Fast variable inversion-recovery time EPI for anatomical reference and quantitative T_1 mapping

Ville Renvall[1,2], Thomas Witzel[1,2], Lawrence L. Wald[1,2], and Jonathan R. Polimeni[1,2]

[1]*Athinoula A. Martinos Center for Biomedical Imaging, Massachusetts General Hospital, Charlestown, MA, United States,* [2]*Department of Radiology, Harvard Medical School, Boston, MA, United States*

TARGET AUDIENCE Researchers/clinicians needing rapid, convenient ultra-high field cortical surface analysis distortion-matched to fMRI.

PURPOSE Recent progress in ultrahigh-field MRI has enabled high-resolution single-shot EPI, developed for fMRI, that exhibits striking anatomical detail. Our aim was to capitalize on the progress and develop a method for fast, quantitative T_1 mapping based on echo planar imaging (EPI) to provide anatomical images that are natively distortion-matched to the fMRI data. Having anatomical data that is geometrically identical to the functional data provides a way to localize brain activations more accurately than what can be achieved with a geometrically dissimilar anatomical template. Our goal was to obtain a full brain image at 1-mm^3 isotropic resolution in < 3 min that can be automatically segmented by FreeSurfer.

METHODS Our IR-EPI acquisition rapidly obtains several inversion times (TI) by placing EPI readouts following a slab-selective inversion pulse and permuting the slice order each TR, as has been previously proposed[1], with a novel reordering scheme with a "skip" option that permits stepping the slice permutation by several slices at a time. For instance, if the imaging volume consists of 9 slices, and the skip factor is set to 3, the slice acquisition order of the first TR with ascending base order would be: 1, 2, 3, 4, 5, 6, 7, 8, 9; the second TR: 4, 5, 6, 7, 8, 9, 1, 2, 3; the final third: 7, 8, 9, 1, 2, 3, 4, 5, 6. This scheme substantially reduces the scan time for a whole-brain 1 mm^3 iso. acquisition from 10–15 minutes to under 3 minutes. Additionally, we employed an adiabatic frequency offset compensated inversion (FOCI) inversion pulse[2] to gain transmit efficiency, and FLEET autocalibration signal acquisition was adopted to improve GRAPPA performance[3]. After acquisition, the data were processed offline using Matlab: each voxel was modeled with a mono-exponential T_1 recovery including a lag term to compensate for incomplete T_1 recovery; unmodelable voxels were identified and filtered by a 3-dimensional 26-neighborhood median; and synthetic IR contrast images with appropriate TI were computed. Finally, fully automatic segmentations and reconstructed cortical surfaces were obtained, using default settings, with FreeSurfer.

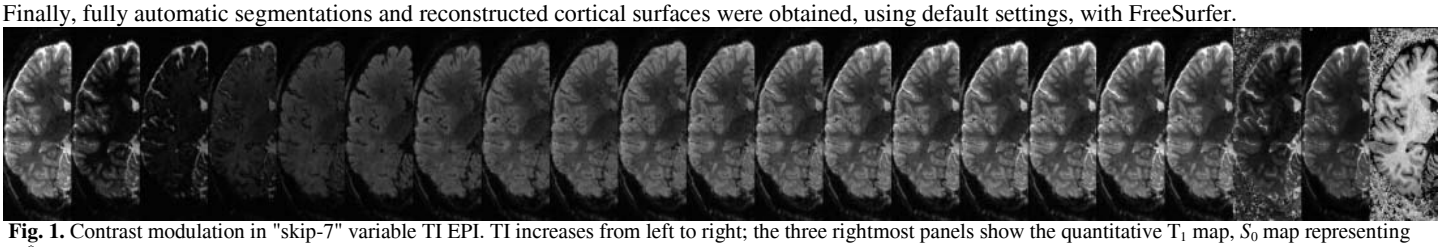

Fig. 1. Contrast modulation in "skip-7" variable TI EPI. TI increases from left to right; the three rightmost panels show the quantitative T_1 map, S_0 map representing T_2^* and spin density components, and an image synthesized from the T_1 map with TI = 2300 ms, magnitude image.

Seven volunteers were scanned on a 7-T whole body MRI scanner (Siemens Healthcare, Erlangen, Germany) using a 32-channel receive array with a birdcage head transmit coil after written informed consent. The skipped variable inversion recovery (IR) time EPI data was acquired at 1-mm^3 isotropic resolution with TR/TE/flip/BW/matrix/slices/skip/R = 8 s / 22 ms / 90° / 1184 Hz/pix / 192×192 / 126 / 7 / 4. The total acquisition time was < 3 min. For comparison, we acquired T_1-weighted multi-echo MPRAGE images utilizing FOCI inversion. The ME-MPRAGE data were bias field corrected using spm12b (FWHM = 18 mm, sampling distance = 2) to improve the image homogeneity especially in temporal lobes.

RESULTS Fig. 1 shows the contrast variation, two computed and one synthesized image for an oblique axial slice of a representative subject. The T_1 modeling remains robust despite the skipping during the sampling of the IR. In Fig. 2, FreeSurfer reconstructions are shown for MEMP RAGE and synthetic EPI scans overlaid on three closely matching orthogonal image slices. The two scans yield comparable results, although differences due to unequal geometric distortions can be observed. In this example, the contrast available in the IR EPI also enables segmentation of subcortical structures (putamen and pallidum) that are not found in the ME-MPRAGE segmentation.

DISCUSSION A drawback of relaxation time mapping is the long scan time. Our IR-EPI method can provide a 1-mm^3 isotropic full brain T_1 map in less than 3 minutes, which is even clinically acceptable. The scan time can be further reduced by using Simultaneous Multi Slice technique, or shortening the TR by omitting the acquisition of the relatively unchanging images in the latter portion of the IR.

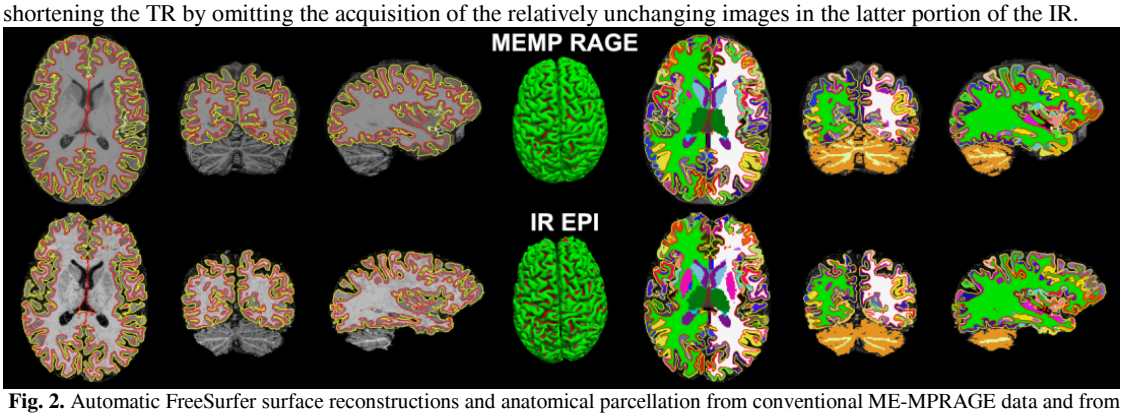

Fig. 2. Automatic FreeSurfer surface reconstructions and anatomical parcellation from conventional ME-MPRAGE data and from synthetic T_1-weighted data from a matching IR-EPI acquisition.

CONCLUSION A method to reduce scan time in EPI-based T_1 mapping was developed and tested on a 7-T scanner. Applications include automatic segmentation of brain structures, quantitative morphometry, and reference for fMRI, where these data may be more relevant than conventional anatomical data. The method provides clean T_1 maps without parasitic T_2 or T_2^* residuals, here segregated into another component.

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