Comparison of cortical surface reconstructions between quantitative T_1 and T_1-weighted volumetric data

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Target audience: Clinicians and researchers using quantitative anatomical measures, especially in the human brain.

Purpose: Automatic cortical surface reconstructions enable quantitative morphometric analyses of brain anatomy that can be sensitive to sub-voxel changes in cortical thickness, and can be used to track or detect brain atrophy or plasticity. Most surface reconstructions are derived from volumetric T_1-weighted data, however changes to the acquisition protocol or imaging hardware can induce changes to image contrast or geometry that can yield inaccurate measures of brain anatomy, therefore it has been suggested that quantitative parameter maps may provide more robust quantification [1]. Generating quantitative parameter maps is time consuming because multiple acquisitions with different contrasts are necessary for the calculation. The MP2RAGE method [2] efficiently acquires two image volumes in each acquisition by including two readouts in each inversion recovery, and therefore can be used to generate a T_1 map quickly and without mis-registration between the volumes. Here we demonstrate cortical surface reconstructions generated directly from the T_1 map generated by the MP2RAGE method and compare the precision and accuracy of these reconstructions with the T_1-weighted MP2RAGE volumes as well as the conventional multi-echo MPRAGE (MEMPRAGE) T_1-weighted volumes [3].

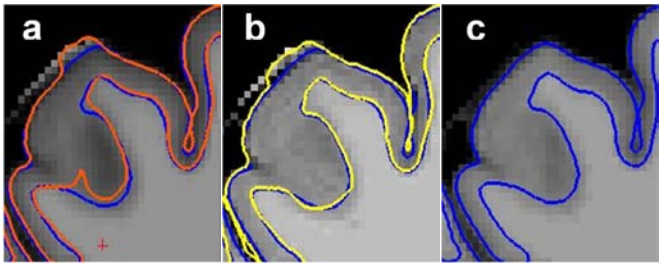

Fig. 1: Surface reconstructions generated from the three volumes tested. (a) MP2RAGE volume. (b) T_1 map volume. (c) MEMPRAGE volume. (Orange contour: MP2RAGE surfaces; blue contour: MEMPRAGE surfaces; yellow contour: T_1 map surfaces.)

	diff. (mm)	std. dev.
T_1 map vs. T_1 map (rescan)	0.16	0.002
MEMPRAGE vs. T_1 map (repeat)	0.41	0.02
MEMPRAGE vs. T_1 map (rescan)	0.40	0.02
MP2RAGE vs. T_1 map (repeat)	0.51	0.02
MP2RAGE vs. T_1 map (rescan)	0.51	0.02

Table 1: Comparison of average absolute thickness difference across four subjects (eight hemispheres) with population standard deviation across the hemispheres.

Methods: Four healthy adult volunteers participated after providing informed consent. Data were acquired on a 3 Tesla whole-body Tim TRIO MR scanner (Siemens Healthcare, Erlangen, Germany) using the vendor-supplied 32-channel head receive coil array. In each session, we acquired two consecutive repetitions of 1 mm isotropic MEMPRAGE data ($TI/TE_1/TE_2/TE_3/TE_4$/TR/flip/BW = 1200ms/2510ms/1.64ms/3.5ms/5.36ms/7.22ms/2510ms/7º/651 Hz/px, 2×GRAPPA, T_{acq} = 6min 2sec) and two consecutive repetitions of 1 mm isotropic MP2RAGE data (TI_1/TI_2/TE/TR/flip/BW = 700ms/2500ms/2.96ms/5000ms/4º/240Hz/px, 3×GRAPPA, T_{acq} = 8min 52sec), termed "*repeats*", then repositioned the subject within the scanner and re-acquired both MEMPRAGE and MP2RAGE data, termed "*rescans*", for a total of six volumes acquired per session. We applied the online 3D gradient nonlinearity distortion correction to all acquisitions. FreeSurfer [4, 5] was used to generate cortical surface reconstructions of the MEMPRAGE data, the T_1-weighted MP2RAGE data, and the quantitative T_1 map volumes calculated online directly from the MP2RAGE acquisition. The T_1 values were negated to generate an image volume with the contrast polarity between white and gray matter seen in T_1-weighted volumes. Conventional white matter edits were required for the T_1 map volumes to remove small white matter misclassifications in regions outside of the brain (caused by the intensity negation).

To quantify the precision of each reconstruction and to compare the reconstructions from the three different volumes, we first aligned all volumes to one another using a robust registration method [6], calculated vertex correspondences between all pairs of surfaces, then calculated the 3D distance and thickness difference between corresponding vertices on the white matter surfaces and on the pial surfaces. Signed distance was calculated by comparing the distance vector to the direction of the surface normal vector.

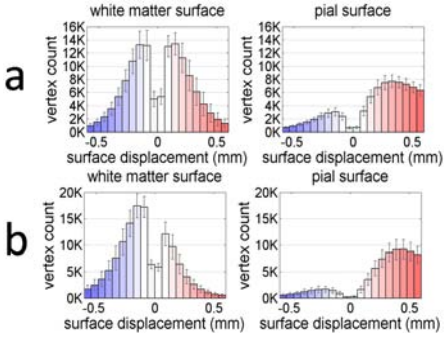

Fig. 2: Histograms of signed distance across four subjects (eight hemispheres) for repeat pairs: (a) MEMPRAGE vs. T_1 map and (b) MP2RAGE vs. T_1 map.

Results: Example surface reconstructions from the three volumes are shown in Fig. 1. The average absolute thickness difference between the rescan T_1 map data was 0.16 mm, comparable to the value 0.12 mm from a previous study at 1.5T [7], indicating a sub-voxel precision of the thickness measure. The average thickness between surfaces generated from the "repeat" and "rescan" acquisitions is summarized in Table 1. The average distance difference across four subjects (eight hemispheres) for the T_1 map rescan pairs was 0.13 mm ± 0.004 mm for the white surface and 0.16 mm ± 0.002 mm for the pial surface; for MEMPRAGE vs. T_1 map, the average distance was 0.20 mm for the white surface, and 0.44 mm for pial surface for both repeat and rescan comparison. However, for MP2RAGE vs. T_1 map pair, the average distance was 0.19 mm for the white surface, and 0.48 mm for the pial surface for both the repeat and rescan comparisons. Histograms of signed distance for between the MEMPRAGE and T_1 map pair (Fig. 2a) show that the pial surface generated from the T_1 map is consistently positioned outward compared to that of the MEMPRAGE data, whereas the white surface is consistently positioned across the MEMPRAGE and the T_1 map data. For the MP2RAGE and T_1 map rescan pair (Fig. 2b), the pial surface of the T_1 map is also shifted outward whereas the white surface of MP2RAGE is placed inward to that of the T_1 map.

Discussion: In both the MP2RAGE T_1-weighted data and the T_1 map derived from it, in some locations the dura adjacent to the pial surface can be mis-classified as gray matter and acts to displace the pial surface outward, thereby increasing the thickness estimate. The consistency of the white matter surface position seen in the MEMPRAGE and the T_1 map, the high reproducibility of the white surface position seen in the MEMPRAGE and the T_1 map, and the disagreement of white matter surface position seen in the MP2RAGE and the derived T_1 all suggest that the T_1 map may provide a more accurate or robust segmentation of the white matter surface than the MP2RAGE T_1-weighted data alone.

Conclusion: The T_1 map produced by the MP2RAGE method can provide an additional anatomical contrast that can be exploited to assist in quantitative measures of cortical morphometry.

References: [1] Fischl *et al.* (2004) *NeuroImage* **23**:S69. [2] Marques *et al.* (2010) *NeuroImage* **2**:1271. [3] van der Kouwe *et al.* (2008) *NeuroImage* **40**:559. [4] Dale *et al.* (1999) *NeuroImage* **9**:179. [5] Fischl *et al.* (1999) *NeuroImage* **9**:195. [6] Reuter *et al.* (2012) *NeuroImage* **61**:1402. [7] Han *et al.* (2006) *NeuroImage* **32**:180.

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