Quantitative Comparison of Extremely Rapid Structural Data Acquisition Compared to Conventional MPRAGE

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Introduction: Automated MRI-derived measurements of in-vivo human brain volumes from anatomical scans can provide novel insights into normal and abnormal neuroanatomy [1], but only a few studies have probed the repeatability and effects of sequence-dependent parameters on these measurements, including scanner changes such as vendor, field strength and gradient strength [2,3], and sequence modification [3-5]. The multi-echo MPRAGE (MEMPRAGE) sequence was implemented to reduce signal distortion by acquiring at a higher bandwidth and averaging multiple echoes to recover SNR while providing additional T_2* information that can enhance cortical segmentation [4]. To ensure minimal impact on subject burden and maximal efficiency, we implemented a rapid 2-minute MEMPRAGE protocol for anatomical scans, which we later showed to yield quantitatively repeatable morphometric information across different scanners and days [6]. Here, we validate the morphometric results obtained from the rapid 2-minute scan by comparison to those from a conventional 6-minute MPRAGE scan acquired in the same session.

Methods: All measurements were made using a 3.0 T MRI scanner (MAGNETOM Trio, A Tim system, Siemens Healthcare, Erlangen, Germany), located at the MGH Martinos Center. The product 12-channel receive-only head coil was used in all cases. 22 subjects (7 female, mean age 21.7 years) were scanned; all gave written informed consent according to a protocol approved by the local IRB. Each session included a conventional T_1-weighted MPRAGE scan acquired in 5 min 29 sec (TE = 2.98 ms, TR = 2300 ms, FOV = 256 x 240 mm, 192 slices, voxel size = 1.0 mm^3, parallel imaging (PI) acceleration = 2, bandwidth = 240 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, bandwidth = 650 Hz/px). An Autoalign procedure was used to ensure reproducible slice and field-of-view positioning for each subject [7,8]. The anatomical scans were analyzed using the FreeSurfer toolkit [9]. An automated parcellation of the cortex, subcortical (without white matter) and white matter structures was performed, and the estimated Total Intracranial Volume (eTIV) was calculated [10]. Correlation plots were made for the volume of each structure independently determined from each scan.

Results: Figure 1 shows plots of Intracranial, Right Hippocampal, Left Pallidum and anterior Corpus Callosum volumes for 22 subjects scanned with the conventional MPRAGE and the rapid MEMPRAGE protocols. Similar volume determinations were made for most cortical and white matter structures in the brain. Volume correlations for key structures are summarized below, along with the correlations for repeat scans with the rapid MEMPRAGE protocol on a different set of subjects performed over two different days, from [6]:

Sequence	**MPR v MEM**		**MEM repeat**	
Structure	*Slope*	R^2	*Slope*	R^2
eTIV	0.91	0.98	1.01	0.99
L Cerebral WM	0.92	0.97	0.97	0.98
L Caudate	0.96	0.96	0.94	0.96
L Putamen	1.05	0.93	0.95	0.91
L Hippocampus	0.92	0.93	1.01	0.94
L Amygdala	0.88	0.76	0.93	0.81
R Cerebral WM	0.91	0.98	0.98	0.98
R Caudate	0.90	0.87	0.97	0.93
R Putamen	0.97	0.95	0.96	0.91
R Hippocampus	1.01	0.95	0.98	0.97
R Amygdala	1.05	0.72	0.83	0.74
CC Posterior	0.99	0.95	1.02	0.98
CC Anterior	1.01	0.97	0.95	0.96

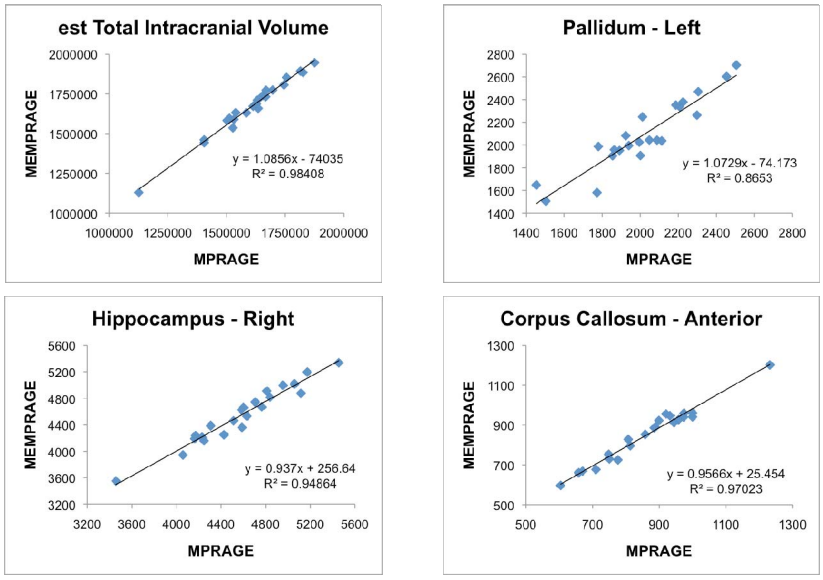

Figure 1: Intracranial (eTIV), Right Hippocampal, Left Pallidum and anterior Corpus Callosum volumes (in mm^3) for 22 subjects scanned with a 5 min 29 sec conventional MPRAGE and the rapid 2 min 12 sec MEMPRAGE protocols. Linear regression data for volume measurements determined from the two different scans are shown.

Discussion: The correlation of volumes determined from data acquired using the conventional 6-minute single-acquisition MPRAGE and the rapid 2-minute MEMPRAGE protocols are very high, and compare with those obtained previously from standard MPRAGE or multi-echo FLASH scans [3], unaccelerated MEMPRAGE scans [4] or 1-mm resolution 6-minute MEMPRAGE scans [5]. Correlations are also similar to those seen for repeat scans of the 2-minute MEMPRAGE on different days and on different scanners [6]. R^2 values above 0.9 are observed for most structures, with values very close to 1.0 for large structures, despite the fact the two scans employ different bandwidths and the MEMPRAGE sequence has a reduced influence from susceptibility-induced gradients. Smaller structures such as the Amygdala and Pallidum showed lower volume correlations, with $R^2 \sim 0.75 - 0.9$, however higher measurement uncertainty for these structures is commonly observed [3,5,6]. The results indicate that the rapid 2-minute MEMPRAGE protocol employing 4-fold acceleration, and benefiting from reduced distortion and improved contrast with the addition of T_2* data can be used in place of conventional longer MPRAGE scans without degradation of the quantitative morphometric results obtained.

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