A direct reconstruction method for blood velocity estimation from phase-contrast MRI data

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Target Audience: Researchers and practitioners interested in developing methods to improve the diagnostic accuracy of phase-contrast MRI (PC-MRI).

Purpose: In PC-MRI, blood velocity is encoded into the phase of the complex MRI images. Since the velocity has multiple directional components (v_x, v_y, v_z, and background v_b), multiple measurements with distinct encoding patterns are necessary. Also, because the parameter of interest is dynamically changing, it is important to encode at multiple time points and with high temporal frequency. Balanced four-point encoding (BFPE)[1] is a commonly used encoding strategy for three-directional PC-MRI. The standard reconstruction of the velocity components from BFPE data is based on the assumption that the velocities do not change significantly during the timespan of four consecutive measurements. A deviation from this assumption leads to both loss in temporal resolution and introduction of oscillatory artifacts. The purpose of this work is to develop and validate a new approach to deriving velocity estimates from PC-MRI data that improves temporal resolution and reduces artifacts without increasing acquisition time.

Methods: The proposed method is based on direct reconstruction (DiR), where all measurements across time are jointly processed, pixel-by-pixel. In this method, each measurement is correctly assumed to be acquired at a unique instant of time; this is a departure from the standard approach where each four consecutive measurements across time are processed together and treated as if they were acquired simultaneously.

The standard approach to velocity estimation from BFPE data can be written as: $\vec{\phi}_i = (A_{i\to i+3})^{+}\vec{\theta}_{i\to i+3}$ (Eq. 1), where $\vec{\theta}_{i\to i+3}$ represents four noisy measurements collected from time interval i to $i+3$, $A_{i\to i+3}$ is a 4×4 encoding matrix, $(\cdot)^{+}$ represents pseudo-inverse, and $\vec{\phi}_i$ represents the estimate of four phase components (three spatial and one background offset). For a total of N measurements, the process is repeated for $i = 1, 2 \ldots N-3$ to obtain phase-time profiles.

The proposed DiR method can be mathematically written as: $\vec{\phi}_{1\to N} = (B^TB + \lambda R^TR)^{-1}B^T\vec{\theta}_{1\to N}$ (Eq. 2), where $\vec{\theta}_{1\to N}$ represents all N measurements across time, B is a $N\times 4N$ underdetermined matrix that represents the forward model, R is a regularization term that provides stability to the underdetermined system of equations, λ controls the extent of regularization, and $\vec{\phi}_{1\to N}$ is a $4N\times 1$ vector that represents estimated directional phase components. Here, we selected matrix R to be a finite difference approximation to the second derivative of $\vec{\phi}$ with respect to time variable, i. Because of its more accurate formulation and ability to incorporate a priori knowledge in terms of regularization, we expect the DiR method to outperform the standard approach.

For both the methods, the estimated phases ($\vec{\phi}$) are scaled to generate velocity estimates based on the magnitude of the encoding gradients. Also, the reconstruction process, for both the methods, is repeated for all pixels.

Results: Four components of velocity (v_x, v_y, v_z, and v_b) were simulated in Matlab using Hann functions. BFPE data were generated from the velocity profiles using the forward operator B. The resulting simulated PC-MRI data were then contaminated with white Gaussian noise, and the two reconstruction methods (standard and DiR) were applied and compared. The results for v_x, v_y, and v_z are shown in Figure 1. The fourth, background component v_b, was simulated to be a constant across time and is not shown. The RMSE value, collectively across all four velocity components, of the DiR method was 45, which is 7-fold lesser compared to the RMSE of 315 for the standard approach.

Experimental data were collected from a healthy volunteer using a 1.5 T clinical scanner (Siemens Medical Solutions, Germany) using body matrix receive coils. BFPE measurements were made using an EPI-PC sequence with echo-train-length of 5, and an ECG-triggered, segmented acquisition was used to acquire a cine series of 192x144 matrix images. Total acquisition time for sixty frames (individual encodings acquired every 14.5 ms) was 15 s (17 heartbeats) with a parallel acceleration factor of 2. First, TGRAPPA[2] was used for frame-by-frame image reconstruction. The standard and proposed methods were then used to reconstruct velocity profiles at each pixel. The computation time of DiR was comparable to that of the standard method. See results in Figure 2.

Discussion: Standard PC-MRI methods process the measured data on a block-by-block basis (Eq. 1), and treat all measurements within each temporal block as if they were collected simultaneously. While this approach may be adequate for two point encoding (single velocity direction), the increased temporal window required for four-point encoding can introduce severe distortion in the velocity esimation. The distortion is evident in both simulation (Figure 1) and experimental results (Figure 2). Although it is possible to improve the temporal resolution of the standard method by reducing the k-space segment size, this remedy comes at the cost of increased acquisition time. The proposed method, by employing the exact forward model, avoids distortion and improves the temporal resolution by upto a factor of 4 without increasing the acquistion time. Also, by controlling λ in Eq. 2, the DiR method provides a principled way to supress noise.

Conclusions: We have presented and validated a new data processing method that improves the reconstruction quality of PC-MRI in terms of SNR, artifacts, and temporal resolution. This same approach may also be applicable to 7D flow, and other phase-based measurements of dynamic processes, such as DENSE and elastography.

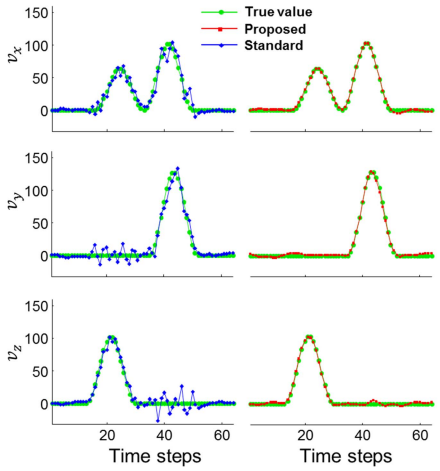

***Figure 1**: Simulation results. The true temporal profiles for the three velocity components (v_x, v_y, v_z) are shown in green along with the reconstructions based on the standard method (blue) and the proposed DiR method (red).*

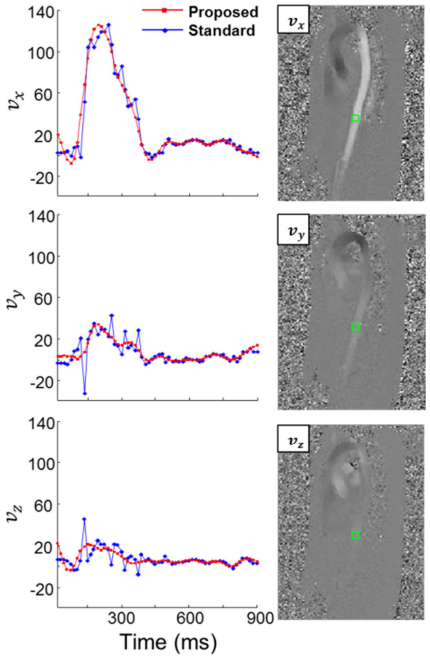

***Figure 2**: Blood velocity measurements from a healthy volunteer. A selected frame (right column) from the DiR method is shown. Velocity-time profiles (left column) at a selected spatial location (green squares) are shown for the two reconstruction methods.*

References: [1] Pelc et al. J. Magn. Reson. Imag. 1991; 1: 405-413. [2] Breuer et al. Megan. Reson. Med. 2005; 53: 981-985.