Accelerated MP2RAGE Imaging Using Sparse Iterative Reconstruction

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Introduction:

MP2RAGE[1] is a T1 imaging method that greatly reduces the B1 bias field as well as T2* and PD contrast compared to standard MPRAGE acquisitions and has the additional advantage to generate T1 maps from the obtained MP2RAGE contrast. To this end, two FLASH images are sampled after inversion, resulting in a prolonged TR and thus long total acquisition times (~8min using GRAPPA x3[2]). For clinical use, examinations of this duration are difficult to conduct. We thus propose to apply sparse iterative reconstruction[3] on MP2RAGE images to reduce the required acquisition time. Results are benchmarked calculating contrast figures for the different acceleration factors as well as assessing the undersampling effects on an automated brain morphometry algorithm.

Materials & Methods:

After obtaining written consent, a fully sampled MP2RAGE (TR 5s, TI_1/TI_2 0.7s/2.5s, flip angles 4 and 5 degrees, resolution 1mm isotropic, acq. matrix 256x240x176, TA=20mn) of one healthy volunteer was acquired at 3T (MAGNETOM Skyra, Siemens Healthcare, Germany) using a 20-channel head/neck coil. Artificial undersampling was performed using a variable-density Cartesian spiral phyllotaxis pattern[4] with different acceleration factors from 1 to 16. The reconstruction of the images from undersampled data was computed by iteratively minimizing the following cost function enforcing both consistency with acquired data and sparsity in the wavelet domain:

$$\min_X \sum_{i=1,2} \left\| PF\{S_c X_i\} - Y_i \right\|_2^2 + \lambda \left| \Psi X_i \right|_1 .$$

with P being the sampling mask, F the discrete Fourier transform, S_c complex coil sensitivities computed with ESPIRiT[5], Y the undersampled k-space, λ a regularization parameter and Ψ the wavelet-transform.

Both the MP2RAGE uniform contrast and the T1 map of the fully sampled dataset were reconstructed and served as ground truth for comparing the obtained undersampling results. Furthermore, the Morphobox prototype[6] was applied on the fully sampled uniform image to obtain six masks of structures of interest for further analysis, namely: thalamus, caudate, putamen, hippocampus, global white matter and global grey matter.

The artificially undersampled datasets were reconstructed using the procedure shown above, obtaining uniform contrasts from which T1 maps were subsequently calculated following [1]. After a first qualitative evaluation, contrast ratios (CR), contrast-to-noise ratios (CNR), root-mean-square difference (RMSD) as well as T1 map differences were quantitatively assessed in the six brain structures defined above. CR and CNR were computed using the definition given by Okubo's comparison of MPRAGE and MP2RAGE[7].

Results and Discussion:

Figure 1 shows reconstructed slices, relative difference to the fully sampled conventional reconstruction and RMSD with increasing acceleration factor R (R = 2.19, 5.23, 7.90). It can be seen that with higher R, edges smooth out and that anatomical information is lost in some structures, e.g. in the caudate or putamen. Similarly, the RMSD is increasing with rising R. Changes in volume estimates of the structures of interest over the different Rs are shown in Figure 2. To note, white-matter estimates considerably drop with R>4. CR and CNR figures, however, remain stable as can be seen in Figure 3. CNR shows a slight increase for R>5 which is probably due to the iterative denoising. T1 maps show that average T1 values remain stable in all structures of interest; in some structures, however, standard deviations increase to up to 10%.

Conclusion:
The application of sparse iterative reconstruction on undersampled MP2RAGE acquisitions allows obtaining images with only minor quality and CNR degradation for a not too high R. Increased blurring might however impede visual reading with higher acceleration factors. Our preliminary data suggests that acceleration factors up to 5.2, corresponding to an acquisition time of 3.8 min, are feasible with acceptable quality penalty. Notably, the iterative reconstruction proposed here has not yet used the redundancy in the two inversion contrasts as proposed by Berkin et al.[8]; exploiting these, further improvements in image reconstruction quality may be feasible.

References:
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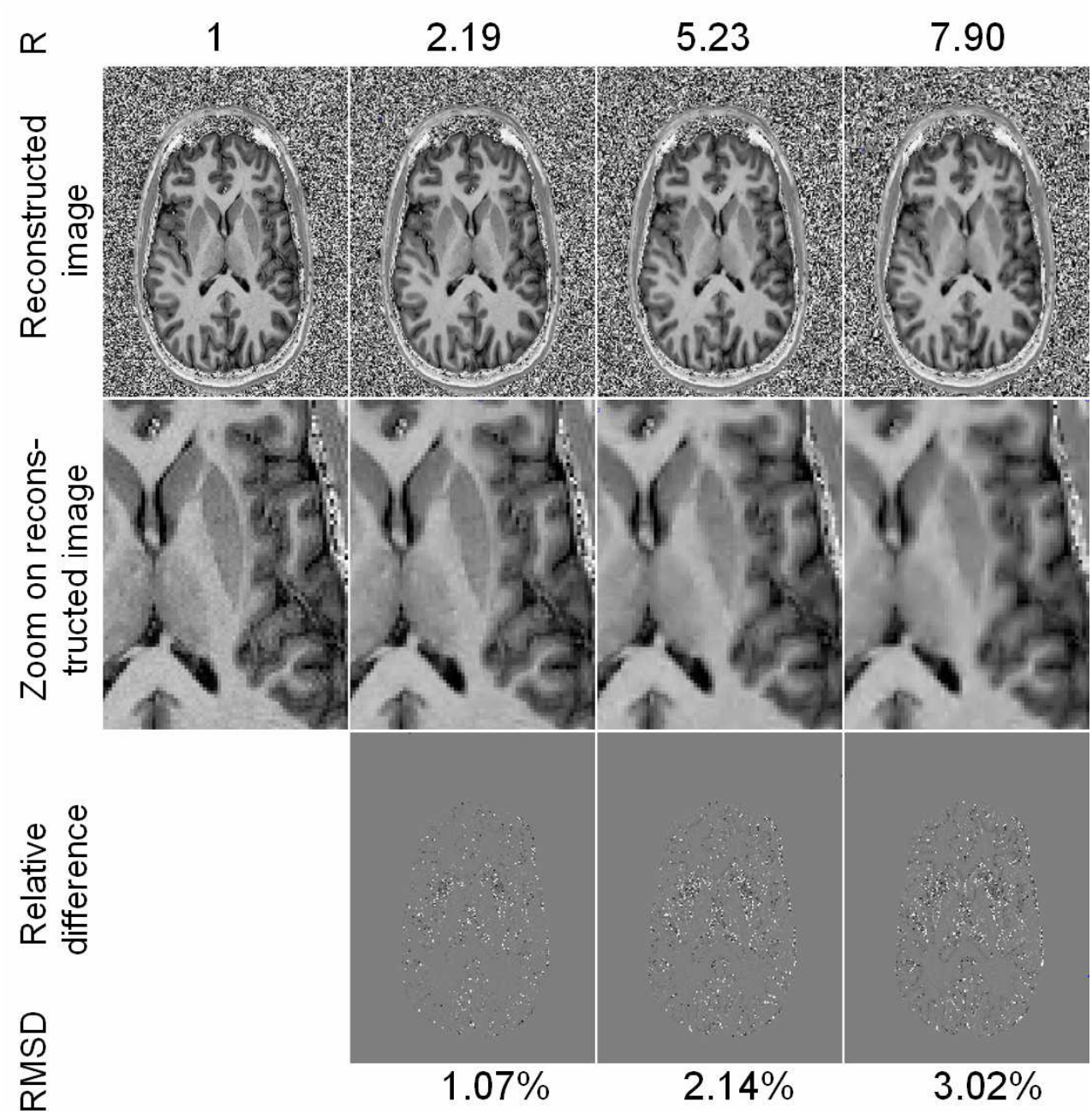

***Figure 1**: MP2RAGE image (R=1) and slice reconstruction of MP2RAGE images at different acceleration factors.*

Undersampling Factor	1	2.19	5.23	6.05	7.90	10.11
White matter	876.7±54.4	883.4±47.7	883.3±48.6	883.3±47.9	883.6±48.0	883.4±48.6
Gray matter	1499.7±182.2	1488.1±165.4	1483.5±159.6	1481.8±156.9	1480.4±154.8	1478.2±152.5
Putamen	1229.9±131.6	1227.3±115.3	1225.8±115.0	1224.3±111.9	1223.6±110.8	1222.4±109.3
Caudate	1321.2±109.5	1313.4±94.8	1313.2±95.7	1311.9±95.5	1311.8±94.3	1310.9±94.6
Hippocampus	1548.9±306.9	1536.3±287.5	1537.3±284.7	1534.6±280.5	1535.7±281.5	1536.12±277.3
Thalamus	1108.2±114.3	1113.6±102.5	1113.5±103.1	1113.2±102.2	1113.2±100.5	1113.3±99.7

***Table 1:** T1 values [ms] obtained using the fully sampled MP2RAGE image (R = 1) and undersampled images with different undersampling factors.*

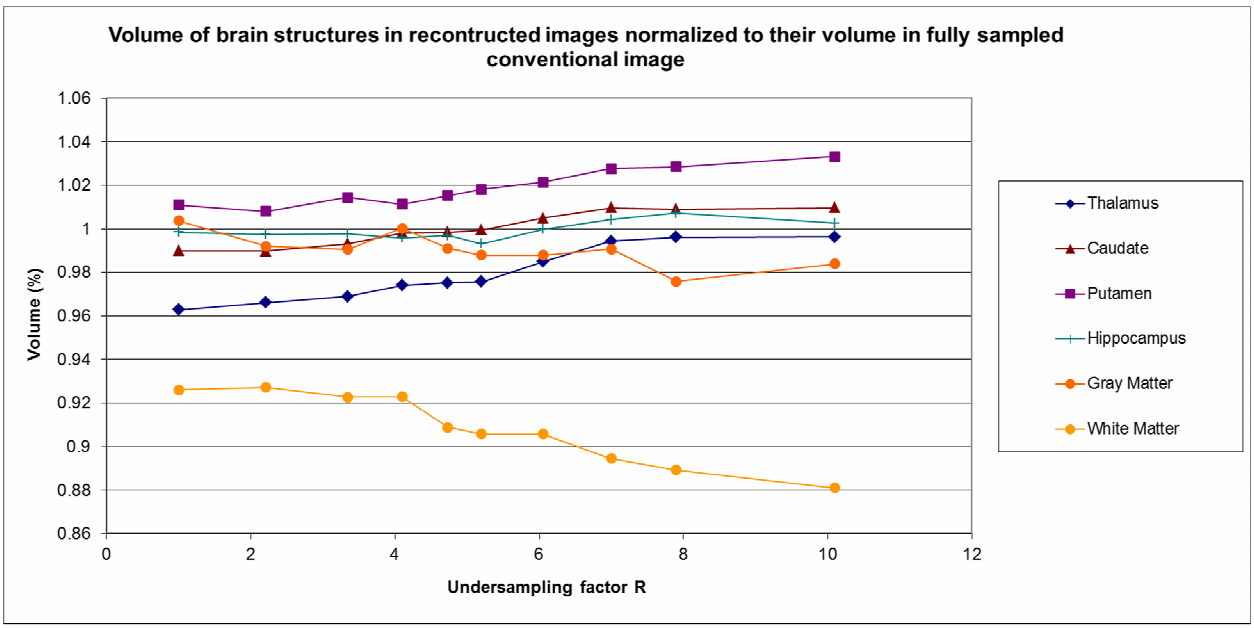

Figure 2: *Volume of selected brain regions obtained by the Morphobox segmentation as a function of undersampling factor normalised to the respective volumes from the conventional MP2RAGE image.*

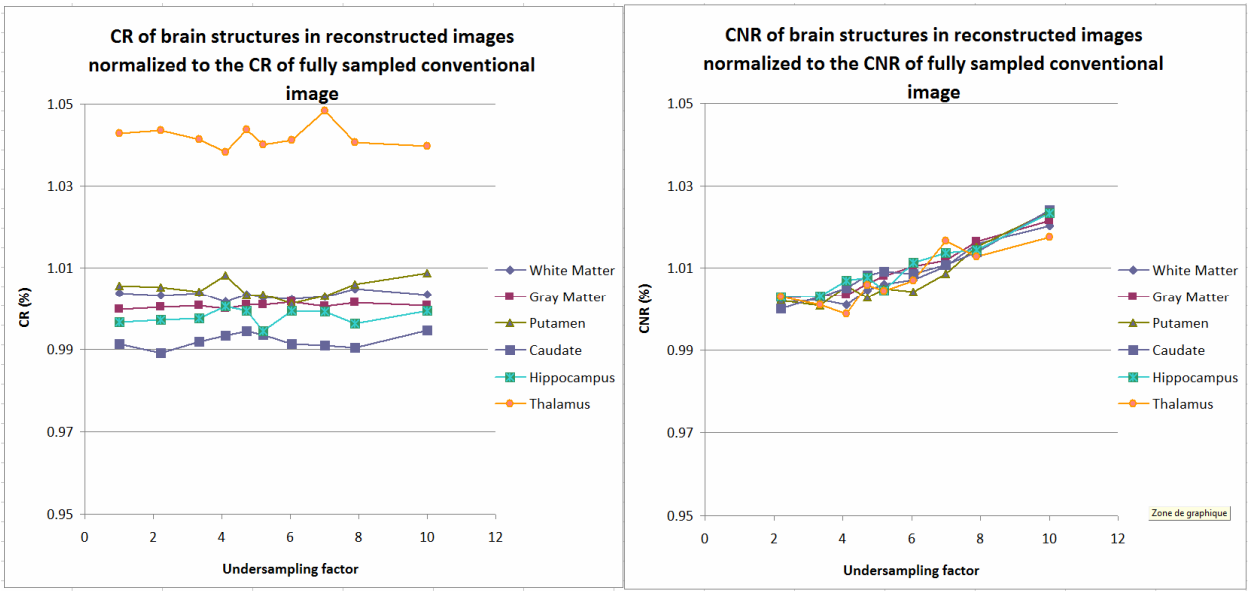

Figure 3: *Relative contrast ratios and contrast to noise ratios of brain structures of interest in reconstructed images with different undersampling factors compared to contrast ratios and contrast to noise ratios in the fully sampled conventional MP2RAGE image.*

Synopsis: MP2RAGE is a T1 imaging method providing greatly reduced B1 bias as well as less T2* and PD-contributions. It requires, however, long acquisition time (standard protocol with GRAPPAx3: ~8min) which hampers its clinical application. This work proposes to use sparse iterative reconstruction techniques to shorten MP2RAGE acquisition times. Resulting images are benchmarked using contrast assessment, changes in obtained T1 values as well as evaluating the effect of undersampling on an automated brain morphometry algorithm. Acceptable penalty in image quality and morphometric outcome was achieved with up to 5-fold acceleration, yielding a measurement time of 3.8min compared to fully sampled 20min.