Fast MRI for repeated scans

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Abstract. Radiological assessment of brain disease progression and response to therapy is often performed with repeated MRI scans acquired every few weeks/months. In these longitudinal studies, each scan is acquired anew without taking into account the information present in previous scans. However, many image regions remain unchanged from one time point to the next, making the difference image between the time points sparse. We present a new algorithm that speeds up the MR acquisition process of the repeated scan by using the data acquired in the baseline scan of the same patient. Our method uses the baseline scan to identify regions of interest in the repeated scan. These regions are partially acquired, followed by reconstruction process that speeds up the entire scanning procedure. Our experimental study on 16 pairs of baseline/follow-up MR scans shows that the image quality of the MR scans produced by our method with a speedup factor of up to 3.5 are within the imaging variability of the scanner.

1 Introduction

Radiological assessment of brain disease progression and response to therapy is often performed with repeated MRI scans acquired every few weeks/months [1, 2]. The MR scanning protocol consists of several pulse sequences, resulting in various imaging contrasts such as T1 and T2 weighted images. At each time point, an entire, multi-sequence scan is acquired anew without taking into account the information present in the previous scans. However, many image regions remain unchanged from one time point to the next. This results in unnecessarily long scanning times. Our hypothesis is that the difference between the current scan and the previous scan data can be sparse, and the previous scan can be advantageously used to speed up the scanning time of a repeated scan with minimal compromise of the image quality.

During the scan acquisition, the MR signals are stored in a spatial frequency domain called *k-space* [3]. The speed at which the k-space values can be acquired is inherently limited by the required image contrast, resolution and coverage, the properties of human tissues, hardware limitations, and safety issues [4]. The demand for multi-sequence MRI under these fundamental speed limits has given rise to plethora of methods for MRI speed-up.

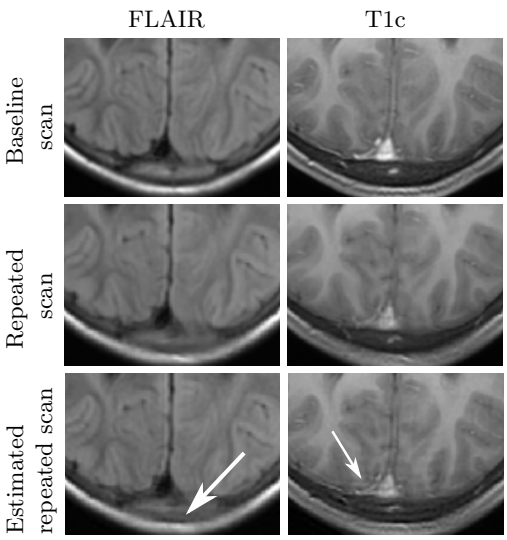

Fig. 1: FLAIR (left) and contrast-enhanced T1 (right) full-time scanning baseline (top) and repeat (middle) slices are presented vs. fast acquired one (bottom), with a speed-up factor of 3.5. Note that the images are very similar with the exception of very small artifacts, indicated by the arrows. The reconstruction quality of contrast-enhanced T1 (T1c) images falls below that of FLAIR images, due to changes in contrast agent injection rate between baseline and repeated scans.

Methods for speeding-up MR acquisition with existing hardware are mostly based of partial k-space acquisition. This approach consists of selectively sampling the k-space followed by the estimation the missing k-space samples using a prior knowledge on the image. Keyhole methods update data in the center of the k-space more frequently than in other parts, thus providing high temporal resolution but lower spatial resolution [3]. Methods for fast dynamic MRI use the previous image frames in the time-series to complete the missing k-space values [5, 6]. However, these methods compromise the spatial coverage and/or spatial image resolution.

In Compressed sensing (CS) MRI [7, 8], the basic premise is that MRI can be sparsely represented in a transform domain, thereby requiring only a subset of the k-space for reconstruction. The sparsity of MRI in different transform domains has been used by others for various applications. For example, Bilgic et al. [9] exploit the fact that certain characteristics of the scanned object do not change across pulse sequences. They propose a reconstruction algorithm that relies on Bayesian compressed sensing to jointly reconstruct a set of images from under-sampled k-space data.

One concept that has not been previously researched is the use of the patient's baseline scan to speed up the acquisition of his/her repeated scan. In many clinical diagnostic applications, patients are longitudinally scanned to determine pathology changes between time points and to evaluate treatment efficacy. In most cases, there is substantial similarity between the baseline and the repeated scans. The changes usually occur in a confined region around the tumor or pathology, while the rest of the image remains the same. Consequently, the data from the baseline scan can be advantageously used to speed up the scanning time of a repeated scan without compromising image quality. Fig. 1 shows representative results of our method.

In this paper we present a new method to effectively exploit the data from the baseline scan to reduce the acquisition time of the repeated scan. The main contributions of this paper are: 1) the use of baseline scan data for repeated scan acquisition speed-up; 2) no compromise on image quality in clinically important regions; and 3) experimental results obtained from 16 MR clinical brain show reliable reconstruction results with speedup factor of 3.5 or less. To the best of our knowledge, this is the first attempt to speed-up an MR scan with the same patient's baseline scan.

2 Method

The inputs to our method are the baseline brain scan of the patient, consisting of two or more MRI pulse sequences with several contrasts, such as T1-weighted and T2-weighted, and a single pulse sequence from a repeated scan. The outputs are the remaining imaging contrasts of the repeated scan, acquired in fast acquisition mode. In the following, we assume for simplicity that: 1) the same MR pulse sequences are acquired in the baseline and repeated scans; 2) all the pulse sequences have same number of slices, denoted by N_s; 3) the k-space is sampled with Cartesian sampling trajectories; 4) the differences between scans of the same patient are mainly due to pathological changes and; 5) the acquisition of the repeated scan is spatially matched to the baseline scan. We discuss the validity of these assumptions later, in Section 4.

The method consists of two step. First, we use the first sequence in the repeated scan to detect the changes from the baseline scan so that slices with significant changes will be acquired in full-time mode. Second, we acquire slices that are similar to their corresponding ones in the baseline scan in fast acquisition mode, thus speeding up the entire scanning process.

2.1 Detection of slices for fast acquisition

This step automatically detects slices with significant changes based on the baseline scan and the first imaging contrast of the repeated scan. We compare the slices with the following measure. The difference between two corresponding s_i-th slices of these pulse sequences is defined as:

$$I_{diff}(s_i) = I_f(s_i) - I_b(s_i) \tag{1}$$

where I_b and I_f are the corresponding baseline and repeated matching imaging contrasts.

We focus on the outliers of $I_{diff}(s_i)$ to define a measure of difference between the scans. In the literature we find many approaches for outliers detection, such as Chauvenet's criterion and Grubbs' test. For simplicity, we use the interquartile range method [10] to identify and reject outliers from data. The outliers in $I_{diff}(s_i)$ are the voxels $O = \{o_1, ..., o_N\}$.

We then perform a connected components analysis on O to obtain $L = \{l_1, ..., l_K\}$ regions of outliers. Regions with less than N_v voxels are automatically rejected and considered to be spatially isolated outliers. For the remaining

regions, $I_b(s_i)$ and $I_f(s_i)$, we model the grey-level distribution of pathologies with a Gamma distribution with parameters k and θ [11]. Since there is no closed form for the parameter's Maximum Likelihood Estimation, we use the approximation in [12]:

$$\hat{k} = \frac{a_0 + a_1 Q + a_2 Q^2}{Q(b_0 + b_1 Q + Q^2)} \tag{2}$$

$$\hat{\theta} = \frac{1}{k \cdot N_{l_j}} \sum_{i=1}^{N_{l_j}} x_i; \tag{3}$$

where $X = \{x_i\}_{i=1}^{N_{l_j}}$ are the outliers of group l_j, Q is :

$$Q = ln(\frac{1}{N_{l_j}} \sum_{i=1}^{N_{l_j}} x_i) - \frac{1}{N_{l_j}} \sum_{i=1}^{N_{l_j}} ln(x_i) \tag{4}$$

and a_i, b_i are as defined in [12]. We estimate these values for both the baseline and the repeated scans imaging contrasts, since we model change as either progression or regression of the pathology.

As was observed by Prastawa et al. [11] the closer the distribution of the outliers group is to the Gamma distribution, the higher the probability that its slice contains changes in pathology. Therefore, to identify outliers that represent pathology changes, we measure the distance of every group of voxels from Gamma distribution defined by the estimated parameters of the group with the KL-distance [13]. The difference measure for slice is the sum of the measurements of different regions in the slice.

This results in a measure of difference between a previously acquired slice and its corresponding repeated scan slice. Slices are then sorted by this measure, and the N_{full} most different slices will be fully scanned in the remaining pulse sequences to avoid compromising image contrast in them. The remaining slices, $G_s^{fast} = s_1, ..., s_{Nfast}$, will be scanned in a fast scanning procedure. The user-defined parameter N_{full} defines the trade-off between the fast acquisition and the number of slices acquired slices in full image scan mode.

2.2 Fast acquisition of selected slices

The input to this step is a list of slices to be acquired in the fast acquisition mode. For these slices, the k-space lines are randomly sampled with variable density, so that the sampling density is higher near the k-space origin. The missing k-space lines are taken directly from the baseline scan.

Specifically, let $S_i^p(k_m)$ and $S_i^r(k_m)$ be the k-spaces of i-th slice of the baseline and the repeated scans, and let m the index of the phase encode line number k_m. Let C be the set of random sampled k-space lines and let N_k be the number of items in C. The estimation of the k-space for the slices rapidly acquired is:

$$\hat{S}_i^r(k_m) = \begin{cases} S_i^r(k_m) \; k_m \in C \\ S_i^p(k_m) \text{ otherwise} \end{cases} \tag{5}$$

for $i \in G_s^{fast}$. The inverse Fourier transform of $\hat{S}_i^r$ is the estimated i-th image slice. The estimated repeated scan, $\hat{I}_f$, consists of N_{full} full-time acquired slices and N_{fast} estimated slices.

2.3 Speed-up factor computation

We compute the speedup of our method at the pulse sequence level, where we assume that the acquisition of a single line in the k-space takes the same time for all pulse sequence types. Let N_l be the number of k-space lines required for Nyquist rate acquisition. We define the speedup factor by the time required to acquire a pulse sequence at Nyquist rate, which is the number of slices, N_s, times N_l, divided by the acquisition time of the new method. This value consists of the number of full-time acquires slice, N_{full} times N_l, plus the number of fast-acquired slices, N_{fast} times the number of k-space lines acquired with the proposed method, N_k:

$$F = \frac{N_s \cdot N_l}{N_{full} \cdot N_l + N_{fast} \cdot N_k} \tag{6}$$

For example, with typical values of $N_s = 40, N_l = 320, N_{full} = 7$, $N_k = 43$, our method can acquire a scan 3.5 times faster than sampling at Nyquist rate.

3 Experimental Results

We conducted a retrospective quantitative evaluation of our method with clinical MRI datasets. Experiments involved six patients, three of them with Optic Pathway Gliomas (OPG) and three with Glioblatoma Multiforme (GBM). Each patient was scanned with a 1.5T General Electric MRI system, with a multi-sequence protocol at intervals of several months at the Tel-Aviv Medical Center, Israel. In total, 16 pairs of scans were acquired. Each scan consisted of T2-weighted, contrast-enhanced T1 (T1c), and FLAIR images. Each dataset has $512 \times 512 \times 38$ voxels with voxel size of $0.5mm \times 0.5mm \times 5.0mm$.

Studies have shown that T2-weighted images are most sensitive for detecting brain pathology [14]. Therefore, we set this image contrast to be fully acquired with no speed-up in the repeated scan. The acquisitions of the remaining imaging contrasts, T1c and FLAIR were accelerated with our method.

The k-space samples of the scans were generated synthetically from images obtained at the Nyquist rate by applying an inverse Fourier transform. We set the minimum number of outlier voxels in a group to $N_v = 100$ and the number of slices to be fully scanned to $N_{full} = 10$. The parameters $N_s = 38$ and $N_l = 512$ are explicitly derived from the dimensions of the data. In our experiments, data intensity values were normalized to the range of $[0, 1]$ to compensate for grey-level variations between time-points. Experiments were performed with the original data, where no noise was added or filtered.

We performed two experiments. First, we set $N_k = 15$ to obtain a speed-up factor of method to 3.5 and visually examined the results. Fig. 1 illustrates

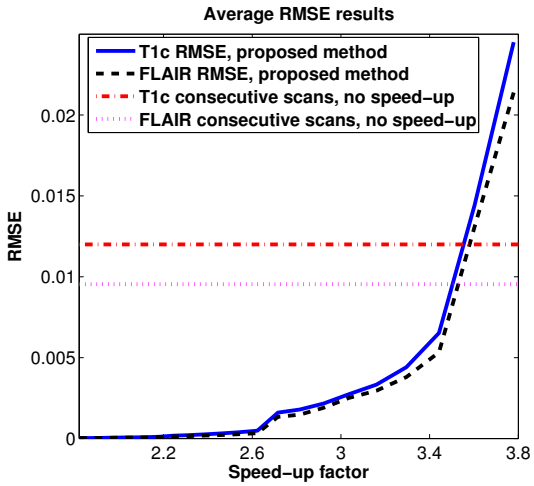

Fig. 2: Average RMSE of 16 baseline-follow-up pairs of scans for various speed-up factors. The horizontal lines are the RMSE values between two scans with no radiological changes.

the resulting images. Note that the images are very similar to each other, with the exception of very small artifacts which arise from misregistration errors and grey-level differences between the baseline and repeated scans.

In the second experiment, we examined values of N_k in the range of 2 and 200, (corresponding to speed-up factors in the range of 1.8 and 3.7), and quantitatively evaluated the performance of the method as a function of the speed-up factor in terms of root mean square error (RMSE) vs. full-time scanning at Nyquist rate. The RMSE is defined as:

$$RMSE = \sqrt{\frac{\sum_j (I_f(j) - \hat{I}_f(j))^2}{\sum_j (I_f(j))^2}} \tag{7}$$

where j is the spatial slice index.

To provide a RMSE reference value, we additionally computed the RMSE between a different set of 16 pairs of registered scans acquired at Nyquist rate of patients who exhibited no radiological changes between scans. The average RMSE values measure the variability between two scans of the same patient in which there are no actual changes between scans. The resulting values, shown as the red and pink horizontal lines in Fig. 2, are $RMSE_v^{T1c} = 1.2 \times 10^{-2}$ for the contrast-enhanced T1, and $RMSE_v^{FLAIR} = 9.5 \times 10^{-3}$ for the FLAIR.

Fig. 2 shows the tradeoff between the speed-up factor and the RMSE. The horizontal lines show the reference RSME values described above. We observe that for a speed-up factor of up to 3.5 the RMSE values are within the variability of the scanner. Our method's performance is higher for the FLAIR images than for the T1c images because the grey-level values of the T1c images are highly depend on the contrast agent injection rate during acquisition, which may vary between scans. As a result, the k-space values of the T1c baseline scan used to estimate part of the repeated scan's k-space of this image produce some imaging

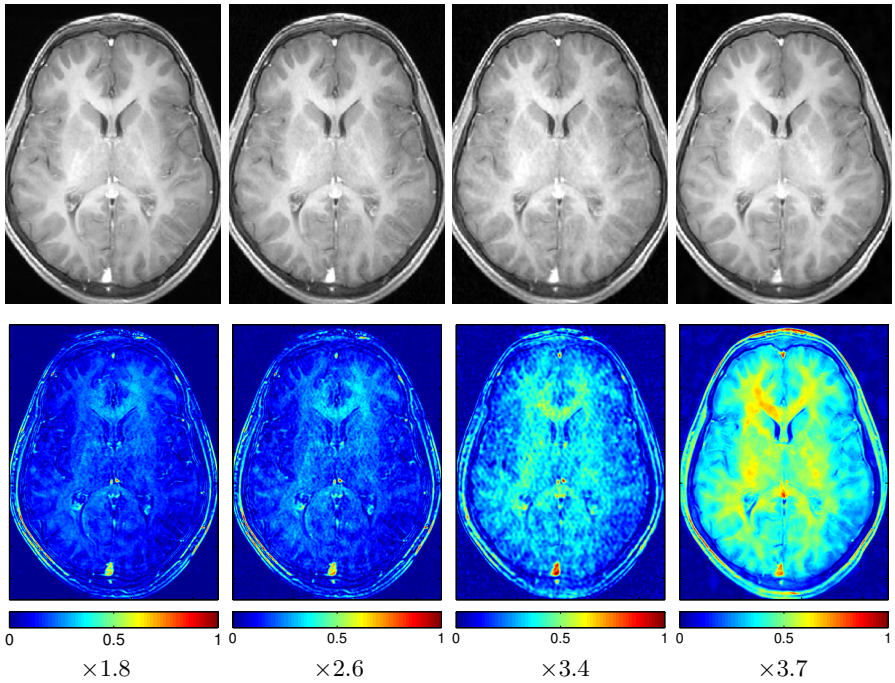

Fig. 3: Reconstruction results (top) and absolute difference images vs. full-time scanned image (bottom) of T1c representative image, for speed-up factors of (left to right): 1.8, 2.6, 3.4 and 3.77. The color bars at the bottom represent the grey level percentage estimation error divided by 100.

artifacts, despite the normalization performed in our experiments. Fig. 3 shows reconstruction results of T1c for representative speed-up factors.

4 Discussion and Conclusions

We have described a new method for MR acquisition speed-up of a repeated brain scan. Our method finds the most similar slices between the baseline scan and the repeated scan and speeds-up their acquisition in the repeated scan. Our results show that a speedup of up to 3.5 is achievable within the imaging scanner variability. To the best of our knowledge, this is the first attempt to speed-up an MR scan with baseline patient scans.

We now address two practical issues regarding the implementation of the method. First, the method assumes that the baseline and repeated scans are spatially matched. This spatial matching can be obtained by reproducing the past scan's slice positions for the scan being acquired. This feature is currently offered by some MRI vendors [15].

Second, we assume that changes between baseline and repeated scans are caused due to pathology changes. However, changes may be the result of dif-

ferences in field inhomogeneity, coil properties, different scanners, different sequences, etc. In our method we normalize the grey level intensity values of the scans to match the same scale, in order to minimize the effect of external resources on the changes between the scans.

We note that in the special case of longitudinal studies, scans are in many cases acquired in the same scanning site with the same scanning protocol to minimize the effect of external parameters on the resulted clinical follow-up. This assumption, together with refined image normalization, is sufficient to avoid reconstruction artifacts which may arise due to mixing k-space samples of two scans acquired with a few months gap.

While our method may compromise on image quality to speed up the acquisition process, this compromise is limited to regions that may have lower clinical relevance, as slices with high clinical importance are fully scanned. This is in contrast to existing methods that make the compromise across the entire image.

In addition, the proposed method is independent with and complimentary to CS methods for rapid MRI and can work in conjunction with them to speed-up the acquisition. Future work includes speeding-up additional pulse sequences and implementing our method on a real MR scanner.

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