

High-Resolution Imaging of Myocardial Perfusion

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INTRODUCTION

Dynamic imaging of myocardial perfusion imaging after injection of a contrast agent is a major tool for noninvasive assessment of the physiological conditions of heart tissues. To make myocardial perfusion imaging more practically useful, the dynamic contrast-enhanced (DCE) images need to have high spatiotemporal resolution, which cannot be achieved by the conventional imaging method due to the slow acquisition speed of MRI. Many methods such as faster pulse sequences and reduced encoding techniques [1, 2] have been proposed to address this problem. Although as high as a factor of eight reduction in imaging time is achieved [2], in some applications (e.g., 3D real-time imaging of cardiac blood perfusion), this reduction is still not sufficient to freeze motion and provide enough spatiotemporal resolution. This paper presents a new generalized-series (GS) model-based method to provide additional improvement in spatiotemporal resolution.

PROPOSED METHOD

The proposed method decomposes the DCE image sequence $\rho(\mathbf{x}, t)$ into two components:

$$\rho(\mathbf{x}, t) = \rho_{tr}(\mathbf{x}, t) + \rho_{ss}(\mathbf{x}, t) \quad (1)$$

where $\rho_{tr}(\mathbf{x}, t)$ is the transient component containing the dynamic contrast wash-in/wash-out information, and $\rho_{ss}(\mathbf{x}, t)$ is the steady-state component containing the anatomical information. Because of the transient nature of the signal changes associated with dynamic wash-in/wash-out, $\rho_{tr}(\mathbf{x}, t)$ cannot be collected using the gating technique. The steady-state component, however, is periodic and therefore can be collected over many cardiac cycles using gating. In the proposed method, we use $\rho_{ss}(\mathbf{x}, t)$ to constrain the reconstruction of $\rho(\mathbf{x}, t)$ so that $\rho(\mathbf{x}, t)$ can be reconstructed in high resolution even with a small number of k-space encodings for each frame.

A. Data Acquisition

We collect two data sets in the proposed method. The first dataset is collected before injection of the contrast agent using gated cine pulse sequence. This dataset is used to reconstruct the steady-state component of the model, i.e., $\rho_{ss}(\mathbf{x}, p\Delta t)$ where p is the frame index and Δt is the time interval between two frames. The second dataset is collected during the dynamic wash-in/wash-out period after injection of the contrast agent. We denote this dataset as $d(\mathbf{k}_n, q\Delta t^*)$ where q is the frame index, Δt^* is usually larger than Δt , and \mathbf{k}_n are spatial frequencies corresponding to a few central k-space samples.

B. Image Reconstruction

The proposed image reconstruction algorithm consists of two key steps. (1) $\rho_{ss}(\mathbf{x}, p\Delta t)$ is interpolated along the time axis to generate a sequence of reference images $\rho_{ref}(\mathbf{x}, q\Delta t^*)$ at the time points where the DCE data are collected. (2) $\rho_{ref}(\mathbf{x}, q\Delta t^*)$ are used to reconstruct $\rho(\mathbf{x}, q\Delta t^*)$. This is done through the use of the generalized-series model [3], which represents $\rho(\mathbf{x}, q\Delta t^*)$ as

$$\rho(\mathbf{x}, q\Delta t) = \sum_{n=1}^M c_n(q)\phi_n(\mathbf{x}, q\Delta t) \quad (2)$$

where M is the model order, $c_n(q)$ are the series coefficients for the q th frame, and $\phi_n(\mathbf{x}, q\Delta t)$ are the basis functions defined as

$$\phi_n(\mathbf{x}, q\Delta t) = (|\rho_{ref}(\mathbf{x}, q\Delta t)| + \lambda) \exp(i2\pi \mathbf{k}_n \cdot \mathbf{x}) \quad (3)$$

with λ being a regularization parameter selected in the same way as in [3]. The series coefficients $c_n(q)$ are determined by fitting $\rho(\mathbf{x}, q\Delta t^*)$ to the measured dynamic data, which amounts to solving a set of simultaneous linear equations [3]. The snapshot images $\rho(\mathbf{x}, q\Delta t^*)$ are then reconstructed using Eq. (2).

RESULTS

Myocardial perfusion imaging experiments were conducted on a healthy rat using Bruker ADVANCE 4.7-T/40-cm system equipped with 12-cm/40-Gauss/cm shielded gradients. Gated cine data were first acquired using a FLASH sequence for a FOV of 5cmx5cm, $\Delta t = 20$ msec, and matrix size 256x256. Omniscan gadodiamide (Gd) was then injected into the vessel of the rat without moving the rat. Started by an R-wave trigger, the DCE data were acquired also using FLASH sequence, with the same FOV, $\Delta t^* = 58.5$ msec (or 17 frames/sec), and matrix size 8x32 (PEXRO, center k-space, reduction factor = 32). Four representative frames (1, 3, 20, and 37) are shown in Fig. 1. Zero-filled Fourier transform on the DCE dataset resulted in very blurred images, as expected. Using the same dynamic encodings, the proposed method significantly enhanced the quality of the images in terms of both the anatomical structure and the dynamic uptake of the contrast agent at various regions. Figure 2 shows the temporal variation of the intensity at three regions-of-interest (right ventricle (RV), left ventricle (LV), and LV wall, shown in the first row of Fig. 1). The anatomical signal is removed from the DCE signal, followed by a polynomial fitting in order to reveal the overall trend of the temporal variations. These curves match well with the expected order of wash-in process for these three regions.

CONCLUSION

This paper proposes a new GS model-based imaging method for high-resolution myocardial perfusion imaging. This method decouples the acquisition of the steady-state component from the transient component, making it possible to obtain high spatial and temporal resolution simultaneously. The proposed method has been validated using experimental data, which produce excellent results. This method is particularly useful for physiological imaging of a beating heart with injection of a contrast agent, where the proposed method can provide additional speedups for the existing methods to achieve 3D "real-time" imaging.

REFERENCES

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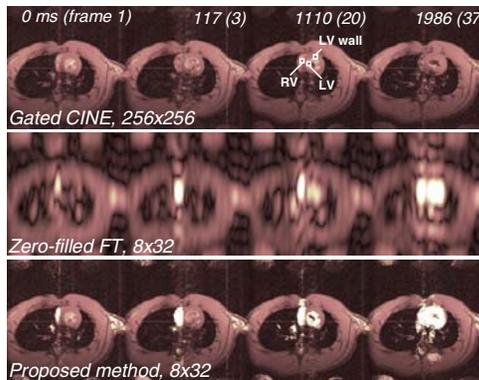


Fig. 1. Four representative frames of DCE images of a rat's heart. Note that the proposed method generates high resolution DCE images.

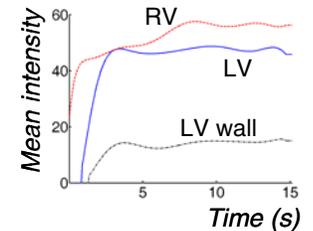


Fig. 2. Mean intensity variation of three ROIs (marked in the first row of Fig. 1) after removal of anatomical signal followed by polynomial fitting. Note that these curves match well with the expected order of wash-in process for the three ROIs.