Quantitative Comparison of Morphometric Data from Multi-Echo MPRAGE with Variable Acceleration and Different Head Coils

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Target Audience: Researcher groups conducting volumetric brain morphometry, with concerns over optimal pulse sequence or hardware.

Purpose: Automated MRI-derived measurements of in-vivo human brain volumes from anatomical scans can provide novel insights into normal and abnormal neuroanatomy, but only a few studies have probed the repeatability and effects of sequence-dependent parameters on these measurements.[1] The multi-echo MPRAGE (MEMPRAGE) sequence was implemented to reduce signal distortion by using a higher bandwidth and averaging multiple echoes to recover SNR while using variable T_2* decays to enhance contrast, and hence, cortical segmentation.[2] To ensure minimal impact on subject burden and maximal efficiency, we implemented a rapid 2-minute MEMPRAGE protocol for anatomical scans, which we have shown yields quantitatively repeatable morphometric information across different scanners and days.[3] Here, we validate the morphometric results obtained from the rapid scan with those from a higher-resolution MEMPRAGE scan with lower image acceleration, acquired in the same session.

Methods: All measurements were performed using a 3.0 T MRI scanner (MAGNETOM Trio, A Tim System, Siemens Healthcare, Erlangen, Germany). 45 subjects (mean age 22.7 years, 26 male) were scanned using the 32-channel head coil, 31 subjects (mean age 21.8 years, 19 female) were scanned using the 12-channel head coil. All gave written informed consent according to a protocol approved by the local IRB. Each session included a high-resolution MEMPRAGE scan acquired in 6 min 44 sec (TE = 1.64, 3.50, 5.36 and 7.22ms, TR = 2530 ms, FOV = 256 x 256 mm, 176 slices, voxel size = 1.0 mm^3, parallel imaging (PI) acceleration = 2 (p2), bandwidth = 651 Hz/px); and a rapid MEMPRAGE scan acquired in 2 min 12 sec (TE = 1.54, 3.36, 5.18 and 7.01ms, TR = 2200 ms, FOV = 230 x 230 mm, 144 slices, voxel size = 1.2 mm^3, PI = 4 (p4), bandwidth = 651 Hz/px). The anatomical scans were analyzed using the FreeSurfer toolkit, after the two scans from each subject were aligned using the FreeSurfer robust registration tool. An automated parcellation of the cortex, subcortical and white matter structures was performed, and the estimated Total Intracranial Volume (eTIV) was calculated. Correlation plots were made for the volume or surface area of each structure determined from each scan.

Results: Figure 1 shows correlation plots of surface area of an example cortical region and volume of an example sub-cortical structure for subjects scanned with the p2 and p4 MEMPRAGE protocols. Similar volume determinations were made for sub-cortical and white matter structures, while cortical area, volume and thickness were determined for grey matter regions. Correlations for key structures and global measures are summarized below, along with those for test/re-test of the p4 MEMPRAGE protocol on a different set of subjects performed over two different days, from[3]:

Sequence:	**p2-p4 12ch**	**p2-p4 32ch**	**p4 test/ retest**
Structure	R^2	R^2	R^2
eTIV	1.00	0.99	0.99
L Caudate	0.96	0.94	0.96
L Putamen	0.83	0.86	0.91
L Hippocampus	0.80	0.92	0.94
L Amygdala	0.84	0.61	0.81
R Caudate	0.89	0.95	0.93
R Putamen	0.86	0.86	0.91
R Hippocampus	0.83	0.77	0.97
R Amygdala	0.76	0.76	0.74
CC Posterior	0.98	0.99	0.98
CC Anterior	0.96	0.95	0.96
Total WM Vol	0.98	0.99	0.98
Total GM Vol	0.98	0.99	-----
Total Cort Surf	0.98	1.00	1.00

Average R^2 for all:

left cort regions - area

p2-p4 12ch: 0.85

p2-p4 32ch: 0.90

p4 test/retest: 0.86

left cort regions - vol

p2-p4 12ch: 0.83

p2-p4 32ch: 0.89

p4 test/retest: 0.85

right cort regions - area

p2-p4 12ch: 0.85

p2-p4 32ch: 0.88

p4 test/retest: 0.85

right cort regions - vol

p2-p4 12ch: 0.85

p2-p4 32ch: 0.88

p4 test/retest: 0.84

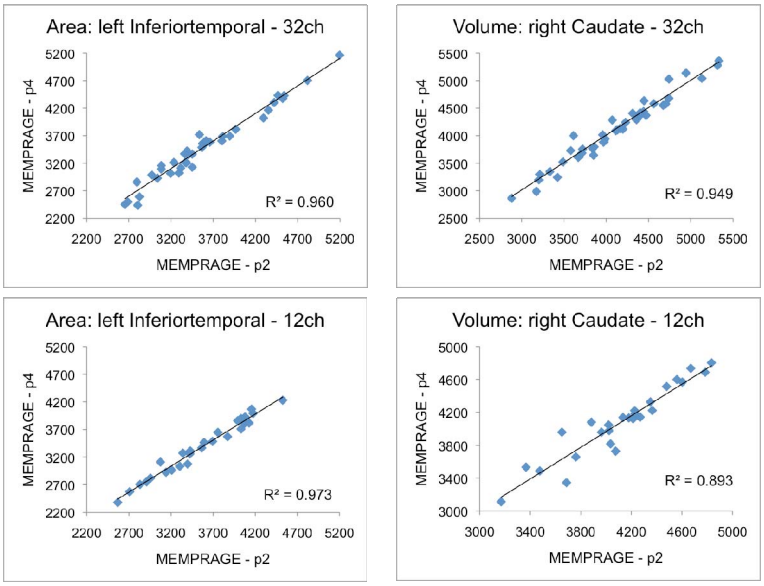

Figure 1: Left Inferiortemporal cortical surface area (mm^2) and right Caudate volume (mm^3) for subjects scanned with a two-fold accelerated MEMPRAGE and the rapid four-fold accelerated MEMPRAGE protocols in either the product 12- or 32-channel head coils. Linear regression data for measurements determined from the two different scans are shown.

Discussion/Conclusion: The correlation of volumes and cortical surface areas determined from data acquired using a 1 mm isotropic p2 MEMPRAGE and the rapid p4 MEMPRAGE protocols are very high, and compare with those obtained previously from standard MPRAGE[1] or unaccelerated MEMPRAGE scans.[2] Correlations are also similar to those seen for repeat scans of the rapid p4 MEMPRAGE on different days.[3] Smaller structures such as the Amygdala showed lower volume correlations, however higher measurement uncertainty for these structures is commonly observed.[1-3] Although this study did not compare the reliability of measures obtained from the 12ch and the 32ch coil on the same subject, we show that the correlation of the p2 and p4 MEMPRAGE scan results are not affected by the head coil used. Four subjects were excluded from analysis in each coil group because of failures in the automated Talaraich transformation. Talaraich failures did not favor the p2 or p4 sequence. Intra-subject correlations of the volume of all sub-cortical/white-matter structures was very high in both coils, with $R^2 \sim 0.998 - 0.999$ for all subjects. The results indicate that the rapid 2-minute MEMPRAGE protocol employing four-fold acceleration can be used in place of longer, higher-resolution MEMPRAGE scans without degradation of the quantitative morphometric results obtained.

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