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Shuffled Magnetization-Prepared Multicontrast Rapid Gradient-Echo Imaging

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Abstract

Purpose—To develop a novel acquisition and reconstruction method for magnetization-prepared 3-dimensional multicontrast rapid gradient-echo imaging, using Hankel matrix completion in combination with compressed sensing and parallel imaging.

Methods—A random k-space shuffling strategy was implemented in simulation and in vivo human experiments at 7 T for 3-dimensional inversion recovery, T_2 /diffusion preparation, and magnetization transfer imaging. We combined compressed sensing, based on total variation and spatial-temporal low-rank regularizations, and parallel imaging with pixel-wise Hankel matrix completion, allowing the reconstruction of tens of multicontrast 3-dimensional images from 3- or 6-min scans.

Results—The simulation result showed that the proposed method can reconstruct signal-recovery curves in each voxel and was robust for typical in vivo signal-to-noise ratio with 16-times acceleration. In vivo studies achieved 4 to 24 times accelerations for inversion recovery, T_2 /diffusion preparation, and magnetization transfer imaging. Furthermore, the contrast was improved by resolving pixel-wise signal-recovery curves after magnetization preparation.

Conclusions—The proposed method can improve acquisition efficiencies for magnetization-prepared MRI and tens of multicontrast 3-dimensional images could be recovered from a single scan. Furthermore, it was robust against noise, applicable for recovering multi-exponential signals, and did not require any previous knowledge of model parameters.

Keywords

shuffled k-space; magnetization-prepared rapid gradient echo; MP-RAGE; high field; Hankel matrix; inversion recovery; T_2 /diffusion preparation; magnetization transfer

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Additional Supporting Information may be found in the online version of this article.

Supporting Methods: Supporting methods include subsections on (i) adiabatic inversion, T_2 /diffusion, and MT preparation pulses; (ii) bias field correction; (iii) reconstruction algorithm; and (iv) reconstruction problem in MT imaging.

Supporting Discussion: Supporting discussion provides a detailed summary of previous Hankel matrix completion studies in comparison with the present study.

Correction added after online publication 15 November 2017. The author updated their Supporting Information file to correct the symbols appearing in their equations and to update reference 25. References 27 and 28 were also removed.

INTRODUCTION

The contrast available with gradient-echo (GRE) MRI acquisitions can be increased by “preparing” the longitudinal magnetization using a magnetization-preparation pulse module. For example, the well-known magnetization-prepared rapid gradient-echo (MP-RAGE) sequence uses an initial inversion radiofrequency (RF) pulse with a delay time to achieve T_1 weighting or a 90° - 180° - 90° -driven equilibrium RF pulse for T_2 weighting (1,2). The T_1 -weighted MP-RAGE is one of the most commonly used sequences for anatomical brain imaging, because of its high contrast between gray and white matter. The T_2 -weighted MP-RAGE has been widely applied in functional MRI (3,4), MR angiography (5), cardiac imaging (6), and quantitative T_2 mapping (7,8). Several other contrast mechanisms, including $T_{1\rho}$, magnetization transfer (MT), and arterial spin labeling, also rely on the use of magnetization-preparation pulses. However, magnetization-preparation pulses perturb the steady state of the acquisition sequence (e.g., spoiled GRE in this study) (9,10), leading to relatively inefficient data acquisition.

Several recent studies demonstrated the rapid acquisition and reconstruction of tens to hundreds of MR images with varied contrasts (11–17). Specifically, a method called “ T_2 shuffling” has exploited the sparse representation of signals for reconstructing multicontrast images, in which a four-atom dictionary was used to approximate T_2 decays in combination with a local (spatial-temporal) low-rank regularization (12). Another approach exploited the linear predictability of the magnetization relaxation (i.e., the exponential decay) through structured matrix completion (15,16). For example, a Hankel matrix completion together with a global (spatial-temporal) low-rank regularization has been successfully applied for the acceleration of T_2 mapping (16). Other studies have shown that inversion-recovery MRI signals naturally can be reconstructed through iterative fitting using an exponential function (14) or by Hankel matrix completion (15). Furthermore, the Hankel matrix completion could be combined with other constrained reconstructions such as compressed sensing (18) and parallel imaging (19).

In this study, we extended the application of Hankel matrix completion to MP 3-dimensional (3D) multicontrast rapid GRE imaging, in which the signal recovery (e.g., T_1 relaxation) was modeled as a sum of exponentials. We also combined this technique with compressed sensing, based on total variation (18) and spatial-temporal low-rank regularizations (12,16,20), and parallel imaging (via ESPIRiT (19)). Our method was based on a standard Cartesian k-space acquisition, with a minor change to the standard MP-RAGE sequence of shuffling the phase-encode ordering (12). The feasibility of the proposed method was demonstrated for inversion recovery, T_2 /diffusion preparation, and MT imaging in simulation and in vivo human experiments at 7 T.

METHODS

Magnetization-Prepared Rapid GRE Sequence

As shown in Figure 1a, the 3D spoiled GRE is segmented by magnetization-preparation pulses, and multiple k_x and k_y phase encodings are acquired per each magnetization-preparation pulse (i.e., the Look-Locker method) (21). The sequence was modified from a

standard inversion recovery sequence with segmented rapid GRE (EFGRE3D, compiler version DV23, GE Healthcare, Waukesha, WI, USA). Adiabatic pulses, which are highly tolerant to B_1 inhomogeneity at 7 T, were used for three magnetization preparation experiments (as detailed in the Supporting Methods).

In this sequence, the major contrast is prepared in M_z and the acquired MR signal is a function of preparation weighting, T_1 , and imaging parameters of the host GRE sequence (21). Specifically, each preparation pulse attenuates the steady state of longitudinal magnetization $M_{z-ss- prep}^-$ by a factor of E_{prep} as given by

$$M_z^+(0) = E_{prep} M_{z-ss- prep}^- \quad [1]$$

where E_{prep} is the efficiency of inversion RF pulse, T_2 weighting factor $e^{-\frac{TE}{T_2}}$, diffusion weighting factor e^{-bD} , or MT weighting factor, depending on the type of magnetization-preparation pulse; and $M_z^+(0)$ is the longitudinal magnetization after the preparation pulse. Then, the longitudinal magnetization of the host GRE sequence $M_z^+(k)$, with $k = 1$ to L as the index of repetition time (TR) in each GRE segment, can be derived as (21)

$$M_z^+(k) = E_{prep} M_{z-ss- prep}^- (\cos\alpha)^k e^{-\frac{TR \cdot k}{T_1}} + \frac{M_0 \left(1 - e^{-\frac{TR}{T_1}}\right) \left[1 - (\cos\alpha)^k e^{-\frac{TR}{T_1}}\right]}{1 - \cos\alpha \cdot e^{-\frac{TR}{T_1}}} \quad [2]$$

where α is the flip angle (FA) of excitation in the host GRE sequence, and M_0 is the equilibrium magnetization. Furthermore, using the steady-state magnetization for GRE

without a preparation pulse, i.e., $M_{z-ss- noprep} := \frac{M_0 \left(1 - e^{-\frac{TR}{T_1}}\right)}{1 - \cos\alpha \cdot e^{-\frac{TR}{T_1}}}$, Equation [2] can be rewritten as

$$M_z^+(k) = M_{z-ss- noprep} - \left(M_{z-ss- noprep} - E_{prep} M_{z-ss- prep}^-\right) (\cos\alpha \cdot e^{-\frac{TR}{T_1}})^k. \quad [3]$$

Finally, the subtraction of MRI images or raw k-space data from two scans with and without preparation pulse (an MP scan and a GRE reference scan), i.e.,

$\left[M_z^+(k) - M_{z-ss- noprep}\right] \sin\alpha$, provides an exponential decay curve for one T_1 component (and one FA) or a linear combination of exponential decays for multiple T_1 components. Note that Equation [3] ignored the influence of MT effects of the excitation pulse and stimulated echoes. More comprehensive modeling/simulation (22,23) could be used in further studies.

Shuffled Cartesian k-Space Encoding

To resolve the signal-recovery curve for each image pixel, a shuffled phase-encode ordering (12) was incorporated with the aforementioned MP-RAGE sequence in this study. A

uniformly distributed random-ordered phase-encoding table for k_x and k_y was used. The k_z dimension was frequency encoding and was fully sampled. Figure 1b shows that the prospectively shuffled phase encoding caused all of the signal-recovery times (RTs) to be mixed in a random order across a full k-space acquisition. After reordering, the k-space was divided into 8 to 32 undersampled segments for specific RTs and undersampling factors of 4 to 24. In each GRE segment, 128 or 256 TRs of the host GRE sequence (GRE-TRs) were acquired, with every 4, 8 or 32 GRE-TRs associated with one specific RT. In the in vivo inversion-recovery retrospective experiment, eight GRE segments were acquired to cover the full k-space with 32 GRE-TRs per segment (i.e., a total of 256 GRE-TRs in one cycle), and 440 cycles during the whole experiment; in the in vivo inversion-recovery prospective experiment, 32 GRE segments were acquired with eight GRE-TRs per segment (i.e., a total of 256 GRE-TRs in one cycle), and 64 cycles during the whole experiment; in the T_2 preparation experiment, 32 GRE segments were acquired with four GRE-TRs per segment (i.e., a total of 128 GRE-TRs in one cycle), and 128 cycles in the whole experiment.

Pixel-wise Hankel Matrix Completion in Combination With Compressed Sensing and Parallel Imaging

The proposed method solves the reconstruction problem for a series of undersampled Cartesian k-space subsets with a known exponential relaxation model (in Eq. [3]). The reconstruction problem can generally be written as

$$\underset{\mathbf{x}}{\operatorname{argmin}} \sum_{t=1}^{N_T+1} \sum_{c=1}^{N_C} \|\mathbf{M}_t \mathbf{F} \mathbf{S}_c \mathbf{B} \mathbf{D}_t \mathbf{x} - \mathbf{D}_t' \mathbf{y}\|_2^2 + \lambda_1 \sum_{i=1}^{N_P} \|h(\mathbf{R}_i \mathbf{Q} \mathbf{x})\|_* + \lambda_2 \|\mathbf{x}\|_{\text{TV}} + \lambda_3 \sum_{b=1}^{N_B} \|\mathbf{C}_b \mathbf{x}\|_* \quad [4]$$

The first term is a least-squares formulation that ensured the estimated MP image $\mathbf{x}$ (dimensions: x-y-RT, $\mathbf{x} = M_z^+ \sin \alpha$ in Eqs. [2] and [3]) to be consistent with the acquired k-space data $\mathbf{y}$ (dimensions: kx-ky-coil-RT). The k-space data are formed as $\mathbf{y} = \operatorname{vec}(\mathbf{K}_m \parallel \mathbf{K}_r)$, with $\mathbf{K}_m$ for the MP k-space and $\mathbf{K}_r$ for the reference k-space, $\parallel$ for concatenation along the RT dimension, and $\operatorname{vec}(\cdot)$ for vectorization. Similarly, each image is formed as the concatenation of two vectors $\mathbf{x} = \mathbf{x}_m \parallel \mathbf{x}_r$, in which $\mathbf{x}_m$ denotes the MP images and $\mathbf{x}_r$ the reference image. This fidelity term performs the evaluation and summation for each RT t and for each coil element c . N_T is the number of RTs, and N_C is the number of coils. $\mathbf{D}_t$ selects an image at t , and $\mathbf{D}_t'$ selects the corresponding k-space data at t . When $t = 1$ to N_T , $\mathbf{D}_t$ and $\mathbf{D}_t'$ select the MP image and k-space; when $t = N_T + 1$, they pick up the reference image and k-space. Other matrices/linear operators are Fourier transform operator $\mathbf{F}$, ESIPRiT coil sensitivity maps as diagonal matrices $\mathbf{S}_c$ for $c = 1$ to N_C (19), and coil bias field as a diagonal matrix $\mathbf{B}$ (24) (as detailed in the Supporting Methods). The diagonal matrix $\mathbf{M}_t$ masks the MP k-space when $t = 1$ to N_T , and becomes an identity matrix for the reference k-space (which is fully sampled) when $t = N_T + 1$.

The second term in Equation [4] is the sum of nuclear norms for the pixel-wise Hankel matrices $\sum_{i=1}^{N_P} \|h(\mathbf{R}_i \mathbf{Q} \mathbf{x})\|_*$, where N_P is the number of pixels, $\|\cdot\|_*$ is the nuclear norm,

$\mathcal{H}(\cdot)$ is the Hankel matrix formation (25), $\mathbf{R}_i$ is an operator that selects the recovery time course for a pixel i from the data $\mathbf{Q} \mathbf{x}$, and $\mathbf{Q} = (\mathbf{D}_1 - \mathbf{D}_{N_T+1})$
 $\|\mathbf{D}_2 - \mathbf{D}_{N_T+1}\| \cdots \|(\mathbf{D}_{N_T} - \mathbf{D}_{N_T+1})\|$ is an linear operator that performs the subtraction of MP image $\mathbf{D}_i \mathbf{x}$ with the reference image $\mathbf{D}_{N_T+1} \mathbf{x}$ for every RT $t = 1 \dots N_T$ and every pixel (as shown in Fig. 1c). Such subtraction in $\mathbf{Q}$ ensures the Hankel matrix for the pixel-wise time course to be rank- r for r T_1 components; otherwise, without this operator, the rank of Hankel matrix for the time course is $r+1$ due to a constant reference term as explained in Equation [3]. However, the subtraction operator $\mathbf{Q}$ is not used in the MT experiment, and the Hankel matrix regularization term without $\mathbf{Q}$ encourages the multi-exponential “decay” curve in each pixel.

The third term is a total variation penalty $\|\mathbf{x}\|_{TV}$, which applies the finite differences as a sparsity transform for a L_1 -norm (26). The total variation penalty was applied spatially for the in vivo inversion recovery and T_2 /diffusion preparation experiments.

The last term is the sum of nuclear norms for matrices containing reshaped images or image patches (as shown in Supporting Fig. S1) (i.e., the global/local spatial-temporal low-rank regularization) (20). This term is written as $\sum_{b=1}^{N_B} \|\mathbf{C}_b \mathbf{x}\|_*$, where $\mathbf{C}_b$ is an operator that selects and reshapes a spatial-temporal block containing signal-recovery curves of its spatial neighbors (as shown in Supporting Fig. S1) (20), and N_B is the number of blocks. For simulation, in vivo inversion recovery, and T_2 /diffusion-preparation experiments, only global low-rank regularization (16) was used (i.e., $N_B = 1$), which was empirically found to reduce the spatial variation in images compared with the local low-rank regularization.

The reconstruction was solved by alternating direction method of multipliers algorithm (27,28) in BART software (<https://github.com/mrirecon/bart>) (details are described in the Supporting Methods). λ_1 , λ_2 , and λ_3 are parameters in association with the aforementioned regularizations. These regularization parameters were empirically chosen, attempting to reduce the undersampling artifacts while avoiding insufficient or excessive smoothing of the data as a result of under- or overregularization. Increasing the penalty (as controlled by the regularization parameter λ_1) on the Hankel low-rank term encouraged exponential curve shape along the RT dimension, and allowed using fewer exponential components. Increasing the optional penalty on the total variation term, λ_2 , promoted spatial smoothness. Increasing the penalty on the spatial low-rank term, λ_3 , improved spatial-dynamic consistency (i.e., along the x/y and RT dimensions). However, all three regularizations may cause oversmoothing of the data, and therefore should be adjusted for each experiment.

Proximal Operator for Pixel-Wise Hankel Matrix Completion—A modified hard-thresholding (29,30) on singular values of pixel-wise Hankel matrix is used as the proximal operator (27,28), in which the rank of Hankel matrix is not fixed but is determined by the threshold level τ , as follows:

$$s_{\tau 1}[h(\mathbf{v}_i)] = \mathbf{U}_i \sum_{\tau 1, i} \mathbf{V}_i^*, \text{ where } \sum_{\tau 1, i}(\mathbf{j}, \mathbf{j}) := \begin{cases} \sum_i(\mathbf{j}, \mathbf{j}) & \sum_i(\mathbf{j}, \mathbf{j}) \geq \tau 1 \\ 0 & \sum_i(\mathbf{j}, \mathbf{j}) < \tau 1 \end{cases}. \quad [5]$$

where $\mathbf{U}_i$, $\mathbf{\Sigma}_i$, and $\mathbf{V}_i^*$ are from singular value decompositions of Hankel matrix $h(\mathbf{v}_i)$ ($\mathbf{v}_i = \mathbf{R}_i \mathbf{Q} \mathbf{x}$ in Eq. [4] or $\mathbf{R}_i \mathbf{x}$ in Eq. [S1]), and $\mathbf{\Sigma}_{\tau 1; i}$ is a diagonal matrix with singular values after the hard-thresholding.

Proximal Operator for Spatial-Temporal Low-Rank Regularization—The proposed double threshold can be described as the concatenation (symbol “||”) of two data matrices along the RT dimension:

$$\begin{aligned} s_{\tau 2(1), \tau 2(2)}(\mathbf{C}_b \mathbf{x}) &= \mathbf{U}_b \sum_{\tau 2(1), b} \mathbf{V}_{1, b} || \mathbf{U}_b \sum_{\tau 2(2), b} \mathbf{V}_{2, b}, \text{ where } \sum_{\tau 2(\cdot), b}(\mathbf{j}, \mathbf{j}) \\ &= \max \left[0, \sum_b(\mathbf{j}, \mathbf{j}) - \tau 2(\cdot) \right] \text{ and } \mathbf{V}_b^* \\ &= \mathbf{V}_{1, b} || \mathbf{V}_{2, b}. \end{aligned} \quad [6]$$

where $\mathbf{U}_b$, $\mathbf{\Sigma}_b$, and $\mathbf{V}_b^*$ are from the singular value decompositions of the image block $\mathbf{C}_b \mathbf{x}$, and $\mathbf{\Sigma}_{\tau 2(1), b}$ and $\mathbf{\Sigma}_{\tau 2(2), b}$ are the diagonal matrices with singular values after soft-thresholding with two threshold levels $\tau 2(1)$ and $\tau 2(2)$ (and $\tau 2(1) > \tau 2(2)$). In addition, $\mathbf{V}_b^*$ contains recovery time courses, and is separated into $\mathbf{V}_{1, b}$ and $\mathbf{V}_{2, b}$, where $\mathbf{V}_{1, b}$ contains the recovery time-course segments of early RTs that are associated with the high threshold level, and $\mathbf{V}_{2, b}$ contains those of the remaining RTs that are associated with the low threshold level (as shown in Supporting Fig. S1). For the T_2 /diffusion experiment, only a single, soft threshold was used (i.e., $\tau 2 = \tau 2(1) = \tau 2(2)$).

Experimental Design

Simulation Experiment—The proposed reconstruction was first tested on simulated individual raw images of 32 receive elements without and with $\pm 10\%$ noise relative to the max signal level at the steady state, resulting in a maximum SNR of 17.3 before coil combination (details are explained in the Supporting Methods).

Human Brain Inversion Recovery Experiments—A retrospective acceleration experiment was performed on a 7T whole-body MRI scanner (GE Healthcare, Waukesha, WI, USA) with a 32-channel head coil (NOVA Medical, Houston, TX, USA) in a healthy volunteer. Three-dimensional inversion recovery GRE images were acquired with the following parameters: echo time (TE)/TR = 1.4/4.6 ms, readout bandwidth = ± 31.25 kHz, matrix size = $172 \times 220 \times 64$, field of view = $220 \times 220 \times 128$ mm³, number of excitations = 1, FA = 8°, and RTs (from 104 to 1587 ms with a step size of 347 ms for every 32 GRE-TRs). All eight 3D images were fully sampled, and the total scan time was 20 min. Only 64 points were sampled on one phase-encoding dimension to reduce scan time, resulting in a resolution of $1.3 \times 1 \times 2$ mm³. During simulation of acceleration, the frequency-encoding

dimension (along which 220 points were sampled) and the aforementioned phase-encoding dimension (the one with 64 points sampled) were swapped to mimic a phase-encoding table of 172×220 points. In addition, the last RT datum was considered as the reference image in the simulation.

A prospective acceleration experiment was performed on the same 7T MRI in one subject who received tumor resection and radiotherapy 5 years ago. Three-dimensional inversion recovery and reference GRE images were acquired with the following parameters: echo time/TR = 2.0/5.9 ms, readout bandwidth = ± 31.25 kHz, matrix size = $128 \times 128 \times 128$, field of view = $220 \times 220 \times 192$ mm³, number of excitations = 1, FA = 8°, and 32 RTs (from 23 to 1432 ms with a step size of 45.5 ms for every eight GRE-TRs). All 32 3D images were reconstructed from one inversion-recovery scan and one GRE reference scan, so the overall acceleration factor was 16. The total scan time was 3 min.

Human Brain T₂/Diffusion-Preparation Experiment—Three-dimensional T₂/diffusion-prepared images were acquired from one healthy volunteer on the same 7T MRI scanner with an acceleration factor of 24. The total scan time was 6 min. The T₂-prepared and reference GRE images were acquired with the following parameters: echo time/TR = 2.0/5.9 ms, $\delta/\tau = 15/36$ ms, readout bandwidth = ± 62.5 kHz, matrix size = $128 \times 128 \times 128$, field of view = $220 \times 220 \times 192$ mm³, number of excitations = 1, FA = 5°, and 32 RTs (from 12 to 739 ms with a step size of 23.5 ms for every four GRE-TRs). For diffusion weighting, two b-values were used, and they were $b_1 = 577$ and $b_2 = 1011$ s/mm², and the images with T₂ preparation but without diffusion weighting were labeled as b_0 . Apparent diffusion coefficient (ADC) maps with different RTs were calculated as $ADC_n = \ln[(S_{b_2, n}/S_{b_2, 32}) / (S_{b_0, n}/S_{b_0, 32})] / (b_2 - b_0)$, where $S_{b_0, n}$ and $S_{b_2, n}$ are signal intensities without and with diffusion weighting for the N th RT, and were normalized by the final RT ($N = 32$).

RESULTS

Simulation Experiments

As shown in Figure 2 and Supporting Figures S2 and S3, the signal intensity and contrast of the accelerated images were comparable with those obtained from the full k-space ground truth. The differences were mostly found on the edges. Pixel-wise signal-recovery curves were resolved for different tissue types. The proposed Hankel matrix completion also showed apparent denoising effects on the signal-recovery curves that contained the added $\pm 10\%$ white noise. The artifact-to-noise ratio (i.e., amplitude of error/standard deviation of background noise) was estimated to be 21. These observations suggest that the proposed reconstruction method was robust against noise.

As shown in Figure 3, retrospective acceleration based on in vivo fully sampled images showed that the proposed method preserved the contrast of the inversion-recovery images in general, and also provided improved reconstruction performance compared with only parallel imaging and compressed sensing (i.e., PI + TV).

Prospective Human Brain Inversion Recovery Experiment

The in vivo results confirmed the capability of this method for recovering multicontrast images and pixel-wise signal-recovery curves. In Figure 4 and Supporting Figure S4, the nulling time for white matter was found to be 300 ms, and the nulling time for gray matter was 400 ms. The images with RTs from 400 to 600 ms were mostly white matter enhanced with apparent T_1 weighting. At the end of the GRE segment, gray matter and white matter had both reached their steady states.

Prospective Human Brain T_2 /Diffusion-Preparation Experiment

In Figure 5 and Supporting Figure S5, T_2 /diffusion weighting at early RTs was resolved. The T_2 /diffusion contrast (e.g., the bright cerebrospinal fluid signal) vanished with increasing RT, demonstrating how resolving the signal recovery can highlight the preparation contrast. Slight contrast loss in T_2 /diffusion-weighted images was observed in the frontal region adjacent to the nasal cavity and temporal lobe. This artifact was likely caused by the B_0 inhomogeneity, and could be resolved by increasing the bandwidth of preparation pulse.

Prospective Human Brain MT Experiment

In Supporting Figure S6, the proposed method is shown to resolve signal recovery and magnetization exchange between macromolecule proton pool and free water pool following a magnetization-preparation pulse.

Comparison of Experiments With/Without Resolving Signal-Recovery Curves

Figure 7a shows severe blurring in the lumped images (reconstructed from all RTs, first column). Such blurring was improved significantly just by using a subset of RT data (Fig. 7a, second column), but there were still residual blurring artifacts even when using a compressed sensing and parallel-imaging reconstruction. The signal recovery-resolved images provided the best contrast with minimal artifacts (Fig. 7a, third column). In Supporting Figure S7c, the simulation shows the increase of effective T_1 blurring with the length of GRE segment, suggesting the need for high acceleration as demonstrated in this study. In Figure 7b, the diffusion contrast, which was prepared in M_z by the diffusion-preparation pulse, vanished with the increase of RT, demonstrating the need to resolve the T_1 -recovery time courses to get an unbiased ADC measurement.

DISCUSSION

Magnetization Preparation and Multicontrast MP-RAGE

This study demonstrated a shuffled 3D MP-RAGE method with whole-brain coverage and rapid acquisition, in which parallel imaging, compressed sensing, and pixel-wise Hankel matrix completion were used together to generate multicontrast images from a single scan. The simulation experiment demonstrated the robustness of the proposed method for a SNR as low as 17.3 in the tested raw images. The in vivo experiments further confirmed the capability of this method for prospective accelerations, recovering tens of multicontrast images in each MP rapid scan. More importantly, the proposed method could improve the contrast of images in vivo by reducing the T_1 blurring artifacts in images, and was able to

resolve the signal-recovery curve in each image pixel. We chose to segment the in vivo data into 8 to 32 segments, to allow sufficient k-space coverage for each segment. If the coverage was insufficient, the method may lose intrinsic sensitivity to differentiate different recovery curves and suffer from spatial blurring. Nevertheless, the reconstruction that exploited exponential recovery signal model was valid for any choice of number of segments. Under certain sampling strategies, such as repeatedly sampling center k-space, one potentially can reconstruct segments with a fewer number of TRs. It is also possible to increase number of segments iteratively until each segment has only one TR (i.e., a pyramidal reconstruction as demonstrated by others (15,31)). Furthermore, this method could be extended to many other imaging applications including myocardial T_1 mapping (32,33) and brain myelin water mapping (8).

In this study, the diffusion-prepared GRE images were acquired at a relatively high spatial resolution (i.e., $1.7 \times 1.7 \times 1.5 \text{ mm}^3/\text{pixel}$). The diffusion-weighted contrast was found to vanish with the increase of RT. Meanwhile, the T_2 and diffusion weighting also attenuated the steady-state signal level (i.e., at the last RT). Therefore, instead of measuring the signal level of one RT like conventional MP-RAGE, measuring the ratio of the signal level of the first RT to that at the last RT, as in Equation [1] in this study, is a more robust way to quantify T_2 and diffusion weightings in magnetization-preparation experiments (6,8,34,35).

In Supporting Figure S6, the proposed reconstruction yielded MT ratios that increased and then decreased with the increase of RT. This is likely due to the magnetization exchange between macromolecule proton pool and free water pool after MT preparation (36,37). The largest MT ratios in white matter was observed at 168 ms. The reconstruction of non-mono-exponential time courses demonstrated the applicability of the proposed method for measuring signal recoveries that deviate from a mono-exponential function.

Shuffled k-Space and Pixel-Wise Hankel Matrix Completion

The combined use of parallel imaging, compressed sensing, and pixel-wise Hankel matrix completion improves acquisition efficiency, as shown by the reconstruction of tens of multicontrast 3D images from a single 3- or 6-min MRI scan. The novelty of the proposed reconstruction method lies in two aspects. First, it does not need prior knowledge on the model parameters (e.g., T_1 values or dictionary of the relaxation curves). Second, it is applicable for multi-exponential signal-recovery curve reconstruction. A detailed summary of previous Hankel matrix completion studies, in comparison with the present study, can be found in the Supporting Discussion.

The proposed method, based on the Look-Locker method, is sensitive to B_1 inhomogeneity from the transmit coil (21). However, the B_1 transmission field can be effectively characterized by a separated B_1 mapping scan (38), and the resulting B_1 map can be used to correct for the B_1 inhomogeneity from the transmit coil using Equation [3]. Another potential solution for decoupling B_1 transmission inhomogeneity with signal-recovery measurement is randomizing the excitation FAs and solving the Bloch equation during reconstruction (i.e., via dictionary matching in MR fingerprinting (39)), and iteratively performing the MR fingerprinting under the compressed-sensing framework as shown by Davies et al. (40).

CONCLUSIONS

In conclusion, the proposed method can improve acquisition efficiencies for magnetization-preparation experiments, and tens of multicontrast 3D images could be recovered from a single scan. We demonstrated this method with several preparation modules, including inversion recovery, T_2 -diffusion and MT, acquired in 3-or 6-min scans. Contrast of the reconstructed images was enhanced, and the signal-recovery curve in each pixel was resolved. More importantly, the proposed reconstruction scheme was robust against noise, applicable for multi-exponential signal, and did not depend on prior knowledge of model parameters.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

Acknowledgments

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FIG. 1.

a: Sequence used in this study was a modified magnetization-preparation sequence with a segmented GRE acquisition. **b:** All data are sampled during the signal recovery. The shuffled phase encoding (in k_x and k_y dimensions) caused the data with different RTs to be mixed in a random order in k -space. **c:** The simplified reconstruction illustration shows the pixel-wise Hankel matrix completion. The Hankel matrix completion encouraged exponential relaxation curves in each pixel. In the inversion recovery and T_2 /diffusion-preparation experiments, the reference signal was subtracted from the signal-recovery curve.

FIG. 2.

Simulated inversion recovery data with $\pm 10\%$ noise (top). The images with 32 RTs (for the shuffled MP-RAGE data, 18 of 32 RTs are shown) were reconstructed with the proposed method (16-fold acceleration for 32 times undersampled MP-RAGE data and a full-k-space reference) (i.e., PI + TV + spatial-temporal low-rank regularization + Hankel matrix completion (bottom)). The images obtained with the proposed method were similar to the full k-space ground truth, and the major differences were mostly near the image edges.

Comparison with conventional parallel imaging and compressed-sensing reconstruction and difference maps for the proposed method can be found in Supporting Figure S2.

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FIG. 3.

Simulation based on fully sampled MPnRAGE data in vivo. The MPnRAGE data were retrospectively separated into eight undersampled k-space data sets with different RTs (top left, 4 of 8 RTs are shown). The k-space sampling patterns followed a uniform distribution. Images were reconstructed with parallel imaging and total variation regularization (PI + TV, top right, four-fold acceleration) or with the proposed method (i.e., PI + TV + spatial-temporal low-rank regularization + Hankel matrix completion) (bottom left, four-fold acceleration for 8 times undersampled MP-RAGE data and a full-k-space reference). The

images obtained with the proposed method were similar to the full k-space ground truth, and the major differences were mostly observed at initial RTs (bottom right).

FIG. 4.

Three-dimensional inversion-recovery images at multiple RTs in a subject at 5 years after tumor resection and radiotherapy. Nine of 32 RTs are shown. The acceleration factor was 16, jointly achieved by compressed sensing, parallel imaging, and Hankel matrix completion.

FIG. 5.

Three-dimensional T_2 -prepared images with 32 RTs in a healthy volunteer. Six of 32 RTs are shown, and diffusion-prepared images are shown in Figure 6. All images were jointly reconstructed from the T_2 -/diffusion-prepared data and one reference data. The acceleration factor was 24, jointly achieved by compressed sensing, parallel imaging, and Hankel matrix completion. Note that the T_2 contrasts vanished with RT, suggesting that resolving the signal recovery can enhance contrast (shown in Fig. 7b).

FIG. 6.

Three-dimensional diffusion-prepared images with 32 RTs in a healthy volunteer. Six of 32 RTs are shown, and T_2 -prepared images (i.e., b_0) are shown in Figure 5. All images were jointly reconstructed from the T_2 -diffusion-prepared data and one reference data. The acceleration factor was 24, jointly achieved by compressed sensing, parallel imaging, and Hankel matrix completion. Note that the diffusion contrasts vanished with RT, suggesting that resolving the signal recovery can enhance contrast (shown in Fig. 7b).

FIG. 7.

Resolving the signal recovery with the proposed method can improve image resolution and contrast. **a:** When the signal recovery was not resolved, there was blurring in the reconstructed images (the first column), as shown in the inversion recovery and T_2 -preparation experiments. To improve contrast, images were reconstructed from a subset of the RT data, shown here with parallel imaging and total variation regularization at acceleration factors of 3 and 4 for up and down plots, respectively (PI + TV, the second column), but there were still residual artifacts. These blurring artifacts were effectively eliminated by the proposed

method (PI + TV + spatial-temporal low-rank regularization + Hankel matrix completion, the third column) with 8 and 16 acceleration factors for up and down plots, respectively (i.e., 16 and 32 RTs resolved). **b:** Apparent diffusion coefficient maps at different RTs. The diffusion contrast vanished and the ADC decreased with the increase of RT, demonstrating the need to resolve the signal-recovery curves in diffusion-prepared imaging.