Accelerated first-pass perfusion MRI using BLOSM: Evaluation using dynamic simulations and patient datasets with prominent respiratory motion

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Target audience: Researchers interested in the technical development of improved cardiac MRI perfusion methods.

Background:

We recently developed a motion-compensated compressed sensing (CS) method to accelerate dynamic MRI of the heart that exploits matrix low-rank sparsity within motion-tracked regions of temporal image sequences (Block LOw-rank Sparsity with Motion guidance, or BLOSM) [1]. Initial results showed that BLOSM appears promising for accelerating first-pass myocardial perfusion imaging, even when patient breathholding is poor and substantial respiratory motion occurs. Presently, we implemented improved motion tracking for BLOSM and compared the improved BLOSM method to other CS methods using computer-simulated motions and using first-pass perfusion datasets from patients with respiratory motion.

Methods:

The BLOSM method divides images into regions, tracks the regions through time using intrinsic motion information, and applies matrix low-rank sparsity to the tracked regions [1]. To obtain motion information, we use the Advanced Normalization Tools (ANTS) registration toolbox [2], which includes a set of state-of-the-art image registration methods. Furthermore, a coarse-to-fine strategy was adopted for the iterative CS reconstruction which uses smaller regions and more detailed image registration techniques as the estimated images become sharper. In the early iterations, global translational shifts are estimated for large regions using a mutual-information-based rigid registration technique. In later iterations, detailed non-rigid deformations are estimated for smaller regions using a cross-correlation-based registration technique when spatial resolution increases.

Computer simulations of heart-like phantoms were implemented with rigid translational shifts, through-plane motion, cardiac contraction and rotation (Figure 1, first column). All the phantoms had quadratically changing signal intensity over time as well. The images were Fourier transformed to generate k-space data, undersampled, and then reconstructed with various CS techniques.

In vivo first-pass cardiac perfusion imaging was performed on a 1.5T system (Avanto, Siemens). In accordance with an IRB approved protocol, 26 slices from 8 patients were collected and each slice was treated as a distinct dataset. The datasets all presented prominent respiratory motion, even though the patients were instructed not to breathe. A saturation-recovery Turbo FLASH sequence was used with parameters as follows: saturation recovery time of 100-120 ms, field of view 240-315×370-410 mm^2, matrix 86-152×128-200, slice thickness 8 mm, flip angle 8-15°, TR 1.9-2.2 ms, and TE 0.9-1.4 ms. Among the 26 datasets, 14 of them were comprised of fully-sampled magnitude-valued images and 12 of them were comprised of fully-sampled complex-valued raw data. The resulting data pool thus contained 26 magnitude-valued images and 12 complex-valued raw datasets. The magnitude images were Fourier transformed to generate k-space data. All k-space data were retrospectively undersampled using a variable density Cartesian k_y-t mask at rate 4, 6, 8 and 10. The undersampled data were reconstructed using BLOSM, k-t SLR [3] which uses whole image low-rank sparsity without motion guidance, and k-t FOCUSS with motion estimation and motion compensation (with ME/MC) [4]. For comparison with BLOSM, k-t SLR was implemented without spatiotemporal total variation constraints. With the fully sampled data as a reference, mean squared error (MSE) was calculated for quantitative analysis.

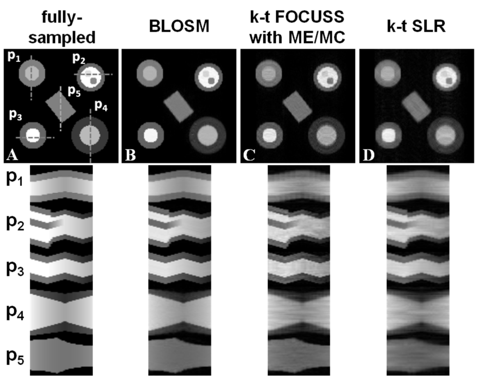

Figure 1. Reconstruction of retrospectively rate-4 undersampled images and x-t profiles from computer-simulated phantoms. Phantom 1 (P1) undergoes rigid translational shifts along the phase-encoding direction. P2 has an abrupt change in size as well as appearance and disappearance of features to mimic through plane motion combined with translational shifts in the readout direction. P3 undergoes rigid translational shifts along the readout direction. P4 undergoes a gradual change in size which can be interpreted as either cardiac contraction or through-plane motion. P5 rotates counterclockwise. BLOSM (column B) provided the most accurate recovery of the fully sampled images. For k-t FOUCSS with ME/MC (column D) and k-t SLR (column E) residual artifacts and motion blurring can be observed.

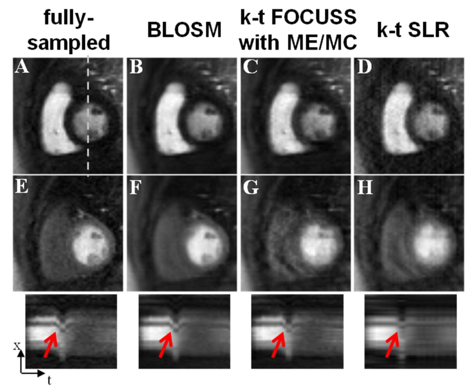

Figure 2. Example images at two time points (rows 1 and 2) from one patient's perfusion CMR. The heart moved at the 2nd row (E-H) due to breathing. BLOSM (B,F) outperformed k-t FOCUSS with ME/MC (C,G) and k-t SLR (D,H), closely matching the fully-sample images (A,E) with the presence or absence of motion. X-t profiles demonstrating similar results are shown on the bottom row, with important dynamic features highlighted by red arrows.

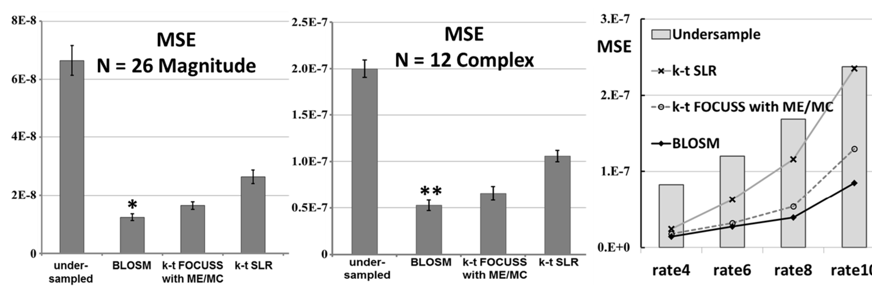

Figure 3. Quantitative analysis of CS-reconstructed first-pass MRI of the heart, comparing BLOSM to k-t FOCUSS with ME/MC and k-t SLR. MSE for 26 magnitude-valued datasets (A) and for 12 complex-valued datasets (B) showed that BLOSM achieved the minimum error. BLOSM also achieved the lowest error at all acceleration rates (C). (* P<0.01 BLOSM vs. the other methods, ANOVA; ** P<0.01 BLOSM vs. all the other methods, paired Student's t-test)

Results:

Both phantom data (Fig. 1) and in vivo perfusion imaging (Fig. 2) showed the best image quality using BLOSM, particularly in the presence of motion. Quantitative analysis (Fig. 3) showed lower MSE for BLOSM compared to other CS methods.

Conclusions and Discussion:

BLOSM (with improved motion tracking) can accelerate first-pass MRI of the heart at rate 4-8, providing better image quality compared to some competing CS methods, even in the presence of respiratory motion. BLOSM can also be combined with parallel imaging [5], and the combined method may provide even higher acceleration rates for first-pass MRI of the heart in the future.

References: [1]Chen et al. ISMRM 2013:4555 [2]Nicholas et al. Proc Workshop Bio Imag Reg 2012;7359:31-39 [3]Lingala et al. IEEE T Med Imaging 2011;30(5):1042-1054 [4]Jung et al. MRM 2009;61(1):103-116 [5]Chen et al. ISMRM 2014 submitted

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