Expanding SMS coverage in cardiac perfusion MRI through deep learning for temporal interpolation

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Target Audience: MR physicists, cardiac radiologists and disease researchers, deep learning researchers and practitioners.

Introduction: Simultaneous multi-slice (SMS) imaging acquires multiple slices in the same duration as single slices[1]. This technique has been expanded to radial imaging[2] for the application of cardiac perfusion MRI. SMS provides increased slice coverage without a loss of temporal resolution. However, radial SMS is currently limited to a multi-band factor of three. To expand coverage, a subsequent acquisition covering the additional area is required. This is problematic as the cardiac phases for each slice are no longer are the same. We propose increasing the number of acquired slices by staggering the SMS slice locations at each heartbeat and using acquired slices at the same location from the previous and subsequent beats to temporally interpolate the missing slices. Fig. 1a shows an illustration of this approach.

Interpolation is an active area of research in both medical imaging[3] as well as traditional image processing fields[4]. In the medical imaging context, increasing the temporal resolution is analogous to video frame rate interpolation. One promising technique, originally proposed for video frame interpolation, is the adaptive separable convolution (ASC) method[5] which uses a deep neural network to determine convolution kernels for each pixel of two adjacent time frames. The convolution problem is simplified by casting a traditional 2-dimensional convolution as separable convolution with a vertical and horizontal kernel for reducing computation. Fig. 1b shows an illustration of this network. We propose applying this adaptive separation convolution interpolation technique to cardiac SMS imaging as a deep slice generation technique (DeepSlice) in order to increase scan coverage from three slices to six without increasing the number of acquisitions.

Methods: DeepSlice (Fig. 1b) used a pre-trained ASC neural network[5] followed by cardiac MRI-specific training to perform the interpolation. Our loss function was based on minimizing the mean absolute error (l_1-loss). Optimization was done through the Adamax algorithm, with a learning rate of 0.001, β_1 of 0.9, and β_2 of 0.999. The batch size was 16. All implementations were done using the PyTorch framework. For the purpose of comparison, we also used a cubic spline interpolation in the temporal domain at each pixel. The DeepSlice network was trained on studies with where five slices were acquired without cardiac gating, with 50 ms readouts. In each study, five slices were acquired approximately four times per second, for 60 seconds[6]. The training data included both at rest and regadenoson stress acquisitions. All images were initially reconstructed as magnitude images using the Spatio-Temporal Constrained Reconstruction (STCR)[7].

The training dataset had a total of 30,000 interpolation image sets (three images of the same slice location at different time points). We used an 80/20 training/validation split. Each slice had a matrix size of 144x144. This method was ultimately applied to SMS datasets with a multi-band factor of 3 acquired twice within a heart beat though at different slice locations. The proposed method was simulated by interpolating alternate frames for both SMS blocks. The DeepSlice approach was compared against this reference standard as well as the linear interpolation using structural similarity (SSIM), peak signal-to-noise ratio (PNSR), and mean squared error (MSE) metrics. DeepSlice was also compared against a temporal cubic spline interpolation at each pixel.

Results: Fig. 2 shows that the DeepSlice approach provides sharp images similar to ground truth. By contrast, the spline interpolation method shows movement-induced ghosting artifacts (red arrows). From a quantitative standpoint, DeepSlice similarly outperforms linear interpolation, giving an SSIM score of 0.989+/-0.02, a PSNR value of 42.5+/4.0, and a MSE value of 0.0010+/-0.0002 compared to the linear interpolation SSIM score of 0.987+/-0.02, a PSNR value of 42.0+/-4.1, and a MSE value of 0.00011+/-0.0002. Fig. 3 gives an example of DeepSlice interpolation over 6 heartbeats. Interpolated frames are observed to be comparatively sharp to physically acquired frames with the absence of ghosting due to movement-induced mis-registration and other obvious interpolation-related artifacts.

Discussion and Conclusion: DeepSlice is a state-of-the-art method to generate missing slices that is well-suited for expanding cardiac SMS coverage while also reducing the number of acquisitions per heartbeat. The results demonstrate the promise of this technique, showing quantitative superiority over standard interpolation methods and presenting visually appealing examples in this initial work. Further work includes generalizing this approach and applying it to other dynamic cardiac imaging applications.

References: 1: Breuer, MRM, 2005. 2: Wang, MRI, 2016. 3: Neubert, CMIG, 2012. 4: Baker, IJCV, 2011. 5: Niklaus, ICCV, 2017. 6: Bieging, IJCI, 2017. 7: Adluru, JMRI, 2009.
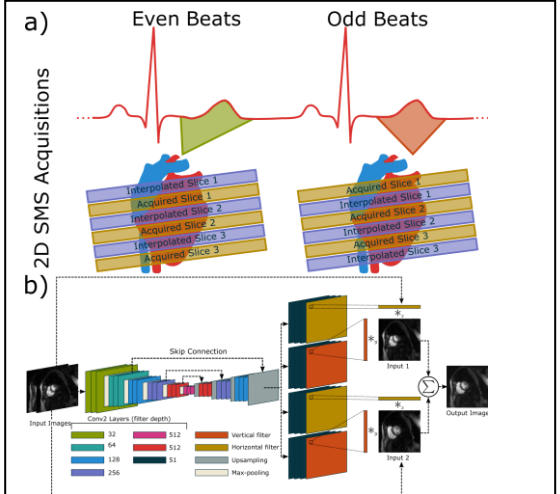
Fig.1: Schematic of proposed method. a) Proposed method to stagger SMS slices every other heart beat and interpolate the missing slices. b) ASC network architecture.
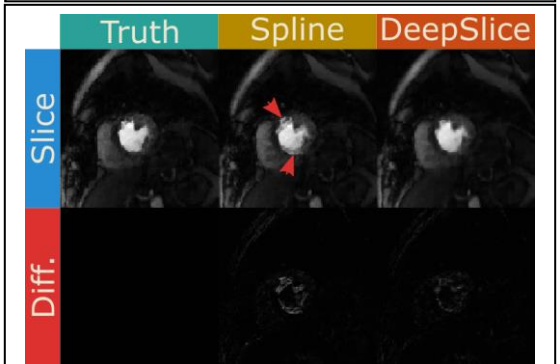

Fig.2: Example interpolated slice showing the ground truth image, spline interpolated image, and slice generated using DeepSlice interpolation. Red arrows highlight ghosting errors seen in the spline case not seen in DeepSlice.
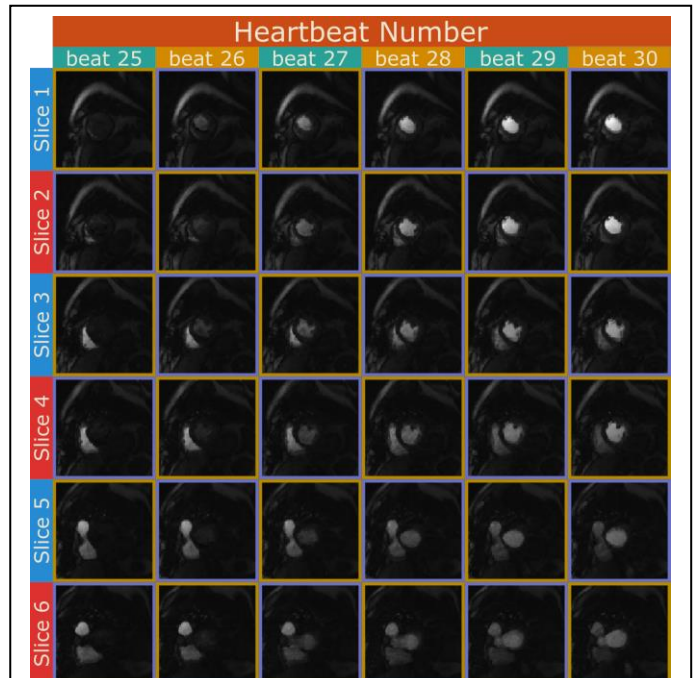

Fig. 3: Example of interpolation on SMS data. Frames bordered in yellow are slices physically acquired. Frames bordered in purple are interpolated.