

Aggregated Motion Estimation for Parallel Real-Time MRI

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Abstract

Many modern applications of magnetic resonance imaging (MRI) require high temporal and spatial resolution. Because the data acquisition speed is fundamentally limited by physical and physiological constraints it is important to find approaches to reduce the amount of acquisitions without deteriorating the image quality. Many existing solution strategies are based on strong *a priori* assumptions about the unknown object, which often introduces undesirable bias in the image. To overcome this difficulty, we have recently introduced a novel algorithm that estimates the deformation between nearby frames and incorporates this information into the reconstruction process. Our method is not restricted to affine or rigid motions, and does not need additional measurements. In the present study, we present further reconstruction results from phantom and *in vivo* cardiac measurements demonstrating the increased temporal and spatial resolution of our approach compared to state-of-the-art algorithms.

Keywords: inverse problems, parallel imaging, nonlinear inversion, aggregated sampling

1. Introduction

High temporal resolution is crucial for many real-time MRI studies of dynamic evolution processes, such as cardiovascular imaging. Achieving high acquisition speed is challenging due to hardware limitations and the risk of peripheral nerve stimulation. Many techniques and strategies have emerged to reduce the amount of acquired data without degrading the image quality. Among these efforts, a recent and important development is the adaptation of a parallel imaging concept that makes use of multiple receiver coils to acquire data simultaneously. The spatial information related to the coil elements is utilized for reducing the amount of conventional Fourier encoding. Due to serious undersampling and because the coil sensitivities are generally unknown the reconstruction problem often reduces to be ill-posed. Regularization methods have to be exploited to obtain plausible solutions, by incorporating *a priori* information about the unknown object (modeled by the proton density function) and the coil profiles (see e.g. Uecker et al 2008; Uecker et al. 2010). In (Knoll et al, 2012) total variation and total generalized variation were used as regularization functional. Such approaches reduce streaking artifacts but also fail to recover tiny details of the object. In seriously undersampled situations, regularization itself is not enough to guarantee high quality images.

To overcome these limitations, in (Li et al, 2013) a novel reconstruction method has been suggested for real-time MRI. This combines the ‘self-navigation’ idea with a nonlinear formulation to simultaneously estimate proton density and coil sensitivity profiles. As is shown there, the method produces superior visual quality images with high temporal fidelity. In this study, we shall further examine this method by comparing it with state-of-art algorithms on more challenging phantom and *in vivo* human cardiac data.

2. Theory

In this section, we will briefly review *Aggregated Motion Estimation* (AME) (Li et al, 2013), see Figure 1. It integrates non-parametric motion correction into the recently developed nonlinear reconstruction method for highly undersampled radial MRI data with multiple receiver coils of (Uecker et al, 2008; Uecker et al, 2010).

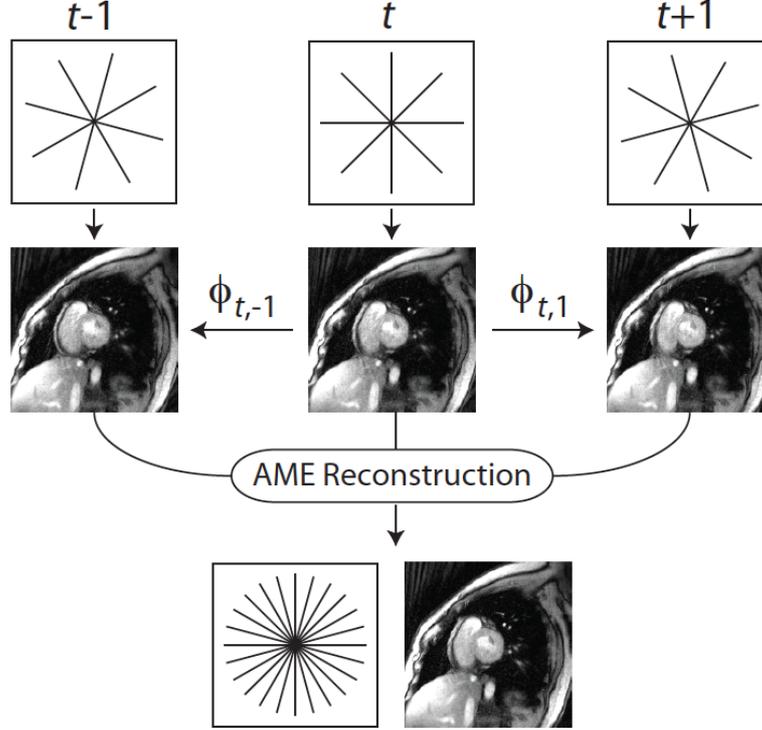


Figure 1. Flow diagram illustrating the AME nonlinear reconstruction method for reconstructing the t -th frame, with $K = \{-1, 0, 1\}$.

2.1. Parallel Real-time Magnetic Resonance Imaging

Based on its mechanism, the measurement model of parallel real-time MRI can be expressed as

$$y_{t,l} = S_t \mathbf{F}(\rho_t \bullet c_{t,l}) + \varepsilon_{t,l}, \quad l \in \Lambda := \{1, \dots, N\}. \quad (1)$$

Here ρ_t denotes the image (spin density) of t -th frame, $c_{t,l}$ the coil profiles, $\varepsilon_{t,l}$ the noise, S_t the sampling operator in k -space, and \mathbf{F} the Fourier transform. The problem is to obtain a series of proper images (ρ_t) from the measured data ($y_{t,l}$). Essentially, the number of samples (M) determines the scanning time for each frame. It follows that the choice of M is a trade-off between temporal and spatial resolution.

2.2. Aggregated Motion Estimation for Nonlinear Reconstruction

Each frame was preliminarily reconstructed by the nonlinear inversion (NLINV) method (Uecker et al, 2008; Uecker et al, 2010). Then, the motion (or deformation) between frames is estimated on these images, via the TV- L^1 optical flow model (cf. Wedel et al, 2009; Chambolle & Pock, 2011). More precisely, the motion field $u_{t,s}(x)$

from ρ_t to ρ_{t+s} is estimated by the solution of

$$\min_{u,v} \|\rho_t + \nabla \rho_t \bullet u - \rho_{t+s} + v\|_1 + \lambda \|\nabla u\|_1 + \mu \|\nabla v\|_1,$$

where v is an assistant variable modeling the changes of artifacts between images.

Let $K \subset \mathbf{Z}$ be of finite elements, such as $\{-1, 0, 1\}$, and $\Phi_{t,s}(\rho_t) = \rho_t(\bullet + u_{t,s}(\bullet))$, for $s \in K$. By variable substitution, we obtain from (1)

$$S_{t+s} \mathbf{F}(\Phi_{t,s}(\rho_t) \bullet c_{t+s,l}) = y_{t+s,l} \quad l \in \Lambda, s \in K. \quad (2)$$

Compared with (1), we see that there are $|K|$ times more samples for solving ρ_t , while preserving the same temporal resolution. As shown in Figure 1, the AME nonlinear reconstruction method (Li et al, 2013) is to solve (2) by the *iteratively regularized Gauss-Newton method* (IRGNM, Bakushinskii, 1992; Bauer et al, 2009) with proper regularizations. In detail, it comes to the following iterations:

$$h_n = \operatorname{argmin}_h \sum_s \|S_{t+s} \mathbf{F}(\Phi_{t,s}(\rho_t) \bullet h_{t+s,l}) + S_{t+s} \mathbf{F}(\Phi_{t,s}(h_0) \bullet c_{t+s,l}) - (y_{t+s,l} - S_{t+s} \mathbf{F}(\Phi_{t,s}(\rho_t) \bullet c_{t+s,l}))\|^2 \\ + \alpha_n \|\rho_t^{(n)} + h_0 - \rho_t^0\| + \alpha_n \sum_s \|a(I + b\|\cdot\|^2)^{m/2} \mathbf{F}(c_{t+s,l}^{(n)} + h_{t+s,l} - c_{t+s,l}^0)\|^2,$$

$$x_{n+1} = x_n + h_n,$$

where $x_n = (\rho_t, (c_{t+s,l}^{(n)}))^T$, $h = (h_0, (h_{t+s,l}))^T$ and the initial guess $x_0 = (\rho_t^0, (c_{t+s,l}^0))^T$.

Concerning the algorithms for solving these minimization problems in this subsection, we refer to (Li et al, 2013).

3. Reconstruction results

In this section, the AME nonlinear inversion method is evaluated on both phantom and *in vivo* human cardiac data. All MRI measurements were performed at a 3T MRI system (Siemens Magnetom TIM Trio, Erlangen, Germany). We used a radio frequency (RF)-spoiled radial FLASH (fast low angle shot) pulse sequence for data acquisition (cf. Zhang et al, 2010). As for phantom study, a 32-channel head coil (Siemens Healthcare, Erlangen, Germany) was used and the rotational speeds were controlled at angular velocities of 0.5 Hz, 1.0 Hz, and 1.5 Hz. Real-time MRI of the human heart without synchronization to the electrocardiogram and during free breathing was performed with a 32-channel cardiac coil consisting of an anterior and posterior 16-coil array.

For comparison, the NLINV method (Uecker et al, 2008; Uecker et al, 2010) was also used for reconstruction. Moreover, the NLINV method incorporating a temporal median filter with a window width corresponding to the interleaved multi-turn arrangement as post-processing would be denoted by NLINV-MED.

The comparison of these methods on phantom data with different speeds is shown in Figure 2. In the slow rotation, the image obtained by NLINV contains noticeable artifacts, which are reduced by NLINV-MED and AME as arrow indicates. In the moderate speed, the image by NLINV shows stronger streaking artifacts than the slow rotation case; the result by NLINV-MED is the worst, where the outmost hole away from rotating center (with fastest line speed) is deteriorated to a worm-like shape, as pointed by the arrow; by contrast, AME still retains the hole shape and suppresses the artifacts. In the fast rotation, the images by NLINV and NLINV-MED contain many prevailing streaking artifacts, and distorts the shape of holes; on the other hand, the result by AME keeps the shape of all three holes with few weak artifacts.

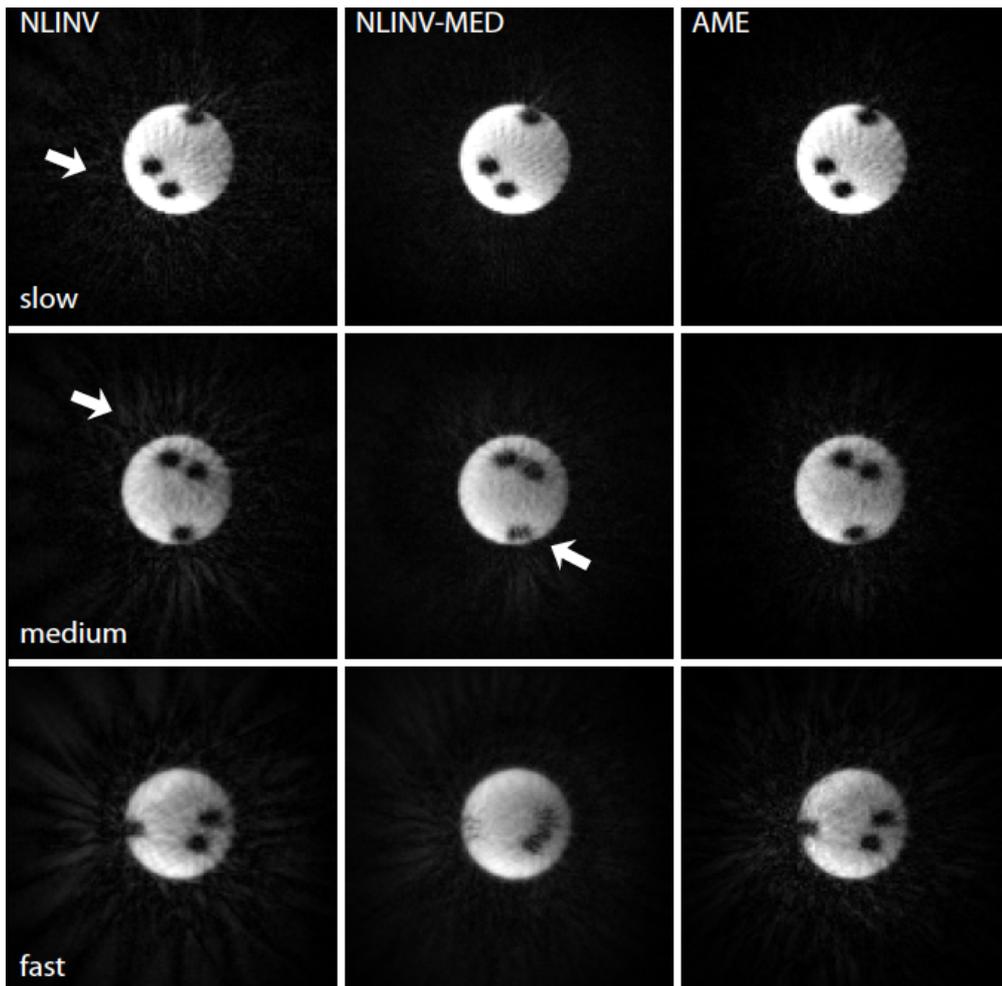


Figure 2. Reconstructions of phantom data by NLINV, NLINV-MED and AME, which are arranged from left to right correspondingly. From upper to lower, it corresponds to different rotating angular speeds of 0.5 Hz, 1.0 Hz, and 1.5 Hz.



Figure 3. Reconstruction of the human heart in a short-axis view at temporal resolutions of 10 ms and 18 ms. The upper row lists the reconstruction results of NLINV, NLINV-MED and AME with 10 ms per frame; the lower one corresponds to 18 ms.

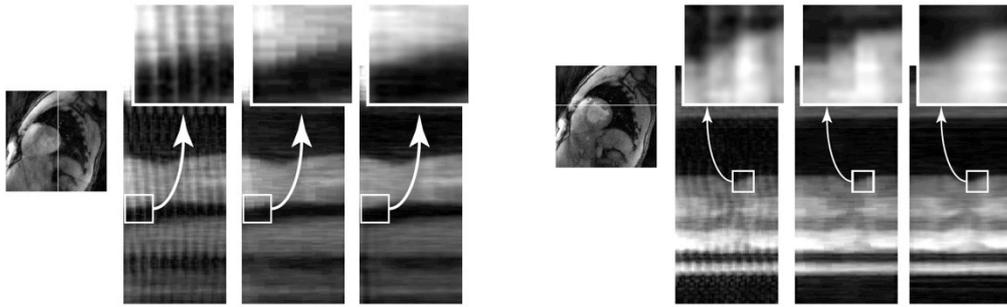


Figure 4. Temporal evolution of the marked line in human heart images in a short-axis view. The temporal resolutions of the left and right subfigures are 10 ms and 18 ms, respectively.

Figure 3 shows a short-axis view of human heart in seriously undersampled situations at temporal resolutions of 10 ms and 18 ms. We clearly see that the images by AME again presents least artifacts (upper-left) of the three. It is also worth noting that the improvement of AME is more significant at much lower sampling rate, compared with NLINV and NLINV-MED. The corresponding temporal profiles of specific lines are shown in Figure 4. The reconstruction by AME gives best temporal continuity and eliminates the scale-like artifacts, which correspond to the flickering artifacts in the sequences of images.

4. Conclusions

This work has further examined our recently proposed reconstruction method for parallel real-time MRI, showing that it offers improved image quality. Experimental results on phantom and *in vivo* human cardiac data demonstrate desirable performance in terms of temporal and spatial resolution. The present results may be even further improved by exploiting other type regularizations, such as sparsity-based ones. Such ideas will be the subject of future work.

References

- Bakushinskii, A.B. (1992). "The problem of the convergence of the iteratively regularized Gauss-Newton methods," *Computational Mathematics and Mathematical Physics*, 32(9): 1353-1359.
- Bauer, F., Hohage, T. and Munk, A. (2009). "Iteratively regularized Gauss-Newton method for nonlinear inverse problems with random noise," *SIAM Journal on Numerical Analysis*, 47(3): 1827–1846.
- Chambolle, A. and Pock, T. (2011). "A First-Order Primal-Dual Algorithm for Convex Problems with Applications to Imaging." *Journal of Mathematical Imaging and Vision* 40(1): 120-145.
- Knoll, F., Clason, C., Bredies, K., Uecker, M. and Stollberger, R. (2012). "Parallel imaging with nonlinear reconstruction using variational penalties." *Magnetic Resonance in Medicine* 67(1): 34-41.
- Li, H., Haltmeier, M., Zhang, S., Frahm, J. and Munk, A. (2013). "Aggregated motion estimation for image reconstruction in real-time MRI." arXiv: 1304.5054.
- Uecker, M., Hohage, T., Block, K.T. and Frahm, J. (2008). "Image reconstruction by regularized nonlinear inversion - Joint estimation of coil sensitivities and image content." *Magnetic Resonance in Medicine* 60(3): 674-682
- Uecker, M., Zhang, S. and Frahm, J. (2010). "Nonlinear Inverse Reconstruction for Real-Time MRI of the Human Heart Using Undersampled Radial FLASH." *Magnetic Resonance in Medicine* 63(6): 1456-1462.

Wedel, A., Pock, T., Zach, C., Bischof, H. and Cremers, D. (2009). "An Improved Algorithm for TV-L1 Optical Flow." *Statistical and Geometrical Approaches to Visual Motion Analysis*, Springer-Verlag: 23-45.

Zhang, S., Uecker, M. Voit, D., Merboldt, K.D. and Frahm, J. (2010). "Real-time cardiovascular magnetic resonance at high temporal resolution: radial FLASH with nonlinear inverse reconstruction," *Journal of Cardiovascular Magnetic Resonance*, 12: 39-45.