ms, BW 650 Hz/px, TI 700/1400/2100 ms, flip angle 7/7/7°, 3× ILG acceleration (40 ref. lines), 176 sagittal slices, 256×256 matrix, 1×1×1 mm^3 resolution, T_{acq} 11:21 min:s. vNav parameters: 3D EPI, TR 11 ms, TE 5.1 ms, 32×32 matrix, 32 sagittal slices, 6/8 partition partial Fourier, 8×8×8 mm^3 voxels, BW 4464 Hz/px, T_{acq}/nav 275 ms.

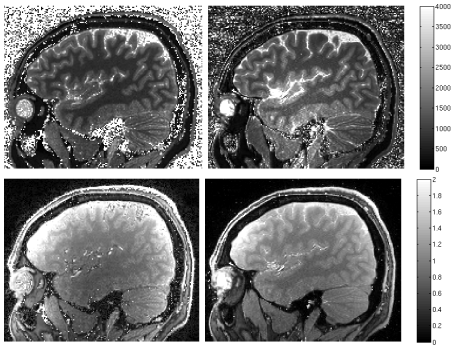

Figure 3: Estimates of T_1 (top) and PD (bottom), from MEMPxRAGE-ILG acquisition/Bloch simulation (left) and multiecho FLASH acquisition/model equation fit (right).

A forward model for signal generation based on Bloch equations was implemented in Matlab (MathWorks, Natick, MA) and used to predict signals for a given T_1 relaxation time[2] (Figure 1). Figure 2 shows corresponding PSFs for each sequence. Note the broader PSF for conventional MPRAGE. The proton density (PD) and T_1 time that best predicted the observed signal evolution was found at each voxel across the range of inversion times. For comparison, two multiecho FLASH (MEF) volumes were acquired on the same subjects: TR 20 ms, TE 1.91+1.9*n*, *n*=0,..,7, BW 650 Hz/px, flip angles 5° and 30° (separate acquisitions), T_{acq} 5:08 min:s, 4× GRAPPA acceleration, geometry matches MEMPxRAGE-ILG. Standard methods[5,6] were used to estimate PD and T_1 from the MEF scans.

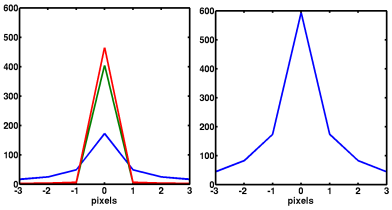

Figure 2: PSF for white matter at 3 T in inner-phase encoding direction for (left) MEMPxRAGE-ILG TI 1 (blue), 2 (green) and 3 (red) and (right) MPRAGE. Profiles scaled by mean modeled signal intensity.

Results: Figure 3 shows T_1 and PD estimates from MEMPxRAGE-ILG using Bloch simulation, and estimates for the same subject derived by fitting the steady-state equation for the MEF scans[5,6]. Figure 4 shows a FreeSurfer surface model/parcellation from the combined MEMPxRAGE-ILG volumes.

Discussion: GRAPPA successfully recovers volumes at all TIs and TEs with minimal residual aliasing. The more uniform signal over the partition at each inversion time (due to acceleration) together with the availability of more than two inversion times better constrains the Bloch simulation and may provide better T_1 fits. Results are comparable to T_1 fitting with MEF, although the latter may be more affected by dielectric resonance effects. The effect of the embedded vNavs is subtle and can be modeled (Figure 1). As in traditional FLASH acquisitions and with appropriate timing, the multiple gradient echoes from the MEMPxRAGE-ILG sequence can be used to estimate the B_0 field map, separate fat from water, and estimate T_2* decay at each voxel using traditional techniques[7,8]. Bloch simulation can also be used to fit T_2*, however more than two echoes would be preferable.

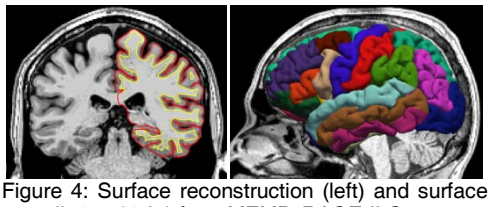

Figure 4: Surface reconstruction (left) and surface parcellation (right) from MEMPxRAGE-ILG.

Conclusion: MEMPxRAGE with ILG and vNavs is an efficient sequence for high quality, low distortion and low blur acquisitions, useful for quantitative tissue parameter mapping and high resolution brain morphometry in a single acquisition.

Acknowledgements: This work was supported by: NIH R21MH096559, R01HD071664, R21EB008547, K01EB011498, K99HD074649, P41RR014075, and the Ellison Medical Foundation. Thanks to Drs. T. Kober and G. Krueger for access to image sorting code.

References: [1] Bakkour et al., Neurology 72(12):1048-55, 2009. [2] Marques et al., Neuroimage 49(2):1271-81, 2010. [3] Tisdall et al., MRM 68(2):389-99, 2012. [4] Van der Kouwe et al., Neuroimage 40(2):559-69, 2008. [5] Deoni et al., MRM 53(1):237-41, 2005. [6] Fischl et al., Neuroimage 23 suppl 1:S69-84, 2004. [7] Glover, JMRI 1(5):521-30. [8] Yu et al., JMRI 26(4):1153-61.